

# Computing a Subtrajectory Cluster from $c$ -Packed Trajectories

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## Abstract

We present a near-linear time approximation algorithm for the subtrajectory cluster problem of  $c$ -packed trajectories. Given a trajectory  $T$  of complexity  $n$ , an approximation factor  $\varepsilon$ , and a desired distance  $d$ , the problem involves finding  $m$  subtrajectories of  $T$  such that their pair-wise Fréchet distance is at most  $(1 + \varepsilon)d$ . At least one subtrajectory must be of length  $l$  or longer. A trajectory  $T$  is  $c$ -packed if the intersection of  $T$  and any ball  $B$  with radius  $r$  is at most  $c \cdot r$  in length.

Previous results by Gudmundsson and Wong [24] established an  $\Omega(n^3)$  lower bound unless the Strong Exponential Time Hypothesis fails, and they presented an  $O(n^3 \log^2 n)$  time algorithm. We circumvent this conditional lower bound by studying subtrajectory cluster on  $c$ -packed trajectories, resulting in an algorithm with an  $O((c^2 n / \varepsilon^2) \log(c/\varepsilon) \log(n/\varepsilon))$  time complexity.

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## 1 Introduction

With the proliferation of location-aware devices comes an abundance of trajectory data. One way to process and make sense of many trajectories is to group long and similar subtrajectories. The analysis of long and similar parts of trajectories can provide insights into behavior and mobility patterns, such as common routes taken and places visited frequently.

Buchin et al. [8] initialised the study of subtrajectory cluster problems to detect and extract common movement patterns. The Subtrajectory Cluster (SC) decision problem is defined as follows. Given one or more trajectories, determine if there exists a cluster of  $m - 1$  non-overlapping subtrajectories and one reference trajectory. The reference trajectory  $T_r$  must be at least of length  $l$ , and the Fréchet distances between  $T_r$  and the other  $m - 1$  subtrajectories must be at most  $d$ . In the case of animals, long and common movement patterns can indicate movement between grazing spots of sheep or the migration flyway of seabirds. In the case of humans, common movement on a Monday morning can show commuting patterns to find the most heavily congested areas.



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Subtrajectory clustering has attracted research from multiple communities. Gudmundsson and Wolle [23] used subtrajectory cluster to analyse the common movement patterns of football players. Buchin et al. [7] applied subtrajectory cluster to map reconstruction by clustering common movement patterns of vehicles into road segments. Researchers in the Geographical Information and Data Mining communities also considered the variants and practical performance of subtrajectory cluster algorithms [11, 29, 21, 22, 26, 1, 17]. In addition, the potential of SC is examined in a wide range of applications, including sports player analysis [30] and human movement analysis [10, 25].

Several theoretical studies of the subtrajectory clustering problem focus on improving the quality of clustering. Agarwal et al. [1] defined a single objective function, the weighted sum of three quality measures of a clustering. These quality measures include the number of clusters chosen, the quality of the cluster, and the size of the trajectories excluded from the clustering. Brüning et al. [6] studied so-called  $\Delta$ -coverage, aiming to find a set  $C$  of curves to cover a polygonal curve such that a curve in  $C$  is fixed in size, and  $|C|$  is minimised.

However, despite considerable attention from multiple communities, there is no subcubic time algorithm that solves the subtrajectory cluster problem, limiting its usefulness on large data sets. Buchin et al. [8] solved the subtrajectory cluster problem in  $O(n^5)$  time when the similarity measurement of two trajectories is the Fréchet distance, and Gudmundsson and Wong [24] further improved the runtime with an  $O(n^3 \log^2 n)$  time algorithm. In addition, Gudmundsson and Wong [24] showed that there is no  $O(n^{3-\delta})$  algorithm for subtrajectory cluster for any  $\delta > 0$  unless the Strong Exponential Time Hypothesis (SETH) fails.

SC is unlikely to have a strongly subquadratic algorithm even if we allow a small approximation factor on the Fréchet distances between subtrajectories. Because given two trajectories  $T_1$  and  $T_2$ , we can structure the SC problem to find two subtrajectories such that their Fréchet distance is at most  $(1 + \epsilon)d$ , and the reference trajectory must be as long as the maximum of  $T_1$  and  $T_2$ . Solving this instance of SC is equivalent to approximating the Fréchet distance of  $T_1$  and  $T_2$ , and Bringmann [4] showed that there is no 1.001-approximation with runtime  $O(n^{2-\delta})$  for the continuous Fréchet distance for any  $\delta > 0$ , unless SETH fails.

Since an exact subcubic and an approximate subquadratic algorithm are unlikely to exist, we study subtrajectory cluster on a realistic family of trajectories, called  $c$ -packed trajectories. A trajectory  $T$  is  $c$ -packed if, for any ball  $B$  of radius  $r$ , the length of  $T$  lying inside  $B$  is at most  $c$  times  $r$ . The packedness value of a trajectory  $T$  is the maximum  $c$  for which  $T$  is  $c$ -packed. Bringmann [4] proved that computing the Fréchet distance has no strong subquadratic algorithm unless SETH fails, and the notion of  $c$ -packedness was introduced by Driemel et al. [15] to circumvent such conditional lowerbound. Since then, the notion of  $c$ -packedness has gained considerable attention from the theory community [20, 4, 2, 12, 5], and several real-world data sets have been shown to have low packedness values [19, 15]. In one particular instance, Gudmundsson et al. [19] approximated the packedness values of several real-world trajectory data sets. In their experiments, several trajectory data sets have low packedness values, such as the movement patterns of people in Beijing, school buses, European football players, and trawling bats.

In this paper, given a  $c$ -packed trajectory  $T$  of complexity  $n$  and a desired multiplicative approximation error  $\epsilon$  on the Fréchet distance between subtrajectories, we present an  $O((c^2 n / \epsilon^2) \log(c/\epsilon) \log(n/\epsilon))$  time algorithm that solves the SC problem. It is worth noting that previous papers considering  $c$ -packed curves typically replace a factor  $n$  with a polynomial of constant degree in  $c$  [13, 18]. We are able to replace a factor of  $n^2$  with  $c^2/\epsilon^2$ , bringing the algorithm's running time from cubic to near-linear, assuming  $c \in O(1)$ .

