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On Lazy Randomized Incremental Construction*

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Abstract. We introduce a new type of randomized incremental algorithms. Contrary to standard randomized incremental algorithms, these *lazy* randomized incremental algorithms are suited for computing structures that have a "nonlocal" definition. In order to analyze these algorithms we generalize some results on random sampling to such situations. We apply our techniques to obtain efficient algorithms for the computation of single cells in arrangements of segments in the plane, single cells in arrangements of triangles in space, and zones in arrangements of hyperplanes.

1. Introduction

Since randomization first appeared in the computational geometry literature in the late eighties, it has had great impact on the field. Currently the best-known algorithms for many problems are randomized. Even when there are deterministic algorithms with the same or a better asymptotic running time, the randomized algorithms are so much simpler and easier to implement that they seem to be the method of choice in practice.

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A popular type of randomized algorithms is *randomized incremental algorithms*. Here a geometric structure induced by a set S of certain geometric objects is computed by adding the objects in S in random order, meanwhile maintaining the structure induced by the current subset. Examples are algorithms for computing arrangements of line segments [9], [15], convex hulls [19], [8], Voronoi diagrams [11], [4], [13], and the union of fat triangles or pseudodisks [14].

Most of these algorithms are based on the theory by Mulmuley [15] and by Clarkson and Shor [9]. They have analyzed random sampling in an abstract setting that applies to a number of geometric problems. Although the settings by Mulmuley and by Clarkson and Shor are formulated in a different way, they both rely on the same basic framework. They consider a set of geometric objects (a set of line segments, say), and define some geometric structure on it (the planar arrangement defined by these segments). This structure is built up from simple elements of constant complexity called *regions* (trapezoids of the trapezoidal map defined by the segments). To analyze the behavior of the structure for a randomly drawn subset of the objects, they define for every regions a set of objects *defining* the region and a set of objects *in conflict with* the region. The assumption they need for their analysis is that a region is present in a geometric structure exactly if all of the defining objects are present, but none of the conflicting objects are. This assumption makes it possible to specify exactly the probability that a certain region appears in the structure induced by a random subset of the given set of objects; it lies at the basis of Mulmuley's as well as Clarkson and Shor's analysis.

Unfortunately, there are geometric structures that do not fit into the framework of Mulmuley and of Clarkson and Shor. One of the most important such structures is a single face in an arrangement of segments in the plane or, in general, a single cell in an arrangement of $(d-1)$-dimensional simplices in d-space. Single cells do not fit into their frameworks because the question of whether a trapezoid defined by some segments in the plane is part of the single cell cannot be answered locally: it depends on the complete configuration of the segments. Therefore it is impossible to define a set of conflicting objects properly.

If we want to develop a randomized incremental algorithm for computing a structure with nonlocal definition—a single cell, for example—then we face two problems. First, the analysis of Mulmuley and of Clarkson and Shor does not apply. Second, because it cannot be decided locally whether a region is part of the structure, it is difficult to maintain the structure efficiently.

Chazelle *et al.* [5] overcame these problems for the computation of a single face in an arrangement of line segments in the plane. They have extended part of Clarkson and Shor's analysis to that case (in fact, our more general analysis borrows several ideas from theirs). They also showed how to find the parts of the single cell that are cut off after the insertion of a new segment, using some auxiliary data structures. (See Section 3 for more details.) This, however, seems to be very difficult in higher dimensions.

This was the motivation for our research: we wanted to devise a randomized incremental algorithm for the computation of a single cell in an arrangement of triangles in 3-space. Because we could not find a way to maintain the single cell efficiently after each insertion, we took the following lazy approach, which appears

to be new. When inserting a triangle we do not attempt to identify and discard the parts of the cell which are cut off; we simply keep everything around, including the parts that are no longer part of the single cell. This way we would, of course, end up constructing the full arrangement of triangles. Therefore we clean up the structure at certain stages (after inserting the 2^ith triangle, for $i = 1, \ldots, \log n$, to be precise). To perform this clean up we just visit everything in the structure that we have constructed so far, discarding the parts outside the single cell. To analyze this algorithm we needed a generalization of Clarkson and Shor's results on random sampling to structures with a nonlocal definition. The result is a new framework and analysis for randomized algorithms, which allows for structures with a "nonlocal" definition. Our analysis shows that the bounds obtained by Mulmuley and by Clarkson and Shor remain valid in our more general framework.[1] In a nutshell, we relax the above-mentioned condition that a region is present in a geometric structure if and only if its defining set is present and none of its conflicting objects are. In our generalization, this is only a necessary and not a sufficient condition.

Using this analysis we show that the lazy algorithm for computing single cells in 3-space runs in expected time $O(\psi(n) \log n)$, where $\psi(n)$ is the maximum number of boxes in the vertical decomposition of a single cell in an arrangement of n triangles. Recently Tagansky [21] proved that $\psi(n) = O(n^2 \log^2 n)$. We thus achieve a running time of $O(n^2 \log^3 n)$. This improves on a result by Aronov and Sharir [1] who gave an algorithm for the single-cell problem with running time $O(n^{2+\varepsilon})$, for any fixed $\varepsilon > 0$. In the two-dimensional case our algorithm for computing a single face runs in time $O(n\alpha(n) \log n)$. (Here and in the rest of the paper $\alpha(n)$ denotes the extremely slowly growing functional inverse of Ackermann's function.) Thus we achieve the same running time as Chazelle *et al.* [5], but with a simpler algorithm.

Our technique extends to various other problems. We illustrate this by giving a simple algorithm for computing zones in arrangements of hyperplanes in d-dimensional space. The algorithm computes the zone of a hyperplane in an arrangement of hyperplanes in d-dimensional space in $O(n^{d-1} + n \log n)$ time. It can also compute zones of curves, surfaces, and so on. To our knowledge no efficient algorithms were known for these problems.

2. Random Sampling with Nonlocal Definition

We present our analysis of random sampling with nonlocal definition in an abstract framework, following the spirit of Clarkson and Shor [9]. This permits us to apply it to different situations.

Let S be a set of n objects. (To keep some life in the following presentation, the reader would be well advised to imagine a concrete example. Assume, for instance, that S is a set of n line segments in the plane.) For every subset $R \subseteq S$, define a collection of "regions" $\mathscr{C}(R)$. (The set of line segments R partitions the plane into

[1] We recently learned that Clarkson and Matoušek independently from each other or us proved similar generalizations of Clarkson and Shor's random sampling results.

faces. Consider the face containing the origin. We partition this face into trapezoids by the usual vertical trapezoidation scheme—see Section 3 for the precise definition. The collection of trapezoids thus obtained is $\mathscr{C}(R)$.) Elements of $\mathscr{C}(R)$ are denoted by Δ. Let $\mathscr{F}$ be the set of all possible regions Δ, that is, all Δ that arise in $\mathscr{C}(R)$ for some subset $R \subseteq S$.

