Reporting Flock Patterns

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Abstract. Data representing moving objects is rapidly getting more available, especially in the area of wildlife GPS tracking. It is a central belief that information is hidden in large data sets in the form of interesting patterns. One of the most common spatio-temporal patterns sought after is flocks. A flock is a large enough subset of objects moving along paths close to each other for a certain pre-defined time. We give a new definition that we argue is more realistic than the previous ones, and by the use of techniques from computational geometry we present fast algorithms to detect and report flocks. The algorithms are analysed both theoretically and experimentally.

1 Introduction

Data related to the movement of objects is becoming increasingly available because of substantial technological advances in position-aware devices such as GPS receivers, navigation systems and mobile phones. The increasing number of such devices will lead to huge spatio-temporal data volumes documenting the movement of animals, vehicles or people. One of the objectives of spatio-temporal data mining [15, 17] is to analyse such data sets for interesting patterns. For example, a group of 25 moose in Sweden was equipped with GPS-GSM collars. The GPS collar acquires a position every half hour and then sends the information to a GSM-modem where the positions are extracted and stored. Analysing this data gives insight into entity behaviour, in particular, migration patterns. There are many other examples where spatio-temporal data is collected [1, 16]. The analysis of moving objects also has applications in sports (e.g. soccer players [11]), in socio-economic geography [8] and in defence and surveillance areas.

We will model a set of moving objects by a set P of n moving point objects $p_1, \ldots, p_n$ whose locations are known at τ consecutive time-steps $t_1, \ldots, t_\tau$ that is, the trajectory of each object is a polygonal line that can self-intersect, see Fig. 1a. For brevity, we will call moving point objects *entities* from now on. It is assumed that the velocity of an entity along a line segment of the trajectory is constant.

There is some research on data mining of moving objects (e.g. [12, 18, 19, 22]) in particular, on the discovery of similar directions or clusters. Verhein and Chawla [22] used associated data mining to detect patterns in spatio-temporal sets.

Laube and Imfeld [13] proposed a different approach in 2002 - the REMO framework (RElative MOtion) which defines similar behaviour in groups of entities. They define a collection of spatio-temporal patterns based on similar direction of motion or change of direction. Laube et al. [14] extended the framework by not only including direction of motion, but also location itself. They defined several spatio-temporal patterns, including *flock*, *leadership*, *convergence* and *encounter*, and gave algorithms to compute them efficiently.

Laube et al. [14] developed an algorithm for finding the largest flock pattern (maximum number of entities) using the higher-order Voronoi diagram with running time $\mathcal{O}(\tau(nm^2+n\log n))$, where m

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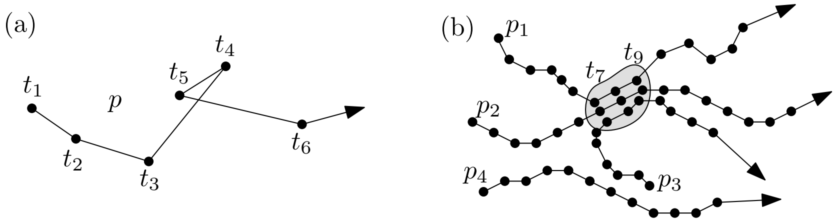

Fig. 1. (a) A polygonal line describing the movement of an entity p in the time interval $[t_1, t_6]$. (b) A flock for p_1, p_2, p_3 in the time interval $[t_7, t_9]$.

is the minimum number of entities that a flock has to contain. They also proved that the detection problem can be answered in $\mathcal{O}(\tau(nm + n \log n))$ time. Applying the paper by Aronov and Har-Peled [5] to the problem gives a $(1+\varepsilon)$-approximation with expected running time $\mathcal{O}(\tau n/\varepsilon^2 \log^2 n)$. Gudmundsson et al. [10] showed that if the disk (i.e. the region in which the entities have to be in order to form a flock) is $(1+\varepsilon)$-approximated then the detection problem can be solved in $\mathcal{O}(\tau(n/\varepsilon^2 \log 1/\varepsilon + n \log n))$ time.

However, the above algorithms only consider each time-step separately, that is, given $m \in \mathbb{N}$ and $r > 0$ a flock is defined by at least m entities within a circular region of radius r and moving in the same direction at some point in time. We argue that this is not enough for most practical applications, e.g. a group of animals may need to stay together for days or even weeks before it is defined as a flock. Therefore we propose the following definition of a flock:

Definition 1. *(m, k, r)-flock$_A$ - Given a set of n trajectories where each trajectory consists of τ line segments, a flock in a time interval $I = [t_i, t_j]$, where $j - i + 1 \geqslant k$, consists of at least m entities such that for every point in time within I there is a disk of radius r that contains all the m entities. Note that $m, k \in \mathbb{N}$ and $r > 0$ are given constants.*

In this model, Gudmundsson and van Kreveld [9] recently showed that computing the longest duration flock and the largest subset flock is NP-hard to approximate within a factor of $\tau^{1-\varepsilon}$ and $n^{1-\varepsilon}$, respectively. They also give a 2-radius approximation algorithm for the longest duration flock with running time $\mathcal{O}(n^2 \tau \log n)$.

We describe efficient approximation algorithms for reporting and detecting flocks, where we let the size of the region deviate slightly from what is specified. Approximating the size of the circular region with a factor of $\Delta > 1$ means that a disk with radius between r and Δr that contains at least m objects may or may not be reported as a flock while a region with a radius of at most r that contains at least m entities will always be reported.

We present several approximation algorithms, for example, a $(2+\varepsilon)$-approximation with running time $T(n) = \mathcal{O}(\tau n k^2 (\log n + 1/\varepsilon^{2k-1}))$ and a $(1+\varepsilon)$-approximation algorithm with running time $\mathcal{O}(1/m\varepsilon^{2k}) \cdot T(n)$.

Our aim is to present algorithms that are efficient not only with respect to the size of the input (which is τn) but also try to keep the dependency on k and m as small as possible. For most of the practical applications we have seen; m will be between a couple of entities to a few hundreds or even thousands, and k is expected to be between 5 and 30 for most applications.

Ib this model a set of entities can have many flocks and even one single entity can be involved in several flocks. For example, a flock involving $m+1$ entities trivially contains $m+1$ flocks of cardinality m. We must specify what we want to find and report in a given data set, see [10] for a discussion. One possibility is simply to detect whether a flock occurs. If so, we may want to report one example of a flock. Secondly, we may want to find all flocks that occur. Thirdly, we may want to report the largest size subset of entities that form a flock. In this paper we deal with the variant of finding all flocks, in Section 4 we will discuss the other variants briefly.

