Competitive Search for Longest Empty Intervals

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Abstract

A problem arising in statistical data analysis and pattern recognition is to find a longest interval free of data points, given a set of data points in the unit interval. We use the inverse length of the empty interval as a parameter in the complexity bounds, since it is small in statistically relevant cases. For sorted point sets we get nearly optimal strategies. While the asymptotic complexities are trivial, achieving an optimal number of operations appears to be difficult. Constant factors can be of practical interest for huge data sets. We derive deterministic and randomized upper and lower bounds. Matching bounds and smooth trade-offs between the different operations (reads, comparisons, subtractions) are open questions. For unsorted point sets, the complexity is at least linear. Therefore we also use statistical inference to get approximate solutions in sublinear time. We also point out some extensions to multidimensional analogues of the problems.

1 Introduction

Given a set of n data points in a finite-size part of a geometric space, we call a subset of this space (with prescribed shape) free of data points an empty region. Searching for largest empty regions is a natural problem in, e.g., data mining [10, 11]. It has been considered for rectangles in the plane [1, 2, 5, 8, 12] and boxes in d dimensions. Usually, the complexity of algorithms is expressed as a function of input size n. However, empty regions are statistically relevant only if they are large compared to the expected size if the data point set were drawn from a uniform distribution. Then, large empty regions may be found faster than in the worst case. Thus it is sensible to measure complexity as a function of both n and a parameter inverse to the size of the empty region. Here we study, as a first step, the 1-dimensional case: empty intervals between n data points in the unit interval. While the worst-case complexity is trivially $\Theta(n)$, the parameterized problem has a different nature. Still, its optimal asymptotic complexity is easy to determine by standard arguments, but the exact number of operations appears to be a surprisingly difficult question. Constant factors can make a difference in practice, not for a single instance, but when huge data sets with many instances are processed. Analyzing the number of operations (e.g., comparisons) without ignoring constant factors is quite common for sorting, searching, and order statistics.

We state our problem Longest Empty Interval more formally. A sorted set of real numbers $0 = x_0 < x_1 < \ldots < x_n = 1$ is given. An *empty interval* is an interval delimited by two consecutive x_i, x_{i+1}. We can access x_i through index i in constant time. (The x_i are either stored in an array or delivered by an oracle.) Our goal is to find a longest empty interval, that is, one with largest difference $\max_i(x_{i+1} - x_i)$. This can be trivially done by n read operations (*reads* for short), subtractions, and comparisons, respectively, and linear time is optimal due to an obvious adversary argument. Define $r := 1/\max_i(x_{i+1} - x_i)$. Supposing that a "very long" empty interval is expected, with $r \ll n$, we want an algorithm that takes advantage of the small r.

Throughout the paper, logarithms are base 2. We call the x_k values *data points*. In our complexity bounds we neglect minor-order terms. To avoid clumsy notation we also silently suppress factors $1 + o(1)$ where $o(1)$ tends to 0 as n grows.

We show that Longest Empty Interval can be solved optimally with $r \log(n/r)$ reads. However, in order to keep the number of other operations within $O(r \log(n/r))$ we need some more reads. We have to add factor 2 (deterministic) or 1.4427 (randomized). We also study the case of unsorted data point sets, called Longest Empty Interval (unsorted). Amazingly, n and r almost switch their roles: We give an algorithm with roughly $n \log r$ comparisons, while the number of reads is trivially n. We remark that a rather obvious RAM algorithm using n equidistant buckets solves Longest Empty Interval (unsorted) in $O(n)$ time, but for comparison-based algorithms $\Theta(n \log r)$ is optimal, and the simple scheme also fails for similar problems in higher dimensions. The problem is also known as *max gap* and has an $\Omega(n \log n)$ lower bound in the algebraic decision tree model [3, 9]. Our algorithms do not assume prior knowledge of r. Another practical advantage is their simplicity, however, several details leading to the constant factors are a bit tricky, and there remain gaps between the current upper and lower bounds. In the unsorted case, approximate solutions, i.e., large

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regions with few data points, can still be obtained in sublinear time. We give a grid-based method to analyze the performance of an obvious sampling method. The last section informally discusses extensions to other geometric set families.

We conclude the introduction with some motivations and further related literature.