To every $\Delta \in \mathscr{F}$ we assign subsets $\mathscr{D}(\Delta)$ and $\mathscr{K}(\Delta)$ of S. We call the set $\mathscr{D}(\Delta)$ the *defining set* of Δ and we call the set $\mathscr{K}(\Delta)$ the *killing set* of Δ. The elements of $\mathscr{K}(\Delta)$ are said to be *in conflict with* Δ. Let $b(\Delta) := |\mathscr{D}(\Delta)|$ and $\omega(\Delta) := |\mathscr{K}(\Delta)|$. First, we require the following:

(i) There is a constant $b > 0$ such that $b(\Delta) \leq b$ for all $\Delta \in \mathscr{F}$.

We also require that the following conditions hold for all $\Delta \in \mathscr{F}$:

(ii) If $\Delta \in \mathscr{C}(R)$, then $\mathscr{D}(\Delta) \subseteq R$.
(iii) If $\Delta \in \mathscr{C}(R)$, then $\mathscr{K}(\Delta) \cap R = \emptyset$.
(iv) If $\Delta \in \mathscr{C}(R)$ and R' is a subset of R with $\mathscr{D}(\Delta) \subseteq R' \subseteq R$, the $\Delta \in \mathscr{C}(R')$.

These conditions are weaker than the conditions of Clarkson and Shor, which require that $\Delta \in \mathscr{C}(R)$ if and only if $\mathscr{D}(\Delta) \in R$ and $\mathscr{K}(\Delta) \cap R = \emptyset$. (In our example, a trapezoid $\Delta \in \mathscr{C}(R)$ is defined by at most four segments: at most two segments bounding Δ from above and below, and at most two other segments defining the left and right edges of Δ. These four segments make up $\mathscr{D}(\Delta)$. The killing set of Δ consists of the segments that intersect Δ. The reader can now easily check conditions (i)–(iv). It is not difficult to verify that there is no way to define $\mathscr{D}(\Delta)$ and $\mathscr{K}(\Delta)$ such that Clarkson and Shor's stronger condition holds.)

Although we want to make statements about random samples, it turns out to be useful to argue about random permutations. When we need a random sample of S of size r, we use the first r elements in a random permutation of S. Thus, let $s_1, \ldots, s_n$ be a random permutation of S. All the probabilities and expectancies studied in the following are with respect to this random permutation. Let $S_r := \{s_1, \ldots, s_r\}$ and $\mathscr{C}_r := \mathscr{C}(S_r)$.

Following Clarkson and Shor we define a function $\tau(r)$ that describes the expected number of regions for a sample of size at most r.

$$\tau(r) := \max_{1 \leq t \leq r} E[|\mathscr{C}_t|].$$

What we want to bound are the higher moments $E[\sum_{\Delta \in \mathscr{C}_r} \omega(\Delta)^d]$ for constant $d > 0$. We first prove two simple lemmas. We use the *falling factorial* notation $n^{\underline{a}} := n \cdot (n-1) \cdots (n-a+1)$, for integers $a \geq 0$.

Lemma 1. *Let $\Delta \in \mathscr{F}$ and $b \leq t \leq r \leq n$. Then*

$$P[\Delta \in \mathscr{C}_r \mid \mathscr{D}(\Delta) \subseteq S_r] \leq P[\Delta \in \mathscr{C}_t \mid \mathscr{D}(\Delta) \subseteq S_t].$$

Proof. We define the sequence $s'_1, s'_2, \ldots, s'_{n-a}$ by taking the sequence $s_1, \ldots, s_n$ and removing the elements of $\mathscr{D}(\Delta)$. We define $S'_r := \{s'_1, s'_2, \ldots, s'_r\}$. Let $\mathscr{S}^{\Delta}$ be the

family of all subsets of S that create Δ in connection with $\mathscr{D}(\Delta)$, that is,

$$\mathscr{S}^{\Delta} := \{R \subseteq S \setminus \mathscr{D}(\Delta) \mid \Delta \in \mathscr{C}(R \cup \mathscr{D}(\Delta))\}.$$

Note that property (iv) implies that any subset of a set in $\mathscr{S}^{\Delta}$ is also in $\mathscr{S}^{\Delta}$. Since $S'_{t-a} \subseteq S'_{r-a}$, this implies

$$\begin{aligned} P[\Delta \in \mathscr{C}_r \mid \mathscr{D}(\Delta) \subseteq S_r] &= P[S'_{r-a} \in \mathscr{S}^{\Delta}] \leq P[S'_{t-a} \in \mathscr{S}^{\Delta}] \\ &= P[\Delta \in \mathscr{C}_t \mid \mathscr{D}(\Delta) \subseteq S_t]. \end{aligned}$$ □

Lemma 2. *Let $\Delta \in \mathscr{T}$. For $b \leq t \leq r \leq n$ we have $P[\Delta \in \mathscr{C}_r] \leq (r^{\underline{b}}/t^{\underline{b}})P[\Delta \in \mathscr{C}_t]$.*

Proof. Let $a := b(\Delta)$. We have

$$\begin{aligned} P[\Delta \in \mathscr{C}_r] &= P[\mathscr{D}(\Delta) \subseteq S_r] \cdot P[\Delta \in \mathscr{C}_r \mid \mathscr{D}(\Delta) \subseteq S_r] \\ &= \frac{r^{\underline{a}}}{n^{\underline{a}}} P[\Delta \in \mathscr{C}_r \mid \mathscr{D}(\Delta) \subseteq S_r] \\ &\leq \frac{r^{\underline{a}}}{n^{\underline{a}}} P[\Delta \in \mathscr{C}_t \mid \mathscr{D}(\Delta) \subseteq S_t] \\ &= \frac{r^{\underline{a}}}{t^{\underline{a}}} \cdot \frac{t^{\underline{a}}}{n^{\underline{a}}} P[\Delta \in \mathscr{C}_t \mid \mathscr{D}(\Delta) \subseteq S_t] \qquad \text{(valid since } a \leq b \leq t\text{)} \\ &= \frac{r^{\underline{a}}}{t^{\underline{a}}} P[\Delta \in \mathscr{C}_t] \\ &\leq \frac{r^{\underline{b}}}{t^{\underline{b}}} P[\Delta \in \mathscr{C}_t]. \end{aligned}$$ □

Before we proceed we need a few definitions, motivated by Chazelle *et al.* [5]. We define the following events:

$$X_t^{\Delta} : \Delta \in \mathscr{C}_r,$$

$$Y_r^{\Delta} : \Delta \in \mathscr{C}_r \quad \text{and} \quad s_{r+1} \in \mathscr{K}(\Delta).$$

Note that

$$P[Y_r^{\Delta}] = P[Y_r^{\Delta} \mid X_r^{\Delta}] \cdot P[X_r^{\Delta}] = \frac{\omega(\Delta)}{n-r} P[X_r^{\Delta}]. \tag{1}$$

Furthermore, from the definition of Y_r^{Δ} and property (iii) we derive

$$Y_r^{\Delta} \subseteq X_r^{\Delta} \cap \overline{X_{r+1}^{\Delta}}. \tag{2}$$

The inclusion can be proper, since there can be other reasons why Δ does not show up in $\mathscr{C}_{r+1}$.