This paper is organised as follows. Next we give a brief description of the skip-quadtree structure used in this paper together with a description of the computational model used. In Section 2 we give a discrete version of the definition of a flock and prove that it is equivalent to the original definition provided that the entities move with constant velocity between consecutive time-steps. Furthermore, we describe our general approach to detect flocks. Then, in Section 3, we give three approximation algorithms which are all based on the general approach. In Section 4 we discuss different ways of pruning the set of flocks reported, and in the final section we discuss the implementations and the experimental results.

1.1 The computational model

One of the main tools used in this paper is the skip-quadtree presented by Eppstein, Goodrich and Sun [7] in 2005. The standard practice [6, 7] in computational geometry using quadtrees or octrees is that certain operations can be done in constant time. In arithmetic terms, the computations needed to perform point location, range queries or nearest neighbour queries in a quadtree, involve finding the most significant binary digit at which two coordinates of two points differ. This can be done using a constant number of machine instructions if we have a most-significant-bit instruction, or by using floating point or extended precision normalisation.

1.2 Skip-quadtree

We will show that approximation algorithms can be obtained by performing a set of range counting queries in higher dimensional space. There are several data structures supporting this type of query; quadtrees, skip-quadtrees, octrees, *kd*-trees, range trees, BBD-trees, BAR-trees and so on. For our requirements we could use either skip-quadtrees or BBD-trees, and since the implementation of the randomised skip-quadtree is very simple we chose to use the skip-quadtree.

The skip-quadtree uses the compressed quadtree as the bottom-level structure. The standard compressed quadtree uses $\mathcal{O}(2^d \cdot n)$ space and the worst-case height is $\mathcal{O}(n)$. We briefly describe the structure and show how to modify the structure so that it uses $\mathcal{O}(dn)$ space while the query time will increase with an $\mathcal{O}(\log d)$-factor.

First, here is the original description of a compressed quadree taken from [7]. Consider the standard quadtree T of the input set S. We may assume that the centre of the root square (containing the set S) is the origin and the half side length for any square in T is a power of 2.

Define an interesting square of a quadtree to be one that is either the root or that has at least two non-empty quadrants. Any quadtree square p containing at least two points contains a unique largest interesting square q in T. The compressed quadtree explicitly only stores the interesting squares, thus removing all the non-interesting squares and deleting their empty children. So for each interesting square p, they store 2^d bi-directed pointers, one for each d-dimensional quadrant. If the quadrant contains at least two points, the pointer goes to the largest interesting square inside the quadrant; if the quadrant contains one point, the pointer goes to that point; and if the quadrant is empty the pointer is NULL.

The above description of a compressed quadtree implies that the size of the tree is $\mathcal{O}(2^d \cdot n)$. Instead of storing information about which children contain points and which children are empty, we modify the tree such that it contains a list containing only the non-empty children. This improves the space complexity to $\mathcal{O}(dn)$, however this modification will increase the cost of a search in the tree since deciding if a child exists or not requires $\mathcal{O}(d)$ time.

The skip-quadtree supports $(1 + \delta)$-approximate range (counting) queries, i.e. the query range Q is approximated by an extended query range Q_δ. The extended query range Q_δ consists of Q and all points within a distance $\delta \cdot w$ from Q, where w is the diameter of Q. The approximate query counts all points in Q, it either counts or does not count points in $Q_\delta \setminus Q$ and it does not count any point in $\mathbb{R}^d \setminus Q_\delta$.

Together with the results of [7], the above discussion can be summarised by the following lemma.

Lemma 1. *Insertion, deletion and search in the modified d-dimensional skip-quadtree using a total of $\mathcal{O}(dn)$ space can be done in $\mathcal{O}(d \log n)$ time. An $(1 + \delta)$-approximate range counting query for any fat convex region of complexity $\mathcal{O}(d)$ can be answered in time $T(n) = \mathcal{O}(d^2(\log n + 1/\delta^{d-1}))$, where $\delta > 0$ is a given constant.*

2 Approximate flocks

The input is a set P of n trajectories $p_1, \ldots, p_n$, where each trajectory p_i is a sequence of τ coordinates in the plane $(x_1^i, y_1^i), (x_2^i, y_2^i), \ldots, (x_\tau^i, y_\tau^i)$, where (x_j^i, y_j^i) is the position of entity p_i at time t_j. We will assume that the movement of an entity from its position at time t_j to its position at time t_{j+1} is described by the straight-line segment between the two coordinates, and that the entity moves along the segment with constant velocity.

2.1 An equivalent definition of flock

Next we will give an alternative and algorithmically simpler, definition of a flock.

Definition 2. *(m, k, r)-flock$_B$ - Given a set of n trajectories where each trajectory consists of τ line segments a flock in a time interval $[t_i, t_j]$, where $j - i + 1 \geqslant k$ consists of at least m entities such that for every discrete time-step t_ℓ, $i \leqslant \ell \leqslant j$, there is a disk of radius r that contains all the m entities.*

Note that the centre of a disk does not have to coincide with one of the positions of the entities, see for example the disk D_5 in Fig. 2.

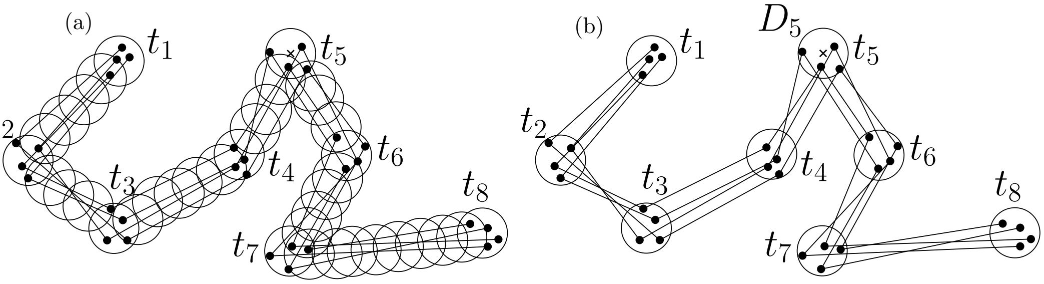

Fig. 2. A flock of four entities in the time interval $[t_1, t_8]$, according to the definitions of (a) flock$_A$ and (b) flock$_B$.

Lemma 2. *If the entities move with constant velocity along the straight line segment between two consecutive time-steps then flock$_A$ and flock$_B$ are equivalent.*

Proof. Consider a given time interval $I = [t_1, t_k]$ and assume that F_A and F_B are the set of all flocks in I according to Definition 1 and 2 respectively. Obviously every flock $f_A \in F_A$ is also a flock in F_B, thus $F_A \subseteq F_B$.

