EXTREMAL EVENT GRAPHS: A (STABLE) TOOL FOR ANALYZING NOISY TIME SERIES DATA

Abstract. Local maxima and minima, or extremal events, in experimental time series can be used as a coarse summary to characterize data. However, the discrete sampling in recording experimental measurements suggests uncertainty on the true timing of extrema during the experiment. This in turn gives uncertainty in the timing order of extrema within the time series. Motivated by applications in genomic time series and biological network analysis, we construct a weighted directed acyclic graph (DAG) called an extremal event DAG using techniques from persistent homology that is robust to measurement noise. Furthermore, we define a distance between extremal event DAGs based on the edit distance between strings. We prove several properties including local stability for the extremal event DAG distance with respect to pairwise $L_\infty$ distances between functions in the time series data. Lastly, we provide algorithms, publicly free software, and implementations on extremal event DAG construction and comparison.

1. Introduction

Experimental time series data are ubiquitous in today’s science and provide a window through which we can observe the underlying dynamics of complex systems, ranging from cells to ecosystems and climate. We study collections of time series which are also referred to as multivariate time series in the literature \[59, 63\]. We construct a weighted directed graph descriptor of a collection of time series data using persistent homology, a technique that belongs to a collection of approaches known as Topological Data Analysis (TDA) that uses algebraic topology \[23, 37\] to extract shape from data. TDA is used to study data from a wide range of applications including material science \[32\], cancer biology \[61\], and political science \[18\]. Some of the classic and foundational papers in TDA include \[66, 24, 20, 16, 44\].

Our descriptor characterizes a collection of time series by the order of their extrema in a way that also captures the robustness of this order with respect to measurement uncertainty. Our motivation comes from the desire to mathematically capture and compare collections of 'omics time series data, such as transcriptomics, proteomics, and others. In particular, the coarse information of orders of extrema have been used to assess regulatory network models of gene/protein interactions \[14\]. Other applications involve quantifying similarity between gene expression time series \[4, 55\] across repeated experiments.

Our mathematical methods are motivated by the combinatorial approaches in \[14, 4, 42\] that use only the approximate timing of time series extrema as the relevant features of experimental data. To take into account the uncertainty of capturing temporal orderings of extrema, \[14\] replaced
the single time point locations of extrema with time intervals that were determined by manual inspection. If the intervals are disjoint, then the ordering of extrema is interpreted to be robust to measurement uncertainty. In the follow-up paper [4], an approach was developed in which the intervals are algorithmically constructed using merge trees [17, 36], branch decompositions [35], and sublevel sets. These intervals are called $\varepsilon$-extremal intervals and have the property that they are the smallest intervals for which all continuous perturbations of a continuous function (with additional technical restrictions) that lie within an $\varepsilon$-band are guaranteed to attain an extremum under measurement uncertainty of size $\varepsilon$. Using the $\varepsilon$-extremal intervals, labeled directed acyclic graphs (DAGs) are constructed to represent the time series data for any fixed value of $\varepsilon$. We refer to these DAGs as $\varepsilon$-DAGs. Vertices or nodes in the $\varepsilon$-DAG represent extrema in the time series data. Directed edges $a \rightarrow b$ indicate that we can unambiguously discern the order (in time) of events corresponding to vertices $a$ and $b$ under measurement uncertainty of size $\varepsilon$.

Continuing this line of research, [42] defined a distance metric that compares two collections of time series by comparing the corresponding $\varepsilon$-DAGs. This metric involves computing the directed maximal common edge subgraph (DMCES) and was applied in [4] to quantify similarity in replicate experiments of microarray yeast cell cycle data. Additionally, the metric was used in [55] to provide quantitative evidence that an intrinsic oscillator drives the blood stage cycle of the malaria parasite Plasmodium falciparum. The metric for $\varepsilon$-DAGs using the DMCES is effective in capturing similarity between the time series, but is computationally expensive. This limits the total number of extrema across all time series that can be effectively analyzed. Another limitation is that the distance can only be measured at a single measurement uncertainty level $\varepsilon$, which is often unknown and thus the distance has to be computed multiple times for a collection of $\varepsilon$ values. A better measurement would incorporate information about changes in similarity as a function of changing $\varepsilon$ in a single value.

We significantly expand and generalize the work of [4] and [42] by constructing a weighted DAG that reflects robustness of the extremal ordering for all levels of measurement error $\varepsilon$. We call this an extremal event DAG. Vertices in this graph again represent extrema in the time series data, and a directed edge $a \rightarrow b$ indicates that extremum $a$ occurs before extremum $b$. The node weights measure prominence of extrema while the edge weights indicate the smallest $\varepsilon$ level for which the relative order between the two associated extrema can no longer be guaranteed. The node weights are computed using sublevel set persistence [17]. After representing the collection of time series as an extremal event DAG, we define a distance between extremal event DAGs as a modified version of the edit distance (Chapter 15 of [13]). The edit distance quantifies similarity of two strings based on the minimum number of operations (e.g., insertion, substitution, and deletion) it takes to align the two strings. This distance is commonly used in many applications including DNA sequence alignment, see [41] for one of the first papers on the topic. The standard algorithm for the edit distance between two strings of length $n$ can be computed via dynamic programming in $\Theta(n^2)$ (Chapter 15 of [13]).

We prove several key properties of the extremal event DAG weights. Most importantly for computability and applications, Theorem 3.4 gives a simple criterion to compute edge weights. Furthermore, we analyze stability properties of distances between extremal event DAGs. Section 5 gives stability results for distances used to compare extremal event DAGs with respect to pairwise $L_\infty$ distance between the underlying continuous functions. These stability results show that small changes within time series data lead to small changes in the corresponding extremal event DAG distances. In Theorem 5.23 we show the extremal event DAG distance is stable in a local case: two paired continuous functions from the two collections of time series must lie within an $\varepsilon$ band that allows for an unambiguous alignment, in the sense of the edit distance, of the minima and maxima between the two time series. Additionally, one of the time series can have small amplitude additional maxima and minima.
Lastly, in Section 6 we provide a polynomial time algorithm to compute the extremal event DAG given collections of discrete time series, and the dynamic program needed to compute the extremal event DAG distance. Free and public software on computing extremal event DAGs and the distance between these descriptors is available at [2].

1.1. TDA in Analyzing Time Series Data. Our use of TDA differs significantly from other approaches that use TDA to study time series data and the dynamics of underlying biological networks. One common method studies single variable time series by using Takens’ embedding theorem [57]. The data is transformed by computing a sliding window embedding of the data into a point cloud in $\mathbb{R}^n$. This point cloud is then analyzed using one dimensional persistent homology to detect and quantify periodicity. Examples that take this or a modified approach include detecting periodicity of genomic time series data [46], studying entropy and the dynamics of the underlying system [53, 1], characterizing gene regulatory networks [5], and distinguishing between audio signals of the same note from different instruments [50].

The second common method to study single variable time series using TDA is to apply sublevel set persistence to detect prominent features. Applications include signal processing [26], Fourier spectrum analysis and parameter detection [39], arrhythmia detection [15], and cancer studies [31]. Furthermore, sublevel set persistence on time series can be used to determine noise that is often seen as small peaks in the time series [40].

Lastly, TDA has been used to study other types of time dependent data. One includes dynamic metric spaces that can be used to describe phenomena such as bird flocks, insect swarms, schools of fish, and aphid trajectories. TDA techniques to study these type of data include vineyards [12], CROCKER plots [58, 60, 64], spatiotemporal filtrations [28] and zig-zag persistence [8, 27]. Furthermore, time series data of fMRI images have been used to construct functional networks, and then applying filtrations on the weights of these networks to extract topological features [56, 47]. A more extensive summary on TDA techniques to study time series can be found in [19].

1.2. Biological Motivation. Extremal event DAGs are developed abstractly for multivariate time series in general, however, we focus on the application of analyzing ‘omics data that measures expression levels of thousands of genes. Transcription of genes produces messenger RNA (mRNA) which are translated to proteins. Gene expression, measured by either the amount of mRNA produced (transcriptomics) or by the amount of corresponding protein (proteomics), can be used to measure the level of activity of a given gene product. There is strong evidence that the relative phases of oscillating regulators are important to controlling important cellular processes such as the cell cycle [30], circadian rhythm, or malaria parasite periodic infection of human blood cells. The assertion of [4, 14] is that the ordering of extrema is a reasonable approximation of control by phase relationship.

For example, it is hypothesized that a small transcriptional regulatory network controlling the cell cycle can activate hundreds of other transcription factors in a phase-specific manner to play a vital role in maintaining the proper progression of DNA replication and cell division [7, 10, 13, 29, 52]. There are still many open questions about the precise role of the transcriptional network in the ordering of cell cycle events [48, 51]. A reproducible ordering of gene expression such as what was observed in [4] provides supporting evidence for the central role of the cell cycle gene regulatory network in orchestrating timely expression of other cell cycle events.

A question of interest in biology is evaluating the similarity of two experiments across labs or experimental conditions. For example, an experimentalist may wish to measure the similarity of expression level of genes driving the cell cycle between replicate experiments between time series collected under different growth conditions, or across organisms and tissues. For example, circadian clock networks in different tissues that control the temporal ordering of phase specific gene expression [38, 65]. Similarity and differences in timing of the same network in tissues like heart and liver can tell us about their mutual coupling as well as coupling to the master circadian clock in
the brain \cite{33, 39}. In summary, mathematically modeling and comparing orders of extremal events in 'omics data is useful for identifying time series differences in multiple biological applications. In particular, extremal event DAGs and distances can be used to study the important biological questions about time dependent cellular processes, some of which we have mentioned here.

2. Preliminaries

We begin by summarizing the necessary background information. We refer the reader to \cite{23, 17} for additional background in algebraic topology, and computational topology respectively.

2.1. Extrema. For a subset $X \subset \mathbb{R}$, $x \in X$ and $\varepsilon > 0$, let $B_\varepsilon(x)$ be the open neighborhood of radius $\varepsilon$ centered at $x$. That is

$$B_\varepsilon(x) := \{ y \in X \mid |y - x| < \varepsilon \}.$$ 

**Definition 2.1** (Local Extrema). Let $f : X \to \mathbb{R}$ be a function. We say $f$ has a local minimum at $x \in X$ if there exists $\varepsilon > 0$ for which $f(x) < f(y)$ for all $y \in B_\varepsilon(x) \setminus \{x\}$. Similarly, $f$ has a local maximum at $x \in X$ if there exists $\varepsilon > 0$ for which $f(x) > f(y)$ for all $y \in B_\varepsilon(x) \setminus \{x\}$. We refer to any local minimum or local maximum as a local extremum of $f$. If $x \in X$ with $f(x) < f(y)$ for all $y \in X \setminus \{x\}$, we say $f$ has a global minimum at $x$. Similarly, for $x \in X$ where $f(x) > f(y)$ for all $y \in X \setminus \{x\}$, we say $f$ has a global maximum at $x$.

We often order the extrema of a function. To ease notation, we write $[n]$ to be the set of the first $n$ integers. That is

$$[n] := \{1, 2, \ldots, n\}.$$ 

2.2. Distances. We use the $L_\infty$ metric to quantify distances between collections of points and functions.

**Definition 2.2** ($L_\infty$ metric). For points $p = (p_1, p_2, \ldots, p_n), q = (q_1, q_2, \ldots, q_n) \in \mathbb{R}^n$, we define the $L_\infty$ distance between points $p$ and $q$ as $\|p - q\|_\infty = \max_i |p_i - q_i|$. For functions $f, g : C \to \mathbb{R}$, we define the $L_\infty$ distance between functions $f$ and $g$ as $\|f - g\|_\infty = \sup_{x \in C} |f(x) - g(x)|$.

For a subset $X \subset \mathbb{R}^n$, $x \in X$ and $\varepsilon > 0$, let $\square_\varepsilon(x)$ be the $L_\infty$ open neighborhood of radius $\varepsilon$ centered at $x$. That is

$$\square_\varepsilon(x) := \{ y \in X \mid \|y - x\|_\infty < \varepsilon \}.$$ 

2.3. $\varepsilon$-Perturbations. We consider perturbations of a function $f$ in order to account for measurement noise in experimental time series data.

**Definition 2.3** ($\varepsilon$-Neighborhood of $f$). Let $f : C \to \mathbb{R}$ be a continuous function, where $C$ is some compact domain. For $\varepsilon \geq 0$, define

$$N_\varepsilon(f) := \{ g : C \to \mathbb{R} \mid g \text{ is continuous, and } \|f - g\|_\infty < \varepsilon \}$$

to be the $\varepsilon$-neighborhood of $f$. A function $g \in N_\varepsilon(f)$ is called an $\varepsilon$-perturbation of $f$.

2.4. Nicely Tame Functions. Given a topological space, $X$ and an integer $k \in \mathbb{Z}$, we denote the $k^{th}$ singular homology group as $H_k(X)$. We assume $\mathbb{Z}/2\mathbb{Z}$ coefficients for this paper.

**Definition 2.4** (Homological Critical Values). Let $X$ be a topological space, $f : X \to \mathbb{R}$ a function. We call $a \in \mathbb{R}$ a homological critical value if there exists $k \in \mathbb{Z}$ and $\delta > 0$ such that for all $0 < \varepsilon < \delta$, the linear map $H_k(f^{-1}(-\infty, a - \varepsilon)) \to H_k(f^{-1}(-\infty, a + \varepsilon))$ induced by the inclusion of sublevel sets is not an isomorphism.

In other words, the homological critical values are the values at which the homology of the sublevel sets change. For Morse functions over $\mathbb{R}$, these points are exactly the heights of the local extrema of $f$ \cite{34}. 

Definition 2.5 (Tameness). Let $X$ be a topological space. A function $f : X \to \mathbb{R}$ is tame if it has a finite number of homological critical values and the homology groups $H_k(f^{-1}(-\infty, a])$ are finite for every $a \in \mathbb{R}$.

Definition 2.6 (Nicely Tame Functions). Let $X \subset \mathbb{R}$ be a topological space. A function $f : X \to \mathbb{R}$ is nicely tame if $f$ is tame, continuous, and for each critical value $y$, the preimage $f^{-1}(y)$ is a finite set.

We work with nicely tame functions on a closed interval, which we denote by $C \subset \mathbb{R}$. Hence, the zeroth dimensional homology group (which captures connectedness) is the only nontrivial group.

2.5. Persistence Diagrams from Sublevel Set Filtrations. Persistent homology tracks how homological features evolve in a nested sequence of topological subspaces. We work with a specific case of persistent homology that encodes the changes of the connectedness of sublevel sets of a function $f : X \to \mathbb{R}$ as the height (domain) parameter ranges from $-\infty$ to $\infty$. This information is encoded in a persistence diagram and encodes the prominence of the local extrema of $f$. Persistent homology is a general mathematical framework and we only provide the definitions necessary for our results here; see [17, 45] for more detailed introductions to persistence.

A filtration of a topological space $X$ is a nested family of subspaces $(X_r)_{r \in T}$ where $T \subseteq \mathbb{R}$, such that for all $r, s \in T$ where $r \leq s$, we have $X_r \subseteq X_s$, and $\bigcup_{r \in T} X_r = X$. For $f : X \to \mathbb{R}$, the sequence of all such sublevel sets $f^{-1}(-\infty, x]$ ordered by inclusion and indexed by $\mathbb{R}$ is the sublevel set filtration.

Given a topological space $X$ and $f : X \to \mathbb{R}$, we study the zeroth dimensional homology of sublevel sets $H(f^{-1}(-\infty, x])$. The topological relationships between homology groups of sublevel sets are encoded in a persistence diagram.

Definition 2.7 (Persistence Diagram $D(f)$). Let $f : C \to \mathbb{R}$ be a nicely tame function. Let $\mathbb{R} = \mathbb{R} \cup \{-\infty, \infty\}$. The persistence diagram $D(f)$ is the multiset set of points in $\mathbb{R}^2$ such that the point $p = (b, d) \in \mathbb{R}^2$ is included with multiplicity,

$$\mu(p) := \lim_{\varepsilon \to 0} \left( \beta(b, d) - \beta(b - \varepsilon, d) - \beta(b, d + \varepsilon) + \beta(b - \varepsilon, d + \varepsilon) \right)$$

where $\beta(b, d)$ is the rank of $H(f^{-1}(-\infty, b]) \to H(f^{-1}(-\infty, d])$. We set $p \in D(f)$ if, and only if, $\mu(p) > 0$.

The persistence diagram summarizes the homology groups as the height parameter ranges from $-\infty$ to $\infty$. Each persistence point $p = (b, d) \in D(f)$ is called a birth-death pair. Colloquially speaking, each $p$ represents a unique generator of the homology groups of the sublevel sets of $f$ that is ‘born’ at parameter $b$ and ‘dies’ going into parameter $d$. If the function values of the local extrema are unique for a function over $\mathbb{R}$, then we have a one-to-one correspondence between persistence points and the local minima of $f$, where $(b, d)$ corresponds to the local minimum $(t, f(t) = b)$. In the event that the values of several minima are the same, this correspondence is not unique. However, a unique correspondence can be induced by fixing an order on the local minima (e.g., the domain coordinates) and using that ordering to break ties.

For a multiset $A$, we write $|A|$ for the total multiplicity of $A$ i.e., $|A| = \sum_{p \in A} \mu(p)$. Figure 1 gives an example of a function and its persistence diagram from a sublevel set filtration.

A key observation is that each point in $D(f)$ has a birth coordinate that is equal to the height of a local minimum and a death coordinate that is equal to the height of a local maximum, except for the point where the death coordinate is $\infty$. This observation is a result of the Critical Value Lemma in [11]. We call the unique point in $D(f)$ with a death coordinate of $\infty$ the essential connected component. From the key observation it follows that if $t$ does not represent the essential component, then there exists a local maximum $(t', f(t'))$ such that $(f(t), f(t')) \in D(f)$. In this case, $f(t')$ is the height at which the connected component of $f^{-1}(-\infty, f(t')]$ containing $t$ merges with another
connected component of the sublevel set \( f^{-1}(-\infty, f(t')] \) represented by a local minimum \( s \) where \( f(s) < f(t) \). We call \( f(t') \) the merge height of \( t \).

![Figure 1](image)

**Figure 1.** Left. A nicely tame function, \( f : [a,b] \to \mathbb{R} \). Right. Persistence diagram of \( f \), \( D(f) \) obtained from a sublevel set filtration of \( f \). The set \( D(f) \) is \( \{(f(t_1), \infty), (f(t_3), f(t_2)), (f(t_5), f(t_4))\} \). The first coordinate of each point in \( D(f) \) is the height of a local minimum, while the second coordinate is the height of a local maximum or \( \infty \).

2.6. \( \varepsilon \)-Extremal Intervals. Let \( \text{INT}(C) \) be the set of relatively open intervals contained in \( C \). To enable comparability between local extrema for functions in \( N_\varepsilon(f) \) for different levels of \( \varepsilon \), we use the following definition.

**Definition 2.8** (\( \varepsilon \)-Extremal Interval at \( t \)). Let \( f : C \to \mathbb{R} \) be a continuous function and \( T = \{t_i\}_{i=1}^n \) be the domain coordinates of all local extrema of \( f \). Let \( \varepsilon > 0 \). Define \( \varphi^f_\varepsilon : T \to \text{INT}(C) \) such that

- **Case 1:** If \( t \in T \) and \((t, f(t))\) is a local minimum, define \( \varphi^f_\varepsilon(t) \) to be the connected component of \((f - \varepsilon)^{-1}(-\infty, f(t) + \varepsilon)\) that contains \( t \).
- **Case 2:** If \( t \in T \) and \((t, f(t))\) is a local maximum, define \( \varphi^f_\varepsilon(t) \) to be the connected component of \((f + \varepsilon)^{-1}(f(t) - \varepsilon, \infty)\) that contains \( t \).

We call \( \varphi^f_\varepsilon(t) \) the \( \varepsilon \)-extremal interval at \( t \) (see Figure 2).

We note that we often refer to the \( \varepsilon \)-extremal intervals as extremal intervals. We also sometimes omit the superscript \( f \) and simply write \( \varphi_\varepsilon \) when the function used to construct the \( \varepsilon \)-extremal intervals is clear.

**Remark 2.9** (Notation for Endpoints of Extremal Intervals). Let \( f : C \to \mathbb{R} \) be a continuous function with a local extremum at \( t \in C \). Suppose \( \varphi^f_\varepsilon(t) \) is the \( \varepsilon \)-extremal interval at \( t \). We define the left endpoint of \( \varphi^f_\varepsilon(t) \) to be \( \text{left}(\varphi^f_\varepsilon(t)) := \inf(\varphi^f_\varepsilon(t)) \). We define the right endpoint of \( \varphi^f_\varepsilon(t) \) to be \( \text{right}(\varphi^f_\varepsilon(t)) := \sup(\varphi^f_\varepsilon(t)) \). Finally, we denote the length of \( \varphi^f_\varepsilon(t_i) \) by \( \text{len}(\varphi^f_\varepsilon(t)) \).

The next Lemma shows that \( \varepsilon \)-extremal intervals are nested as a function of increasing \( \varepsilon > 0 \).

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The choice of pairings in \( D(f) \) follows the Elder Rule (See section 7.1 of [17]): when two sublevel sets merge together, the connected component born at the lowest height 'continues', while the other connected component 'dies'. In the case where both connected components are born at the same height, we arbitrarily choose to continue the connected component that occurs first in the domain.
Figure 2. The $\varepsilon$-extremal intervals at $t_3$ and $t_4$. The $\varepsilon$-extremal interval at $t_3$ is the connected component of $(f + \varepsilon)^{-1}(f(t_3) - \varepsilon, \infty)$ that contains $t_3$ (Case 2). The $\varepsilon$-extremal interval at $t_4$ is the connected component of $(f - \varepsilon)^{-1}(-\infty, f(t_4) + \varepsilon)$ that contains $t_4$ (Case 1).

Lemma 2.10 (Nesting of $\varepsilon$-Extremal Intervals). Let $f : C \to \mathbb{R}$ be a nicely tame function. Let $t$ be the domain coordinates of a local extrema of $f$. If $0 < \varepsilon_0 < \varepsilon_1$, then,

$$\varphi_{\varepsilon_0}(t) \subset \varphi_{\varepsilon_1}(t).$$

Proof. Since sublevel sets of a function form a filtration, we have

$$(f - \varepsilon_0)^{-1}(-\infty, f(t) + \varepsilon_0) \subset (f - \varepsilon_0)^{-1}(-\infty, f(t) + \varepsilon_1).$$

At the same time, because $\varepsilon_0 < \varepsilon_1$,

$$(f - \varepsilon_0)^{-1}(-\infty, f(t) + \varepsilon_1) \subset (f - \varepsilon_1)^{-1}(-\infty, f(t) + \varepsilon_1).$$

Combining these two statements we find that

$$(f - \varepsilon_0)^{-1}(-\infty, f(t) + \varepsilon_0) \subset (f - \varepsilon_1)^{-1}(-\infty, f(t) + \varepsilon_1).$$

Note that $\varphi_{\varepsilon_0}(t) \cap \varphi_{\varepsilon_1}(t) \neq \emptyset$ because they are connected components of $(f - \varepsilon_0)^{-1}(-\infty, f(t) + \varepsilon_0)$ and $(f - \varepsilon_1)^{-1}(-\infty, f(t) + \varepsilon_1)$ respectively that contain $t$. Therefore (1) implies $\varphi_{\varepsilon_0}(t) \subset \varphi_{\varepsilon_1}(t)$. \qed

2.7. Node Lives. Given a function $f : C \to \mathbb{R}$ and the domain coordinate $t$ of a local extremum, any continuous function $g \in N_{\varepsilon}(t)$ is guaranteed to have the same type of extremum in the interval $\varphi_{\varepsilon}(t)$. At some value of $\varepsilon$, however, this is no longer guaranteed. We use the persistence diagram $D(f)$ to assist us with understanding when this occurs.
Definition 2.11 (Birth-Death Pairing Map). Let \( C \subset \mathbb{R} \) and \( f : C \to \mathbb{R} \) be a nicely tame function. Let \( \{t_i\}_{i=1}^n \) be the set of domain coordinates of the local minima of \( f \). Define the birth-death pairing map to be \( \zeta_f : \{t_i\}_{i=1}^n \to \mathbb{R}_{>0} \) such that
\[
\zeta_f(t_i) = \begin{cases} 
\max(f) & \text{if } t_i \text{ represents the essential component} \\
f(t_j) & \text{otherwise},
\end{cases}
\]
where \( f(t_j) \) is the merge height of the minimum at \( t_i \).

Observe the minima for \( f \) are the maxima of \(-f\) and vice-versa. Additionally, the absolute difference in heights between extrema of \( f \) remain the same in both \( f \) and \(-f\). Hence, we can study the prominence of maxima of \( f \) by studying the minima of \(-f\). This follows from [3] which discusses the symmetry between persistence diagrams computed from height filtrations that are ascending versus descending.

Definition 2.12 (Persistence of Extrema). Let \( X \subset \mathbb{R} \) and \( f : X \to \mathbb{R} \) be a nicely tame function, and let \((b, d) \in D(f)\). The persistence of \((b, d)\) is the difference between the birth and death times, \( d - b \). Suppose \( t \) is the domain coordinate such that \( f(t) = b \) and \((t, f(t))\) is the local minimum of \( f \) representing the pair \((b, d)\). We define the persistence of the extremum \((t, f(t))\), denoted \( \text{pers}_f(t) \), as
\[
\text{pers}_f(t) := \begin{cases} 
\max(f) - f(t), & \text{if } (t, f(t)) \text{ is the global minimum of } f \\
d - b, & \text{if } (t, f(t)) \text{ is a local (and not global) minimum of } f \\
\text{pers}_{-f}(t), & \text{if } (t, f(t)) \text{ is a local maximum of } f.
\end{cases}
\]

See Figure 3 for an example of computing the persistence of local extrema.

Definition 2.13 (Node Life). Let \( f : C \to \mathbb{R} \) be a nicely tame function with a local extremum at domain coordinate \( t \). The node life of \( t \) is \( \text{pers}_f(t)/2 \).

We sometimes omit the subscript \( f \) from \( \text{pers}_f(t) \) when the function we are computing the node life from is clear. Proposition 2 and Corollary 1 from [4] states that \( \varphi_f^\varepsilon(t) \) is the smallest interval for which any nicely tame \( \varepsilon \)-perturbation of \( f \) is guaranteed to have at least one local extremum of the same type as \( t \), as long as \( \varepsilon \) is less than the node life.

3. Extremal Event DAG

To define the extremal event DAG, that will capture information about extrema of multiple time series, we need a notion of comparability of local extrema.

Definition 3.1 (Comparability of Extrema). Let \( f, g : C \to \mathbb{R} \) be nicely tame functions. Let \( t_f, t_g \) be local extrema of \( f \) and \( g \) respectively. Let \( \varepsilon > 0 \). We declare \( t_f \prec_\varepsilon t_g \) if for every nicely tame \( \varepsilon \)-perturbation of \( f \) and \( g \) there exists \( \varepsilon \)-perturbed extrema \( t'_f \) and \( t'_g \) such that \( t'_f \in \varphi_f^\varepsilon(t_f), t'_g \subset \varphi_g^\varepsilon(t_g), \) and \( t'_f < t'_g \). We say \( t_f \) and \( t_g \) are comparable at \( \varepsilon \) if all of the following hold.

1. \( \text{pers}_f(t_f) > 2\varepsilon \)
2. \( \text{pers}_g(t_g) > 2\varepsilon \)
3. \( t_f \prec_\varepsilon t_g \) or \( t_g \prec_\varepsilon t_f \)

If at least one of these conditions does not hold, then \( t_f \) and \( t_g \) are incomparable at \( \varepsilon \).

Definition 3.1 relates order of extrema to possible \( \varepsilon \)-perturbations of functions. Using this definition, we are ready to define the extremal event DAG.

Definition 3.2 (Extremal Event DAG). Let \( F = \{f_i : C \to \mathbb{R}\}_{i=1}^k \) be a collection of nicely tame functions. For \( i \in [n] \), let \( t_1^i < t_2^i < \cdots < t_{l_i}^i \) be the domain coordinates for the local extrema of \( f_i \). The extremal event DAG of \( F \) is the directed graph, \( \text{DAG}(F) := (V, E, \omega_V, \omega_E) \), where
Figure 3. Top. A nicely tame function $f$ and its persistence diagram from a sublevel set filtration. In this example, $\text{pers}_f(t_1) = \max(f) - f(t_1)$, $\text{pers}_f(t_3) = f(t_2) - f(t_3)$, and $\text{pers}_f(t_5) = f(t_4) - f(t_5)$. Bottom. $-f$ and its persistence diagram from a sublevel set filtration. Now we can compute the persistence of the local maxima of $f$. $\text{pers}_f(t_4) = f(t_4) - \min(f)$ and $\text{pers}_f(t_2) = f(t_2) - f(t_3)$.