We observe that the sum $\sum_{t=A}^{B} P[Y_t^\Delta]$, for $1 \le A \le B \le n$, is bounded by the probability that Δ appears in at least one of the sets $\mathscr{C}_A, \mathscr{C}_{A+1}, \ldots, \mathscr{C}_B$. The latter event can be expressed as

$$X_A^\Delta \cup \bigcup_{t=A+1}^{B} \left(\overline{X_{t-1}^\Delta} \cap X_t^\Delta\right).$$

However, what is the probability $P[\overline{X_{t-1}^\Delta} \cap X_t^\Delta]$ that Δ gets "inserted" in step t? By (iv), the only reason for some $\Delta \in \mathscr{C}_t$ not to be in $\mathscr{C}_{t-1}$ is that $s_t \in \mathscr{D}(\Delta)$. Hence, we have

$$\begin{aligned} P\left[\overline{X_{t-1}^\Delta} \cap X_t^\Delta\right] &= P\left[\overline{X_{t-1}^\Delta} \cap X_t^\Delta \mid X_t^\Delta\right] \cdot P[X_t^\Delta] \\ &= P[s_t \in \mathscr{D}(\Delta)] \cdot P[X_t^\Delta] \le \frac{b}{t} P[X_t^\Delta]. \end{aligned} \tag{3}$$

Here we used a technique called *backward analysis*, introduced by Chew [6] and made popular by Seidel [19], [20].

Putting everything together, we have

$$\sum_{t=A}^{B} P[Y_t^\Delta] \le P[X_A^\Delta] + \sum_{t=A+1}^{B} P\left[\overline{X_{t-1}^\Delta} \cap X_t^\Delta\right] \le P[X_A^\Delta] + \frac{b}{A} \sum_{t=A+1}^{B} P[X_t^\Delta]. \tag{4}$$

We can now prove the main theorem of this section.

Theorem 3. *For $1 \le r \le n$ and constant $d \ge 0$ there is a constant $C_d > 0$ such that*

$$E\left[\sum_{\Delta \in \mathscr{C}_r} \omega(\Delta)^d\right] \le C_d \left(\frac{n}{r}\right)^d \tau(r).$$

Proof. For $r < 2b$ the theorem holds with $C_d = (2b)^d$, so we assume that $r \ge 2b$. We proceed by induction on d. For $d = 0$ the sum whose expected value we want to bound is just the complexity of $\mathscr{C}_r$; by the definition of $\tau(r)$ the claim holds with $C_0 = 1$.

Now assume that the claim holds for powers less than d. We first prove by (a second level of) induction that for $r/2 \le r_0 \le r$ and $0 \le j \le d$ a constant $C_j' > 0$ exists such that

$$\sum_{\Delta \in \mathscr{F}} \left\{ \omega(\Delta)^j \sum_{t=r_0}^{r} P[X_t^\Delta] \right\} \le C_j' r \left(\frac{n}{r}\right)^j \tau(r). \tag{5}$$

To do so, we define

$$F_j := \sum_{\Delta \in \mathscr{F}} \left\{ \omega(\Delta)^j \sum_{t=r_0}^{r} P[X_t^\Delta] \right\}.$$

Clearly, $F_0 \le \sum_{t=r_0}^{r} \tau(t) \le r\tau(r)$. Assume now that (5) holds for $j-1$, and consider F_j. We have

$$\begin{aligned}
F_j &= \sum_{\Delta \in \mathscr{F}} \left\{ \omega(\Delta)^j \sum_{t=r_0}^{r} P[X_t^\Delta] \right\} \\
&\overset{(1)}{\le} \sum_{\Delta \in \mathscr{F}} \left\{ \omega(\Delta)^{j-1} \sum_{t=r_0}^{r} (n-t) P[Y_t^\Delta] \right\} \\
&\le n \sum_{\Delta \in \mathscr{F}} \left\{ \omega(\Delta)^{j-1} \sum_{t=r_0}^{r} P[Y_t^\Delta] \right\} \\
&\overset{(4)}{\le} n \sum_{\Delta \in \mathscr{F}} \omega(\Delta)^{j-1} P\left[X_{r_0}^\Delta\right] + \frac{bn}{r_0} \sum_{\Delta \in \mathscr{F}} \left\{ \omega(\Delta)^{j-1} \sum_{t=r_0+1}^{r} P[X_t^\Delta] \right\} \\
&\le nC_{j-1} \left(\frac{n}{r_0}\right)^{j-1} \tau(r_0) + b\frac{n}{r_0} F_{j-1} \\
&\le r_0 C_{j-1} \left(\frac{n}{r_0}\right)^{j} \tau(r_0) + b\frac{n}{r_0} C'_{j-1} r \left(\frac{n}{r}\right)^{j-1} \tau(r) \\
&\le \left(2^{j-1} C_{j-1} + 2bC'_{j-1}\right) r \left(\frac{n}{r}\right)^{j} \tau(r) \\
&\le C'_j r \left(\frac{n}{r}\right)^{j} \tau(r)
\end{aligned}$$

for a $C'_j = 2^{j-1} + 2bC'_{j-1}$. This proves claim (5). We can now consider $E[\Sigma_{\Delta \in \mathscr{C}_r} \omega(\Delta)^d]$. Let $r_0 := \lfloor r/2 \rfloor + 1$ and note that $r_0 \ge b$.

$$\begin{aligned}
\sum_{\Delta} \left\{ \omega(\Delta)^d P[X_r^\Delta] \right\} &\le \sum_{\Delta} \left\{ \omega(\Delta)^d \frac{2}{r} \sum_{t=r_0}^{r} P[X_r^\Delta] \right\} \\
&\le C\frac{1}{r} \sum_{\Delta} \left\{ \omega(\Delta)^d \sum_{t=r_0}^{r} P[X_t^\Delta] \right\} = C\frac{1}{r} F_d
\end{aligned}$$

for some $C > 0$ by Lemma 2. Using (5), the theorem follows with $C_d = CC'_d$. □

3. A Lazy Randomized Incremental Algorithm: Computing a Single Face in an Arrangement of Line Segments

The computation of single cells in two- and higher-dimensional spaces is important for motion-planning problems: a single cell in the arrangement of constraint surfaces in configuration space corresponds to the reachable region for the robot in the workspace. The two-dimensional problem has already been solved quite satisfactorily by Chazelle *et al.* [5]. The algorithm that we present has the same running time as theirs and is slightly simpler. More importantly, it introduces a new technique called *lazy randomized incremental construction*, which can be used to solve a variety of other problems—see Section 5.

