STABLE AND CONSISTENT DENSITY-BASED CLUSTERING

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Abstract. We present a multiscale, consistent approach to density-based clustering that satisfies stability theorems—in both the input data and in the parameters—which hold without distributional assumptions. The stability in the input data is with respect to the Gromov–Hausdorff–Prokhorov distance on metric probability spaces and interleaving distances between (multi-parameter) hierarchical clusterings we introduce. We prove stability results for standard simplification procedures for hierarchical clusterings, which can be combined with our approach to yield a stable flat clustering algorithm. We illustrate the stability of the approach with computational examples. Our framework is based on the concepts of persistence and interleaving distance from Topological Data Analysis.

1. Introduction

1.1. Motivation. Let $f : \mathbb{R}^d \to \mathbb{R}$ be a probability density function, and let $Z$ be its support. There is a hierarchical clustering $H(f)$ of $Z$ where, for $r > 0$, $H(f)(r)$ is the set of connected components of $\{x \in Z : f(x) \geq r\}$. This construction has a long history; following Hartigan [Har75], we call $H(f)$ the density-contour hierarchical clustering of $f$. The central problem of density-based clustering is to approximate $H(f)$, given finite samples drawn from $f$.

A large amount of work has been done on the related problem of estimating the density $f$ itself, given finite samples. If one constructs an estimate $\hat{f}$ of $f$ from a sample $X$, then filtering the sample points by their $\hat{f}$ values gives an estimate of the order in which sample points appear in $H(f)$. To then estimate the clustering structure of $H(f)$ at a threshold $r$, a natural approach is to construct a graph on the vertices $\{x \in X : \hat{f}(x) \geq r\}$ that encodes distance relations, and then take the connected components of this graph. This is the approach of, e.g., Cuevas–Febrero–Fraiman [CFF00]; for more references see Related Work, below.

Another popular approach to density-based clustering, which is orthogonal to the previous one in a sense we will make precise below, is the robust single-linkage algorithm of Chaudhuri–Dasgupta [CD10]. The algorithm takes a parameter $k \in \mathbb{N}$, and constructs a hierarchical clustering of the sample $X$ by taking the single-linkage clustering, with respect to the distance scale $t > 0$, of the set $\{x \in X : x \text{ has at least } k \text{ neighbors within distance } t\}$. As the parameter $t$ increases, one obtains a hierarchical clustering of the sample. Since this hierarchical clustering is indexed by a spatial parameter, it is remarkable that Chaudhuri–Dasgupta prove that this method is Hartigan consistent: as the size of the sample tends to infinity, the robust single-linkage of a sample of $f$ converges in probability to $H(f)$, using a criterion of Hartigan to compare the density-contour hierarchical clustering with a hierarchical clustering produced from a sample.

In their work on the HDBSCAN clustering algorithm [MH18], McInnes–Healy observed that robust single-linkage is a “horizontal” slice of the two-parameter hierarchical clustering $\pi_0 \text{DR}(X)$ one gets by taking the path components of the Degree-Rips bifiltration from Topological Data Analysis ([LW15]). The two parameters of Degree-Rips are a distance scale $t > 0$...
and a degree threshold $k \in \mathbb{N}$: if one considers $\pi_0^{\text{DR}}(X)$ of a sample $X$ and fixes $k$, one recovers the robust single-linkage of $X$; if one takes a vertical slice by fixing $t$, one recovers the first approach we discussed, where the density estimate $\hat{f}$ is a kernel density estimate computed with the uniform (i.e. square) kernel and bandwidth $t$, and the graph is the Rips graph with distance scale $t$.

A drawback to both of these approaches is their sometimes pathological stability properties. In their work on the stability of single-linkage [CM10a], Carlsson–Mémoli define a metric on dendrograms; using a natural generalization of this metric to arbitrary hierarchical clusterings, one can see that neither approach is stable to Gromov–Hausdorff–Prokhorov-small perturbations to the input $X$, or to small changes in their parameters (the Rips parameter $t$ or the robust single-linkage parameter $k$).

In this paper, we define a three-parameter hierarchical clustering that we call kernel linkage\(^1\), which is a natural generalization of $\pi_0^{\text{DR}}$. Kernel linkage adds an additional real parameter $s > 0$ so that the bandwidth of the kernel density estimate does not need to be equal to the Rips parameter, and it allows for more general choices of kernel. Further, kernel linkage takes as input any metric probability space (such as a finite metric space with the normalized counting measure) and lets the density threshold $k > 0$ be real-valued.

Despite the behavior of the horizontal and vertical slices, we show that kernel linkage, as a three-parameter hierarchical clustering, is Gromov–Hausdorff–Prokhorov stable. This suggests that one should consider slices of kernel linkage in which all parameters vary, as such slices of multi-parameter objects inherit stability. These slices are the main topic of this paper.

\(^1\)Called robust linkage in a previous version of this paper.

1.2. Contributions.

1.2.1. Theoretical framework. If $X$ is a set, then the collection of all possible clusterings of $X$ (i.e. families of disjoint and non-empty subsets of $X$) is partially ordered by the refinement relation. We write $\mathcal{C}(X)$ for the poset of clusterings of $X$ (Definition 2.2). A contravariant hierarchical clustering of $X$ is given by an order-reversing map $H : \mathbb{R}_{>0} \to \mathcal{C}(X)$. A motivating

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**Figure 1.** On the left, a probability density function $f$ on the real line. On the right, a heat map representing the bifiltration of the support $X$ of $f$ defined in Eq. (1). The intensity of color at a point $(s,k)$ in the heat map indicates the proportion of points in $X$ that are in $X_{[s,k]}$. The dashed line across the heat map indicates a possible choice of $\gamma$. 

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1.2. Contributions.
example is the density-contour hierarchical clustering $H(f)$. There is a natural generalization of this definition to multi-parameter hierarchical clusterings (Definition 2.3), which are moreover allowed to be covariant in some parameters and contravariant in others. We show that one can use correspondences and interleavings to obtain a distance between multi-parameter hierarchical clusterings that generalizes the Carlsson–Mémoli distance on dendrograms. We call this the correspondence-interleaving distance (Definition 2.13), denoted $d_{CI}$. When considering hierarchical clusterings of measure spaces, one can require the interleavings that appear in the definition of $d_{CI}$ to respect the measures. In this way, one obtains the measured-interleaving distance (Definition 2.18) on multi-parameter hierarchical clusterings of measure spaces, denoted $d_{MI}$.

Given a metric probability space $X$, we define a three-parameter hierarchical clustering of $X$, which we call the kernel linkage of $X$ (Definition 2.25). This construction is based on a two-parameter filtration of $X$, which we call the kernel filtration (Definition 2.24), which has at index $(s, k)$ the following subset of $X$:

\[ X_{[s,k]} = \left\{ x \in X : \int_{y \in X} K \left( \frac{d_X(x,y)}{s} \right) d\mu_X \geq k \right\} , \]

where $K$ is a choice of kernel satisfying mild hypotheses. See Fig. 1 for an example. The kernel linkage of $X$ has at index $(s, t, k)$ the single-linkage clustering at distance scale $t$ of $X_{[s,k]}$.  

1.2.2. Stability. The first main result of the paper is a stability theorem for kernel linkage:

**Result A** (Theorem 3.6). Kernel linkage is uniformly continuous with respect to the Gromov–Hausdorff–Prokhorov distance on compact metric probability spaces, and the measured-interleaving distance. If kernel linkage is defined using the uniform kernel, then it is 2-Lipschitz.

We obtain one-parameter hierarchical clusterings of the input $X$ by taking slices of kernel linkage: if $I \subseteq \mathbb{R}_{>0}$ is an interval and $\gamma : I \to \mathbb{R}^3_{>0}$ is a function that is non-increasing in its first two coordinates and non-decreasing in the third, the slice of kernel linkage along $\gamma$ has, at the parameter $r \in I$, the kernel linkage at $\gamma(r)$. We call the resulting one-parameter hierarchical clustering the $\gamma$-linkage, or $\gamma$-link for short (Definition 3.8).

For concreteness, in this introduction we restrict attention to straight lines in $\mathbb{R}^3_{>0}$, and to further simplify things, we assume the spatial parameters are equal, $s = t$. In detail, we specify a line $\lambda^{x,y}$ in $\mathbb{R}^3_{>0}$ by choosing an $s$-intercept $x > 0$ and a $k$-intercept $y > 0$, and we parametrize this line with the $k$-coordinate (Notation 3.13). Let $\mu = -y/x$ be the slope of $\lambda^{x,y}$. We let $\lambda$-link be the resulting hierarchical clustering algorithm. As a consequence of Result A, we get the following stability result:

**Result B** (Corollary 3.15). Assume kernel linkage is defined using the uniform kernel. Let $\lambda = \lambda^{x,y}$ and let $\mu$ be the slope of $\lambda$. Then, with respect to the Gromov–Hausdorff–Prokhorov distance and the measured-interleaving distance, $\lambda$-link is $\max(2|\mu|, 1)$-Lipschitz.

Furthermore, $\lambda$-link is stable in the choice of $\lambda$:

**Result C** (Corollary 3.17). Let $X$ be a metric probability space, let $\lambda = \lambda^{x,y}$ with slope $\mu$, and let $\lambda' = \lambda^{x',y'}$ with slope $\mu'$. Then

\[ d_{MI} (\lambda$-link$(X), \lambda'$-link$(X)) \leq \max \left( |y - y'|, |x - x'| \cdot \min(|\mu|, |\mu'|) \right) . \]
**Result D** (Proposition 4.7 and Theorem 4.11). The algorithm $\lambda$-link is Hartigan consistent with respect to any continuous and compactly supported probability density function $f : \mathbb{R}^d \rightarrow \mathbb{R}$.

1.2.4. Stability of pruning and flattening. After constructing a hierarchical clustering of a dataset, one often wants to simplify this hierarchical clustering, either for visualization, to remove spurious features that may reflect noise in the data, or to extract a flat (i.e., non-hierarchical) clustering. The final results of this paper concern the stability properties of simplification procedures. Because these results are stated in terms of interleavings, one can apply these simplification procedures to the output of $\gamma$-link, and our stability and consistency results for $\gamma$-link imply such results for the simplification.

Perhaps the most interesting of these is a “flattening” procedure inspired by the ToMATo clustering algorithm of Chazal–Guibas–Oudot–Skraba [CGOS13]. Given a one-parameter hierarchical clustering $H$, this procedure constructs a flat clustering of the underlying data by taking the clusters corresponding to the high persistence points in the persistence diagram of $H$ (in the sense of persistent homology; see Section 5.3). Following Chazal et al., we say that $H$ is $(a,b)$-separated for $0 < a < b$ if the region in the persistence diagram of $H$ between the diagonals with $y$-intercept $a$ and $b$ is empty (roughly speaking, if $a \ll b$, then the significant features of $H$ are well separated from the “topological noise”); see Fig. 3 of Section 5. The algorithm takes a persistence threshold $\tau > 0$ as a parameter, and we call the result the persistence-based flattening of $H$, denoted $\text{PF}(H,\tau)$. The ideas behind this flattening procedure come from the ToMATo clustering algorithm, but Chazal et al. do not study this flattening procedure in isolation.

As a consequence of the stability of persistence-based flattening (Proposition 5.15) and Result B, we obtain the following stability result for the combination of $\lambda$-link and $\text{PF}$ (see Section 5.1 for the notion of interleaving used in this result).

**Result E** (Corollary 5.16). Assume kernel linkage is defined using the uniform kernel. Let $X$ be a compact metric probability space, let $\lambda = \lambda_{x,y}$ with slope $\mu$, and assume $\lambda$-link($X$) is $(a,b)$-separated. Let $X'$ be a compact metric probability space with

$$d_{\text{GHP}}(X,X') < \frac{b-a}{3 \max(2|\mu|,1)}$$

and let $\varepsilon = d_{\text{GHP}}(X,X') \cdot \max(2|\mu|,1)$. Then, for any $\tau \in (a+\varepsilon,b-2\varepsilon)$, there is a correspondence $R \subseteq X \times X'$ and a bijection $m : \text{PF}(\lambda\text{-link}(X),\tau) \rightarrow \text{PF}(\lambda\text{-link}(X'),\tau)$ such that, for all $C \in \text{PF}(\lambda\text{-link}(X),\tau)$, $C$ and $m(C)$ are $\varepsilon$-interleaved with respect to $R$.

We remark that, as a consequence of Proposition 5.15 and Result C, one gets a similar stability result for the combination of $\lambda$-link and $\text{PF}$ with respect to the parameter $\lambda$.

We also study a well-known pruning procedure for hierarchical clusterings of a measure space, used, for instance, in [SN10] and by the HDBSCAN algorithm [CMS13], and we prove a stability theorem for this pruning procedure with respect to the measured-interleaving distance (Proposition 5.26).

1.2.5. Computational examples. Finally, we run $\gamma$-link on synthetic data with several families of $\gamma$. We illustrate the stability that is gained by using curves $\gamma$ in which all the parameters of kernel linkage vary, and explain how this stability can be exploited for parameter selection. An implementation of $\gamma$-link is available at [RS21].

1.3. Related work. Distances between (one- and two-parameter) hierarchical clusterings have been studied by Carlsson and Mémoli [CM10a, CM10b]. The notions of hierarchical clustering we consider and the correspondence-interleaving distance are generalizations of the notions in
Parameter: A curve $\gamma = (s, t, k) : (0, \max_\gamma) \to \mathbb{R}^3_{>0}$ such that $s$ and $t$ are non-increasing and $k$ is non-decreasing.

Input: A finite metric space $X$.

Output: A hierarchical clustering $\gamma$-link$(X)$ of $X$.

For $r \in (0, \infty)$:
1. If $\max_\gamma \leq r$, let $G_r$ be the empty graph.
   If $r < \max_\gamma$, let $G_r$ be the graph with vertices
   \[
   \left\{ x \in X : \frac{1}{|X|} \sum_{y \in X} K\left( \frac{d(x, y)}{s(r)} \right) \geq k(r) \right\},
   \]
   and edges $(x, y)$ if $d(x, y) \leq t(r)$.

2. Let $\gamma$-link$(X)(r)$ be the connected components of $G_r$.

Algorithm 1. The $\gamma$-link algorithm when the input is a finite metric space.

their work: in particular, if $D_1$ and $D_2$ are dendrograms on finite sets, then $d_{CI}(D_1, D_2)$ is twice the distance between $D_1$ and $D_2$ defined in [CM10a].

The formigram distance, introduced by Kim and Mémoli [KM18], can also be seen as a particular instance of the correspondence-interleaving distance.

The papers [RSNW12, CGOS13] address the stability of consistent hierarchical clustering methods. In their frameworks, stability is guaranteed when their assumptions on the underlying distribution are satisfied. In contrast, our stability results hold without distributional assumptions.

Combining density estimates and graphs that encode distance relations to estimate the density-contour hierarchical clustering has a long history, and several methods based on this idea have been proposed. See, e.g., [BCP07, RW10, SN10, CGOS13] and [BMT17] for the case of persistent homology.

The consistency of robust single-linkage was first established by Chaudhuri–Dasgupta [CD10], and then generalized to density functions supported on manifolds in [BNR⁺13]. In [EBW15], the consistency of hierarchical clustering algorithms is formulated using a notion of distance that is closely related to the correspondence-interleaving distance, and, building on results of Chaudhuri–Dasgupta, they show that robust single-linkage is consistent in their sense.

When the input data is a finite subset of Euclidean space, and $\gamma$ is a line with constant $s$-component, the algorithm $\gamma$-link recovers the connected components of the weighted Čech filtration introduced in [ACG⁺19], when their parameter $p$ is set to $\infty$. In particular, their stability result applies to this instance of $\gamma$-link.

A successful reduction of multi-parameter persistence to 1-parameter persistence using slices is introduced and studied by Cagliari, Di Fabio, and Ferri in [CDFF10].

In [BL21], Blumberg and Lesnick prove a stability result for Degree-Rips. The hypotheses for their result are weaker than the hypotheses for our stability result for kernel linkage (they use the Gromov–Prokhorov distance instead of the Gromov–Hausdorff–Prokhorov distance), and the bounds in their conclusion are correspondingly weaker, since Degree-Rips is not continuous with respect to the Gromov–Prokhorov distance. Jardine has also proved results about the stability of Degree-Rips [Jar20], using a hypothesis involving configuration spaces, rather than a distance on metric probability spaces.
In [Sco20, Section 6.5], building on the results presented in this paper, the author shows that the stability of kernel linkage can be lifted to the stability of the kernel filtration (Definition 2.24), which in particular implies that other topological invariants of this multi-filtration are Gromov–Hausdorff–Prokhorov stable.