In the sorted case one may argue that the longest empty interval *could have been* computed on the fly, when the set has been sorted, and this makes up a minor part of the calculations. But what if distances in our huge sorted point sets *have not been* computed earlier, simply because there was no interest in such analysis? Then we want to solve the *actual* problem as efficiently as possible. There may also arise machine learning problems where we know that some unknown "empirical" function is monotone, values are not explicitly stored but can be queried by experiments, and we are mainly interested in large jumps of this function.

In fact, Longest Empty Interval exhibits striking similarities to a well-known problem in combinatorial search: competitive group testing [6, 7]. The classical *group testing* problem asks to find r defective elements out of n elements. Here the computational primitives are group tests: We may query arbitrary subsets Q, and the test says whether Q has some defective. In the additive model of group testing, a test returns the number of defectives in Q. In the more general weighted version, defectives have weights, and a group test returns the sum of weights. Group testing has an asymptotic complexity of $\Theta(r \log(n/r))$ tests, even if the set is linearly ordered and query sets Q must be intervals, i.e., contiguous subsets. However, if r is not known in advance, it is very difficult to figure out the constant factor [6, 7]. The similarity between Longest Empty Interval and group testing is explained by the observation that we can "measure" the distance between two data points by two reads and one subtraction. Thus, $O(1)$ operations correspond to "something like" an interval group test. On the other hand, of course, our primitive operations are different, and we are also looking for a different type of object. Although the techniques are somewhat similar, we cannot simply transfer known results for group testing to our problem.

In [4] we gave algorithms for finding at most s disjoint intervals of maximum total length that contain at most p data points (s, p are fixed parameters). Finding longest empty intervals in sorted point sets is part of the preprocessing. Then, it is proved that the optimal solutions are composed of such intervals from a certain candidate set whose size depends only on s and p, and it can be computed by dynamic programming. Only the time for preprocessing depends on n, therefore we save a significant fraction of the overall running time by log-time preprocessing. In range prediction applications as in [4], the data points come as previously sorted sets.

Some aspects addressed in this work are also apparent in [11], but more from a heuristic and machine learning perspective.

2 The Sorted Case

Theorem 1 Longest Empty Interval *can be solved using* $r \log(n/r)$ *reads, and this bound is optimal.*

Proof. An adversary may divide the data points into r sets of roughly n/r consecutive data points, and hide an empty interval slightly shorter than $1/r$ in every subset. Then, the searcher has to find the (indices of) data points delimiting these long empty intervals, in order to be able to compare their lengths and determine the longest one. Hence the searcher is forced to do binary search in every subset. This shows the lower bound.

The proposed algorithm maintains, in a linked list, the ordered sequence of data points x_k already read. In every step we take two consecutive data points in this list with currently largest distance, say x_a and x_b, read the data point $x_{\lfloor (a+b)/2 \rfloor}$ and insert it in our list. We stop as soon as $a + 1 = b$. Since $x_b - x_a$ is the maximal distance in the sequence, we have found the longest empty interval at this moment.

To analyze the number of reads, think of this splitting process as a binary tree of segments of data points, in the obvious sense. One read is associated with every non-leaf node. Consider the tree upon termination of the algorithm. A *long* node represents an interval of length at least $1/r$, other nodes are called *short*. We prune the tree as follows. Any pair of short leaf siblings is removed, making their parent a leaf. The parent node is always long, since the algorithm has considered intervals by decreasing lengths and stopped at $1/r$. After pruning, one read is associated with every long node. Since the leaves represent pairwise disjoint intervals, at most r leaves are long nodes. Every long non-leaf node is on some path from the root to some long leaf (otherwise we could continue pruning). It follows that all reads are associated with nodes on paths to at most r of the leaves. The path length in the tree is trivially bounded by $\log n$. At most r nodes have depth $\log r$, and the remaining subpaths from level $\log r$ to the leaves have length at most $\log n - \log r$. Since at most r such paths exist, we get the claimed bound. □

However we have to worry about the other operations, too. Upon every read we also need two subtractions to get the lengths of the two new intervals. Thus, the method needs $2r \log(n/r)$ subtractions. The catch is that we need to know the longest interval for the next split. Using a heap for at most r interval lengths (the current leaves of the tree), we make, for every read, up to $4 \log r$ length comparisons to include the two new

interval lengths in the heap (and also $5 \log r$ copy operations in the heap). Thus the method in this form costs $4r \log r \log(n/r)$ comparisons. An optimal number of reads is good if data access is very expensive, e.g., if data reside in some external memory. But usually the costs of reads, comparisons, and subtractions should be similar. Thus we will next aim at $O(r \log(n/r))$ operations in total, with small constant factors. We now propose a method that still uses repeated halving, but on the range of values rather than indices. The number of reads is only doubled.