Let S be a set of n line segments in the plane. We wish to compute the face $\mathscr{C}(S)$ in the arrangement of S which contains the origin. Actually, we compute the vertical decomposition of this face. This decomposition is obtained by extending vertical segments from any vertex of the single cell upward and/or downward, as illustrated in Fig. 1. The number of trapezoids in the vertical decomposition of a single cell in the plane is linear in the complexity of the cell. Hence, for a single cell defined by m segments it is $O(m\alpha(m))$.

Our basic algorithm follows the general framework for randomized incremental algorithms described by Boissonnat *et al.* [2], which was also followed by Chazelle *et al.* These algorithms maintain a data structure, the so-called *history graph*. The history graph for an insertion sequence $s_1, s_2, \ldots, s_n$ of the segments of S is a rooted, directed, and acyclic graph, whose nodes correspond to trapezoids that have been created during the incremental construction. In the following we often do not distinguish between a node and its corresponding trapezoid. The trapezoids of the current single cell are leaf nodes in the history graph. The addition of a segment s_r is done as follows. The trapezoids of the current face that are intersected by s_r are determined by searching in the history graph. The new trapezoids that arise because of the insertion of s_r are computed, and their corresponding nodes are added to the history graph as leaves below the nodes (which are now no longer leaves) corresponding to the intersected trapezoids—see below for details.

In a standard randomized incremental algorithm this is basically all that has to be done: update the history graph locally where regions are destroyed by the newly

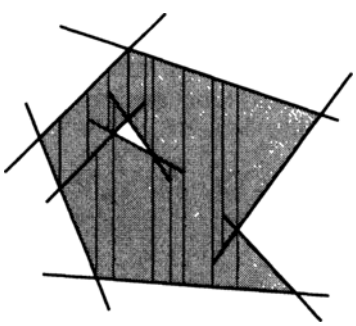

Fig. 1. The vertical decomposition of a single cell.

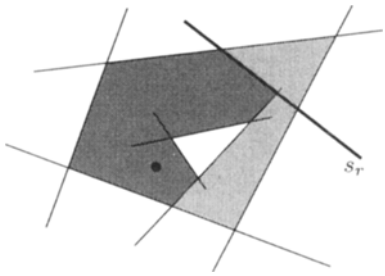

Fig. 2. A new segment cuts off part of the single face.

inserted object. However, since single cells are not defined locally, this is not sufficient here: those trapezoids that are no longer in the single face should be determined, because they lie in a part that is cut off by s_r.

Figure 2 illustrates this. The dot in this figure indicates the origin. Trapezoids in the lightly shaded region are cut off when s_r is inserted.

The leaves in the history graph corresponding to these trapezoids then have to be marked—we say that they are colored red—so that they will not be refined in future steps. This is the approach taken by Chazelle *et al.* In order to identify the trapezoids that have been cut off they need some extra tricks: they maintain a union-find structure on the boundary components of the single face so that they can detect when s_r cuts off part of the single face, and they apply a tandem search on the adjacency graph of the trapezoids in the current face to determine the parts that are cut off. Unfortunately, this approach does not seem to work in 3-space, where it is difficult to detect whether a new triangle cuts off a portion of the single cell.

We propose a much simpler strategy, which also works in 3-space: we simply skip this second step, that is, after an insertion we do not attempt to identify the trapezoids that are no longer part of the single cell. Of course, we would end up constructing the full arrangement of line segments if we always keep all the trapezoids around. So we sometimes perform a "clean-up step" to eliminate the trapezoids that are not part of the current single cell, but we do this only a small number of times. In particular, we perform a clean-up step after inserting the 2^ith segment, for $1 \leq i \leq \lfloor \log n \rfloor$. The rationale behind this is that we are now allowed to perform the clean-up in a brute-force way, by visiting all the leaves in the history graph.

The global framework of a lazy randomized incremental algorithm is thus as follows:

Let $s_1, s_2, \ldots, s_n$ be a random permutation of S.
last_cleanup := 1
for $r := 1$ **to** n
do perform an update step to insert object s_r;
  if $r = 2 \cdot$ *last_cleanup*
  then perform a clean-up step; *last_cleanup* := r.

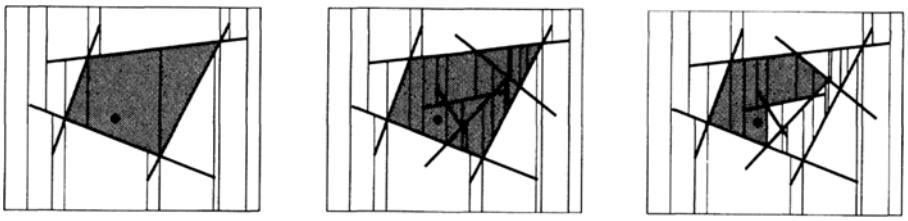

Fig. 3. Computing a single face lazily.

Figure 3 illustrates the lazy approach for the single-face algorithm. The shaded trapezoids are the ones corresponding to green leaves. After we have inserted the first four segments and we have done the clean-up step, the shaded trapezoids are exactly the ones in the single face defined by the origin (the small dot in the figure). After inserting some more segments this is no longer true. However, after inserting the eighth segment we do another clean-up, where we color the trapezoids outside the single face red. For readers who are not familiar with the algorithm of Chazelle *et al.* we give a more detailed description of the update step and the clean-up step for the computation of a single face in an arrangement of line segments.

We maintain two data structures: the history graph and an adjacency graph $\mathscr{G}$. The leaves of the history graph correspond to trapezoids. Leaves whose trapezoids need no further refinement because they are already known to be outside the current face are *red*; the other leaves are *green*. The nodes of the graph $\mathscr{G}$ correspond to trapezoids in the current structure that can still be in the single face. In other words, they correspond to green leaves of the history graph. There is an arc between two nodes in $\mathscr{G}$ if and only if the corresponding trapezoids share a vertical edge. This graph makes it possible to go from a trapezoid to its neighbors in the same face of the decomposition. We maintain cross-pointers between nodes in $\mathscr{G}$ and the corresponding green leaves in the history graph. We denote the trapezoid corresponding to a node v in the history graph or the adjacency graph by $\Delta(v)$.