1.4. Structure of the paper. In Section 2.1 and Section 2.2, we define hierarchical clusterings and the distances $d_{CI}$ and $d_{MI}$. In Section 2.3, we define the kernel linkage of a metric probability space. In Section 3.1, we prove a stability theorem for kernel linkage (Theorem 3.6), and in Section 3.2, we define $\gamma$-link and prove stability results for it (Proposition 3.10 and Proposition 3.12). In Section 4 we introduce two notions of consistency, compare them to notions in the literature, and prove that $\gamma$-link is consistent (Theorem 4.11). In Section 5, we study pruning and flattening procedures for hierarchical clusterings and prove stability results for them (Proposition 5.6, Proposition 5.15, Proposition 5.26). In Section 6 we give computational examples that illustrate the stability properties of $\gamma$-link. Appendix A contains standard but technical arguments for results in Section 4. Appendix B contains a table with notation.

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2. Hierarchical clusterings

In this section, we define (multi-parameter) hierarchical clusterings, and the correspondence-interleaving distance between them. We discuss hierarchical clusterings of measure spaces, and define the measured-interleaving distance between them. Finally, we present our main example of a multi-parameter hierarchical clustering, the kernel linkage of a metric probability space.

2.1. The correspondence-interleaving distance.

Definition 2.1. Let $X$ be a set. A clustering of $X$ is a set of non-empty, disjoint subsets of $X$. The elements of a clustering are called clusters.

Definition 2.2. Let $X$ be a set. The poset of clusterings of $X$, denoted $C(X)$, is the poset whose elements are the clusterings of $X$, and where $S \preceq T \in C(X)$ if, for each cluster $A \in S$, there is a (necessarily unique) cluster $B \in T$ such that $A \subseteq B$.

In the next definition, we consider the strictly positive real numbers $\mathbb{R}_{>0}$ as a poset with its usual ordering. Given a poset $P$, let $P^{\text{op}}$ denote the poset with the opposite order.

Definition 2.3. Let $X$ be a set. A covariant hierarchical clustering of $X$ is an order-preserving map $H : \mathbb{R}_{>0} \to C(X)$. A contravariant hierarchical clustering of $X$ is an order-preserving map $H : \mathbb{R}^{\text{op}}_{>0} \to C(X)$.

Unless otherwise stated, the term hierarchical clustering will mean contravariant hierarchical clustering. An important motivating example is the following:

Example 2.4. If $f : \mathbb{R}^d \to \mathbb{R}$ is a probability density function, and $X = \text{supp}(f)$, then there is a hierarchical clustering $H(f)$ of $X$, where, for $r > 0$, $H(f)(r)$ is the set of connected
components of \( \{ x \in X : f(x) \geq r \} \). Following Hartigan [Har75], we call this the **density-contour** hierarchical clustering of \( f \).

A well-known covariant hierarchical clustering is given by the single-linkage hierarchical clustering algorithm:

**Example 2.5.** Let \( X \) be a metric space. We denote by \( \text{SL}(X) \) the **single-linkage** covariant hierarchical clustering of \( X \), where, for \( r > 0 \), \( \text{SL}(X)(r) \) is the partition of \( X \) defined by the smallest equivalence relation \( \sim_r \) on \( X \) with \( x \sim_r y \) if \( d_X(x, y) \leq r \).

In this paper, we will consider multi-parameter hierarchical clusterings that are covariant in some parameters, and contravariant in others. We formalize this as follows.

**Definition 2.6.** Let \( n \geq 1 \), and let \( \vec{v} \in \{-1, 1\}^{\times n} \). Let \( \mathbb{R}_{>0}^{\vec{v}} \) be the product poset \( \mathbb{R}_{>0}^{\vec{v}} = R_1 \times \cdots \times R_n \), where

\[
R_i = \begin{cases} \mathbb{R}_{>0} & \text{if } v_i = 1 \\ \mathbb{R}_{>0}^{\bar{v}} & \text{if } v_i = -1 \end{cases}.
\]

**Definition 2.7.** Let \( X \) be a set, let \( n \geq 1 \), and let \( \vec{v} \in \{-1, 1\}^{\times n} \). A **\( \vec{v} \)-hierarchical clustering** of \( X \) is an order-preserving map \( H : \mathbb{R}_{>0}^{\vec{v}} \to C(X) \).

**Notation 2.8.** Let \( \vec{v} \in \{-1, 1\}^{\times n} \). We write \( \vec{\varepsilon} = (\varepsilon_1, \ldots, \varepsilon_n) \geq 0 \) if \( \varepsilon_i \geq 0 \) for \( 1 \leq i \leq n \). For \( \vec{r} = (r_1, \ldots, r_n) \in \mathbb{R}_{>0}^{\vec{v}} \), we write \( \vec{r} + \vec{\varepsilon} \) for \( (r_1 + v_1 \varepsilon_1, \ldots, r_n + v_n \varepsilon_n) \) and we write \( \vec{r} + \vec{\varepsilon} > 0 \) if \( r_i + v_i \varepsilon_i > 0 \) for all \( 1 \leq i \leq n \).

**Definition 2.9.** Let \( H \) and \( E \) be \( \vec{v} \)-hierarchical clusterings of a set \( X \), and let \( \varepsilon' \geq 0 \). We say that \( H \) and \( E \) are **\( \varepsilon' \)-interleaved** if, for all \( \vec{r} \in \mathbb{R}_{>0}^{\vec{v}} \) such that \( \vec{r} + \vec{\varepsilon} > 0 \), we have the following relations in \( C(X) \):

\[
H(\vec{r}) \preceq E(\vec{r} + \vec{\varepsilon}) \quad \text{and} \quad E(\vec{r}) \preceq H(\vec{r} + \vec{\varepsilon}).
\]

Interleavings between hierarchical clusterings let us quantify how similar two hierarchical clusterings of the same set are. As an example, we have the following straightforward stability result.

**Lemma 2.10.** Let \( f, g : \mathbb{R}^d \to \mathbb{R}_{>0} \) be probability density functions with the same support and let \( \varepsilon \geq 0 \). Then \( \|f - g\|_\infty \leq \varepsilon \) if and only if \( H(f) \) and \( H(g) \) are \( \varepsilon \)-interleaved. \( \square \)

Since our goal is to approximate the density-contour hierarchical clustering using a sample, we need to be able to compare hierarchical clusterings of different sets. We do this by using correspondences.

**Definition 2.11.** A **correspondence** \( R \) between sets \( X \) and \( Y \) is given by a set \( R \subseteq X \times Y \) such that the projections \( \pi_X : R \to X \) and \( \pi_Y : R \to Y \) are surjective.

If \( \psi : Y \to X \) is a function between sets, and \( S = \{ C_i \}_{i \in I} \) is a clustering of \( X \), then \( \psi^*(S) = \{ \psi^{-1}(C_i) \}_{i \in I} \) is a clustering of \( Y \). This defines an order-preserving map \( \psi^* : C(X) \to C(Y) \). So if \( H \) is a \( \vec{v} \)-hierarchical clustering of \( X \), then there is a \( \vec{v} \)-hierarchical clustering \( \psi^*(H) \) of \( Y \), defined by the composite \( \psi^*(H) : \mathbb{R}_{>0}^{\vec{v}} \xrightarrow{H} C(X) \xrightarrow{\psi^*} C(Y) \).

**Definition 2.12.** Let \( H \) and \( E \) be \( \vec{v} \)-hierarchical clusterings of sets \( X \) and \( Y \) respectively, and let \( R \subseteq X \times Y \) be a correspondence. Let \( \varepsilon \geq 0 \). We say that \( H \) and \( E \) are **\( \varepsilon \)-interleaved with respect to \( R \)** if \( \pi_X^*(H) \) and \( \pi_Y^*(E) \) are \( \varepsilon \)-interleaved as \( \vec{v} \)-hierarchical clusterings of \( R \).
**Definition 2.13.** Let $H$ and $E$ be $\vec{v}$-hierarchical clustering of sets $X$ and $Y$ respectively. Define the correspondence-interleaving distance

$$d_{CI}(H, E) = \inf\{\varepsilon \geq 0 : \text{there is a correspondence } R \subseteq X \times Y \text{ such that } H, E \text{ are } (\varepsilon, \ldots, \varepsilon)\text{-interleaved with respect to } R\}.$$  

Aside from set-theoretic concerns, $d_{CI}$ defines an extended pseudo metric on $\vec{v}$-hierarchical clusterings:

**Proposition 2.14.** The distance $d_{CI}$ satisfies the following properties, for all $\vec{v}$-hierarchical clusterings:

1. For any $H$, $d_{CI}(H, H) = 0$.
2. For any $H, E$, $d_{CI}(H, E) = d_{CI}(E, H)$.
3. For any $H, E, F$, $d_{CI}(H, F) \leq d_{CI}(H, E) + d_{CI}(E, F)$.  

**2.2. The measured-interleaving distance.** Recall that a measurable space $(X, \mathcal{S})$ consists of a set $X$ together with a $\sigma$-algebra $\mathcal{S}$ of subsets of $X$, and that a measure space $(X, \mathcal{S}, \mu_X)$ consists of a measurable space $(X, \mathcal{S})$ together with a measure $\mu_X$ defined on $\mathcal{S}$. We usually suppress the $\sigma$-algebra $\mathcal{S}$ from the notation. We will be interested in the case where $X$ is a metric space and $\mathcal{S}$ is the Borel $\sigma$-algebra.

**Definition 2.15.** Let $X$ be a measurable space and let $H$ be a $\vec{v}$-hierarchical clustering of $X$. We say that $H$ is measurable if every cluster of $H$ is a measurable subset of $X$.

We now introduce the distance we will use between measurable hierarchical clusterings of measure spaces. The idea is to use correspondences and interleavings as before, but to keep track of how much the interleavings distort the measures.

**Notation 2.16.** Let $H$ and $E$ be $\vec{v}$-hierarchical clusterings of sets $X$ and $Y$ respectively. Let $\vec{v} \geq 0$, and let $R \subseteq X \times Y$ be a correspondence such that $H$ and $E$ are $\vec{v}$-interleaved with respect to $R$. For $\vec{r} \in \mathbb{R}^d_{\geq 0}$ such that $\vec{r} + \vec{v} \vec{e} > 0$, we write $R_X : H(\vec{r}) \to E(\vec{r} + \vec{v} \vec{e})$ for the function such that $\pi_X^{-1}(A) \subseteq \pi_Y^{-1}(R_X(A))$ for all $A \in H(\vec{r})$.

**Definition 2.17.** Let $H$ and $E$ be measurable $\vec{v}$-hierarchical clusterings of measure spaces $(X, \mu_X)$ and $(Y, \mu_Y)$ respectively. Let $\vec{v} \geq 0$, $m \geq 0$, and let $R \subseteq X \times Y$ be a correspondence. We say that $H$ and $E$ are $(\vec{v}; m)\text{-measured-interleaved with respect to } R$ if $H$ and $E$ are $\vec{v}$-interleaved with respect to $R$, and, for all $\vec{r} \in \mathbb{R}^d_{\geq 0}$ such that $\vec{r} + \vec{v} \vec{e} > 0$, we have

$$\mu_X \left( \bigcup_{i \in I} A_i \right) \leq \mu_Y \left( \bigcup_{i \in I} R_X(A_i) \right) + m \text{ and } \mu_Y \left( \bigcup_{j \in J} B_j \right) \leq \mu_X \left( \bigcup_{j \in J} R_Y(B_j) \right) + m$$

for all finite collections $\{A_i \in H(\vec{r})\}_{i \in I}$ and all finite collections $\{B_j \in E(\vec{r})\}_{j \in J}$.

**Definition 2.18.** Let $H$ and $E$ be measurable $\vec{v}$-hierarchical clusterings of measure spaces $(X, \mu_X)$ and $(Y, \mu_Y)$ respectively. Define the measured-interleaving distance

$$d_{MI}(H, E) = \inf\{\varepsilon \geq 0 : \text{there is a correspondence } R \subseteq X \times Y \text{ such that } H, E \text{ are } (\varepsilon, \ldots, \varepsilon; \varepsilon)\text{-measured-interleaved with respect to } R\}.$$  

As in Proposition 2.14, it is easy to show that the measured-interleaving distance defines an extended pseudo metric on measurable $\vec{v}$-hierarchical clusterings of measure spaces.
2.3. The kernel linkage of a metric probability space.

**Definition 2.19.** A metric probability space consists of a metric space $X$ together with a Borel probability measure $\mu_X$ on $X$.

**Definition 2.20.** A kernel is a non-increasing function $K : \mathbb{R}_{\geq 0} \to \mathbb{R}_{\geq 0}$ that is continuous from the right and such that $0 < \int_0^\infty K(r) \, dr < \infty$.

Note that, in particular, $K(0) > 0$ and $\lim_{r \to \infty} K(r) = 0$.

**Example 2.21.** Many kernels used for density estimation are kernels in the above sense. We will be particularly interested in

$$K(x) = \begin{cases} 1 & x < 1 \\ 0 & \text{otherwise} \end{cases} : \mathbb{R}_{\geq 0} \to \mathbb{R}_{\geq 0},$$

with $K(x) = 1$ if $x < 1$ and $K(x) = 0$ otherwise. We refer to this as the uniform kernel.

**Definition 2.22.** Let $K$ be a kernel, and let $X$ be a metric probability space. Define the local density estimate of a point $x \in X$ at scale $s > 0$ as

$$(\mu_X \ast K_s)(x) := \int_{x' \in X} K \left( \frac{d_X(x, x')}{s} \right) \, d\mu_X.$$

**Remark 2.23.** In the special case where $Z \subset \mathbb{R}^d$ is a finite set of points, and $X$ is Euclidean space $\mathbb{R}^d$ equipped with the normalized counting measure defined by $Z$, the formula for the local density estimate becomes

$$(\mu_X \ast K_s)(x) = \frac{1}{|Z|} \sum_{z \in Z} K \left( \frac{||x - z||}{s} \right).$$

Based on the usual formula for kernel density estimates, one might expect a factor of $1/s^d$ here. However, we need our local density estimate to be monotonic in $s$, in order to define the kernel filtration, below. In effect, one can re-introduce the factor $1/s^d$ after taking one-parameter slices of the kernel filtration, and this is what we do to prove our consistency result (see Definition 4.9).

**Definition 2.24.** Let $K$ be a kernel, let $X$ be a metric probability space, and let $s, k > 0$. Let $X_{[s,k]} \subseteq X$ be the sub-metric space:

$$X_{[s,k]} = \{ x \in X : (\mu_X \ast K_s)(x) \geq k \}.$$

Note that, since $K$ is non-increasing, we have $X_{[s,k]} \subseteq X_{[s',k']} \subseteq X$ whenever $s' \geq s$ and $k' \leq k$. This forms a 2-parameter filtration of $X$, which we call the kernel filtration of $X$.

We combine the kernel filtration of a metric probability space with the single-linkage construction to define the following $(1,1,-1)$-hierarchical clustering (recall Definition 2.7).

**Definition 2.25.** Let $K$ be a kernel, and let $X$ be a metric probability space. Define the kernel linkage of $X$ as the $(1,1,-1)$-hierarchical clustering of $X$:

$$L^K(X) : \mathbb{R}_{>0} \times \mathbb{R}_{>0} \times \mathbb{R}_{>0}^{\text{op}} \to \mathcal{C}(X)$$

$$(s,t,k) \mapsto \text{SL} \left( X_{[s,k]} \right) (t).$$

If there is no risk of confusion, we suppress $K$ from the notation, and write $L(X)$.

We now provide a formula for the local density estimate that we will need for proving the stability of kernel linkage. In the statement, and throughout the paper, $B(x,r)$ denotes the open ball centered at $x$ of radius $r$. 