- $V := \{v(i, j) \mid i \in [m] \text{ and } j \in [k_i]\}$. In particular $v(i, j) \in V$ corresponds to the extremum of $f_i$ at $t_{i}^j$.
- $\mathcal{E} := \{(v(i, j), v(r, s)) \mid t_{i}^j < t_{r}^s\}$.
- $\omega_{V} : V \to \mathbb{R}_{\geq 0}$ is defined by the node life $\omega_{V}(v(i, j)) := \frac{1}{2} \text{pers}_{f_i}(t_{i}^j)$. We call $\omega_{V}$ the node weights.
- $\omega_{E} : E \to \mathbb{R}_{\geq 0}$ is defined by $\omega_{E}(v(i, j), v(r, s)) := \inf\{\varepsilon \mid t_{i}^j \text{ and } t_{r}^s \text{ are incomparable}\}$. We call $\omega_{E}$ the edge weights.

Given $\varepsilon > 0$, we can easily recover $\varepsilon$-DAG$(F)$ from DAG$(F)$ where $\varepsilon$-DAG$(F)$ is defined in [4]. Specifically, $\varepsilon$-DAG$(F)$ is the subgraph of the DAG$(F)$ that consists of vertices and edges with a weight less than or equal to $\varepsilon$. Hence, DAG$(F)$ is a stronger descriptor since it is not dependent on $\varepsilon$.

Computing the vertices and directed edges of the extremal event DAG can be done directly from the graphs of the functions in $F$. Computing the weights requires more information. Expanding upon earlier observation about node lives, we note that we choose to define the node weights as the node lives for the following reason. If $(t, f(t))$ is a local extremum of a nicely tame function $f$, then Proposition 2 of [4] states that if $|J_t| > 2\varepsilon$, then every nicely tame $\varepsilon$-perturbation of $f$ has a local
extremum of the same type as \( t \) contained in \( \varphi^\ell_t(t) \). Noting that \( |J_t| = \text{pers}_f(t) \), this means that every nicely tame \( g \in N_\varepsilon(f) \) has a local extremum of the same type as \( t \), say \( t' \in \varphi^\ell_t(t) \) as long as \( \varepsilon < \frac{1}{2}\text{pers}_f(t) \). Furthermore, Proposition 1 of \([4]\) states that for any two local extrema at \((s,f(s))\), and \((t,f(t))\) of \( f \) of the same type, we have \( \varphi^\ell_t(t) \cap \varphi^\ell_s(s) = \emptyset \). Hence, when \( \varepsilon < \frac{1}{2}\text{pers}_f(t) \), we guarantee a relative ordering of extrema for \( \varepsilon \)-perturbations of \( f \).

If \( \varepsilon > \frac{1}{2}\text{pers}_f(t) \), Proposition 1 of \([4]\) does not apply and we lose the association between the extrema of the perturbed function of \( g \in N_\varepsilon(f) \) and the extremum of \( f \) at \( t \).

### 3.1. Properties of Extremal Intervals

Next, we prove some properties of the extremal intervals that are useful for computing the edge weights. For Lemma 3.3 we omit the superscript and subscript \( f \) from \( \varphi^\ell_t \) and \( \text{pers}_f \) since \( f \) is the only function we are considering.

**Lemma 3.3** (Properties of \( \varphi^\varepsilon_t(t) \)). Let \( f : C \to \mathbb{R} \) be a nicely tame function. Let \( t_1 < t_2 < \ldots < t_n \) be the domain coordinates of the local extrema of \( f \). The following statements hold.

1. The length \( \text{len}(\varphi^\varepsilon_t(t)) \) increases as a function of \( \varepsilon \).
2. For \( i < n \), \( \varepsilon \leq \frac{1}{2}|f(t_i) - f(t_{i+1})| \) if and only if \( t_{i+1} \notin \varphi^\varepsilon_t(t_i) \) and \( t_i \notin \varphi^\varepsilon_t(t_{i+1}) \).
3. For \( i < n \), if \( \varepsilon \leq \frac{1}{2}\min\{\text{pers}_t, \text{pers}_{t_{i+1}}\} \), then \( t_{i+1} \notin \varphi^\varepsilon_t(t_i) \) and \( t_i \notin \varphi^\varepsilon_t(t_{i+1}) \).

**Proof.** Let \( f \) and \( T = \{t_i\}_{i=1}^n \) be defined as in the lemma statement. We prove the three statements for local minima first. Let \( i \in [n] \). Assume that \((t_i, f(t_i))\) is a local minimum. Note that, since minimum and maximum alternate in \( T \), we know that \( t_{i+1} \) (if it exists) is a local maximum.

**Proof of Statement [1] for minima.** Consider two values \( 0 < \varepsilon_0 < \varepsilon_1 \). By Lemma 2.10, we find \( \varphi_{\varepsilon_0}(t_i) \subseteq \varphi_{\varepsilon_1}(t_i) \).

Therefore \( \text{len}(\varphi_{\varepsilon_0}(t_i)) \leq \text{len}(\varphi_{\varepsilon_1}(t_i)) \).

**Proof of Statement [2] for minima.** For the forward direction, we assume \( i < n \) and \( \varepsilon \leq \frac{1}{2}|f(t_i) - f(t_{i+1})| \). Since \( t_i \) is a local minimum and \( t_{i+1} \) is a local maximum, we have \( \varepsilon \leq \frac{1}{2}(f(t_{i+1}) - f(t_i)) \), which implies

\[
 f(t_{i+1}) - \varepsilon \geq f(t_i) + \varepsilon.
\]

By definition of \( \varepsilon \)-extremal intervals (Definition 2.3) and since \( t_i \) is a local minimum, any point \( x \in \varphi^\varepsilon_t(t_i) \) satisfies \( f(x) - \varepsilon < f(t_i) + \varepsilon \). Since we already established that \( f(t_{i+1}) - \varepsilon \geq f(t_i) + \varepsilon \) in Equation [2], we know that \( t_{i+1} \notin \varphi^\varepsilon_t(t_i) \). Similarly, since \( t_{i+1} \) is a maximum, for any point \( y \in \varphi^\varepsilon_t(t_{i+1}) \), we know that \( f(y) + \varepsilon > f(t_{i+1}) - \varepsilon \). Along with Equation [2], we conclude \( t_i \notin \varphi^\varepsilon_t(t_{i+1}) \).

Next, we prove the backward direction by contrapositive. Assume \( i < n \) and \( \varepsilon > \frac{1}{2}|f(t_i) - f(t_{i+1})| \). Since \( t_i \) is a local minimum and \( t_{i+1} \) is a local maximum, we have

\[
 f(t_{i+1}) - \varepsilon < f(t_i) + \varepsilon.
\]

Therefore, \( t_{i+1} \in (f - \varepsilon)^{-1}(-\infty,f(t_i) + \varepsilon) \). In order for \( t_{i+1} \in \varphi^\varepsilon_t(t_i) \), we need to show that \( t_{i+1} \) is in the connected component of \((f - \varepsilon)^{-1}(-\infty,f(t_i) + \varepsilon)\) containing \( t_i \). Recalling that left(\( \ast \)) denotes the left endpoint of an interval and since \( t_i \in \varphi^\varepsilon_t(t_i) \), we have left(\( \varphi^\varepsilon_t(t_i) \)) < \( t_i < t_{i+1} \). In addition, since \( t_i \) and \( t_{i+1} \) are adjacent, right(\( \varphi^\varepsilon_t(t_i) \)) > \( t_{i+1} \). We conclude that \( t_{i+1} \in \varphi^\varepsilon_t(t_i) \). Therefore, Statement [2] holds for minima.

**Proof of Statement [3] for minima.** Statement [3] follows directly from [4] Proposition 4.

For the case where \((t_i, f(t_i))\) is a local maximum, we substitute \(-f\) for \( f \) and follow the proofs above. \( \square \)

### 3.2. Computing Edge Weights

Next, we state a condition for checking that requirement 3 of Definition 3.1 is met.
**Theorem 3.4 (Computing Edge Weights).** Let $F = \{f_i : C \to \mathbb{R}\}_{i=1}^n$ be a collection of nicely tame functions where $t_1^i < t_2^i < \cdots < t_n^i$ are all the domain coordinates of the local extrema of $f_i$. Let $\text{DAG}(F) := (V, E, \omega_V, \omega_E)$ be the extremal event DAG of $F$. For all edges $(v(i, j), v(c, d)) \in E$, the following statements hold

1. If $i = c$, then
   \[ \omega_E(v(i, j), v(c, d)) = \min\{\omega_V(v(i, j)), \omega_V(v(c, d))\}. \]

2. If $i \neq c$, then
   \[ \omega_E(v(i, j), v(c, d)) = \min\{\omega_V(v(i, j)), \omega_V(v(c, d)), \varepsilon^*(t_j^i, t_d^c)\}, \]

   where
   \[ \varepsilon^*(t_j^i, t_d^c) := \inf\{\varepsilon \mid \varphi_{\varepsilon}^l(t_j^i) \cap \varphi_{\varepsilon}^r(t_d^c) \neq \emptyset\}. \]

**Proof.** Assume all hypotheses.

First, we prove Statement [1]. Since $i = c$ in this case, we omit the superscripts $i$ and $c$ of $t_j^i$ and $t_d^c$. Additionally we set $f := f_i$. Furthermore, we omit the subscript and superscript $f$ from the functions $\text{pers}_f$ and $\varphi_f$. We consider two cases.

Suppose $\varphi_{\varepsilon}(t_j^i) \cap \varphi_{\varepsilon}(t_d^c) = \emptyset$. Without loss of generality, assume $t_j < t_d$. Let $g \in N_\varepsilon(f)$. Using Proposition 2 and Corollary 2 of [4], we get that $\varphi_{\varepsilon}(t_j)$ and $\varphi_{\varepsilon}(t_d)$ contain local extrema $t_j^i$ and $t_d^c$ of the same type as $t_j$ and $t_d$. Since $\varphi_{\varepsilon}(t_j) \cap \varphi_{\varepsilon}(t_d) = \emptyset$, $t_j < t_d$ implies $t_j^i < t_d^c$. Therefore, $t_j$ and $t_d$ are comparable.

Next suppose $\varphi_{\varepsilon}(t_j^i) \cap \varphi_{\varepsilon}(t_d^c) \neq \emptyset$. This is the content of Lemma 9.1 in Appendix 9.1. Altogether we find that if $\varepsilon < \min\{\omega_V(v(i, j)), \omega_V(v(c, d))\}$, then $t_j$ and $t_d$ are comparable.

Lastly, we consider the case that $\varepsilon \geq \min\{\omega_V(v(i, j)), \omega_V(v(c, d))\}$. By Definition 3.1, $t_j$ and $t_d$ are incomparable.

We have shown that $t_j, t_d$ are comparable for all $\varepsilon < \min\{\omega_V(v(i, j)), \omega_V(v(c, d))\}$ and $t_j, t_d$ are incomparable for all $\varepsilon \geq \min\{\omega_V(v(i, j)), \omega_V(v(c, d))\}$. Therefore,
\[ \min\{\omega_V(v(i, j)), \omega_V(v(c, d))\} = \inf\{\varepsilon \mid t_j \text{ and } t_d \text{ are incomparable}\}. \]

We conclude $\omega_E(v(i, j), v(c, d)) = \min\{\omega_V(v(i, j)), \omega_V(v(c, d))\}$.

Next, we prove Statement [2]. Let $(t_j^i, f_i(t_j^i))$ and $(t_d^c, f_c(t_d^c))$ be extrema. First, let
\[ \varepsilon \leq \min\{\omega_V(v(i, j)), \omega_V(v(c, d))\}, \varepsilon^* \} \]

Then, by definition of $\varepsilon^*$, the intervals $\varphi_{\varepsilon}^l(t_j^i)$ and $\varphi_{\varepsilon}^r(t_d^c)$ are disjoint. Additionally, from Proposition 2 and Corollary 2 of [4], both intervals guarantee existence of local extrema of the appropriate type under any $\varepsilon$-perturbation. Therefore, $t_j^i$ and $t_d^c$ are comparable.

Next, if $\varepsilon^* < \varepsilon \leq \min\{\omega_V(v(i, j)), \omega_V(v(c, d))\}$, then $\varphi_{\varepsilon}^l(t_j^i) \cap \varphi_{\varepsilon}^r(t_d^c) \neq \emptyset$. Since a local extremum of an $\varepsilon$-perturbation can happen anywhere in $\varphi_{\varepsilon}^l(t_j^i)$ and $\varphi_{\varepsilon}^r(t_d^c)$, then $t_j^i$ and $t_d^c$ are incomparable at $\varepsilon$.

Lastly, if $\varepsilon \geq \min\{\omega_V(v(i, j)), \omega_V(v(c, d))\}$, then by Definition 3.1 $t_j^i$ and $t_d^c$ are incomparable.

We conclude that $\omega_E(v(i, j), v(c, d)) = \min\{\omega_V(v(i, j)), \omega_V(v(c, d)), \varepsilon^*(t_j^i, t_d^c)\}$. \qed
3.3. Example of Extremal Event DAG Construction. We give an example of constructing an extremal event DAG.

**Example 3.5.** We construct the extremal event DAG for \( \sin(x) : [0, 2\pi] \rightarrow \mathbb{R} \), \( \cos(x) : [0, 2\pi] \rightarrow \mathbb{R} \) as illustrated in Figure 4. First we compute the persistence diagram from a sublevel set filtration of \( \sin(x) \), \( -\sin(x) \), \( \cos(x) \), and \( -\cos(x) \). This computes the node lives of all local extrema in \( \sin(x) \) and \( \cos(x) \). These node lives are the node weights in the extremal event DAG. Next we compute edge weights between nodes based on Theorem 3.4(1).

For an illustration of this, consider the local extrema at \( x = 0 \) and \( x = \frac{\pi}{2} \) of \( \sin(x) \). The node lives of these two local extrema are 0.5 and 1 respectively. The edge weight between the two corresponding vertices in the extremal event DAG is the minimum of these two node lives: 0.5.

Computing the edge weights between two vertices corresponding to different functions is more involved. We need to apply Theorem 3.4(2). To illustrate this, consider the local extrema at \( x = \frac{\pi}{2} \) of \( \sin(x) \) and \( x = \pi \) of \( \cos(x) \). Since \( \sin(x) \) and \( \cos(x) \) are translations of one another, the extremal intervals grow at the same rate for both \( \sin(x) \) and \( \cos(x) \). We know that \( \varphi_{\varepsilon}^{\sin}(\pi/2) \) and \( \varphi_{\varepsilon}^{\cos}(\pi) \) first intersect at the half-way point of the domain coordinates, which is \( \frac{3\pi}{4} \). Using the definition of the \( \varepsilon \)-extremal intervals we find

\[
\sin(\pi/2) - \varepsilon = \sin(3\pi/4) + \varepsilon
\]

\[
\varepsilon = \frac{1}{4}(2 - \sqrt{2}) \approx 0.14
\]

\[
\cos(\pi) + \varepsilon = \cos(3\pi/4) - \varepsilon
\]

\[
\varepsilon = \frac{1}{4}(2 - \sqrt{2}) \approx 0.14
\]

The epsilon value computed is the infimum \( \varepsilon \) for which \( \varphi_{\varepsilon}^{\sin}(\pi/2) \) and \( \varphi_{\varepsilon}^{\cos}(\pi) \) both contain \( \frac{3\pi}{4} \). Hence this is also the infimum \( \varepsilon \) for which \( \varphi_{\varepsilon}^{\sin}(\pi/2) \cap \varphi_{\varepsilon}^{\cos}(\pi) \neq \emptyset \). Since 0.14 is less than the node life of either extrema, then by Theorem 3.4(2), the edge weight between the vertices corresponding to \( x = \pi/2 \) in \( \sin(x) \) and \( x = \pi \) in \( \cos(x) \) is 0.14. Applying a similar process to all edges, we get the extremal event DAG.

4. Extremal Event DAG Distance

In this section, we define distances between extremal event DAGs representing different collections of time series, or *datasets*. In particular, we first discuss the alignment of nodes between different collections of time series and then the alignment of edges. We call the result an *extremal event supergraph*. The weights on the nodes and edges of the extremal event supergraph are determined by the weights on the two extremal event DAGs. The distance between the extremal event DAGs is then computed from the weights on the extremal event supergraph.

4.1. Backbone Distance. From Figure 4 one can see that each time series is translated into an ordered linear sequence of alternating minima and maxima. These linear sequences greatly simplify the comparison between datasets assuming that there is a one-to-one correspondence between the identifications of each of the time series in each dataset. For example, consider two gene expression datasets under different experimental conditions. In this case, each time series has a unique identity corresponding to the gene that it represents. Our primary task in this section is to perform a matching operation between the extrema of two time series with matching identities. To perform the matching, we use a modified version of the DNA alignment algorithm from [41]. Throughout this section, we refer to Figure 5 for illustrations of definitions.
Figure 4. Extremal Event DAG for $\sin(x) : [0, 2\pi] \to \mathbb{R}$ and $\cos(x) : [0, 2\pi] \to \mathbb{R}$. The nodes on the left represent the local extrema of $\sin(x)$ while the nodes on the right represent the local extrema of $\cos(x)$. The node weights are the node lives of the corresponding local extrema while the edge weights are computed using Theorem 3.4.

**Definition 4.1** (Backbones). A **backbone** is a finite sequence $x = (x_1, x_2, \ldots, x_n)$, where each $x_i$ is a tuple $x_i = (s_i, w_i)$ with $s_i$ a string, and $w_i \in \mathbb{R}_{\geq 0}$. The empty string is denoted by 0. The **length** of $x$ is denoted $\text{len}(x)$, and is equal to the number of elements in the sequence (here, $\text{len}(x) = n$). We call each $x_i$ a **node** and we denote the first $k$ terms of $x$ by $x[1 : k]$.

**Remark 4.2** (Constructing Backbones from Nicely Tame Functions). In what follows, we construct a backbone from a nicely tame function $f : C \to \mathbb{R}$ by computing $\text{DAG}\{f\} = (V, E, \omega_V, \omega_E)$ and removing all edges and edge weights; the nodes are ordered by their corresponding domain coordinates. Then, the data associated to each node $v \in V$ is a string representing which type of local maxima (min or max) along with the node weight $\omega_V(v)$. This backbone for $f$ is denoted $B(f)$. See Figure 6 for an example.

**Remark 4.3** (Backbones as Sets). We consider functions over backbones to other spaces. For these settings, we think of a backbone as an ordered multiset, $x = \{x_1, x_2, \ldots, x_n\}$, (i.e., repeated elements are allowed) equipped with an injective index function, $\iota_x : x \to \{1, 2, \ldots, n\}$ where $\iota_x(x_i) = i$. Let $0 := (0, 0)$. We also define $\bar{x} = \{0\} \cup x$, where $0$ is the **empty node**. The function $\iota$ is not extended to $\bar{x}$.

Next we discuss alignments and how to compute a distance between two backbones using an optimal alignment.

**Definition 4.4** (Alignment). Let $x = (x_1, x_2, \ldots, x_m)$ and $y = (y_1, y_2, \ldots, y_n)$ be backbones. Let $[k]$ denote the first $k$ natural function; that is, $[k] := \{1, 2, \ldots, k\} \subset \mathbb{N}$. An **alignment** is a totally ordered correspondence between $\bar{x}$ and $\bar{y}$ that does not repeat elements of $x$ or $y$ and respects the labels (or strings) of the backbones. We say that the number of pairs in the correspondence is the **length** of the alignment. In particular, we represent an alignment of length $k$ between $x$ and $y$ as a function $\alpha : [k] \to \bar{x} \times \bar{y}$, where $\alpha(i)$ can be written as two coordinate functions $\alpha(i) := (\alpha_x(i), \alpha_y(i))$, such that

1. **No Null Alignments.** The pair $(0, 0)$ is not in the image of $\alpha$, which we denote by $\text{im}(\alpha)$. 


Figure 5. Time Series Data and Corresponding Extremal Event DAGs. We consider two datasets consisting of two functions, $\frac{1}{2}\sin(x)$ and $\frac{1}{2}\cos(x)$ over $[0, 2\pi]$ with some added noise. In Figure 5a and Figure 5b, we label the blue curve as “sine” and green curve as “cosine”. Figure 5c is the extremal event DAG for Dataset 1 while Figure 5d is extremal event DAG for Dataset 2.

(2) **Preserves Order of Backbones.** The coordinate functions $\alpha_x : [k] \rightarrow \tilde{x}$, $\alpha_y : [k] \rightarrow \tilde{y}$ are partially monotone. The function $\alpha_x$ is partially monotone if and only if for every $i, j \in [k]$ such that $\alpha_x(i) \neq 0$ and $\alpha_x(j) \neq 0$, we have

$$\iota_x(\alpha_x(i)) < \iota_x(\alpha_x(j))$$

if and only if $i < j$.

An analogous definition applies to $\alpha_y$.

(3) **No Misalignments.** For each $((s_x, w_x), (s_y, w_y)) \in \text{im}(\alpha)$, we either have equality in strings $s_x = s_y$, or one of $(s_x, w_x)$, $(s_y, w_y)$ is equal to $0$. 


(4) Restriction to Matching. Each element of \( x \) and \( y \) appears in the image of \( \alpha_x \) and \( \alpha_y \) exactly once. That is, for each \( x_i \in x \), there exists exactly one \( j \in [k] \) for which \( \alpha_x(j) = x_i \).

The analogous statement holds for each \( y_i \in y \).

If \( \alpha(i) = (\alpha_x(i),0) \), we say that \( \alpha_x(i) \) is aligned with an insertion; similarly for \( \alpha(i) = (0,\alpha_y(i)) \). We denote the restriction of \( \alpha \) to the first \( h \) integers, \( [h] = \{1,2,\ldots,h\} \subset [k] \) as \( \alpha[1:h] \).

Notation 4.5 (Elements in \( \text{im}(\alpha) \)). When we use the notation \( (x,y) \in \text{im}(\alpha) \), we always assume that \( x \neq 0 \) and \( y \neq 0 \). We also use notation \( (x,0) \in \text{im}(\alpha) \) and \( (0,y) \in \text{im}(\alpha) \) to denote that \( x \) or \( y \) is aligned with an insertion.

Note that the restriction of \( \text{im}(\alpha) \cap (x \times y) \) is a partial matching (that is, each element in \( x \times y \), if not aligned with an insertion, is aligned with a distinct element of the other backbone). We call any pair \( (x,y) \in \text{im}(\alpha) \cap (x \times y) \) a nontrivial match. An example of two different alignments of the sine backbones shown in Figure 6 is given in Figure 7. Figure 7a is aligned without insertions, while Figure 7b has two insertions in each of the backbones. Notice that the insertions occur at the small noisy extrema in each of the time series.

Definition 4.6 (Cost of Alignment). Let \( x \) and \( y \) be backbones and \( \alpha : [k] \to \mathbb{R} \times \mathbb{R} \) be an alignment of length \( k \). The cost of \( \alpha \) is defined as

\[
\text{cost}(\alpha) := \sum_{(x,y) \in \text{im}(\alpha)} |w_x - w_y|,
\]

where \( x = (s_x,w_x) \) and \( y = (s_y,w_y) \). We define the cost of the partial alignment \( c_{x,y}(i,j) \) to be the minimum cost of aligning \( x[1:i] \) with \( y[1:j] \), that is,

\[
c_{x,y}(i,j) := \min\{\text{cost}(\alpha) \mid \alpha \text{ is an alignment of } x[1:i] \text{ and } y[1:j]\}.
\]

Referring again to Figure 7a we compute that the alignment in Figure 7b has a lower cost, 0.116, than that in Figure 7a 0.932.

Definition 4.7 (Optimal Alignment). Let \( x = (x_1,x_2,\ldots,x_m) \) and \( y = (y_1,y_2,\ldots,y_n) \) be backbones. We call an alignment \( \alpha : [k] \to \mathbb{R} \times \mathbb{R} \) optimal if \( \text{cost}(\alpha) = c_{x,y}(m,n) \).

An optimal alignment minimizes cost. We note that there could be multiple alignments that minimize cost and so an optimal alignment is not necessarily unique.
that are aligned with nodes in \( \tilde{L} \) be the
are aligned with an insertion, and the third term accounts for the cost of the nodes in \( y \).

\( \text{Definition 4.8} \) (Backbone Distance). The backbone distance between backbones \( x \) and \( y \) is defined as

\[
d_B(x, y) = \inf_{\alpha} \left( \sum_{(x, y) \in \im(\alpha)} |w_x - w_y| + \sum_{(x, 0) \in \im(\alpha)} w_x + \sum_{(0, y) \in \im(\alpha)} w_y \right)
\]

where \( \alpha \) ranges over all alignments between \( x \) and \( y \).

The backbone distance finds the best alignment between \( x \) and \( y \), then defines the distance to be the \( L_1 \)-norm between a vector consisting of the node weights in \( \tilde{x} \) and a vector consisting of the matching node weights in \( \tilde{y} \). The first term of Equation (3) accounts for the cost of the nodes in \( x \) that are aligned with nodes in \( y \), the second term accounts for the cost of the nodes in \( x \) that are aligned with an insertion, and the third term accounts for the cost of the nodes in \( y \) that are aligned with an insertion.

We show that this distance is in fact a metric. In order to show the triangle inequality, \( d_B(x, z) \leq d_B(x, y) + d_B(y, z) \), we need a way of composing an alignment between \( x \) and \( y \) with an alignment between \( y \) and \( z \). This is the content of Construction 4.9 and Lemma 4.10.

\( \text{Construction 4.9} \) (Composition of Alignments). Let \( x, y, z \) be backbones and \( \alpha_1: [k] \to \tilde{x} \times \tilde{y} \), \( \alpha_2: [l] \to \tilde{y} \times \tilde{z} \) be alignment maps. The composition of \( \alpha_1 \) and \( \alpha_2 \) induces an ordered correspondence between \( \tilde{x} \) and \( \tilde{z} \) whose nontrivial pairs are given by

\[
A := \{ (x, z) \mid \exists y \in y \text{ s.t. } (x, y) \in \im(\alpha_1) \text{ and } (y, z) \in \im(\alpha_2) \}.
\]

The pairs in \( A \) are ordered using the order given in \( x \). The set \( A \), however does not form a complete alignment of \( x \) and \( z \) because \( x_i \in x \) with \( (x_i, 0) \in \im(\alpha_1) \) and \( z_j \in z \) with \( (0, z_j) \in \im(\alpha_2) \) are not
accounted for in pairs in \(A\). We include all such pairs \((x_i, 0)\) and \((0, z_j)\) to construct a function \(\alpha_2 \circ \alpha_1 : [s] \rightarrow \tilde{x} \times \tilde{z}\) in such a way that each pair satisfies

(a) If \(\iota_x(x_i) < \iota_x(x)\) (\(\iota_x(x) < \iota_x(x_j)\)) and \((x_i, z_i) \in A\) then for

\[
\alpha_2 \circ \alpha_1(s_1) = (x_i, z_i), \quad \alpha_2 \circ \alpha_1(s_2) = (x, 0), \quad \alpha_2 \circ \alpha_1(s_3)(x_j, z_j)
\]

we have the order \(s_1 < s_2 < s_3\).

(b) If \(\iota_z(z_i) < \iota_z(z)\) (\(\iota_z(z) < \iota_z(z_j)\)) and \((x_i, z_i) \in A\) then for

\[
\alpha_2 \circ \alpha_1(s_1) = (x_i, z_i), \quad \alpha_2 \circ \alpha_1(s_2) = (0, z), \quad \alpha_2 \circ \alpha_1(s_3)(x_j, z_j)
\]

we have the order \(s_1 < s_2 < s_3\).

An extension of \(A\) to an alignment \(\alpha_2 \circ \alpha_1 : [s] \rightarrow \tilde{x} \times \tilde{z}\) exists, but also that it may not be unique since there may be multiple options on where to place consecutive insertions. We resolve this ambiguity arbitrarily in the following way. If there is a set of consecutive insertions \(\{(x_i, 0), (x_i, 0), \ldots, (x_i, 0), (0, z_j), \ldots, (0, z_j)\}\) between a pair \((x_i, z_i)\) and a pair \((x_j, z_j)\), then we order them starting with the insertions \(\{(x_i, 0)\}_{r=1}^k\) ordered by the order given in \(x\), followed by the insertions \(\{(0, z_j)\}_{r=1}^k\) insertions ordered by the order given in \(z\). We hastened to point out that the following results (Lemma 4.10, Lemma 4.11, and Lemma 9.2) hold for \(\alpha_2 \circ \alpha_1\) defined using any choice of order of such consecutive insertions.

The ordered correspondence \(\alpha_2 \circ \alpha_1\) constructed in Construction 4.9 is, in fact, an alignment:

**Lemma 4.10** (Composition is an Alignment). Let \(x, y, z\) be backbones and \(\alpha_1 : [k] \rightarrow \tilde{x} \times \tilde{y}\), \(\alpha_2 : [l] \rightarrow \tilde{y} \times \tilde{z}\) be alignment maps. Then, \(\alpha_2 \circ \alpha_1\) defined in Construction 4.9 is an alignment between \(x\) and \(z\).

