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A GPU-accelerated Framework for Processing Trajectory Queries

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Abstract—**The increasing amount of trajectory data facilitates a wide spectrum of practical applications. In many such applications, large numbers of trajectory range and similarity queries are issued continuously, which calls for high-throughput trajectory query processing. Traditional in-memory databases lack considerations of the unique features of trajectories, thus suffering from inferior performance. Existing trajectory query processing systems are typically designed for only one type of trajectory queries, i.e., either range or similarity query, but not for both. Inspired by the massive parallelism on GPUs, in this paper, we develop a GPU-accelerated framework, named GAT, to support both types of trajectory queries (i.e., both range and similarity queries) with high throughput. For similarity queries, we adopt the Edit Distance on Real sequence (EDR) as the similarity measure which is accurate and robust to noise in real-world trajectories. GAT employs a GPU-friendly index called GTIDX to effectively filter invalid trajectories for both range and similarity queries, and exploits the GPU to perform parallel verifications. To accelerate the verification process on the GPU, we apply the Morton-based encoding method to reorganize trajectory points and facilitate coalesced data accesses for individual point data in global memory, which reduces the global memory bandwidth requirement significantly. We also propose a technique of grouping size-varying cells into balanced blocks with similar numbers of trajectory points, to achieve load balancing among the Streaming Multiprocessors (SMs) of the GPU. We conduct extensive experiments to evaluate the performance of GAT using two real-life trajectory datasets. The results show that GAT is scalable and achieves high throughput with acceptable indexing cost.**

I. Introduction

Recent years have witnessed a surge of trajectories being continuously generated from every corner around the world. For instance, DiDi Chuxing, China's largest online ride-sharing platform, processes over three million trip requests every day, suggesting that thousands of trajectories are generated in every second [1]. A *trajectory* is typically represented by a sequence of successive points of moving objects, where each point consists of geospatial coordinates and the corresponding timestamp. Large trajectory data facilitate a wide spectrum of real-world applications, such as route planing [2], trajectory pattern mining [3] and travel time prediction [4]. In these applications, two types of trajectory queries, i.e., *range query* and *similarity query*, serve as primitive, yet essential operations.

A range query aims to identify trajectories overlapping a given bounding area, while a similarity query determines the k trajectories that are most similar to the query trajectory (the similarity is typically measured by a certain distance function). Both types of trajectory queries are expensive to compute, in face of hundreds of millions of trajectories. Furthermore, in many real-world applications, large numbers of trajectory queries may be continuously generated and should be efficiently processed in order to fulfill application requirements. Take the taxi fleet management in Shanghai for example. Detour detections pose top-k similarity queries on historical trajectories to determine if the ride trajectory of a given taxi is an outlier, comparing against the historical trajectories sharing similar origins and destinations. And lost found services raise range queries in order to locate all taxis that traversed in a given region. There are around 50,000 taxis in Shanghai, the largest metropolitan in China, and hundreds of range and top-k similarity queries may be generated in every minute, which should be processed efficiently in support of the management of such a large taxi fleet. *Therefore, processing trajectory queries in high throughput has become significantly important.*

While traditional in-memory databases (e.g., HStore [5]) or data processing frameworks (e.g., SparkSQL [6]) provide generic solutions that can process the two types of trajectory queries, their performance is typically suboptimal, due to the lack of considerations on the unique features of trajectories. Recently, considerable research efforts have been devoted to developing specialized trajectory query processing systems (e.g., Simba [7], SharkDB [8]). However, these existing solutions are typically designed for answering only a certain type of queries, either range or similarity queries, but not both. To process both types of queries together, a possible extension to these solutions is to build separate indices with different parameter settings for each type of queries, but resulting in problems such as extra memory cost.

To scale up the performance, a natural solution is to exploit GPUs to accelerate trajectory query processing. GPUs have recently been widely applied in some practical applications, thanks to their massive parallelism. To the best of our knowledge, however, only one recent work [9] attempted at leveraging GPUs for processing trajectory similarity queries. They employ the Hausdorff distance function [10] for measuring the

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similarity between two trajectories. This distance function can easily be decomposed into independent computations, hence facilitating the parallel processing on the GPU. However, the major disadvantages of this work are three-fold. First, the underlying Hausdorff distance function is sensitive to location noise and local time shifting (which is common in real-world trajectories), which may return some trajectories that are not similar to the query trajectory [11]. Second, its parallel query processing on the GPU is highly coupled with the Hausdorff distance function, making it inextensible to more realistic distance functions such as EDR [12]. Finally, it is designed for only one type of queries, i.e., similarity queries, and cannot be easily extended for efficient processing of range queries.

In this paper, we develop a GPU-accelerated framework, named GAT, for processing the two types of trajectory queries (i.e., both range and similarity queries). To return high-quality similar trajectories, we adopt the EDR [12] as the distance function, which is an accurate and robust similarity measure for searching for similar trajectories [11]. Generally, GAT follows the filtering-and-verification framework where the CPU is responsible for generating candidate trajectories via effective pruning rules and the GPU performs parallel candidate verifications for final resulting answers. The filtering basis of GAT is a GPU-friendly index called GTIDX that fuses the merits of the cell-level trajectory representations and the quadtree-like index, and reduces the number of candidates for both types of trajectory queries effectively. The candidate trajectories are then be transferred to the GPU for verifications. We find that there exists overlap among the candidates of different queries. This inspires us to propose a Memory Allocated Table (MAT) for checking the existence of data in global memory of the GPU, thus avoiding redundant data transfer over PCIe bus. During verification, for range queries, we leverage the GPU to determine whether a candidate trajectory overlaps a given bounding area in parallel; For top-k similarity queries, we iteratively supply the GPU with a set of candidate trajectories based on the lower bound of EDR distance, parallelize each EDR distance computation, and progressively refine a priority queue that maintains the possible top-k answers according to the computed EDR values.

To exploit GPUs for efficient candidate verification, we have to address two practical issues. The first issue is the *limited global memory bandwidth* of the GPU. Threads running on different GPU cores access trajectory data from the shared global memory concurrently. Numerous individual data requests from thousands of cores may easily compromise the verification performance due to the limited bandwidth of global memory. The second issue is *load balancing among the Streaming Multiprocessors (SMs) of the GPU*. The GPU follows the Single Instruction Multiple Data parallelism model and it is critical to assign similar amount of computational workload among the SMs on the GPU for high processing performance. Any SMs with heavier workloads may become stragglers, hindering the overall performance.

In GAT, we provide a data placement strategy to facilitate *coalesced global memory data access* among GPU cores. We apply the Morton-based encoding method [13] to reorder a set of cells and reorganize trajectory points according to these cells. The Morton's codes ensure that trajectory points to be verified by the GPU cores in the same SM are stored continuously in global memory, and the individual accesses to these points can be coalesced into a single access request to significantly reduce the global memory bandwidth requirement. To achieve load balancing, we deliberately *group size-varying cells into balanced blocks*, where different balanced blocks involve similar numbers of trajectory points. By assigning the balanced blocks with similar numbers of trajectory points to the SMs, we avoid overloading some SMs to a great extent.

The main contributions of this work are the following.

• We develop a GPU-accelerated framework GAT to support the two types of queries, including both range and top-k similarity queries over trajectories. GAT follows the filtering-and-verification framework, where we identify candidates on the CPU and leverage the GPU to perform parallel verifications to increase the overall throughput of query processing.

• We design a GPU-friendly index GTIDX that organizes trajectory points into geospatial cells, which is effective in pruning invalid candidates for both types of trajectory queries and generating similar-sized candidates for achieving load balance among the SMs on the GPU.

• It is the first work, to the best of our knowledge, that adopts the EDR distance function for processing similarity queries using the GPU. The EDR distance function is accurate for measuring the similarity between trajectories, and robust to location noises. We decompose the EDR calculation into independent components to exploit the GPU.

• We propose two techniques of accelerating the verification process on the GPU. We employ the Morton-based encoding to facilitate coalesced individual accesses from cores to reduce the global memory bandwidth requirement. And we propose a technique of grouping size-varying cells into balanced blocks to achieve load balancing among the GPU SMs.

• We conduct extensive experiments to evaluate the performance of GAT using two real-life trajectory datasets. The results show that our framework is efficient, scalable and with high throughput. It runs about 6.9x and 4.5x faster than CPU-based multi-threaded methods on range and top-k similarity queries, respectively, and outperforms the adaptations of GPU solutions to range queries.

The remainder of this paper is organized as follows. Section II gives preliminaries. Section III provides an overview of GAT. Section IV presents the index structure. Section V provides GPU-accelerated query processing approaches. We show experimental results in Section VI, review related works in Section VII and conclude this paper in Section VIII.