The Update Step. Starting at the root we propagate the segment s_r that has to be inserted down the history graph: from a node v we proceed recursively to all children of v whose trapezoids are intersected by s_r and that have not been visited before in this update step. This way we find all the leaves γ in the history graph such that the trapezoid $\Delta(\gamma)$ is intersected by s_r. The red leaves we have found need not be refined. For each green leaf γ we have found we split $\Delta(\gamma)$ with segment s_r to obtain a number of new trapezoids. The number of new trapezoids is at most four; Chazelle *et al.* give a detailed description of the different cases that can occur when a trapezoid is split. Some (at most two) of these new trapezoids are not properly defined trapezoids yet. More precisely, each vertical edge which does not contain a vertex of the new arrangement must be removed, and the two trapezoids that share this edge must be merged. In the history graph a green leaf is created for each new trapezoid, and there is an arc from a trapezoid $\Delta(\gamma)$ that has been split to a new trapezoid Δ if the interiors of $\Delta(\gamma)$ and Δ intersect. Note that a node γ has at most

four out-going arcs. Finally, we update the adjacency graph $\mathscr{G}$: we remove the nodes corresponding to intersected trapezoids, and we add the newly created trapezoids with the appropriate adjacency relations.

The Clean-Up Step. Let v_0 be the node in $\mathscr{G}$ whose trapezoid contains the origin. (This trapezoid can either be maintained during the update steps, or we can simply check all nodes of $\mathscr{G}$ to find it.) Perform a graph traversal on $\mathscr{G}$ to identify the connected component of $\mathscr{G}$ containing v_0, and delete the other components from $\mathscr{G}$. Color all the nodes of the history graph red that correspond to nodes of $\mathscr{G}$ which are not in the same component as v_0.

In the next section we give a general analysis of lazy randomized algorithms. This analysis is then used to prove that the expected running time of the above single-face algorithm is $O(n\alpha(n)\log n)$. Anticipating this result we state the following theorem.

Theorem 4. *Given a set of n line segments in $\mathbb{R}^2$, the face in the arrangement containing the origin can be computed in $O(n\alpha(n)\log n)$ expected time using $O(n\alpha(n))$ storage.*

Remarks. The algorithm of Chazelle *et al.* is "on-line" in the sense that at any point during the construction, they can use the current history graph to determine whether a query point lies in the current single cell. Our algorithm does not give us this possibility, since we have no way of knowing which trapezoids of the current subdivision are part of the single cell that we want to maintain. However, we can always report the current single face by doing a graph traversal, as in a clean-up step.

Our algorithm as well as the algorithm by Chazelle *et al.* also works for curves of bounded degree. The time bound becomes $O(\lambda_{s+2}(n)\log n)$. This bound is asymptotically the same as for the worst-case size of a single cell times a logarithmic factor.

Finally, note that our algorithm departs from previous work on randomized incremental algorithms as the structure maintained at time r is *not* independent of the order in which the segments have been inserted. More precisely, it depends on which of the objects were inserted before the most recent clean-up step and which objects were inserted after the most recent clean-up step.

4. The Analysis of Lazy Randomized Incremental Algorithms

Below we give a general analysis of lazy randomized incremental algorithms. We then use this general result to analyze the example algorithm that we gave in the previous section, namely the computation of a face in an arrangement of line segments.

4.1. *A General Analysis*

As in Section 2, we formulate the analysis in an abstract framework. This allows us to apply it to several different cases. Again we advise the reader to keep a concrete example in mind, such as the computation of a face in an arrangement of line segments.

Let S be a set of n objects (a set of line segments, say), and let $\mathscr{F}$ be a set of *regions* (trapezoids defined by at most four of the segments). For every region $\Delta \in \mathscr{F}$, we assign subsets $\mathscr{D}(\Delta)$ and $\mathscr{K}(\Delta)$ of S, called the *defining set* and the *killing set*. Furthermore, for every $R \subseteq S$ we define two subsets $\mathscr{T}(R) \subset \mathscr{F}$ and $\mathscr{M}(R) \subset \mathscr{F}$. Finally, for $R' \subseteq R \subseteq S$ we define $\mathscr{C}(R, R') := \mathscr{T}(R) \cap \mathscr{M}(R')$. The idea is that the set $\mathscr{C}(R, R')$ corresponds to the structure maintained by the lazy algorithm: in our analysis R is the current subset and R' is the subset for which the last clean-up was performed.

To illustrate these definitions, we apply them to our line-segments example. Here $\mathscr{T}(R)$ is the set of *all* trapezoids in the full arrangement $\mathscr{A}(R)$, while $\mathscr{M}(R)$ is the set of trapezoids in $\mathscr{F}$ that are contained in the face of $\mathscr{A}(R)$ which contains the origin —note that a region $\Delta \in \mathscr{M}(R)$ does not have to be defined by segments in R, so $\mathscr{M}(R)$ is *not* a subset of $\mathscr{T}(R)$. The set $\mathscr{C}(R, R)$, however, corresponds exactly to the trapezoidation of the face containing the origin.

As in Section 2, we let $b(\Delta) := |\mathscr{D}(\Delta)|$ and $\omega(\Delta) := |\mathscr{K}(\Delta)|$. We require that:

(i′) There is a constant $b > 0$ such that $b(\Delta) \leq b$ for all $\Delta \in \mathscr{F}$.
(ii′) A region $\Delta \in \mathscr{F}$ is in $\mathscr{T}(R)$ if and only if $\mathscr{D}(\Delta) \subseteq R$ and $\mathscr{K}(\Delta) \cap R = \emptyset$.
(iii′) For $R' \subseteq R \subseteq S$ we have $\mathscr{M}(R) \subseteq \mathscr{M}(R')$.

Note that conditions (i′) and (ii′) are exactly Clarkson's condition for the set $\mathscr{T}(R)$.

Let $s_1, \ldots, s_n$ be a random permutation of S, and let $S_r := \{s_1, \ldots, s_r\}$. Define $\mathscr{C}_r := \mathscr{C}(S_r, S_p)$, where p is the largest power of two that is less than r. Furthermore, for $1 \leq q < r \leq n$, we define the function

$$\tau(r, q) := \max_{q < t \leq r} E\big[|\mathscr{C}(S_t, S_q)|\big]. \tag{6}$$

Theorem 5. *Let $3 \leq r \leq n$ and let p be the largest power of two that is less than r. The expected size of $\mathscr{C}_r$ is at most $\tau(r, p)$. The expected number of regions in $\mathscr{C}_r \setminus \mathscr{C}_{r-1}$ is bounded by $O((1/r)\tau(r, p/2))$. The expected total conflict size of these regions is bounded as*

$$E\left[\sum_{\Delta \in \mathscr{C}_r \setminus \mathscr{C}_{r-1}} \omega(\Delta)\right] \leq O\left(\frac{n}{r^2}\tau\left(r, \frac{p}{2}\right)\right).$$

Proof. The first claim follows immediately from the definition of $\tau(r, p)$. The other two results follow from the following bound, which holds for constant $d \geq 0$:

$$E\left[\sum_{\Delta \in \mathscr{C}_r \setminus \mathscr{C}_{r-1}} \omega(\Delta)^d\right] \leq O\left(\frac{1}{r}\left(\frac{n}{r}\right)^d \tau\left(r, \frac{p}{2}\right)\right). \tag{7}$$