Theorem 2 LONGEST EMPTY INTERVAL *can be solved using* $2r \log(n/r)$ *reads,* $2r \log(n/r)$ *comparisons, and* $O(r)$ *subtractions.*

Proof. In the jth phase ($j = 1, 2, 3 \ldots$), we declare every $i/2^j$ (i odd, $0 < i < 2^j$) a *grid point*. For every new grid point g, binary search finds k with $x_k \le g < x_{k+1}$. We call $[x_k, x_{k+1}]$ the *empty interval around* g. We compute the lengths of empty intervals around all grid points and determine the longest one.

Let p be the exponent with $1/2^p \le 1/r < 1/2^{p-1}$. Then, a longest empty interval (of length $1/r$) contains a grid point in phase p. Since we have computed the lengths of empty intervals around all grid points, $1/r$ is among these values, and it is the maximum length. Since every empty interval without grid points is entirely between two consecutive grid points, its length is at most $1/2^p \le 1/r$, hence we know at this moment that a longest empty interval is found.

In order to find the empty interval around any new grid point introduced in phase j, it suffices to do binary search on the data points between the two neighbored old grid points. (Recall that we already know the indices of the leftmost and rightmost data point in this range.) Since all these search spaces do not overlap, we perform 2^{j-1} binary search procedures on a total of n elements in phase j. By concavity of log, the total number of search steps in phase j is maximized if all search spaces have equal size $n/2^{j-1}$. Summation over all phases yields the number of operations: $\sum_{j=1}^{p} 2^{j-1}(\log \frac{n}{2^{j-1}} + O(1)) = 2^p(\log n - p + O(1))$.

The worst case is $1/r < 1/2^{p-1}$, with an arbitrarily small difference. Now $2^p < 2r$ yields the upper bound of $2r \log(n/r)$ search steps. Every search step requires one read and one comparison. Subtractions are only used to compute the lengths of empty intervals around the $O(r)$ grid points. Only $O(r)$ comparisons are needed to determine the maximum length among them. □

The worst case in the above analysis suggests that randomization on the grid size might improve the constant factor in the number of reads. In fact, we obtain:

Theorem 3 LONGEST EMPTY INTERVAL *can be solved using an expected number of* $(1/\ln 2)r \log(n/r)$ *reads,* $(1/\ln 2)r \log(n/r)$ *comparisons, and* $O(r)$ *subtractions. (Remark:* $1/\ln 2 < 1.4427$*.)*

Proof. We sample a random $t \in [1, 2)$ according to some probability density function q that we specify below, multiply the grid point distances by t, and continue deterministically as in Theorem 2. For formal clarity: We construct the grid on an interval of length t including $[0, 1]$, but then we ignore all grid points outside $[0, 1]$.

As in Theorem 2, let p be the exponent with $1/2^p \le 1/r < 1/2^{p-1}$. If $t \le 2^p/r$ then we also have $t/2^p \le 1/r < t/2^{p-1}$. Now we argue, as in Theorem 2, that an empty interval of length $1/r$ is identified in phase p. However, since grid points outside the unit interval are ignored, we perform only $2^{j-1}/t$ binary search procedures on disjoint subsets of a set of n elements, in phase j. The total number of search steps in phase j is maximized if all search spaces have equal size $tn/2^{j-1}$. Summing over all phases we get $\frac{1}{t}\sum_{j=1}^{p} 2^{j-1}\left(\log \frac{tn}{2^{j-1}} + O(1)\right) = \frac{2^p}{t}(\log n - p + O(1))$.

If $t > 2^p/r$ then $t/2^{p+1} \le 1/r < t/2^p$. Still we can argue as above, but with $p + 1$ in the role of p, which yields the result $(2/t)2^p(\log n - p + O(1))$.