It remains to prove that $F_B \subseteq F_A$. Let f_B be an arbitrary flock in F_B, and let D_ℓ and $D_{\ell+1}$ be disks of radius r that include the entities of f_B at time t_ℓ and $t_{\ell+1}$ respectively, see Fig. 3a. It is enough to consider every two discrete time-steps t_ℓ and $t_{\ell+1}$ in I separately.

Next we prove that at every point in time $\gamma \in I' = [t_\ell, t_{\ell+1}]$ there is a disk $\mathcal{D}_\gamma$ that contains all the entities $\{p_1, \ldots, p_m\}$ in f_B. Let c_ℓ and $c_{\ell+1}$ be the centres of D_ℓ and $D_{\ell+1}$ respectively, and let h be the straight-line segment with endpoints at c_ℓ and $c_{\ell+1}$, as illustrated in Fig. 3a. An entity q that moves with constant velocity on h has a well-defined position at time $\gamma \in I'$, we denote this position by c_γ. Next we show that the disk $\mathcal{D}_\gamma$ with centre at c_γ and radius r contains all the entities of f_B. Let p_i be an arbitrary entity of f_B. Since both, the movement of q and the movement of p_i during I' follows a straight-line and since both move with constant velocity the relative trajectory of p_i in relation to q is a straight-line as shown in Fig. 3b. Since a disk is convex and since $p_i(t_\ell)$ and $p_i(t_{\ell+1})$ are points within D_ℓ and $D_{\ell+1}$, respectively, it holds that $p_i(\gamma)$ must lie within $\mathcal{D}_\gamma$. Consequently, $f_B \in F_A$ and therefore $F_B \subseteq F_A$ which completes the proof of the lemma. □

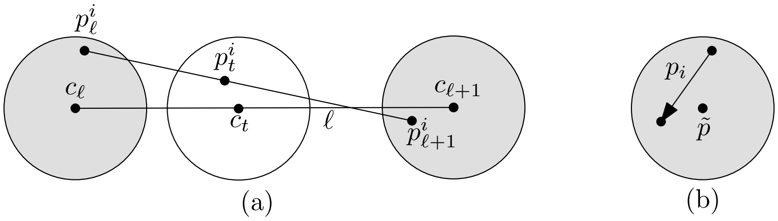

Fig. 3. Illustration for the proof of Lemma 2.

In the remainder of this paper we refer to Definition 2 whenever we talk about flocks. Definition 2 immediately suggests a new approach; for each time interval $[t_i, t_{i+k-1}]$ check whether there is a set of m entities $F = \{p_1, \ldots, p_m\}$ that can be covered by a disk of radius r at each discrete time-step in $[t_i, t_{i-1+k}]$. Next we will show how this observation allows us to develop an approximation algorithm.

2.2 The general approach

When developing an algorithm for this problem one of the main hurdles that we encountered was to detect flocks without having to keep track of all the objects in a potential flock. That is, when we consider a specific time-step; the number of potential flocks can be very large and the number of objects that one needs to keep track of for each potential flock might be $\Omega(n)$. In general this problem occurs whenever one attempts to develop a method that processes the input time-step by time-step. In this paper we avoid this problem by transforming the trajectories into higher dimensional space. Note that the gain is that we only need to count the number of points in a region, instead of keeping track of the actual objects. This might seem like overkill but both the theoretical bounds and the experimental bounds support this approach, at least as long as k is fairly small.

The basic idea builds upon the fact that a polygonal line with d vertices in the plane can be modelled as a point in $2d$ dimensions. The trajectory of an entity p in the time interval $[t_i, t_j]$ is described by the polygonal line

$$p(i, j) = \langle (x_i, y_i), (x_{i+1}, y_{i+1}), \ldots, (x_j, y_j) \rangle,$$

which corresponds to a point

$$p'(i, j) = (x_i, y_i, x_{i+1}, y_{i+1}, \ldots, x_j, y_j)$$

in $2(j - i + 1)$-dimensional space.

The first step when checking whether there is a flock in the time interval $[t_i, t_{i+k-1}]$ is to map the polygonal lines of all entities to $\mathbb{R}^{2k}$. Equivalence 1 gives the key characterisation of flocks. First, we define an (x, y, i, r)-*pipe* which is an unbounded region in $\mathbb{R}^{2k}$. Such a pipe contains all the points that are only restricted in two of the $2k$ dimensions (namely in dimensions i and $i+1$) and when projected on those two dimensions lie in a circle of radius r around the point (x, y). Formally, a (x, y, i, r)-pipe is the following region:

$$\big\{(x_1, \ldots, x_{2k}) \in \ \mathbb{R}^{2k} \mid \ (x_i - x)^2 + (x_{i+1} - y)^2 \leqslant r^2\big\}.$$

Equivalence 1 *Let $F = \{p_1, \ldots, p_m\}$ be a set of entities and let $I = [t_1, t_k]$ be a time interval. Let $\{p'_1, \ldots, p'_m\}$ be the mappings of F to $\mathbb{R}^{2k}$ w.r.t. I. It holds that:*

$$F \textit{ is a } (m, k, r)\textit{-flock} \iff \exists x_1, y_1, \ldots, x_k, y_k : \ \forall p \in F : \ p' \in \bigcap_{i=1}^{k} (x_i, y_i, 2i-1, r)\textit{-pipe}.$$

To see that this equivalence holds we observe the following: for each time-step $t_i \in I$ the disk with radius r and centre (x_i, y_i) contains the entity positions $p_1^i, \ldots, p_m^i$.

We will show that approximation algorithms can be obtained by performing a set of range counting queries in higher dimensional space.

3 Approximation algorithms

We now give approximation algorithms where the radius r is approximated. A $\varDelta$-approximation (with $\varDelta > 1$) here means that every (m, k, r)-flock will be reported, an $(m, k, \varDelta r)$-flock may or may not be reported, while no (m, k, r')-flock where r' exceeds $\varDelta r$ will be reported.

3.1 Method 1: A $(\sqrt{8} + \varepsilon)$-approximation algorithm

By Equivalence 1 it is fairly straight-forward to develop a $(\sqrt{8} + \varepsilon)$-approximation algorithm. For each time interval $I = [t_i, t_{i+k-1}]$, where $1 \leqslant i \leqslant \tau - k + 1$, we will do the following computations.

For each entity p let p' denote the mapping of p to $\mathbb{R}^{2k}$ with respect to I. We construct a skip-quadtree T for the point set $P' = \{p'_1, \ldots, p'_n\}$. Then, for each point $p' \in P'$ and an appropriately chosen $\delta > 0$ we perform a $(1 + \delta)$-approximate range counting query in T where the query range $Q(p')$ is a $2k$-dimensional cube of side length $4r$ and centre at p'. That is, we approximate the $2k$-dimensional cube which is itself an approximation for the query region. Every counting query containing at least m entities corresponds to an $(m, k, \sqrt{8} + \varepsilon)$-flock as Lemma 3 will show. Note that the same flock may be reported several times.