To prove (7), let $q := p/2$, and fix a set $S^* \subset S$ of size q. We first restrict ourselves

to those random permutations $s_1, \ldots, s_n$ of S with $S_q = S^*$. We denote by $P^*[X]$ the probability of an event X with respect to this restricted sample space.

$$
\begin{aligned}
E\left[\sum_{\Delta \in \mathscr{C}_r \setminus \mathscr{C}_{r-1}} \omega(\Delta)^d \,\middle|\, S_q = S^*\right] &= \sum_{\Delta \in \mathscr{T}} \omega(\Delta)^d P^*[\Delta \in \mathscr{C}_r \wedge \Delta \notin \mathscr{C}_{r-1}] \\
&\overset{\text{(iii')}}{\leq} \sum_{\Delta \in \mathscr{T}} \omega(\Delta)^d P^*\left[\Delta \in \mathscr{C}(S_r, S_p) \wedge \Delta \notin \mathscr{T}(S_{r-1})\right] \\
&\overset{\text{(iii')}}{\leq} \sum_{\Delta \in \mathscr{T}} \omega(\Delta)^d P^*\left[\Delta \in \mathscr{C}(S_r, S_q) \wedge \Delta \notin \mathscr{T}(S_{r-1})\right] \\
&= \sum_{\Delta \in \mathscr{M}(S^*)} \omega(\Delta)^d P^*[\Delta \in \mathscr{T}(S_r) \wedge \Delta \notin \mathscr{T}(S_{r-1})] \\
&\overset{\text{(ii')}}{\leq} \sum_{\Delta \in \mathscr{M}(S^*)} \omega(\Delta)^d P^*[\Delta \in \mathscr{T}(S_r) \wedge s_r \in \mathscr{D}(\Delta)] \\
&\overset{\text{(i')}}{\leq} \frac{b}{r-q} \sum_{\Delta \in \mathscr{M}(S^*)} \omega(\Delta)^d P^*[\Delta \in \mathscr{T}(S_r)] \\
&\leq \frac{2b}{r} E\left[\sum_{\Delta \in \mathscr{C}(S_r, S_q)} \omega(\Delta)^d \,\middle|\, S_q = S^*\right].
\end{aligned}
$$

To bound the expected value in the last expression, we apply Theorem 3 to the restricted sample space where $S_q = S^*$. Let $\bar{S} := S \setminus S^*$. For $\bar{R} \subseteq \bar{S}$, we define a set of regions as

$$\bar{\mathscr{C}}(\bar{R}) := \mathscr{C}(\bar{R} \cup S^*, S^*) = \mathscr{M}(S^*) \cap \mathscr{T}(S^* \cup \bar{R}).$$

The defining and killing sets of a region Δ are given as $\overline{\mathscr{D}(\Delta)} := \mathscr{D}(\Delta) \setminus S^*$ and $\overline{\mathscr{K}(\Delta)} := \mathscr{K}(\Delta) \setminus S^*$. It is not difficult to check that conditions (i)–(iv) of Section 2 hold for the space defined in this way: condition (i) follows from our condition (i') and, since S^* is fixed, conditions (ii), (iii), and (iv) follow from (ii'). We can thus use Theorem 3 to conclude that there is a constant $C_d > 0$ such that

$$
\begin{aligned}
&E\left[\sum_{\Delta \in \mathscr{C}(S_r, S_q)} \omega(\Delta)^d \,\middle|\, S_q = S^*\right] \\
&\quad = E\left[\sum_{\Delta \in \bar{\mathscr{C}}(\bar{R} \cup S^*, S^*)} \omega(\Delta)^d \,\middle|\, \bar{R} \subseteq \bar{S}, |\bar{R}| = r - q\right] \\
&\quad \leq C_d \left(\frac{n-q}{r-q}\right)^d \max_{1 < t \leq r-q} E\left[|\bar{\mathscr{C}}(\bar{R} \cup S^*, S^*)| \;\; \bar{R} \subseteq \bar{S}, |\bar{R}| = t\right] \\
&\quad = C_d \left(\frac{n-q}{r-q}\right)^d \max_{q < t \leq r} E[|\mathscr{C}(R, S^*)| \mid S^* \subseteq R \subseteq S, |R| = t].
\end{aligned}
$$

The expectancy on the left-hand side is still with respect to all random permutations of S with $S_q = S^*$. Taking the average over all possible choices of $S^* \subset S$ proves inequality (7). □

Note that we did not actually need the full generality of Theorem 3 to prove this result. In fact, we could have referred to Clarkson and Shor's results [9] as well. To keep this paper self-contained, however, we have chosen to apply our more general Theorem 3.

4.2. *The Analysis of the Single-Face Algorithm*

We apply the abstract analysis given above to bound the expected running time of the lazy randomized incremental algorithm for computing a single face that we presented in the previous section.

Here S is the given set of n line segments and $\mathcal{T}$ is the set of trapezoids that can be defined by any four of them. Thus condition (i') holds with $b = 4$. As mentioned above, we define $\mathcal{T}(R)$, for $R \subseteq S$, to be the set of all trapezoids in the vertical decomposition of the full arrangement $\mathcal{A}(R)$. Clearly, condition (ii') holds for $\mathcal{T}(R)$. Our clean-up steps are modeled using the set $\mathcal{M}(R)$, which we define to contain all trapezoids that lie in the single face of $\mathcal{A}(R)$ containing the origin. Then $\mathcal{C}_r = \mathcal{T}(S_r) \cap \mathcal{M}(S_p)$, where p is the largest power of two smaller than r, is exactly the set of trapezoids present after the insertion of s_r (but before doing any clean-up step). Notice that the single face shrinks when extra segments are added, so condition (iii') is satisfied.