**Proof.** We show that all properties of Definition 4.4 hold. Since \(\alpha_1, \alpha_2\) are alignments, they contain no null alignments or misalignments. This implies that \(\alpha_2 \circ \alpha_1\) also contains no null alignments or misalignments. Furthermore, \(\text{im}(\alpha_2 \circ \alpha_1)\) contains all \(x \in x\) that are nontrivially aligned with \(y \in y\) along with all \(x \in x\) that are aligned with an insertion. Hence all \(x \in x\) appear in the image of \((\alpha_2 \circ \alpha_1)\) exactly once. The same can be said for all \(z \in z\). Therefore, Property (1), Property (3), and Property (4) of Definition 4.4 hold.

Lastly, we show that \(\alpha_2 \circ \alpha_1\) preserves order of the backbones \(x\) and \(z\). First consider the set of nontrivial pairs \(A\). We show the order of the (partial) backbones \(x\) and \(z\) is preserved in this set. By construction, we know the order of \(x\) is preserved. Replacing each pair \((x, z) \in A\) by \((x, y) \in \text{im}(\alpha_1)\) where \((y, z) \in \text{im}(\alpha_2)\), we see the order of \(y\) is preserved because \(\alpha_1\) is an alignment. Next, replacing each of these pairs with \((y, z)\) where \((y, z) \in \text{im}(\alpha_2)\), we see that order \(z\) is preserved in \(A\) because \(\alpha_2\) is an alignment. Hence, the order of the backbones \(x\) and \(z\) are preserved in \(A\). By Construction 4.9 each remaining trivial pair is added to the set \(A\) so that the order of the backbones \(x\) and \(z\) are preserved. Thus, Property (2) of Definition 4.4 also holds and we have an alignment \(\alpha_2 \circ \alpha_1\) between \(x\) and \(z\).

Next, we prove that the backbone distance satisfies the triangle inequality. We consider three backbones \(x, y,\) and \(z\). We use optimal alignments between \(x\) and \(y\), and \(y\) and \(z\), to construct an alignment between \(x\) and \(z\). We show that the constructed alignment between \(x\) and \(z\) satisfies the triangle inequality. Since the alignment between \(x\) and \(z\) that we find is an upper bound of an optimal alignment between \(x\) and \(z\), the backbone distance must also satisfy the triangle inequality.

**Lemma 4.11** (Backbone Distance Satisfies Triangle Inequality). Let \(x, y, z\) be backbones. Then,

\[
d_B(x, z) \leq d_B(x, y) + d_B(y, z).
\]

**Proof.** Let \(\alpha_1 : [k] \rightarrow \tilde{x} \times \tilde{y}\), \(\alpha_2 : [m] \rightarrow \tilde{y} \times \tilde{z}\) be optimal alignments. Consider the composition alignment \(\alpha_2 \circ \alpha_1\) from Construction 4.9. Define \(A\) as in Construction 4.9

\[
A_x := \{(x, y) \in \text{im}(\alpha_1) \mid \exists z \in z \text{ s.t. } (y, z) \in \text{im}(\alpha_2)\},
\]
and

\[ A_z := \{(y, z) \in \text{im}(\alpha_2) \mid \exists x \in X \text{ s.t. } (x, y) \in \text{im}(\alpha_1)\}. \]

We start by considering and justifying all the relations we need in the triangle inequality computation. Since \( d_B(x, z) \) is computed using an optimal alignment between \( x \) and \( z \) and \( \alpha_2 \circ \alpha_1 \) is one alignment,

\[
(4) \quad d_B(x, z) \leq \sum_{(x, z) \in \text{im}(\alpha_2 \circ \alpha_1)} |w_x - w_z| + \sum_{(x, 0) \in \text{im}(\alpha_2 \circ \alpha_1)} w_x + \sum_{(0, z) \in \text{im}(\alpha_2 \circ \alpha_1)} w_z.
\]

We apply the \( L_1 \)-norm triangle inequality to the first term in (4) to get

\[
(5) \quad \sum_{(x, z) \in \text{im}(\alpha_2 \circ \alpha_1)} |w_x - w_z| \leq \sum_{(x, y) \in A_x} |w_x - w_y| + \sum_{(y, z) \in A_y} |w_y - w_z|.
\]

Now we discuss the second term in (4). Define

\[ X_{(y, 0)} := \{(x, 0) \in \text{im}(\alpha_2 \circ \alpha_1) \mid \exists y \in Y \text{ s.t. } (x, y) \in \text{im}(\alpha_1) \setminus A_x\}. \]

Observe, if \((x, y) \in \text{im}(\alpha_1) \setminus A_x\), then for all \( z \in Z \), \((y, z) \notin \text{im}(\alpha_2)\). Hence, \((y, 0) \in \text{im}(\alpha_2)\). This implies the set

\[
(x \times \{0\}) \cap \text{im}(\alpha_2 \circ \alpha_1) = ((x \times \{0\}) \cap \text{im}(\alpha_1)) \cup X_{(y, 0)}
\]

and this union is disjoint. Thus,

\[
(6) \quad \sum_{(x, 0) \in \text{im}(\alpha_2 \circ \alpha_1)} w_x = \sum_{(x, 0) \in \text{im}(\alpha_1)} w_x + \sum_{(x, 0) \in X_{(y, 0)}} w_x.
\]

By definition of \( X_{(y, 0)} \), for each \((x, 0) \in X_{(y, 0)}\), there exists \( y \in Y \) such that \((x, y) \in \text{im}(\alpha_1) \setminus A_x\) and, at the same time, \((y, 0) \in \text{im}(\alpha_2)\). Noting this observation and applying the triangle inequality from the \( L_1 \)-norm to the last term of Equation (6), gives

\[
(7) \quad \sum_{(x, 0) \in \text{im}(\alpha_2 \circ \alpha_1)} w_x \leq \sum_{(x, 0) \in \text{im}(\alpha_1)} w_x + \sum_{\text{im}(\alpha_1) \setminus A_x} |w_x - w_y| + \sum_{(y, 0) \in \text{im}(\alpha_2) \text{ s.t. } (x, y) \in \text{im}(\alpha_1)} w_y.
\]

Now we discuss the third term in (4). Define

\[ Z_{(0, y)} := \{\{0, z\} \in \text{im}(\alpha_2 \circ \alpha_1) \mid \exists y \in Y \text{ s.t. } (y, z) \in \text{im}(\alpha_2) \setminus A_x\}. \]

Similarly, the set

\[
(\{0\} \times Z) \cap \text{im}(\alpha_2 \circ \alpha_1) = ((\{0\} \times Z) \cap \text{im}(\alpha_2)) \cup Z_{(0, y)}.
\]

This implies

\[
(8) \quad \sum_{(0, z) \in \text{im}(\alpha_2 \circ \alpha_1)} w_z = \sum_{(0, z) \in \text{im}(\alpha_2)} w_z + \sum_{(0, z) \in Z_{(0, y)}} w_z.
\]

By definition, for each \((0, z) \in Z_{(0, y)}\), there exists \( y \in Y \) such that \((y, z) \in \text{im}(\alpha_2) \setminus A_x\) and \((0, y) \in \text{im}(\alpha_1)\). Applying the triangle inequality from the \( L_1 \)-norm to the last term of Equation
\[ \sum_{(0,z) \in \text{im}(\alpha_2 \circ \alpha_1)} w_z \leq \sum_{(0,z) \in \text{im}(\alpha_2)} w_z + \sum_{(y,z) \in \text{im}(\alpha_2) \setminus A_x} |w_z - w_y| + \sum_{(0,y) \in \text{im}(\alpha_1) \text{ s.t. } (y,z) \in \text{im}(\alpha_2)} w_y. \]  

We derive two additional sets of relationships that will be used in the final estimate. We first note that since \( \text{im}(\alpha_1) \cap (x \times y) = A_x \cup ((\text{im}(\alpha_1) \cap (x \times y)) \setminus A_x) \) and this union is disjoint,

\[ \sum_{(x,y) \in A_x} |w_x - w_y| + \sum_{(x,y) \in \text{im}(\alpha_1) \setminus A_x} |w_x - w_y| = \sum_{(x,y) \in \text{im}(\alpha_1)} |w_x - w_y|. \]

Analogously, since \( \text{im}(\alpha_2) \cap (y \times z) = A_z \cup ((\text{im}(\alpha_2) \cap (y \times z)) \setminus A_z) \) and this union is disjoint. Thus,

\[ \sum_{(y,z) \in A_z} |w_y - w_z| + \sum_{(y,z) \in \text{im}(\alpha_2) \setminus A_z} |w_y - w_z| = \sum_{(y,z) \in \text{im}(\alpha_2)} |w_y - w_z|. \]

The second set of relationships are inequalities. First, notice if \((y, z) \in \text{im}(\alpha_2) \setminus A_z\), then \(y\) must align with an empty node in the alignment \(\alpha_1\). Hence, \(\{(0, y) \mid (y, z) \in \text{im}(\alpha_2) \setminus A_z\} \subset \{(0, y) \in \text{im}(\alpha_1)\}\). This implies

\[ \sum_{(y,0) \text{ s.t. } (y,z) \in \text{im}(\alpha_2) \setminus A_z} w_y \leq \sum_{(0,y) \in \text{im}(\alpha_1)} w_y. \]

Finally, we note that \(\{(y, 0) \in \text{im}(\alpha_2) \mid (x, y) \in \text{im}(\alpha_1)\} \subset \text{im}(\alpha_2) \cap (y \times \{0\})\). Therefore,

\[ \sum_{(y,0)\in \text{im}(\alpha_2) \text{ s.t. } (x,y)\in \text{im}(\alpha_1)} w_y \leq \sum_{(y,0)\in \text{im}(\alpha_2)} w_y \]

Now we can put all these relations together to prove the backbone distance satisfies the triangle inequality.
\[
\begin{align*}
d_B(x, z) &\leq \sum_{(x,z) \in \text{im}(\alpha_{001})} |w_x - w_z| + \sum_{(x,0) \in \text{im}(\alpha_{001})} w_x + \sum_{(0,z) \in \text{im}(\alpha_{001})} w_z \\
&\quad \text{by Equation (4)} \\
&\leq \sum_{(x,y) \in A_x} |w_x - w_y| + \sum_{(y,z) \in A_z} |w_y - w_z| + \sum_{(x,0) \in \text{im}(\alpha_{001})} w_x \\
&\quad + \sum_{(0,z) \in \text{im}(\alpha_{001})} w_z \text{ by Equation (5)} \\
&\leq \sum_{(x,y) \in A_x} |w_x - w_y| + \sum_{(x,y) \in \text{im}(\alpha_1) \setminus A_x} |w_x - w_y| \\
&\quad + \sum_{(x,0) \in \text{im}(\alpha_1)} w_x + \sum_{(y,0) \in \text{im}(\alpha_2) \text{ s.t. } (x,y) \in \text{im}(\alpha_1)} w_y \\
&\quad + \sum_{(y,z) \in A_z} |w_y - w_z| + \sum_{(y,0) \in \text{im}(\alpha_2)} |w_z - w_y| \\
&\quad + \sum_{(0,z) \in \text{im}(\alpha_2)} w_z \text{ by Equations (7) and (9)} \\
&\leq \sum_{(x,y) \in \text{im}(\alpha_1)} |w_x - w_y| + \sum_{(x,0) \in \text{im}(\alpha_1)} w_x + \sum_{(0,y) \in \text{im}(\alpha_1)} w_y \\
&\quad + \sum_{(y,z) \in \text{im}(\alpha_2)} |w_y - w_z| + \sum_{(y,0) \in \text{im}(\alpha_2)} w_y + \sum_{(0,z) \in \text{im}(\alpha_2)} w_z \\
&\quad \text{by Equations (10), (12), (11), and (13)} \\
&= d_B(x, y) + d_B(y, z).
\end{align*}
\]

Hence, \(d_B(x, z) \leq d_B(x, y) + d_B(y, z)\).

We can now prove the backbone distance is a metric.

**Proposition 4.12 (Backbone Distance is a Metric).** The backbone distance (Definition 4.8) is a metric.

**Proof.** Let \(x, y\) be backbones. Recall that for each \(x \in x\), we can write \(x = (s_x, w_x)\); likewise for \(y \in y\). Let \(\alpha : [k] \to x \times y\) be an optimal alignment. We verify all properties of a metric.

**Non-Negativity.** Since all node weights are non-negative, \(d_B(x, y) \geq 0\).

**Symmetry.** By construction, \(d_B\) is symmetric; see [3].

**Definiteness.** If \(x = y\), then the optimal alignment aligns each node with itself, and there are no insertions. Hence, all node weights match and \(d_B(x, y) = 0\).

On the other hand, assume \(d_B(x, y) = 0\). This implies

\[
0 = \sum_{(x,y) \in \text{im}(\alpha)} |w_x - w_y| + \sum_{(x,0) \in \text{im}(\alpha)} w_x + \sum_{(0,y) \in \text{im}(\alpha)} w_y.
\]

Since all weights are non-negative, the latter two summands (corresponding to nodes aligned with insertions) sum to zero. Since there are no null alignments (Definition 4.4 Property (1)), every
node in \( x \) is aligned with a node in \( y \). We have
\[
0 = \sum_{(x,y) \in \text{im}(\alpha)} |w_x - w_y|
\]
and so \( w_x = w_y \) for all nontrivial pairs \((x,y)\). Additionally, if \((x,y) \in \text{im}(\alpha)\), we know that \( s_x = s_y \). Since this is true for all nodes, we must have \( x = y \).

\textbf{Triangle Inequality.} By Proposition Lemma 4.11, the triangle inequality holds. Therefore, the backbone distance is a metric.

\[\square\]

4.2. Extremal Event DAG Distance. Using the backbone distance, we define a distance between two extremal event DAGs, \( D \) and \( D' \), constructed from comparable datasets. In other words, the number and identity of the time series are the same between the two datasets so that the choice of which backbones to align is clear. Once the alignments have been computed, we construct a supergraph based on \( D \) and \( D' \) where there is a vertex for each node pair from each alignment. We add a directed edge between two vertices if the edge exists between the two vertices in either \( D \) or \( D' \). After we construct the supergraph, we impose two weight functions on the vertices and nodes given by the weights of the nodes and edges in \( D \) and \( D' \) respectively. The difference between these weight vectors is the extremal event DAG distance between \( D \) and \( D' \).

\textbf{Definition 4.13 (Extremal Event Supergraph).} Let \( D = (V, E, \omega_V, \omega_E) \) and \( D' = (V', E', \omega_{V'}, \omega_{E'}) \) be two extremal event DAGs with \( n \) pairs of aligned backbones. Let \( x_1, x_2, \ldots, x_n \) be the backbones of \( D \), and \( y_1, y_2, \ldots, y_n \) be the backbones of \( D' \) and, for each \( i \in [k] \), let \( \alpha^{(i)} : [k] \rightarrow \bar{x}_i \times \bar{y}_i \) be the corresponding alignments where \( k_i = \text{len}(\alpha^i) \). Just as we expanded \( \alpha \) to two coordinate functions in Definition 4.4, \( \alpha^{(i)} \) can be expanded into two coordinate functions \( \alpha^{(i)} := (\alpha_{x_i}, \alpha_{y_i}) \). The extremal event supergraph determined by the alignments \( \{\alpha^{(i)}\}_{i=1}^n \) of \( D \) and \( D' \) is a doubly weighted directed graph \((V_\alpha, E_\alpha, \omega_\alpha, \omega'_\alpha)\), where

- \( V_\alpha := \{v(i,j) | i \in [n], j \in [k_i]\} \). That is, the vertices of \( V_\alpha \) are in one-to-one correspondence with each element of every alignment. Note \( V \cup V' \subset V_\alpha \).
- An ordered pair of vertices \((v(i,j), v(k,l)) \in V_\alpha \times V_\alpha \) is a directed edge in \( E_\alpha \) if and only if either one or both of the following is true
  - \((\alpha_{x_i}(j), \alpha_{x_k}(l)) \in E\)
  - \((\alpha_{y_i}(j), \alpha_{y_k}(l)) \in E'\).
  Note \( E \cup E' \subset E_\alpha \).
- The weight function \( \omega_\alpha : V_\alpha \cup E_\alpha \to \mathbb{R}_{\geq 0} \) is defined by
  \[
  \omega_\alpha(x) = \begin{cases}
  \omega_V(v(i,j)), & v(i,j) \in V_\alpha \\
  \omega_E(v(i,j), v(k,l)), & x = (v(i,j), v(k,l)) \in E \subseteq E_\alpha \\
  0, & \text{otherwise}.
  \end{cases}
  \]
- The weight function \( \omega'_\alpha : V_\alpha \cup E_\alpha \to \mathbb{R}_{\geq 0} \) is defined by
  \[
  \omega'_\alpha(x) = \begin{cases}
  \omega_V(v((i,j)), & v(i,j) \in V_\alpha \\
  \omega_E(v(i,j), v(k,l)), & x = (v(i,j), v(k,l)) \in E' \subseteq E_\alpha \\
  0, & \text{otherwise}.
  \end{cases}
  \]

We give an example of an extremal event supergraph and its weights in Figure 8.

We define the extremal event DAG distance to be the sum of absolute differences in node and edge weights from the extremal event supergraph determined by the best alignment we can easily compute.
Figure 8. Extremal event supergraph of DAG1 and DAG2 from Figure 5. The nodes on the left represent the optimal alignment between the sine backbones in DAG1 and DAG2. The nodes on the right represent the optimal alignment between the cosine backbones in DAG1 and DAG2. The node weights are listed on the node where the upper node weight comes from the weight function for DAG1 and the lower node eight comes from the weight function for DAG2. For readability, we present only one edge weight pair, associated to the bold edge. The edge weight on the left is from DAG1 and the edge weight on the right is from DAG2.

Definition 4.14 (Extremal Event DAG Distance). Let $D$ and $D'$ be two extremal event DAGs where $x_1, x_2, \ldots, x_n$ are the backbones of $D$ and $y_1, y_2, \ldots, y_n$ are the backbones of $D'$. The extremal event DAG distance is defined as:

$$d_{ED}(D, D') = \sum_{i=1}^{n} d_G(x_i, y_i) + \inf_{\{\alpha_i\}_{i=1}^{n}} \sum_{(u, v) \in E_{\alpha}} |\omega_D(u, v) - \omega_{D'}(u, v)|,$$

where $\{\alpha_i\}_{i=1}^{n}$ ranges over all sets of optimal alignments between the backbones.
We define extremal event DAG distance using optimal alignments between backbones because of its computability. As we show in Section 6, we use modified edit distance alignment algorithms to efficiently compute backbone alignments.

An open conjecture is that the sum of differences of edge weights is minimized only under an optimal alignment; that is,

$$d_{ED}(D, D') = \inf_{\{\alpha_i\}_{i=1}^n} \left( \sum_{u \in V_D} |\omega_D^\alpha(u) - \omega_{D'}^\alpha(v)| + \sum_{(u, v) \in E_D} |\omega_D^\alpha(u, v) - \omega_{D'}^\alpha(u, v)| \right)$$

where $\{\alpha_i\}_{i=1}^n$ ranges over all sets of alignments between the backbones.

If this conjecture is true, then we can prove the triangle inequality for the extremal event DAG distance using the same composition of alignments that we used for showing the triangle inequality holds for the backbone metric. If the conjecture is not true, then it is possible that the triangle inequality does not hold for the extremal event DAG distance. For the biological applications we have in mind, the key property that we desire is from a distance is not the triangle inequality, but rather stability, which is the property that small changes in two datasets does not cause a large jump in the distance between the associated extremal event DAGs. We show this property holds in Section 5 when the functions are “close” to one another.

5. Stability Results

In this section, we prove a Lipschitz stability result: that small changes in functions that are sufficiently close result in small distances between the corresponding extremal event DAGs. Our results are similar in flavor to stability for persistence diagrams [11].

5.1. Stability in Backbone Distance. We begin by proving stability results for the backbone distance. The main result of this section is Corollary 5.13 which states the backbone distance between backbones of two nicely tame real valued functions defined on a closed interval is bounded by a constant times the $L_\infty$ distance between the two functions. That is,

$$d_B(B(f), B(f')) \leq K \|f - f'\|_\infty.$$ 

5.1.1. Backbone Infinity Distance. To prove backbone stability, we show that the maximum difference in node weights arising from an optimal alignment is bounded by the $L_\infty$-distance of the two corresponding functions (Theorem 5.12). This leads us to comparing the backbone distance to the following that looks at the maximum distance between aligned node weights that arises from an optimal backbone alignment.

**Definition 5.1 (Backbone Infinity Distance).** Let $x$, $y$ be backbones. We define the backbone infinity distance between $x$ and $y$ as

$$d_{B_\infty}(x, y) = \inf_{\alpha} \max_i |\omega_x(\alpha_x(i)) - \omega_y(\alpha_y(i))|$$

where $\alpha$ ranges over all alignments of $x$ and $y$.

In Appendix 9.2 we prove the backbone infinity distance is a metric. The proof is a simplified version of the proof that the backbone distance is a metric (Proposition 4.12).

We prove backbone distance stability by moving between concepts of local extrema of functions, points in persistence diagrams, and backbone nodes. We describe the relationship between these three concepts next.

Let $f : C \to \mathbb{R}$ be a nicely tame function and $(t, f(t))$ be a local minimum of $f$ that does not represent the essential component in $D(f)$. Recall from Section 2.7 that at a height of $f(t)$ in the sublevel set filtration, a new connected component is born. The death of this connected component happens at the height of a local maximum denoted as $\zeta_f(t)$ (recall Definition 2.11). This implies existence of a point $(f(t), \zeta_f(t)) \in D(f)$ in the persistence diagram. We then compute the node
To make the correspondence between nodes in backbones, extrema, and points in persistence diagrams more precise, we define the following.

Definition 5.2 (Truncated Persistence Points). Let \( f : C \to \mathbb{R} \) be a nicely tame function. Let \( (t, f(t)) \) be a local minimum of \( f \). The point \( (f(t), \zeta_f(t)) \) is the truncated persistence point of \( (t, f(t)) \).

We often refer to the truncated persistence points as persistence points. We note that if \( (t, f(t)) \) is a local maximum of \( f \), then we declare the point \( (-f(t), \zeta_{-f}(t)) \) as the persistence point of \( (t, f(t)) \). Because of the correspondence between extrema, persistence points, and backbone nodes, we discuss pairings of extrema or persistence points to get aligned pairs in backbone alignments.

Remark 5.3 (Persistence Diagram Containing Diagonal). Persistence diagrams are often defined as in Definition 2.7, along with a union of all points on the diagonal \( \Delta = \{(x, x) \in \mathbb{R}^2\} \) counted with infinite multiplicity. The addition of the diagonal is useful for defining distances between persistence diagrams. For the remainder of this section, we assume that persistence diagrams contain all points on the diagonal counted with infinite multiplicity. This representation is useful for constructing alignments between backbones.

5.1.2. Stability in Backbone Infinity Distance. A key result that we use is the **Box Lemma**, that is proved in [11] to prove stability for persistence diagrams.
Lemma 5.4 (Box Lemma ([11])). Let $X$ be a topological space, $f, g : X \to \mathbb{R}$ be tame functions and let $\varepsilon = \|f - g\|_\infty$. For $a < b < c < d$, let $R = [a, b] \times [c, d]$ be a box in the extended plane, $\mathbb{R}^2$, and $R_\varepsilon = [a + \varepsilon, b - \varepsilon] \times [c + \varepsilon, d - \varepsilon]$ be the box obtained by shrinking $R$ by $\varepsilon$ on all sides. Then, 
$$|D(f) \cap R_\varepsilon| \leq |D(g) \cap R|.$$ 

The next result is similar in flavor to the Easy Bijection Lemma from [11]. We first prove stability for the backbone infinity distance in a special case. The result will depend on two constants.

Definition 5.5 (Constants $\delta_{\min}, \delta_{\max}$). Let $X$ be a topological space and $f : X \to \mathbb{R}$ be a tame function. Define $\delta_{\min}$ to be half of the smallest distance between two distinct off-diagonal points, or a point in $D(f)$ and a point on the diagonal, that is, 
$$\delta_{\min} := \frac{1}{2} \min\{\|p - q\|_\infty \mid p \in D(f) \setminus \Delta, q \in D(f), p \neq q\}.$$ 

The constant $\delta_{\max}$ is defined analogously using $D(-f)$.

Next, we note a relationship between Definition 5.5 and the minimum node life of extrema of $f$.

Lemma 5.6 (Minimum of Node Lives is Bounded Below by $\delta_{\min}$). Let $f : C \to \mathbb{R}$ be a nicely tame function. Let $\{t_i\}_{i=1}^n$ be the domain coordinates for local minima of $f$. Define $\delta$ to be half the minimum of the node lives of $t_i$, that is, 
$$\delta := \frac{1}{2} \min\{|\text{pers}_f(t_i)|\}_{i=1}^n.$$ 

Then $\delta_{\min} \leq \delta$.

Proof. Let $t \in \{t_i\}_{i=1}^n$ such that $\frac{1}{2}\text{pers}_f(t) = \delta$. Observe the point $(\frac{1}{2}\text{pers}_f(t), \frac{1}{2}\text{pers}_f(t))$ is the orthogonal projection of $(f(t), \zeta_f(t))$ onto the diagonal. In particular, $(\frac{1}{2}\text{pers}_f(t), \frac{1}{2}\text{pers}_f(t))$ is the closest point on the diagonal to $(f(t), \zeta_f(t))$. Notice, 
$$\left\| (f(t), \zeta_f(t)) - \left(\frac{1}{2}\text{pers}_f(t), \frac{1}{2}\text{pers}_f(t)\right) \right\|_\infty = \frac{1}{2}\text{pers}_f(t) = \delta.$$ 

Additionally, since for all $t_i \in \{t_i\}_{i=1}^n$ where $t_i \neq t$, we have $\frac{1}{2}\text{pers}_f(t_i) \geq \delta$, it must be the case that 
$$\left\| (f(t_i), \zeta_f(t_i)) - \left(\frac{1}{2}\text{pers}_f(t_i), \frac{1}{2}\text{pers}_f(t_i)\right) \right\|_\infty \geq \delta.$$ 

This implies that half the minimum distance between a point $p \in D(f) \setminus \Delta$ and a point on the diagonal is equal to $\delta$, that is, 
$$\frac{1}{2} \min\{\|p - q\|_\infty \mid p \in D(f) \setminus \Delta, q \in \Delta\} = \delta.$$ 

Lastly, since 
$$\{\|p - q\|_\infty \mid p \in D(f) \setminus \Delta, q \in \Delta\} \subseteq \{\|p - q\|_\infty \mid p \in D(f) \setminus \Delta, q \in D(f), p \neq q\}$$ 
we conclude $\delta_{\min} \leq \delta$. \hfill $\square$

Using the same proof but with $-f$ and $D(-f)$, we find $\delta_{\max} \leq \delta$. We use the two constants $\delta_{\min}$ and $\delta_{\max}$ to determine when functions are “close”.

Definition 5.7 (Very Close). Let $f : C \to \mathbb{R}$ be a nicely tame function. Let $\delta_f = \min\{\delta_{\min}, \delta_{\max}\}$. A nicely tame function $f' : C \to \mathbb{R}$ is very close to $f$ if $\|f - f'\|_\infty < \delta_f$.

Next we prove an analogue of the Easy Bijection Lemma [11] for backbones. We start by constructing an alignment between two backbones arising from nicely tame functions $f$ and $f'$ where $f'$ is very close to $f$. Figure 10 shows an example on how to construct the direct alignment between very close functions.
Construction 5.8 (Direct Alignment). Let \( f, f' : C \to \mathbb{R} \) be nice tame functions such that \( f' \) is very close to \( f \). Let \( \varepsilon = \|f - f'\|_{\infty} \). Note, that since \( f, f' \) are very close, we have \( \varepsilon < \delta_f \). The direct alignment construction consists of two steps:

1. **Pairing nodes in \( B(f) \) with \( B(f') \).** Recall that each node in \( B(f) \) and \( B(f') \) corresponds to a local extremum of \( f \) and \( f' \), respectively. We begin by pairing local minima of \( f \) with local minima of \( f' \). By definition of persistence diagrams, there is a one-to-one correspondence between the local minima of \( f \) and the points in \( D(f) \). Thus, we can pair local minima of \( f \) and \( f' \) by pairing off diagonal points in \( D(f) \) and \( D(f') \), respectively.

   Let \( p = (p_1, p_2) \in D(f) \setminus \Delta \). We describe what point in \( D(f') \) is paired with \( p \). Since \( p \in \square_{\varepsilon}(p) \), the Box Lemma tells us that the multiplicity \( \mu(p) \) of \( p \) satisfies

   \[
   \mu(p) \leq |D(f') \cap \square_{\varepsilon}(p)| \leq |D(f) \cap \square_{2\varepsilon}(p)|.
   \]

   By definition of \( \delta_f \) and the assumption \( \varepsilon < \delta_f \), we know that \( p \) is the only point contained in the set \( D(f') \cap \square_{2\varepsilon}(p) \). Therefore, \( |D(f') \cap \square_{\varepsilon}(p)| = \mu(p) \). Furthermore, since \( p \in D(f) \cap \square_{\varepsilon}(p) \), there is the same number of points, with multiplicity, in \( D(f') \cap \square_{\varepsilon}(p) \) and in \( D(f) \cap \square_{\varepsilon}(p) \).