Lemma 3. *The algorithm is a $(\sqrt{8} + \varepsilon)$-approximation algorithm.*

Proof. First we show that each (m, k, r)-flock f is reported by the algorithm. Let p_f be an arbitrary entity of f and assume that f is a flock in the time interval $I = [t_i, t_{i+k-1}]$. We will prove that the approximation algorithm returns an $(m, k, (\sqrt{8} + \varepsilon)r)$-flock g such that $f \subseteq g$.

According to Definition 2 there exists a disk D_l with radius r that contains the entities in f for each discrete time-step t_l in I. The algorithm performs a counting query for each point in P' w.r.t. $[t_i, t_{i+k-1}]$, in particular for p'_f. The query range $Q(p'_f)$ is a $2k$-dimensional cube of side length $4r$ and centre at p'_f, where p'_f is the point in $2k$-dimensions corresponding to p_f. For a discrete time l, the query range corresponds to a square Q' in two dimensions with centre at p and side length $4r$, where the dimensions mark the $x-$ and $y-$positions of the entities at time l. As every entity of f has distance at most $2r$ to p_f this implies that every entity in f lies within $Q(p'_f)$. Thus, when p_f is queried, the algorithm reports an $(m, k, (\sqrt{8} + \varepsilon)r)$-flock g such that $f \subseteq g$.

To establish the approximation bound we still have to show that no (m, k, r')-flock g where r' exceeds $(\sqrt{8}+\varepsilon)r$ is reported. Let g be a reported flock w.r.t. the time interval $I = [t_i, t_{i+k-1}]$. We have to show that for every time-step t_l in I there exists a disk of radius $(\sqrt{8} + \varepsilon)r$ that contains the entities in g. This follows trivially by the choice of δ. If we choose δ to be $\varepsilon/\sqrt{8}$, the square of side length $4(1 + \delta)r$ is contained in the disk with radius $(\sqrt{8} + \varepsilon)r$ centred at p'_f, as illustrated in Fig. 4a. This completes the proof of the lemma. □

Lemma 4. *The algorithm reports at most τn $(m, k, (\sqrt{8} + \varepsilon)r)$-flocks. It runs in $\mathcal{O}(\tau n k^2(\log n + 1/\varepsilon^{2k-1}))$ time and requires $\mathcal{O}(\tau n)$ space.*

Proof. The number of reported flocks is trivially bounded by n, the number of entities, times τ, the number of time-steps. At each of the $(\tau - k + 1)$ time intervals the algorithm builds a skip-quadtree of the n elements from scratch. In total this requires $\mathcal{O}(\tau k n \log n)$ time, according to Lemma 1. Next a $(1 + \delta)$ counting query is performed for each of the n entities; each query requires $\mathcal{O}(k^2(\log n + 1/\varepsilon^{2k-1}))$ time as $\delta = \frac{\varepsilon}{\sqrt{8}}$. Hence, the total time needed to perform all the $n(\tau - k')$ queries is bounded by $\mathcal{O}(\tau k^2 n(\log n + 1/\varepsilon^{2k-1}))$ and thus dominates the running time as stated in the lemma.

The space needed to build the skip-quadtree for each time interval is $\mathcal{O}(kn)$, and since we only maintain one tree at a time the bound follows. □

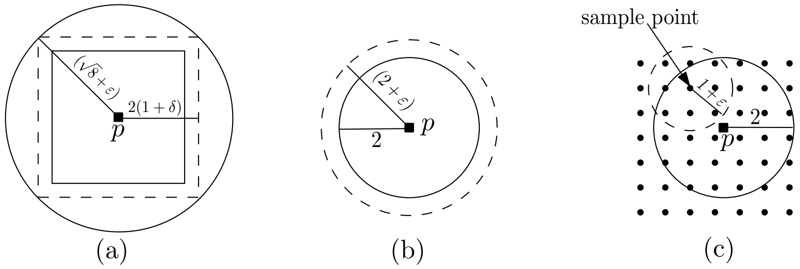

Fig. 4. Illustration of the query ranges of methods 1,2 and 3 for $r = 1$. The approximative query ranges are marked by dashed lines.

3.2 Method 2: A $(2 + \varepsilon)$-approximation algorithm

The algorithm is similar to the above algorithm. The main difference is that we will use the intersection of k pipes as the query regions instead of the $2k$-dimensional box. For each time interval $I = [t_i, t_{i+k-1}]$, where $1 \leqslant i \leqslant \tau - k + 1$, we will do the following computations.

For each entity p let p' denote the mapping of p to $\mathbb{R}^{2k}$ with respect to I. We construct a skip-quadtree T for the point set $P' = \{p'_1, \ldots, p'_n\}$. Then, for each point $p' \in \mathcal{P}'$ we perform a $(1 + \varepsilon)$-approximate range counting query in T where the query range $Q(p')$ is the intersection of the k pipes $(x_i, y_i, 2i - 1, 2r)$ where (x_i, y_i) is the position of entity p at time-step t_i.

The definition of fatness we use was introduced by Van der Stappen [20]. For convex objects it is basically equivalent to other definitions [2, 4, 21].

Definition 3. *[20] Let $\alpha > 1$ be a real value. An object s is α-fat if for any d-dimensional ball D whose centre lies in s and whose boundary intersects s, we have* $\text{volume}(D) \leqslant \alpha \cdot \text{volume}(s \cap D)$.

Lemma 5. *The intersection of d pipes $(x_i, y_i, 2i - 1, 2r)$, $1 \leqslant i \leqslant k$, in $2d$-dimensional space is a bounded convex 4^d-fat region whose boundary consists of $\mathcal{O}(d)$ surfaces of quadratic complexity.*

Proof. W.l.o.g. we assume that the centre of the intersection $\mathcal{I}$ of the d pipes is the origin, then $\mathcal{I}$ can be described by the following d inequalities:

$$\begin{aligned} x_1^2 + x_2^2 &\leqslant r^2 \\ x_3^2 + x_4^2 &\leqslant r^2 \\ &\cdots \\ x_{d-1}^2 + x_d^2 &\leqslant r^2. \end{aligned}$$

The set of inequalities together with the fact that the inequalities are pairwise independent immediately gives that $\mathcal{I}$ is bounded, convex and its boundary consists of $\mathcal{O}(d)$ surfaces of quadratic complexity. Thus it remains to prove that $\mathcal{I}$ is 4-fat. The definition of α-fat says that a d-dimensional region R is α-fat if for every d-dimensional ball B with centre within R and whose boundary intersects R the volume of R within B is at least $1/\alpha$ of the total volume of B. We place an arbitrary ball whose centre lies in $\mathcal{I}$ and consider the intersection of the ball and $\mathcal{I}$ projected onto two dimensions, say dimension $2i - 1$ and $2i$. The projection of the ball is a disk whose centres lies within the projection of $\mathcal{I}$ which is also a disk. Thus, it is obvious that at least $1/4$ of the projected ball lies in the projected region of $\mathcal{I}$. Taking all dimensions into account this yields that $\mathcal{I}$ is 4^d-fat. □

Recall that since the query range is convex and fat we can use the result stated in Lemma 1.