We first bound the function $\tau(r, q)$, for $1 \le q \le n$ and $q < r \le 4q$. Thus we have to bound the expected number of trapezoids in the trapezoidation $\mathcal{T}(S_t)$ that lie in the single face of $\mathcal{A}(S_q)$ containing the origin, for $q < t \le r \le 4q$. For this it is sufficient to bound the expected number of vertices of $\mathcal{A}(S_t)$ that lie in the face or on its boundary. Recall that $\mathcal{C}(S_q, S_q)$ denotes the trapezoids of the trapezoidation of the single face of $\mathcal{A}(S_q)$, and let $\omega(\Delta)$ be the number of segments in S_t intersecting trapezoid Δ. Then it is easy to see that the number of vertices we have to consider is bounded by

$$O\left(\sum_{\Delta \in \mathcal{C}(S_q, S_q)} (1 + \omega(\Delta) + \omega(\Delta)^2)\right). \tag{8}$$

To bound the expected value of this sum we note that the complexity of the single face is $O(q\alpha(q))$ [12], [17], and we use that S_q is a random sample of S_t of size q with $q \ge t/4$. We have seen in Section 2 that the set $\mathcal{C}(S_q, S_q)$ fulfills conditions (i)–(iv). Hence, Theorem 3 tells us that

$$E\left[\sum_{\Delta \in \mathcal{C}(S_q, S_q)} (1 + \omega(\Delta) + \omega(\Delta)^2)\right] = O\left(\left(1 + \frac{t}{q} + \left(\frac{t}{q}\right)^2\right) q\alpha(q)\right) = O(t\alpha(t)).$$

It follows that the expected size of $\mathscr{C}(S_t, S_q)$ is $O(t\alpha(t))$. Hence, $\tau(r, q) = O(r\alpha(r))$ for $q \leq r < 4q$. By Theorem 5, this implies that the expected size of $\mathscr{C}_r$ is $O(r\alpha(r))$, so the structure we are maintaining is asymptotically not larger than the face we actually want to maintain.

The history graph constructed by the algorithm contains a node for every created trapezoid. The number of out-going edges for every node is at most four, so it suffices to bound the total number of trapezoids created by the algorithm to bound the expected size of the history graph. By Theorem 5, this is

$$\begin{aligned}\sum_{r=1}^{n} E[|\mathscr{C}_r \setminus \mathscr{C}_{r-1}|] &= \sum_{r=1}^{n} O\left(\frac{\tau(r, p/2)}{r}\right) \\ &= \sum_{r=1}^{n} O\left(\frac{r\alpha(r)}{r}\right) \\ &= O(n\alpha(n)).\end{aligned}$$

This bounds the expected amount of storage used by the algorithm. We can turn this into a worst-case bound by changing the algorithm slightly: as soon as we use too much storage we stop the algorithm and start with a new random permutation. We expect to succeed in a constant number of trials.

To bound the running time, we have to consider two different steps. First, consider the update steps. During update step r we spend time to find the trapezoids of $\mathscr{C}_{r-1}$ that are intersected by s_r, and we spend time to split certain trapezoids, update the history graph, and update the graph $\mathscr{G}$. More precisely, we spend constant time for each node of the history graph that we visit. (Here we use that a node in the history graph has constant degree, so that we can check all its children to see which ones to visit.) Observe that we visit a node v of the history graph only if s_r intersects the trapezoid $\Delta(v)$. It follows that we can bound the time necessary for *all* history searches by

$$\sum_{\Delta \in \mathscr{T}} \omega(\Delta) P[\Delta \text{ is created by the algorithm}].$$

This we can rewrite and bound using Theorem 5:

$$\begin{aligned}\sum_{r=1}^{n} E\left[\sum_{\Delta \in \mathscr{C}_r \setminus \mathscr{C}_{r-1}} \omega(\Delta)\right] &= \sum_{r=1}^{n} O\left(\frac{n}{r^2}\tau\left(r, \frac{p}{2}\right)\right) \\ &= \sum_{r=1}^{n} O\left(\frac{n}{r^2} r\alpha(r)\right) \\ &= O(n\alpha(n)\log n).\end{aligned}$$

It remains to bound the time needed for the clean-up steps. A clean-up in step $p = 2^i$ takes time proportional to the number of trapezoids in $\mathscr{C}_p$. By the above, the

expected number of trapezoids in $\mathscr{C}_p$ is $O(p\alpha(p))$ and, hence, the total expected work for the clean-up steps is

$$\sum_{i=1}^{\lfloor \log n \rfloor} O(2^i \alpha(2^i)) = O(n\alpha(n)).$$

This finishes the proof of Theorem 4.

5. More Lazy Randomized Algorithms: Computing Single Cells and Zones

We now apply our technique to solve the problem that initiated our research: the computation of a single cell in an arrangement of triangles in 3-space. We also describe an algorithm for computing zones in arrangements of lines in the plane and arrangements of hyperplanes in d-dimensional space.

5.1. *Vertical Decompositions in 3-Space*

To be able to use a randomized incremental algorithm for computing single cells in 3-space we need a decomposition scheme for arrangements of triangles. Therefore we first recall the notion of vertical decompositions in 3-space introduced by Clarkson *et al.* [7], before we present our algorithm and its analysis.

Let $S = \{s_1, \ldots, s_n\}$ be a set of n possibly intersecting triangles in 3 space. The *vertical decomposition* of the arrangement $\mathscr{A}(S)$ decomposes each cell of $\mathscr{A}(S)$ into subcells, the *boxes*, and is defined as follows: from every point on an edge of $\mathscr{A}(S)$—this can be a part of a triangle edge or of the intersection of two triangles—we extend a vertical ray in positive and negative x_3-direction to the first triangle above and the first triangle below this point. This way we create for every edge a vertical wall, which we call a *primary wall*. We obtain a *cylindrical decomposition* of $\mathscr{A}(S)$ into cells, the *cylinders*, with a unique bottom and top face; the vertical projections of both faces are exactly the same. However, the number of vertical walls of a cylinder need not be constant and the cylinder may not be simply connected. So we decompose the vertical projection of its bottom face into trapezoids as in the planar case, that is, we draw segments parallel to the x_2-axis from the vertices of the face. These segments are extended vertically upward until they meet the top face; the walls thus erected are the *secondary walls*. Each cell of the vertical decomposition is now a box with a trapezoidal base and top—which may degenerate to a triangle—that are connected by vertical walls. Tagansky [21] proved the following bound on the complexity of vertical decompositions.

Theorem 6 [21]. *The maximum combinatorial complexity $\psi(n)$ of the vertical decomposition of a single cell in an arrangement of n triangles is lower bounded by $\Omega(n^2\alpha^2(n))$ and upper bounded by $O(n^2 \log^2 n)$.*

5.2. *Computing Single Cells in Arrangements of Triangles*

Our algorithm for the computation of the vertical decomposition of a single cell in an arrangement of n triangles in 3-space follows the lazy approach described in Section 3. When adding a triangle we do not seek to discard the boxes which are no longer in the cell; instead we keep even boxes that are no longer part of the single cell, and clean up the decomposition only after inserting the 2^ith triangle, for $i = 1, \ldots, \lfloor \log n \rfloor$.