   We explain how to define a bijection by pairing the points in the squares \( D(f) \cap \square_{\varepsilon}(p) \) and \( D(f') \cap \square_{\varepsilon}(p) \). Let \( n = \mu(p) \) and let \( \{t_i\}_{i=1}^n \) be the set of the domain coordinates of the local minima of \( f \) for which \( f(t_i) = p_1 \). Let \( q = (q_1, q_2) \in D(f') \cap \square_{\varepsilon}(p) \). Observe \( q_1 = f'(t) \) for some local minimum \( (t, f'(t)) \) of \( f' \). Because \( p, q \in \square_{\varepsilon}(p) \), we have \( \|p - q\|_{\infty} \leq \varepsilon < \delta_f \).

   In particular,

   \[
   |p_1 - q_1| = |f(t_i) - f'(t)| < \delta_f, \text{ for all } i \in [n].
   \]

   This implies that

   \[
   f(t_i) - \delta_f < f'(t) < f(t_i) + \delta_f, \text{ for all } i \in [n].
   \]

   This inequality, the fact that \( \delta_f \leq \delta_2 \), and \( f(t_i) = p_1 \) for all \( i \in [n] \) implies

   \[
   t \in A := (f - \delta_f)^{-1}(-\infty, p_1 + \delta_f).
   \]

   By Lemma 5.6, \( \delta_f \leq \frac{1}{3} \min\{\text{pers}_f(t_i)\}_{i=1}^n \). Applying Proposition 1 of \([4]\), we find \( A \) is a disjoint union of intervals and each contains exactly one \( t_i \), i.e., \( A = \bigcup_{i=1}^n \varphi_{\delta_f}(t_i) \). Let \( t^*_i \in \{t_i\}_{i=1}^n \) such that \( t \in \varphi_{\delta_f}(t^*_i) \). For our alignment, we pair the local minima \( (t^*_i, f(t^*_i)) \) with \( (t, f'(t)) \). Iterating this process for all points \( q \in D(f') \cap \square_{\varepsilon}(p) \) results in a bijection between points in the squares \( D(f) \cap \square_{\varepsilon}(p) \) and \( D(f') \cap \square_{\varepsilon}(p) \).

   Iterating the above procedure for all points \( p \in D(f) \setminus \Delta \), we pair all local minima of \( f \) with local minima of \( f' \). All remaining local minima of \( f' \) are paired with an empty node. The order of the alignment is given by the domain coordinates of \( f' \). What remains are the local maxima of \( f \) and \( f' \). To pair these extrema, we apply the same exact process to minima of \( -f \) and \( -f' \) since they are local maxima of \( f \) and \( f' \).

2. **Indexing the pairs so that order of the backbones for \( B(f) \) and \( B(f') \) are preserved.** Let \( x = B(f) \) and \( x' = B(f') \). Since extrema in \( f \) (and \( f' \)) are in one-to-one correspondence with nodes in \( x \) (and \( x' \), respectively), we know that each pair of aligned extrema in Step 1 corresponds to a pair of nodes in \( x \times x' \). To construct the direct alignment \( \alpha : [k] \to x \times x' \), we order the pairs found in Step 1 based on the order of the domain coordinates of the local extrema of \( f' \). It follows that \( k \) is the number of local extrema of \( f' \). Let \( (t^*_i, f'(t^*_i)) \) be the \( i \)-th extremum based on order of domain coordinates of \( f' \), and assume, without loss of generality, that this extremum is a local minimum. Then, \( \alpha(i) = (\alpha_x(i), \alpha_{x'}(i)) \) is given by \( \alpha_x(i) = \min \frac{1}{2} \text{pers}_f(t^*_i) \) and \( \alpha_{x'}(i) \) is the paired node pair from Step 1.

Lemma 5.9 (Direct Alignment is an Alignment). Let \( f, f' : C \to \mathbb{R} \) be nice tame functions such that \( f' \) is very close to \( f \). Let \( x = B(f) \) and \( x' = B(f') \). The direct alignment, \( \alpha : [k] \to x \times x' \) constructed in Construction 5.8 is an alignment.
Proof. We show Definition 4.4 holds. By Construction 5.8 we immediately see we have no null alignments, misalignments, and have a restriction to matching. Hence, Property (1), Property (3), and Property (4) hold. What remains is showing the alignment preserves order of backbones.

Since the nodes of \( x' \) are ordered by domain coordinates of local extrema of \( f' \), the alignment \( \alpha \) preserves the order of nodes of \( x' \). We now show that the alignment \( \alpha \) also preserves the order of nodes in \( B(f) \). Consider nodes \( \alpha_x(i), \alpha_x(j) \in x = B(f) \) such that \( i < j \) and \( \alpha_x(i), \alpha_x(j) \) map to local extrema \( (t, f(t)) \) and \( (s, f(s)) \), respectively. Trivially, \( t, s \) are contained in \( \varphi_{\delta_j}(t) \) and \( \varphi_{\delta_j}(s) \), respectively. Since \( \|f - f'\|_\infty < \delta_f \leq \min\{\frac{1}{2}\text{pers}(f(t_i))\}_i \) by Lemma 5.6 then if \( t \) and \( s \) are not adjacent, \( \varphi_{\delta_j}(t) \cap \varphi_{\delta_j}(s) = \emptyset \) by Proposition 1 of [4]. Otherwise \( t \) and \( s \) are adjacent and by Lemma 3.3 Statement (3), we have \( t \notin \varphi_{\delta_j}(s) \) and \( s \notin \varphi_{\delta_j}(t) \). Either way, we find \( \iota(\alpha_x(i)) < \iota(\alpha_x(j)) \) implies \( \iota(\alpha_x(i)) < \iota(\alpha_x(j)) \). Therefore, the order of the backbones \( B(f) \) and \( B(f') \) is preserved and we have constructed an alignment between \( B(f) \) and \( B(f') \).

Next, we prove a bound on the absolute difference between aligned weights in the Direct alignment.

**Lemma 5.10 (Bound in Difference in Node Weights in Direct Alignment).** Let \( f, f' : C \to \mathbb{R} \) be nicely tame functions such that \( f' \) is very close to \( f \). Let \( \varepsilon := \|f - f'\|_\infty \). Let \( x = B(f) \) and \( x' = B(f') \), and \( \alpha : [k] \to \bar{x} \times \bar{x}' \) be the direct alignment as defined in Construction 5.8. Then, the absolute difference in weights among aligned nodes is bounded by \( \varepsilon \); that is, for all \( (x, x') \in \text{im}(\alpha) \), \( |w_x - w_{x'}| \leq \varepsilon \).

**Proof.** Let \( (x, x') \in \text{im}(\alpha) \). Either both represent extrema from \( f \) and \( f' \), or the node \( x \) is the empty node.

First, assume that both nodes represent extrema. For this proof, we assume they are minima and note an analogous argument holds for maxima. Let \( (t, f(t)) \) and \( (t', f'(t')) \) be the local minima corresponding to nodes \( x \) and \( x' \), respectively. Either both of these extrema do not represent the essential component in \( D(f) \) and \( D(f') \) or at least one of them does. Suppose neither represents the essential component. Consider the persistence points \( p = (f(t), \zeta_f(t)), q = (f'(t'), \zeta_{f'}(t')) \) in \( D(f) \setminus \Delta \) and \( D(f') \setminus \Delta \) respectively. From Construction 5.8 we know that both \( p, q \in \square_{\varepsilon}(p) \). This implies \( \|p - q\|_\infty \leq \varepsilon \).

Hence, \( |w_x - w_{x'}| = \frac{1}{2}|\text{pers}(f(t) - \text{pers}(f'(t'))| = \frac{1}{2}|(\zeta(t) - f(t)) - (\zeta'(t') - f'(t'))| = \frac{1}{2}|(\zeta(t) - f(t)) + (f'(t') - f(t))| \leq \frac{1}{2}|\zeta(t) - f(t)| + \frac{1}{2}|f'(t') - f(t)| \leq \frac{\varepsilon}{2} + \frac{\varepsilon}{2} = \varepsilon. \)

Next, consider the case at least one of \( (t, f(t)) \) or \( (t', f'(t')) \) represents the essential component. By the Box Lemma, we can infer that both points have to represent the essential component. Then we know these points are global minima of \( f \) and \( f' \). Since \( (f(t), \infty) \) and \( (f'(t'), \infty) \) are both contained in the square of radius \( \varepsilon \) centered at \( (f(t), \infty) \) in the extended plane, \( |f(t) - f'(t')| \leq \varepsilon \).

Additionally, by Construction 5.8 we know that \( t_{\text{max}}, \) a global maximum of \( f \), is paired with \( t'_{\text{max}}, \) a global maximum of \( f' \) such that \( t'_{\text{max}} \in \varphi_{\delta_j}(t_{\text{max}}) \). This implies \( |f(t_{\text{max}}) - f'(t'_{\text{max}})| \leq \varepsilon \). Applying the same computation as above, we see \( |w_x - w_{x'}| \leq \varepsilon. \)

Lastly, consider the case \( (t', f'(t')) \) is paired with an empty node. Consider the point \( (f'(t'), \zeta_{f'}(t')) \in D(f') \). The Box Lemma implies \( \square_{\varepsilon}((f'(t'), \zeta_{f'}(t'))) \) must contain at least one point from \( D(f) \). By
assumption \((t', f'(t'))\) is paired with an empty node, and so \(\boxtimes_\varepsilon((f'(t'), \zeta_{f'}(t'))\) must contain a point on the diagonal. Therefore, \((f'(t'), \zeta_{f'}(t'))\) is within an \(L_\infty\) distance of \(\varepsilon\) from a point on the diagonal. Because the point \((\frac{1}{2} \text{pers}_f(t'), \frac{1}{2} \text{pers}_f(t'))\) is the orthogonal projection of \((f'(t'), \zeta_{f'}(t'))\) onto
the diagonal, it is the closest point on the diagonal in \(\mathbb{R}^2\) to \((f'(t'), \zeta_{f'}(t'))\). Therefore

\[
\left\|(f'(t'), \zeta_{f'}(t')) - \left(\frac{1}{2} \mathrm{pers}_{f'}(t'), \frac{1}{2} \mathrm{pers}_{f'}(t')\right)\right\|_{\infty} \leq \varepsilon.
\]

Comparing the \(x\)-coordinates of pair of points in (14), we find \(\frac{1}{2} \mathrm{pers}_{f'}(t') - f'(t') \leq \varepsilon\) and comparing the \(y\)-coordinates we find \(\zeta_{f'}(t') - \frac{1}{2} \mathrm{pers}_{f'}(t') \leq \varepsilon\). Therefore,

\[
\zeta_{f'}(t') \leq \frac{1}{2} \mathrm{pers}_{f'}(t') + \varepsilon, \quad f'(t') \geq \frac{1}{2} \mathrm{pers}_{f'}(t') - \varepsilon.
\]

Altogether we find

\[
\mathrm{pers}_{f'}(t') = \zeta_{f'}(t') - f'(t') \leq \left(\frac{1}{2} \mathrm{pers}_{f'}(t') + \varepsilon\right) - \left(\frac{1}{2} \mathrm{pers}_{f'}(t') - \varepsilon\right) = 2\varepsilon,
\]

and, therefore, \(\frac{1}{2} \mathrm{pers}_{f'}(t') \leq \varepsilon\).

We conclude that for all paired extrema,

\[
|w_x - w_{x'}| \leq \varepsilon.
\]

\[\square\]

We can now prove local stability for the backbone infinity distance.

**Lemma 5.11 (Local Backbone Infinity Stability).** Let \(f, f' : C \to \mathbb{R}\) be nicely tame functions such that \(f'\) is very close to \(f\). Then,

\[
d_{B_\infty}(B(f), B(f')) \leq \|f - f'\|_{\infty}.
\]

*Proof.* In Lemma 5.10, we showed that using the direct alignment between \(B(f)\) and \(B(f')\), the absolute difference in aligned node weights is bounded by \(\|f - f'\|_{\infty}\). Since the backbone infinity distance is defined by using an optimal alignment, we get

\[
d_{B_\infty}(B(f), B(f')) \leq \|f - f'\|_{\infty}.
\]

\[\square\]

To remove the assumption that \(f\) and \(f'\) are very close and thus to globalize the backbone infinity stability result, we construct a straight-line homotopy between \(f\) and \(f'\) and consider a finite number of functions within this homotopy for which every two successive functions are very close. For each such pair of functions, Lemma 5.11 applies and we are able to apply almost the same argument as the proof of the Interpolation Lemma in [11]. Because we sample functions between \(f\) and \(f'\) in the homotopy, we are able to conclude that \(d_{B_\infty}(B(f), B(f')) \leq \|f - f'\|_{\infty}\).

**Theorem 5.12 (Backbone Infinity Stability).** Let \(f, f' : C \to \mathbb{R}\) be nicely tame functions. Then,

\[
d_{B_\infty}(B(f), B(f')) \leq \|f - f'\|_{\infty}.
\]

*Proof.* Let \(c := \|f - f'\|_{\infty}\). Define \(h_\lambda := (1 - \lambda)f + \lambda f'\) where \(\lambda \in [0, 1]\). This is the family of convex combinations of \(f\) and \(f'\) forms a linear interpolation between the two functions, starting at \(h_0 = f\) and ending at \(h_1 = f'\). Furthermore, we define \(\delta(\lambda) := \delta_{h_\lambda}\) as in Definition 5.7. Consider the open cover \(U\) of \([0, 1]\) by open intervals \(J_\lambda = (\lambda - \delta(\lambda)/2c, \lambda + \delta(\lambda)/2c)\) for all \(\lambda \in [0, 1]\). The compactness of \([0, 1]\) implies the existence of a finite subcover \(U'\) of \(U\). Let \(\lambda_1 < \lambda_2 < \cdots < \lambda_n\) be
the midpoints of the open intervals in $U'$. Observe, that half the length of $J_\lambda$ is equal to $\delta(\lambda)/2c$. Since any two consecutive intervals $J_{\lambda_i}$ and $J_{\lambda_{i+1}}$ have a non-empty intersection,

$$\lambda_{i+1} - \lambda_i \leq \delta(\lambda_i)/2c + \delta(\lambda_{i+1})/2c$$

$$\leq 2 \max\{\delta(\lambda_i)/2c, \delta(\lambda_{i+1})/2c\}$$

$$= \max\{\delta(\lambda_i), \delta(\lambda_{i+1})\}/c$$

Furthermore, note

$$|h_{\lambda_i} - h_{\lambda_{i+1}}| = |((1 - \lambda_i)f + \lambda_if') - ((1 - \lambda_{i+1})f + \lambda_{i+1}f')|$$

$$= |f(\lambda_{i+1} - \lambda_i) - f'(\lambda_{i+1} - \lambda_i)|$$

$$= \|f - f'\|_{\infty} (\lambda_{i+1} - \lambda_i).$$

This implies

$$\|h_{\lambda_i} - h_{\lambda_{i+1}}\|_{\infty} = c(\lambda_{i+1} - \lambda_i) \leq \max\{\delta(\lambda_i), \delta(\lambda_{i+1})\}.$$

Therefore, $h_{\lambda_i}$ is very close to $h_{\lambda_{i+1}}$ or vice-versa. Either way, Lemma 5.11 applies and we have

$$d_{B_\infty}(h_{\lambda_i}, h_{\lambda_{i+1}}) \leq \|h_{\lambda_i} - h_{\lambda_{i+1}}\|_{\infty}$$

for all $1 \leq i \leq n - 1$. Setting $\lambda_0 = 0$ and $\lambda_{n+1} = 1$, we see the inequality also holds for $i = 0$ and $i = n$ because $h_{\lambda_i}$ is very close to $h_{\lambda_0}$, and $h_{\lambda_{n+1}}$ is very close to $h_{\lambda_n}$. Therefore,

$$d_{B_\infty}(B(f), B(f')) \leq \sum_{i=0}^{n} d_{B_\infty}(B(h_{\lambda_i}), B(h_{\lambda_{i+1}}))$$

$$\leq \sum_{i=0}^{n} \|h_{\lambda_i} - h_{\lambda_{i+1}}\|_{\infty}$$

$$= \|f - f'\|_{\infty}.$$

The first inequality follows from the triangle inequality of the backbone infinity distance (Lemma 9.2). The last equality follows from how the collection $h_{\lambda_i}$ samples the straight line homotopy from $f$ to $f'$. Thus $d_{B_\infty}(B(f), B(f')) \leq \|f - f'\|_{\infty}$. \qed

5.1.3. Backbone Stability. Using Theorem 5.12 we also get stability results for the backbone distance. If the alignment that realizes the backbone infinity distance between two backbones, $B(f)$ and $B(f')$ is of length $K$, then the sum of absolute differences of node weights is bounded by $K \|f - f'\|_{\infty}$. This is because the backbone distance is bounded by the sum of absolute differences in node weights from the alignment realizing the backbone infinity distance.

**Corollary 5.13** (Backbone Stability). Let $f, f' : C \to \mathbb{R}$ be nicely tame functions. Let $K$ be the length of the alignment realizing the backbone infinity distance between $B(f)$ and $B(f')$. Then,

$$d_B(B(f), B(f')) \leq K \|f - f'\|_{\infty}.$$

If we are unable to compute $K$, note that we can bound $K$ by the number of extrema of $f$ plus the number of extrema of $f'$ because that is the longest possible length of an alignment between $B(f)$ and $B(f')$. 
5.2. Local Stability in Extremal Event DAG Distance. We showed stability between backbones. In this section, we extend those results to the entire extremal event DAG in a local case (when \( f' \) is extremely close to \( f \)). We start by proving that the direct alignment for functions we call extremely close is the optimal backbone alignment for the backbones of those two functions.

**Definition 5.14** (Extremely Close). Let \( f : C \to \mathbb{R} \) be a nicely tame function. Let \( \delta_f \) be as defined in Definition 5.5. A nicely tame function \( f' : C \to \mathbb{R} \) is extremely close to \( f \) if \( \|f - f'\|_\infty < \delta_f/2 \).

The difference between functions that are very close and extremely close is that the constant is \( \delta_f \) is divided by two for functions that are extremely close. This is needed in order for the following lemma to hold.

**Lemma 5.15** (Extremal Pairs With Node Life Differences Greater Than \( \varepsilon \)). Let \( f, f' : C \to \mathbb{R} \) be nicely tame functions such that \( f' \) is extremely close to \( f \). Let \( \varepsilon := \|f - f'\|_\infty \). Suppose \( p := (f(t), \zeta_f(t)) \in D(f) \setminus \Delta \) and \( q := (f'(t'), \zeta_{f'}(t')) \in D(f') \cap \Box_e(p) \). Then,

1. \( \frac{1}{2} \text{pers}_{f'}(t') > \varepsilon \). Consider \( \Box_{4\varepsilon}(p) \). Since \( f' \) is extremely close to \( f \), \( \varepsilon < \delta_f/2 \). Hence, \( 4\varepsilon < 2\delta_f \). Recall \( 2\delta_f \) is at most the smallest distance between any two points in \( D(f) \), provided that at least one point is not on the diagonal. Therefore, \( \Box_{4\varepsilon}(p) \) does not intersect the diagonal. Consider a square of radius \( 4\varepsilon \) where the right bottom corner is the point \((f(t) + 4\varepsilon, f(t) + 4\varepsilon)\), that is, \( \Box_{4\varepsilon}(f(t), f(t) + 8\varepsilon) \). Since \( q \in D(f') \cap \Box_e(p) \), the difference of the \( y \)- and \( x \)-coordinates of \( q \) (which is the persistence of \( q \)) is bounded below by the difference of \( y \)- and \( x \)-coordinates of the point \((f(t) + \varepsilon, f(t) + 7\varepsilon)\), see Figure 11a.

Hence,

\[
\frac{1}{2} \text{pers}_{f'}(t') > \frac{1}{2} ((f(t) + 7\varepsilon) - (f(t) + \varepsilon)) = 3\varepsilon > \varepsilon.
\]

2. Let \((f(s), \zeta_f(s)) \in D(f) \setminus \Box_e(p) \). Since \( f' \) is extremely close to \( f \), \( \varepsilon < \delta_f/2 \) and hence \( 2\varepsilon < \delta_f \). Since \( \delta_f \) is at most half the smallest distance between two points in \( D(f) \) where at least one point is not on the diagonal, the squares of radius \( 2\varepsilon \) centered at different points in \( D(f) \setminus \Delta \) are all disjoint. This implies

\[
\| (f(t), \zeta_f(t)) - (f(s), \zeta_f(s)) \|_\infty > 2\varepsilon.
\]

Furthermore, by the direct alignment, we know \( q \in \Box_e(p) \). This implies \( q \notin \Box_{2\varepsilon}((f(s), \zeta_f(s))) \). Consider the point \(((f(s) - 2\varepsilon), \zeta_f(s))) \). From planar geometry (See Figure 11b),

\[
|\text{pers}_{f'}(t') - \text{pers}_f(s)| > |(\zeta_f(s) - f(s)) - (\zeta_f(s) - (f(s) - 2\varepsilon))| = 2\varepsilon.
\]

Therefore, \( \frac{1}{2} |\text{pers}_{f'}(t') - \text{pers}_f(s)| > \varepsilon \).

\( \square \)

Now we prove the direct alignment gives an optimal backbone alignment when two functions are extremely close.

**Lemma 5.16** (Direct Alignment Gives Optimal Backbone Alignment). Let \( f, f' : C \to \mathbb{R} \) be nicely tame functions such that \( f' \) is extremely close to \( f \). Then, the direct alignment defined in Construction 5.8 is the unique optimal alignment that realizes \( \delta_B(B(f), B(f')) \).

**Proof.** Let \( \alpha \) be the direct alignment between \( x := B(f) \) and \( x' := B(f') \). Recall in Definition 4.1 that each \( x \in x \) can be written as a tuple \( x = (s_x, w_x) \); likewise, we can write \( x' \in x' \) as \( x' = (s_{x'}, w_{x'}) \). By way of contradiction, suppose \( \eta \) is a different alignment between \( x \) and \( x' \) such that \( \text{cost}(\eta) \leq \text{cost}(\alpha) \). Recall from the construction of the direct alignment (Construction 5.8) that...
the length of the direct alignment is the number of nodes in $x'$. By Construction 5.8, for each $x' \in \mathbf{x}'$, there exists a unique $x_\alpha \in \mathbf{x}$ such that $(x_\alpha, x') \in \text{im}(\alpha)$. Hence, we can write

$$\text{cost}(\alpha) = \sum_{(x,x') \in \text{im}(\alpha)} |w_x - w_{x'}| = \sum_{x' \in \mathbf{x}'} |w_{x'} - w_{x_\alpha}|.$$ 

Since $\eta$ is an alignment, it must align all nodes of $\mathbf{x}'$. Hence, we have $\text{len} \eta \geq \text{len} \mathbf{x}' = \text{len} \alpha$. Let $x_\eta$ denote the unique element of $\mathbf{x}$ such that $(x_\eta, x') \in \text{im}(\eta)$. We now discuss the following logical dichotomy: either

Case 1: for all $x' \in \mathbf{x}'$, $|w_{x'} - w_{x_\eta}| > |w_{x'} - w_{x_\alpha}|$, or

Case 2: there exists at least one $x' \in \mathbf{x}'$ for which $|w_{x'} - w_{x_\eta}| \leq |w_{x'} - w_{x_\alpha}|$.

We first consider Case 1. Suppose, for all $x' \in \mathbf{x}'$, we have $|w_{x'} - w_{x_\eta}| > |w_{x'} - w_{x_\alpha}|$. Since $\eta$ aligns all nodes of $\mathbf{x}'$, we have the first inequality below

$$\text{cost}(\eta) \geq \sum_{x' \in \mathbf{x}'} |w_{x'} - w_{x_\eta}|$$
$$> \sum_{x' \in \mathbf{x}'} |w_{x'} - w_{x_\alpha}|$$
$$= \text{cost}(\alpha).$$

This is a contradiction with $\text{cost}(\eta) \leq \text{cost}(\alpha)$.

Now, we consider Case 2. Suppose there exists $x' \in \mathbf{x}'$ for which

$$|w_{x'} - w_{x_\eta}| \leq |w_{x'} - w_{x_\alpha}|.$$  

(15)

If $x_\eta = x_\alpha$ for all such $x' \in \mathbf{x}'$, then we get that either $\eta$ is the same alignment as $\alpha$ or there must exist $y' \in \mathbf{x}'$ for which (15) is not true and hence $|w_{y'} - w_{y_\eta}| > |w_{y'} - w_{y_\alpha}|$. In particular, since for all instances where $|w_{x'} - w_{x_\eta}| \leq |w_{x'} - w_{x_\alpha}|$, $x_\eta = x_\alpha$, this implies $|w_{x'} - w_{x_\eta}| = |w_{x'} - w_{x_\alpha}|$. For
Putting this all together, we obtain
\[ \text{cost}(\eta) > \text{cost}(\alpha). \]
In either case, we have a contradiction with \( \text{cost}(\eta) \leq \text{cost}(\alpha). \)

Hence, there must exist some \( x' \in x' \) for which (15) holds and \( x_\eta \neq x_\alpha. \)

In Lemma 9.4 in Appendix 9.3, we show that both of the following statements are true:
\[
\begin{align*}
&\text{(a)} \quad |w_{x'} - w_{x_\eta}| = |w_{x'} - w_{x_\alpha}|. \\
&\text{(b)} \quad \text{There exists a } z' \in x' \text{ for which } |w_{x'} - w_{x_\eta}| > \varepsilon \text{ where } \varepsilon := \|f - f'\|_\infty.
\end{align*}
\]
From (a) and (b), we find that for all \( x' \in x' \) for which \( |w_{x'} - w_{x_\eta}| \leq |w_{x'} - w_{x_\alpha}| \) and \( x_\eta \neq x_\alpha, \) the equality \( |w_{x'} - w_{x_\eta}| = |w_{x'} - w_{x_\alpha}| \) must hold. Furthermore, there exists \( z' \in x' \) for which
\[ |w_{x'} - w_{x_\eta}| > |w_{x'} - w_{x_\alpha}|. \]
For all remaining \( y' \in x', \) we have
\[ |w_{y'} - w_{y_\eta}| \geq |w_{y'} - w_{y_\alpha}|. \]
Putting this all together, we obtain
\[
\text{cost}(\eta) \geq \sum_{x' \in x'} |w_{x'} - w_{x_\eta}|
\[ > \sum_{x' \in x'} |w_{x'} - w_{x_\alpha}|
\[ = \text{cost}(\alpha),
\]
which again contradicts the assumption that \( \text{cost}(\eta) \leq \text{cost}(\alpha). \)

We conclude that any alignment that is different from the direct alignment has a higher cost. Therefore, the direct alignment is the unique optimal alignment that realizes \( d_G(x, x') = d_G(B(f), B(f')). \)

We next prove a few lemmas that bound differences in node weights of aligned extrema.

For the rest of this subsection, we use the following assumptions and notation:

**Assumptions 5.17** (Local Stability Assumptions). Let \( F = \{f_i\}_{i=1}^n \) and \( F' = \{f'_i\}_{i=1}^n \) be collections of nicely tame functions from \( C \) to \( \mathbb{R}. \) Furthermore, suppose \( f'_i \) is extremely close to \( f_i \) for each \( i \in [n]. \)
\( D = (V, E, \omega_V, \omega_E) \) and \( D' = (V', E', \omega'_{V'}, \omega'_{E'}) \) be the extremal event graph DAGs of \( F \) and \( F', \) respectively. Let \( S_\alpha = (V_\alpha, E_\alpha, \omega_\alpha, \omega'_\alpha) \) be the extremal event supergraph arising from the set of alignments \( \alpha = \{\alpha_i\}_{i=1}^n \) that is used to compute the extremal event DAG distance between \( D \) and \( D'. \)

**Lemma 5.18** (Bound on Difference in Node Lives). Assume Assumptions 5.17. Let \( v(i, j) \in V_\alpha. \)
Then,
\[ |\omega_\alpha(v(i, j)) - \omega'_\alpha(v(i, j))| \leq \|f_i - f'_i\|_\infty. \]

**Proof.** By Lemma 5.16, the alignment \( \alpha_i \) between \( B(f_i) \) and \( B(f'_i) \) is the direct alignment. In Lemma 5.10, we showed the absolute difference in node weights between aligned nodes is bounded by \( \|f_i - f'_i\|_\infty. \)
Therefore,
\[ |\omega_\alpha(v(i, j)) - \omega'_\alpha(v(i, j))| \leq \|f_i - f'_i\|_\infty. \]

From Lemma 5.18, we can conclude that if \( f' \) is extremely close to \( f, \) then the backbone distance between \( B(f) \) and \( B(f') \) is bounded by the number of extrema in \( f' \) multiplied by \( \|f - f'\|_\infty. \) This is because the direct alignment has a length of \( B(f') \) and the absolute difference in aligned node weights for each pair is bounded by \( \|f - f'\|_\infty. \)
Corollary 5.19 (Bound on Backbone Distance for Extremely Close Functions). Let \( f, f' : C \to \mathbb{R} \) be nicely tame functions such that \( f' \) is extremely close to \( f \). Let \( k \) be the number of extrema of \( f' \). Then,
\[
d_B(B(f), B(f')) \leq k \| f - f' \|_\infty.
\]

Next we give a bound on the absolute difference in heights of aligned extrema when every pair of functions is extremely close. In the following lemma we simplify notation as follows:

- \( u_j := \alpha_{B(f_i)}(j) \)
- \( u'_j := \alpha_{B(f'_i)}(j) \).