Lemma 2.26. Let $K$ be a kernel, and let $X$ be a metric probability space. Let $K^{-1} : \mathbb{R}_{>0} \to \mathbb{R}_{\geq 0}$ be defined as $K^{-1}(t) = \min\{u : K(u) \leq t\}$. Then $K^{-1}$ is a non-increasing function with compact support, and we have, for every $x \in X$,

$$
(\mu_X * K_s)(x) = \int_0^\infty \mu_X(B(x, sK^{-1}(r))) \, dr.
$$

Proof. Since $K(r) \to 0$ as $r \to \infty$, for every $t > 0$ the set $\{u : K(u) \leq t\}$ is non-empty. Moreover, $K$ is continuous from the right, so the set has a minimum, and thus $K^{-1}$ is well-defined. The fact that $K^{-1}$ is non-increasing is clear, and the fact that it has compact support follows from the fact that $K$ is bounded.

To prove the statement about $(\mu_X * K_s)$, we need the following straightforward fact about $K^{-1}$: for every $s, t \in \mathbb{R}_{\geq 0}$ we have $K^{-1}(t) > s$ if and only if $t < K(s)$. We finish the proof by computing

$$
\int_{x' \in X} K\left(\frac{d(x, x')}{s}\right) \, d\mu_X = \int_{x' \in X} \int_0^\infty 1_{\{r < K\left(\frac{d(x, x')}{s}\right)\}} \, dr \, d\mu_X
$$

$$
= \int_{x' \in X} \int_0^\infty 1\{d(x, x') < sK^{-1}(r)\} \, dr \, d\mu_X
$$

$$
= \int_0^\infty \int_{x' \in X} 1\{d(x, x') < sK^{-1}(r)\} \, d\mu_X \, dr
$$

$$
= \int_0^\infty \mu_X\left(B(x, sK^{-1}(r))\right) \, dr. \quad \square
$$

Using Lemma 2.26, one proves that the kernel linkage of a metric probability space is a measurable $(1, 1, -1)$-hierarchical clustering:

Lemma 2.27. If $X$ is a metric probability space, $s,t,k > 0$, and $C \in \mathbb{L}(X)(s,t,k)$, then $C$ is a Borel subset of $X$. \quad \square

3. Stability

We now prove a stability theorem for the kernel linkage of a metric probability space, which was defined in Section 2.3. We then define the hierarchical clustering algorithm $\gamma$-link by taking slices of kernel linkage, and we prove stability results for $\gamma$-link.

3.1. Stability of kernel linkage.

Definition 3.1. Let $A, B$ be compact subsets of a metric space $Z$. The Hausdorff distance between $A$ and $B$ is

$$
d_{H}(A, B) = \inf\{\varepsilon > 0 : A \subseteq B^{\varepsilon} \text{ and } B \subseteq A^{\varepsilon}\}
$$

where $W^{\varepsilon} = \{z \in Z : \exists w \in W, d_Z(z, w) < \varepsilon\}$ for any $W \subseteq Z$.

Definition 3.2. Let $\mu, \nu$ be Borel probability measures on a metric space $Z$. The Prokhorov distance between $\mu$ and $\nu$ is

$$
d_{P}(\mu, \nu) = \inf\{\varepsilon > 0 : \mu(A) \leq \nu(A^{\varepsilon}) + \varepsilon \text{ and } \nu(A) \leq \mu(A^{\varepsilon}) + \varepsilon \text{ for all Borel sets } A \subseteq Z\}.
$$

Definition 3.3. Let $(X, \mu_X), (Y, \mu_Y)$ be compact metric probability spaces. The Gromov–Hausdorff–Prokhorov distance between $(X, \mu_X)$ and $(Y, \mu_Y)$ is

$$
d_{GHP}(X,Y) = \inf_{i,j} \left\{ \max\left\{ d_{H}(i(X), j(Y)), d_{P}(i_*\mu_X, j_*\mu_Y)\right\} \right\},
$$

where the infimum is taken over all isometric embeddings $i : X \to Z$ and $j : Y \to Z$ into a common metric space $Z$. 10
The Gromov–Hausdorff–Prokhorov distance is a metric on the set of isometry-equivalence classes of compact metric probability spaces; see, e.g., [Mie09].

**Lemma 3.4.** Let $K$ be a kernel and let $r' \in (0, K(0))$. Let $Z$ be a compact metric space and let $\mu$ and $\nu$ be Borel probability measures on $Z$ such that $d_p(\mu, \nu) < \varepsilon$ for $\varepsilon > 0$. Let $x, y \in Z$ such that $d_Z(x, y) < \varepsilon'$. Then, for all $s > 0$, we have

$$(\mu \ast K_s)(x) \leq (\nu \ast K_{s + \varepsilon_s})(y) + \varepsilon_k,$$

for $\varepsilon_s = \frac{\varepsilon + \varepsilon'}{K^{-1}(r')} + K(0)\varepsilon$.

**Proof.** Using the formula of Lemma 2.26, we know that $(\mu \ast K_s)(x) = \int_0^K(0) \mu(B(x, sK^{-1}(r))) \, dr$, since, if $r > K(0)$, then $K^{-1}(r) = 0$. Note that, for any radius $R \geq 0$, we have

$$\mu(B(x, R)) \leq \nu(B(x, R)\varepsilon) + \varepsilon \leq \nu(B(x, R + \varepsilon)) + \varepsilon \leq \nu\left(B(y, R + \varepsilon + \varepsilon')\right) + \varepsilon,$$

so we can bound the local density estimate of $x$ as follows.

$$(\mu \ast K_s)(x) \leq \int_0^K(0) \nu(B(y, sK^{-1}(r) + \varepsilon + \varepsilon')) + \varepsilon \, dr = \int_0^K(0) \nu(B(y, sK^{-1}(r) + \varepsilon + \varepsilon')) \, dr + K(0)\varepsilon.$$

Since $K^{-1}$ is non-increasing, and $r' < K(0)$, it follows that $K^{-1}(rr'/K(0)) \geq K^{-1}(r)$ for every $r \geq 0$. Moreover, for any $0 \leq r \leq K(0)$, we have $K^{-1}(rr'/K(0)) \geq K^{-1}(r')$. These two considerations imply that, for $0 \leq r \leq K(0)$, we have

$$sK^{-1}(r) + \varepsilon + \varepsilon' \leq (s + (\varepsilon + \varepsilon')/K^{-1}(r')) K^{-1}(rr'/K(0)).$$

Combining this with the above bound for the local density estimate of $x$ we get

$$(\mu \ast K_s)(x) \leq \int_0^K(0) \nu\left(B(y, (s + (\varepsilon + \varepsilon')/K^{-1}(r')) K^{-1}(rr'/K(0)))\right) \, dr + K(0)\varepsilon$$

$$= \frac{K(0)}{r'} \int_0^{r'} \nu\left(B\left(y, (s + (\varepsilon + \varepsilon')/K^{-1}(r')) K^{-1}(r)\right)\right) \, dr + K(0)\varepsilon$$

$$\leq \frac{K(0)}{r'} \left(\nu \ast K_{(s + (\varepsilon + \varepsilon')/K^{-1}(r'))}\right)(y) + K(0)\varepsilon.$$

Finally, note that, for $0 \leq a \leq M < \infty$ and $c \geq 1$, we have $ca \leq a + M(c - 1)$. As $\nu$ is a probability measure, any local density estimate is bounded by $K(0)$. This implies that

$$(\mu \ast K_s)(x) \leq \left(\nu \ast K_{(s + (\varepsilon + \varepsilon')/K^{-1}(r'))}\right)(y) + K(0) \left(\frac{K(0)}{r'} - 1\right) + K(0)\varepsilon,$$

as required. \qed

Before proving the stability of kernel linkage, we define a canonical correspondence between two compact metric spaces embedded in a common metric space.

**Definition 3.5.** Let $X$ and $Y$ be compact metric spaces, let $Z$ be any metric space, and let $i : X \to Z$ and $j : Y \to Z$ be isometric embeddings. Define the **closest point correspondence** $R_c \subseteq X \times Y$, where $(x, y) \in R_c$ if and only if $d_Z(i(x), j(y)) = \min_{y' \in Y} d_Z(i(x), j(y'))$ or $d_Z(i(x), j(y)) = \min_{x' \in X} d_Z(i(x'), j(y))$.

**Theorem 3.6.** Kernel linkage is uniformly continuous with respect to the Gromov–Hausdorff–Prokhorov distance on compact metric probability spaces, and the measured-interleaving distance. If kernel linkage is defined using the uniform kernel, then it is 2-Lipschitz.
Proof. Let $K$ be a kernel. We prove the following: for every $\varepsilon > 0$, there exists $\delta > 0$ such that if $X$ and $Y$ are compact metric probability spaces and $i : X \to Z$ and $j : Y \to Z$ are isometric embeddings into a metric space $Z$ with $d_H(i(X), j(Y)), d_P(i_x \mu_X, j_x \mu_Y) < \delta$, then $\mathbb{L}^K(X)$ and $\mathbb{L}^K(Y)$ are $(\varepsilon, \varepsilon, \varepsilon, \varepsilon)$-measured-interleaved with respect to the closest point correspondence $R_c \subseteq X \times Y$.

Let $r' \in (0, K(0))$ and $\delta > 0$, and define $\delta_0 = \frac{2r'}{K^{-1}(r')} \text{ and } \delta_k = K(0)^2/r' - K(0) + K(0)\delta$. We now prove that if $X$ and $Y$ are compact metric probability spaces and $i : X \to Z$ and $j : Y \to Z$ are isometric embeddings with $d_H(i(X), j(Y)), d_P(i_x \mu_X, j_x \mu_Y) < \delta$, then $\mathbb{L}^K(X)$ and $\mathbb{L}^K(Y)$ are $(\delta_0, 2\delta, \delta_0, \delta)$-measured-interleaved with respect to $R_c$. This implies the statement of the previous paragraph, by taking $r' \in (0, K(0))$ such that $K(0)^2/r' - K(0) < \varepsilon/2$, and $\delta > 0$ such that $2\delta/k^{-1}(r') < \varepsilon, 2\delta < \varepsilon$, and $K(0)\delta < \varepsilon/2$.

We start by showing that, for any $s, t > 0$ and $k > \delta_k$, we have relations in $C(R_c)$:

$$
\pi^\ast_X(\mathbb{L}^K(X)) (s, t, k) \preceq \pi^\ast_Y(\mathbb{L}^K(Y)) (s + \delta_0, t + 2\delta_0, k - \delta_k)
$$

$$
\pi^\ast_Y(\mathbb{L}^K(Y)) (s, t, k) \preceq \pi^\ast_X(\mathbb{L}^K(X)) (s + \delta_0, t + 2\delta_0, k - \delta_0).
$$

We show that the first relation holds, and the second relation follows from a symmetric argument. Let $(x, y) \in R_c$. If $(x, y)$ belongs to a cluster of $\pi^\ast_X(\mathbb{L}^K(X))(s, t, k)$, then it belongs to a cluster of $\pi^\ast_Y(\mathbb{L}^K(Y))(s + \delta_0, t + 2\delta_0, k - \delta_k)$, by Lemma 3.4. Now, assume that $(x, y)$ and $(x', y') \in R_c$ belong to the same cluster in $\pi^\ast_X(\mathbb{L}^K(X))(s, t, k)$. This means that $x \simeq x'$ in $X_{[s, k]}$. Since $|d_X(x_1, x_2) - d_Y(y_1, y_2)| < 2\delta$ for every $(x_1, y_1), (x_2, y_2) \in R_c$, we have that $y \simeq t + 2\delta y'$ in $Y_{[s + \delta_0, k - \delta_0]}$ as required.

Now let $C_n \in \mathbb{L}^K(X)(s, t, k)$ be a finite collection of clusterings. It follows from the previous paragraph that there are $D_n \in \mathbb{L}^K(Y)(s + \delta_0, t + 2\delta_0, k - \delta_k)$ with $\pi^{-1}(C_n) \subseteq \pi^{-1}(D_n)$. It remains to show that $\mu_Y(\cup_n D_n) \geq \mu_X(\cup_n C_n) - \delta$.

In general, if $M$ is a metric probability space, and $p : M \to N$ is an isometric embedding into a metric space $N$, we can give $N$ the pushforward measure $p_\ast(\mu_M)$, and we get a function $p_\ast : \mathbb{L}^K(M)(s, t, k) \to \mathbb{L}^K(N)(s, t, k)$ such that $p(E) \subseteq p_\ast(E)$ for all $E \in \mathbb{L}^K(M)(s, t, k)$. Write $i_\ast : \mathbb{L}^K(X)(s, t, k) \to \mathbb{L}^K(Y)(s, t, k)$ for the function induced by $i : X \to Z$, and write $A = \cup_n C_n$. By the Prokhorov assumption, $i_\ast(\mu_X)(A) \leq j_\ast(\mu_Y)(A^\delta) + \delta$. Below, we show that $j^{-1}(A^\delta) \subseteq \cup_n D_n$, and therefore $\mu_Y(\cup_n D_n) \geq \mu_Y(j^{-1}(A^\delta)) = j_\ast(\mu_Y)(A^\delta) \geq i_\ast(\mu_X)(A) - \delta \geq \mu_X(\cup_n C_n) - \delta$.

Finally, we show that $j^{-1}(A^\delta) \subseteq \cup_n D_n$. We say that a finite sequence of points in a metric space $(x_0, \ldots, x_n)$ is a $t$-chain if $d(x_i, x_{i+1}) \leq t$ for all $0 \leq i < n$. Now, let $y_0 \in j^{-1}(A^\delta)$, so that there is $a_0 \in A$ with $d_Z(j(y_0), a_0) < \delta$. As $a_0 \in A$, there is a $t$-chain $(a_0, a_1, \ldots, a_m, i(x))$ in $Z$, where $x \in C_n$, for some $n$, and $(i_\ast(\mu_X) + K_s)(a_\ell) \geq k$ for all $0 \leq \ell \leq m$.

Without loss of generality, we may assume $Z = \text{Im}(i) \cup \text{Im}(j)$, and thus that each $a_\ell$ is in the image of $i$ or $j$, so for $1 \leq \ell \leq m$, choose $y_\ell \in Y$ with $d_Z(j(y_\ell), a_\ell) < \delta$. By Lemma 3.4, we have $\mu_X + K_{s+\delta_0}(y_\ell) \geq k - \delta_0$ for all $0 \leq \ell \leq m$. By the triangle inequality, $(j(y_0), j(y_1), \ldots, j(y_m), i(x))$ is a $(t + 2\delta)$-chain in $Z$, and $d_Z(j(y_m), i(x)) < t + \delta$. Choose $y \in Y$ with $(x, y) \in R_c$. Then $d_Z(i(x), j(y)) < \delta$, so $d_Y(y_m, y) < t + 2\delta$. Therefore, $(y_0, y_1, \ldots, y_m, y)$ is a $(t + 2\delta)$-chain in $Y$. As $x \in C_n$, we have $y \in D_n$, so that $y_0 \in D_n$ as well.

It remains to consider the case where $K$ is the uniform kernel. Then $K(0) = 1$, and, for every $r' \in (0, 1)$ we have $K^{-1}(r') = 1$, since $K^{-1} = K$. Letting $r' \to 1$, the interleaving we constructed above approaches a $(2\delta, 2\delta, \delta, \delta)$-interleaving, as needed. □

3.2. Stability of $\gamma$-linkage.

Definition 3.7. Let $H$ be a $(1, 1, -1)$-hierarchical clustering of a set $X$. A curve $\gamma$ in the $(1, 1, -1)$-parameter space is given by an interval $I_\gamma = (0, \max_\gamma) \subseteq \mathbb{R}_{>0}$ and a continuous
function $\gamma : I_\gamma \to \mathbb{R}_{>0} \times \mathbb{R}_{>0} \times \mathbb{R}_{>0}$ which is non-increasing in its first two coordinates, and non-decreasing in its third coordinate. The slice of $H$ by $\gamma$ is the following hierarchical clustering of $X$:

$$H^\gamma(r) = \begin{cases} \emptyset & \text{if } r \geq \max_\gamma \\ H(\gamma(r)) & \text{if } r \in I_\gamma. \end{cases}$$

**Definition 3.8.** Let $K$ be a kernel, and let $\gamma$ be a curve in the $(1,1,-1)$-parameter space. If $X$ is a metric probability space, we let $\gamma\text{-link}(X) := \mathbb{L}^K(X^\gamma)$.

Interleavings between multi-parameter hierarchical clusterings restrict to interleavings between slices, provided the slice does not fix any parameters. We make this precise in the next proposition. We prove the technical statement Proposition 3.10(2) for use in the consistency results.