II. Preliminaries

A. Trajectory Range and Similarity Queries

Definition 1 (Trajectory T): A trajectory T is a sequence of points that captures the trace of a moving object over time, i.e., $T = [(p_1, t_1), \cdots, (p_n, t_n)]$, where $p_i = (x_i, y_i)$ records the geospatial coordinates and t_i is a timestamp, for $i \in [1, n]$.

Let $|T|$ denote the number of points in T and $\mathcal{T}$ be the set of all trajectories.

Definition 2 (Trajectory Range Query $\mathcal{Q}_r$): Given a query region R and a trajectory dataset $\mathcal{T}$, a range query $\mathcal{Q}_r(R)$ returns a set of trajectories overlapped with R, i.e.,

$$\mathcal{Q}_r(R) = \{T \in \mathcal{T} | \exists p_i \in T, \ s.t. \ p_i \in R\} \tag{1}$$

For simplicity, we consider query regions as two-dimensional rectangles in this paper, but our approach can be adapted to handle regions in arbitrary shapes.

We use *Edit Distance on Real sequence* (EDR) to measure the similarity between two trajectories, which is robust and accurate than other distance functions [12].

Definition 3 (EDR δ): Given two trajectories T and T', the EDR between T and T' is the minimum number of insert, delete or replace operations needed to transform T to T':

$$\delta(T, T') = \begin{cases} |T| & \text{if } |T'| = 0 \\ |T'| & \text{if } |T| = 0 \\ \min\{\delta(\bar{T}, \bar{T}') + subcost, & \\ \delta(\bar{T}, T') + 1, \delta(T, \bar{T}') + 1\} & \text{otherwise} \end{cases} \tag{2}$$

where $\bar{T} = [(p_2, t_2), \cdots, (p_n, t_n)]$, (resp. $\bar{T}'$), and $subcost = 0$ if $|x_1 - x_1'| \leq \epsilon \wedge |y_1 - y_1'| \leq \epsilon$, or 1 otherwise. ϵ is a matching threshold.

Definition 4 (Top-k Trajectory Similarity Query $\mathcal{Q}_k$): Given $\mathcal{T}$, a query trajectory T_q and a positive integer k, the top-k trajectory similarity query $\mathcal{Q}_k$ return the k most similar trajectories in $\mathcal{T}$, denoted by $\mathcal{Q}_k(T_q) \subseteq \mathcal{T}$, satisfying: $\forall T' \in \mathcal{Q}_k(T_q)$, $\forall T'' \in \mathcal{T} - \mathcal{Q}_k(T_q)$, $\delta(T_q, T') \leq \delta(T_q, T'')$.

B. GPUs

A GPU typically consists of tens of SMs where each SM includes a number of cores running threads concurrently. All threads execute the same set of instructions over different data, following the Single Instruction Multiple Data (SIMD) parallelism model. Each SM has its shared memory and multiple cores, and all SMs share global memory. Data used by threads are usually transferred from main memory to global memory first, via PCIe bus (the typical bandwidth is lower than 10GB/s). We adopt CUDA [14] proposed by NVIDIA as our programming model over GPUs. A GPU program is also referred to as a *kernel*. When executing a kernel program, a grid of CUDA threads are launched immediately. All CUDA threads are divided into blocks and further into warps explicitly. During GPU computing, each CUDA block is assigned to one SM which maintains a warp scheduler to determine which warp to be executed on the cores in the SM in the next clock cycle.

III. Overview of GAT

The overview of GAT is depicted in Figure 1, which consists of two main components, i.e., Cell-based Index Construction and Trajectory Query Processing (including Range Query Processing and Similarity Query Processing).

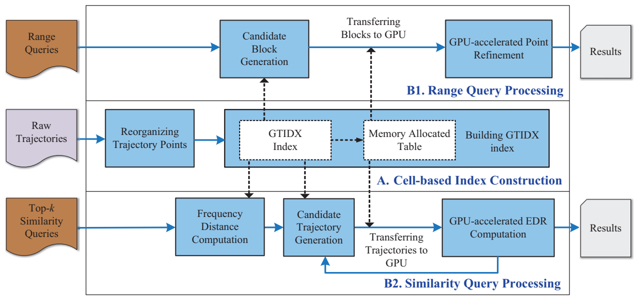

Range Queries
Candidate Block Generation
Transferring Blocks to GPU
GPU-accelerated Point Refinement
Results
B1. Range Query Processing
Raw Trajectories
Reorganizing Trajectory Points
GTIDX Index
Memory Allocated Table
Building GTIDX index
A. Cell-based Index Construction
Top-k Similarity Queries
Frequency Distance Computation
Candidate Trajectory Generation
Transferring Trajectories to GPU
GPU-accelerated EDR Computation
Results
B2. Similarity Query Processing

Fig. 1. The overview of GAT

A. Cell-based Index Construction

There are two main steps in this component:

• **Reorganizing trajectory points**: As discussed in Section I, our index structure depends on cell-level trajectory representation. This is achieved by constructing a square called *whole region* covering all the trajectory points. We divide the whole region into 4^n disjoint *cell*s of the same size along the two geospatial coordinates, where n can be pre-defined to control the total number of cells. Given the raw trajectories, we map each trajectory point to its covering cell. All the points in the same cell are sorted by their belonging trajectory IDs and timestamps in ascending order. Let $\mathcal{C}$ denote all the cells and $P(C)$ denote the set of points residing in cell $C \in \mathcal{C}$.

• **Building GTIDX index**: Our index structure contains three parts: the cell-based trajectory table, the trajectory index and the quadtree-like index. The cell-based trajectory table stores all the points organized by cells, acting as the storage of raw trajectories. The trajectory index is used to reconstruct trajectories from the cell-based trajectory table, which facilitates efficient processing of top-k similarity queries. The quadtree-like index organizes cells into *block*s. Each leaf node in this index corresponds to a block. While the number of cells in each block may differ, the number of the involving trajectory points per block is similar. Organizing cells into blocks helps achieve load balanceing for efficient query processing.

B. Trajectory Query Processing

Without loss of generality, we illustrate the major steps of trajectory query processing by considering a single query. The processing of different queries is independent and concurrent. We first introduce how to perform trajectory range queries, which involves two steps.

• **Candidate block generation**: The input to this step is a query region R and the output is a set of blocks containing several cells with candidate trajectory points, denoted by $\mathcal{Q}_r^c$. First, we traverse the quadtree-like index to locate leaf nodes where the corresponding blocks overlap R. Then, these blocks are identified as candidate blocks and put into $\mathcal{Q}_r^c$.

• **GPU-accelerated point verification**: In this step, we verify whether each point in the candidate blocks $\mathcal{Q}_r^c$ is within the query region using GPU. We first transfer the point to global memory of the GPU if it is not yet in global memory according to the MAT. When a point resides in R, we retrieve

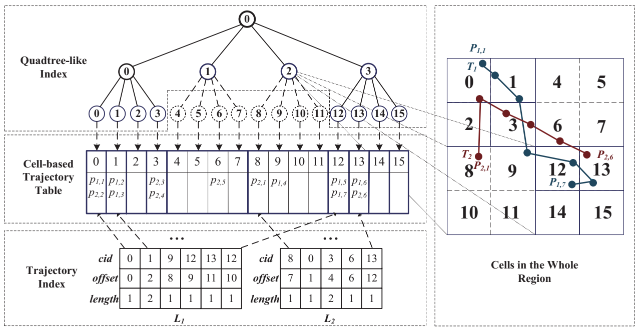


Fig. 2. The structure of GTIDX

the corresponding trajectory based on trajectory ID and add it into the final result set $\mathcal{Q}_r(R)$. For load balance purpose, we assign a block of trajectory points to one SM for verification.

To handle trajectory top-k similarity queries, we maintain a k-sized priority queue Q_k^r for k trajectories with the smallest computed EDR distances, and perform the following three steps, where Step 2 and 3 are executed iteratively.

• **Frequency distance (FD) computation**: The input to this step is a query trajectory T_q and a positive integer k. In this step, we compute a *lower bound* of $\delta(T_q, T)$ [12] for each $T \in \mathcal{T}$, which will be used for reducing unnecessary EDR computations.

• **Candidate trajectory generation**: In each iteration of this step, we select a set of trajectories with the smallest EDR lower bounds, because they are more likely to be in the top-k results. We then reconstruct these candidate trajectories, denoted by $\mathcal{Q}_k^c$, from the points stored in cells via our index.

• **GPU-accelerated EDR computation**: In each iteration, the input to this step is a query trajectory T_q and candidate trajectories $\mathcal{Q}_k^c$, to compute EDR distances for all the candidates. We transfer candidate trajectories to global memory if they are not in global memory, and update the MAT accordingly. We distribute EDR computations among CUDA blocks, and each EDR calculation is decomposed into independent components to be performed by CUDA threads concurrently.