Along the way, we develop a tool for simplifying the free space diagram that may be of independent interest. To efficiently approximate the Fréchet distance, Driemel et al. [15] showed that the free space complexity, i.e., the number of non-empty cells, is  $O(cn/\varepsilon)$  for two simplified  $c$ -packed trajectories (see Section 2 for an overview of the free space, or [3] for a formal definition). However, simplifying a trajectory by taking shortcuts between vertices can yield a much shorter trajectory, and the SC problem is sensitive to the length of the trajectories since the reference trajectory has to have a length at least  $l$ . To tackle this problem, we developed a tool to construct the free space diagram in  $O((cn/\varepsilon) \log(cn/\varepsilon))$  time, preserving the length of two trajectories while benefiting from the  $O(cn/\varepsilon)$  free space complexity. Our tool can be of value for problems in which the length of a trajectory is important, such as subtrajectory cluster [8], partial curve matching [9], and Fréchet distance with speed limit [27].

In Section 2, we will formally define the subtrajectory cluster problem and outline the greedy plane sweep algorithms by Buchin et al. [8] and Gudmundsson and Wong [24], which our approach builds on. In Section 3, we provide a technical overview of our main results. In Section 4, we will discuss how to simplify the free space diagram to achieve a lower complexity while preserving trajectory lengths.

In Section 5, we will consider the restricted case when the reference trajectory must be vertex-to-vertex. In Section 6, we will remove this restriction by considering arbitrary reference trajectory.

## 2 Preliminaries

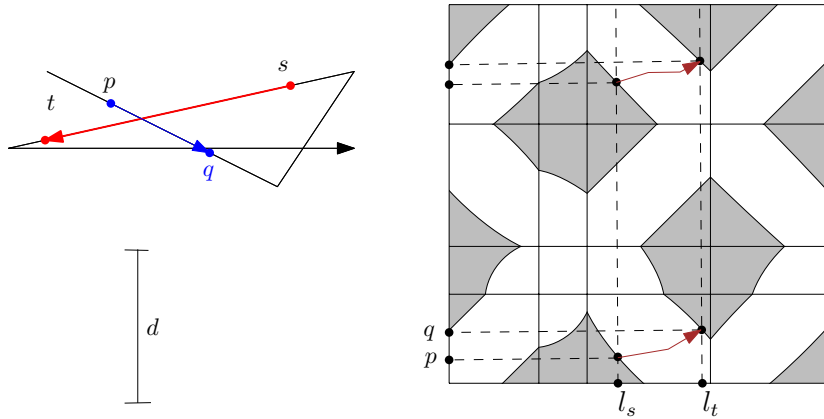
In this section, we will outline the previous algorithms for the subtrajectory cluster problem. The subtrajectory cluster problem was first introduced by Buchin et al. [8], and later improved by Gudmundsson and Wong [24]. But instead of looking for a subtrajectory where the Fréchet distances between the reference trajectory and the subtrajectories are exact, we aim to find a solution that approximates the Fréchet distance between subtrajectories in the cluster.

► **Problem 1** ([24]). *Given trajectory  $T$  of complexity  $n$ , a positive integer  $m$ , positive real numbers  $d$ ,  $l$  and  $\varepsilon$ , decide if there exists a subtrajectory cluster of  $T$  such that:*

- *the cluster consists of one reference subtrajectory and  $m - 1$  other subtrajectories of  $T$ ,*
- *the reference subtrajectory has Euclidean length at least  $l$ ,*
- *the Fréchet distance between the reference subtrajectory and any other subtrajectory is at most  $(1 + \varepsilon)d$ ,*
- *any pair of subtrajectories in the cluster overlap in at most one point.*

Buchin et al. [8] solved the exact SC problem by using a plane sweep algorithm on the free space diagram  $\mathcal{F}_d(T, T)$ . Let  $s$  and  $t$  be two points on  $T$ , and we denote  $T_{st}$  as the subtrajectory of  $T$  starting from  $s$  and ending on  $t$ . Let  $l_s$  and  $l_t$  be the vertical sweep lines  $x = s$  and  $x = t$  on  $\mathcal{F}_d(T, T)$ , respectively (see Figure 1). An  $xy$ -monotone path in  $\mathcal{F}_d(T, T)$ , or monotone path for short, is a continuous path that is non-decreasing in both  $x$ - and  $y$ -coordinates. To solve SC( $m$ ,  $d$ ,  $l$ ), the lines  $l_s$  and  $l_t$  sweep from left to right while making sure that  $l_s$  is to the left of  $l_t$ , and the reference trajectory  $T_{st}$  is at least  $l$  long, i.e.,  $t - s \geq l$ . In each interval  $[l_s, l_t]$ , they compute the maximum number of monotone paths in  $\mathcal{F}_d(T, T)$  starting at  $l_s$  and ending at  $l_t$ .

Let  $p$  and  $q$  be two points on  $T$ , and let  $(s, p)$  and  $(t, q)$  be two coordinates on  $\mathcal{F}_d(T, T)$ . As we only consider monotone paths starting from  $l_s$  and ending on  $l_t$ , we call the monotone path from  $(s, p)$  to  $(t, q)$  the  $pq$  monotone path. First, a monotone path  $pq$  must traverse only



■ **Figure 1** The free space diagram  $\mathcal{F}_d(T, T)$ , and interval  $[l_s, l_t]$  defined by two points  $s$  and  $t$  on  $T$ . If there exists a monotone path (marked in brown) from  $(s, p)$  to  $(t, q)$  through the free space, then the Fréchet distance between subtrajectories  $T_{st}$  and  $T_{pq}$  is at most  $d$ .

the free space. Second, two monotone paths  $pq$  and  $ab$  must not overlap along the  $y$ -interval in more than a single point. Third, the  $y$ -coordinates of any  $pq$  monotone path cannot overlap the  $[s, t]$  interval in more than a single point. We obtain the following subproblem.

▶ **Subproblem 2** ([24]). *Given a trajectory  $T$  of complexity  $n$ , a positive integer  $m$ , a positive real value  $d$ , and a reference subtrajectory of  $T$  starting at  $s$  and ending at  $t$ , let  $l_s$  and  $l_t$  be two vertical lines in  $\mathcal{F}_d(T, T)$  representing the points  $s$  and  $t$ . Decide if there exist:*

- $m - 1$  distinct paths starting at  $l_s$  and ending at  $l_t$ , such that
- the  $y$ -coordinate of any two monotone paths overlap in at most one point, and
- the  $y$ -coordinate of any monotone path overlaps the  $y$ -interval from  $s$  to  $t$  in at most one point.