**Definition 3.9.** A curve $\gamma = (\gamma_s, \gamma_t, \gamma_k) : I_\gamma \to \mathbb{R}^3$ in the $(1,1,-1)$-parameter space is **non-singular in each component** if it is continuously differentiable and $\gamma'_s, \gamma'_t, \gamma'_k < 0$ and $\gamma'_k > 0$.

**Proposition 3.10.** Let $\gamma$ be a curve in the $(1,1,-1)$-parameter space that is non-singular in each component. Let $H$ and $E$ be measurable $(1,1,-1)$-hierarchical clusterings of measure spaces $X$ and $Y$ respectively, and let $R \subseteq X \times Y$ be a correspondence.

1. Assume $0 < c = \inf_{r \in I_\gamma} \{\min (|\gamma'_s(r)|, |\gamma'_t(r)|, |\gamma'_k(r)|)\}$. If $\varepsilon > 0$ and $H$ and $E$ are $(\varepsilon, \varepsilon, \varepsilon, \varepsilon)$-measured-interleaved with respect to $R$, then $H^\gamma$ and $E^\gamma$ are $(\varepsilon/c, \varepsilon)$-measured-interleaved with respect to $R$.

2. Assume there exists $r \in I_\gamma$ with $H^\gamma(r) = \emptyset$. For every $\varepsilon > 0$ there is $\delta > 0$ such that, if $H$ and $E$ are $(\delta, \delta, \delta, \varepsilon, \delta)$-measured-interleaved with respect to $R$, then $H^\gamma$ and $E^\gamma$ are $(\varepsilon, \varepsilon, \varepsilon, \delta)$-measured-interleaved with respect to $R$.

**Proof.** We start by proving (1). Let $\varepsilon > 0$. From the conditions on the derivatives, we deduce

\[ \gamma_s(r) + \varepsilon \leq \gamma_s(r - \varepsilon/c), \quad \gamma_t(r) + \varepsilon \leq \gamma_t(r - \varepsilon/c), \quad \text{and} \quad \gamma_k(r) - \varepsilon \geq \gamma_k(r - \varepsilon/c) \]

for every $r \in (\varepsilon/c, \max_\gamma)$. By assumption, we have

\[ \pi_X^s(H)(s,t,k) \leq \pi_X^s(E)(s + \varepsilon, t + \varepsilon, k - \varepsilon), \]

\[ \pi_Y^t(E)(s,t,k) \leq \pi_Y^t(H)(s + \varepsilon, t + \varepsilon, k - \varepsilon) \]

for all $s,t,k > 0$ with $k - \varepsilon > 0$. We show that for all $r$ such that $r - \varepsilon/c > 0$ we have $\pi_X^s(H^\gamma)(r) \leq \pi_X^s(E^\gamma)(r - \varepsilon/c)$. The other inclusion works analogously. It is enough to consider $r < \max_\gamma$, since for $r \geq \max_\gamma$, we have $\pi_X^s(H^\gamma)(r) = \emptyset$ by definition of slicing. So let $r \in (\varepsilon/c, \max_\gamma)$, and compute

\[ \pi_X^s(H^\gamma)(r) = \pi_X^s(H)(\gamma_s(r), \gamma_t(r), \gamma_k(r)) \leq \pi_X^s(E)(\gamma_s(r) + \varepsilon, \gamma_t(r) + \varepsilon, \gamma_k(r) - \varepsilon) \]

\[ \leq \pi_Y^t(E)(\gamma_s(r - \varepsilon/c), \gamma_t(r - \varepsilon/c), \gamma_k(r - \varepsilon/c)) \]

\[ = \pi_Y^t(E^\gamma)(r - \varepsilon/c), \]

where the first inequality is by the $(\varepsilon, \varepsilon, \varepsilon)$-interleaving and the second one is by Eq. (1).
\[ r \geq r_1. \] This is because Eq. (\ast) holds for any \( r \in (\varepsilon, r_1) \) and thus we can repeat the argument given for (1) to show that, since \( \delta \leq \min(\varepsilon, r) \), \( H^\varepsilon \) and \( E^\gamma \) are \((\varepsilon, \varepsilon)\)-measured-interleaved with respect to \( R \). We conclude the proof by showing that \( E^\gamma(r_1) = \emptyset \); this implies that \( E^\gamma(r) = \emptyset \) for every \( r \geq r_1 \), while \( H^\gamma(r) = \emptyset \) for every \( r \geq r_1 \) by assumption. As \( \delta \leq c(r_1 - r_0) \), we have

\[
\pi^\gamma_1(H)(\gamma(r_1)) \leq \pi^\varepsilon_1(H)(\gamma_1(r_1) + c(r_1 - r_0), \gamma_1(r_1) + c(r_1 - r_0), \gamma_1(r_1) - c(r_1 - r_0)) \leq \pi^\varepsilon_1(H^\varepsilon)(r_1 - (r_1 - r_0)) = \pi^\varepsilon_1(H^\varepsilon)(r_0) = \emptyset,
\]

where in the second step we used the fact that Eq. (\ast) holds for \( r_1 \), since \( r_1 \in (\varepsilon, r_2) \). \hfill \Box

**Definition 3.11.** Let \( \gamma_1 \) and \( \gamma_2 \) be curves in the \((1, 1, -1)\)-parameter space. For \( \varepsilon > 0 \), we say that \( \gamma_1 \) and \( \gamma_2 \) are \( \varepsilon \)-interleaved if \( |\max_{1} - \max_{\gamma_2}| \leq \varepsilon \) and for every \( r \in (\varepsilon, \max_{\gamma_1}) \) we have \( \gamma_1(r) \leq \gamma_2(r - \varepsilon) \), and for every \( r \in (\varepsilon, \max_{\gamma_2}) \) we have \( \gamma_2(r) \leq \gamma_1(r - \varepsilon) \).

The following stability result is then straightforward to prove.

**Proposition 3.12.** Let \( X \) be a metric probability space, and let \( H \) be a \((1, 1, -1)\)-hierarchical clustering of \( X \). If \( \varepsilon \geq 0 \) and \( \gamma_1 \) and \( \gamma_2 \) are curves in the \((1, 1, -1)\)-parameter space that are \( \varepsilon \)-interleaved, then \( d_{\text{MH}}(H^\gamma_1, H^\gamma_2) \leq \varepsilon. \)

An interesting feature of \( \gamma \)-link is its flexibility: the stability results of this section hold for a large class of curves \( \gamma \). For concreteness, we now explain what these stability results imply when we restrict attention to lines in the kernel linkage parameter space. To simplify the class of curves further, we assume that the two spatial parameters of kernel linkage are equal, \( s = t \).

**Notation 3.13.** We specify a line \( \lambda \) by choosing an \( s \)-intercept \( x > 0 \) and a \( k \)-intercept \( y > 0 \). Let \( \mu = -y/x \) be the slope of \( \lambda \). We write \( \lambda_{x,y} \) if we need to specify the intercepts. If we parametrize \( \lambda \) with the \( k \) coordinate, we get a curve in the \((1, 1, -1)\)-parameter space, in the sense of Definition 3.7: \( \lambda : (0, y)^{\text{op}} \to \mathbb{R}_{>0} \times \mathbb{R}_{>0} \times \mathbb{R}_{\geq 0}^{\text{op}} \) defined by \( \lambda(r) = ((r/\mu) + x, (r/\mu) + x, r) \). We write \( \lambda_{x,\infty} : \mathbb{R}_{\geq 0}^{\text{op}} \to \mathbb{R}_{>0} \times \mathbb{R}_{>0} \times \mathbb{R}_{>0}^{\text{op}} \) for the vertical line defined by \( \lambda_{x,\infty}(r) = (x, x, r) \).

If we parametrize with the \( s \) coordinate, we get the poset map \( \lambda_{\text{cov}} : (0, x) \to \mathbb{R}_{>0} \times \mathbb{R}_{>0} \times \mathbb{R}_{\geq 0}^{\text{op}} \) defined by \( \lambda_{\text{cov}}(r) = (r, r, \mu r + y) \). One can take the slice of kernel linkage by \( \lambda_{\text{cov}} \), except now one obtains a covariant one-parameter hierarchical clustering. By an abuse of notation, we call this \( \lambda_{\text{cov}} \)-link. As before, we write \( \lambda_{\text{cov}}^{y} : \mathbb{R}_{>0} \to \mathbb{R}_{>0} \times \mathbb{R}_{>0} \times \mathbb{R}_{\geq 0}^{\text{op}} \) for the horizontal line defined by \( \lambda_{\text{cov}}^{y}(r) = (r, r, y) \).

**Remark 3.14.** For a finite metric space \( X \) endowed with the normalized counting measure, the covariant hierarchical clustering \( \lambda_{\text{cov}}^{y} \)-link(\( X \)) is equal to the robust single-linkage hierarchical clustering of \( X \) with parameter \( y \cdot |X| \) (it is worth noting, however, that robust single-linkage is often re-parametrized; for example, the version of robust single-linkage that is used by the HDBSCAN clustering algorithm is contravariant, and is parametrized by \( 1/s \)). Meanwhile, \( \lambda_{x,\infty} \)-link(\( X \)) is an instance of the first approach to density-based clustering mentioned in the introduction.

The stability results Proposition 3.10 and Proposition 3.12 do not apply to these slices, and it is easy to construct examples that show that, in fact, for fixed \( x \) and \( y \), the algorithms \( \lambda_{x,\infty} \)-link and \( \lambda_{\text{cov}}^{y} \)-link are not continuous with respect to the Gromov–Hausdorff–Prokhorov distance and the correspondence-interleaving distance. Similarly, when applied to a fixed metric probability space, the algorithms are not continuous with respect to changes in \( x \) or \( y \) (see Section 6).

We now explain what the stability results for \( \gamma \)-link imply for lines \( \gamma = \lambda \) with non-zero, finite slope.
Corollary 3.15. Assume kernel linkage is defined using the uniform kernel. Let $0 < x, y < \infty$, let $\lambda = \lambda^{x,y}$, and let $\mu = -y/x$ be the slope of $\lambda$. Then, with respect to the Gromov–Hausdorff–Prokhorov distance and the measured-interleaving distance:

1. $\lambda$-link is $\max(2|\mu|, 1)$-Lipschitz,
2. $\lambda_{\text{cov}}$-link is $\max(|1/\mu|, 2)$-Lipschitz. \qed

Remark 3.16. The Lipschitz constants in Corollary 3.15 require some comments. Because this kind of stability result does not hold for horizontal or vertical lines through the kernel linkage parameter space, one should expect that, asymptotically, the stability of $\lambda$-link becomes worse as $\mu \to -\infty$ or $\mu \to 0$. This is evident for $\mu \to -\infty$ in Corollary 3.15(1), but it is not clear for $\mu \to 0$ in Corollary 3.15(1). To see what is happening in this case, fix a compact metric probability space $X$, choose $\lambda^{x,y}$ such that $|\mu| < 1/2$, and let $x \to \infty$, so that $\mu \to 0$. Then, the length of the interval of $r$-values where $\lambda$-link($X$) can vary goes to 0. So, even though $\lambda$-link is 1-Lipschitz for all $\lambda$ in this family, the bound given by the 1-Lipschitz property becomes less meaningful as $\mu \to 0$. Similar considerations apply to $\lambda_{\text{cov}}$-link.

Finally, Proposition 3.12 implies a stability result for the choice of $\lambda$:

Corollary 3.17. Let $X$ be a metric probability space. Let $\lambda = \lambda^{x,y}$ with slope $\mu = -y/x$ be defined by intercepts $0 < x, y < \infty$, and let $\lambda' = \lambda^{x',y'}$ with slope $\mu' = -y'/x'$ be defined by intercepts $0 < x', y' < \infty$.

1. $d_{\text{MI}}(\lambda$-link($X$), $\lambda'$-link($X$)) $\leq \max(|y - y'|, |x - x'| \cdot \min(|\mu|, |\mu'|))$.
2. $d_{\text{MI}}(\lambda_{\text{cov}}$-link($X$), $\lambda'_{\text{cov}}$-link($X$)) $\leq \max(|x - x'|, |y - y'| \cdot \min(|1/\mu|, |1/\mu'|))$. \qed

4. Consistency

Once one has the correspondence-interleaving distance and the measured-interleaving distance, there is a natural notion of consistency for hierarchical clustering algorithms associated to each of these distances. In this section, we define these notions, and show that both imply Hartigan consistency. Then, we show that $\gamma$-link is consistent with respect to both distances.

4.1. Notions of consistency of hierarchical clustering algorithms.

Definition 4.1. A hierarchical clustering algorithm $\mathcal{A}$ with parameter space $\Theta$ is a mapping that assigns to each finite metric space $X$ and each parameter $\theta \in \Theta$ a hierarchical clustering $\mathcal{A}^\theta(X)$ of $X$.

In the next definition, we use the closest point correspondence $R_c$ of Definition 3.5.

Definition 4.2. Let $f : \mathbb{R}^d \to \mathbb{R}$ be a probability density function, with $X = \text{supp}(f)$. A hierarchical clustering algorithm $\mathcal{A}$ with parameter space $\Theta$ is CI-consistent (respectively MI-consistent) with respect to $f$ if for every $n \in \mathbb{N}$ there exists a parameter $\theta_n \in \Theta$ such that, for every $\varepsilon > 0$ and $X_n$ an i.i.d. $n$-sample of $X$ with distribution $f$, the probability that $\mathcal{A}^\theta_n(X_n)$ and $H(f)$ are $\varepsilon$-interleaved (respectively $\varepsilon$-measured-interleaved) with respect to $R_c$ goes to 1 as $n$ goes to $\infty$. In the case of MI-consistency, $X_n$ is endowed with the normalized counting measure $\mu_n$ and $X$ with the measure $\mu_f$ defined by $f$.

Clearly MI-consistency implies CI-consistency. We shall see that CI-consistency implies Hartigan consistency. In order to define Hartigan consistency, we define the notion of cluster tree algorithm.
**Definition 4.3.** Let \( X \) be a set. A cluster tree of \( X \) is given by a family \( \mathcal{T} \) of subsets of \( X \) with the property that whenever \( A \) and \( B \) are distinct elements of \( \mathcal{T} \), then one of the following is true: \( A \cap B = \emptyset \), \( A \subseteq B \), or \( B \subseteq A \). The elements of \( \mathcal{T} \) are called clusters of \( \mathcal{T} \).

**Example 4.4.** Let \( H \) be a hierarchical clustering of a set \( X \). We can define an associated cluster tree \( \mathcal{F}H = \{ C \in H(\gamma) : \gamma > 0 \} \).

**Definition 4.5.** A cluster tree algorithm \( \mathcal{A} \) with parameter space \( \Theta \) is a mapping that assigns to each finite metric space \( X \) and each parameter \( \theta \in \Theta \) a cluster tree \( \mathcal{A}^\theta(X) \) of \( X \).

**Definition 4.6** (cf. [Har81]). Let \( f : \mathbb{R}^d \to \mathbb{R} \) be a probability density function, with \( X = \text{supp}(f) \). A cluster tree algorithm \( \mathcal{A} \) with parameter space \( \Theta \) is Hartigan consistent with respect to \( f \) if for every \( n \in \mathbb{N} \) there exists a parameter \( \theta_n \in \Theta \) such that, given \( A \) and \( A' \) distinct elements of \( H(f)(r) \) for some \( r > 0 \), and \( X_n \) an i.i.d. \( n \)-sample of \( X \) with distribution \( f \) we have

\[
P(A_n \cap A'_n = \emptyset) \xrightarrow{n \to \infty} 1,
\]

where \( A_n \) is the smallest cluster in \( \mathcal{A}^{\theta_n}(X_n) \) that contains \( A \cap X_n \), and \( A'_n \) is the smallest cluster in \( \mathcal{A}^{\theta_n}(X_n) \) that contains \( A' \cap X_n \).

The proof of the following result is in Appendix A.

**Proposition 4.7.** Let \( f : \mathbb{R}^d \to \mathbb{R} \) be a continuous and compactly supported probability density function. If a hierarchical clustering algorithm \( \mathcal{A} \) is CI-consistent with respect to \( f \), then the associated cluster tree algorithm \( \mathcal{F}\mathcal{A} \) is Hartigan consistent with respect to \( f \).