Lemma 5.20 (Bound on Difference in Heigths of Aligned Extrema). Assume Assumptions 5.17. Let \( v(i, j) \) be a vertex in \( S_\alpha \). Let \( \{\alpha_i\}_{i=1}^n \) be the set of backbone alignments between \( B(f_i) \) and \( B(f'_i) \) that determines \( S_\alpha \). Let \( u_j \in B(f_i) \) and \( u'_j \in B(f'_i) \). Let \( (t, f_i(t)) \) and \( (t', f'_i(t')) \) be the local extrema corresponding to \( u_j \) and \( u'_j \), respectively. Then,
\[
|f_i(t) - f'_i(t')| \leq \| f_i - f'_i \|_\infty.
\]

Proof. By Lemma 5.16 \( \alpha_i \) is the direct alignment for all \( i \in [n] \). Recall from Construction 5.8 that both \((f_i(t), \zeta_{f_i}(t))\) and \((f'_i(t'), \zeta_{f'_i}(t'))\) are contained in the square centered at \((f_i(t), \zeta_{f_i}(t))\) of radius \( \| f_i - f'_i \|_\infty \). Hence, \(|f_i(t) - f'_i(t')| \leq \| f_i - f'_i \|_\infty \). \( \square \)

We now have a bound on the maximum difference between node weights in extremal event DAGs. What remains is bounding the difference in edge weights between extremal event DAGs when each pair of functions is extremely close. Let \( (v(i, k), v(j, m)) \) be an edge in the extremal event supergraph. We show
\[
|\omega(\alpha_i, v(i, k), v(j, m)) - \omega(\alpha'_i, v(i, k), v(j, m))| \leq \max\{ \| f_i - f'_i \|_\infty, \| f_j - f'_j \|_\infty \}.
\]

For Lemma 5.21, recall from Theorem 3.4 that \( \varepsilon^*(t, s) \) is the infimum \( \varepsilon \) for which \( \varphi_{\varepsilon}(t) \cap \varphi_{\varepsilon}(s) \neq \emptyset \). Furthermore, we simplify notation as follows:

- \( u_k := \alpha_{B(f_i)}(k) \)
- \( u'_k := \alpha_{B(f'_i)}(k) \)
- \( s_m := \alpha_{B(f_j)}(m) \)
- \( s'_m := \alpha_{B(f'_j)}(m) \).

Lemma 5.21 (Bound on Difference of Extremal Interval Intersection Values). Assume Assumptions 5.17. Let \( (v(i, k), v(j, m)) \in E_\alpha \) such that \( i \neq j \), and all four nodes defining these two edges, \( u_k, u'_k, s_m, s'_m \) are not empty nodes. Suppose the extrema these nodes represent are \((t, f_i(t)), (s, f_j(s))\), \((t', f'_i(t'))\), and \((s', f'_j(s'))\), respectively. Then,
\[
|\varepsilon^*(t, s) - \varepsilon^*(t', s')| \leq \varepsilon_{i,j}
\]
where \( \varepsilon_{i,j} := \max\{ \| f_i - f'_i \|_\infty, \| f_j - f'_j \|_\infty \} \).

Proof. Consider the case that both \((t, f_i(t))\) and \((s, f_j(s))\) are local minima. In the case that one or both are local maxima, we replace one, or both \( f_i, f_j \) by the corresponding negative function and convert the problem to a problem about two minima. Hence, only considering the case that both are local minima is sufficient. Additionally, we omit superscripts on \( \varepsilon \)-extremal intervals to avoid notational clutter. An input of \( t \) or \( s \) indicates the \( \varepsilon \)-extremal interval is computed from \( f_i \) or \( f_j \), respectively. An input of \( t' \) or \( s' \) indicates the \( \varepsilon \)-extremal interval is computed from \( f'_i \) or \( f'_j \), respectively. For convenience of exposition, let \( \varepsilon_i = \| f_i - f'_i \|_\infty \), \( \varepsilon_j = \| f_j - f'_j \|_\infty \), and \( \varepsilon_{i,j} := \max\{ \varepsilon_i, \varepsilon_j \} \).
Combining these two cases, we conclude

\[ f(x) \]

Therefore,

\[ \phi \]

Hence,

\[ \epsilon \]

In the case \( \epsilon \), plies

\[ \phi^t \]

\[ \phi^{t'} \]

\[ \epsilon_{i,j} \]

Suppose \( \epsilon^*(t, s) < \epsilon^*(t', s') \). Let \( \epsilon > \epsilon^*(t, s) \). Then \( \varphi_{\epsilon}(t) \cap \varphi_{\epsilon}(s) \neq \emptyset \). By Lemma 5.20

\[ |f_i(t) - f_i'(t')| \leq \epsilon_{i,j}. \]

Hence, \( f_i(t) \leq f_i'(t') + \epsilon_{i,j} \). Additionally, since \( \|f_i - f_i'\|_\infty \leq \epsilon_{i,j} \),

\[ (f_i' - \epsilon_{i,j})(x) \leq f_i(x) \text{ for all } x \in C. \]

These two inequalities imply \( f_i(t) + \epsilon \leq f_i'(t') + \epsilon + \epsilon_{i,j} \) and \( (f_i' - \epsilon - \epsilon_{i,j})(x) \leq f_i(x) - \epsilon \) for all \( x \in C \). Recall

\( \varphi_{\epsilon}(t) \) is the connected component of \( (f_i - \epsilon)^{-1}(f_i(t) + \epsilon) \) containing \( t \),

\( \varphi_{\epsilon + \epsilon_{i,j}}(t') \) is the connected component of \( (f_i' - \epsilon - \epsilon_{i,j})^{-1}(f_i'(t') + \epsilon + \epsilon_{i,j}) \) containing \( t' \).

Therefore, \( \text{left}(\varphi_{\epsilon + \epsilon_{i,j}}(t')) < \text{left}(\varphi_{\epsilon}(t)) \) and \( \text{right}(\varphi_{\epsilon + \epsilon_{i,j}}(t')) > \text{right}(\varphi_{\epsilon}(t)) \). We get \( \varphi_{\epsilon}(t) \subset \varphi_{\epsilon + \epsilon_{i,j}}(t') \). Similarly, we get \( \varphi_{\epsilon}(s) \subset \varphi_{\epsilon + \epsilon_{i,j}}(s') \). The non-empty intersection of \( \varphi_{\epsilon}(t) \cap \varphi_{\epsilon}(s) \) implies \( \varphi_{\epsilon + \epsilon_{i,j}}(t') \cap \varphi_{\epsilon + \epsilon_{i,j}}(s') \neq \emptyset \). This non-empty intersection holds true for all \( \epsilon > \epsilon^*(t, s) \). Since

\[ \epsilon^*(t, s) < \epsilon^*(t', s'), \]

we get

\[ \epsilon^*(t', s') \leq \epsilon_{i,j} + \epsilon^*(t, s). \]

Therefore,

\[ \epsilon^*(t', s') - \epsilon^*(t, s) \leq \epsilon_{i,j}. \]

In the case \( \epsilon^*(t', s') < \epsilon^*(t, s) \), we get \( \varphi_{\epsilon}(t') \subset \varphi_{\epsilon + \epsilon_{i,j}}(t) \) and \( \varphi_{\epsilon}(s') \subset \varphi_{\epsilon + \epsilon_{i,j}}(s) \) by symmetry. Therefore,

\[ \epsilon^*(t, s) - \epsilon^*(t', s') \leq \epsilon_{i,j}. \]

Combining these two cases, we conclude

\[ |\epsilon^*(t, s) - \epsilon^*(t', s')| \leq \epsilon_{i,j}. \]

Next, we can bound the absolute difference in aligned edge weights.
Lemma 5.22 (Bound on Differences in Edge Weights). Assume Assumptions 5.17. Then,
\[
|\omega_\alpha(v(i, k), v(j, m)) - \omega'_\alpha(v(i, k), v(j, m))| \leq \max\{\|f_i - g_i\|_\infty, \|f_j - g_j\|_\infty\}.
\]

Proof. Let \(\varepsilon_{i,j} := \max\{\|f_i - g_i\|_\infty, \|f_j - g_j\|_\infty\}\). Let \((t, f_i(t)), (s, f_j(s)), (t', f'_i(t'))\), and \((s', f'_j(s'))\) be the local extrema corresponding to nodes \(\alpha_{B(f_i)}(k), \alpha_{B(f_j)}(m), \alpha_{B(f'_i)}(k),\) and \(\alpha_{B(f'_j)}(m)\), respectively. Additionally, we omit superscripts on \(\varepsilon\)-extremal intervals to avoid notational clutter. An input of \(t\) or \(s\) indicates the \(\varepsilon\)-extremal interval is computed from \(f_i\) or \(f_j\), respectively. An input of \(t'\) or \(s'\) indicates the \(\varepsilon\)-extremal interval is computed from \(f'_i\) or \(f'_j\), respectively.

We prove this lemma by discussing several cases. First, we assume that \(\omega_\alpha(v(i, k), v(j, m))\) and \(\omega'_\alpha(v(i, k), v(j, m))\) are non-zero. Then, by definition,
\[
E_{\text{diff}} := |\omega_\alpha(v(i, k), v(j, m)) - \omega'_\alpha(v(i, k), v(j, m))|
\]
\[
= |\min\{\frac{1}{2}\text{pers}(t), \frac{1}{2}\text{pers}(s), \varepsilon^*(t, s)\} - \min\{\frac{1}{2}\text{pers}(t'), \frac{1}{2}\text{pers}(s'), \varepsilon^*(t', s')\}|.
\]

Let \(\varepsilon_i := \|f_i - g_i\|_\infty\), \(\varepsilon_j := \|f_j - g_j\|_\infty\), and \(\varepsilon_{i,j} = \max\{\varepsilon_i, \varepsilon_j\}\). Now we begin to go through the cases. Note that \(E_{\text{diff}}\) can be one of nine absolute differences depending on which value the minimum is achieved. In the cases where the difference comes from node weights of the same node or the extremal intersection values, we can apply either Lemma 5.18 or Lemma 5.21. In all other cases we split the equality \(E_{\text{diff}} = |U_1 - U_2|\) into two cases \(E_{\text{diff}} = U_1 - U_2\) or \(E_{\text{diff}} = U_2 - U_1\). We replace the larger term with one of the possible values from \(E_{\text{diff}}\) so that we can apply Lemma 5.18 or Lemma 5.21. For example, in one of the cases, if we assume \(E_{\text{diff}} = \frac{1}{2}(\text{pers}(s') - \text{pers}(t))\). Then, \(\text{pers}(s') \leq \text{pers}(t')\). Applying Lemma 5.18, we find
\[
E_{\text{diff}} = \frac{1}{2}(\text{pers}(s') - \text{pers}(t)) \leq \frac{1}{2}(\text{pers}(t') - \text{pers}(t)) \leq \varepsilon_i \leq \varepsilon_{i,j}.
\]

All together, we have 15 cases. We explicitly write these 15 cases out in Appendix 9.4. Based on these bounds, we conclude in the case that \(\omega_\alpha(v(i, k), v(j, m))\) and \(\omega'_\alpha(v(i, k), v(j, m))\) are non-zero, \(E_{\text{diff}} \leq \varepsilon_{i,j}\).

Now assume one of \(\omega_\alpha(v(i, k), v(j, m))\) or \(\omega'_\alpha(v(i, k), v(j, m))\) is equal to zero. Without loss of generality, suppose \(\omega'_\alpha(v(i, k), v(j, m)) = 0\). Then,
\[
E_{\text{diff}} = \min\{\frac{1}{2}\text{pers}(t), \frac{1}{2}\text{pers}(s), \varepsilon^*(t, s)\}.
\]

Applying Lemma 5.18, we find
\[
\frac{1}{2}\text{pers}(t) \leq \varepsilon_i \leq \varepsilon_{i,j}, \quad \frac{1}{2}\text{pers}(s) \leq \varepsilon_j \leq \varepsilon_{i,j}.
\]

If \(E_{\text{diff}} = \varepsilon^*(t, s)\), then \(\varepsilon^*(t, s) \leq \frac{1}{2}\text{pers}(t) \leq \varepsilon_i \leq \varepsilon_{i,j}\). Hence, \(E_{\text{diff}} \leq \varepsilon_{i,j}\).

Combining all the cases, we can conclude
\[
|\omega_\alpha(v(i, k), v(j, m)) - \omega'_\alpha(v(i, k), v(j, m))| \leq \varepsilon_{i,j}.
\]

□

Using the bounds we established between aligned node and edge weights in the extremal event supergraph arising from extremely close functions, we can bound the extremal event DAG distance.

Theorem 5.23 (Extremal Event DAG Stability). Assume Assumptions 5.17. Let \(k_i\) be the number of extrema in \(f_i\). Let \(\varepsilon_i := \|f_i - f'_i\|_\infty\) and \(\varepsilon_{i,j} := \max\{\varepsilon_i, \varepsilon_j\}\). Let \(P\) be the set of unordered pairs between the first \(n\) positive integers. Let \(S_{\alpha|\alpha_i}\) be the restricted subgraph of \(S_{\alpha}\) that is induced by
Theorem 5.23 without restrictions on closeness of \( \alpha_i \). Furthermore, let \( i \neq j \) and denote \( E_{i,j} \) to be the set of cross edges in \( S_{\alpha} \), that is, \( (u, v) \in E_{i,j} \) if \( u \in S_{\alpha|\alpha_i} \) and \( v \in S_{\alpha|\alpha_j} \). Then,

\[
d_{ED}(D, D') \leq \sum_{i=1}^{n} \varepsilon_i \left( k_i + \frac{k_i}{2} \right) + \sum_{(i,j) \in P} |E_{i,j}| \varepsilon_{i,j}.
\]

**Proof.** Let \( E_i \) be the set of edges in the extremal event supergraph restricted to the subgraph induced by \( \alpha_i \). Hence, for each edge \( (u, v) \in E_i \), we have \( u, v \in S_{\alpha|\alpha_i} \). The extremal event DAG distance between \( D \) and \( D' \) can be expressed as the sum of three terms.

\[
d_{ED}(D, D') = \sum_{i=1}^{n} d_B(B(f_i), B(f'_i)) + \sum_{(u,v) \in E_i} |\omega_\alpha(u, v) - \omega'_\alpha(u, v)|
+ \sum_{(u,v) \in E_{i,j}} |\omega_\alpha(u, v) - \omega'_\alpha(u, v)|.
\]

The first term is the sum of backbone distances between \( B(f_i) \) and \( B(f'_i) \) for each \( i \in [n] \). The second term is the sum of the absolute difference in edge weights where the nodes defining each edge are from the same backbone alignment. The third term is the sum of the absolute difference in edge weights where the nodes defining each edge are contained in different backbones.

Applying Corollary 5.19 we know that \( d_B(B(f_i), B(f'_i)) \leq k_i \varepsilon_i \). Hence, we can bound the first term

\[
\sum_{i=1}^{n} d_B(B(f_i), B(f'_i)) \leq \sum_{i=1}^{n} k_i \varepsilon_i.
\]

Applying Lemma 5.22 we know that if \( (u, v) \in E_i \), then \(|\omega_\alpha(u, v) - \omega'_\alpha(u, v)| \leq \varepsilon_i \). There are \( \binom{k_i}{2} \) edges in \( E_i \). Hence, we can bound the second term by

\[
\sum_{(u,v) \in E_i} |\omega_\alpha(u, v) - \omega'_\alpha(u, v)| \leq \sum_{i=1}^{n} \binom{k_i}{2} \varepsilon_i.
\]

Let \( |E_{i,j}| \) be the cardinality of the set \( E_{i,j} \). Applying Lemma 5.22 we can bound the third term

\[
\sum_{(u,v) \in E_{i,j}} |\omega_\alpha(u, v) - \omega'_\alpha(u, v)| \leq \sum_{(i,j) \in P} |E_{i,j}| \varepsilon_{i,j}.
\]

Combining the three bounds we find that

\[
d_{ED}(D, D') \leq \sum_{i=1}^{n} \left( k_i + \frac{k_i}{2} \right) \varepsilon_i + \sum_{(i,j) \in P} |E_{i,j}| \varepsilon_{i,j}.
\]

Note that Theorem 5.23 requires that in collections \( \{f_i\}_{i=1}^{n} \) and \( \{f'_i\}_{i=1}^{n} \) each pair \( (f_j, f'_j) \) is extremely close. Therefore this a local stability result. Theorem 5.12 offers an approach to use a local result (Lemma 5.11) to prove a global result. This globalization approach uses a homotopy that is sampled sufficiently densely so that each consecutive pair satisfies the assumptions of the local result. However, the key ingredient used to aggregate the local results to a global estimate is a triangle inequality. It remains an important open question whether extremal event DAG distance satisfies the triangle inequality. If so, than a similar globalization process would yield a version of Theorem 5.23 without restrictions on closeness of \( f_j \) and \( f'_j \).
6. Computations of Extremal Event DAGs and Extremal Event Supergraphs

We describe how to compute the extremal event DAG and extremal event DAG distance. Since experimental time series data often collects discrete time points as opposed to continuous functions, we first take a detour to discuss \( \varepsilon \)-extremal intervals and their associated properties in the discrete setting.

6.1. Discrete \( \varepsilon \)-Extremal Intervals.

**Definition 6.1** (Collection of Time Series). A set \( D = \{ D_j \}_{j=1}^K \) is a dataset composed of time series \( D_j \) on the closed interval \( C := [a, b] \) where \( D_j = \{(z_i, h_i^j)\}_{i=1}^N \) with
\[
Z := \{z_1 = a, z_2, \ldots, z_{N-1}, z_N = b\},
\]
is an ordered set with \( z_j < z_{j+1} \) and the heights \( h_j^i \) are the heights of the \( j^{th} \) points at \( z_j \) of time series \( i \).

For our purposes, we assume that \( Z \) denotes the progression of time. However, the following results hold even when \( Z \) denotes some ordered quantity other than time, for example, distance.

**Definition 6.2** (Discrete \( \varepsilon \)-Extremal Intervals). Let \( f_i : [a, b] \to \mathbb{R} \) be the linear interpolation of the time series \( D_i \). Let \( \varepsilon > 0 \), and suppose \( f_i \) has a local extremum at \( t \). Define the discrete \( \varepsilon \)-extremal interval to be a relatively open interval \( d^D_i(t) \subset [a, b] \) with endpoints in \( Z \) such that
\[
\begin{align*}
(1) & \quad d^D_i(t) \ni \varphi^f_i(t) \\
(2) & \quad d^D_i(t) is the minimal such interval, meaning there does not exist an interval \( I \) with endpoints in \( Z \) such that \( d^D_i(t) \supset I \ni \varphi^f_i(t) \).
\end{align*}
\]

We note that we omit the superscript \( D_i \) from \( d^D_i \) if the function is clear.

A few properties of \( \varepsilon \)-extremal intervals still hold in the discrete case. Namely, Propositions 1 and 2 of [4]. Proposition 1 implies that as long as \( \varepsilon \) does not exceed the node life of two local minima \((t_j, f_i(t_j)), (t_k, f_i(t_k))\) of \( D_i \), then \( d^\varepsilon(t_j) \cap d^\varepsilon(t_k) = \emptyset \). Proposition 2 implies that as long as \( \varepsilon \) does not exceed the node life of the extremum at \( t_j \), then any \( \varepsilon \)-perturbation of \( f_i \) has a local minimum contained in \( d^\varepsilon(t_j) \). The \( \varepsilon \)-extremal interval property that is lost is minimality, which is Proposition 3 of [4]. This proposition states that the \( \varepsilon \)-extremal intervals are the smallest intervals to guarantee extrema of \( \varepsilon \)-perturbations of \( f_i \), given the node life of extrema is less than \( \varepsilon \). Since discrete \( \varepsilon \)-extremal intervals contain the ones we would get from the linear interpolations, we cannot guarantee minimality. A more thorough discussion of these properties in the discrete case can be found in Section 4.2 of [4].

In regards to properties mentioned in this paper, Statement [1] of Lemma 3.3 states \( \varepsilon \)-extremal intervals grow as \( \varepsilon \) increases also holds in the discrete setting. This is because the computation of the discrete \( \varepsilon \)-extremal intervals is the same as the continuous case except that the intervals are widened so that the endpoints are contained in the domain of the time series. This added computation does not affect the monotonicity of growth in the \( \varepsilon \)-extremal intervals.

**Lemma 6.3** (Monotonicity of \( d^\varepsilon(t_i) \)). Let \( D_j \) be a time series with \( t_1 < t_2 < \ldots < t_n \) the domain coordinates of the local extrema. Then, for each \( i \in [n] \), the length \( \text{len}(d^\varepsilon(t_i)) \) is increasing with respect to \( \varepsilon \).

Additionally, Statement [2] of Lemma 3.3 holds in the discrete case. We prove that here since we apply it in Section 6.2.

**Lemma 6.4** (Containment Property of Discrete \( \varepsilon \)-Extremal Intervals). Let \( D_j \) be a time series with domain coordinates \( \{t_i\}_{i=1}^n \) for \( i \in [n] \) where \( t_1 < t_2 < \ldots < t_n \). Suppose \( D_j \) has a local minimum at \( t_i \) where \( i \leq n-1 \). Then, \( \varepsilon \leq \frac{1}{2} |f_j(t_i) - f_j(t_{i+1})| \) if and only if \( t_{i+1} \notin d^\varepsilon(t_i) \).
Proof. Let \( t_i \) be the domain coordinate of a local minimum of \( D_j \). For this proof we omit the subscript \( j \) from \( D_j \) and its linear interpolation \( f_j \).

First assume \( \varepsilon \leq \frac{1}{2}|f(t_i) - f(t_{i+1})| \). We show \( t_{i+1} \notin d_\varepsilon(t_i) \). Since \( t_i \) is the domain coordinate of a local minimum, \( f(t_i) < f(t_{i+1}) \). Thus,

\[
\varepsilon \leq \frac{1}{2}(f(t_{i+1}) - f(t_i)) \]

\[
f(t_i) + \varepsilon \leq f(t_{i+1}) - \varepsilon.
\]

This implies \( t_{i+1} \notin (f - \varepsilon)^{-1}(-\infty, f(t_i) + \varepsilon) \). Hence, \( t_{i+1} \notin \varphi_\varepsilon(t_i) \). By Definition 6.2 the right endpoint of \( d_\varepsilon(t_i) \) is equal to \( t_{i+1} \), and the right half of this interval is open. Hence, \( t_{i+1} \notin d_\varepsilon(t_i) \).

Next we prove that \( t_{i+1} \notin d_\varepsilon(t_i) \) implies \( \varepsilon \leq \frac{1}{2}|f(t_i) - f(t_{i+1})| \). We do this by proving the contrapositive. Assume \( \varepsilon > \frac{1}{2}|f(t_i) - f(t_{i+1})| \). Since \( t_i \) is the domain coordinate of a local minimum, \( f(t_i) < f(t_{i+1}) \). Thus,

\[
\varepsilon > \frac{1}{2}(f(t_{i+1}) - f(t_i)) \]

\[
f(t_i) + \varepsilon > f(t_{i+1}) - \varepsilon.
\]

This implies \( t_{i+1} \in (f - \varepsilon)^{-1}(-\infty, f(t_i) + \varepsilon) \). Furthermore, \( t_{i+1} \) must be in the same connected component as \( t_i \) in \( (f - \varepsilon)^{-1}(-\infty, f(t_i) + \varepsilon) \) since \( t_{i+1} \) is adjacent to \( t_i \). Therefore, \( t_{i+1} \in \varphi_\varepsilon(t_i) \).

By Definition 6.2 \( d_\varepsilon(t_i) \supseteq \varphi_\varepsilon(t_i) \). Therefore, \( t_{i+1} \in d_\varepsilon(t_i) \).

Applying a symmetric argument as in Lemma 6.4 we see that \( \varepsilon \leq \frac{1}{2}|f_j(t_i) - f_j(t_{i-1})| \) if and only if \( t_{i-1} \notin d_\varepsilon(t_i) \) and \( i \geq 2 \).

In discrete time series, the idea of incomparability is reduced to intersections between a finite number of intervals. Generically speaking, any continuous, monotone interpolation of a time series giving rise to \( \varepsilon \)-extremal intervals \( \varphi_\varepsilon \) results in greater values of \( \varepsilon^* \) than the discrete intervals \( d_\varepsilon \). In a loose sense, the \( \varepsilon^* \) determined by \( d_\varepsilon \) is the infimum \( \varepsilon^* \) over all smooth, monotone interpolations of the discrete time series. Therefore \( \varepsilon^* \) determined by \( d_\varepsilon \) is the most conservative estimate of incomparability available from the time series information.

Lastly, we remark that local stability of the extremal event DAG distance extends to the discrete case. To see this, note the node lives of extrema in discrete functions can be computed from the sublevel set persistence diagram obtained through linearly interpolating the values of the discrete function. Therefore, Lemma 5.15 Lemma 5.16 Lemma 5.18 Corollary 5.19 Lemma 5.20 that are all statements about node lives and differences in aligned node lives all extend to the discrete case. Furthermore, the proof of Lemma 5.21 (that bounds the difference between \( \varepsilon \)-extremal intersection values between aligned edge weights) relies on the nesting property of \( \varepsilon \)-extremal intervals. This property still holds in the discrete case and so Lemma 5.21 also extends in the discrete case. The proofs of Lemma 5.22 and Theorem 5.23 use the aforementioned lemmas. Therefore local stability for extremal event DAGs holds for discrete time series.

6.2. Computing the Extremal Event DAG. In this section, we describe Algorithm 5 which computes the extremal event DAG from a collection of time series over a closed interval. This algorithm is based on two key insights. First, the edge weight between two local extrema from the same function is the minimum of the node lives of the two local extrema (Statement 1 of Theorem 3.4). Second, the edge weight between two local extrema from different functions is the minimum of the two node lives and the infimum \( \varepsilon \) for when the two \( \varepsilon \)-extremal intervals intersect (Statement 2 of Theorem 3.4). We first describe the computation of merge trees that are used to compute the node lives of local extrema.
Definition 6.5 (Merge Tree). Let \( f \) be a real-valued function. Let \( \Gamma(f) \) be the graph of \( f \). We declare \( x \sim y \) if there exists an \( h \in \mathbb{R} \) for which \( x, y \in f^{-1}(h) \) and \( x, y \) are in the same connected component of \( f^{-1}(-\infty, h) \). The **merge tree** of \( f \), denoted \( M_f \), is defined to be the quotient space

\[
M_f := \Gamma(f)/\sim.
\]

Given a nicely tame function, \( f : C \to \mathbb{R} \), we construct the structure of the merge tree, \( G = (V, E) \), by [54]. This structure consists of a list of **merge triplets** where each triplet is a three-tuple of real numbers \((u, s, v)\) such that \( u \) represents the connected component containing itself for \( a \in [f(u), f(s)) \) and \( v \) becomes the representative of the connected component at a height of \( f(s) \).

In relation to zeroth-dimensional persistence diagram from a sublevel set filtration, \((f(u), f(s))\) is a birth-death pair and the two connected components represented by \( u \) and \( v \) merge into the connected component represented by \( v \) at a height of \( f(s) \). If the merge triplet has identical components denoted as \((u, u, u)\), then \( u \) is the global minimum of its connected component in \( G \). The time complexity of computing the Merge Tree using Kruskal’s algorithm for a function represented as a graph, \( G = (V, E) \) is \( O(m \log n) \) where \( n = |V| \) and \( m = |E| \) [54]. In our setting, the number of edges is bounded by \( n \) and so the time complexity is \( O(n \log n) \).

We describe how we compute the node lives and node labels of the extremal event DAG, using the triplets computed from the merge trees. Algorithm 1 (GetMinLives) takes input a merge tree \( M \) for a time series \( D = \{(z_i, h_i)\}_{i=1}^N \). Algorithm 1 outputs the node lives of the local minima of \( D \). For each merge triplet with distinct components, \((z_i, z_j, z_k)\) in \( M \), \((h_i, h_j)\) is a point in the zeroth-dimensional persistence diagram from the sublevel set filtration. By Definition 2.13 we get that \( \frac{1}{2} \text{pers}_D(z_i) = (h_j - h_i)/2 \). If the merge triplet has all identical components, \((z_j, z_j, z_j)\), then \( \frac{1}{2} \text{pers}_D(z_j) = \frac{1}{2} \text{max}\{(h_i)_{i=1}^N - \text{min}\{(h_i)_{i=1}^N\}) \). Applying one of these two computations to all merge triplets computes node lives for all local minima in \( D \). To compute the node lives of the local maxima, we apply the same process to \(-D\), where we take the negative of all heights \( h_i \).