At the end of each iteration, we keep the IDs of k trajectories with the smallest EDR distances computed so far using priority queue Q_k^r. The iteration terminates iff all the EDR lower bounds for the unchecked trajectories are larger than the k distances of trajectories belonging to Q_k^r. Finally, we put the k trajectories based on the IDs in Q_k^r into $\mathcal{Q}_k$.

IV. GPU-friendly Cell-based Index

A. The Structure of GTIDX

Our index GTIDX is developed based on a set of cells, covering all the trajectories. Figure 2 shows an example of 16 cells in the whole region including two trajectories marked with red and blue lines. Each cell C has an identifier cid, which is determined by the Morton-based encoding method [13].

We develop our index GTIDX following a three-part structure: the cell-based trajectory table $\mathcal{S}$, the trajectory index $\mathcal{I}_T$ and the quadtree-like index $\mathcal{I}_Q$. Figure 2 shows the index structure.

1) Cell-based trajectory table $\mathcal{S}$: This table is used to store all trajectories in cell-level representation. We adopt such representation to facilitate pruning strategies for both types of queries. To get the cell-level representation for any trajectory in $\mathcal{T}$, we map each trajectory point to its covering cell. We then define a cell-based trajectory table $\mathcal{S}$ including all the cells in ascending order of cell identifiers. Within each cell $C \in \mathcal{C}$, we keep all the trajectory points covered by it, denoted by $\phi_p(C)$, in ascending order of (trajectory ID, timestamp). In this manner, $\mathcal{S}$ stores points from the same trajectory in each cell continuously.

2) Trajectory index $\mathcal{I}_T$: We associate the table $\mathcal{S}$ with a trajectory index $\mathcal{I}_T$ to reconstruct any trajectory efficiently. The index maps a trajectory ID tid to a vector L_{tid}. Each element in L_{tid} is a triplet of $(cid, offset, length)$, representing a subsequence of the raw trajectory T_{tid}. Specifically, $offset$ and $length$ specify a continuous part of $\mathcal{S}$ starting from $offset$ to $offset + length - 1$, in which all the points in the subsequence are within C_{cid}. By traversing all the elements in L_{tid}, we are able to obtain the correct sequence of points in trajectory T_{tid}. Note that the size of L_{tid} is typically smaller than the number of trajectory points, especially when the points from a trajectory are aggregated into a few cells.

Figure 2 shows an example of $\mathcal{S}$ and $\mathcal{I}_T$ for two trajectories T_1 and T_2, where $p_{i,j}$ is the j-th point in T_i. We take T_1 as an example. The seven points of T_1 are split into five cells, and the points within each cell are stored in the corresponding item of $\mathcal{S}$. We obtain six subsequences from T_1 according to $\mathcal{C}$ and create six elements in L_1. For instance, the second element $\mathcal{S}[2] = (1, 2, 2)$ corresponds to the subsequence with two points $p_{1,2}$ and $p_{1,3}$ in C_1. Note that $p_{1,5}$ and $p_{1,7}$ in C_{12} are covered by two elements in L_1 because they belong to different subsequences.

3) Quadtree-like index $\mathcal{I}_Q$: While the cell-based trajectory table provides a way to organize trajectory points, it is easy to see that the number of points per cell may differ greatly. Such differences result in unbalanced workloads among GPU SMs during query processing (see details in Section V). To alleviate the problem, we propose to group cells into *balanced block*s using a quadtree-like index $\mathcal{I}_Q$, which can be viewed as a subtree of the complete quadtree QT, as described below.

QT organizes all the 4^n cells using $n + 1$ levels and each node in it corresponds to a *block* of cells, e.g., the root node corresponds to the whole set of cells, and each leaf node is a block with one cell. We define the number of points covered by the cells in a block as the *size* of this block. A node in QT is denoted by $N = (l, nid, isLeaf)$, where l is the node level identifier from 0 to n, nid is the node ID in this level and $isLeaf$ is a binary variable indicating whether N is a leaf or not. Note that (l, nid) uniquely identifies a node in QT. Interestingly, by employing Morton codes as cell identifiers, we can directly compute the set $\phi_c(N)$ of cells covered by any node N in QT:

$$\phi_c(N) = \{C \in \mathcal{C} \mid 4^{n-l} \times nid \leq C.cid < 4^{n-l} \times (nid + 1)\} \quad (3)$$

The above equation is guaranteed by the well-known relationship between Morton codes and quadtree structural properties [15]. More importantly, the cells in $\phi_c(N)$ reside continuously in the trajectory table $\mathcal{S}$.

We construct $\mathcal{I}_Q$ by pruning QT in a bottom-up way. That is, we recursively prune all the child nodes of N iff the total number of trajectory points covered by the child nodes is lower than a threshold θ_p called the *block size threshold*. The resulting tree is recognized as $\mathcal{I}_Q$ with a set of new leaf nodes, denoted by $\phi_l(\mathcal{I}_Q)$, which cannot be pruned further. For instance, in Figure 2, we set $\theta_p = 3$, then the new leaf nodes of $\mathcal{I}_Q$ are $\{(1, 1, true), (1, 2, true)\}$ as the total numbers of points in the child nodes for each of them are below three. One can verify that the new leaf nodes in $\mathcal{I}_Q$ provide a grouping over cells, and they are the only nodes in $\mathcal{I}_Q$ covering less than θ_p trajectory points:

$$\bigcup_{N \in \phi_l(\mathcal{I}_Q)} \phi_c(N) = \mathcal{C} \wedge \phi_c(N) \cap \phi_c(N') = \emptyset, \forall N, N' \in \phi_l(\mathcal{I}_Q) \quad (4)$$

$$|\phi_p(N)| < \theta_p, \forall N \in \phi_l(\mathcal{I}_Q) \wedge |\phi_p(N)| \geq \theta_p, \forall N \in \mathcal{I}_Q - \phi_l(\mathcal{I}_Q) \quad (5)$$

Note that the original quadtree QT satisfies two properties: (1) the nids of leaf nodes in QT have a 1-to-1 mapping to cell identifiers cids; (2) if node N' is the parent of N, we have $N'.level = N.level - 1 \wedge N'.nid = \lfloor N.nid/4 \rfloor$. Based on these properties, for any cell $C \in \mathcal{C}$, we can compute the leaf node in $\mathcal{I}_Q$ covering cell C based on the following theorem.

Theorem 1: Given $\mathcal{I}_Q$ over $\mathcal{C}$ and a cell $C \in \mathcal{C}$, a leaf node $N \in \phi_l(\mathcal{I}_Q)$ covers C iff $\lfloor C.cid/4^{n-N.l} \rfloor = N.nid$.

Benefits of GTIDX. There are three benefits of GTIDX: (1) the cell-based trajectory table $\mathcal{S}$ facilitates the fast pruning of invalid trajectories for range queries and the computation of EDR lower bounds for similarity queries. And the lightweight index $\mathcal{I}_T$ enables fast reconstruction of trajectories; (2) in each cell, points from the same trajectory are stored continuously in S, which enables coalesced data accesses in global memory; (3) the quadtree-like index $\mathcal{I}_Q$ groups size-varying cells into balanced blocks. This grouping balances the verification workload among GPU SMs for range queries.

Space complexity. We now discuss the space requirement of GTIDX. First, the trajectory table $\mathcal{S}$ contains all the trajectory points and hence the space cost of $\mathcal{S}$ is O($\sum_{T \in \mathcal{T}} |T|$). Second, the trajectory index $\mathcal{I}_T$ maintains a vector of $(cid, offset, length)$ triplets for each trajectory in $\mathcal{T}$. Thus, the space cost of $\mathcal{I}_T$ is O($\sum_{T \in \mathcal{T}} |T|$). Third, the tree index $\mathcal{I}_Q$ contains at most 2×4^n nodes with the fields of $(l, nid, isLeaf)$. Hence, the space cost of $\mathcal{I}_Q$ is O(4^n). In practice, $4^n \ll \sum_{T \in \mathcal{T}} |T|$ and the total number of triplets in $\mathcal{I}_T$ is much smaller than that of trajectory points. These two factors make the actual space requirement of GTIDX close to the size of trajectories. Note that we do not need to keep the original trajectories as $\mathcal{S}$ has already contained all the data. Hence, GTIDX is space-efficient.