To look for a set  $\{p_1q_1, p_2q_2, \dots, p_{m-1}q_{m-1}\}$  of monotone paths, both algorithms use a greedy approach. First, set  $p_1$  to be the lowest feasible point on  $l_s$ , and compute  $p_1q_1$  by searching for a lowest monotone path through the free space. Inductively, with  $p_{i-1}q_{i-1}$  computed, set  $p_i$  to the lowest feasible point on  $l_s$  that is on or above  $q_{i-1}$ , and do the same. If a search from  $p_i$  leads to a dead end, we simply set  $p_i$  to the next lowest feasible point on  $l_s$ , and search again.

The sweep lines stop at all  $O(n^3)$  critical points, and for each critical point there is a  $[l_s, l_t]$  interval to consider. Buchin et al. [8] solved each instance in  $O(nm) \subseteq O(n^2)$  time. Gudmundsson and Wong [24] improved the efficiency by connecting the critical points efficiently in a tree-like data structure which allows them to reuse computed monotone paths from previous interval instances. They showed that, in their construction, there are at most  $O(n^3 \log n)$  edges, and each edge takes at most  $O(\log n)$  time to add, remove, or access. This brings down the complexity of the algorithm from  $O(n^5)$  to  $O(n^3 \log^2 n)$  time.

### 3 Technical Overview

Our technical overview is divided into three parts. In Sections 3.1, 3.2, and 3.3, we summarise the main result of Sections 4, 5, and 6 respectively.

### 3.1 Computing the Free Space Diagram

Our algorithm constructs a simplified free space diagram that preserves trajectory lengths. The size (in terms of Euclidean length) of the simplified free space diagram is the same as the size of the unsimplified free space diagram. The only difference between the two diagrams is that approximate distances are used in the simplified diagram. In particular, we define a function that uniformly maps a trajectory to its simplification, and we calculate the distance between the mapped simplification points instead of points on the original trajectory. We prove that the complexity of the simplified free space diagram will be at most  $O(cn/\varepsilon)$ , and that the trajectory lengths in the diagram are preserved. Next, we build the simplified free space diagram. We use an algorithm by Conradi and Driemel [13] to query pairs of nearby segments. Finally, we construct a data structure on the free space diagram so that we can access the closest non-empty cells below, above, to the left, and to the right in constant time. Putting this all together, we obtain Theorem 1. For a full proof, see Section 4.

► **Theorem 1.** *Given a pair of trajectories, one can construct a simplified free space diagram in  $O((cn/\varepsilon) \log(cn/\varepsilon))$  time, so that the simplified free space has complexity  $O(cn/\varepsilon)$ , it approximates the Fréchet distance to within a factor of  $(1 + \varepsilon)$ , and it preserves the trajectory lengths of the original trajectory.*

### 3.2 Reference trajectory is vertex-to-vertex

Next, we focus on the special case where the reference trajectory is vertex-to-vertex. Three data structures are used in the vertex-to-vertex subtrajectory cluster algorithm of Gudmundsson and Wong [24] – a directed graph, a range tree, and a link-cut tree. For an overview of these data structures, see the full version. Originally, the number of leaves per range tree is  $O(n)$ , and the directed graph has complexity  $O(n^2)$ . We use the  $c$ -packedness property to prove that, in our simplified free space diagram, the number of leaves per range tree is  $O(c/\varepsilon)$ , and the directed graph has complexity  $O((cn/\varepsilon) \log(c/\varepsilon))$ . The link-cut tree data structure can be used without modification. Putting this all together, we obtain Theorem 2. Recall that  $m$  is the desired number of subtrajectories in the cluster. For a full proof, see Section 5.

► **Theorem 2.** *There is an  $O(nm \log(c/\varepsilon) \log(n/\varepsilon))$  time algorithm that solves  $\text{SC}(\mathbb{T}, m, 1, (1 + \varepsilon)d)$  in the case that the reference trajectory is vertex-to-vertex.*

### 3.3 Reference trajectory is arbitrary

Finally, we tackle the general case where the reference trajectory is arbitrary. The main obstacle in the general case is that there are  $\Theta(n^3)$  internal critical points that correspond to potential starting and ending positions of the reference trajectory. In fact, Gudmundsson and Wong [24] show that, for general (not  $c$ -packed) curves, these internal critical points are essentially unavoidable. They use the  $\Theta(n^3)$  internal critical points to show that under the Strong Exponential Time Hypothesis (SETH), there is no  $O(n^{3-\delta})$  time algorithm for subtrajectory cluster for any  $\delta > 0$ .

Our main lemma in this section is to bound the number of internal critical points for subtrajectory cluster on  $c$ -packed trajectories. The lemma uses the  $c$ -packedness property in two different ways. First, the  $c$ -packedness property bounds the complexity of the simplified free space diagram to linear. This replaces one of the factors of  $n$  with  $c/\varepsilon$ . Second, the  $c$ -packedness property is used to prove that in any horizontal strip, only a constant number of cells have free space. This replaces another factor of  $n$  with  $c/\varepsilon$ , resulting in  $O(c^2n/\varepsilon^2)$

internal critical points. Finally, we prove that the interval management data structure can be used in the same way as in Gudmundsson and Wong's algorithm [24]. Putting this all together, we obtain Theorem 3. For a full proof, see Section 6.

► **Theorem 3.** *There is an  $O((c^2n/\varepsilon^2)\log(c/\varepsilon)\log(n/\varepsilon))$  time algorithm that solves SC(T, m, l,  $(1 + \varepsilon)d$ ) in the case that the reference trajectory is arbitrary.*

## 4 Computing the Free Space Diagram

In this section, we will explain the process of constructing a simplified free space diagram for two  $c$ -packed polygonal curves  $P$  and  $Q$ . The free space  $\mathcal{D}_d(P, Q)$  describes all pairs of points, one on  $P$ , one on  $Q$ , whose distance is at most  $d$  [3]. With slight abuse of notation, we parameterise the polygonal curve  $P$  such that  $P(x)$  is a point on  $P$ , where  $x \in [0, \|P\|]$ . Formally,

$$\mathcal{D}_d(P, Q) = \{(x, y) \in [0, \|P\|] \times [0, \|Q\|] \mid \text{dist}(P(x), Q(y)) \leq d\}.$$