Lemma 6. *The algorithm is a $(2 + \varepsilon)$-approximation algorithm.*

Proof. The proof follows from the same arguments as used in the proof of Lemma 3. When approximately evaluating the query range $Q(p')$ which is the intersection of the k pipes $(x_i, y_i, 2i-1, 2r)$, $1 \leqslant i \leqslant k$ where (x_i, y_i) is the position of entity p at time-step t_i, we test whether there is an $(m, k, (2+\varepsilon)r)$-flock which p is part of. If p is part of an (m, k, r)-flock f in the time interval I, the disk with radius r containing all the entities in f at time-step $t_i \in I$ is contained in the disk with radius $2r$ centred at (x_i, y_i). Thus, when querying p, the algorithm reports an $(m, k, (2+\varepsilon)r)$-flock g with $f \subseteq g$. □

Lemma 7. *The algorithm reports at most* τn $(m, k, (2+\varepsilon)r)$*-flocks. It runs in* $\mathcal{O}(\tau n k^2(\log n + 1/\varepsilon^{2k-1}))$ *time and requires* $\mathcal{O}(\tau n)$ *space.*

Proof. The number of reported flocks is trivially bounded by n, the number of entities, times τ, the number of time-steps. At each of the $(\tau - k + 1)$ time intervals the algorithm builds a skip-quadtree of the n elements from scratch. In total this requires $\mathcal{O}(\tau k n \log n)$ time, according to Lemma 1. Next a counting query is performed for each point in $\mathcal{P}'$; each query requires $\mathcal{O}(k^2(\log n + 1/\varepsilon^{2k-1}))$ time, thus the total time needed to perform all the n queries is bounded by $\mathcal{O}(k^2 n(\log n + 1/\varepsilon^{2k-1}))$ time and thus dominates the running time as stated in the lemma.

The space needed to build the skip-quadtree for each time interval is $\mathcal{O}(kn)$, and since we only maintain one tree at a time the bound follows. □

Remark 1. A quick comparison between Lemmas 4 and 7 reveals that even though the approximation factor of the second method is smaller the running time is identical. However, this is a theoretical bound, in practice we chose to implement the second method using a compressed quadtree. The reason for this is that the skip-quadtree computes the volume between a d-dimensional cell (orthogonal box) and $Q(p')$, where $Q(p')$ is the intersection of the k pipes, which is possible in theory but hard in practice. The query data structure of a compressed quadtree only checks whether the intersection is non-empty which is much easier to implement. Consequently, the experiments performed with methods 1 and 2 use a different query data structure.

3.3 Method 3: A $(1+\varepsilon)$-approximation algorithm

We use the same approach as above but instead of querying only the input points in $\mathbb{R}^{2k}$ we will now query $\mathcal{O}(1/\varepsilon^{2k})$ sample points for each entity point. For each time interval $I = [t_i, t_{i+k'}]$, where $1 \leqslant i \leqslant \tau - k + 1$ and $k' = k - 1$, we will do the following computations.

For each entity p let p' denote the mapping of p to $\mathbb{R}^{2k}$ with respect to I. Construct a skip-quadtree T for the point set $P' = \{p'_1, \ldots, p'_n\}$. Let Γ be the intersection points of a regular grid in $\mathbb{R}^{2k}$ of spacing $\varepsilon \cdot r/2$. Each input point p'_i generates the sample set $\Gamma \cap D(p'_i)$ where $D(p'_i)$ is the $2k$-dimensional ball of radius $2r$ centred at p'_i. Clearly, this gives rise to $\mathcal{O}(1/\varepsilon^{2k})$ sample points for each entity p.

Next, we perform a $1+\varepsilon/(2+\varepsilon)$-approximate range counting query in T for each sample point $(x_1, y_1, \ldots, x_k, y_k)$ where the query range is the intersection of the k pipes $(x_i, y_i, 2i-1, (1+\varepsilon/2)r)$, $1 \leqslant i \leqslant k$. However, a necessary condition for a sample point q to induce an (m, k, r)-flock is that there are at least m entities in the disk D_q of radius $2r$ centred at q. During the processing of the sample points we can count how many entities indeed lie in D_q for each sample point q. As we generate at most $\mathcal{O}(n/\varepsilon^{2k})$ sample points, this means that we have to check at most $\mathcal{O}(n/(m\varepsilon^{2k}))$ candidate sample points for inducing a flock. Next we prove the approximation bound.

Lemma 8. *The algorithm is a* $(1+\varepsilon)$*-approximation algorithm.*

Proof. The $1+\varepsilon/(2+\varepsilon)$-approximation of the range query ensures that no (m, k, r')-flock with $r' > (1+\varepsilon)r$ is reported: as we query pipes of radius $(1+\varepsilon/2)r$, the maximum distance from a grid query point to a counted entity could be $(1+\varepsilon/2) \cdot (1+\varepsilon/(2+\varepsilon))r = (1+\varepsilon)r$.

Next, we show that each (m, k, r)-flock is reported by the algorithm. Assume that f is an (m, k, r)-flock in the time interval I. We prove that the approximation algorithm returns an $(m, k, (1+\varepsilon)r)$-flock g such that $f \subseteq g$.

Let $(x_1, y_1, \dots, x_k, y_k) \in \mathbb{R}^{2k}$ be a point that induces an (m, k, r)-flock f with respect to I. We look only at one time-step $t_i \in I$. By the cell spacing it is obvious that there are sample points $(\dots, x_i^q, y_i^q, \dots) \in \Gamma$ such that the Euclidean distance from (x_i^q, y_i^q) to (x_i, y_i) is less than $\varepsilon r/2$. This means that the disk (in $\mathbb{R}^2$) with radius $(1+\varepsilon/2)r$ centred at q completely contains the disk with radius r centred at (x_i, y_i). Thus, when checking the sample points $(\dots, x_i^q, y_i^q, \dots)$ all entities of f are in range for time-step t_i. As this holds analogously for all other time-steps the algorithm reports an $(m, k, (1+\varepsilon)r)$-flock g such that $f \subseteq g$. □

Lemma 9. *The algorithm reports at most τn $(m, k, (1+\varepsilon)r)$-flocks. It runs in $\mathcal{O}(\frac{\tau n k^2}{m\varepsilon^{2k}}(\log n + 1/\varepsilon^{2k-1}))$ time and requires $\mathcal{O}(\tau n)$ space.*

Proof. The number of reported flocks is trivially bounded by n, the number of entities, times τ, the number of time-steps. At each of the $(\tau - k + 1)$ time intervals the algorithm builds a skip-quadtree of the n elements from scratch. In total this requires $\mathcal{O}(\tau k n \log n)$ time, according to Lemma 1. Next a counting query is performed for each of the $\mathcal{O}(n/(m\varepsilon^{2k}))$ candidate sample points in Γ; each query requires $\mathcal{O}(k^2(\log n + 1/\varepsilon^{2k-1}))$ time, thus the total time needed to perform all $n(\tau - k + 1)$ queries is as stated in the lemma.