Define $x := 2^p/r$, and note that $1 \le x < 2$. We express the number of reads as $(x/t)r \log(n/r)$ if $t \le 2^p/r$, and $2(x/t)r \log(n/r)$ if $t > 2^p/r$. Specifically, we use density $q(t) = 1/(t \ln 2)$ for sampling. (In fact, q is a density function, due to $\int_1^2 dt/t = \ln 2$). Thus we obtain in front of $r \log(n/r)$ the following expected factor: $x\left(\int_1^x \frac{1}{t} q(t)dt + 2\int_x^2 \frac{1}{t} q(t)dt\right) = \frac{x}{\ln 2}\left(\int_1^x \frac{1}{t^2}dt + 2\int_x^2 \frac{1}{t^2}dt\right) = \frac{x}{\ln 2}\left(\frac{1}{1} - \frac{1}{x} + \frac{2}{x} - \frac{2}{2}\right) = \frac{1}{\ln 2}$. The other bounds follow as in Theorem 2. □

It remains open, even in the randomized case, whether $r \log(n/r)$ reads are sufficient together with $O(1)r \log(n/r)$ other operations. More generally, a smooth trade-off between reads and comparisons would be nice. Apparently this would require to "bridge" somehow between repeated halving on the range of indices and values.

3 The Unsorted Case

In order to solve LONGEST EMPTY INTERVAL (UNSORTED), we have to read all n data points x_i, since any missing x_i could fall into the largest empty interval of the rest of the data set. Hence the number of reads is not interesting. We focus on comparisons and subtractions. Trivially, sorting the x_i solves the problem by $n \log n$ comparisons and n subtractions, but for $r \ll n$ we can avoid sorting and save almost a $\log n$ factor:

Theorem 4 LONGEST EMPTY INTERVAL (UNSORTED) *can be solved using* $n(\log r + 3) + 4r$ *comparisons and*

$O(r)$ subtractions, and $n \log r$ is a lower bound for the number of comparisons.

Proof. Again we perform repeated halving on $[0,1]$, inserting grid points $i/2^j$ (i odd) in phase j, but this time we divide the data points recursively into subsets situated between any two neighbored grid points. If j phases are needed, this costs altogether nj comparisons between data points and grid points. After each phase we check which of the mentioned subsets became empty. This step is simple: To every new grid point we attach a discrete variable that tells us whether some data point went to the left and to the right subset. As soon as we get some empty subset(s) in our partitioning, we know that the largest empty interval is formed by the rightmost data point in some nonempty subset and the leftmost data point in the next nonempty subset to the right. All candidates are found by n comparisons in total, because the linear order of subsets is known, and minimum resp. maximum search is done on disjoint subsets. If j is the final phase, at most 2^j subtractions yield the interval lengths, and 2^j further comparisons return the result.

Once more, let p be the exponent with $1/2^p \le 1/r < 1/2^{p-1}$. We detect an empty subset when two grid points hit the largest empty interval, which happens in phase $j \le p+1$. Hence $j < \log r + 2$, furthermore $2^j \le 2^{p+1} < 4r$. Summation of comparisons in binary search and candidate selection yields the upper bound.

As for the lower bound, an adversary may split the unit interval into r pieces of equal size and place $r-1$ data points at their borders. If any of these pieces remains free of data points, it is the largest empty interval. For a data point d define, at any moment, $I(d) \subseteq [0,1]$ as the interval of possible values of d's coordinate according to the searcher's current knowledge. Basically, the adversary answers to any comparison of d to a point in $[0,1]$ so that $I(d)$ keeps at least half of its length. Then, in order to determine which piece a data point belongs to, the searcher must compare its coordinate with $\log r$ numbers; comparisons between points are not more powerful. A slight difficulty is that the adversary must make sure that no piece becomes disjoint to all intervals $I(d)$ prematurely, because then the searcher would know the solution. However, before the searcher can "empty" a piece P, the adversary "sacrifices" one data point d with $I(d) \supseteq P$ and places d in the middle of P. □

A question is whether $n \log r$ comparisons is a lower bound also for randomized strategies.

It is not possible to find exactly the largest empty interval in sublinear time. On the other hand, for statistical inference and data mining, a relaxed optimization goal is still appropriate: Find a large interval containing at most a given fraction of data points (as in [4]). Then we can sample from the data points and estimate the point numbers in intervals. The question is how reliable the inferred "sparse" intervals are.