To circumvent the quadratic free space complexity, Driemel et al. [15] showed that the free space complexity of two simplified  $c$ -packed curves is  $O(cn/\varepsilon)$ . Given a  $c$ -packed curve  $P = p_1p_2\dots p_n$ , we simplify  $P$  into its  $\varepsilon d$ -simplification  $P' = q_1q_2\dots q_k$  as follows. Let  $B(a, r)$  be the ball centered at  $a$  with radius  $r$ . First, set  $q_1 = p_1$ . With  $q_i$  defined, traverse  $P$  from  $q_i$  until a vertex  $v$  is outside  $B(q_i, \varepsilon d)$ , or  $v$  is the last vertex of  $P$ , and set  $q_{i+1} = v$ . Continue until all vertices of  $P$  are exhausted. Driemel et al. [15] showed that the  $\varepsilon d$ -simplification of a  $c$ -packed curve is at most  $6c$ -packed [15, Lemma 4.3], and the Fréchet distance between  $P$  and  $P'$  is at most  $(1 + \varepsilon)d$ . A simplified curve has the useful property that every segment but the last is at least  $\varepsilon d$  long. We assume for simplicity that the last one is at least  $\varepsilon d$  long as well, since otherwise one can backtrack and modify the simplified curve such that each segment is at least  $\varepsilon d/2$  long, and our arguments can be extended to such case.

► **Observation 4.** *One can simplify a polygonal curve  $P$  into its  $\varepsilon d$ -simplification  $P'$  such that the Fréchet distance between  $P$  and  $P'$  is at most  $(1 + \varepsilon)d$ , and each segment in  $P'$  is at least  $\varepsilon d$  long.*

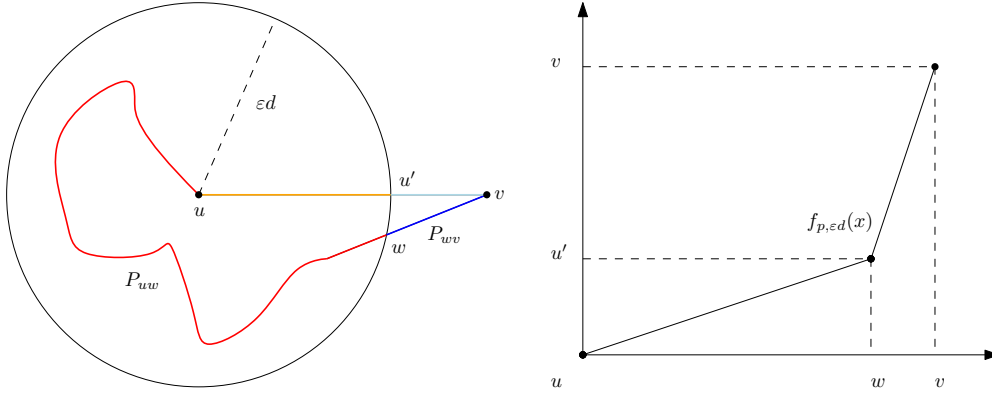
Simplifying two  $c$ -packed curves can reduce the free space complexity, but using the plane-sweep algorithm to solve the SC problem on the resulting free space diagram is unfortunately infeasible. This is because the total length of the simplified trajectories can be much shorter, making it impossible to slide a window of width  $l$  on the free space diagram  $\mathcal{F}_{(1+\varepsilon)d}(P', Q')$ . To address this issue, we developed a tool that enables the construction of a free space diagram that maintains the original curve length, while also benefiting from the reduced free space complexity.

### 4.1 Simplifying the Free Space

In this section, we introduce a method that simplifies the free space. We show that we can construct the *simplified free space*  $\mathcal{D}'_{(1+\hat{\varepsilon})d}(P, Q)$ , where  $\hat{\varepsilon}$  is at most  $8\varepsilon$ , such that the complexity of the simplified free space is at most  $O(cn/\hat{\varepsilon})$ . In addition,  $\mathcal{D}'_{(1+\hat{\varepsilon})d}(P, Q)$  contains  $\mathcal{D}_d(P, Q)$  as a subset, but it is not bigger than the free space of  $P$  and  $Q$  if we approximate their Fréchet distance, i.e.,  $\mathcal{D}'_{(1+\hat{\varepsilon})d}(P, Q) \subseteq \mathcal{D}_{(1+\hat{\varepsilon})d}(P, Q)$ .

We will first define a function that uniformly maps parts of the polygonal curve  $P$  to segments of  $P'$  in Definition 5, using which we will formally define the simplified free space in Definition 6. We will then formally prove the set inclusions mentioned above in Lemma 7.

► **Definition 5.** Let  $\text{simpl}(P, \varepsilon d)$  be the  $\varepsilon d$ -simplification of a polygonal curve  $P$ . Let  $P_{uv}$  be the subcurve of  $P$  from point  $u$  to  $v$  that are simplified into the segment  $(u, v) \in \text{simpl}(P, \varepsilon d)$ . Let  $w$  be the first intersection point of  $P_{uv}$  and the boundary of the ball  $B(u, \varepsilon d)$  along  $P_{uv}$ , and let  $u'$  be the intersection of  $(u, v)$  and the boundary of the ball  $B(u, \varepsilon d)$ . Define the mapping  $f_{P, \varepsilon d} : P \rightarrow \text{simpl}(P, \varepsilon d)$  such that  $f_{P, \varepsilon d}$  maps  $[u, w)$  to  $[u, u')$  uniformly, and  $[w, v]$  to  $[u', v]$  uniformly (see Figure 2).



■ **Figure 2** A figure showcasing the function in Definition 5. The point  $u'$  is the intersection of the segment  $(u, v)$  and the ball  $B(u, \varepsilon d)$ , and the point  $w$  is the intersection of subtrajectory  $P_{uv}$  and  $B(u, \varepsilon d)$ . The function  $f_{P, \varepsilon d}$  uniformly maps  $P_{uw}$  (red) to  $(u, u')$  (orange), not including  $u'$  and  $w$ . The function  $f_{P, \varepsilon d}$  uniformly maps  $P_{wv}$  (blue) to  $(u', v)$  (light blue).

► **Definition 6.** Define the simplified free space of  $P$  and  $Q$  with respect to the Fréchet distance  $d > 0$ , and a parameter  $\varepsilon > 0$  as

$$\mathcal{D}'_{(1+\varepsilon)d}(P, Q) = \{(x, y) \in [0, \|P\|] \times [0, \|Q\|] \mid \text{dist}(f_{P, \varepsilon d}(P(x)), f_{Q, \varepsilon d}(Q(y))) \leq (1 + \varepsilon)d\}.$$

Similarly, let  $\mathcal{F}'_{(1+\varepsilon)d}(P, Q)$  be the simplified free space diagram.