Algorithm 1 GetMinLives(D, M)

1. **Input:** Array of merge tree triplets and time series \( D = \{(z_i, h_i)\}_{i=1}^N \).
2. **Output:** Dictionary of node lives for each point in curve.
3. minlives ← Initialize dictionary keyed by locations of extrema
4. for \((z_i, z_j, z_k)\) ∈ \( M \) do
5.   if \( z_j = z_k \) then
6.       minlives\((z_i) = \text{max}\{(h_i)_{i=1}^N - \text{min}\{(h_i)_{i=1}^N\})/2 \)
7. else
8.       minlives\((z_i) = |h_j - h_i|/2 \)
9. end if
10. end for
11. return minlives

The algorithm GetNodeLives\( (D, M_{\text{min}}, M_{\text{max}}) \) applies GetMinLives twice for both \( D \) and \(-D\) with merge trees \( M_{\text{min}} \) and \( M_{\text{max}} \) respectively. Suppose \( D \) has \( n \) local extrema. Each line in Algorithm 1 takes constant time. Since the loop has at most \( n \) iterations, then the total time complexity of Algorithm 1 is \( O(n) \). Hence, the time complexity of GetNodeLives is also \( O(n) \).

6.2.2. Computing Edge Weights. We explain how to compute the edge weights of the extremal event DAG. First consider the edge weight between two nodes in \( B(f) \), a single backbone. By
Statement \([1]\) of Theorem \([3.4]\) we know the edge weight is the minimum node life between the two extrema. Computing the minimum between two values takes constant time.

Next, we describe how we compute the edge weight between two nodes from different backbones. In order to do this, we must first compute the infimum \(\varepsilon\) for which two \(\varepsilon\)-extremal intervals intersect. In the discrete setting, the growth of the \(\varepsilon\)-extremal intervals only change at a finite number of \(\varepsilon\). We refer to the \(\varepsilon\) values where discontinuous changes in length occur as *jumps*. Algorithm \([2]\) \((\text{GetEpsJumpsRight})\) computes the \(\varepsilon\) jumps for the right endpoint of an \(\varepsilon\)-extremal interval. We recall in the discrete setting, connected components are determined by the linear interpolation of points in the image of \(f\). In Lemma \([6.6]\) we use \(\sim\) to denote the equivalence relation given by connected components i.e., for a time series \(D_i = \{(z_j, h_j^i)\}_{j=1}^N\), and \(z_j, z_k \in Z\), we declare \(z_j \sim z_k\) at \(\varepsilon > 0\) if both \(z_j, z_k\) are contained in the same connected component of \((f_i - \varepsilon)^{-1}(-\infty, f_i(x) + \varepsilon)\) where \(f_i\) is the linear interpolation of \(D_i\) and \(x \in Z\).

**Algorithm 2** \(\text{GetEpsJumpsRight}(D, z_i)\)

**Input:** Time series \(D = \{(z_i, h_i)\}_{i=1}^N\) and domain point \(z_i \in Z\).

**Output:** Vector of real numbers indicating values for which the right endpoint of \(d_\varepsilon(z_i)\) jumps.

1: Initialize epsilon array and jump height
2: if \(i \neq N\) then
3:   epsilons ← \(|h_{i+1} - h_i|/2\)
4:   levelheight ← \(h_{i+1}\)
5:   for \(j ← (i + 2) \ldots N\) do
6:     if (extremum(\(z_i\)) = min \(\wedge h_j \geq\) levelheight)
7:     \(\lor\) (extremum(\(z_i\)) = max \(\wedge h_j \leq\) levelheight) then
8:       epsilons append \(|h_j - h_i|/2\)
9:     levelheight ← \(h_j\)
10: end if
11: end for
12: end if
13: return epsilons

**Lemma 6.6** (Correctness of Algorithm \([2]\)). Let \(D = \{(z_i, h_i)\}_{i=1}^N\) be a time series. Let \(z_i\) be the domain coordinate of a local extremum of \(D\). Let \(r_i(\varepsilon) : \mathbb{R}_{>0} \rightarrow \mathbb{R}\) denote the right endpoint of \(d_\varepsilon(z_i)\). Then, \(\text{GetEpsJumpsRight}(D, z_i)\) Algorithm \([2]\) returns all \(\varepsilon\) values for which \(r_i\) has a jump discontinuity.

Proof. We note that if \(i = N\), then \(r_i(\varepsilon) = z_i\) for all \(\varepsilon \geq 0\). Hence, there are no jumps. \(\text{GetEpsJumpsRight}\) returns the empty array, which is correct. For the rest of this proof, we assume \(i \neq N\). To prove correctness, we show that we have the following loop invariant. At the start of each iteration of the for loop, the array epsilons consists of jumps of \(r_i(\varepsilon)\) in sorted order. We first remark that jump discontinuities of \(r_i(\varepsilon)\) occur at the infimum \(\varepsilon\) for which a point \(z_j \in Z\) is contained in \(d_\varepsilon(z_i)\) with \(j > i\). This is because in the discrete setting, the \(\varepsilon\)-extremal intervals only grow when a new point in \(Z\) is contained in \(d_\varepsilon(z_i)\). In particular, we show the loop invariant that \(z_{i+j} \in d_{\varepsilon'}(z_i)\), where \(\varepsilon'\) is the maximum of the array named epsilons after the \(j^{th}\) iteration.

**Initialization:** First, consider \(\varepsilon_1 = |h_i - h_{i+1}|/2\). By Lemma \([6.4]\) \(z_{i+1} \notin d_{\varepsilon_1}(z_i)\) and for all \(\varepsilon > \varepsilon_1, z_{i+1} \in d_\varepsilon(z_i)\). Hence, \(\varepsilon_1\) is the infimum \(\varepsilon\) for which \(z_{i+1} \in d_\varepsilon(z_i)\). This implies that \(\varepsilon_1\) is a jump discontinuity of \(r_i\). From Lemma \([6.3]\) we know that \(d_\varepsilon(z_i)\) increases monotonically. Hence no other point in \(Z\) is contained in \(d_\varepsilon(z_i)\) at a smaller value of \(\varepsilon\). Therefore, \(\varepsilon_1\) is the smallest jump discontinuity of \(r_i(\varepsilon)\) and so the loop invariant holds before the first iteration.
Maintenance: Assume the loop invariant holds after the \( j^{th} \) iteration. We show it also holds after the \( j+1^{st} \) iteration. First assume \( z_i \) is a local minimum. Then,

\[
\text{levelheight} = \max\{h_k \mid k \in [i + 1, i + j]\}.
\]

Denote \( z_* := z_{i+(j+1)} \). We want to find the infimum \( \varepsilon > 0 \) for which \( z_* \in d_\varepsilon(z_i) \).

Suppose \( h_* < \text{levelheight} \). We claim that \( z_* \in d_{\varepsilon'}(z_i) \) where \( \varepsilon' := \max\{\text{epsilons}\} \). This means that no new \( \varepsilon \) value needs to be added to the epsilons vector in Algorithm 3. Let

\[
z' := \arg\max\{h_k \mid k \in [i + 1, i + j]\}.
\]

Thus \( h' = \text{levelheight} \). Since \( h_* < \text{levelheight} = h' \) and \( \varepsilon' = (h' - h_i)/2 \), then

\[
\begin{align*}
h_* - h_i &< h' - h_i = 2\varepsilon' \\
h_* - \varepsilon' < h_i + \varepsilon'
\end{align*}
\]

This implies that \( z_* \in (f - \varepsilon')^{-1}(\mathbb{R}^\mathbb{R}, f(z_i) + \varepsilon') \) (recall \( f \) is the linear interpolation of \( D \)). Observe, \( z_{i+j} \in d_{\varepsilon'}(z_i) \) by the assumption that the loop invariant holds at the \( j^{th} \) iteration. Since \( z_* \) is adjacent to \( z_{i+j} \), \( z_* \) must be in the same connected component of \( (f - \varepsilon')^{-1}(\mathbb{R}^\mathbb{R}, f(z_i) + \varepsilon') \) as \( z_i \), i.e., \( z_* \sim z_i \). Therefore, \( z_* \in d_{\varepsilon'}(z_i) \) and the loop invariant holds.

Next suppose \( h_* \geq \text{levelheight} \). Let \( \varepsilon' \) be as before. Applying a similar computation as above we find that \( z_* \notin (f - \varepsilon')^{-1}(\mathbb{R}^\mathbb{R}, f(z_i) + \varepsilon') \). Observe that at \( \varepsilon^* := (h_* - h_i)/2 \) we have

\[f(z_*) - \varepsilon^* = f(z_i) + \varepsilon^*.
\]

This leads to the observation that \( z_* \in (f - \varepsilon)^{-1}(\mathbb{R}^\mathbb{R}, h_i + \varepsilon) \) for any \( \varepsilon > \varepsilon^* \) by Lemma 6.3. Since \( \varepsilon^* > \varepsilon' \), \( z_{i+j} \in (f - \varepsilon)^{-1}(\mathbb{R}^\mathbb{R}, f(z_i) + \varepsilon) \) as well. Since \( z_i \sim z_{i+j} \) by the loop invariant and \( z_{i+j} \sim z_* \) by adjacency, \( z_i \sim z_* \) as desired for any \( \varepsilon > \varepsilon^* \). These two observations tell us that \( \varepsilon^* \) is the infimum \( \varepsilon \) for which \( z_* \in d_\varepsilon(z_i) \). Therefore, \( \varepsilon^* \) should indeed be added to the epsilons array and is larger than all other values in the array. By assumption, the epsilons array is sorted. Hence, the loop invariant holds.

In the case that \( (z_i, h_i) \) is a local maximum, we apply a symmetric argument by noting that \( d_\varepsilon(z_i) \) is the (expanded out) connected component of \( (f + \varepsilon)^{-1}(f(z_i) - \varepsilon, \mathbb{R}^\mathbb{R}) \) containing \( z_i \) and a new value is added to the \( \varepsilon \) vector if \( h_j \leq \text{levelheight} \).

End: Note that the for loop terminates since there are only a finite number of iterations.

Since the number of jumps of \( r_i(\varepsilon) \) is bounded by \( N - i + 1 \), and epsilons consists of all infimum \( \varepsilon \) for which a point in \( N \) and greater than \( z_i \) is contained in \( d_\varepsilon(z_i) \), then Algorithm 2 is correct.

Next, we analyze the time complexity of Algorithm 2. Every line takes constant time. Since the for loop (Line 3–Line 11) has at most \( N - 1 \) iterations, then the total time complexity of Algorithm 2 is \( O(N) \).

Furthermore, we can apply the same algorithm but with going through points on the left of \( z_i \) to find all the points for which the left endpoint of \( d_\varepsilon(z_i) \) changes. Note that there are \( N - 1 \) points to the left and right of \( z_i \) combined, and so finding all \( \varepsilon \)-jumps of \( d_\varepsilon(z_i) \) takes \( O(N) \). We call this combined function, GETEPSJUMPS (Algorithm 3). Lastly, to find the infimum \( \varepsilon \) for which two \( \varepsilon \)-extremal intervals intersect, we apply Algorithm 4. Algorithm 4 takes input of two time series \( D_j, D_k \), two domain coordinates of local extrema of \( D_j, D_k \), and merge trees of \( D_j, -D_j, D_k, -D_k \). Algorithm 3 (GETEPSJUMPS) is applied to both functions and extrema. Then, Algorithm 4 goes through all jumps in order to find the smallest one for which the two \( \varepsilon \)-extremal intervals intersect.

Next, we discuss the time complexity of Algorithm 4. The number of jumps is bounded by the number of points in the domains of the two functions. Additionally, at each jump, we compute


Algorithm 3 GetEpsJumps($D, z_i$)

Input: Time series $D = \{(z_i, h_i)\}_{i=1}^N$ and domain point $z_i \in Z$.

Output: Vector of real numbers indicating values for which the left or right endpoint of $d_\varepsilon(z_i)$ jumps.

1: Initialize epsilon array and jump height
2: epsilons ← \{GetEpsJumpsLeft($D, z_i$)\}
3: epsilons append GetEpsJumpsRight($D, z_i$)
4: return epsilons

Algorithm 4 GetEpsIntersection($D_j, D_k, z_j, z_k, M_{D_j}, M_{-D_j}, M_{D_k}, M_{-D_k}$)

Input: Time series $D_j = \{(z_i, h_i^j)\}_{i=1}^N$, $D_k = \{(z_i, h_i^k)\}_{i=1}^N$ and domain points of extrema in $D_j$ and $D_k$, denoted $z_j, z_k \in Z$. $M_{D_j}$, $M_{-D_j}$, $M_{D_k}$, $M_{-D_k}$ are merge trees of $D_j$, $-D_j$, $D_k$, $-D_k$ respectively.

Output: $\inf_\varepsilon d^D_j(z_j) \cap d^D_k(z_k) \neq \emptyset$

1: Initialize epsilon array
2: epsilons ← \{GetEpsJumps($D_j, z_j$)\}
3: epsilons append GetEpsJumps($D_k, z_k$)
4: sort epsilons
5: for $\varepsilon \in$ epsilons do
6: $d^D_j(z_j)$ ← GetExtremalInterval($D_j, z_j, M_{D_j}, M_{-D_j}, \varepsilon$)
7: $d^D_k(z_k)$ ← GetExtremalInterval($D_k, z_k, M_{D_k}, M_{-D_k}, \varepsilon$)
8: if $d^D_j(z_j) \cap d^D_k(z_k) \neq \emptyset$ then
9: return $\varepsilon$
10: end if
11: end for

GetExtremalInterval for the two extrema, where the computation of the discrete extremal intervals are discussed in [4] and implemented in [2]. In particular, the time complexity for computing GetExtremalInterval($D, z_i, M_D, M_{-D}$) is $O(N)$. This is because computing the $\varepsilon$-extremal interval requires evaluating $f$ at points in $Z$ near $z_i$. In summary

- Line 2 and Line 3 each take $O(N)$.
- Line 4 takes $O(N \log N)$.
- Line 6 and Line 7 take $O(N)$.
- All other lines take constant time.

- The number of iterations of the for loop in Line 5-Line 11 is bounded by $2N$.

All together we compute the time complexity of GetEpsIntersection($D_j, D_k, z_j, z_k, M_{D_j}, M_{-D_j}, M_{D_k}, M_{-D_k}$) as

$$2O(N) + O(N \log N) + 2N(O(N)) = O(N \log N) + O(N^2).$$

6.2.3. Computing Extremal Event DAG. Algorithm 5 computes the extremal event DAG from a collection of time series $D = \{D_j\}_{j=1}^K$. Algorithm 5 uses previously defined algorithms and functions from this section along with InitializeGraph. This algorithm is designed and implemented in [2]. InitializeGraph takes a collection of time series $D$ as input and outputs $(T, H, V, E)$ where $V, E$ are vertices and directed edges of the extremal event DAG of $D$, $T$ is the domain coordinates of the local extrema, and $H$ is the heights of local extrema. This function checks through all points in $Z$ for extrema to record as vertices and then goes through all vertex pairs to check for edges. Let $N = |Z|$. The number of vertices is bounded by $NK$ and the number of edges is bounded by
\( \binom{NK}{2} \). Hence, the time complexity of \texttt{InitializeGraph} is

\[
O(NK + \frac{(NK)(NK - 1)}{2}) = O((NK)^2).
\]

\[\text{Algorithm 5 } \texttt{GetExtremalEventDAG}(\mathcal{D})\]

\begin{algorithmic}
\Input A collection of time series \( \mathcal{D} = \{D_j\}_{j=1}^K \).
\Output The extremal event DAG of \( \mathcal{D} \).
\end{algorithmic}

1: \( M_{D_j} \leftarrow \) merge tree for \( D_j \)
2: \( M_{-D_j} \leftarrow \) merge tree for \(-D_j \)
3: \( \text{NodeLives}_j \leftarrow \text{GetNodeLives}(D_j, M_{D_j}, M_{-D_j}) \)
4: \( (T, V, E) \leftarrow \text{InitializeGraph}(\mathcal{D}) \) \quad \text{Initialize unweighted extremal event DAG.}
5: \text{Initialize function } \omega_V : V \rightarrow \mathbb{R} \text{ with all values set to zero.}
6: \text{Initialize function } \omega_E : E \rightarrow \mathbb{R} \text{ with all values set to zero.}
7: \For \( v \in V \)
8: \quad \text{if } (T(v), H(v)) \in D_j \text{ then}
9: \quad \quad \omega_V(v) \leftarrow \text{NodeLives}_j(v)
10: \quad \text{end if}
11: \EndFor
12: \For \( e = (u, v) \in E \)
13: \quad \text{if } (T(u), H(u)), (T(v), H(v)) \in D_j \text{ then}
14: \quad \quad \omega_E(e) \leftarrow \min(\text{NodeLives}_j(u), \text{NodeLives}_j(v))
15: \quad \text{else if } (T(u), H(u)) \in D_j, (T(v), H(v)) \in D_k \text{ then}
16: \quad \quad \varepsilon \leftarrow \text{GetEpsIntersection}(D_j, D_k, T(u), T(v), M_{D_j}, M_{-D_j}, M_{D_k}, M_{-D_k})
17: \quad \quad \omega_E(e) \leftarrow \min(\text{NodeLives}_j(u), \text{NodeLives}_k(v), \varepsilon)
18: \quad \text{end if}
19: \EndFor
20: \Return \( (V, E, \omega_V, \omega_E) \)
\end{algorithmic}

The correctness of Algorithm 5 follows from the correctness of all our other previously defined algorithms. Next we analyze the time complexity.

- Line 1 and Line 2 each take \( KO(N \log N) \).
- Line 3 takes \( KO(N) \).
- Initializing the extremal event DAG in Line 4 takes \( O((NK)^2) \).
- Computing all the node weights in Line 7-Line 12 has a time complexity of \( O(NK) \).
- Each iteration in the for loop between Line 13-Line 21 takes at most \( O(N \log N) + O(N^2) \), since the number of vertices is bounded above by \( NK \), then the number of edges is bounded above by \( \binom{NK}{2} = \frac{(NK)(NK - 1)}{2} \). Thus, the number of iterations of this for loop is bounded by \( \binom{NK}{2} \).

In total, we get the time complexity to be

\[
KO(N \log N) + KO(N) + O((NK)^2) + O(NK) + \frac{(NK)(NK - 1)}{2}(O(N \log N) + O(N^2)) = O(N^2K^2 \log N) + O(N^4K^2).
\]

6.3. Computing Optimal Backbone Alignments. To compute a distance between extremal event DAGs, we align backbones in the extremal event DAGs in an optimal manner. Here, we describe how the alignment is computed and prove that the alignment is optimal. Recall, that \( \alpha \) denotes an alignment between two backbones (Definition 4.4).
Definition 6.7 (Alignment Matrix). Let \( \mathbf{x} = (x_1, x_2, \ldots, x_m) \), \( \mathbf{y} = (y_1, y_2, \ldots, y_n) \) be backbones. Note that each \( x_i \) can be written as the pair \( x_i = (s_{x,i}, w_{x,i}) \); likewise each \( y_i \) can be written as the pair \( y_i = (s_{y,i}, w_{y,i}) \). The alignment matrix, denoted \( \mathbf{mat} \), is an \((m+1) \times (n+1)\) matrix recursively defined as follows:

\[
\mathbf{mat}[i, j] = \begin{cases} 
0 & \text{if } i = j = 1 \\
\sum_{k=1}^{i-1} w_{x,k}, & \text{if } i > 1, j = 1 \\
\sum_{k=1}^{j-1} w_{y,k}, & \text{if } i = 1, j > 1 \\
\min \left\{ \begin{array}{l} 
\mathbf{mat}[i-1, j] + w_{x,i-1} \\
\mathbf{mat}[i, j-1] + w_{y,j-1} \\
\mathbf{mat}[i-1, j-1] + \text{diff}(x_{i-1}, y_{j-1}) \end{array} \right\} & \text{otherwise,}
\end{cases}
\]

where \( \text{diff}: \mathbf{x} \times \mathbf{y} \rightarrow \mathbb{R}_{\geq 0} \cup \{\infty\} \) is defined by

\[
\text{diff}((s_x, w_x), (s_y, w_y)) = \begin{cases} 
|w_x - w_y|, & \text{if } s_x = s_y \\
\infty, & \text{otherwise.}
\end{cases}
\]

Next we note that the bottom right entry in the alignment matrix is the minimum cost of aligning two backbones \( \mathbf{x} \) and \( \mathbf{y} \). This follows from [62]. Recall the definition of the cost function in Definition 6.6. We also prove Proposition 6.8 in Appendix 9.5.

Proposition 6.8 (Alignment Matrix Finds Minimum Cost). Let \( \mathbf{x} = (x_1, x_2, \ldots, x_m) \) and \( \mathbf{y} = (y_1, y_2, \ldots, y_n) \) be backbones. Let \( \mathbf{mat} \) be the \((m+1) \times (n+1)\) alignment matrix. Then, \( \mathbf{mat}[m+1, n+1] = c_{\mathbf{x}, \mathbf{y}}(m, n) \).

6.3.1. Finding Optimal Alignment from Alignment Matrix.

Definition 6.9 (Path). Let \( M \) be an \( m \times n \) matrix with real valued entries. A path in \( M \) is an injective function \( p: [k] \rightarrow M \) such that \( p(i) \) and \( p(i+1) \) are adjacent values in a row, column, or diagonal for all \( i \in \{1, 2, \ldots, k-1\} \).

To find an optimal alignment from the alignment matrix we construct a path via backtracking.

Path via Backtracking. Let \( \mathbf{x} = (x_1, x_2, \ldots, x_m) \) and \( \mathbf{y} = (y_1, y_2, \ldots, y_n) \) be backbones. Let \( \mathbf{mat} \) be the corresponding alignment matrix. We construct a path \( p \) in \( \mathbf{mat} \) recursively as follows:

- \( p(1) = \mathbf{mat}[m+1, n+1] \)
- If \( p(h) = \mathbf{mat}[i, j] \) for \( h \geq 1 \) and \( i, j > 1 \), then,

\[
p(h+1) = \begin{cases} 
\mathbf{mat}[i-1, j] & \text{if } \mathbf{mat}[i, j] = \mathbf{mat}[i-1, j] + w_{x,i-1} \\
\mathbf{mat}[i, j-1] & \text{if } \mathbf{mat}[i, j] = \mathbf{mat}[i, j-1] + w_{y,j-1} \\
\mathbf{mat}[i-1, j-1] & \text{if } \mathbf{mat}[i, j] = \mathbf{mat}[i-1, j-1] + \text{diff}(x_{i-1}, y_{j-1}) \end{cases}
\]

If multiple of the conditions hold, then define \( p(h+1) \) to be any one of them. We call \( p \) a backtracking path.

In summary, we are undoing the matrix construction to figure out which matrix entries lead to the cost in \( \mathbf{mat}[m+1, n+1] \). Once we apply backtracking, we have at least one path from \( \mathbf{mat}[m+1, n+1] \) to \( \mathbf{mat}[1, 1] \). We remark that backtracking is well-defined. For any entry \( p(h) = \mathbf{mat}[i, j] \), one of the three upper left entries \( \mathbf{mat}[i-1, j], \mathbf{mat}[i, j-1], \mathbf{mat}[i-1, j-1] \) equals \( p(h+1) \) by construction of the alignment matrix (Definition 6.7). Since we have a finite matrix, we eventually end at \( \mathbf{mat}[1, 1] \). We note that a path constructed from backtracking is not necessarily unique. For describing the alignment from a backtracking path \( p: [k] \rightarrow \mathbf{mat} \), we consider the reverse path \( p': [k] \rightarrow \mathbf{mat} \) where \( p'(i) = p(k - (i-1)) \).

Alignment from Backtracking. Let \( \mathbf{x} = (x_1, x_2, \ldots, x_m) \) and \( \mathbf{y} = (y_1, y_2, \ldots, y_n) \) be backbones. Let \( \mathbf{mat} \) be the corresponding alignment matrix. Let \( p : [k] \rightarrow \mathbf{mat} \) be a path computed from
backtracking and $p': [k] \to \text{mat}$ be the reverse path. We construct an alignment $\alpha: [k-1] \to \tilde{x} \times \tilde{y}$ such that

$$\alpha(h) = \begin{cases} (x_i, 0) & \text{if } p'(h) = \text{mat}[i, j] \text{ and } p'(h + 1) = \text{mat}[i + 1, j] \\ (0, y_j) & \text{if } p'(h) = \text{mat}[i, j] \text{ and } p'(h + 1) = \text{mat}[i, j + 1] \\ (x_i, y_j) & \text{if } p'(h) = \text{mat}[i, j] \text{ and } p'(h + 1) = \text{mat}[i + 1, j + 1] \end{cases}.$$ 

In other words, the following moves of $p'$ through the matrix $\text{mat}$ mean:

- Vertical move from $\text{mat}[i, j]$ to $\text{mat}[i + 1, j]$ indicates an alignment of $x_i$ with an insertion.
- Horizontal move from $\text{mat}[i, j]$ to $\text{mat}[i, j + 1]$ indicates an alignment of $y_j$ with an insertion.
- Diagonal move from $\text{mat}[i, j]$ to $\text{mat}[i + 1, j + 1]$ indicates an alignment of $x_i$ with $y_j$.

Next we verify that an alignment found from backtracking is indeed an alignment.

**Proposition 6.10 (Backtracking Finds an Alignment).** Let $x = (x_1, x_2, \ldots, x_m)$ and $y = (y_1, y_2, \ldots, y_n)$ be backbones. Let $\text{mat}$ be the $(m+1) \times (n+1)$ alignment matrix. Let $\alpha: [k] \to \tilde{x} \times \tilde{y}$ be an alignment found from backtracking. Then, $\alpha$ is an alignment.

**Proof.** We verify that $\alpha$ is well-defined, and $\alpha$ satisfies all four properties of being an alignment (Definition 4.4). Let $p': [k + 1] \to \text{mat}$ be the path used to construct $\alpha$.

First we show $\alpha$ is well-defined. Let $h \in [k - 1]$ and consider $\alpha(h)$. Observe exactly one of the three conditions (vertical move, horizontal move, diagonal move) that define $\alpha(h)$ holds by the construction of $p'$, and $\alpha(h) \in \tilde{x} \times \tilde{y}$. Hence, $\alpha$ is well-defined.

Observe by construction, $\alpha$ has no null alignments. Hence, Property (1) of Definition 4.4 holds. Next we show the remaining properties.
Property [2] (Preserves Order of Backbones). We use the index function $i_x$ and the coordinate function $\alpha_x$ from Definition 4.1. Suppose $\alpha_x(i), \alpha_x(j) \in \mathbf{x}$ where $i < j$. Suppose further that $p'(i) = \text{mat}[q,r]$ and $p'(j) = \text{mat}[s,t]$, indicating that $\alpha_x(i) = x_q, \alpha_x(j) = x_s$. By construction of $p'$ and the fact that $i < j$, either (1) $q = s$ and $r < t$ or (2) $q < s$. We claim that only (2) holds in our setting.

Assume for a contradiction that $q = s$ and $r < t$. By construction of $p'$, this means that there are only horizontal moves between $p'(i)$ and $p'(j)$. Hence, $\alpha_x(i)$ or $\alpha_x(j)$ must be the empty node. This contradicts the assumption that both $\alpha_x(i)$ and $\alpha_x(j)$ are in $\mathbf{x}$. Therefore $q < s$, and in particular, $q < s$ if and only if $i < j$.

Since $\alpha_x(i) = x_q$ and $\alpha_x(j) = x_s$, we have the index function $i_x(\alpha_x(i)) = q$ and $i_x(\alpha_x(j)) = s$ if and only if $i_x(\alpha_x(i)) < i_x(\alpha_x(j))$. Therefore $i_x(\alpha_x(i)) < i_x(\alpha_x(j))$ if and only if $i < j$, so that $\alpha$ preserves the order of nodes in the backbone $\mathbf{x}$. The same argument substituting $y$ for $x$ also shows that $\alpha$ preserves the order of nodes in the backbone $\mathbf{y}$.

Property [3] (No Misalignments). By design of $\text{mat}$, a misalignment has an infinite cost. Since each entry in the alignment matrix is a minimum of three values where at least two values are finite, then $\text{mat}$ does not contain any infinite entries. This implies that when applying backtracking, we never have a diagonal move corresponding to a misalignment.

Property [4] (Restriction to Matching). Let $x_i \in \mathbf{x}$. By definition of backtracking, there exists exactly one $j \in [k+1]$ such that $p'(j) = \text{mat}[i+1,h]$ where $h \in [n+1]$. This implies that $x_i$ appears in $\text{im}(\alpha_x)$ exactly once. Similarly, for $y_i \in \mathbf{y}$, there exists exactly one $j \in [k+1]$ such that $p'(j) = \text{mat}[h,j+1]$ where $h \in [m+1]$. Hence $y_i$ appears in $\text{im}(\alpha_y)$ exactly once. Therefore we have a restriction to matching.

We now prove that an alignment found using this backtracking has a cost equal to $\text{mat}[m + 1, n + 1]$.