The space needed to build the skip-quadtree for each time interval is $\mathcal{O}(kn)$, and since we only maintain one tree at a time the bound follows. □

4 Minimise the number of reported flocks

The general (theoretical) approach described in Section 3 has the following disadvantage: As every entity is tested, a flock consisting of exactly m elements can be reported up to m times. This may get even worse if a flock is found whose number of entities exceeds m. Below we briefly discuss three approaches how reporting this redundant information could be avoided. The main idea for all of them is to prune the number of reported flocks, the last approach abandons the restriction that a flock defining region always has to be disk.

Each entity is part of at most one flock. In theory one object can be part of many flocks at the same time which, in practice, this seems unreasonable. Thus, the first method we propose guarantees that an object belongs to at most one flock at a time.

The strategy for this approach is very simple. If a counting query reports a flock then the entities involved in the flock are marked and the skip-quadtree is updated so that the marked entities will not be counted again. The additional time that we have to spend updating the tree is $\mathcal{O}(nk \log n)$ per time-step, thus $\mathcal{O}(\tau nk \log n)$ in total. The number of reported flocks is trivially bounded by $\tau n/m$.

Each entity is part of at most a constant number of flocks. The above approach minimises the number of reported flocks; however, it also overlooks a lot of flocks. Therefore we chose to use a different approach in the experiments which guarantees a higher level of correctness while bounding the number of flocks that an entity may belong to simultaneously.

The idea is that when a flock is found every input point within the query region will be marked, so that no query will be performed with those points as centres. Using a simple packing argument it follows that the maximal number of flocks an entity can be part of during a time-step is bounded by $\mathcal{O}(2^{2k})$. The additional time that we have to spend updating the tree is $\mathcal{O}(nk \log n)$ per time-step, thus $\mathcal{O}(\tau nk \log n)$ in total.

Extending flocks that have been found. In such an approach we also assume that each entity can only be part of at most one flock. Once a flock is found, we first check whether we can reasonably extend it, which means we may manipulate the disk as flock-defining region if it seems reasonable to join objects closeby. There are many ways to do this that work in practice, however, guaranteed theoretical bounds are hard to prove.

5 Experiments

In this section we report on the performed experiments. We describe the experimental setup, i.e. the hard- and software used for the experiments, we briefly explain the algorithms and we present and discuss the running times of them with respect to different parameters of the input.

5.1 Setup

We used a Linux operated off-the-shelf PC with an Intel Pentium-4 3.6 GHz processor and 2 GB of main memory. The data structures and algorithms were implemented in C++ and compiled with the Gnu C++ compiler. The running times are reported as seconds. All our point sets used in the experiments were created artificially. The point sets differ in size (10,000 - 160,000 points; one algorithm was run with more than 1 million points), in length of the time interval (4 - 16 time-steps) and also in the distribution of the points (uniformly random or clustered).

To ensure that our algorithms indeed find flocks, we arranged 10% of the points in each point-set in such a way that they form randomly positioned flocks. Each of the flocks has $m = 50$ entities in a circle of radius $r = 50$ (hence the number of artificially inserted flocks is 0.002 times the total number of points). As it is unlikely to have flocks that were generated by accident, we inserted those artificial flocks to make sure that the methods correctly find them.

The remaining 90% of the points were randomly distributed, either uniformly or in clusters. The purpose of the clustered point sets is that they are more likely to resemble real data, and hence it is interesting to compare the impact of different distributed point sets on the running times of our methods. Each cluster was generated by choosing randomly a cluster centre and then distributing (with a Gaussian distribution) a number of points around that centre. However, the number, distribution, radius and density of the clusters was chosen that it is unlikely (although it can happen) to create flocks by accidents, i.e. a cluster is not dense enough to form a flock because its radius is much larger than the flock radius. Choosing the clusters in this way makes a comparison between the results for clustered and uniformly randomly distributed point sets easier, as the differently distributed points can have a strong effect on the height and width of the created tree structures.

Each point coordinate of an input point is an integer taken from the interval $\left[0, ..., 2^{13}\right]$ or $\left[0, ..., 2^{16}\right]$, respectively. Note that each generated data instance contains the coordinates of points for a certain number of time-steps τ, and in the experiments on that instance, we always looked for flocks of at least $m = 50$ entities in a circle with radius $r = 50$ and of length k with $k = \tau$.

5.2 Methods

We compare the results of four methods called 'box', 'pipe', 'no-tree' and 'pruning'. All of them mark points that were found to belong to a flock, and in the further course of the algorithm those marked points are not used as a potential flock centre, see Section 4 for a discussion. The output of the algorithms are the centres of the found flocks. The box and pipe method are named after their query region and are explained in Sections 3.1 and 3.2, respectively.

The no-tree method (which was implemented for the sake of comparison) does not use a tree as underlying structure. It contains two nested loops, the outer one (running over all input points) specifying a potential flock centre and the inner one (running again over all input points) computing the distance between a point and the potential flock centre. If there are enough points within a ball (around the potential flock centre) of double flock-radius (see the proof of Lemma 3 for an explanation why the radius is doubled) then we found a flock. Hence, the no-tree method is a 2-approximation.