► **Lemma 7.** Let  $\mathcal{D}_d(P, Q)$  be the free space of curves  $P$  and  $Q$  with respect to the Fréchet distance  $d$ , and let  $\mathcal{D}'_{(1+\varepsilon)d}(P, Q)$  be their simplified free space with an approximation error  $\varepsilon > 0$ . Then  $\mathcal{D}_d(P, Q) \subseteq \mathcal{D}'_{(1+4\varepsilon)d}(P, Q) \subseteq \mathcal{D}_{(1+8\varepsilon)d}(P, Q)$ .

**Proof.** With slight abuse of notation, let  $x = P(x)$ , and  $y = Q(y)$ , for  $x \in [0, \|P\|]$ , and  $y \in [0, \|Q\|]$ . Let  $x' = f_{P, \varepsilon d}(x)$ , and let  $y' = f_{Q, \varepsilon d}(y)$ . Observe that  $\text{dist}(x, x') \leq 2\varepsilon d$  for all  $x \in P$  because if  $x$  is within the ball  $B(u, \varepsilon d)$ , then  $x$  is at most  $2\varepsilon d$  apart from  $x'$ . If  $x$  is outside  $B(u, \varepsilon d)$ , it is at most  $\varepsilon d$  apart from  $x'$ , due to the simplification.

- $\mathcal{D}_d(P, Q) \subseteq \mathcal{D}'_{(1+4\varepsilon)d}(P, Q)$ . If a point  $(x, y) \in \mathcal{D}_d(P, Q)$  is white, then  $\text{dist}(x, y) \leq d$ . By the triangle inequality,  $\text{dist}(x', y') \leq \text{dist}(x', x) + \text{dist}(y', y) + \text{dist}(x, y) \leq 2\varepsilon d + 2\varepsilon d + d = (1 + 4\varepsilon)d$ , hence  $(x', y')$  must also be white.
- $\mathcal{D}'_{(1+4\varepsilon)d}(P, Q) \subseteq \mathcal{D}_{(1+8\varepsilon)d}(P, Q)$ . Similarly, if a point  $(x', y') \in \mathcal{D}'_{(1+4\varepsilon)d}(P, Q)$  is white, then  $(x, y) \in \mathcal{D}_{(1+8\varepsilon)d}(P, Q)$  must also be white, because  $\text{dist}(x, y) \leq \text{dist}(x', x) + \text{dist}(y', y) + \text{dist}(x', y') \leq 2\varepsilon d + 2\varepsilon d + (1 + 4\varepsilon)d = (1 + 8\varepsilon)d$ . ◀

Similar to how we defined the  $(u, v)$  cell, let the  $(P_{uv}, Q_{ab})$  cells be the cells in the free space diagram defined by the subcurves  $P_{uv}$  and  $Q_{ab}$ . We show that we can compute the intersection of the simplified free space with  $(P_{uv}, Q_{ab})$  cells in constant time. Please see the full version for a proof of below lemma.

► **Lemma 8.** *Given vertices  $u, v$  on  $P$  and  $a, b$  on  $Q$ , one can construct the cells in  $\mathcal{F}'_{(1+\varepsilon)d}(P, Q)$  defined by  $P_{uv}$  and  $Q_{ab}$  in constant time.*

The complexity of the simplified free space  $\mathcal{D}'_{(1+\varepsilon)d}(P, Q)$  is  $O(cn/\varepsilon)$  if  $P$  and  $Q$  are  $c$ -packed. Assuming that  $P_{uv}$  and  $Q_{ab}$  are simplified into segments  $(u, v) \in P'$  and  $(a, b) \in Q'$ , respectively, the simplified free space intersects  $(P_{uv}, Q_{ab})$  cells if and only if the distance between  $(u, v)$  and  $(a, b)$  is at most  $(1 + \varepsilon)d$ . The rest follows by modifying the proof of [15, Lemma 4.4].

► **Corollary 9.** *Let  $P$  and  $Q$  be two  $c$ -packed curves with complexity  $n$ , and let  $\hat{\varepsilon}$  be a constant times a parameter  $\varepsilon > 0$ . The complexity of the simplified free space  $\mathcal{D}'_{(1+\hat{\varepsilon})d}(P, Q)$  is  $O(cn/\varepsilon)$ .*

## 4.2 Compute the Non-empty Cells

To take advantage of the near-linear complexity of the simplified free space, we use an algorithm by Conradi and Driemel [13] to efficiently compute the non-empty cells without inspecting all pairs of segments.

► **Fact 10** ([13, Lemma 59]). *Given two  $c$ -packed curves  $P$  and  $Q$  in  $\mathbb{R}^2$ , a parameter  $d \geq 0$ , and let  $P'$  and  $Q'$  be their  $\varepsilon d$ -simplifications. In  $O((cn/\varepsilon) \log(cn/\varepsilon))$  time, one can find all pairs of segments  $(u, v) \in P'$  and  $(a, b) \in Q'$  such that the distance between  $(u, v)$  and  $(a, b)$  is at most  $d$ .*

To construct the simplified free space diagram efficiently, we first observe the following.

► **Observation 11.** *If segments  $(u, v) \in P'$  and  $(a, b) \in Q'$  are more than  $(1 + 2\varepsilon)d$  apart, then  $P_{uv}$  and  $Q_{ab}$  are more than  $d$  apart.*

The above observation enables us to determine if  $(P_{uv}, Q_{ab})$  cells are empty by determining if  $(u, v)$  and  $(a, b)$  are near.

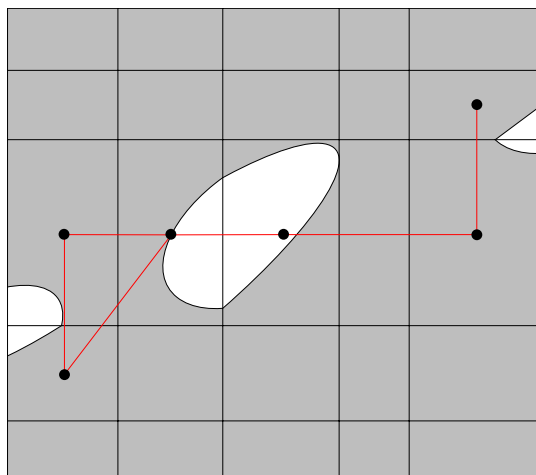
## 4.3 Constructing the Simplified Free Space Diagram

Given two  $c$ -packed polygonal curves  $P$  and  $Q$ , we will use the results from previous subsections to construct the simplified free space diagram using the below steps. In Lemma 8, we showed that if  $P_{uv}$  and  $Q_{ab}$  are simplified into segments  $(u, v) \in P'$  and  $(a, b) \in Q'$ , respectively, we can compute  $(P_{uv}, Q_{ab})$  cells in constant time. Such aggregation of  $(P_{uv}, Q_{ab})$  cells is an *aggregated non-empty cell*, and we will treat them as one cell for simplicity.