Proposition 6.11 (Backtracking Finds Alignment with Cost Computed from Alignment Matrix). Let $\mathbf{x} = (x_1, x_2, \ldots, x_m)$ and $\mathbf{y} = (y_1, y_2, \ldots, y_n)$ be backbones. Let $\text{mat}$ be the $(m + 1) \times (n + 1)$ alignment matrix. Let $\alpha : [k] \rightarrow \mathbf{x} \times \mathbf{y}$ be an alignment found from backtracking. Then, $\text{cost}(\alpha) = \text{mat}[m + 1, n + 1]$.

Proof. We show $\text{cost}(\alpha) = \text{mat}[m + 1, n + 1]$. To do this, we prove $\text{cost}(\alpha[1 : h]) = p'(h + 1)$ for all $h \leq k$ by induction. For the base case, consider $\alpha[1 : 1] = \alpha(1)$. There are three possibilities for $\alpha(1)$. Either:

1. $\alpha(1) = (x_1, 0)$
2. $\alpha(1) = (0, y_1)$
3. $\alpha(1) = (x_1, y_1)$.

Recall that $x_i \in \mathbf{x}$ can be expanded as $x_i = (s_{x,i}, w_{x,i})$; likewise, for $y_i \in \mathbf{y}$, we can write $y_i = (s_{y,i}, w_{y,i})$. If (1), then $\text{cost}(\alpha(1)) = w_{x,1} = \text{mat}[2, 1] = p'(2)$. If (2), then $\text{cost}(\alpha(1)) = w_{y,1} = \text{mat}[1, 2] = p'(2)$. If (3), then $\text{cost}(\alpha(1)) = \text{diff}(x_1, y_1) = \text{mat}[2, 2] = p'(2)$. In all three cases we find $\text{cost}(\alpha(1)) = p'(2)$.

Next, we assume the induction hypothesis that $\text{cost}(\alpha[1 : h]) = p'(h + 1)$ for some $h < k$.

Suppose $p'(h + 1) = \text{mat}[i, j]$. There are three possibilities for $\alpha(h + 1)$. Either

1. $\alpha(h + 1) = (x_i, 0)$
2. $\alpha(h + 1) = (0, y_j)$
3. $\alpha(h + 1) = (x_i, y_j)$.

If (1), then

$\text{cost}(\alpha[1 : h + 1]) = \text{cost}(\alpha[1 : h]) + w_{x,i} = p'(h + 1) + w_{x,i} = \text{mat}[i, j] + w_{x,i} = p(h + 2)$.
If (2), then
\[ \text{cost}(\alpha[1:h+1]) = \text{cost}(\alpha[1:h]) + w_{y,j} = p'(h+1) + w_{y,j} = \text{mat}[i,j] + w_{y,j} = p'(h+2). \]

If (3), then
\[ \text{cost}(\alpha[1:h+1]) = \text{cost}(\alpha[1:h]) + \text{diff}(x_i,y_j) = p'(h+1) + \text{diff}(x_i,y_j) = \text{mat}[i,j] + \text{diff}(x_i,y_j) = p'(h+2). \]

All equalities follow from either the induction hypothesis or construction of \( p' \).

By induction, \( \text{cost}(\alpha[1:h]) = p'(h+1) \) for all \( h \leq k \). In particular,
\[ \text{cost}(\alpha[1:k]) = \text{cost}(\alpha) = p'(k+1) = \text{mat}[n+1,n+1]. \]

Observe that Proposition 6.8 and Proposition 6.11 give the following corollary.

**Corollary 6.12** (Backtracking Finds Optimal Alignment). Let \( \mathbf{x} = (x_1, x_2, \ldots, x_m) \) and \( \mathbf{y} = (y_1, y_2, \ldots, y_n) \) be backbones. Let \( \text{mat} \) be the \((m+1) \times (n+1)\) alignment matrix. Let \( \alpha : [k] \rightarrow \tilde{x} \times \tilde{y} \) be an alignment found from backtracking. Then \( \text{cost}(\alpha) = c_{x,y}(m,n) \).

6.3.2. **Time Complexity of Computing Backbone and Extremal Event DAG Distance.** Using the dynamic program above, we can compute the backbone distance in \( O(mn) \) time where \( m \) and \( n \) are the lengths of the two backbones. However, since backbone alignments are not always unique, then computing all optimal backbone alignments can become costly.

When computing the extremal event DAG distance, we must compute the optimal backbone alignments that minimize the difference in weights over all possible aligned edges. Since we could have multiple optimal backbone alignments, then computing the extremal event DAG distance in the worst case is expensive. However, we have found empirically for the applications below that almost always there is a unique optimal alignment. This then results in a polynomial time complexity for computing the extremal event DAG distance.

7. **Applications**

We apply the extremal event DAG construction and distance to two applications: (1) quantifying similarity in replicate experiments of microarray yeast cell cycle data and (2) providing quantitative evidence that an intrinsic oscillator drives the blood stage cycle of the malaria parasite \( Plasmodium falciparum \). These two datasets were analyzed in \([4]\) and \([55]\), respectively, using a directed maximal common edge subgraph (DMCES) metric that compared \( \varepsilon \)-DAGs (recall \( \varepsilon \)-DAGs described after Definition 3.2) with a sequence of fixed \( \varepsilon \). Because of the computational complexity of computing the DMCES metric, these calculations were done on a limited number of time series with a limited number of extrema per time series, i.e., on less noisy data. Additionally, since the \( \varepsilon \)-DAGs specify a value of a parameter \( \varepsilon \), the experiments were performed over a range of \( \varepsilon \) between 0 and 0.15. The construction of extremal event DAGs does not need the value of \( \varepsilon \) to be specified. Additionally, both the extremal event DAG construction and distance are computed in polynomial time as opposed to the exponential time complexity of the DMCES metric. This all means we can compute distances over much larger sets of genes in a significantly shorter amount of time.

7.1. **Yeast Cell Cycle Data.** The first dataset consists of microarray time series transcriptomics from the yeast \( Saccharomyces cerevisiae \), published in \([43]\). The yeast cell cycle is well studied and has experimental validation \([21, 9, 22, 52]\). The amplitude of the data has been normalized between -0.5 and 0.5 and its phase has been shifted by alignment using CLOCCS analysis, see “Appendix A: Yeast Data Analysis” in \([4]\). Using the CLOCCS analysis, the replicate experiments were aligned so that the time series start at the same point in the yeast cell cycle. Furthermore, the data were truncated to one period so that the data analysis focuses on the extrema from a
synchronized cell population, since the production of daughter cells causes increasing levels of cell
division asynchrony that reduces the periodic signal. We analyze two collections of time series data
$D_1$ and $D_2$ that each consists of 16 genes and 265 time points.

We perform three different comparison computations:

1. We focus on a subset of $D_1$ and $D_2$ that consists of the time series for four genes: SWI4,
   YOX1, NDD1, and HCM1. We denote these sub-datasets as $D'_1$ and $D'_2$ respectively. We
   then compute the extremal event DAG distance between the extremal event DAGs of $D'_1$
   and $D'_2$,

   $$d_{ED}(\text{DAG}(D'_1), \text{DAG}(D'_2)).$$

2. We consider dataset $D'_2$ but switch labels between time series for CLB2 and YOX1. We
   call this mislabeled dataset $D'_3$. Then we compute

   $$d_{ED}(\text{DAG}(D'_1), \text{DAG}(D'_3)).$$

   The comparison between $d_{ED}(\text{DAG}(D'_1), \text{DAG}(D'_2))$ to $d_{ED}(\text{DAG}(D'_1), \text{DAG}(D'_3))$ indicates
   the impact of the replacement of one time series by another on the extremal event DAG
   distance.

3. Lastly, we assess the distance between the full datasets $D_1$ and $D_2$ by constructing a baseline
   distribution for the expected distance. We do this by first by scrambling the gene names in
   $D_2$ to create a dataset $\hat{D}_2$. We then compute

   $$d_{ED}(\text{DAG}(D_1), \text{DAG}(\hat{D}_2)).$$

   We repeat this computation 100 times for 100 random name assignments. This experiment
   gives us an idea on the range of possible distances between $D_1$ and $D_2$. We then compare
   this distribution to the actual distance

   $$d_{ED}(\text{DAG}(D_1), \text{DAG}(D_2)).$$

Since the extremal event DAG distance can be any non-negative number, it can be difficult to
discern how similar $D_1$ and $D_2$ are solely based on computing $d_{ED}(\text{DAG}(D_1), \text{DAG}(D_2))$. To gain
a better understanding of how similar $D_1$ and $D_2$ are, we perform computation (3) to get a baseline
distribution of distances between the time series in $D_1$ and time series in $D_2$. This distribution can
then be used as a null hypothesis $H_0$ for testing $H_1$ that $D_1$ and $D_2$ measure gene expression in the
identically behaving cell in the same environmental condition.

**Computations 1 & 2.** We computed

$$d_{ED}(\text{DAG}(D'_1), \text{DAG}(D'_2))) = 10.34$$

$$d_{ED}(\text{DAG}(D'_1), \text{DAG}(D'_3))) = 15.48.$$ 

The mismatched gene dataset causes a 50% increase in distance even though only 25% of the dataset
was perturbed, a substantial change. This result is consistent with the result from numerical
experiment 3 in [4] where the same data were analyzed using $\varepsilon$-DAGs and the DMCES metric.
Specifically, DMCES similarity was computed between the $\varepsilon$-DAGs at $\varepsilon$ values ranging between 0
and 0.15. A similarity score of one indicated that the $\varepsilon$-DAGs are equal whereas a similarity score
of 0 indicates the $\varepsilon$-DAGs are very dissimilar. The similarity ranged between 0.7 and 1 for $D'_1$
and $D'_2$, whereas the similarity ranged between 0.4 and 0.6 for $D'_1$ and $D'_3$. The same qualitative
conclusion can be drawn from our results and the earlier work; namely that replacing one time
series with another decreases similarity, or increases distance, between datasets.

**Computation 3.** After computing $d_{ED}(\text{DAG}(D_1), \text{DAG}(D_2))$ 100 times we get the distribution
of distances shown in Figure 14 with the following statistics

- Maximum Distance = 384.30
- Mean Distance = 341.90
Figure 14. Extremal Event DAG Distances in Experiment 3. The red bar is $d_{ED}(\text{DAG}(D_1), \text{DAG}(D_2))$, the distance between the two yeast datasets without any scrambling of genes.

- Minimum Distance = 273.95
- Standard Deviation = 23.14

We found $d_{ED}(\text{DAG}(D_1), \text{DAG}(D_2)) = 150.44$. Therefore $d_{ED}(\text{DAG}(D_1), \text{DAG}(D_2))$ is roughly eight standard deviations (see Figure 14) below the mean of the estimated null distribution, which suggests that there is a significant amount of similarity between $D_1$ and $D_2$. In numerical experiment 4 in [4], the same goal of measuring replicate similarity was approached using a different technique. Subsets of 4 and 8 genes out of the 16 total were used to construct $\varepsilon$-DAGs over the range of $\varepsilon$ 0-0.15. No baseline was calculated, but the computations showed a mean similarity that was usually over the relatively high value of 80% and frequently over 90%.

Overall, the results of these three computations are consistent with the numerical experiments in [4]. We offer the significant improvement that we did not need to run each of these computations over a range of $\varepsilon$ because the extremal event DAG construction does not depend on $\varepsilon$. Because of the vast increase in computational efficiency, we were able to perform computation 3 using all 16 genes in the two datasets instead of randomly sampled subsets. It was shown in [4] that using subsets of increasing size decreased variance in the subsampled computations rather than substantially changing mean performance, which was taken to be evidence that subsampling was a good proxy for the distance between $D_1$ and $D_2$. In other words, if the DMCES method could have computed the distance between $D_1$ and $D_2$, then increasing the size of the subsamples would show convergence to that value. We offer a method that does not require a convergence argument, but rather can compute the value directly.

7.2. Malaria Parasite Data. In this application, we seek to show that oscillatory genes in strains of Plasmodium falciparum maintain as much of a phase ordering as well known circadian genes across various mouse tissues. This provides circumstantial evidence that malaria parasites have an internal clock that is at least as conserved as that of the circadian oscillator, as shown in [55]. The mouse data comes from [65] that contains the circadian transcriptomes of 12 mouse organ tissues every two hours for 48 hours. In [55], similarity between datasets within malaria or mouse was determined by choosing “reference datasets” to which the other strains and tissues were compared,
as opposed to computing all pairwise comparisons. The 3D7 strain and the liver tissue were chosen as the reference datasets in \textit{Plasmodium falciparum} and the mouse tissues respectively.

In both collections of time series, subsets of periodic genes were selected that peak at similar times across parasite strains or mouse tissues. These genes are called “in-phase” subsets. After this subset of genes was found, all datasets were interpolated with piecewise cubic Hermite interpolating polynomial spline to one hour intervals. The data were wrapped so that there could be a common starting point. Furthermore, \textit{Plasmodium falciparum} was down-sampled by removing every odd datapoint. More details on the experiments and data preprocessing can be found in the supplementary materials of [55]. After the pre-processing steps, our time series contain 119 parasite genes and 107 mouse genes.

To gain a better understanding of how similar our datasets are, we created a baseline distribution for each strain or tissue by randomly interchanging gene names and shifting each time series by a random amount, using the same random shifts as in [55]. Specifically, if we view the values of a time series as an ordered list \( h_1, h_2, \ldots, h_n \) of length \( n \), we randomly select \( 1 \leq m \leq n \) to create a new shifted time series
\[
( h_m, h_{m+1}, \ldots, h_n, h_1, h_2, \ldots, h_{m-1} ).
\]
The phase shift operation preserves characteristics of the dataset except for the ordering of extrema. For each strain and tissue, the baseline distance was computed between the unpermuted and unshifted reference dataset and the permuted and shifted datasets.

We use the following notation for the parasite datasets:
- Let \( D_1 \) be the collection of time series from strain 3D7. This is the reference dataset.
- Let \( D_2 \) be the collection of time series from strain FVO-NIH.
- Let \( D_3 \) be the collection of time series from strain SA250.
- Let \( D_4 \) be the collection of time series from strain D6.
- Let \( D'_2 \) be the collection of shifted and permuted time series of \( D_2 \).
- Let \( D'_3 \) be the collection of shifted and permuted time series of \( D_3 \).
- Let \( D'_4 \) be the collection of shifted and permuted time series of \( D_4 \).

We perform the following computations to study the parasite data.

1. Pick 1500 random subsets of 15 genes. With the arbitrary choice of 15 genes fixed, let \( \hat{D}_i \) denote the subset of the corresponding time series from \( D_i \) for \( i \in \{1, 2, 3, 4\} \). Compute
\[
d_{ED}(\text{DAG}(\hat{D}_1), \text{DAG}(\hat{D}_j))
\]
for each random subset and each \( j \in \{2, 3, 4\} \).

2. Pick a new set of 1500 random subsets of 15 genes, where \( \hat{D}_i \) for \( i \in \{1, 2, 3, 4\} \) is defined as above for each subset. Let \( \hat{D}'_j \) denote the subset of the shifted and permuted time series \( D'_j \) for \( j \in \{2, 3, 4\} \). Compute \( d_{ED}(\text{DAG}(\hat{D}_1), \text{DAG}(\hat{D}'_j)) \) for each random subset and \( j \in \{2, 3, 4\} \).

We do analogous experiments to study the mouse gene data. We use the following notation.
- Let \( D_a \) be the collection of time series recorded from liver tissue. This is the reference dataset.
- Let \( D_b \) be the collection of time series recorded from kidney tissue.
- Let \( D_c \) be the collection of time series recorded from lung tissue.
- Let \( D'_b \) be the collection of shifted and permuted time series of \( D_b \).
- Let \( D'_c \) be the collection of shifted and permuted time series of \( D_c \).

We perform the following experiments to study the mouse tissue data.

1. Pick 1500 random subsets of 15 genes. Let \( \hat{D}_i \) denote the subset of the corresponding time series from \( D_i \) for \( i \in \{a, b, c\} \). Compute \( d_{ED}(\text{DAG}(\hat{D}_a), \text{DAG}(\hat{D}_j)) \) for each random subset and \( j \in \{b, c\} \).
(2) Pick a new set of 1500 random subsets of 15 genes, where \( \hat{D}_i \) for \( i \in \{1, 2, 3, 4\} \) is defined as above for each subset. Let \( \hat{D}'_j \) denote the subset of the shifted and permuted time series \( \mathcal{D}'_j \) for \( j \in \{b, c\} \). Compute \( d_{ED}(\text{DAG}(\hat{D}_a), \text{DAG}(\hat{D}'_j)) \) for each random subset and \( j \in \{b, c\} \).

We summarize the results of the experiments below and provide more statistics in Appendix 9.6.

In Figure 15 and Figure 16, we see in general that the baseline distances are larger than the distances between cell lines and reference cell line.

**Figure 15.** Histograms from *Plasmodium falciparum* experiments. The reference strain was 3D7 for all experiments. The distribution of baseline extremal event DAG distances is shown in blue for each graph and the distribution of extremal event DAG distances is shown in purple. In all three plots, the extremal event DAG distances are smaller than the corresponding baseline distances. Performing a paired t-test to the blue and purple distributions with a null hypothesis that the distributions are the same in all three plots resulted in a \( p \)-value below machine precision.

**Figure 16.** Histograms from mouse experiments. The reference cell line was liver for all experiments. The distribution of baseline extremal event DAG distances is shown in blue for each graph and the distribution of extremal event DAG distances is shown in purple. In all three plots, we see the extremal event DAG distances are smaller than the corresponding baseline distances. Performing a paired t-test to the blue and purple distributions with a null hypothesis that the distributions are the same in all three plots resulted in a \( p \)-value below machine precision.

Overall, we find the extremal event DAG distances from the parasite experiments to be smaller than the extremal event DAG distances from the mouse experiments, both in absolute value and in terms of distribution overlap, as found in [55], indicating support for a malarial clock. Additionally, Figure 15 shows another pattern seen in [55], which is that the D6 data have the smallest distance to
the 3D7 reference data and that SA250 has the largest distance to 3D7 compared both in absolute value and to their respective baselines.

In this computation, we used subsampling to computationally handle the size of dataset, as in [55], and computed 1500 samples instead of 5000. However, we used more than double the genes in our samples, 15 versus 6, and incorporated information about all levels of \( \varepsilon \) instead of only a small fixed subset of \( \varepsilon \). The consistency of results found between the computations validates the methodology of using extremal event DAGs in place of \( \varepsilon \)-DAGs.

8. Conclusion

We constructed a weighted directed graph descriptor of collections of time series data that keeps track of the order and prominence of extrema, and is robust to experimental noise that arises from taking discrete time samples of a continuous process. Furthermore, we define a distance between these extremal event DAGs that constructs an extremal event supergraph using a modified version of the edit distance and then computes the distance by taking the \( L_1 \) distance between aligned node and edge weights in the extremal event supergraph. The benefit of this distance is that it can be computed via dynamic programming and therefore can be computed efficiently. We used this distance to compare the similarity of experimental replicates in yeast cell cycle data, the similarity of circadian gene expression in different mouse tissues, and the similarity of gene expression across malaria parasite strains. Our results are consistent with results from other literature [4, 55] that used directed maximal common edge subgraphs of \( \varepsilon \)-DAGs [42]. The benefit to using the extremal event DAG methodology is that the savings in memory and computation speed facilitates the analysis of significantly larger datasets.

Furthermore, we prove several stability results. In particular, the backbone distance arising from two functions is bounded by the \( L_\infty \) distance of the two functions multiplied by the number of nodes in the backbone infinity alignment. Using backbone stability, we prove the extremal event DAG distance is stable in a local case. Local here means that the individual time series in one collection differs from the corresponding time series in the other collection by the amount that allows direct alignment of the minima and maxima between the two time series. Additionally, one of the time series can have small amplitude additional maxima and minima. Extension of the local stability result to a stability between arbitrary multivariate time series is challenging. Theoretically, one needs a way to globally compare distances between multivariate time series. If the triangle inequality for the extremal event DAG distance holds, then the local stability of the extremal event DAG can be used to prove a global stability result using the same technique as in the proof of backbone stability (Theorem 5.12). While in this paper we define the extremal event DAG distance using the \( L_1 \) norm, we suspect that stability also holds if we use any \( L_p \) norm. We leave this generalization as future work.

We focus on a descriptor that is robust to measurement error that arises from taking discrete time samples of a continuous process. However, there can be other types of uncertainty present in the data. One type is related to signal processing and is seen as small peaks in the data. If we want to remove this type of measurement errors from our analysis, we can apply a preprocessing step using techniques from [40]. This technique applies sublevel set persistence to a time series to determine a node life threshold. Nodes with a node life below the threshold are classified as results of signal processing errors, or as noise. Eliminating nodes classified as noise and then computing extremal event DAGs gives a smaller descriptor of a collection of time series that further increases the size of computationally feasible datasets. Similar preprocessing steps to remove small peaks can be made using Fourier transforms [6, 25].

In summary, extremal event DAGs are a new computational tool that can be used alone or in combination with noise reduction algorithms to summarize and compare collections of time series data.
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Let $F$ be a collection of nicely tame functions where $t^i_1 < t^i_2 < \cdots < t^i_{k_i}$ are all the domain coordinates of the local extrema of $f_i$. Let $\text{DAG}(F) := (V,E,\omega_V,\omega_E)$ be the extremal event $\text{DAG}$ of $F$. Let $(v(i,j),v(c,d)) \in E$. Suppose $i = c$, $\varepsilon < \min\{\omega_V(v(i,j)),\omega_V(v(c,d))\}$, and $\phi^c_{\varepsilon}(t^i_j) \cap \phi^c_{\varepsilon}(t^i_d) = \emptyset$. Then $t^i_j$ and $t^i_d$ are comparable.

Proof. Since $i = c$ in this case, we omit the superscripts $i$ and $c$ of $t^i_j$ and $t^i_d$. Additionally we set $f := f_i$. Furthermore, we omit the subscript and superscript $f$ from the functions $\text{pers}_f$ and $\phi^f_{\varepsilon}$.

By Proposition 1 and Theorem 2 of [4], one of $t_j$ or $t_d$ is the domain coordinate of a local maximum while the other is the domain coordinate of a local minimum, and these two extrema are adjacent, i.e., there are no extrema of $f$ between $t_j$ and $t_d$. Without loss of generality, suppose $(t_j,f(t_j))$ is a local maximum, $(t_d,f(t_d))$ is a local maximum, and $t_j < t_d$. By way of contradiction, suppose $t_j$ and $t_d$ are incomparable. Since we assume that the first two requirements of Definition 3.1 are satisfied, it is the third condition that is violated. Therefore it is not true that $t_j \preceq_{\varepsilon} t_d$ nor is it true that $t_d \preceq_{\varepsilon} t_j$. Since $t_j < t_d$, there exists $g \in N_\varepsilon(f)$ such that for every $t^i_j \in \varphi^c_\varepsilon(t_j)$ that is a domain coordinate of a local minimum of $g$, and $t^i_d \in \varphi^c_\varepsilon(t_d)$ that is a domain coordinate of a local maximum of $g$, we have $t^i_j > t^i_d$. Consider such $t^i_j$ and $t^i_d$ that are adjacent.

We claim that $g(t^i_j) > f(t_d) - \varepsilon$. On the contrary, suppose $g(t^i_j) \leq f(t_d) - \varepsilon$. We show there exists a local maximum $(t^i_g,g(t^i_g))$ such that $t^i_g \in \varphi^c_\varepsilon(t_d)$ and $t^i_g < t^i_j$, which contradicts the assumption $t_j$ and $t_d$ are incomparable.

Since $g \in N_\varepsilon(f)$, we have $f(t_d) - \varepsilon < g(t_d)$. Hence, $g(t^i_j) < g(t_d)$. Suppose $C = [a,b]$ where $a,b \in \mathbb{R}$. We discuss two cases: either $t_d = b$ or $t_d \neq b$. We prove Case 1 that $t_d \neq b$. By definition of $\varepsilon$-extremal intervals, $f\left(\text{right}(\varphi^c_\varepsilon(t_d))\right) + \varepsilon = f(t_d) - \varepsilon$. Since $g \in N_\varepsilon(f)$,

$$g\left(\text{right}(\varphi^c_\varepsilon(t_d))\right) < f\left(\text{right}(\varphi^c_\varepsilon(t_d))\right) + \varepsilon = f(t_d) - \varepsilon.$$
Recall, \( f(t_d) - \varepsilon < g(t_d) \). Therefore, \( g(\varphi(\varepsilon(t_d))) < g(t_d) \). By Statement (3) of Lemma 3.3, we have \( t_d \notin \varphi(\varepsilon(t_d)) \). Hence, \( t_j' < t_d \). Furthermore, by assumption \( t_d' < t_j' \) where \( t_d' \in \varphi(\varepsilon(t_d)) \). Hence, \( t_j' > t_d' > \left( \varphi(\varepsilon(t_d)) \right) \) and \( t_j' < t_d < \right( \varphi(\varepsilon(t_d)) \). Thus, \( t_j' \in \varphi(\varepsilon(t_d)) \). All together we have, 
\[
\begin{align*}
t_j' &< t_d < \right( \varphi(\varepsilon(t_d)) ), \\
g(t_j') &< g(t_d), \\
g(t_d) &> g(\right( \varphi(\varepsilon(t_d)) )).
\end{align*}
\]
This and the assumption \( g \) is nicely tame implies there exists a local maximum \((t'_g, g(t'_g))\) such that \( t_g' \in (t_j', \right( \varphi(\varepsilon(t_d)) )) \). Hence, \( t_g' \in \varphi(\varepsilon(t_d)) \) and \( t_j' < t_g' \).

We prove Case 2 \( t_d = b \). Since \( g \in N(\epsilon)(f) \), \( g(t_d) = g(b) \in (f(b) - \epsilon, f(b) + \epsilon) \). By assumption, \( g(t_j') \leq f(b) - \epsilon < g(b) \). Using the same reasoning as in the case \( t_d \neq b \), we find \( t_j' > \left( \varphi(\varepsilon(b)) \right) \) and \( t_j' < b \). Altogether we can conclude there exists a local maximum \( t_g' \in (t_j', b) \subset \varphi(\varepsilon(b)) \) of \( g \).

In both cases \( t_d = b \) and \( t_d \neq b \) we find there exists a local maximum \((t'_g, g(t'_g))\) such that \( t'_g \in \varphi(\varepsilon(t_d)) \) and \( t_j' < t_g' \). This shows that \( t_j \leq \epsilon \) \( t_d \), which is a contradiction.

Therefore the claim 
\[
g(t_j') > f(t_d) - \epsilon
\]
holds. A similar argument can be used to show 
\[
g(t_j) < f(t_j) + \epsilon.
\]
By Statement (3) of Lemma 3.3, \( t_j \notin \varphi(\varepsilon(t_d)) \) since \( \epsilon \leq \min \{ \omega(x(j)), \omega(x(c, d)) \} = \frac{1}{2} \min \{ \text{pers}(t_j), \text{pers}(t_d) \} \).

Applying Statement (2) of Lemma 3.3, we get \( \epsilon \leq \frac{1}{2} (f(t_d) - f(t_j)) \). Hence,
\[
\begin{align*}
g(t_j) &> f(t_d) - \epsilon \geq \frac{1}{2} (f(t_d) + f(t_j)) \\
g(t_j') &< f(t_j) + \epsilon \leq \frac{1}{2} (f(t_d) + f(t_j))
\end{align*}
\]
This implies that 
\[
g(t_j') < g(t_j')
\]
Since \( t_j < t_j' \) and \((t'_g, g(t'_g))\) is a local maximum while \((t_j', g(t_j'))\) is local minimum of \( g \), there must exist domain coordinates of a local minimum and maximum of \( g \) between \( t_j' \) and \( t_j' \). Hence, we reach a contradiction with the assumption that \( t_j' \) and \( t_j' \) are adjacent extrema. Therefore, we conclude that \( t_j \) and \( t_d \) are comparable.

\[
\square
\]

9.2. Backbone Infinity Distance is A Metric. We show the backbone infinity distance is a metric. We start by proving that the triangle inequality holds.