Algorithm 1: Index Construction

```
Input: raw trajectories $\mathcal{T}$, $n$, $\theta_p$
Output: $\mathcal{S}$, $\mathcal{I}_T$, $\mathcal{I}_Q$
1  for $tid \in [1, |\mathcal{T}|]$ do
2      $\mathcal{M} \leftarrow$splitTraj($T, n$);
3      for $M \in \mathcal{M}$ do
4          $\mathcal{I}_T[tid]$.insert($cid, \mathcal{S}[cid].size(), |M|$);
5          $\mathcal{S}[cid] \leftarrow \mathcal{S}[cid] \cup M$;
6  $QT \leftarrow$buildFullQuadTree($n$);
7  for $l = n$ to $0$ do
8      $terminate \leftarrow True$;
9      for $nid = 0$ to $4^l - 1$ do
10         $N \leftarrow$getNode($QT, l, nid$);
11         if $|\phi_p(N)| < \phi_p$ then
12             $terminate \leftarrow False$;
13             pruneChildren($QT, N$);
14             $N.isLeaf \leftarrow True$;
15     if $terminate = True$ then
16         break;
17 $\mathcal{I}_Q \leftarrow QT$;
```

B. GTIDX Construction

Algorithm 1 provides the details of constructing GTIDX. To compute $\mathcal{S}$ and $\mathcal{I}_T$, we traverse all the trajectories in $\mathcal{T}$ (line 1). Given a trajectory T, we first split T into a set of subsequences $\mathcal{M}$, ensuring points in each subsequence belong to the same cell (line 2). For each subsequence M in $\mathcal{M}$, we append a triplet to $\mathcal{I}_T[T.tid]$ recording the information that $|M|$ points in M from the trajectory T are covered by the cell cid (line 4). We also update $\mathcal{S}$ accordingly (line 5).

Next, we construct a complete quadtree QT (line 6) and perform a bottom-up pruning to obtain $\mathcal{I}_Q$ (line 7-17). We start from the nodes in the deepest level of QT (line 7). If the cells covered by a node N contain less than θ_p points, we prune its child nodes in QT (line 13) and mark N as a leaf node (line 14). The process is repeated from level n to level 0 of QT and we perform early termination if no pruning is conducted at a certain level (line 15-16).

V. GPU-accelerated Query Processing

A. Motivation and Overview

GAT follows the filtering-and-verification framework, where the filtering step prunes invalid trajectories and the verification step verifies all the candidates to get the final results. While various spatial indices [16] [17] have been proposed to reduce the number of candidate trajectories, it is worth mentioning that the filtering step is usually efficient and represents a small fraction of the overall query processing time. In contrast, the verification step is typically very expensive to compute. For range queries, the number of candidate trajectories is determined by the size and the location of the query region R, which can be huge especially in the presence of batch queries. For top-k similarity queries, the quadratic time complexity of EDR computation may become the bottleneck of query processing. We hence focus on accelerating candidate verification. An important observation is that *the verification step involves executing the same procedure over different data.*

Algorithm 2: Range Query

```
Input: a set of query regions $\{R\}$, $\mathcal{S}$, $\mathcal{I}_T$, $\mathcal{I}_Q$;
Output: a result set of trajectories $\{\mathcal{Q}_r(R)\}$;
1  for $R \in \{R\}$ parallelly do
2      // (1) filtering by CPU
3      $Q_c \leftarrow$ createQueue();
4      $Q_c$.push($\mathcal{I}_Q.root$);
5      while $Q_c \neq \phi$ do
6          $N \leftarrow Q_c$.pop();
7          $isOverlap \leftarrow$ checkOverlap($R, N$);
8          if $isOverlap = True$ and $N.isLeaf = True$ then
9              $\mathcal{Q}_r^c$.insert(extractBlock($N$));
10         if $isOverlap = True$ and $N.isLeaf = False$ then
11             $\{N_{child}\} \leftarrow$ findChildNodes($N$);
12             $Q_c$.push($\{N_{child}\}$);
13     // (2) verification by GPU
14     copyBlockToGPU($\mathcal{Q}_r^c, \mathcal{S}$);
15     $\mathcal{B}_r \leftarrow$ initBitMap($|\mathcal{T}|$);
16     for CUDA block $bID \in [0, size(\mathcal{Q}_r^c) - 1]$ parallelly do
17         $\mathcal{P} \leftarrow$ extractPoints();
18         for $i \in [0, size(\mathcal{P})/N_{th} - 1]$ do
19             for CUDA thread $thID \in [0, N_{th} - 1]$ parallelly
               do
20                 $p \leftarrow \mathcal{P}[i * N_{th} + thID]$;
21                 $\mathcal{B}_r[p.tID] \leftarrow$ pointVerify($p$, $R$);
22     $\mathcal{Q}_r(R) \leftarrow$ recoverTraj($\mathcal{B}_r, \mathcal{S}, \mathcal{I}_T$);
```

For instance, we need to check whether each of the candidate trajectory points is within a query region or not, or compute EDR distances for a large number of trajectory pairs. This possibility of data-level parallelism inspires us to leverage GPU techniques to speed up the verification step.

A straightforward way to perform verifications for batch queries on GPUs is to treat each query independently using one CUDA thread. However, the verification workloads among different queries may vary a lot and the overlap of candidate trajectory data accessed by many queries may cause redundant data transfer between main memory and global memory. Both factors reduce query processing throughput significantly. A fine-grained task assignment is thus required to address the problem. In what follows, we present our GPU-accelerated method for trajectory query processing.

B. Trajectory Range Query

Algorithm 2 illustrates the pseudo code of trajectory range query processing in GAT. We perform range queries in two steps: (1) filtering invalid trajectories by CPU and (2) verifying candidates by GPU. For Step 1, we traverse the tree index $\mathcal{I}_Q$ to identify the blocks spatially overlapping the query region. We define that a block *overlap*s a region if there exists at least one cell in this block overlapping the region. It is better to use the CPU to perform the filtering due to the complex branch instructions involved in this step.

1) Filtering by CPU: The input to this step is a set of query regions $\{R\}$ of the range queries $\{\mathcal{Q}_r\}$ and the output is a set $\mathcal{Q}_r^c$ of candidate blocks (i.e., sets of cells) overlapping the query region R for each $\mathcal{Q}_r$. Each block in $\mathcal{Q}_r^c$ corresponds to a leaf node in $\mathcal{I}_Q$ and spatially overlaps the query region R. The points covered by a candidate block in $\mathcal{Q}_r^c$ will be processed by a GPU SM for verification. We consider leaf nodes since they are balanced in size and each of them contains less than θ_p points according to Formula 5. For illustration purpose, we first describe how to perform filtering for one range query $\mathcal{Q}_r$. We denote by (r_0, r_1) the top-left and bottom-right points of the query region R.

A naïve way to compute $\mathcal{Q}_r^c$ for $\mathcal{Q}_r$ is to check all the leaf nodes in $\mathcal{I}_Q$. For a leaf node $N \in \phi_l(\mathcal{I}_Q)$, if the corresponding block overlaps the query region R, we add the block to $\mathcal{Q}_r^c$. However, we observe that the query region is typically small and most leaf nodes in $\mathcal{I}_Q$ are not candidates. To speed up the process, we perform a breath-first search over $\mathcal{I}_Q$ (line 3-12) and apply the following pruning rule (line 7) during traversing, to avoid examining descendants of a non-candidate node.

Theorem 2: Given any node N in $\mathcal{I}_Q$, if the corresponding block does not overlap the query region R, all the blocks corresponding to the descendants of N are not candidates.

The only missing part of our filtering step is how to quickly determine whether a block overlaps R. In $\mathcal{I}_Q$, by applying the Morton-based encoding on nodes in each level, we can traverse all nodes and for each node, check whether its corresponding block overlaps the query region via several efficient bit manipulations. We provide the details as follows.

Consider a node $N = (l, nid, isLeaf)$ in $\mathcal{I}_Q$. Since all the nodes in level l of the original quadtree virtually partition the whole region into $2^l \times 2^l$ virtual blocks, we denote the virtual block in the i-th row and j-th column by (i, j). For example, in Figure 3, the 4 nodes in level 1 of $\mathcal{I}_Q$ partition the whole region into 4 virtual blocks $(0, 0)$, $(0, 1)$, $(1, 0)$, and $(1, 1)$.

Theorem 3: Given a virtual block (i, j) of node $N = (l, nid, isLeaf)$ in quadtree QT, the following equations hold:

$$
\begin{aligned}
i &= \sum_{k \in [0, 2l-1] \wedge (k\%2=1)} (\lfloor nid/2^k \rfloor \%2) \times 2^{\lfloor k/2 \rfloor} \\
j &= \sum_{k \in [0, 2l-1] \wedge (k\%2=0)} (\lfloor nid/2^k \rfloor \%2) \times 2^{\lfloor k/2 \rfloor}
\end{aligned}
\tag{6}
$$

which can be computed efficiently via bit manipulations.