For technical reasons we further modify the problem statement in two ways, without changing its "essence": Firstly, instead of a huge set of data points we assume an unknown *continuous* probability distribution on $[0,1]$ to sample from. Secondly, instead of searching for an interval with given probability mass q and maximum length L, we search for an interval with given L and minimum q. (Note that the length of an interval is "observable", whereas probability mass can only be estimated.) Now we can measure the performance simply by the competitive ratio q_A/q, where q_A is the probability mass of the interval selected by the algorithm, and q is the minimal probability mass among all intervals of length L. We get the following trade-off, with $\delta = q_A/q - 1$:

Theorem 5 *Given some $L < 1$ and an unknown probability distribution on the unit interval, let q be the minimum probability mass of the intervals of length L. Then one can, in $O(m \log m)$ time, sample an expected number of m points and specify an interval of length L with probability mass smaller than $(1+\delta)q$, subject to an error probability less than*

$$\frac{h}{q}(1+1/\delta)\exp\left(-mq\frac{(\delta-2/h)^2}{4+2\delta}\right),$$

for any positive δ and h.

Proof. The algorithm as such is trivial: Sample a number of points that follows a Poisson distribution with expectation m, then take an interval A of length L that contains a minimum number of sampled points. Finding A is straightforward, we just spend $O(m \log m)$ time on sorting. The concern is to analyze the probability mass of A. (We use the Poisson distribution only because this greatly simplifies the argument. In practice we may sample a fixed number m of points instead, the difference is negligible.)

For any deviation δ and expectation μ we bound the probability that, given two Poisson distributed random variables with expectation μ and $(1+\delta)\mu$, the former variable is *not* smaller than the latter one, i.e., the order of sizes is switched. (For the following we may also apply Chernoff bounds to certain cut-off points, but still we had to add products of tail probabilities, and the whole calculation does not seem to become simpler, nor is the result better. Therefore we prefer a direct way.)

The aforementioned switch probability is clearly

$$\exp(-(2+\delta)\mu)\sum_{j=0}^{\infty}\frac{((1+\delta)\mu)^j}{j!}\sum_{i=j}^{\infty}\frac{\mu^i}{i!}.$$

Using $k = j + i$ as summation index, substituting i and observing $j \le i$, we transform this expression into

$$\exp(-(2+\delta)\mu) \sum_{k=0}^{\infty} \mu^k \sum_{j=0}^{k/2} \frac{(1+\delta)^j}{j!(k-j)!}.$$

To be precise, summation limit $k/2$ should read $\lceil (k+1)/2 \rceil$, but this "sloppiness" lightens the notation and will not affect the final bound. We further rewrite the expression as

$$\exp(-(2+\delta)\mu) \sum_{k=0}^{\infty} \frac{\mu^k}{k!} \sum_{j=0}^{k/2} (1+\delta)^j \binom{k}{j}.$$

Stirling's formula yields $\binom{k}{k/2} \approx 2^k\sqrt{2}/\sqrt{\pi k}$. For decreasing $j < k/2$, the binomial coefficients become only smaller, and a factor $1+\delta$ is lost in each step to a smaller j, hence the inner sum is bounded by

$$\frac{2^k\sqrt{2}}{\sqrt{\pi k}}(1+\delta)^{k/2} \left(1 + \frac{1}{1+\delta} + \left(\frac{1}{1+\delta}\right)^2 + \dots\right)$$

$$= (1+1/\delta)\frac{2^k\sqrt{2}}{\sqrt{\pi k}} \left(\sqrt{1+\delta}\right)^k.$$

To get rid of the $1\sqrt{k}$ term we bound $\sqrt{2}/\sqrt{\pi k}$ just by 1. Thus, our probability bound simplifies to an exponential function:

$$(1+1/\delta)\exp(-(2+\delta)\mu) \sum_{k=0}^{\infty} \frac{\left(2\mu\sqrt{1+\delta}\right)^k}{k!}$$

$$= (1+1/\delta)\exp(-\mu(2+\delta))\exp(2\mu\sqrt{1+\delta})$$
$$< (1+1/\delta)\exp(-\mu\delta^2/(4+2\delta)).$$

Back to the main proof, let B be an optimal solution, that is, an interval of length L with minimum probability mass q. We split B into h pieces, each with probability mass q/h. We extend this partition to both sides of B, that means, we cut off pieces of probability mass q/h successively to the left and right, starting at the left and right endpoint of B, respectively. (The last pieces at both ends of the unit interval may have smaller probability mass.) Now assume that the selection algorithm has chosen an interval A with probability mass at least $(1+\delta)q$. We cut away both ends of A which are, in general, not complete pieces in our partition. The shortened interval $G \subset A$ has still a probability mass $(1+\delta-2/h)q$ or larger. The number of sampled points in G and B follows a Poisson distribution with expectation $m(1+\delta-2/h)q$ or larger, and mq, respectively.