1. Simplify  $P$  and  $Q$  into their  $\varepsilon d$ -simplifications  $P'$  and  $Q'$ .
2. Find all pairs of nearby segments from  $P'$  and  $Q'$  that are at most  $(1 + \varepsilon)d$  apart using Fact 10.
3. For each pair of nearby segments  $(u, v) \in P'$  and  $(a, b) \in Q'$ , compute the  $(P_{uv}, Q_{ab})$  cells using Lemma 8.
4. Sort all non-empty cells horizontally and vertically.
5. Connect non-empty cells in a graph fashion such that a non-empty cell is connected to the first non-empty cells to its top, bottom, left, and right.

Given two polygonal curves  $P$  and  $Q$  of complexity  $n$ , simplifying them (step 1) takes  $O(n)$  time. By Fact 10, step 2 takes  $O((cn/\varepsilon) \log(cn/\varepsilon))$  time. Computing a cell in  $\mathcal{F}'_{(1+\varepsilon)d}(P, Q)$  takes  $O(1)$  time by Lemma 8.  $\mathcal{F}'_{(1+\varepsilon)d}(P, Q)$  has at most  $O(cn/\varepsilon)$  non-empty cells, which takes  $O(cn/\varepsilon)$  time to compute in step 3; sorting them in step 4 takes  $O((cn/\varepsilon) \log(cn/\varepsilon))$  time. Connecting each cell to at most four other cells takes  $O(cn/\varepsilon)$  time in step 5. Putting this together, we obtain Lemma 12, and we summarise our result in Theorem 1.





■ **Figure 3** The non-empty cells are connected horizontally and vertically to skip empty cells.

► **Lemma 12.** *Let  $P$  and  $Q$  be two  $c$ -packed curves of complexities  $n$ . Let  $\varepsilon > 0$  and  $d > 0$  be two parameters, and let  $\hat{\varepsilon} \leq 8 \cdot \varepsilon$ . One can construct and connect  $O(cn/\varepsilon)$  aggregated non-empty cells of the simplified free space diagram  $\mathcal{F}'_{(1+\hat{\varepsilon})d}(P, Q)$  in  $O((cn/\varepsilon) \log(cn/\varepsilon))$  time such that  $\mathcal{D}_d(P, Q) \subseteq \mathcal{D}'_{(1+\hat{\varepsilon})d}(P, Q) \subseteq \mathcal{D}_{(1+\hat{\varepsilon})d}(P, Q)$ . Given an aggregated non-empty cell  $C$ , one can access the first aggregated non-empty cells below, above, to the left, and to the right of  $C$  in  $O(1)$  time.*

► **Theorem 1.** *Given a pair of trajectories, one can construct a simplified free space diagram in  $O((cn/\varepsilon) \log(cn/\varepsilon))$  time, so that the simplified free space has complexity  $O(cn/\varepsilon)$ , it approximates the Fréchet distance to within a factor of  $(1 + \varepsilon)$ , and it preserves the trajectory lengths of the original trajectory.*

## 5 Reference trajectory is vertex-to-vertex

Throughout the rest of the paper we assume that the free space diagram is the simplified free space diagram  $\mathcal{F}'_{(1+\varepsilon)d}$  in Lemma 12. Next, we will use the algorithm by Gudmundsson and Wong [24] to determine whether there is a solution to  $\text{SC}(T, m, 1, (1 + \varepsilon)d)$  where  $T$  is a  $c$ -packed trajectory, and the reference subtrajectory  $T_{st}$  is vertex-to-vertex, i.e., both  $s$  and  $t$  must be an endpoint of some segment of  $T$ .

Three data structures are used in the vertex-to-vertex subtrajectory cluster algorithm of Gudmundsson and Wong [24] – a directed graph, a range tree, and a link-cut tree. For an overview of these data structures, see the full version. In Section 5.1, we show that the number of leaves per range tree is  $O(c/\varepsilon)$ , and the directed graph has complexity  $O((cn/\varepsilon) \log(c/\varepsilon))$ . In Section 5.2, we show that the link-cut tree data structure can be used without modification.

### 5.1 Using a Directed Graph to Store Candidate Monotone Paths

To show that the range tree has at most  $O(c/\varepsilon)$  leaves, it suffices to show that there exist at most  $O(c/\varepsilon)$  critical points on each horizontal or vertical boundary of the simplified free space diagram.

► **Lemma 13.** *In the simplified free space diagram  $\mathcal{F}'_{(1+\hat{\varepsilon})d}(T, T)$ , let  $H$  be a horizontal (resp. vertical) strip that is at least  $\varepsilon d$  wide on its  $y$ -span (resp.  $x$ -span). The intersection of  $H$  and the simplified free space  $\mathcal{D}'_{(1+\hat{\varepsilon})d}(T, T)$  exists in at most  $O(c/\varepsilon)$  aggregated cells.*

**Proof.** Let  $T'$  be the  $\varepsilon d$ -simplification of  $T$ , and let  $T_{uv}$  simplify into segment  $(u, v) \in T'$ . Let  $u' \subseteq (u, v)$  be a small part that is at least  $\varepsilon d$  long. Let  $S_{u'} = u' \oplus B(0, (1 + \hat{\varepsilon})d)$ .

Using similar construction, and arguments of [15, Lemma 4.4], one can prove that at most  $O(c/\varepsilon)$  segments in  $T'$  intersects  $S_{u'}$ . Based on the construction of the simplified free space  $\mathcal{D}'_{(1+\hat{\varepsilon})d}(T, T)$ , a point  $(x, y) \in \mathcal{D}'_{(1+\hat{\varepsilon})d}(T, T)$  is white if and only if  $\text{dist}(f_{T, \varepsilon d}(T(x)), f_{T, \varepsilon d}(T(y))) \leq (1 + \hat{\varepsilon})d$ . As such, at most  $O(c/\varepsilon)$  aggregated cells have simplified free space intersecting  $H$ . ◀

Next, bound the construction time and space complexity of the directed graph in [24].