The pruning method takes advantage of the fact that each flock of a certain length k is also a flock of length $k^* < k$. Therefore all points not involved in flocks of length k^* cannot be involved in flocks of length k. The method works as follows. As a first step we compute flocks of length 4 using the box method. Then we build a new tree containing only those points that were contained in flocks during the first step. This drastically reduces the number of points. We then again apply the box method on the new tree for the entire length k.

input		uniformly						clustered					
		box		pipes		no-tree		box		pipes		no-tree	
n	k	flocks	time	flocks	time	flocks	time	flocks	time	flocks	time	flocks	time
10K	4	20	0	20	0	20	5	20	0	20	1	20	5
10K	8	20	2	20	1	20	5	20	1	20	0	20	5
10K	16	20	2	20	1	20	6	20	1	20	0	20	5
20K	4	40	1	*41*	0	40	21	40	0	40	1	40	20
20K	8	40	7	40	5	40	21	40	1	40	0	40	22
20K	16	40	13	40	10	40	25	40	3	40	2	40	25
40K	4	80	0	80	1	80	83	80	1	80	0	80	83
40K	8	80	32	80	22	80	87	80	2	80	2	80	87
40K	16	80	62	80	44	80	99	80	8	80	7	80	101
80K	4	160	3	*163*	3	160	332	160	3	160	2	160	332
80K	8	160	129	160	88	160	347	160	6	160	4	160	346
80K	16	160	244	160	182	160	392	160	30	160	29	160	392
160K	4	320	8	*321*	10	320	1326	320	8	320	5	320	1327
160K	8	320	441	320	316	320	1391	320	20	320	15	320	1384
160K	16	320	986	320	768	320	1576	320	102	320	93	320	1564

Table 1. Results for $\varepsilon = 0.05$ and point-sets with coordinates from $\left[0, ..., 2^{16}\right]$.

5.3 Results

We run the experiments with a couple of generated point-sets for each combination of point-set characteristics, such as number of points, number of time-steps and point distribution. The results were very similar for fixed characteristics and hence the tables below show the numbers for only one collection of point-sets with the specified characteristics. The results of the algorithms are depicted in Table 1, where the coordinates of the points are chosen from the interval $\left[0, ..., 2^{16}\right]$. The columns below 'input' specify the number of points and the number of time-steps, and the columns below 'uniformly' and 'clustered' show the number of flocks found and the running times needed when performing the box-, pipes- and no-tree-algorithm on the corresponding input. We also performed the same experiments on point-sets where the coordinates where chosen from $\left[0, ..., 2^{13}\right]$. Table 2 shows those results. The results for the method with pruning are given in Table 3. Because of the similarity of the results for a different number of time-steps, we only report the results for 16 time-steps in that table. Table 4 shows the results of the no-tree method for a large number of time-steps and a small number of entities. All tables show the results, i.e. the number of flocks found and the running time in seconds, only for $\varepsilon = 0.05$, because no big influence of different values of ε could be observed. From our point of view the running times are much more important than the number of flocks found. Hence, the number of flocks are shown here only for the sake of completeness. These numbers are indicated in *italics* in case they deviate from the number of artificially inserted flocks. (In most cases the methods found exactly as many flocks as were artificially inserted.)

5.4 Discussion

Flat trees in high dimensions. One general observation is that the running times of our algorithms are increasing with the number of time-steps (i.e. with the number of dimensions). Recall that an internal node of an octree has 2^d children where d is the number of dimensions. Using 16 time-steps means 32 dimensions which translates to more than 4 billion quadrants, i.e. children of an internal node (in our approach we only store non-empty children in a list, which reduces storage space but increases time complexity). In an experiment with 160,000 points in 32 dimensions it is very unlikely that many of the randomly distributed points (not in flocks) fall into the same quadrant. Therefore the tree is very flat, i.e. have only a very small depth, which results in high running times.

input		uniformly						clustered					
		box		pipes		no-tree		box		pipes		no-tree	
n	k	flocks	time	flocks	time	flocks	time	flocks	time	flocks	time	flocks	time
10K	4	20	1	20	0	20	5	20	2	20	1	20	4
10K	8	20	8	20	6	20	6	20	2	20	2	20	6
10K	16	20	14	20	11	20	6	20	5	20	11	20	6
20K	4	40	1	40	4	40	20	40	2	40	1	40	20
20K	8	40	52	40	35	40	22	40	6	40	4	40	22
20K	16	40	83	40	58	40	25	40	17	40	44	40	25
40K	4	80	4	80	15	80	83	*81*	6	80	2	80	83
40K	8	80	237	80	166	80	87	80	16	80	21	80	87
40K	16	80	347	80	244	80	99	80	55	80	177	80	99
80K	4	160	10	160	57	160	333	*206*	16	160	8	160	332
80K	8	160	932	160	696	160	348	160	45	160	77	160	348
80K	16	160	1411	160	1124	160	394	160	164	160	594	160	395
160K	4	320	29	320	201	320	1326	*1317*	42	320	27	320	1331
160K	8	320	3179	320	2658	320	1393	320	124	320	238	320	1392
160K	16	320	6015	320	4226	320	1575	320	692	320	2306	320	1576

Table 2. Results for $\varepsilon = 0.05$ and point-sets with coordinates from $\left[0, ..., 2^{13}\right]$.

Error value ε. When performing a range query, ε influences the approximate region to be queried. One could expect that a larger value of ε can lead to shorter running times and more flocks that are found, because the descent in the tree can be stopped earlier and the query region can become larger. However, apart from very marginal fluctuations, this behaviour could not be observed in our experiments. Our point sets and therefore our trees in the experiments are rather sparsely filled. Hence, the squares corresponding to most of the leaves in the tree (which correspond to single points in a point set) are still quite large compared to the flock radius r and also to $(1+\varepsilon)r$. Furthermore, it often seems that the point sets are too sparse to find any random flocks. Therefore we refrained from reporting results for different ε and only used $\varepsilon = 0.05$.

Number of flocks. Most of the times the algorithms found exactly as many flocks as were artificially put into the point-sets. A few times more flocks were found but only in instances with a small number of time-steps, which is reasonable since if the points that are not belonging to an artificially inserted flock, form a flock at all, then it is more likely that this happened for only a small number of time-steps. In one case (see Table 2, box method on clustered points, $n = 160K$, $k = 4$) more than 1300 flocks were found (where only 320 were artificially inserted) which indicates that for that instance the distribution of the points and clusters (in combination with a high number of points and a small coordinate space) reached a limit were the clusters are dense enough to often create random flocks. In some of our experiments we observed that the algorithms found less flocks than artificially were inserted. This can happen if two flocks are close to each other and fall into one query region and hence will be counted as one flock by the algorithm.

Coordinate space $\left[\mathbf{0, ..., 2^{13}}\right]$ vs. $\left[\mathbf{0, ..., 2^{16}}\right]$. Somewhat surprising might be that the experiments with point-sets with coordinates in $\left[0, ..., 2^{16}\right]$ were much faster than those with point-sets with coordinates in $\left[0, ..., 2^{13}\right]$ (all other parameters were the same). One explanation is that in a bigger underlying space (i.e. where the coordinates are in $\left[0, ..., 2^{16}\right]$) it is more likely that the query region falls into a single square corresponding to a quadtree node. Due to the sparseness of the point-sets the algorithms are likely to find just a single point in that square. On the other hand in a smaller underlying space the query region might intersect more squares, which results in more subsequent queries, which in turn takes more time.