### 4.2. Consistency of \( \gamma \)-linkage

We now prove that the hierarchical clustering algorithm \( \gamma \)-link is MI-consistent with respect to any probability density function \( f : \mathbb{R}^d \to \mathbb{R} \) that is continuous and compactly supported. The strategy is to find curves \( \gamma \) such that the \( \gamma \)-link of the metric probability space \( (\text{supp}(f), \mu_f) \) is a good approximation of \( H(f) \). Then, the stability of \( \gamma \)-link implies that, for a sufficiently good sample \( X_n \) of \( f \), the \( \gamma \)-link of \( X_n \) is a good approximation of the \( \gamma \)-link of \( (\text{supp}(f), \mu_f) \).

To identify curves \( \gamma \) that we can use to approximate \( H(f) \), we introduce the notion of an admissible family of curves in the \((1,1,-1)\)-parameter space. An example of an admissible family is given by the family of lines \( \lambda \) defined in Notation 3.13.

**Definition 4.8.** Let \( \gamma : I_\gamma \to \mathbb{R}^3_{>0} \) be a curve in the \((1,1,-1)\)-parameter space. We say that \( \gamma \) is covering if \( \gamma_s \) is strictly decreasing and \( \gamma_s(r) \to 0 \) as \( r \to \max_{\gamma} \), and \( \gamma_k \) is strictly increasing and \( \gamma_k(r) \to 0 \) as \( r \to 0 \).

**Definition 4.9.** Let \( K \) be a kernel, and let \( \gamma \) be a curve in the \((1,1,-1)\)-parameter space. For \( s > 0 \), we write \( v_s = \int_\mathbb{R}^d K(||x||/s) \, dx \). Define a non-decreasing function \( \varphi : I_\gamma \to \mathbb{R}_{>0} \) by

\[
\varphi(r) = \frac{\gamma_k(r)}{v_{\gamma_s(r)}}.
\]

If \( \gamma \) is covering, then \( \varphi \) is a bijection. In that case, we write \( \overline{\gamma} = \gamma \circ \varphi^{-1} \).

If \( \gamma \) is a curve in the \((1,1,-1)\)-parameter space that is covering, then \( \overline{\gamma} \) is also a curve in the \((1,1,-1)\)-parameter space, and for \( X \) a metric probability space, we say that the \( \overline{\gamma} \)-link of \( X \) is the hierarchical clustering \( \mathbb{L}(X)^{\overline{\gamma}} \).

**Definition 4.10.** We say that a family \( \{ \gamma^\theta \}_{\theta \in \Theta} \) of curves in the \((1,1,-1)\)-parameter space is an admissible family if each \( \gamma^\theta \) is covering and non-singular in each component, and if, for every \( b > 0 \), there is \( \theta \in \Theta \) such that for all \( r \in I_{\gamma^\theta} \), we have \( \gamma_s^\theta(r), \gamma_k^\theta(r) < b \).
Clearly, the family \( \{ x^y \}_{x>0, y>0} \) is an admissible family. In fact, for any fixed \( \alpha > 0 \), the family \( \{ x^{\alpha y} \}_{y>0} \) is admissible. The proof of the following result is in Appendix A.

**Theorem 4.11.** Let \( \{ \gamma^\theta \}_{\theta \in \Theta} \) be an admissible family of curves in the \((1, 1, -1)\)-parameter space. The hierarchical clustering algorithm \( \gamma \)-link with parameter space \( \Theta \) is MI-consistent with respect to any continuous, compactly supported probability density function \( f : \mathbb{R}^d \to \mathbb{R} \).

**Remark 4.12.** For any covering curve \( \gamma \) in the \((1, 1, -1)\)-parameter space, \( \gamma \)-link and \( \gamma \)-link produce the same underlying cluster tree. So, it follows from the preceding theorem that if \( \{ \gamma^\theta \}_{\theta \in \Theta} \) is an admissible family of curves in the \((1, 1, -1)\)-parameter space, then the algorithm \( \gamma \)-link with parameter space \( \Theta \) is Hartigan consistent with respect to any continuous, compactly supported probability density function \( f : \mathbb{R}^d \to \mathbb{R} \).

5. **Pruning and flattening hierarchical clusterings**

After constructing a hierarchical clustering of a dataset, one often wants to simplify this hierarchical clustering. A *pruning* procedure removes clusters from a hierarchical clustering, leaving a simpler hierarchical clustering. A *flattening* procedure extracts a single clustering of the underlying dataset from a hierarchical clustering.

In this section, we consider three well-known simplification procedures (two pruning and one flattening) and prove stability results for them. Because these results are stated in terms of interleavings, one can apply these simplification procedures to the output of \( \gamma \)-link, and our stability and consistency results for \( \gamma \)-link imply such results for the simplification.

We first consider persistence-based pruning and flattening procedures that are inspired by the ToMATo clustering algorithm of Chazal, Guibas, Oudot, and Skraba [CGOS13]. The basic idea is to first prune the hierarchical clustering according to persistence, removing those clusters that have only recently appeared in the hierarchy, and then to extract a flat clustering by simply taking the leaves of the pruned hierarchical clustering. The pruning procedure resembles also the pruning of [KCB+16]. We show in Section 5.2 that these procedures can be applied to any hierarchical clustering, and that they have compelling stability properties. By taking a modular approach—studying the stability properties of the procedures in isolation—we hope to make clear just how strong these stability properties are. Following the methodology of [CGOS13], in Section 5.3 we explain how the persistence diagram of a hierarchical clustering can be used for selecting the parameter of these procedures.

The third simplification procedure we consider is a measure-based pruning of measurable hierarchical clusterings, in which one removes those clusters whose measure is below a certain threshold. This pruning is well-known, and is a key step of the HDBSCAN algorithm [CMS13]. Our stability result for this procedure requires measured-interleavings, and this is one of our motivations for considering such interleavings.

5.1. **The persistent clusters of a hierarchical clustering.** There are many ways to measure the similarity of two clusterings of a dataset (see, e.g., [Mei07] and references therein), so there are many possible ways one could try to formulate a stability result for a flattening procedure. Our approach is based on the fact that the persistence-based flattening procedure we consider actually produces more than a flat clustering: it produces a set of pairwise disjoint persistent clusters, in the sense of the following:

**Definition 5.1.** Let \( X \) be a set. A persistent cluster \( C \) of \( X \) consists of an interval \( \text{life}(C) \subseteq \mathbb{R}_{>0} \) together with a map of posets \( C : \text{life}(C)^{\text{op}} \to \mathcal{P}(X) \), where \( \mathcal{P}(X) \) is the power set of \( X \).
We have a stability result for the persistence-based flattening. Let \( \tau \) be persistent clusters of \( X \) and \( Y \) respectively, and let \( \pi \) be a correspondence between sets \( X \) and \( Y \). We now define a notion of interleaving between persistent clusters; we will use this notion to formulate a stability result for the persistence-based flattening.

**Notation 5.2.** Let \( H \) be a hierarchical clustering of a set \( X \). For \( r \geq r' \) we write \( H(r) \rightarrow H(r') \) for the function that takes \( C \in H(r) \) to the unique \( D \in H(r') \) such that \( C \subseteq D \).

**Definition 5.3.** Let \( C \) and \( D \) be persistent clusters of a set \( X \), and let \( \varepsilon \geq 0 \). We say that \( C \) and \( D \) are \( \varepsilon \)-interleaved if \( |\text{birth}(C) - \text{birth}(D)|, |\text{death}(C) - \text{death}(D)| \leq \varepsilon \), and for every \( r \in (\text{death}(C) + 2\varepsilon, \text{birth}(C)) \) we have \( C(r) \subseteq D(r - \varepsilon) \) and for every \( r \in (\text{death}(D) + 2\varepsilon, \text{birth}(D)) \) we have \( D(r) \subseteq C(r - \varepsilon) \). Let \( R \subseteq X \times Y \) be a correspondence between sets \( X \) and \( Y \), let \( C \) and \( D \) be persistent clusters of \( X \) and \( Y \) respectively, and let \( \varepsilon \geq 0 \). We say that \( C \) and \( D \) are \( \varepsilon \)-interleaved with respect to \( R \) if \( \pi_X^{-1}(C) \) and \( \pi_Y^{-1}(D) \) are \( \varepsilon \)-interleaved as persistent clusters of \( R \).

We now define a fundamental object associated to any hierarchical clustering, which we call the poset of persistent clusters. This object, or something equivalent, appears in many works on hierarchical clustering (e.g., [KCB+16, Appendix A], [MH18, Section 2.3], or [Jar19] for an approach in the multi-parameter setting). See Fig. 2 for an example of this construction.

**Definition 5.4.** Let \( H \) be a hierarchical clustering of a set \( X \). Define the poset of persistent clusters of \( H \), denoted \( \text{PC}(H) \), as the poset with underlying set the following quotient set:

\[
\text{PC}(H) = \left( \prod_{r > 0} H(r) \right) / \sim,
\]

where \( \sim \) is the symmetric closure of the relation where, for \( C \in H(r) \) and \( C' \in H(r') \) with \( r \geq r' \), we have that \( C \) and \( C' \) are related if \( C \subseteq C' \) and for every \( r'' \in [r', r] \), there is exactly one cluster \( C'' \in H(r'') \) such that \( C'' \subseteq C' \). Each \( C \in \text{PC}(H) \) is a persistent cluster in the sense of Definition 5.1, with \( \text{life}(C) = \{ r > 0 : \exists C \in H(r) \text{ with } C = [C] \} \). The partial order on \( \text{PC}(H) \) is defined by \( C \leq D \) if \( \text{U}(C) \subseteq \text{U}(D) \).

### 5.2. Persistence-based pruning and flattening.

**Definition 5.5.** Let \( H \) be a hierarchical clustering of a set \( X \). For \( r > 0 \), and \( C \in H(r) \), let

\[
\text{pers}(C) = \sup \{ i > 0 : \exists A \in H(i) \text{ with } A \subseteq C \} - r.
\]

For \( \tau \geq 0 \), the persistence-based pruning of \( H \) with respect to the threshold \( \tau \) is the hierarchical clustering \( H_{\text{pers} \geq \tau} \) of \( X \) with

\[
H_{\text{pers} \geq \tau}(r) = \{ C \in H(r) : \text{pers}(C) \geq \tau \}.
\]

See Fig. 3 for a diagrammatic example of this pruning. By design, this operation is stable with respect to interleavings.

**Proposition 5.6.** Let \( H \) and \( E \) be hierarchical clusterings of sets \( X \) and \( Y \) respectively, and let \( \tau \geq 0 \). The hierarchical clusterings \( H_{\text{pers} \geq \tau} \) and \( H \) are \( \tau \)-interleaved and, if \( H \) and \( E \) are \( \varepsilon \)-interleaved with respect to a correspondence \( R \subseteq X \times Y \), then \( H_{\text{pers} \geq \tau} \) and \( E_{\text{pers} \geq \tau} \) are \( \varepsilon \)-interleaved with respect to \( R \).
In order to prove a stability result for the persistence-based flattening procedure, we will need some finiteness assumptions for hierarchical clusterings:

**Definition 5.7.** We say that a hierarchical clustering \( H \) of a set \( X \) is **finite** if \( \text{PC}(H) \) is finite, and there is \( r > 0 \) such that \( H(r) = \emptyset \). We say that \( H \) is **essentially finite** if, for every \( \tau > 0 \), we have that \( H_{\text{pers} \geq \tau} \) is finite.

All the hierarchical clusterings relevant to us are essentially finite:

**Example 5.8.** It is easy to see that, for any \( \gamma \) and any compact metric probability space, \( \gamma \text{-link}(X) \) is essentially finite. From Lemma 5.17, below, and [CdSGO16, Theorem 3.33], it follows that if \( f : \mathbb{R}^d \to \mathbb{R} \) is continuous and compactly supported, then \( H(f) \) is essentially finite.

The persistence-based flattening is defined in terms of the *leaves* of the hierarchical clustering. We now develop the terminology we need to define this flattening procedure and prove its stability result.

An interval of a poset \( P \) consists of a subset \( I \subseteq P \) such that whenever we have \( x \leq y \leq z \in P \) with \( x, z \in I \), we also have \( y \in I \). Let \( \text{TOI}(P) \) denote the set of totally-ordered intervals of \( P \).

**Notation 5.9.** Let \( H \) be a hierarchical clustering of a set \( X \). Note that the poset \( \text{PC}(H) \) has the property that, for all \( C \in \text{PC}(H) \), the set \( \text{PC}(H)_{\geq C} = \{ D \in \text{PC}(H) : D > C \} \) is totally-ordered. If \( H \) is finite, and \( C \in \text{PC}(H) \) is such that \( \text{PC}(H)_{> C} \) is non-empty, we let \( \text{succ}(C) \) be the minimum of \( \text{PC}(H)_{> C} \). A leaf of a hierarchical clustering \( H \) is a minimal element of \( \text{PC}(H) \), and we write \( \text{leaves}(H) \) for the set of leaves of \( H \).

Let \( H \) and \( E \) be hierarchical clusterings of sets \( X \) and \( Y \) respectively, and assume there is \( \varepsilon \geq 0 \) such that \( H \) and \( E \) are \( \varepsilon \)-interleaved with respect to a correspondence \( R \subseteq X \times Y \). For \( C \in \text{PC}(H) \), let \( \text{life}(C)_{> \varepsilon} = \text{life}(C) \cap R_{> \varepsilon} \). Define a function \( i_X : \text{PC}(H) \to \text{TOI}(\text{PC}(E)) \) by mapping a persistent cluster \( C \) to the totally-ordered interval \( \{ [R_X(C(r))] \}_{r \in \text{life}(C)_{> \varepsilon}} \). If \( H \) and \( E \) are finite, then we get a partial map \( m_X : \text{PC}(H) \to \text{PC}(E) \) by mapping \( C \) to \( \min(i_X(C)) \). Note that this partial map is order-preserving and depends on \( \varepsilon \). Define, analogously, a partial map \( m_Y : \text{PC}(E) \to \text{PC}(H) \).

In the following lemma, whose proof is straightforward, we collect simple properties of the maps \( m_X \) and \( m_Y \).
Lemma 5.10. Let $H$ and $E$ be finite hierarchical clusterings of sets $X$ and $Y$ respectively, and assume there is $\varepsilon \geq 0$ such that $H$ and $E$ are $\varepsilon$-interleaved with respect to a correspondence $R \subseteq X \times Y$. Let $C \in \text{PC}(H)$.

(1) If $\text{birth}(C) > \varepsilon$, then $m_X(C)$ is defined, and $\text{birth}(m_X(C)) \geq \text{birth}(C) - \varepsilon$.

(2) Assume all the leaves of $H$ and $E$ have length strictly greater than $\varepsilon$. If $C \in \text{leaves}(H)$ and $D \in \text{leaves}(E)$, then $D \leq m_X(C)$ if and only if $C \leq m_Y(D)$.

Lemma 5.11. Let $H$ and $E$ be finite hierarchical clusterings of sets $X$ and $Y$ respectively, and assume there is $\varepsilon \geq 0$ such that $H$ and $E$ are $\varepsilon$-interleaved with respect to a correspondence $R \subseteq X \times Y$. If the leaves of $H$ and $E$ all have length strictly greater than $\varepsilon$, then $m_X$ restricts to a bijection $\text{leaves}(H) \to \text{leaves}(E)$ such that $C$ and $m_X(C)$ are $\varepsilon$-interleaved with respect to $R$ for every $C \in \text{leaves}(H)$.

Proof. If $C \in \text{leaves}(H)$, then $\text{life}(C) > \varepsilon$, so $m_X(C)$ is defined. We start by proving that $m_X(C)$ is a leaf; a symmetric argument shows that $m_Y$ sends leaves to leaves. So, let $D \in \text{leaves}(E)$ with $D \leq m_X(C)$, so that we also have $C \leq m_Y(D)$, by Lemma 5.10 (2). Note that we have $\text{birth}(m_Y(D)) \geq \text{birth}(D) - \varepsilon$. So if $D \neq m_X(C)$, then $\text{birth}(D) - \varepsilon > \text{birth}(m_X(C)) \geq \text{birth}(C) - \varepsilon \geq \text{birth}(m_Y(D))$, which contradicts Lemma 5.10 (1).

It follows that we have $m_Y(m_X(C)) = C$ for any leaf $C$, since $C \leq m_Y(m_X(C))$ and $C$ and $m_Y(m_X(C))$ are both leaves. Together with a symmetric argument, this shows that $m_X$ and $m_Y$ restrict to inverse bijections on leaves.