► **Lemma 14.** *Given a  $c$ -packed trajectory  $T$  of complexity  $n$ , constructing  $G$  for the simplified free space diagram  $\mathcal{F}'_{(1+\hat{\varepsilon})d}(T, T)$  takes  $O((cn/\varepsilon) \log(n/\varepsilon))$  time.  $G$  has  $O(cn/\varepsilon)$  nodes and  $O((cn/\varepsilon) \log(c/\varepsilon))$  edges.*

**Proof.** Let  $n_k$  be the number of non-empty aggregated cells in the  $j$ th row in  $\mathcal{F}'_{(1+\hat{\varepsilon})d}(T, T)$ . Construction of the range tree for the top (resp. right) boundary of a row (resp. column) takes  $O(n_k \log n_k)$  time [14]. For all  $p_i$ , finding  $q_i$  takes  $O(n_k \log n_k)$  time

and recall that there are  $O(cn/\varepsilon)$  critical points in  $\mathcal{F}'_{(1+\hat{\varepsilon})d}(T, T)$ . The total construction time is as follows.

$$\sum_{j=0}^{n+1} n_k \log n_k \leq \log\left(\frac{cn}{\varepsilon}\right) \sum_{j=0}^{n+1} n_k = \log\left(\frac{cn}{\varepsilon}\right) O\left(\frac{cn}{\varepsilon}\right) \in O\left(\left(\frac{cn}{\varepsilon}\right) \log\left(\frac{n}{\varepsilon}\right)\right)$$

By Corollary 9, the simplified free space diagram has  $O(cn/\varepsilon)$  non-empty aggregated cells, therefore  $G$  has  $O(cn/\varepsilon)$  nodes. In a range tree, given a continuous interval  $[q_k, q_i]$ , one can find  $O(\log n)$  nodes such that these nodes include  $[q_k, q_i]$  in their canonical subset, where  $n$  is the total number of items in the leaves [14]. There are at most  $O(c/\varepsilon)$  nodes on a horizontal or vertical boundary by Lemma 13, and each critical point  $p_i$  on a vertical (resp. horizontal) cell boundary connects to  $O(\log(c/\varepsilon))$  nodes, therefore the total number of edges is  $O((cn/\varepsilon) \log(c/\varepsilon))$ . ◀

## 5.2 Storing and Reusing Pre-computed Paths

A link-cut tree [28] maintains a forest that allows the link/cut operations of subtrees in  $O(\log n)$  amortised time. In addition, a link-cut tree allows finding the root of a node in  $O(\log n)$  amortised time. The algorithm by Gudmundsson and Wong [24] used a link-cut tree to store and re-use monotone paths. Consider when a sweepline, either  $l_s$  or  $l_t$ , stops at a new critical point  $p$ . Instead of recomputing the monotone paths, they need only to add  $p$  to the existing link-cut tree they maintained in the previous instances.

With graph  $G$  defined, we can analyse the total running time of the algorithm by Gudmundsson and Wong [24] on the simplified free space diagram. The key to observe the running time is that in their algorithm, if an edge leads to a dead-end, it is marked and will not be used in future searches. Furthermore, inserting or removing an edge takes  $O(\log n)$  amortised time in a link-cut tree.

► **Theorem 2.** *There is an  $O(nm \log(c/\varepsilon) \log(n/\varepsilon))$  time algorithm that solves  $\text{SC}(\mathbf{T}, m, 1, (1 + \varepsilon)d)$  in the case that the reference trajectory is vertex-to-vertex.*

**Proof.** Construction of the simplified free space diagram takes  $O((cn/\varepsilon) \log(cn/\varepsilon))$  time by Theorem 1. Construction of  $G$  takes  $O((cn/\varepsilon) \log(n/\varepsilon))$  time by Lemma 14. The graph  $G$  has at most  $O(nm \log(c/\varepsilon))$  edges, see the full version. Gudmundsson and Wong [24] showed that

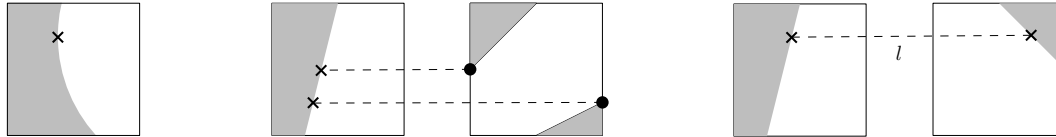
an edge is added to and removed from the link-cut tree at most once, and adding/removing an edge from the link-cut tree takes  $O(\log(n/\varepsilon))$  time since the maximum number of nodes in the link-cut tree is upperbounded by the number of nodes in  $G$ . Therefore maintaining the link-cut tree takes  $O(nm \log(c/\varepsilon) \log(n/\varepsilon))$  time. ◀

## 6 Reference trajectory is arbitrary

Our results in this section rely heavily on the work of Gudmundsson and Wong [24]. Due to space constraints, we can only highlight important parts of their algorithm, and the analysis of our improvements.

When the reference trajectory is arbitrary, a monotone path can start and finish at arbitrary positions in the non-empty cells. Therefore, in addition to the critical points in the free space diagram and the greedy critical points, Gudmundsson and Wong defined three new types of *internal critical points* [24, Definition 25]. An internal critical point must lie in the interior of a non-empty cell, and lie on the boundary of the free space. They made the following distinction (see Figure 4).

1. End-of-cell critical point: the leftmost and rightmost white point of a non-empty cell.
2. Propagated critical point: a point on the boundary of the free space that shares a  $y$ -coordinate with a critical point.
3.  $l$ -apart critical points: two points on the boundaries of free space that are a distance of  $l$  apart horizontally.



■ **Figure 4** The three types of internal critical points are illustrated using a cross in the left, middle, and right figures, respectively. From left to right, they are the end-of-cell critical points (left), propagated critical points (middle) and  $l$ -apart critical points (right).

There could be an infinite number of  $l$ -apart critical points in a pair of non-empty cells. However, if this is the case, we can simply perturb the input by a miniscule amount so that there are no longer an infinite number of  $l$ -apart critical points. See the full version for an example and a figure. Therefore, for the rest of the paper, we can assume that there are at most a constant number of  $l$ -apart critical points per pair of cells.