By projecting the query region $R = (r_0, r_1)$ onto level-l virtual block unit coordinates, we can represent R as a pair $\{(i_0, j_0), (i_1, j_1)\}$ of virtual blocks, where (i_0, j_0) and (i_1, j_1) cover points r_0 and r_1, respectively. Hence, the virtual block (i, j) of N is overlapped with R iff $i \in [i_0, i_1] \wedge j \in [j_0, j_1]$.

Figure 3 shows an example for searching nodes in $\mathcal{I}_Q$. The query region is identified as the yellow dash line in level 1 and the blue dash line in level 2. Level 1 involves $2^1 \times 2^1$ virtual blocks, and R is represented as a pair of $\{(i_0, j_0), (i_1, j_1)\}$, where $(i_0, j_0) = (0, 1)_2$ and $(i_1, j_1) = (1, 1)_2$. Consider the 4 nodes in level 1 first. Node $N_1 = (1, 1, True)$ corresponds to the virtual block $(0, 1)$. Since the block is overlapped with R and N_1 is a leaf node, we insert N_1 into $\mathcal{Q}_r^c$. The virtual block for the non-leaf node $N_2 = (1, 3, False)$ is also overlapped with R, and we will verify its child nodes in level 2 later. The other two nodes in level 1 are not overlapped with R and we stop examining their descendants. We next examine the 4 child nodes of N_2, and insert $(2, 12, True)$ and $(2, 13, True)$ into $\mathcal{Q}_r^c$ as they are overlapped with R.

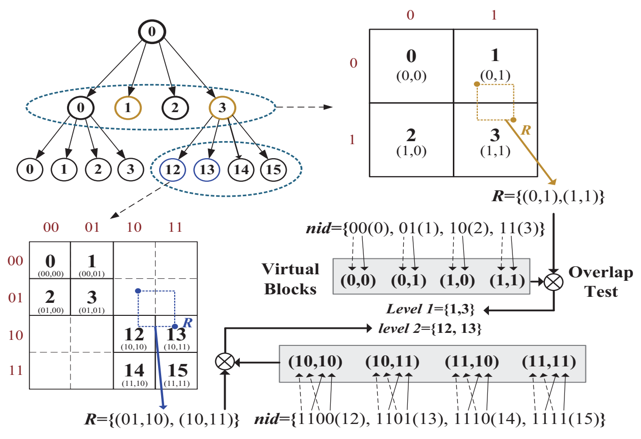


Fig. 3. An example of filtering in processing range queries

2) Verifying by GPU: The input to this step is a set $\mathcal{Q}_r^c$ of candidate blocks and the corresponding query region R. The output is a $|\mathcal{T}|$-wide bitmap $\mathcal{B}_r$ where the i-th bit equals to 1 iff trajectory $T_i \in \mathcal{Q}_r(R)$. $\mathcal{B}_r$ is initially set to 0s. After verification, it will be parsed by CPU to get the final result $\mathcal{Q}_r(R)$. The procedure of this step is shown in Algorithm 2 (line 14-22).

We first retrieve points covered by candidate blocks from the cell-based trajectory table $\mathcal{S}$ based on Equation 3, and transfer them to global memory of the GPU (line 14). Note that points covered by a candidate block are stored continuously in $\mathcal{S}$ owing to the Morton codes, and after transferring, they are still stored continuously in global memory. To avoid redundant data transfer (i.e., overlap of candidate blocks among different queries), we maintain a bitmap table MAT recording the existence of each cell of points in global memory of the GPU. The total number of points in global memory is also recorded in the MAT, and the classical Least Recently Used (LRU) swapping strategy is used to swap cells out of global memory when it is nearly full.

We then perform verification for the retrieved points on the GPU in parallel (line 16-22). We assign points covered by a candidate block to one CUDA block (handled by a GPU SM), which will then be distributed uniformly among CUDA threads. Since each candidate block corresponds to a leaf node in $\mathcal{I}_Q$ which is obtained by grouping size-varying cells, distributing candidate blocks among GPU SMs facilitates load balance. In a CUDA block, for each retrieved point, a CUDA thread tries to check whether the point resides in R or not. If so, we set the corresponding bit in $\mathcal{B}_r$ to 1 (line 17-21). Note that in this step, data requests from CUDA threads can be coalesced, because points in the same candidate block are stored continuously in global memory.

C. Top-k Similarity Query

Given a query trajectory T_q, the goal of top-k similarity query processing is to find the k trajectories closest to T_q using EDR as the distance function efficiently. In GAT, we consider a batch of similarity queries $\{T_q\}$ and execute them concurrently. The computational cost of trajectory similarity queries comes from two aspects. First, the large number of trajectories in $\mathcal{T}$ makes it infeasible to compute the EDR distance for each trajectory against T_q, i.e., $\delta(T_q, T), \forall T \in \mathcal{T}$. Second, the computational complexity of EDR is quadratic, i.e., $O(|T_q| \times |T|)$.

To avoid computing EDR distances for all trajectories, we leverage the lower bound of EDR distance, which is also known as *frequency distance* (FD) [12]. FD(T_q, T) is computed based on the *frequency vector*s (FV) of trajectories. In our context, we can consider each cell in $\mathcal{C}$ as a bin, and the FV of trajectory T over $\mathcal{C}$, denoted by FV$(T, \mathcal{C})$, is a histogram recording the number of points in T belonging to each cell. We apply the same algorithm in [12] to compute FDs and the time complexity is linear to the number of bins in FVs.

Theorem 4: Given two trajectories T_q and T, we have FD$(T_q, T) \leq \delta(T_q, T)$ [12].

Inspired by Theorem 4, we propose to compute $\mathcal{Q}_k$ progressively. Given a query trajectory T_q and k, we first compute FD(T_q, T) for each trajectory $T \in \mathcal{T}$ and sort all the trajectories in ascending order of their FD values. We then iteratively choose $m(\geq k)$ trajectories with the smallest FDs as candidates $\mathcal{Q}_k^c$ and compute their EDR distances against T_q using the GPU. We keep k trajectories with the smallest EDR distances among all the distances computed so far. If all these k distances are no larger than FDs of the remaining trajectories (whose EDR distances have not been computed yet), the k trajectories are the top-k answers to $\mathcal{Q}_k$.

Corollary 1: For any subset $\mathcal{L}_\delta \subseteq \mathcal{T}$ of trajectories, all of

Algorithm 3: Top-k Similarity Query

```
   Input: a set of query trajectories $\{T_q\}$, $\mathcal{S}$, $k$, $\epsilon$, $\mathcal{I}_T$;
   Output: a result set of $k$-sized trajectory sets $\{\mathcal{Q}_k(T_q)\}$
1  for $T_q \in \{T_q\}$ parallelly do
2      $Q_{FD} \leftarrow$ initPriorityQueue("lowestOnTop");
3      $Q_k^r \leftarrow$ initPriorityQueue("highestOnTop", $k$);
4      // (1) computing frequency distance by CPU
5      for $T_i \in \mathcal{T}$ do
6          $FD(T_q, T_i) \leftarrow$ computeFD($FV(T_q, \mathcal{C})$, $FV(T_i, \mathcal{C})$);
7          $Q_{FD}$.push($T_i$, $FD(T_q, T_i)$);
8      $Terminate \leftarrow False$;
9      while $Terminate = False$ do
10         // (2) identifying candidate trajectories by CPU
11         $\mathcal{Q}_k^c \leftarrow Q_{FD}$.popTraj($m$);
12         // (3) EDR calculation by GPU
13         transferTrajToGPU($\mathcal{Q}_k^c$, $\mathcal{I}_T$, $\mathcal{S}$);
14         for CUDA block $bID \in [0, |\mathcal{Q}_k^c| - 1]$ parallelly do
15             $|T_q| \leftarrow$len($T_q$); $|T| \leftarrow$len($\mathcal{Q}_k^c[bID]$);
16             $S \leftarrow$ createArray($(|T_q| + 1) \times (|T| + 1)$);
17             for $i \in [1, (|T_q| + |T| - 1)]$ do
18                 for CUDA thread $thID$ parallelly do
19                     $sl_0, sl_1, sl_2 \leftarrow$getSlashOffset($S$, $i - 2$, $i$);
20                     $S[sl_0 + thID] \leftarrow$ computeState($S$, $sl_1$,
                       $sl_2$, $T_q$, $\mathcal{Q}_k^c[bID]$, $\epsilon$);
21             $Q_k^r$.push($\mathcal{Q}_k^c[bID]$, $S[(|T_q| + 1) \times (|T| + 1) - 1]$);
22         if $(|Q_{FD}| = 0) \vee ((|Q_k^r| = k) \wedge (Q_{FD}.top().FD \geq Q_k^r.top().\delta))$ then
23             $Terminate \leftarrow True$;
24             break;
25     $\mathcal{Q}_k(T_q) \leftarrow Q_k^r$.popTraj($k$);
```

them have smaller EDR distances than those in $\mathcal{T} - \mathcal{L}_\delta$ iff the maximum EDR distance of $\mathcal{L}_\delta$ is no larger than the minimum FD value of trajectories in $\mathcal{T} - \mathcal{L}_\delta$.