The proof that $C$ and $m_X(C)$ are $\varepsilon$-interleaved is straightforward.

Definition 5.12. Let $H$ be a hierarchical clustering of a set $X$, and let $0 < a < b$. We say $H$ is $(a, b)$-separated if $\text{length}(C) \geq b - a$ for all $C \in \text{leaves}(H_{\text{pers} \geq a})$.

Definition 5.12 is an adaptation of the notion of separatedness for persistence diagrams of [CGOS13, Definition 4.1] to hierarchical clusterings. We make this precise in Lemma 5.20, below.

Definition 5.13. Let $H$ be a hierarchical clustering of a set $X$, and let $\tau \geq 0$. The persistence-based flattening of $H$ with respect to the persistence threshold $\tau$ is the set of pairwise-disjoint persistent clusters of $X$

$$\text{PF}(H, \tau) = \text{leaves}(H_{\text{pers} \geq \tau}).$$

The flattening procedure $H \mapsto \text{PF}(H, \tau)$ is stable, provided that $H$ is $(a, b)$-separated and that $\tau \in (a, b)$ is sufficiently far away from the endpoints $a$ and $b$. One can prove the following result directly, or one can appeal to Lemma 5.19 and Lemma 5.20, below.

Lemma 5.14. Let $H$ and $E$ be essentially finite hierarchical clusterings of sets $X$ and $Y$ respectively, and assume there is $\varepsilon \geq 0$ such that $H$ and $E$ are $\varepsilon$-interleaved with respect to a correspondence $R \subseteq X \times Y$. If $H$ is $(a, b)$-separated, and $\varepsilon < (b - a)/2$, then $E$ is $(a + \varepsilon, b - \varepsilon)$-separated.

We are ready to prove the stability result for the persistence-based flattening procedure. The stability we prove is in the input hierarchical clustering, but it is straightforward to formulate and prove a stability result in the parameter $\tau$.

Proposition 5.15. Let $H$ and $E$ be essentially finite hierarchical clusterings of sets $X$ and $Y$ respectively. Assume that $H$ is $(a, b)$-separated, and that there is $\varepsilon < (b - a)/3$ such that $H$ and $E$ are $\varepsilon$-interleaved with respect to a correspondence $R \subseteq X \times Y$. Let $\tau \in (a + \varepsilon, b - 2\varepsilon)$. Then there is a bijection $m_X : \text{PF}(H, \tau) \to \text{PF}(E, \tau)$ such that, for all $C \in \text{PF}(H, \tau)$, $C$ and $m_X(C)$ are $\varepsilon$-interleaved with respect to $R$. 

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Proof. By Proposition 5.6, $H_{\text{pers} \geq \tau}$ and $E_{\text{pers} \geq \tau}$ are $\varepsilon$-interleaved with respect to $R$. By Lemma 5.14, $E$ is $(a+\varepsilon, b-\varepsilon)$-separated. It follows that all the leaves of $E_{\text{pers} \geq \tau}$ have length at least $b-\varepsilon-\tau > \varepsilon$. Clearly, the same is true for $H$, so the result follows from Lemma 5.11. □

Because this stability result for persistence-based flattening is stated in terms of interleavings, it can be combined with the stability and consistency results for $\gamma$-link proved earlier in this paper. As an example, we state the following stability result for the combination of $\lambda$-link (Notation 3.13) and persistence-based flattening.

**Corollary 5.16.** Assume kernel linkage is defined using the uniform kernel. Let $X$ be a compact metric probability space, let $\lambda = \lambda^x$ with slope $\mu$, and assume $\lambda$-link ($X$) is $(a,b)$-separated. Let $X'$ be a compact metric probability space with $d_{\text{GHP}}(X,X') < \frac{b-a}{3\max(2|\mu|,1)}$ and let $\varepsilon = d_{\text{GHP}}(X,X') \cdot \max(2|\mu|,1)$. Then, for any $\tau \in (a+\varepsilon, b-2\varepsilon)$, there is a correspondence $R \subseteq X \times X'$ and a bijection $m_X : \text{PF}(\lambda$-link($X$),$\tau$) $\rightarrow$ $\text{PF}(\lambda$-link($X'$),$\tau$) such that, for all $C \in F(\lambda$-link($X$),$\tau$), $C$ and $m_X(C)$ are $\varepsilon$-interleaved with respect to $R$.

**Proof.** If $X'$ satisfies $d_{\text{GHP}}(X,X') < (b-a)/(3\max(2|\mu|,1))$, then by Corollary 3.15(1), $d_{\text{CI}}(\lambda$-link($X$),$\lambda$-link($X'$)) < $\varepsilon < (b-a)/3$, so the result follows from Proposition 5.15. □

5.3. **The persistence diagram of a hierarchical clustering.** In this section, we recall the notions of persistence module and persistence diagram, and associate a persistence diagram to each essentially finite hierarchical clustering. See Fig. 3 for a pictorial representation of this procedure. The persistence diagram of a hierarchical clustering $H$ is an efficiently computable invariant of $H$ that contains important information about its poset of clusterings (Lemma 5.20). In particular, one can check if $H$ is $(a,b)$-separated simply by looking at the persistence diagram of $H$; this makes the persistence diagram a helpful tool for choosing the parameter $\tau$ of the persistence-based pruning and flattening procedures (see Remark 5.21). The idea of using persistence diagrams for clustering is from [CGOS13].

![Figure 3](image-url)

**Figure 3.** On the left, a hierarchical clustering $H$ and its persistence diagram, which is $(a,b)$-separated. On the right, the persistence-based pruning of $H$ with a parameter $\tau \in (a,b)$, and its persistence diagram. See Remark 5.18 for our conventions regarding $\text{PD}(H)$.

Since introducing the framework of topological persistence in detail is outside the scope of this paper, we refer the interested reader to [CdSGO16].

Fix a field $F$. Let $H$ be a hierarchical clustering of a set $X$. For each $r > 0$, consider the vector space $F^H(r)$ that has as basis the clusters of $H(r)$. For $r > r'$, there is a linear
map \( F H(r) \rightarrow F H(r') \) defined on the basis given above by mapping \( C \in H(r) \) to the only cluster \( D \in H(r') \) such that \( C \subseteq D \). It is clear that these linear maps assemble into a functor \( F H : \mathbb{R}_{\geq 0}^{\text{op}} \rightarrow \mathbb{F}-\text{vec} \). Functors of this form are called persistence modules. A persistence module \( M \) is \textbf{q-tame} if for every \( r > r' \) the rank of the structure map \( M(r) \rightarrow M(r') \) is finite.

**Lemma 5.17.** A hierarchical clustering \( H \) is essentially finite if and only if \( F H \) is q-tame and there exists \( r > 0 \) such that \( H(r) = \emptyset \).

**Proof.** Assume \( H \) is essentially finite. The structure maps of \( F H \) send generators to generators, so the rank of \( F H(r) \rightarrow F H(r') \) is equal to the number of clusters in the image of the map \( H(r \geq r') : H(r) \rightarrow H(r') \). Let \( r > r' > 0 \) and let \( 0 < \tau < (r - r')/2 \). If a cluster is in the image of \( H(r \geq r') \), then it is in the image of \( H_{\text{pers} \geq \tau}(r - \tau \geq r') \), which is finite by assumption. So \( H \) essentially finite implies that \( F H \) is q-tame. The fact that there exists \( r > 0 \) such that \( H(r) = \emptyset \) follows directly from \( H \) being essentially finite.

For the converse, assume \( H \) is q-tame and let \( \tau > 0 \). Assume \( \text{PC}(H_{\text{pers} \geq \tau}) \) is infinite, and let \( \{C_n\}_{n \geq 0} \) be a countable infinite family of elements of \( \text{PC}(H_{\text{pers} \geq \tau}) \). Each interval \( \text{life}(C_n) \) must be contained in the interval \( (0, r - \tau) \) since \( H(r) = \emptyset \). Without loss of generality, we may assume that \( \text{birth}(C_n) \rightarrow b \) and \( \text{death}(C_n) \rightarrow d \) for \( d \leq b \), when \( n \rightarrow \infty \). Let \( d \leq s \leq b \). By the definition of \( H_{\text{pers} \geq \tau} \), there must exist clusters \( \{C_n \in H(s + \tau/2)\} \) such that, for every \( n \geq 0 \), there exists \( \varepsilon_n > 0 \) such that \( [H(s + \tau/2 \geq s + \varepsilon_n)(C_n)] = C_n \). It follows that the family \( \{H(s + \tau/2 \geq s + \tau/4)(C_n)\}_{n \geq 0} \) is countable infinite, and thus that the rank of \( F H(s + \tau/2) \rightarrow F H(s + \tau/4) \) is infinite, a contradiction. \( \square \)

For our purposes, a **persistence diagram** consists of a multi-set of points \( \{(x_i, y_i) \in [0, \infty] \times [0, \infty]\}_{i \in I} \) such that \( y_i > x_i \). The **total persistence** of a point \((x_i, y_j)\) of a persistence diagram is the number \( y_i - x_i \in [0, \infty] \). A persistence diagram is \((a, b)\)-**separated** if it contains no point \((x, y)\) with \( a < y - x \leq b \).

An important construction associates a persistence diagram to every q-tame persistence module, in such a way that isomorphic persistence modules have the same persistence diagram. In the generality of q-tame persistence modules, this is done in \([\text{CdSGO}16, \text{Formula 3.4}]\).

If \( H \) is essentially finite, let \( \text{PD}(H) \) be the persistence diagram of \( F H \). One should note that \( \text{PD}(H) \) is independent of the choice of field \( \mathbb{F} \). When \( H \) is finite, \( \text{PD}(H) \) can be easily constructed using the **Elder rule** \([\text{Cur}18, \text{Definition 3.5}]\).

**Remark 5.18.** For \( H \) a contravariant hierarchical clustering, the \( x \)-axis of \( \text{PD}(H) \) corresponds to homological death, while the \( y \)-axis corresponds to homological birth. The opposite convention is used for covariant \( H \).

Often, the indexing category of a persistence module is taken to be the poset \((\mathbb{R}, \leq)\). All relevant results apply to \( \mathbb{R}_{\geq 0}^{\text{op}}\)-indexed modules as well, since one can extend them with the trivial vector space to get a \( \mathbb{R}_{\geq 0}^{\text{op}}\)-indexed module, and use the isomorphism of posets \( \mathbb{R}_{\geq 0}^{\text{op}} \cong \mathbb{R} \) given by taking negative.

Persistence diagrams can be compared using the **bottleneck distance** \([\text{CdSGO}16, \text{Section 5.2}]\), denoted \( d_B \).

**Lemma 5.19.** Let \( H \) and \( E \) be essentially finite hierarchical clusterings of sets \( X \) and \( Y \). Then \( d_B(\text{PD}(H), \text{PD}(E)) \leq d_{\text{ch}}(H, E) \).

**Proof.** This follows directly from functoriality and the isometry theorem for q-tame persistence modules \([\text{CdSGO}16, \text{Theorem 5.14}]\). \( \square \)

We conclude by giving a result that lets us recover important information about the poset of clusters \( \text{PC}(H) \) from the persistence diagram \( \text{PD}(H) \). The proof for \( H \) finite follows directly
from the construction of $\text{PD}(H)$ using the Elder rule. The proof for an essentially finite $H$ uses the finite case and the fact that $d_B(\text{PD}(H_{\text{pers} \geq \tau}), \text{PD}(H)) \to 0$ as $\tau \to 0$, by Proposition 5.6 and Lemma 5.19.

Lemma 5.20. Let $H$ be essentially finite.

1. For every $\tau > 0$, there is a bijection between $\text{PF}(H, \tau)$ and the points of $\text{PD}(H)$ with total persistence greater than $\tau$.
2. $H$ is $(a, b)$-separated if and only if $\text{PD}(H)$ is $(a, b)$-separated.

Remark 5.21. We now explain how Proposition 5.15 and Lemma 5.20 can be used to guide the choice of the parameter $\tau$ of the persistence-based flattening. Starting from a hierarchical clustering $H$, one can efficiently compute the persistence diagram $\text{PD}(H)$, which provides the following information:

1. The number of clusters of $\text{PF}(H, \tau)$ is equal to the number of points in $\text{PD}(H)$ with total persistence greater than $\tau$.
2. The further $\tau$ is from the set of total persistences $\{y - x : (x, y) \in \text{PD}(H)\}$, the more stable the flattening procedure is.

See Fig. 3 for an example.

5.4. Measure-based pruning. We now consider measurable hierarchical clusterings of measure spaces. A simple way to prune such hierarchical clusterings is to choose a minimum cluster size $m > 0$, and remove clusters from the hierarchy with measure less than $m$. This procedure is not stable if the hierarchical clustering contains clusters that persist for a significant life-span with measure near to the threshold $m$: we quantify this behavior in Definition 5.22. In the absence of such clusters, we show that this measure-based pruning is stable with respect to the measured-interleaving distance.

Definition 5.22. Let $H$ be a measurable hierarchical clustering of a measure space $X$, and let $m, \kappa, \rho > 0$. We say $H$ is $(\kappa, \rho)$-non-compressing around the minimum cluster size $m$ if, given $r > r', C \in H(r), C' \in H(r')$ such that $C \subseteq C'$ and such that $|\mu_X(C) - m| < \kappa$ and $|\mu_X(C') - m| < \kappa$, we have $r - r' < \rho$.

Definition 5.23. Let $H$ be a measurable hierarchical clustering of a measure space $X$. For $m > 0$, the measure-based pruning of $H$ with respect to the minimum cluster size $m$ is the measurable hierarchical clustering $H_{\mu \geq m}$ of $X$ with

$$H_{\mu \geq m}(r) = \{C \in H(r) : \mu_X(C) \geq m\}.$$ 

Lemma 5.24. Let $H$ and $E$ be measurable hierarchical clusterings of measure spaces $X$ and $Y$ respectively. Assume $H$ and $E$ are $(\kappa, \rho)$-non-compressing around the minimum cluster size $m$, and that $H$ and $E$ are $(\varepsilon; \varepsilon)$-measured-interleaved with respect to a correspondence $R \subseteq X \times Y$ for some $\varepsilon < \kappa$. Then $H_{\mu \geq m}$ and $E_{\mu \geq m}$ are $(\varepsilon + \rho; \varepsilon)$-measured-interleaved with respect to $R$.

Proof. Let $r > \varepsilon + \rho$ and let $C \in H(r)$ with $\mu_X(C) \geq m$. Then, $\mu_Y(R_X(C)) \geq m - \varepsilon$. As $r - \varepsilon - \rho > 0$, there is $D \in E(r - \varepsilon - \rho)$ with $R_X(C) \subseteq D$, and by the assumption that $E$ is $(\kappa, \rho)$-non-compressing around $m$, we have $\mu_Y(D) > m + \kappa - \varepsilon$. As $\pi_X^{-1}(C) \subseteq \pi_Y^{-1}(D)$, this gives one direction of the $(\varepsilon + \rho; \varepsilon)$-measured-interleaving with respect to $R$, and the other direction follows from a symmetric argument.

Lemma 5.25. Let $H$ and $E$ be measurable hierarchical clusterings of measure spaces $X$ and $Y$ respectively. Assume $H$ is $(\kappa, \rho)$-non-compressing around the minimum cluster size $m$, and that $H$ and $E$ are $(\varepsilon; \varepsilon)$-measured-interleaved with respect to a correspondence $R \subseteq X \times Y$ for some $\varepsilon < \kappa$. Then $E$ is $(\kappa - \varepsilon, \rho + 2\varepsilon)$-non-compressing around $m$. 