Uniformly vs. clustered. When comparing the results of the uniformly distributed point-sets with the clustered point-sets it becomes evident that our tree-based algorithms always perform better on the clustered data. This behaviour could be expected because, as we have seen from the experiments in general, uniformly distributed points result in octrees that are rather flat (especially for higher dimensions). But it is a 'good balance' between height and width of a tree that allows fast query times. Clustered data sets are more likely to create trees that are deeper on some branches or subtrees, and therefore the algorithm will descent on those subtrees cutting off everything not contained in them. The no-tree method (which is not using a tree) is not affected by the two different types of data.

No-tree vs. box vs. pipe. We observe that the no-tree method's running times are quadratic in the number of points and not influenced by the number of time-steps, as expected. On the other hand the box and pipe algorithms are strongly influenced by the number of time-steps and the number of points. As discussed above for high dimensions the box and pipe methods operate on an underlying tree that is very flat. A large query region in combination with a small coordinate space causes their behaviour to become similar (although with a big overhead) to the no-tree method. The difference between the box and pipe method is caused by the different data structure they use. The box method uses the more complex skip-quadtree, while the pipe method incorporates a compressed quadtree.

Pruning. Table 3 shows the running times of the pruning method for $k = 16$ and $\varepsilon = 0.05$. The impressive impact of the pruning step is illustrated in Figure 5 where the running times of the usual box and the pruning method are shown for point sets with coordinates in $\left[0, ..., 2^{13}\right]$.

Depending on the density and distribution, even some point-sets with more than 1 million points can be dealt by the pruning method within a couple of minutes. Furthermore, we observed that the number of time-steps hardly has an influence on the running times. An exception are the clustered point sets with coordinates in $\left[0, ..., 2^{13}\right]$ and a large number of points, where we experienced much longer running times and a strong correlation between the number of time-steps and running time. Also the point distribution (uniformly or clustered) does not affect the running times of the point-sets with coordinates in $\left[0, ..., 2^{16}\right]$. However, for the point-sets with coordinates in $\left[0, ..., 2^{16}\right]$, we observe much longer running times for the clustered point-sets. This can be explained by noting that after the pruning step it is likely that the remaining points form a flock also for more time-steps. Therefore, almost every query to the data structure gives a flock and hence, the number of queries is drastically decreased. For the clustered point sets with coordinates in $\left[0, ..., 2^{13}\right]$, however, the probability of random flocks is much higher. The fact that the pruning method sometimes finds less flocks than the box method can be explained by noting that the pruning method performs two runs of the box method each of which can handle the points in a different order. Therefore the second run of the box method can encounter points which will not belong to any flock.

6 Concluding remarks

This paper is a first step towards practical algorithms for finding spatio-temporal patterns, such as flocks, encounters and convergences. Future research does not only include more efficient approaches to compute these patterns but also more complicated patterns, e.g. hierarchical patterns or repetitive patterns. In this paper we have presented different algorithms for finding flock patterns and analysed them theoretically as well as experimentally. From the experiments we have seen that our tree-based algorithms can perform very well. Especially for a small number of time-steps the resulting running times are often very small, however, they depend very much on the characteristics of the input point-sets, which motivates more research and experiments, preferably on real-world data.

For a larger number of time-steps the no-tree method can be used. This method's running time is mainly influenced by the number of entities and not by the number of dimensions. Table 4

input		coordinates from $\left[0,...,2^{13}\right]$				coordinates from $\left[0,...,2^{16}\right]$			
		uniformly		clustered		uniformly		clustered	
		pruning		pruning		pruning		pruning	
n	k	flocks	time	flocks	time	flocks	time	flocks	time
10K	16	20	0	20	1	20	1	20	0
20K	16	40	1	40	2	40	1	40	0
40K	16	80	3	80	6	80	2	80	2
80K	16	160	11	160	15	160	3	160	3
160K	16	320	30	320	45	320	9	320	9
320K	16	*639*	82	*633*	303	640	26	640	25
640K	16	*1271*	194	*1268*	1796	1280	75	1280	75
1280K	16	*2501*	533	*2507*	9213	2560	249	2560	246

Table 3. Results for pruning method, $\varepsilon = 0.05$.

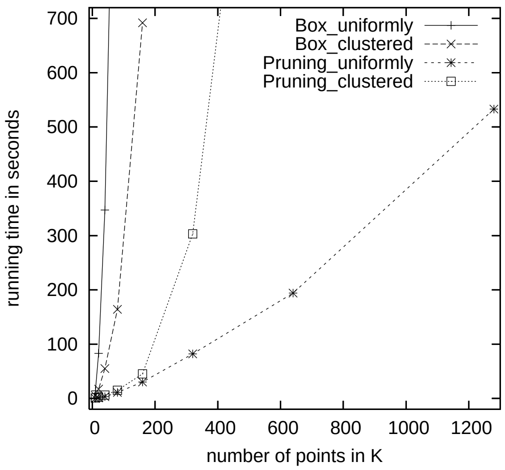

Fig. 5. Running times for $k = 16$, $\varepsilon = 0.05$ and point coordinates from $\left[0,...,2^{13}\right]$.

shows the performance of this algorithm for up to 40000 entities and up to 1000 time-steps. As we have seen from Tables 1 and 2, the characteristics (such as distribution and coordinate space) of the point sets has no influence on the running time of the no-tree method and therefore, Table 4 only shows the results for uniformly distributed points with coordinates in $[0,...,2^{16}]$. We see that also point sets with 1000 time-steps can be searched for flocks of length 1000 within a couple of minutes.

Hence, for a small number n of entities and many time-steps, we can use the no-tree method, which has a running time quadratic in n. For many entities and few time-steps k our tree based methods perform very well, which have a running time exponential in the number of dimensions of the tree, i.e. exponential in k. Thus, we are faced with a trade-off. One approach to tackle the case of many entities and many time-steps has recently been developed by Al-Naymat et al. [3], where the data is preprocessed. In this preprocessing step the number of dimensions (i.e. time-steps) is reduced by random projection. In experiments it was shown [3] that the tree-based methods perform very well on the data with reduced dimensionality. As a conclusion we see that the idea of projecting trajectories into points in higher dimensional space is very viable for finding flocks in spatio-temporal data.

input	uniformly distributed, coordinates from $[0, ..., 2^{16}]$											
	$k = 32$		$k = 64$		$k = 125$		$k = 250$		$k = 500$		$k = 1000$	
n	flocks	time	flocks	time	flocks	time	flocks	time	flocks	time	flocks	time
10K	20	14	20	16	20	15	20	15	20	18	20	21
20K	40	59	40	67	40	69	40	73	40	85	40	88
40K	80	235	80	265	80	278	80	294	80	332	80	337

Table 4. Results of the no-tree method, $\varepsilon = 0.05$.

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