We will first bound the number of internal critical points and the time it takes to compute them. One can compute the end-of-cell and  $l$ -apart critical points in linear time with respect to the number of non-empty cells since there are at most a constant number of them per pair of cells. In Lemma 13, we showed that in a narrow horizontal strip, only a small number of cells intersect free space. An output-sensitive query algorithm would be efficient to find the non-empty cells that a critical point  $p$  propagates to. Therefore, we can use an interval tree [14] to store the  $y$ -spans of all non-empty cells in a row, and query the intersecting intervals of  $y(p)$  in logarithmic time. We formalise the above arguments in the below Lemma 15.

► **Lemma 15.** *Assume that there is a constant number of  $l$ -apart critical points per pair of cells, it takes  $O(cn \log(n/\varepsilon) + c^2n/\varepsilon^2)$  time to compute  $O(c^2n/\varepsilon^2)$  internal critical points in the simplified free space diagram  $\mathcal{F}'_{(1+\varepsilon)d}(T, T)$ .*

**Proof.** There are  $O(cn/\varepsilon)$  non-empty aggregated cells in  $\mathcal{F}'_{(1+\varepsilon)d}(T, T)$ , or non-empty cells for short, and  $O(cn/\varepsilon)$  end-of-cell critical points in  $\mathcal{F}'_{(1+\varepsilon)d}(T, T)$ . Each critical point propagates  $O(c/\varepsilon)$  times by Lemma 13, therefore there are  $O(c^2n/\varepsilon^2)$  propagated critical points. We can charge a cell with a constant number of  $l$ -apart critical points. Therefore, there are at most  $O(cn/\varepsilon)$   $l$ -apart critical points. In total, there are  $O(c^2n/\varepsilon^2)$  internal critical points.

One can compute the end-of-cell critical points by iterating through the free space diagram in  $O(cn/\varepsilon)$  time. To compute the  $l$ -apart critical points, we can start from the first non-empty cell  $C$  in a row and find the first cell that is  $l$ -apart from  $C$ , and solve a constant number of quadratic equations. We can then slide this  $l$ -apart line and do the same for all pairs of cells that are  $l$ -apart in all rows in  $O(cn/\varepsilon)$  time in total.

To compute the propagated critical points, we construct an interval tree [14] for each row in  $\mathcal{F}'_{(1+\varepsilon)d}(T, T)$  to store the maximum and minimum  $y$ -coordinates of the free space in the non-empty cells. Let  $n_i$  be the number of non-empty cells in the  $i$ th row. We can sum the construction time of the interval trees.

$$\sum_{i=1}^n n_i \log n_i \leq \frac{cn}{\varepsilon} \log \left( \frac{cn}{\varepsilon} \right) \in O \left( \left( \frac{cn}{\varepsilon} \right) \log \left( \frac{cn}{\varepsilon} \right) \right)$$

Given a critical point  $p$  in the  $i$ th row, one can query the interval tree in  $O(\log n_i + c/\varepsilon) \in O(\log n + c/\varepsilon)$  time to compute the propagated critical points from  $p$  using Lemma 13 and [14]. With  $O(cn/\varepsilon)$  critical points, computing the propagated critical points takes  $O(cn \log(n)/\varepsilon + c^2n/\varepsilon^2)$  time. ◀

With the additional internal critical points, the number of reference trajectories and the number of greedy critical points increases. We can use the algorithm in the previous section, and obtain the following result.

► **Lemma 16.** *There is an  $O((c^2mn/\varepsilon^2) \log(c/\varepsilon) \log(n/\varepsilon))$  time algorithm that solves  $\text{SC}(\mathbb{T}, m, 1, (1 + \varepsilon)d)$  in the case that the reference trajectory is arbitrary.*

**Proof.** See the full version. ◀

## 6.1 Improve Further with an Interval Management Data Structure

The bottleneck in the above Lemma 16 is operating the outgoing edges of the  $O(c^2mn/\varepsilon^2)$  greedy critical points, which are generated from  $O(c^2n/\varepsilon^2)$  propagated critical points. To avoid computing the greedy critical points, Gudmundsson and Wong [24] used a dynamic monotonic interval data structure [16] to store overlapping monotonic intervals that represent the  $y$ -spans of monotone paths between  $l_s$  and  $l_t$ . Instead of searching for a set of monotone paths between each window greedily, they showed that one can update and query the interval data structure to retrieve  $m - 1$  non-overlapping intervals, all in  $O(\log n)$  amortised time.

► **Theorem 3.** *There is an  $O((c^2n/\varepsilon^2) \log(c/\varepsilon) \log(n/\varepsilon))$  time algorithm that solves  $\text{SC}(\mathbb{T}, m, 1, (1 + \varepsilon)d)$  in the case that the reference trajectory is arbitrary.*

**Proof.** Constructing the simplified free space diagram takes  $O((cn/\varepsilon) \log(cn/\varepsilon))$  time by Theorem 1. Computing and sorting the internal critical points takes  $O((c^2n/\varepsilon^2) \log(n/\varepsilon))$  time by Lemma 15. There are  $O((c^2n/\varepsilon^2) \log(c/\varepsilon))$  edges in total by Lemma 13, and each

edge takes  $O(\log(n/\varepsilon))$  time to insert or remove since there are at most  $O(c^2n/\varepsilon^2)$  nodes in the link-cut tree. In total, we spend  $O((c^2n/\varepsilon^2) \log(c/\varepsilon) \log(n/\varepsilon))$  time to maintain the edges in  $G$ .

Each internal critical point is treated as an event, and maintaining the interval data structure takes  $O(\log n)$  amortised time per event point (see [24, Theorem 2]), and thus  $O((c^2n/\varepsilon^2) \log n)$  in total. The overall complexity is dominated by maintaining the edges. ◀

## 7 Conclusion

We presented an algorithm that solves the subtrajectory cluster problem on  $c$ -packed trajectories  $T$  with an approximation error on the Fréchet distance, achieving an  $O((c^2n/\varepsilon^2) \log(c/\varepsilon) \log(n/\varepsilon))$  time complexity. Our algorithm builds upon the near-optimal algorithm proposed by Gudmundsson and Wong [24], but with significant improvements. By carefully analysing the properties of  $c$ -packed trajectories, we have shown that important parameters such as the number of propagated critical points are significantly lower than the theoretical  $O(n)$  upperbound for realistic trajectories. As a result, our algorithm improves upon the near-optimal algorithm by replacing a factor of  $n^2$  with  $c^2/\varepsilon^2$ , leading to more efficient subtrajectory cluster of realistic trajectories.

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