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Proof. Say \( r > r' \) with \( r - r' \geq \rho + 2\varepsilon \) and we have \( D \in E(r), D' \in E(r') \) with \( D \subseteq D' \), and \( |\mu_Y(D) - m| < \kappa - \varepsilon \) and \( |\mu_Y(D') - m| < \kappa - \varepsilon \). Let \( C = H(r - \varepsilon > r - \varepsilon - \rho)(R_Y(D)) \). As \( H \) and \( E \) are \((\varepsilon; \varepsilon)\)-measured-interleaved with respect to \( R \), we have
\[
m - (\kappa - \varepsilon) < \mu_Y(D) \leq \mu_X(R_Y(D)) + \varepsilon \\
\leq \mu_X(C) + \varepsilon \leq \mu_Y(R_X(C)) + 2\varepsilon \leq \mu_Y(D') + 2\varepsilon < m + (\kappa - \varepsilon) + 2\varepsilon,
\]
and so \( m - \kappa < \mu_X(R_Y(D)) \leq \mu_X(C) < m + \kappa \), contradicting the assumption that \( H \) is \((\kappa, \rho)\)-non-compressing around \( m \).
\[\square\]

Combining these lemmas, we have the stability result for measure-based pruning:

**Proposition 5.26.** Let \( H \) and \( E \) be measurable hierarchical clusterings of measure spaces \( X \) and \( Y \) respectively. Assume \( H \) is \((\kappa, \rho)\)-non-compressing around the minimum cluster size \( m \), and that \( H \) and \( E \) are \((\varepsilon; \varepsilon)\)-measured-interleaved with respect to a correspondence \( R \subseteq X \times Y \) for some \( \varepsilon < \kappa/2 \). Then \( H_{\mu \geq m} \) and \( E_{\mu \geq m} \) are \((3\varepsilon + \rho; \varepsilon)\)-measured-interleaved with respect to \( R \).
\[\square\]

6. **Computational examples**

In this section, we run \( \gamma\text{-link} \) on synthetic datasets with different choices of \( \gamma \) in order to illustrate the stability that is gained by using curves \( \gamma \) in which all the parameters of kernel linkage vary, and we explain how this can be exploited for parameter selection. We will refer to lines with non-zero, finite slope as *skew lines*. The examples in this section were computed using the implementation of \( \gamma\text{-link} \) available at [RS21].

6.1. **(In)stability in the choice of curve.** We apply \( \gamma\text{-link} \) to the dataset \( X \) of Fig. 4 with different families of curves \( \gamma \), and summarize the effect of varying the curve within each family. We consider five families: \( F_1 \) consists of horizontal lines, \( F_2 \) of skew but almost horizontal lines, \( F_3 \) of vertical lines, \( F_4 \) of skew but almost vertical lines, and \( F_5 \) of skew lines. Each family is parametrized by a real parameter \( \theta \) that varies in an interval \( \min_\theta \leq \theta \leq \max_\theta \). The endpoints of the intervals for \( F_1, F_3, \) and \( F_5 \) are chosen so that \( \text{PD}(\gamma^\theta\text{-link}(X)) \) has three points at \( \min_\theta \) and one point at \( \max_\theta \).

![Figure 4](image_url)  
A sample of 500 points of a mix of three Gaussians in \( \mathbb{R}^2 \). The covariance matrix is \( 0.01 \times \text{Id}_2 \) for the three Gaussians, the weights are \( 10/16, 5/16, \) and \( 1/16 \), for the left, top-right, and bottom-right Gaussian, respectively.

In order to visualize the evolution of \( \gamma^\theta\text{-link}(X) \) as we vary \( \theta \), we introduce the following notion. The **total persistence diagram** of a persistence diagram \( \{(x_i, y_i)\}_{i \in I} \) is the multiset of total persistences \( \{y_i - x_i\}_{i \in I} \). In Remark 5.21, we explained how the persistence diagram \( \text{PD}(H) \) encodes important information about \( H \), and how this can be used to choose the parameter \( \tau \) for the persistence-based flattening. In fact, the total persistence diagram of \( \text{PD}(H) \) also contains this information. For this reason, we visualize the evolution of \( \gamma^\theta\text{-link}(X) \) by plotting its total persistence diagram as a function of \( \theta \). By Lemma 5.19, if \( \gamma^\theta\text{-link}(X) \) varies continuously (resp. Lipschitz continuously) with \( \min_\theta \leq \theta \leq \max_\theta \), then the plot of total persistences must consist of a finite union of continuous (resp. Lipschitz continuous) curves.
defined over the interval $[\min_\theta, \max_\theta]$ (see, e.g., bottom of Fig. 5). We use the contrapositive of this fact to detect instability of $\gamma^\theta$-link with respect to $\theta$. Although we will not use this, we remark that this kind of analysis is based on the notion of vineyard [CSEM06]. To simplify plots, we do not display the total persistence of the most persistent point, so that for any line in the families above and any fixed parameter $\min_\theta \leq \theta \leq \max_\theta$ there are at most two points in $\text{PD}(\gamma^\theta$-link).

We now specify the five families mentioned above. Define $v^{s,t} : \mathbb{R}^{op} \rightarrow \mathbb{R} \times \mathbb{R} \times \mathbb{R}^{op}$ by $v^{s,t}(r) = (s, t, r)$ and, similarly, $v^{s,t,\beta}(r) = (s, t - r/\beta, r)$. Let $F_1 = \{\lambda_{\text{cov}}^{y,y}\}^{0.05 \leq y \leq 0.5}$, $F_2 = \{\lambda_{\text{cov}}^{y,y}\}^{0.5 \leq y \leq 1.7}$, $F_3 = \{v^{0.25,t}\}^{0.5 \leq t \leq 1.7}$, $F_4 = \{v^{s,0.25,t,10}\}^{0.5 \leq t \leq 1.7}$, and $F_5 = \{\lambda_{\text{cov}}^{y,y}\}^{0.5 \leq y \leq 1.5}$.

When running $\gamma$-link with curves of the families $F_1$, $F_2$, and $F_5$, we use the uniform kernel. For families $F_3$ and $F_4$ we use the Epanechnikov kernel, which is continuous, as this is a common choice for density estimation. For each family, we sample 1000 equally spaced parameters between $\min_\theta$ and $\max_\theta$.

We see in the top row of Fig. 5 that the set of total persistences is not continuous in the $k$-intercept for horizontal curves, and that, by making the slope different from 0, we get a very similar diagram that is now continuous (in fact Lipschitz) in the $k$-intercept. The center row shows similar behavior for vertical slices.

**Figure 5.** Evolution of the total persistences of the points of $\text{PD}(\gamma$-link$(X))$.
Top left $\gamma \in F_1$, top right $\gamma \in F_2$, center left $\gamma \in F_3$, center right $\gamma \in F_4$, bottom $\gamma \in F_5$.

### 6.2. Application to parameter selection

We now explain how the total persistence vs. parameter plot for $\gamma$-link can be helpful during parameter selection, and how stability in $\gamma$ can be exploited for this task.
Figure 6. A synthetic dataset $Y$ borrowed from [MHA17]. The dataset has 2309 points and was designed to be easily visualizable, but to break as many assumptions of traditional clustering algorithms as possible. The clustering of $Y$ indicated by colors is $PF(\lambda_{\text{cov}}^{0.1,0.03}, \text{link}(Y), \tau = 0.01)$ with the uniform kernel. The parameters $\lambda$ and $\tau$ were chosen by inspecting the plot for the family $G_3$ in Fig. 7. Grey points do not belong to any cluster.

We consider the dataset $Y$ of Fig. 6 and three families of lines: horizontal lines $G_1 = \{\lambda_{\text{cov}}^{0.01}, y \} \leq y \leq 0.1$, vertical lines $G_2 = \{v^{1/2}, t \} \leq t \leq 0.2$, and skew lines $G_3 = \{\lambda_{\text{cov}}^{0.01, 0.1}, y \} \leq y \leq 0.1$. We let $x = 0.1$ for the skew lines since it is around this value that SL($Y$) becomes one single cluster. We sample 500 equally spaced parameters.

We see in Fig. 7 that, for the three families of lines, there is a wide range of parameters for which there are 6 high persistence points well separated from low persistence points (recall that we are not plotting the most persistent point, so there are actually 5 well-separated curves in the plots). Nevertheless, as we have observed before, the plots for the non-skew lines consist of discontinuous curves, so, a priori, we do not have any guarantee that there is a relationship between the hierarchical clusterings obtained using different curves in the family. In contrast, not only do we have such a guarantee for $G_3$, but using the stability result Corollary 3.17, we can construct a “100%-confidence region” to which the true total persistence curves of the family $G_3$ must belong. This is done in the bottom right of Fig. 7. The confidence region of the figure was computed using only 50 equally spaced parameters, which, in this case, is sufficient to detect good separation in total persistence across parameters. Since horizontal and vertical slices are not stable in their parameters, there is no analogous method for constructing confidence regions for these slices.

7. Conclusions and future work

We have defined a three-parameter hierarchical clustering of a metric probability space, which we call kernel linkage, from which one can recover well-known hierarchical clustering methods by taking one-parameter slices. We defined a hierarchical clustering algorithm $\gamma$-link by taking one-parameter slices of kernel linkage. We proved that kernel linkage satisfies a stability theorem that holds without any distributional assumptions, and as a corollary, we deduced a stability theorem for $\gamma$-link for curves $\gamma$ in which all parameters of kernel linkage vary. We proved that $\gamma$-link is consistent with respect to continuous and compactly supported probability density functions on Euclidean space. Finally, we proved stability results for three standard methods to simplify hierarchical clusterings, which can be combined with our stability results for $\gamma$-link. We have tried to be as modular as possible, since we believe that the stability results for kernel linkage and for the simplification procedures are of independent interest.

We have given computational examples that show that other popular hierarchical clustering methods do not enjoy the same stability properties as $\gamma$-link, and we have explained how these stability properties can be exploited during parameter selection.

We hope that the consistency of $\gamma$-link can be generalized to the case where the probability density function is supported on a (possibly non-compact) lower-dimensional manifold. We have proved a consistency result for general choices of the parameter $\gamma$; it would be interesting
Figure 7. Evolution of the total persistences of the points of PD(\(\gamma\)-link(Y)).

Top left \(\gamma \in G_1\), bottom left \(\gamma \in G_2\), top and bottom right \(\gamma \in G_3\).

to restrict attention to simple classes of curves, and establish rates of convergence for \(\gamma\)-link
in these cases.

An implementation of \(\gamma\)-link is available [RS21]; an optimized implementation and an
empirical comparison with related hierarchical clustering algorithms will be addressed in future
work.

References

[ACG+19] Hirokazu Anai, Frédéric Chazal, Marc Glisse, Yuichi Ike, Hiroya Inakoshi, Raphaël Tinarrage,
and Yuhei Umeda. DTM-based filtrations. In 35th International Symposium on Computational
Geometry, volume 129 of LIPIcs. Leibniz Int. Proc. Inform., pages Art. No. 58, 15. Schloss Dagstuhl.
Leibniz-Zent. Inform., Wadern, 2019.

[BCP07] Gérard Biau, Benoît Cadre, and Bruno Pelletier. A graph-based estimator of the number of clusters.
ESAIM: Probability and Statistics, 11:272–280, 6 2007.

[BL21] Andrew J. Blumberg and Michael Lesnick. Stability of 2-parameter persistent homology, 2021.

[BMT17] Omer Bobrowski, Sayan Mukherjee, and Jonathan E. Taylor. Topological consistency via kernel
estimation. Bernoulli, 23(1):288–328, 2017.

[BNR+13] Sivaraman Balakrishnan, Srivatsan Narayanan, Alessandro Rinaldo, Aarti Singh, and Larry Wasser-
man. Cluster trees on manifolds. In C. J. C. Burges, L. Bottou, M. Welling, Z. Ghahramani, and
K. Q. Weinberger, editors, Advances in Neural Information Processing Systems 26, pages 2679–
2687. Curran Associates, Inc., 2013.

[CD10] Kamalika Chaudhuri and Sanjoy Dasgupta. Rates of convergence for the cluster tree. In J. D.
Lafferty, C. K. I. Williams, J. Shawe-Taylor, R. S. Zemel, and A. Culotta, editors, Advances in
Neural Information Processing Systems 23, pages 343–351. Curran Associates, Inc., 2010.

[CDFF10] Francesca Cagliari, Barbara Di Fabio, and Massimo Ferri. One-dimensional reduction of multidimen-
sional persistent homology. Proc. Amer. Math. Soc., 138(8):3003–3017, 2010.

[CdSGO16] Frédéric Chazal, Vin de Silva, Marc Glisse, and Steve Oudot. The structure and stability of persis-
tence modules. SpringerBriefs in Mathematics. Springer, [Cham], 2016.

[CFF00] Antonio Cuevas, Manuel Febrero, and Ricardo Fraiman. Estimating the number of clusters. The
Canadian Journal of Statistics / La Revue Canadienne de Statistique, 28(2):367–382, 2000.
APPENDIX A. PROOFS OF SECTION 4

Before we can prove that CI-consistency implies Hartigan consistency, we need a lemma, which is similar to [CD10, Lemma 14, Appendix: Consistency], and follows from the continuity of \( f \) and the fact that clusters of \( f \) are compact.

**Lemma A.1.** Let \( f : \mathbb{R}^d \to \mathbb{R} \) be a continuous, compactly supported probability density function, let \( r > 0 \) and \( A \neq A' \in H(f)(r) \). There exists \( \varepsilon > 0 \) and \( B, B' \in H(f)(r - \varepsilon) \) with \( B \neq B' \) such that \( A \subseteq B \) and \( A' \subseteq B' \).

**Proof of Proposition 4.7.** Given \( r > 0 \) and distinct path components \( A \) and \( A' \) of \( H(f)(r) \), we show that the probability of \( A_n \cap A'_n = \emptyset \) goes to 1 as \( n \to \infty \), where \( A_n \) is the smallest cluster in \( A_n^{\theta_n}(X_n) \) that contains \( A \cap X_n \) and likewise for \( A' \), and the \( \theta_n \) are the parameters whose existence is given by CI-consistency of \( A \).

From Lemma A.1 it follows that there exists \( \varepsilon > 0 \) and distinct connected components \( B, B' \in H(f)(r - \varepsilon) \) such that \( A \subseteq B \) and \( A' \subseteq B' \). Let \( \delta \in (0, 1) \). By assumption, there exists \( N \) such that, if \( n \geq N \), then the probability that \( A_n^{\theta_n}(X_n) \) and \( H(f) \) are \( \varepsilon/2 \)- interleaved with respect to the closest point correspondence \( R_c \subseteq X_n \times X \) is greater than \( 1 - \delta \). As \( R_c \) contains the pairs \( (x, x) \) for \( x \in X_n \), if \( A_n^{\theta_n}(X_n) \) and \( H(f) \) are \( \varepsilon/2 \)- interleaved with respect to \( R_c \), then \( A_n^{\theta_n} \) and \( i^*(H(f)) \) are \( \varepsilon/2 \)- interleaved as hierarchical clusterings of \( X_n \), where \( i : X_n \to X \) is the inclusion. It is therefore enough to show that if \( A_n^{\theta_n} \) and \( i^*(H(f)) \) are \( \varepsilon/2 \)- interleaved, then \( A_n \cap A'_n = \emptyset \). Now, if \( A_n^{\theta_n} \) and \( i^*(H(f)) \) are \( \varepsilon/2 \)- interleaved, then there exist \( C, C' \subseteq A_n^{\theta_n}(X_n) \) \( (r - \varepsilon/2) \) such that \( A \cap X_n \subseteq C \subseteq B \) and \( A' \cap X_n \subseteq C' \subseteq B' \). As \( A_n \subseteq C \) and \( A'_n \subseteq C' \), and \( B \cap B' = \emptyset \), we have \( A_n \cap A'_n = \emptyset \).

For the rest of this section, we fix a continuous, compactly supported probability density function \( f : \mathbb{R}^d \to \mathbb{R} \).

**Notation A.2.** For \( s > 0 \), define \( f_s : \text{supp}(f) \to \mathbb{R} \) by

\[
f_s(x) = \int_{\mathbb{R}^d} K\left(\frac{|x - y|}{s}\right) f(y) \, dy.
\]

Note that \( f_s(x) = (f * K_s)(x) = (\mu_f * K_s)(x) \). As \( \text{supp}(f) \) is compact, the continuous function \( f \) is uniformly continuous. An elementary consequence (see e.g. [Fol13, Theorem 8.14]) is that \( f_s/v_s \) approximates \( f \) for small enough \( s \):

**Lemma A.3.** For every \( \varepsilon > 0 \) there exists \( \delta > 0 \) such that if \( s < \delta \) then \( ||f_s/v_s - f||_\infty < \varepsilon \).

**Definition A.4.** Let \( H \) be a hierarchical clustering of a set \( X \). The density estimate given by \( H \) is the function \( \eta_H : X \to [0, \infty] \) defined by

\[
\eta_H(x) = \text{sup}\{r > 0 : \exists C \in H(r), x \in C\}.
\]

**Notation A.5.** We write \( L(f) \) for the kernel linkage of \( \text{supp}(f) \), with respect to the probability measure \( \mu_f \). For any curve \( \gamma \) in the (1, 1, -1)-parameter space, we write \( h^\gamma = \eta_{L(f)}^\gamma \). If \( \gamma \) is covering, we write \( h^\gamma = \eta_{L(f)}^\gamma \).