If G and B are disjoint, the numbers of sampled points in G and B are independent random variables. Thus, the probability of G having no more data points than B is bounded by $(1+1/\delta)\exp(-mq\frac{(\delta-2/h)^2}{4+2\delta})$.

If G intersects B, then $G \cap B$ has probability mass iq/h, for some positive integer $i < h$. The probability of G having no more data points than B equals the probability of $G \setminus B$ having no more data points than $B \setminus G$. Since the point samples in the two set differences are independent, we can use the switch probability bound, with appropriate modifications: We have to replace q with the probability mass on $B \setminus G$, which is $q' := \frac{h-i}{h}q$. On the other hand, the deviation is the ratio of probability masses on $G \setminus B$ and $B \setminus G$, minus 1, which evaluates to at least $\frac{h+\delta h-2-i}{h-i} - 1 = \frac{\delta h-2}{h-i}$. Thus the switch probability bound becomes

$$\left(1 + \frac{h-i}{\delta h-2}\right)\exp\left(-mq\frac{(\delta h-2)^2}{(4+2\delta)h(h-i)}\right).$$

In summary, if the algorithm has chosen any interval A as specified above, then A contains some interval G according to one of the above cases. Since A has been selected, A contains no more data points than B, and neither does G. Thus, we get a bound for the error probability by summing up the contributions of all possible G (union bound). Since the absolute value of the exponent is larger if G intersects B, this case is dominated by the former case with G and B disjoint. Note that h/q intervals G exist. This finally yields an error bound $\frac{h}{q}(1+1/\delta)\exp(-mq\frac{(\delta-2/h)^2}{4+2\delta})$. □

After a slight refinement of the proof we can replace factor $\frac{h}{q}$ with the smaller $\frac{h}{L}$. The free parameter h may be choosen so as to minimize the error bound. In particular, taking $h = mq\delta$ gives the best asymptotics for large m. Here we obtain $m(1+\delta)\exp(-mq\frac{\delta^2}{4+2\delta})$. For a given sample size m, the bound can also be used to compute $1+\delta$ that are achievable with high probability, depending on q. For very small q, these δ are large, however, the "absolute" probability mass $q(1+\delta)$ of the returned interval is more interesting than the competitive ratio in this case.

4 Extensions and Further Research: Other Geometric Set Families

It remains to improve the various complexity and probability bounds and to close the gaps. In the main part of this paper we focused on intervals, but the ideas are much more general.

One extension is to find several longest empty intervals, as needed in [4]. We state the problem k LONGEST EMPTY INTERVALS as follows. A sorted set of real numbers $0 = x_0 < x_1 < \dots < x_n = 1$ and some $k < n$ is given. Our goal is to find k intervals with the k largest differences $x_{i+1} - x_i$. (These differences are not necessarily distinct numbers.) Define $1/r$ as the kth largest number in the multiset of all $x_{i+1} - x_i$.

Theorem 6 *Problem k Longest Empty Intervals can be solved using $r\log(n/r)$ reads, or alternatively with $2r\log(n/r)$ reads and $2r\log(n/r)$ comparisons, or with an expected number of $(1/\ln 2)r\log(n/r)$ reads and $(1/\ln 2)r\log(n/r)$ comparisons. Problem k Longest Empty Intervals (unsorted) can be solved using $n(\log r + 3) + 4r$ comparisons*

Proof. We get away with $r\log(n/r)$ reads as in Theorem 1, where we stop only when the kth largest interval is found. The analysis relies on the fact that we stopped at length $1/r$, hence the bound (with re-defined r) is the same. Similar reasoning applies to Theorem 2 and 3, where we determine the k longest intervals around grid points, and to Theorem 4, where we wait for k empty subsets in the partitioning. □

A scheme as in Theorem 4 still works for higher-dimensional problems, although with some relaxation: Since we lack total order, we can hardly get optimal results in $o(n\log n)$ time, but we get approximations. We illustrate the issue for the system of axis-parallel boxes in, say, the d-dimensional unit hypercube $[0,1]^d$. Let $1/r$ be the volume of some largest empty box B. (Volume is a meaningful measure in the statistical and data mining context, as the ratio of volumes is invariant under stretching of axes.) For any fixed d we have:

Theorem 7 *A $(1-1/s)$-approximation to the empty box with largest volume can be computed in time $O(n(\log r + \log s))$.*

Proof. We split the unit hypercube by recursive halving into smaller and smaller, equally sized hypercubes called cells. As soon as we have $\Theta(r^d)$ cells, we can identify a box of empty cells containing most of B. With $\Theta((drs)^d)$ cells, some box of empty cells contains at least $1-1/s$ of the volume of B. Note that every data point can be assigned to the correct cell in a time logarithmic in the number of cells, and the time for operations with cells (building empty boxes, etc.) depends only on the number of cells, but not on n. □

The hidden factors are left as a topic of further research. They depend on d and implementation details.