**Lemma 9.2** (Backbone Infinity Distance Satisfies Triangle Inequality). Let \( x, y, z \) be backbones. Then,
\[
d_{B_{\infty}}(x, z) \leq d_{B_{\infty}}(x, y) + d_{B_{\infty}}(y, z)
\]

**Proof.** Let \( \alpha_1 : [k] \to \bar{x} \times \bar{y}, \alpha_2 : [m] \to \bar{y} \times \bar{z} \) be optimal alignments. Consider the composition alignment \( \alpha_2 \circ \alpha_1 \) from Construction 4.9. Define \( A \) as in Construction 4.9.
\[
A_{A_{x}} := \{(x, y) \in \text{im}(\alpha_{1}) | \exists z \in z \text{ s.t. } (y, z) \in \text{im}(\alpha_{2})\},
\]
and
\[
A_{A_{z}} := \{(y, z) \in \text{im}(\alpha_{2}) | \exists x \in x \text{ s.t. } (x, y) \in \text{im}(\alpha_{1})\}.
\]

Let
\[
C_1 := \max_{(x, z) \in \text{im}(\alpha_{2})\text{im}(\alpha_{1})} \{|w_x - w_z|\}, \quad C_2 = \max_{(x, 0) \in \text{im}(\alpha_{2}) \text{im}(\alpha_{1})} \{|w_x|\}, \quad C_3 = \max_{(0, z) \in \text{im}(\alpha_{2}) \text{im}(\alpha_{1})} \{|w_z|\}.
\]
Because \( d_{B_{\infty}}(x, z) \) is computed from an optimal alignment between \( x \) and \( z \), then
\[
d_{B_{\infty}}(x, z) \leq \max\{C_1, C_2, C_3\}.
\]
Suppose \( \max\{C_1, C_2, C_3\} = C_1 \). Let \((x, z) \in \im(\alpha_2 \circ \alpha_1)\) such that \(|w_x - w_z| = C_1\). Observe since \((x, z) \in \im(\alpha_2 \circ \alpha_1)\) then there exists \(y \in y\) such that \((x, y) \in \im(\alpha_1)\) and \((y, z) \in \im(\alpha_2)\). This observation and the triangle inequality from the \(L_1\)-norm implies
\[
|w_x - w_z| \leq |w_x - w_y| + |w_y - w_z| \leq d_{B_\infty}(x, y) + d_{B_\infty}(y, z).
\]
Hence, in the case \(\max\{C_1, C_2, C_3\} = C_1\), we have \(d_{B_\infty}(x, z) \leq d_{B_\infty}(x, y) + d_{B_\infty}(y, z)\).

Next, suppose \(\max\{C_1, C_2, C_3\} = C_2\). Let \((x, 0) \in \im(\alpha_2 \circ \alpha_1)\) such that \(w_x = C_2\). Define
\[
X_{(y, 0)} := \{(x, 0) \in \im(\alpha_2 \circ \alpha_1) \mid \exists y \in y \text{ s.t. } (x, y) \in \im(\alpha_1) \setminus A_x\}.
\]
Observe, if \((x, y) \in \im(\alpha_1) \setminus A_x\), then for all \(z \in z\), \((y, z) \notin \im(\alpha_2)\). Hence, \((y, 0) \in \im(\alpha_2)\). This implies the set
\[
(x \times \{0\}) \cap \im(\alpha_2 \circ \alpha_1) = ((x \times \{0\}) \cap \im(\alpha_1)) \cup X_{(y, 0)}
\]
and this union is disjoint. Either \((x, 0) \in (x \times \{0\}) \cap \im(\alpha_1)\) or \((x, 0) \in X_{(y, 0)}\). If \((x, 0) \in (x \times \{0\}) \cap \im(\alpha_1)\), then
\[
C_2 = w_x \leq d_{B_\infty}(x, y) \leq d_{B_\infty}(x, y) + d_{B_\infty}(y, z).
\]
Now suppose \((x, 0) \in X_{(y, 0)}\). By definition of \(X_{(y, 0)}\), there exists \(y \in y\) such that \((x, y) \in \im(\alpha_1) \setminus A_x\) and, at the same time, \((y, 0) \in \im(\alpha_2)\). Noting this observation and applying the triangle inequality from the \(L_1\)-norm gives
\[
w_x \leq |w_x - w_y| + w_y \leq d_{B_\infty}(x, y) + d_{B_\infty}(y, z).
\]
We can conclude that in the case \(\max\{C_1, C_2, C_3\} = C_2\) that \(d_{B_\infty}(x, z) \leq d_{B_\infty}(x, y) + d_{B_\infty}(y, z)\).

Lastly, suppose \(\max\{C_1, C_2, C_3\} = C_3\). Let \((0, z) \in \im(\alpha_2 \circ \alpha_1)\) such that \(w_z = C_3\). Define
\[
Z_{(0, y)} := \{(0, z) \in \im(\alpha_2 \circ \alpha_1) \mid \exists y \in y \text{ s.t. } (y, z) \in \im(\alpha_2) \setminus A_y\}.
\]
Similarly, the set
\[
(\{0\} \times z) \cap \im(\alpha_2 \circ \alpha_1) = ((\{0\} \times z) \cap \im(\alpha_2)) \cup Z_{(0, y)}
\]
and this union is disjoint. Either \((0, z) \in (\{0\} \times z) \cap \im(\alpha_2)\) or \((0, z) \in Z_{(0, y)}\). If \((0, z) \in (\{0\} \times z) \cap \im(\alpha_2)\), then
\[
C_3 = w_z \leq d_{B}(y, z) \leq d_{B}(x, y) + d_{B}(y, z).
\]
Now suppose \((0, z) \in Z_{(0, y)}\). By definition of \(Z_{(0, y)}\), there exists \(y \in y\) such that \((y, z) \in \im(\alpha_2) \setminus A_y\) and \((0, y) \in \im(\alpha_1)\). Noting this observation and applying the triangle inequality from the \(L_1\)-norm, we get
\[
w_z \leq |w_z - w_y| + w_y \leq d_{B_\infty}(y, z) + d_{B_\infty}(x, y).
\]
We can conclude in the case \(\max\{C_1, C_2, C_3\} = C_3\) that \(d_{B_\infty}(x, z) \leq d_{B_\infty}(x, y) + d_{B_\infty}(y, z)\).

Therefore, the backbone infinity distance satisfies the triangle inequality. \(\square\)

**Proposition 9.3 (Backbone Infinity Distance is a Metric).** Let \(x, y, z\) be backbones. The backbone infinity distance (Definition 5.3) satisfies all properties of a metric.

**Proof.** Recall that for each \(x \in x\), we can write \(x = (s_x, w_x)\); likewise for \(y \in y\). Let \(\alpha : [k] \to \bar{x} \times \bar{y}\) be an optimal alignment. We verify all properties of a metric.

**Non-Negativity.** Since all node weights are non-negative, \(d_{B_\infty}(x, y) \geq 0\).

**Symmetry.** By construction, \(d_{B_\infty}\) is symmetric; see Definition 5.1.

**Definiteness.** If \(x = y\), then the optimal alignment aligns each node with itself, and there are no insertions. Hence, all node weights match and \(d_{B_\infty}(x, y) = 0\).
On the other hand, assume \( d_{B_\infty}(x,y) = 0 \). This implies
\[
0 = \inf_{\alpha} \max_i |\omega_x(\alpha_x(i)) - \omega_y(\alpha_y(i))|.
\]
Therefore, \(|\omega_x(\alpha_x(i)) - \omega_y(\alpha_y(i))| \leq 0 \) for all \( i \in [n] \). Furthermore, \(|\omega_x(\alpha_x(i)) - \omega_y(\alpha_y(i))| \geq 0 \) for all \( i \in [n] \). Hence, each aligned pair of nodes must have the same node weight. By Definition 4.4, we never align two empty nodes. This implies each node in \( x \) is aligned with a node in \( y \). Furthermore, each aligned pair must have the same label by Definition 4.4. We can conclude \( x = y \).

**Triangle Inequality.** By Proposition Lemma 9.2, the triangle inequality holds.

Therefore, the backbone infinity distance is a metric. \(\square\)

9.3. **Lemma Used For Proving Lemma 5.16**

**Lemma 9.4 (Bijections Within Boxes).** Let \( f, f' : C \to \mathbb{R} \) be nicely tame functions such that \( f' \) is extremely close to \( f \). Let \( \alpha \) be the direct alignment defined in Construction 5.8 between \( x := B(f) \) and \( \alpha \) in \( B(f') \). Suppose \( \eta \) is a different alignment between \( x \) and \( x' \) such that \( \text{cost}(\eta) \leq \text{cost}(\alpha) \).

For each \( x' \in x' \), let \( x_\alpha \in \alpha \) be the unique element such that \( (x_\alpha, x') \in \text{im}(\alpha) \). For each \( x' \in x' \), define \( x_\eta \) similarly. Suppose there exists \( x' \in x' \) such that
\[
|w_{x'} - w_{x_\eta}| \leq |w_{x'} - w_{x_\alpha}|
\]
and \( x_\eta \neq x_\alpha \). Then

1. \( |w_{x'} - w_{x_\eta}| = |w_{x'} - w_{x_\alpha}| \).
2. There exists \( z' \in x' \) for which \( |w_{z'} - w_{x_\eta}| > \varepsilon \) where \( \varepsilon := \|f - f'\|_\infty \).

**Proof.** We prove Statement 1.

Let \( (t', f'(t')) \) be the local extremum of \( f' \) associated with node \( x' \), and let \( (t, f(t)) \) be the local extremum of \( f \) associated with \( x_\alpha \). Without loss of generality, we assume \( (t', f'(t')) \) is a local minimum. (Note that if \( (t', f'(t')) \) is a local maximum, then we apply the same argument with \(-f'\) and \(-f\).) Since \( (x_\alpha, x') \in \text{im}(\alpha) \), we know that \( (t, f(t)) \) is also a local minimum. We first prove, by the way of contradiction, that neither \( x_\eta \) nor \( x_\alpha \) is the empty node.

If \( x_\eta \) is the empty node, then, by the assumption \( x_\eta \neq x_\alpha \), it follows that \( x_\alpha \) is not the empty node. From Construction 5.8, we know that \((f'(t'), \zeta_f(t')) \in D(f') \cap \Box_e(f(t), \zeta_f(t))\).

Applying Lemma 5.15, we find
\[
|w_{x'} > \varepsilon.
\]
On the other hand, by assumption,
\[
|w_{x'} - w_{x_\eta}| \leq |w_{x'} - w_{x_\alpha}| \leq \varepsilon,
\]
where the last inequality follows from Lemma 5.10. Finally, using (16) and that \( w_{x_\eta} = 0 \), we have
\[
|w_{x'} - w_{x_\eta}| = w_{x'} > \varepsilon,
\]
giving a contradiction. Therefore, we conclude that \( x_\eta \) is not the empty node.

If \( x_\alpha \) is the empty node, then by the same argument as above, we arrive at contradiction. Therefore, \( x_\alpha \) is also not the empty node.

Therefore, neither \( x_\eta \) nor \( x_\alpha \) is an empty node. Let \((s_\eta, f(s_\eta)) \) be the local extremum of \( f \) associated with node \( x_\eta \). By Lemma 5.10, \( w_{x'} - w_{x_\eta} \leq \varepsilon \). Additionally, consider the point \( p = (f(s_\eta), \zeta_f(s_\eta)) \in D(f) \cap \Box_e(p) \). In Construction 5.8, we established a bijection between the multiplicity of \( p \), denoted \( \mu(p) \), and the number of points contained in \( D(f') \cap \Box_e(p) \). Additionally, in Lemma 5.10, we showed for all points \((f'(x), \zeta_{f'}(x)) \in D(f') \cap \Box_e(p) \), we have \( \frac{1}{2} |\text{pers}_{f'}(x) - \text{pers}_f(s)| \leq \varepsilon \). Furthermore, by Lemma 5.15, \( \frac{1}{2} |\text{pers}_{f'}(y) - \text{pers}_f(s)| > \varepsilon \) for all \((f'(y), \zeta_{f'}(y)) \in D(f') \setminus \Box_e(p) \). By assumption,
\[
|w_{x'} - w_{x_\eta}| \leq |w_{x'} - w_{x_\alpha}| \leq \varepsilon.
\]
Let \((s_\alpha, f(s_\alpha))\) be the local extremum of \(f\) associated with node \(x_\alpha\). Since the only point of \(D(f)\) contained in the square \(\square_\varepsilon(p)\) is the point \(p\) with multiplicity \(\mu(p)\), we must have \((\xi f(s_\alpha), \zeta f(s_\alpha)) = (f(s_\alpha), f(s_\alpha))\) in order for (1) to hold. Therefore, the two extrema of \(f\) have the same node lives and thus \(w_{x_\alpha} = w_{x_\alpha}\). We can conclude
\[
|w_{x'} - w_{x_\alpha}| = |w_{x'} - w_{x_\alpha}|
\]
as was to be shown to prove Statement (1).

Next we prove Statement (2). We note that the \(\varepsilon\)-extremal intervals discussed in this proof are all constructed from \(f\). We claim there exists a local extremum \((s', f'(s'))\) of \(f'\) such that \((\xi f'(s'), \zeta f'(s')) \in D(f') \cap \square_\varepsilon(p)\) and is aligned via \(\eta\) with an extremum \((s, f(s))\) such that \((f(s), \zeta f(s)) \in D(f) \setminus \square_\varepsilon(p)\). By way of contradiction, suppose that is not the case. Hence, all persistence points in \(D(f') \cap \square_\varepsilon(p)\) are paired with persistence points in \(D(f) \cap \square_\varepsilon(p)\). Since \(\eta \neq \alpha\), \(\eta\) restricted to \(D(f) \cap \square_\varepsilon(p)\) is a bijection onto \(D(f') \cap \square_\varepsilon(p)\) that is different from the bijection \(\alpha\). In other words, if we denote \(\gamma := \alpha|_{D(f) \cap \square_\varepsilon(p)}\) and \(\gamma' := \eta|_{D(f) \cap \square_\varepsilon(p)}\), we have \(\gamma \neq \gamma'\). By Construction 5.8 of \(\alpha\) and noting \(\eta \neq \alpha\), there exists an extremum \((s', f'(s'))\) that aligns via \(\eta\) with an extremum \((s, f(s))\) such that \(s'\) does not belong to interval of size \(\varepsilon\) around \(s\); that is, \(s', f'(s') \notin \varphi_\varepsilon(s)\). Without loss of generality, suppose \(s < s'\). Since \(f'\) is extremely close to \(f\), the number of extrema with persistence points contained in \((D(f) \cup D(f')) \cap \square_\varepsilon(p)\) where the domain coordinates are greater than \(s\) is the same for both \(f\) and \(f'\). Let
\[
A := \{(t, f(t)) \mid (f(t), \zeta f(t)) \in D(f) \cap \square_\varepsilon(p) \text{ and } t > s\}
\]
be the set of extrema of \(f\) whose persistence points are contained in \(D(f) \cap \square_\varepsilon(p)\) such that the domain coordinates of these extrema are greater than \(s\). Additionally, let
\[
B := \{(t, f'(t)) \mid (f'(t), \zeta f'(t)) \in D(f') \cap \square_\varepsilon(p) \text{ and } t > s'\}
\]
To preserve order in \(\eta\), elements of \(A\) must be aligned with the elements of \(B\). Since \(|A| > |B|\), by the pigeonhole principle, at least two extrema of \(f\) are aligned by \(\eta\) with the same extremum of \(f'\). This contradicts the fact that \(\eta\) is a bijection. This contradiction shows that there exists a \(z \in x'\) for which \(|w_{x'} - w_{z_\eta}| > \varepsilon\). By construction of the direct alignment, \(|w_{x'} - w_{z_\eta}| \leq \varepsilon\). Therefore, \(|w_{x'} - w_{z_\eta}| > |w_{x'} - w_{z_\eta}|\).

\[\square\]

9.4 Cases for Bound Differences in Edge Weights in Lemma 5.22

(1) \(E_{\text{diff}} = \frac{1}{2}|\text{pers}(t) - \text{pers}(t')|\). Applying Lemma 5.18, we find
\[
E_{\text{diff}} = \frac{1}{2}|\text{pers}(t) - \text{pers}(t')| \leq \varepsilon_{i,j}.
\]

(2) \(E_{\text{diff}} = \frac{1}{2}|\text{pers}(s) - \text{pers}(s')|\). Applying Lemma 5.18, we find
\[
E_{\text{diff}} = \frac{1}{2}|\text{pers}(s) - \text{pers}(s')| \leq \varepsilon_{j} \leq \varepsilon_{i,j}.
\]

(3) \(E_{\text{diff}} = |\varepsilon^*(t, s) - \varepsilon^*(t', s')|\). Applying Lemma 5.21, we find
\[
E_{\text{diff}} = |\varepsilon^*(t, s) - \varepsilon^*(t', s')| \leq \varepsilon_{i,j}.
\]

(4) \(E_{\text{diff}} = \frac{1}{2}(\text{pers}(t) - \text{pers}(s'))\). Then, \(\text{pers}(t) \leq \text{pers}(s)\). Applying Lemma 5.18, we find
\[
E_{\text{diff}} = \frac{1}{2}(\text{pers}(t) - \text{pers}(s')) \leq \frac{1}{2}(\text{pers}(s) - \text{pers}(s')) \leq \varepsilon_{j} \leq \varepsilon_{i,j}.
\]
(5) \( E_{\text{diff}} = \frac{1}{2} (\text{pers}(s') - \text{pers}(t)). \) Then, \( \text{pers}(s') \leq \text{pers}(t'). \) Applying Lemma 5.18, we find
\[
E_{\text{diff}} = \frac{1}{2} (\text{pers}(s') - \text{pers}(t)) \leq \frac{1}{2} (\text{pers}(t') - \text{pers}(t)) \leq \varepsilon_i \leq \varepsilon_{i,j}.
\]

(6) \( E_{\text{diff}} = \frac{1}{2} (\text{pers}(s) - \text{pers}(t')). \) Then, \( \text{pers}(s) \leq \text{pers}(t). \) Applying Lemma 5.18, we find
\[
E_{\text{diff}} = \frac{1}{2} (\text{pers}(s) - \text{pers}(t')) \leq \frac{1}{2} (\text{pers}(t) - \text{pers}(t')) \leq \varepsilon_i \leq \varepsilon_{i,j}.
\]

(7) \( E_{\text{diff}} = \frac{1}{2} (\text{pers}(t') - \text{pers}(s)). \) Then, \( \text{pers}(t') \leq \text{pers}(s'). \) Applying Lemma 5.18, we find
\[
E_{\text{diff}} = \frac{1}{2} (\text{pers}(t') - \text{pers}(s)) \leq \frac{1}{2} (\text{pers}(s') - \text{pers}(s)) \leq \varepsilon_j \leq \varepsilon_{i,j}.
\]

(8) \( E_{\text{diff}} = \varepsilon^*(t, s) - \frac{1}{2} \text{pers}(t'). \) Then, \( \varepsilon^*(t, s) \leq \frac{1}{2} \text{pers}(t). \) Applying Lemma 5.18, we find
\[
E_{\text{diff}} = \varepsilon^*(t, s) - \frac{1}{2} \text{pers}(t') \leq \frac{1}{2} (\text{pers}(t) - \text{pers}(t')) \leq \varepsilon_i \leq \varepsilon_{i,j}.
\]

(9) \( E_{\text{diff}} = \frac{1}{2} \text{pers}(t') - \varepsilon^*(t, s). \) Then, \( \frac{1}{2} \text{pers}(t') \leq \varepsilon^*(t', s'). \) Applying Lemma 5.21, we find
\[
E_{\text{diff}} = \frac{1}{2} \text{pers}(t') - \varepsilon^*(t, s) \leq \varepsilon^*(t', s') - \varepsilon^*(t, s) \leq \varepsilon_{i,j}.
\]

(10) \( E_{\text{diff}} = \varepsilon^*(t, s) - \frac{1}{2} \text{pers}(s'). \) Then, \( \varepsilon^*(t, s) \leq \frac{1}{2} \text{pers}(s). \) Applying Lemma 5.18, we find
\[
E_{\text{diff}} = \varepsilon^*(t, s) - \frac{1}{2} \text{pers}(s') \leq \frac{1}{2} (\text{pers}(s) - \text{pers}(s')) \leq \varepsilon_j \leq \varepsilon_{i,j}.
\]

(11) \( E_{\text{diff}} = \frac{1}{2} \text{pers}(s') - \varepsilon^*(t, s). \) Then, \( \frac{1}{2} \text{pers}(s') \leq \varepsilon^*(t', s'). \) Applying Lemma 5.21, we find
\[
E_{\text{diff}} = \frac{1}{2} \text{pers}(s') - \varepsilon^*(t, s) \leq \varepsilon^*(t', s') - \varepsilon^*(t, s) \leq \varepsilon_{i,j}.
\]

(12) \( E_{\text{diff}} = \varepsilon^*(t', s') - \frac{1}{2} \text{pers}(t). \) Then, \( \varepsilon^*(t', s') \leq \frac{1}{2} \text{pers}(t'). \) Applying Lemma 5.18, we find
\[
E_{\text{diff}} = \varepsilon^*(t', s') - \frac{1}{2} \text{pers}(t) \leq \frac{1}{2} (\text{pers}(t') - \text{pers}(t)) \leq \varepsilon_i \leq \varepsilon_{i,j}.
\]

(13) \( E_{\text{diff}} = \frac{1}{2} \text{pers}(t) - \varepsilon^*(t', s'). \) Then \( \frac{1}{2} \text{pers}(t) \leq \varepsilon^*(t, s). \) Applying Lemma 5.21, we find
\[
E_{\text{diff}} = \frac{1}{2} \text{pers}(t) - \varepsilon^*(t', s') \leq \varepsilon^*(t, s) - \varepsilon^*(t', s') \leq \varepsilon_{i,j}.
\]

(14) \( E_{\text{diff}} = \varepsilon^*(t', s') - \frac{1}{2} \text{pers}(s). \) Then, \( \varepsilon^*(t', s') \leq \frac{1}{2} \text{pers}(s'). \) Applying Lemma 5.18, we find
\[
E_{\text{diff}} = \varepsilon^*(t', s') - \frac{1}{2} \text{pers}(s) \leq \frac{1}{2} (\text{pers}(s') - \text{pers}(s)) \leq \varepsilon_j \leq \varepsilon_{i,j}.
\]

(15) \( E_{\text{diff}} = \frac{1}{2} \text{pers}(s) - \varepsilon^*(t', s'). \) Then \( \frac{1}{2} \text{pers}(s) \leq \varepsilon^*(t, s). \) Applying Lemma 5.21, we find
\[
E_{\text{diff}} = \frac{1}{2} \text{pers}(s) - \varepsilon^*(t', s') \leq \varepsilon^*(t, s) - \varepsilon^*(t', s') \leq \varepsilon_{i,j}.
\]
9.5. Proof of Proposition 6.8

**Proposition 6.8.** (Alignment Matrix Finds Minimum Cost) Let \( x = (x_1, x_2, \ldots, x_m) \) and \( y = (y_1, y_2, \ldots, y_n) \) be backbones. Let \( \text{mat} \) be the \((m+1) \times (n+1)\) alignment matrix. Then, \( \text{mat}[m+1, n+1] = c_{x,y}(m,n) \).

**Proof.** For \( i \in [n] \), let \( x_i = (s_{x,i}, w_{x,i}) \) and \( y_i = (s_{y,i}, w_{y,i}) \).

We proceed by induction. For the base case, first observe that \( c_{x,y}(1,0) = w_{x,1} \) and \( c_{x,y}(0,1) = w_{y,1} \). By construction, \( \text{mat}[2,1] = w_{x,1} = c_{x,y}(1,0) \) and \( \text{mat}[1,2] = w_{y,1} = c_{x,y}(0,1) \). Next consider \( c_{x,y}(1,1) \). The possible alignments (see Definition 4.4) of \( x_1 := x[1 : 1] \) and \( y_1 := y[1 : 1] \) are

1. \( \alpha_1 : \{1, 2\} \rightarrow \tilde{x}_1 \times \tilde{y}_1 \), where \( \alpha_1(1) = (x_1, 0) \) and \( \alpha_1(2) = (0, y_1) \).
2. \( \alpha_2 : \{1, 2\} \rightarrow \tilde{x}_1 \times \tilde{y}_1 \), where \( \alpha_2(1) = (0, y_1) \) and \( \alpha_2(2) = (x_1, 0) \).
3. \( \alpha_3 : \{1\} \rightarrow \tilde{x}_1 \times \tilde{y}_1 \), where \( \alpha_3(1) = (x_1, y_1) \) is a possible alignment.

Observe \( \text{cost}(\alpha_1) = \text{cost}(\alpha_2) = w_{x,1} + w_{y,1} \) and \( \text{cost}(\alpha_3) = \text{diff}(x_1, y_1) = |w_{x,1} - w_{y,1}| \). Therefore,

\[
c_{x,y}(1,1) = \min \left\{ \frac{w_{x,1} + w_{y,1}}{2}, \frac{\text{cost}(\alpha_2)}{2}, \frac{\text{cost}(\alpha_3)}{2} \right\}
\]

By construction,

\[
\text{mat}[2, 2] = \min \left\{ \frac{\text{mat}[2, 1] + w_{y,1}}{2}, \frac{\text{mat}[1, 2] + w_{x,1}}{2}, \frac{\text{mat}[1, 1] + \text{diff}(x_1, y_1)}{2} \right\}
\]

Substituting \( w_{x,1} \) for \( \text{mat}[2, 1] \), \( w_{y,1} \) for \( \text{mat}[1, 2] \) and zero for \( \text{mat}[1, 1] \), we find \( c_{x,y}(1,1) = \text{mat}[2, 2] \). This shows the base case holds.

For the induction hypothesis we assume that \( \text{mat}[h, k] = c_{x,y}(h-1, k-1) \) for all \( h \leq i \) and \( k \leq j \) where \( i \leq m \) and \( j \leq n \).

In the induction step, we show \( \text{mat}[i+1, j] = c_{x,y}(i, j-1) \), \( \text{mat}[i, j+1] = c_{x,y}(i-1, j) \), and \( \text{mat}[i+1, j+1] = c_{x,y}(i, j) \). First consider \( c_{x,y}(i, j-1) \). Let \( \alpha : [k] \rightarrow \tilde{x}[1 : i] \times \tilde{y}[1 : j-1] \) be an alignment of the first \( i \) nodes of \( x \) with the first \( j-1 \) nodes of \( y \) with cost \( c_{x,y}(i, j-1) \). Consider the last pair of nodes aligned via \( \alpha(k) \). The cost of these two nodes is either (a) the cost of \( x_i \) aligned with an insertion, (b) the cost of \( y_{j-1} \) aligned with an insertion, or (c) the cost of \( x_i \) aligned with \( y_{j-1} \). Note, by Definition 4.4, we never have an insertion aligned with an insertion. Since the cost is the minimum across these three possibilities, the cost is

\[
c_{x,y}(i, j-1) = \min \left\{ c_{x,y}(i-1, j-1) + w_{x,i}, c_{x,y}(i, j-2) + w_{y,j-1}, c_{x,y}(i-1, j-2) + \text{diff}(x_i, y_{j-1}) \right\}
\]

Applying the induction hypothesis, we find

\[
c_{x,y}(i, j-1) = \min \left\{ \frac{\text{mat}[i, j] + w_{x,i}}{2}, \frac{\text{mat}[i+1, j-1] + w_{y,j-1}}{2}, \frac{\text{mat}[i, j-1] + \text{diff}(x_i, y_{j-1})}{2} \right\}
\]

By construction of \( \text{mat} \) (Definition 6.7), we see that \( c_{x,y}(i, j-1) = \text{mat}[i+1, j] \). Using a similar approach, we find \( \text{mat}[i, j+1] = c_{x,y}(i-1, j) \), and \( \text{mat}[i+1, j+1] = c_{x,y}(i, j) \).

This concludes the induction argument. Thus, \( \text{mat}[i, j] = c_{x,y}(i-1, j-1) \) for all \( i \leq m+1 \) and \( j \leq n+1 \). In particular, \( \text{mat}[m+1, n+1] = c_{x,y}(m,n) \). \( \square \)

9.6. Applications. We provide tables summarizing the results of the computations described in Section 7.2.
### Table 1. Summary of Results from Parasite Data.

| Distance       | Mean  | Median | Standard Deviation |
|----------------|-------|--------|--------------------|
| $d_{ED}(\text{DAG}(\hat{D}_1), \text{DAG}(\hat{D}_2))$ | 123.13 | 122.68 | 22.12              |
| $d_{ED}(\text{DAG}(\hat{D}_1), \text{DAG}(\hat{D}_3))$ | 267.97 | 268.18 | 28.68              |
| $d_{ED}(\text{DAG}(\hat{D}_1), \text{DAG}(\hat{D}_4))$ | 143.44 | 142.20 | 30.37              |
| $d_{ED}(\text{DAG}(\hat{D}_1), \text{DAG}(\hat{D}_5))$ | 301.70 | 302.38 | 30.55              |
| $d_{ED}(\text{DAG}(\hat{D}_1), \text{DAG}(\hat{D}_6))$ | 282.00 | 279.72 | 56.59              |
| $d_{ED}(\text{DAG}(\hat{D}_1), \text{DAG}(\hat{D}_7))$ | 424.06 | 421.20 | 53.24              |

### Table 2. Summary of Results from Mouse Data.

| Distance       | Mean  | Median | Standard Deviation |
|----------------|-------|--------|--------------------|
| $d_{ED}(\text{DAG}(\hat{D}_8), \text{DAG}(\hat{D}_9))$ | 493.40 | 490.88 | 71.38              |
| $d_{ED}(\text{DAG}(\hat{D}_8), \text{DAG}(\hat{D}_10))$ | 642.51 | 640.78 | 66.70              |
| $d_{ED}(\text{DAG}(\hat{D}_8), \text{DAG}(\hat{D}_11))$ | 436.17 | 432.42 | 59.62              |
| $d_{ED}(\text{DAG}(\hat{D}_8), \text{DAG}(\hat{D}_12))$ | 607.97 | 607.06 | 60.33              |

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