**Lemma A.6.** Let \( \gamma \) be a curve in the (1, 1, -1)-parameter space that is covering. Then, for any \( x \in \text{supp}(f) \), the quantity \( h^\gamma(x) \) satisfies \( f_{\gamma_1(h^\gamma(x))}(x) = \gamma_k(h^\gamma(x)) \). And, there exists \( r_1 \in I_\gamma \) such that \( h^\gamma(x) < r_1 \) for every \( x \in \text{supp}(f) \).

**Proof.** Note first that, for any \( x \in \text{supp}(f) \), \( h^\gamma(x) = \text{sup}\{r > 0 : f_{\gamma_1(r)}(x) \geq \gamma_k(r)\} \). We begin the proof by showing the following: there is \( r_1 \in I_\gamma \) such that \( \{x \in \text{supp}(f) : f_{\gamma_1(r_1)}(x) \geq \gamma_k(r_1)\} = \emptyset \), and there is \( r_0 \in I_\gamma \) such that \( \{x \in \text{supp}(f) : f_{\gamma_1(r_0)}(x) \geq \gamma_k(r_0)\} = \text{supp}(f) \). For
the existence of $r_1$, note that $f_{\gamma_s(r)}(x) \leq v_s(r) \cdot \max(f)$ for all $x \in \text{supp}(f)$ and $r \in I_\gamma$. So $r_1$ exists, since, as $r \to \max \gamma$, we have $v_{\gamma_s(r)} \cdot \max(f) \to 0$ while $\gamma_k(r)$ is increasing. For the existence of $r_0$ note that, for every $r \in I_\gamma$, the function $f_{\gamma_s(r)}(x)$ is continuous in $x$ and strictly positive for every $x \in \text{supp}(f)$, so we have $\min(f_{\gamma_s(r)}(x)) > 0$ for any $r \in I_\gamma$. So $r_0$ exists since, as $r \to 0$, we have $\gamma_k(r) \to 0$ while $\min(f_{\gamma_s(r)}(x))$ is increasing.

Now, the function $f_{\gamma_s(r)}(x)$ is decreasing and continuous in $r$, and $\gamma_k(r)$ is continuous and strictly increasing in $r$. Since $f_{\gamma_s(r_0)}(x) \geq \gamma_k(r_0)$ and $f_{\gamma_s(r_1)}(x) < \gamma_k(r_1)$, we have that $h^{\gamma}(x)$ is the unique number $r \in [r_0, r_1]$ such that $f_{\gamma_s(r)}(x) = \gamma_k(r)$, as required. □

Lemma A.7. Let $\varepsilon > 0$, and let $\gamma$ be a curve in the $(1, 1, -1)$-parameter space that is covering. There is $\delta > 0$ such that, if $\gamma_s(r) < \delta$ for every $r \in I_\gamma$, then $|h^{\gamma} - f|_\infty < \varepsilon$.

Proof. Using Lemma A.3, let $\delta$ be such that if $s < \delta$, then, for all $x \in \text{supp}(f)$, we have $|f_s(x)/v_s - f(x)| < \varepsilon$. By definition of $\gamma$, we have $h^{\gamma}(x) = \varphi(h^{\gamma}(x))$. Using Lemma A.6, this implies that, for all $x \in \text{supp}(f)$,

$$h^{\gamma}(x) = \varphi(h^{\gamma}(x)) = \frac{\gamma_k(h^{\gamma}(x))}{v_{\gamma_s(h^{\gamma}(x))}} = \frac{f_{\gamma_s(h^{\gamma}(x))}(x)}{v_{\gamma_s(h^{\gamma}(x))}},$$

So, if $\gamma_s(r) < \delta$ for every $r \in I_\gamma$, then $|h^{\gamma} - f(x)| < \varepsilon$ as $\gamma_s(h^{\gamma}(x)) < \delta$. □

In order to state the next lemma, we need a construction. Let $T$ be a topological space, and let $\mathcal{U} = \{U_i\}_{i=0}^n$ be an open cover of $T$, with $U_i \neq \emptyset$ for all $i$. There is a graph $G_{\mathcal{U}}$ associated to $\mathcal{U}$, with vertex set $\{0, \ldots, n\}$, and with an edge $(i, j)$ if $U_i \cap U_j \neq \emptyset$. It’s easy to show that if $T$ is connected, so is this graph:

**Lemma A.8.** If $T$ is a connected topological space, and $\mathcal{U} = \{U_i\}_{i=0}^n$ is a finite open cover of $T$ with $U_i \neq \emptyset$ for all $i$, then the graph $G_{\mathcal{U}}$ is connected. □

**Lemma A.9.** Let $\varepsilon > 0$ and let $\gamma$ be a curve in the $(1, 1, -1)$-parameter space that is covering. There is $\delta > 0$ such that, if $\gamma_s(r), \gamma_t(r) < \delta$ for every $r \in I_\gamma$, then $L(f)^{\gamma}$ and $H(f)$ are $\varepsilon$-interleaved.

Proof. Using the fact that $f$ is uniformly continuous, Lemma A.7, and Lemma A.3, choose $\delta > 0$ such that, for all $x, y \in \mathbb{R}^d$, if $||x - y|| < \delta$, then $|f(x) - f(y)| < \varepsilon/2$, and such that, if $\gamma_s(r) < \delta$ for all $r \in I_\gamma$, then $|h^{\gamma} - f|_\infty < \varepsilon/2$, and such that, if $s < \delta$, then $|f_s/v_s - f|_\infty < \varepsilon/2$. Write $X = \text{supp}(f)$. Let $\gamma$ be a curve in the $(1, 1, -1)$-parameter space that is covering, and such that $\gamma_s(r), \gamma_t(r) < \delta$ for every $r \in I_\gamma$. We show that we have the following relations in $C(X)$:

$$L(f)\gamma(r) \preceq H(f)(r - \varepsilon) \quad \text{and} \quad H(f)(r) \preceq L(f)^{\gamma}(r - \varepsilon)$$

for all $r > \varepsilon$. By Lemma A.7, for any $x \in X$, if $x$ is contained in a cluster of $L(f)^{\gamma}(r)$, then $x$ is contained in a cluster of $H(f)(r - \varepsilon)$; and if $x$ is contained in a cluster of $H(f)(r)$, then $x$ is contained in a cluster of $L(f)^{\gamma}(r - \varepsilon)$.

Next, say $x, y \in C \in L(f)^{\gamma}(r)$ for $r > \varepsilon$. We show that $x$ and $y$ belong to the same cluster of $H(f)(r - \varepsilon)$. Let $r_0 = \varphi^{-1}(r), s_0 = \gamma_s(r_0), t_0 = \gamma_t(r_0)$, and $k_0 = \gamma_k(r_0)$. So, by the definition of $\varphi$, we have $r = k_0/v_{s_0}$. Note we have $s_0, k_0 < \delta$. As $x, y \in C$, there is a chain $x_0, \ldots, x_n \in X$ with $x = x_0, y = x_n$, such that $f_{s_0}(x_i) \geq k_0$ and $||x_i - x_{i+1}|| \leq t_0$ for all $i$. Dividing by $v_{s_0}$, we have $f_{s_0}(x_i)/v_{s_0} \geq k_0/v_{s_0} = r$. Let $0 \leq i \leq n - 1$, and let $\alpha_i : [0, 1] \to \mathbb{R}^d$ parametrize the straight-line path from $x_i$ to $x_{i+1}$. Let $q \in [0, 1]$. Because $||x_i - \alpha_i(q)|| \leq t_0 < \delta$, we have $|f(x_i) - f(\alpha_i(q))| < \varepsilon/2$. As $s_0 < \delta$, we have $|f_{s_0}(x_i)/v_{s_0} - f(x_i)| < \varepsilon/2$. So, we have $f(\alpha_i(q)) > r - \varepsilon$. The concatenation of the $\alpha_i$ is therefore a path in $X$ from $x$ to $y$ such that $f(p) > r - \varepsilon$ for all points $p$ on the path. So, $x$ and $y$ belong to the same cluster of $H(f)(r - \varepsilon)$.  

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Finally, let \( x, y \in C \in H(f)(r) \). So, \( C \) is a connected component of \( \{ f \geq r \} \). We show that \( x \) and \( y \) belong to the same cluster of \( L(f)^\gamma(r - \varepsilon) \) for \( r > \varepsilon \). Write \( t_\varepsilon = \gamma_\varepsilon(\varphi^{-1}(r - \varepsilon)) > 0 \); we will show that there is a \( t_\varepsilon \)-chain \( (x = x_0, \ldots, x_n = y) \in C \). Let \( \{ P^i \}_{i \in I} \) be the set of path components of \( C \). For each \( i \in I \), let \( P_i^\varepsilon \cup a \in P_i B_C(a, t_\varepsilon) \). Then, \( \{ P_i^\varepsilon \}_{i \in I} \) is an open cover of \( C \). Since \( C \) is compact, there is a finite \( J \subseteq I \) such that \( \mathcal{U} = \{ P_i^\varepsilon \}_{i \in J} \) is an open cover of \( C \).

Now, say \( i, j \in J \), and \( P_i^\varepsilon \cap P_j^\varepsilon \neq \emptyset \). We show that for any \( a \in P_i \) and any \( b \in P_j \), there is a \( t_\varepsilon \)-chain in \( C \) connecting \( a \) and \( b \). Choose \( w \in P_i^\varepsilon \cap P_j^\varepsilon \); by definition, there is \( w_i \in P_i \) and \( w_j \in P_j \) such that \( ||w - w_i|| < t_\varepsilon \), and \( ||w - w_j|| < t_\varepsilon \). Then, there is a \( t_\varepsilon \)-chain in \( P_i \) connecting \( a \) to \( w_i \), and a \( t_\varepsilon \)-chain in \( P_j \) connecting \( b \) to \( w_j \), which together give a \( t_\varepsilon \)-chain in \( C \) connecting \( a \) and \( b \). By Lemma A.8, the graph \( G_\mathcal{U} \) is connected. So, there is a \( t_\varepsilon \)-chain in \( C \) connecting \( x \) and \( y \).

**Proposition A.10.** Let \( \{ \gamma^\theta \}_{\theta \in \Theta} \) be an admissible family of curves in the \((1, 1, -1)\)-parameter space, and let \( X_n \) be a sample of \( f \). For every \( \varepsilon > 0 \) there exist \( \theta \in \Theta \) and \( \delta > 0 \) such that, if \( d_p(\mu_n, \mu_f), d_H(X_n, \text{supp}(f)) < \delta \), then \( L(X_n)^{\gamma^\theta} \) and \( H(f) \) are \((\varepsilon; \varepsilon)\)-measured-interleaved with respect to the closest point correspondence \( R_c \subseteq X_n \times X \).

**Proof.** By Lemma A.9, and the fact that the family \( \{ \gamma^\theta \}_{\theta \in \Theta} \) is admissible, we can fix the parameter \( \theta \) so that \( H(f) \) and \( L(f)^{\gamma^\theta} \) are \( \varepsilon/2 \)-interleaved. It is then enough to show that we can choose \( \delta > 0 \) such that, if \( d_p(\mu_n, \mu_f) < \delta \) and \( d_H(X_n, \text{supp}(f)) < \delta \), then \( L(f)^{\gamma^\theta} \) and \( L(X_n)^{\gamma^\theta} \) are \((\varepsilon/2; \varepsilon)\)-measured-interleaved with respect to the closest point correspondence. To see that this can be done, note that the operation \( L(\cdot)^{\gamma^\theta} \) is the composite of \( L(\cdot) \) and slicing by \( \gamma^\theta \), and apply Theorem 3.6 (note that the interleaving constructed in the proof is with respect to the closest point correspondence) and Proposition 3.10(2), where the last result applies by Lemma A.6, since \( \gamma^\theta \) is covering.

The following result is standard.

**Lemma A.11.** Let \((X, d, \mu)\) be a compact metric probability space with full support and let \( X_n \) be an i.i.d. \( n \)-sample of \( X \), seen as a subspace of \( X \). Let \( \varepsilon > 0 \). Then, the probability that \( \max(d_p(\mu_n, \mu), d_H^\gamma(X_n, X)) > \varepsilon \) goes to 0 as \( n \to \infty \). Here \( \mu_n \) is the normalized counting measure given by the sample \( X_n \).

**Proof of Theorem 4.11.** The theorem follows from Proposition A.10 and the fact that samples converge to the space being sampled, Lemma A.11.
## Appendix B. Notation

| Symbol | Definition |
|--------|------------|
| $f : \mathbb{R}^d \to \mathbb{R}$ | Typical probability density function. |
| $\text{supp}(f)$ | Support of density function. |
| $\mathbb{R}_{>0}, \mathbb{R}_{>0}^{\text{op}}$ | Poset of strictly positive real numbers with standard and opposite order. |
| $C(X)$ | Poset of clusterings of a set $X$ (Definition 2.2). |
| $S \preceq T \in C(X)$ | Order relation in poset of clusterings of a set $X$ (Definition 2.2). |
| $H : \mathbb{R}_{>0}^{\text{op}} \to C(X)$ | Typical hierarchical clustering. |
| $C \in H(r)$ | Typical cluster of hierarchical clustering $H$ at scale $r \in \mathbb{R}_{>0}$. |
| $H(f) : \mathbb{R}_{>0}^{\text{op}} \to C(\text{supp}(f))$ | Density-contour hierarchical clustering of density $f$ (Example 2.4). |
| $\text{SL}(X) : \mathbb{R}_{>0} \to C(X)$ | Single-linkage hierarchical clustering of metric space $X$ (Example 2.5). |
| $H(\gamma)$ | Typical parameter curve (Definition 3.7). |
| $\lambda_x^y$ | Line parameter curve with $x$ and $y$ as intercepts (Notation 3.13). |
| $H^\gamma : \mathbb{R}_{>0}^{\text{op}} \to C(X)$ | Slice of multi-parameter h.c. by curve $\gamma$ (Definition 3.7). |
| $K : \mathbb{R}_{>0} \to \mathbb{R}_{>0}$ | Typical kernel (Definition 2.20). |
| $L^K(X)$ | Kernel linkage of metric probability space $X$ (Definition 2.25). |
| $\gamma\text{-link}(X)$ | $\gamma$-linkage of metric probability space (Definition 3.8). |
| $C,D,E \in \text{PC}(H)$ | Poset of persistent clusters of hierarchical clustering $H$ (Definition 5.4). |
| $\text{life}(C), \text{birth}(C), \text{death}(C)$ | Typical persistent clusters of hierarchical clustering $H$ (Definition 5.4). |
| $C(r) \in H(r)$ | Life, birth, and death, of persistent cluster $C$ (Definition 5.1). |
| $\text{PC}(H)$ | Value of persistent cluster $C$ at scale $r$ (Definition 5.1). |
| $\text{leaves}(H)$ | The successor of $C$ in $\text{PC}(H)$ (defined above Lemma 5.10). |
| $H_{\text{c}, \text{p}}(r)$ | Flat clustering given by the minimal elements of $\text{PC}(H)$ (Section 5.2). |
| $\text{PF}(H, \tau)$ | Persistence-based pruning of h.c. with threshold $\tau$ (Definition 5.5). |
| $\text{PD}(H)$ | Persistence-based flattening of h.c. $H$ with threshold $\tau$ (Definition 5.13). |
| $R \subseteq X \times Y$ | Persistence diagram of hierarchical cluster $H$ (Section 5.3). |
| $\pi_X : R \to X$, $\pi_Y : R \to Y$ | Typical correspondence between sets $X$ and $Y$ (Definition 2.11). |
| $R_X : H(\vec{r}) \to E(\vec{r} + \vec{\epsilon})$ | Map defined when $H$ and $E$ are $\epsilon$-interleaved w.r.t. $R$ (Notation 2.16). |
| $d_{CI}$ | Correspondence-interleaving distance (Definition 2.13). |
| $d_{MI}$ | Measured-interleaving distance (Definition 2.18). |
| $d_{GHP}$ | Gromov–Hausdorff–Prokhorov distance (Definition 3.3). |
| $d_{B}$ | Bottleneck distance (Section 5.3). |