The sampling approach of Theorem 5 works similarly for other geometric set families $\mathcal{F}$, once there exists an efficient algorithm for finding large sets in $\mathcal{F}$ with few data points. A technical difficulty of the analysis is to define suitable "grids": For any probability distribution we need a finite family $\mathcal{G}$ so that every set of $\mathcal{F}$ has a subset in $\mathcal{G}$ with small loss of probability mass. Granularity can be chosen so as to minimize the union bound. The cardinality of $\mathcal{G}$ appears as a factor, but the loss affects the negative exponent in the exp term. We give two examples.

Theorem 8 *Given some $L < 1$, an integer s, and an unknown probability distribution on the unit interval, let q be the minimum probability mass of unions of s intervals of total length L. Then one can, in $O(sqm^2\log m)$ time, sample an expected number of m points and specify s intervals of total length L with total probability mass smaller than $(1+\delta)q$, subject to an error probability less than*

$$\frac{(h/q)^{2s-1}}{(2s-1)!}(1+1/\delta)\exp\left(-mq\frac{(\delta-2s/h)^2}{4+2\delta}\right),$$

for any positive δ and h.

Proof. We choose s intervals of total length L, containing the minimum number p of sampled points. To this end we may fix p and compute s intervals with maximum total length, in $O(spm)$ time (or alternatively in $O(pm + s^2p^3)$ time) as shown in [4]. The suitable p for length L is found by doubling and binary search, hence $O(\log p)$ guesses are enough. Since $p = O(qm)$ with high probability, the overall time amounts to $O(sqm^2\log m)$.

The analysis proceeds as in Theorem 5, with some adaptations: The loss is $2s/h$ rather than $2/h$, since we cut the s intervals at both ends, and the cardinality of $\mathcal{G}$ is smaller than $(h/q)^{2s-1}/(2s-1)!$, since s intervals have $2s$ endpoints from the grid, but one coordinate is determined by the other $2s-1$ endpoints and the total length L. □

Theorem 9 *Given some $L < 1$ and an unknown probability distribution on the d-dimensional unit hypercube, let q be the minimum probability mass of the boxes of volume L. Then one can sample an expected number of m points and specify a box of volume L with probability mass smaller than $(1+\delta)q$, subject to an error probability less than*

$$\frac{1}{2}\left(\frac{h}{2q}\right)^{2d-1}(1+1/\delta)\exp\left(-mq\frac{(\delta-2d/h)^2}{4+2\delta}\right),$$

for any positive δ and h. The time complexity depends on the time needed to determine a box of volume L that contains a minimum number of sampled points.

Proof. We choose a box of volume L, containing the minimum number of sampled points. The analysis proceeds again as in Theorem 5, with some adaptations: In each of the d axis directions we split the hypercube into h/q slices of probability mass q/h. The loss is $2d/h$ rather than $2/h$, since we cut a box at its $2d$ sides. The cardinality of $\mathcal{G}$ is about $(h/2q)^{2d-1}/2$, since one of the $2d$ coordinates of a box G is determined by the given volume L. □

The algorithmic problem mentioned in Theorem 9 seems to be interesting in itself.

For families $\mathcal{F}$ like disks or balls, grid construction is possible, too, but more complex, since "heavy" borders of sets in $\mathcal{F}$ must be sliced.

On the other hand, one has to be careful: We point out that some prominent set families are structurally too large to be used as empty regions in data mining. For example, we can fool the family $\mathcal{F}$ of orthoconvex polygons as follows. Consider a distribution on a rectangle where all probability mass is concentrated on a diagonal. (This is not an artificial example. Think of two numerical attributes correlated by a linear function). Then, a largest empty orthoconvex polygon would avoid all data points but still have probability mass 1. By a similar argument, the family $\mathcal{F}$of convex polygons is too large, as the probability mass could be concentrated on a large circle.

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