Algorithm 3 summarizes the pseudo code of executing similarity queries on the CPU-GPU environment in GAT. The details of the three major steps are provided as follows.

1) Computing Frequency Distances by CPU (line 5-7*):* To obtain FD for a trajectory $T \in \mathcal{T}$, we first compute FV($T, \mathcal{C}$) based on the trajectory index $\mathcal{I}_T$. Recall that $\mathcal{I}_T$ maps a trajectory ID tid to a vector of $(cid, offset, length)$ triplets, i.e., L_{tid}. By traversing L_{tid} once, we can calculate the total $length$s for each cid, which is exactly FV($T, \mathcal{C}$). Specifically, for each $C \in \mathcal{C}$, we have:

$$FV(T, \mathcal{C})[C] = \sum_{i=1}^{|L_{tid}|} \mathbb{1}_{L_{tid}.cid = C.cid} \times L_{tid}[i].length \tag{7}$$

Note that the FVs for trajectories in $\mathcal{T}$ can be computed and materialized before query processing. For the query trajectory T_q, we first map each of its points to the covering cell according to the coordinates and then compute the number of points per cell to get FV($T_q, \mathcal{C}$). After that, for each trajectory $T \in \mathcal{T}$, we apply the algorithm in [12] to compute the frequency distance FD(T_q, T) based on FV($T_q, \mathcal{C}$) and FV($T, \mathcal{C}$). We maintain a priority queue Q_{FD} for T_q which contains the IDs of all the trajectories in ascending order of their FDs with respect to T_q.

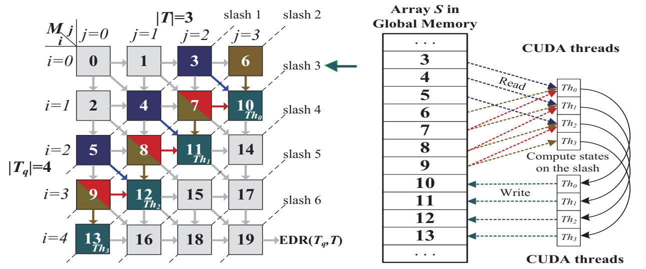
2) Generating candidate trajectories by CPU (line 11*):* In this step, we pop out $m(\geq k)$ $tids$ from Q_{FD} with the smallest FD values and put the corresponding trajectories into $\mathcal{Q}_k^c$ as candidates. If Q_{FD} contains less than m tids, all these remaining trajectories become candidates.

3) Computing EDR distances by GPU (line 13-24*):* This step computes EDR distances for trajectories in $\mathcal{Q}_k^c$ by GPU. We maintain a k-sized priority queue Q_k^r for T_q to store k trajectory IDs with the smallest EDR distances computed so far.

We first retrieve the original trajectories whose IDs belong to $\mathcal{Q}_k^c$ based on $\mathcal{S}$ and the corresponding L_{tid} in $\mathcal{I}_T$. We then transfer these candidate trajectories together with the query trajectory T_q to global memory of the GPU for EDR computations. Similar to the range query, we maintain an MAT to record the existence of trajectories in global memory, and apply the LRU strategy to swap some trajectories out of global memory when it is nearly full.

We then compute EDR distances in parallel on the GPU. We use one CUDA block to compute the EDR distance between a candidate trajectory $T \in \mathcal{Q}_k^c$ and the query trajectory T_q, i.e., $\delta(T_q, T)$ (line 14-21). Without loss of generality, we mainly describe the procedure of computing $\delta(T_q, T)$ in a CUDA block with the assumption that $|T_q| \geq |T|$. For $|T_q| < |T|$, we can compute $\delta(T, T_q)$ instead since EDR is symmetric.

EDR distances can be computed through a *dynamic programming* prodedure. Let $\bar{T}(k)$ denote the subsequence of trajectory T from the k-th point to the end point. We maintain a $(|T_q|+1) \times (|T|+1)$ matrix M, where $M[i][j] = \delta(\bar{T}_q(i), \bar{T}(j))$. According to Definition 3, M satisfies:



(a) Computing EDR on GPU in slash order (b) Data accessed by CUDA threads

Fig. 4. An example of computing EDR on the GPU for top-k similarity queries

$$M[i][j] = \begin{cases} i & \text{if } j = 0 \\ j & \text{if } i = 0 \\ \min\{M[i-1][j]+1, M[i][j-1]+1, \\ \quad M[i-1][j-1] + subcost\} & \text{otherwise} \end{cases} \tag{8}$$

The procedure of computing EDR can be divided into $(|T_q| + |T| - 1)$ iterations. We illustrate the idea using Figure 4(a), where each element in M is represented by a rectangle and called a *state*. We link the states computed in the n-th iteration using slash n. The computations of states in slash n are independent of each other, and only depend on the states in slash $n-1$ and $n-2$. Hence, we use one CUDA thread to compute individual state in each slash. For example, we use CUDA threads Th_0, Th_1, Th_2, Th_3 to compute $M[1][3], M[2][2], M[3][1], M[4][0]$ in slash 3, respectively. By doing this, the EDR distance $\delta(T_q, T)$ can be computed in $|T_q|+|T|-1$ iterations. This is smaller than $|T_q| \times |T|$ iterations required by computing states in a row-major order.

In our implementation, we store all the states of M into a *state array* S in global memory. To facilitate coalesced data access, states in the same slash are stored continuously in S. Specifically, denoting $\alpha = (i+j-1)$ and $\beta = (|T_q|+|T|-\alpha)$, $M[i][j]$ is stored in the $S[v]$, where:

$$v = \begin{cases} \frac{(\alpha+1)(\alpha+2)}{2} + i, & \text{if } \alpha \leq |T|-1 \\ (|T|+1)(|T_q|+1) - \frac{(\beta+1)\beta}{2} + (|T|-j) & \text{if } \alpha \geq |T_q|-1 \\ \frac{|T|(|T|+1)}{2} + (|T+1|)(\alpha+1-|T|) + (|T|-j) & \text{otherwise} \end{cases} \tag{9}$$

Figure 4 (a) shows an example of the location of each state in array S. Offsets of states are labeled in the corresponding rectangle. From Figure 4(b), we can see that in each slash, the accesses to global memory from CUDA threads Th_0, Th_1, Th_2, Th_3 are continuous based on the data placement in array S. To facilitate efficient access to points in T_q and T, we store the points from each trajectory successively in the smaller but faster shared memory associated with each GPU SM. This allows the threads in a warp to access consecutive shared memory addresses for computing states, and reduces bank conflicts effectively [14].

After computing $\delta(T_q, T)$ for all $T \in \mathcal{Q}_k^c$, we put their trajectory IDs with the corresponding EDR distances into Q_k^r (line 21). If the maximum EDR distance is larger than the minimum FD in Q_{FD}, we continue to Step 2. Otherwise, the process terminates and outputs trajectories in Q_k^r as $\mathcal{Q}_k$.

TABLE I
STATISTICS OF DATASETS

	#Trajectories	#Points	#Cells
SHCAR	327,474	75,188,293	262,144
GeoLife	30,325	19,143,208	262,144

TABLE II
PARAMETER RANGES AND DEFAULT VALUES

Parameter	Description	Range
θ_p	Block size threshold	200, 2000, $\underline{20000}$, 200000
S_R	Query region area (km^2)	10, $\underline{20}$, 30, 40
k	Top-k for similarity query	5, 10, 15, $\underline{20}$, 25
ζ	Avg. query trajectory length	200, 400, 600, $\underline{800}$, 1000
$N_{\mathcal{Q}_r}$	#range queries	40, 60, $\underline{80}$, 100, 120
$N_{\mathcal{Q}_k}$	#similarity queries	20, $\underline{40}$, 60, 80, 100
$\|D\|$	dataset size (GB)	3, 4.5, 6, $\underline{7.5}$, 9

VI. EXPERIMENTAL EVALUATION

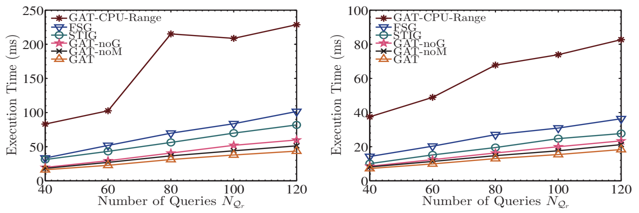
A. Experiment Setup

Datasets. We use two real-life trajectory datasets: SHCAR and GeoLife [18]. SHCAR contains trajectories of 9,446 private cars in Shanghai, China, collected from 2014 to 2015. GeoLife contains trajectories from 182 users during Apr. 2007 – Aug. 2012, where most trajectory points are within Beijing, China. The original datasets contain one complete trajectory for each user. We split the sequence of trajectory points from each user into several subsequences, to obtain trajectories as $\mathcal{T}$. If two consecutive points have a time gap more than 30 minutes, we split them into two trajectories. Table I provides the details of two datasets.

Baselines. For range query, we compare GAT with its CPU version, and two adapted GPU approaches: STIG [19] and FSG [20], which are originally designed for individual points. To illustrate the effectiveness of grouping cells into balanced blocks and the Morton-based encoding, we also consider two variants of GAT: GAT-noG and GAT-noM as follows.

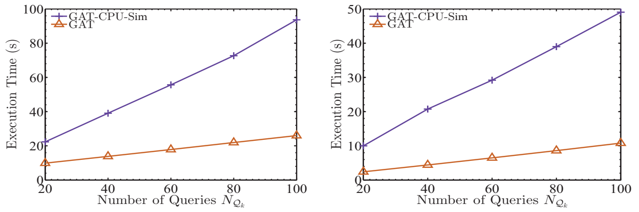
- **GAT-CPU-Sim.** This is a multi-threaded CPU version of GAT, based on histogram sequential scan [12].
- **STIG [19].** This approach leverages kd-tree [21], where the leaf nodes correspond to blocks of points. We keep kd-tree in memory and use the CPU to compute candidate blocks, which will be refined by GPUs to get final results.
- **FSG [20].** This approach uses a flat grid-file based index to accelerate point-in-polygon queries over taxi trips. Similar to our approach, it first finds cells overlapped with the query region, then generates candidate cell-polygon pairs and sends them to the GPU for parallel verifications.
- **GAT-noG.** This is GAT without the grouping strategy, where the leaf nodes in $\mathcal{I}_Q$ are single cells.
- **GAT-noM.** This is GAT without the Morton-based encoding. The cells in $\mathcal{S}$ are sorted in row-major order of the region. We implement $\mathcal{I}_Q$ as a conventional linked tree where each node is associated with a minimum bounding rectangle.
- **GAT-CPU-Range.** This is the CPU version of GAT using multi-threading, where each candidate block is assigned to a thread running on the CPU for verification.

To the best of our knowledge, we are the first to exploit



(a) SHCAR (b) GeoLife

Fig. 5. Comparison of performance on range queries



(a) SHCAR (b) GeoLife

Fig. 6. Comparison of performance on similarity queries

the GPU to accelerate top-k similarity query using EDR as the distance function. Hence, we only compare GAT with its multi-threaded CPU version.

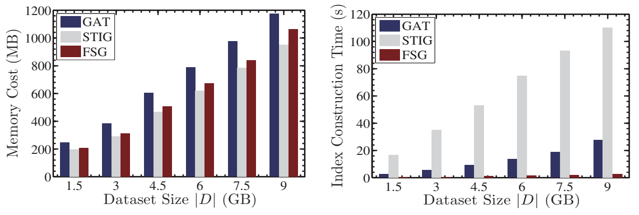
Metrics. We measure the performance of the approaches by the total execution time over a batch of queries. We measure the construction time and memory cost for the indexing cost.

We run all the experiments on a server equipped with two 10-core Xeon E5-2650 v3 processors clocked at 2.3GHz, 64GB of RAM, 4TB of disk storage and a two-chip NVIDIA Tesla K80 GPU. Each chip has 2,496 CUDA cores and 12GB graphical memory. We implement GAT in C++ with CUDA 8.0, running on CentOS 7. We conduct our experiments under various parameter settings. Table II shows the meaning and the range of all parameters, where the default values are underlined. All the results are averaged over 10 runs.

B. Comparison of Various Approaches

Range Query. Figure 5(a) and Figure 5(b) show the execution time with different numbers of range queries on SHCAR and Geolife, respectively. The execution time in all approaches increases when the number of queries becomes larger. Our approach outperforms the other five baselines in all cases and the advantage becomes more significant with more queries. On average, GAT runs 2.28x and 1.89x faster than FSG and STIG, respectively. We observe that GAT incurses lower data transfer cost due to the use of the memory allocation table, while the cost in FSG and STIG is relatively high. STIG performs better than FSG. This is because STIG uses a kd-tree like index to ensure similar number of trajectory points among blocks, leading to more balanced workload. For the same reason, both GAT-noM and GAT run faster than GAT-noG. GAT-noM runs slightly slower than GAT, because data access requests in GAT-noM cannot be coalesced and the performance is restricted by the limited global memory bandwidth. GAT-CPU-Range requires the longest execution time in all cases due to the limited multi-core parallelism.

Similarity Query. Figure 6(a) and Figure 6(b) show the



(a) Memory Cost (b) Index Construction Time

Fig. 7. Indexing cost

execution time with different number of similarity queries on SHCAR and Geolife, respectively. GAT runs up to 4.5x faster than GAT-CPU-Sim over all the query numbers, indicating higher throughput of our approach using GPU. While the number of GPU cores is 100x more than that of CPU cores, the throughput can be compromised by various factors such as the different clock rates of CPU and GPU, and the high latency of PCIe bus for data transfer. On two datasets, the execution time of GAT and GAT-CPU-Sim increases linearly as the number of queries becomes larger. Both approaches require longer execution time on SHCAR which contains more trajectories.

C. Indexing Cost

We evaluate the indexing cost for three GPU approaches. We randomly select the subsets of trajectories from SHCAR, and build indices for each subset.

Memory Cost. Figure 7(a) shows the index memory cost w.r.t. different data sizes. For all the approaches, the size of indices becomes larger when the data size increases. GAT requires slightly more memory cost (8%-22%) compared with other two methods. The main reason is that GAT involves a trajectory index to perform histogram-based pruning for similarity queries, while STIG and FSG can only process range queries and do not maintain such an index. On average, the overhead of GTIDX is merely 12.8% of the data size, which is acceptable and space-efficient.

Index Construction Time. Figure 7(b) provides the index construction time for different data sizes. The construction time increases as the data size becomes larger. For 9GB data, GAT takes only 27.7 seconds for the index construction, which is efficient. GAT requires 75.2% less index construction time than STIG over all the data sizes. This is because STIG needs to compute a large number of medium values when generating kd-tree. The index construction time of GAT is longer than that of FSG due to the additional tree index $\mathcal{I}_Q$ in GAT.

D. Speedup

We next study the speedup achieved by GAT with default parameter values on one and two GPUs. For comparison, we use a single thread to execute all the queries on CPU. The speedup is computed as the ratio of execution time against the single-thread approach. Table III shows the results on two datasets. For range queries, GAT with one GPU achieves 20.07x and 18.03x speedups on SHCAR and GeoLife, respectively, owning to the high parallelism of GPU. Using two GPUs achieves about 1.76x to 1.92x speedup than using one GPU over both datasets. This indicates that GAT can achieve almost linear speedup with more GPUs. For similarity queries, GAT with one GPU achieves 35.54x and 38.94x speedups on SHCAR and GeoLife, respectively. The speedups are higher than those for range queries. Compared with similarity queries, range query processing involves simpler comparison operations. Therefore, the data transfer cost between main memory and global memory may become more significant in the overall execution time, which restricts the increase of speedup. The reasons why GAT with two GPUs fails to achieve 2x speedup are three-fold. First, the total executing time includes the filtering phase performed by multi-threading on the CPU, which makes it not possible to achieve a speedup that is directly proportional to the number of GPUs. Second, in the verification phase, two GPUs maintain independent MATs, which results in a lower hit rate and higher data transfer overhead. Third, the workloads on the two GPUs may not be absolutely balanced. In GAT, when the total number of CUDA blocks is odd, one GPU needs to handle one more CUDA block than the other.

TABLE III
SPEEDUP ACHIEVED ON TWO DATASETS

Dataset	**SHCAR**		**GeoLife**	
#GPUs	**1GPU**	**2GPU**	**1GPU**	**2GPU**
Range Query	20.07	37.63	18.03	32.43
Top-k Similarity Query	35.54	68.53	38.94	74.95

E. Scalability

We investigate the scalability of different approaches by varying the data size from 3GB to 9GB. Figure 8(a) shows the execution time of 80 range queries over different data sizes. All the approaches require longer execution time when the dataset becomes larger. This is determined by the fact that large datasets typically involve more candidates to be verified. GAT scales better than FSG and GAT-noG, as GAT groups cells into blocks to achieve load balance. This phenomenon is more obvious on larger datasets. Figure 8(b) reports the execution time of similarity queries over different data sizes. As data volume grows, both GAT and GAT-CPU-Sim require longer execution time. However, the execution time of GAT grows much slower than that of GAT-CPU-Sim, indicating better scalability using the GPU.

F. Parameter Tuning

In this section, we study the effects of different parameter values on the performance of GAT, as listed in Table II.

Effect of query region area S_R (km^2). The area of query region S_R controls the selectivity of range query. All the query regions are generated by extending from a point in the city center. Figure 9 shows the results with different S_R. The execution time of all approaches increases when the area of R varies from $10km^2$ to $40km^2$. As the query region becomes larger, more blocks overlap with R, leading to more candidates for verification. GAT performs the best over all the areas on GeoLife, but runs slightly slower than FSG and GAT-noG for

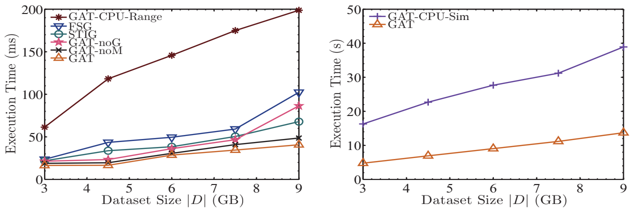

(a) Range Query (b) Similarity Query

Fig. 8. Scalability

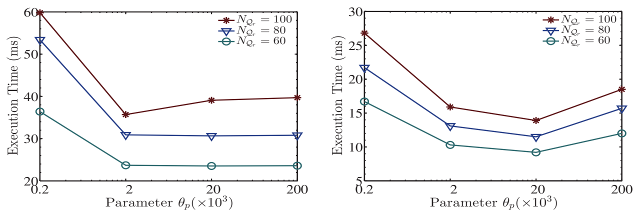

(a) SHCAR (b) GeoLife

Fig. 10. Effect of block size threshold (θ_p)

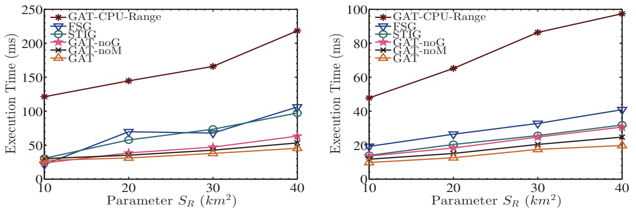

(a) SHCAR (b) GeoLife

Fig. 9. Effect of query region area (S_R)

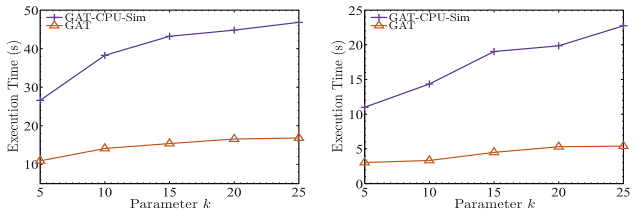

(a) SHCAR (b) GeoLife

Fig. 11. Effect of k

$S_R = 10km^2$ on SHCAR. The reason may be that SHCAR involves a few points residing in a small query region, but GAT verifies the whole block if any of its cells is overlapped with R. The GPU solutions outperform GAT-CPU-Range in all cases, due to the superior of the GPU in parallel computations.

Effect of block size threshold θ_p. Figure 10 shows the execution time of range queries with various values of θ_p. Recall that a large value of θ_p means that more cells are grouped into a large block, while the total number of blocks is reduced. For both datasets, we observe that the execution time of GAT decreases significantly when θ_p varies from 200 to 2000. When θ_p is too small, the number of points per block becomes smaller and verifying a few points in a candidate block cannot fully utilize the parallelism of GPU SM. We also observe a slight increase in execution time when θ_p varies from $20,000$ to $200,000$. This is because larger θ_p results in more points per block and the size difference among blocks becomes larger. Such variance causes unbalanced workloads.

Effect of k. Figure 11 shows the execution time of similarity queries under different values of k. As k becomes larger, both GAT and GAT-CPU-Sim require longer execution time. This is because larger k requires more EDR distances to be computed. However, for GAT, the increase in the execution time is small as the EDR computations are performed by thousands of GPU cores and the extra cost with larger k can be amortized.

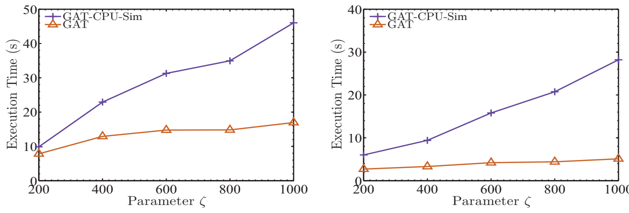
Effect of average query trajectory length ζ. We study the effect of average query trajectory length on similarity query processing. For each length, we randomly choose 50 trajectories and report the averaged result. Figure 12 shows the results. For both SHCAR and GeoLife, GAT outperforms GAT-CPU-Sim over all the trajectory lengths. The reason is that GAT computes each EDR distance with one SM and the computational cost is proportional to the sum of two trajectory lengths in our proposed algorithm. However, GAT-CPU-Sim adopts the original dynamic programming method and the complexity of computing EDR distance is proportional to the multiplication of two trajectory lengths. The advantage of GAT thus becomes more significant for larger ζ.

VII. Related Work

We review related works divided into two categories: trajectory indexing and GPU-based trajectory query processing.

Trajectory indexing. R-Tree [22] is one of most classical indices for spatial data, which is a two-dimensional generalization of B-Tree [23]. After that, some indices such as 3D-RTree [24], TB-Tree [25] and TPR-Tree [26] have been proposed to index trajectory data. SETI [17] proposed a two-level indexing scheme by decoupling spatial and temporal dimensions for spatial queries. PIST [27] developed a cost model to measure the I/O cost of different partitioning over spatial-temporal data, in order to reduce the number of disk accesses. TrajStore [16] proposed an adaptive griding scheme for indexing, clustering and storing trajectory data. Wang et al. developed an in-memory column-oriented storage called SharkDB [8] for trajectories, where range and similarity queries can be executed in memory efficiently. Trajtree [11] was designed to index the computation of EDwP, a similarity metric for trajectories under inconsistent sampling rates. All these indexing schemes are designed for spatial query processing on CPU, which can be incorporated into the filtering part of our framework. However, they are not optimized for GPU-accelerated verification, thus inspiring us to develop GTIDX.

GPU-based trajectory query processing. The GPU has been used for accelerating query processing over trajectory data. Zhang et al. [28] proposed a system called U$_2$STRA to manage large-scale trajectory data efficiently on GPU. They proposed to split trajectories with a four-level hierarchy and index them by a grid-file based data structure. Based on this system, an algorithm called TKSimGPU [9] was developed for top-k similarity queries. The idea is to compute similarity for pairs of trajectories using GPU. However, this approach adopted Hausdorff distance as the similarity measure, which



(a) SHCAR (b) GeoLife

Fig. 12. Effect of query trajectory length (ζ)

is not robust to noise in real trajectories. And the solution cannot support more accurate similarity metrics such as EDR distance [12]. Lettich et al. [15] proposed the PR-quadtree to process stream spatial k-nearest neighbor queries, where a quadtree was developed to achieve load balance in query processing. However, they require to load all the data into global memory for processing, which cannot scale to large datasets. Zhang et al. [20] developed a system to manage taxi trips with a grid-file based data structure. Doraiswamy et al. [19] generalized the kd-tree to STIG to support iterative spatial-temporal queries using the GPU. However, these approaches do not support trajectory similarity queries, and the performance on range queries is inferior to GAT.

VIII. Conclusion

This paper has presented GAT, a GPU-accelerated framework to support two types of trajectory queries together (i.e., both range and similarity queries) over trajectory data. GAT follows the generic filtering-and-verification framework, where the candidates are computed on the CPU, and the massive parallel verifications are performed on the GPU. To accelerate query processing on the GPU, we introduce a space-efficient index to effectively filter invalid trajectories for both types of trajectory queries. The Morton-based encoding is applied to coalesce data access requests from the GPU cores, which alleviates the limited global memory bandwidth problem. To achieve load balancing among GPU SMs, we group size-varying cells into balanced blocks with similar numbers of trajectory points. Extensive experiments are conducted using two real-life trajectory datasets. The results demonstrate that GAT achieves significant performance advantages over CPU-based solutions, and runs about 2x faster than the adaptations of the state-of-the-art GPU-based methods.

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