The algorithm we describe is a natural generalization of the algorithm of Section 3 to three dimensions. Thus it maintains a history graph and an adjacency graph. The red leaves of the history graph correspond to boxes that need no further refinement because they are already *known* to be outside the current cell; the other leaves are green. The boxes of the current decomposition are the green leaves of the history graph. The nodes of the adjacency graph $\mathcal{G}$ correspond to these boxes. There is an arc between two nodes in $\mathcal{G}$ if the corresponding boxes share a vertical secondary wall. These arcs make it possible to go from a box to its neighbors in the same cylinder of the cylindrical decomposition. A box has at most four such neighbors. In addition, we have to store adjacencies between boxes that share a vertical primary wall. If we stored the adjacencies between all these boxes, then the number of neighbors might not be constant. Therefore, we only store the adjacencies between two nodes if the associated boxes share a portion of a vertical primary wall and have either a vertex of the three-dimensional arrangement of triangles or a vertical edge which is the intersection of two primary walls in common. A box has at most two such neighbors. These adjacencies allow us to visit all cylinders in the same cell of the decomposition. Thus, the degree of every node in the graph $\mathcal{G}$ is constant, and it is possible to go from a box to its neighbors in the same cell of the decomposition. We maintain cross-pointers between nodes in $\mathcal{G}$ and the corresponding green leaves in the history graph. Next we describe the actions we have to take when adding a new triangle s_r. We start with the description of the update step, and then we describe the clean-up step.

The Update Step. We propagate the segment s_r down the history graph to determine the leaves whose corresponding boxes intersect s_r, as in Section 3. The red leaves we find need not be refined. For all green leaves γ that we find we decompose the box $\Delta(\gamma)$ into a constant number of new boxes (at most 19, to be precise). A green leaf of the history graph is created for each new box and linked to γ. The adjacency relations are updated at the same time.

As in the planar case, the new set of boxes need not be a proper (vertical) decomposition. So our next step should be to merge the boxes which are separated by wall portions that must be removed. In the planar case the merging was a straightforward operation, but now it imposes a technical difficulty that requires some care.

Recall that there are two types of walls in the vertical decomposition: primary walls and secondary walls. Primary walls are erected from edges of the arrangement. Secondary walls are obtained as follows. After adding the primary walls, the bottom

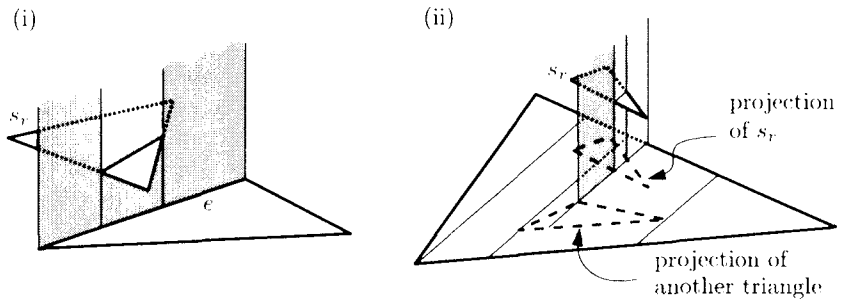

Fig. 4. The lightly shaded wall portions have to be removed because of the new triangle s_r.

faces of the cylinders in the cylindrical decomposition are decomposed into trapezoids; the segments added in the trapezoidation are extended vertically upward until they meet the top face to obtain the secondary walls. Observe that any secondary wall must contain either a vertex of the three-dimensional arrangement of triangles or a vertical edge which is the intersection of two primary walls. Consider a wall intersected by s_r. The wall is cut into at most four pieces by s_r and the primary walls from its edges: a portion below s_r, a portion above s_r, and two other portions, one on either side of s_r. If the wall is a primary wall erected from an edge e of the arrangement, we have to remove the portion of the wall lying on the opposite side of s_r (as seen from e). Figure 4(i) illustrates this. The lightly shaded part of the wall erected for edge e must be removed when s_r is inserted. If the wall is a secondary wall, as in Fig. 4(ii), then the only portion that remains is the portion containing either a vertex of the new arrangement or a vertical edge which is the intersection of two new primary walls. Note that a secondary wall may even disappear completely. Now that we have seen which walls to remove, we examine the merging in more detail.

We distinguish two types of boxes in the merging step: the boxes that have neither a bottom nor a top face contained in s_r, and the boxes that do have their top or bottom face contained in s_r. Notice that two boxes of a different type never have to be merged, since any box has its top and bottom face contained in a single triangle.

It is not difficult to see that the merging of the boxes of the first type only involves the removal of portions of secondary walls. This makes the merging easy. We simply check which portions contain either a vertex of the new arrangement or a vertical edge which is the intersection of two new primary walls (this information is easy to maintain). All other wall portions are removed, that is, we merge the corresponding boxes and we update the links in the history graph and the adjacency graph accordingly. Note that the boxes only grow, so the out-degree of the nodes in the history graph does not increase.

Next, we consider the boxes of the second type, whose bottom or top face is contained in s_r. Here we have to remove portions of primary walls as well as portions of secondary walls. The removal of portions of primary walls is problematic: it may happen that some of the secondary walls were "stopped" by the portions of

primary walls that we are going to remove. This means that these secondary walls now have to be extended. However, then an old box can be cut into many pieces by the extended secondary walls, increasing the out-degree of the corresponding node in the history graph. In other words, we are not allowed to link an old box to all the boxes in the new vertical decomposition that it intersects. Fortunately, this problem can be solved using a trick proposed by Boissonnat and Dobrindt [3]. The idea is to "encode" the links from an old box to all the new boxes it intersects in a rooted graph—the *secondary history graph*. The leaves of the secondary history graph correspond to the new boxes. Instead of having links to all the new boxes the out-degree of the nodes is kept constant. Next we describe the construction of this secondary history graph in more detail.

Let B_b (B_t) denote the set of boxes whose bottom (top) face is contained in s_r, after we have split the boxes with s_r, but before we have started the merging process. We construct two secondary history graphs, one for the boxes in B_b and one for the boxes in B_t. We describe how to construct the secondary history graph for B_b; the construction for B_t is similar.

The union of the bottom faces of the boxes in B_b is the part of the top side of s_r that is inside the current single cell (that is, the single cell of the latest clean-up step). Notice that this union is not necessarily connected, and that its components are not necessarily simply connected. Consider all faces of the boxes in B_b which are contained in a still existing primary wall,[2] and let S_b be the set of bottom edges of these faces. Such a bottom edge is the intersection of the face with the triangle s_r, since the boxes have s_r as their bottom face. We merge collinear segments of S_b if they share an endpoint and there is no third segment with this endpoint. Observe that the segments in S_b have disjoint interiors. Also observe that the cells of the arrangement $\mathcal{A}(S_b)$ on s_r defined by S_b are exactly the bottom faces of the cylinders of the cylindrical decomposition of the current arrangement that are contained in s_r. Now, in order to obtain a correct vertical decomposition we have to compute a (two-dimensional) trapezoidation of $\mathcal{A}(S_b)$, and extend the extra segments thus created vertically upward to obtain the new secondary walls. This trapezoidation is computed using a two-dimensional randomized incremental algorithm by Boissonnat *et al.* [2]. The history graph that results from this construction is our secondary history graph for the set B_b. We also store the adjacency graph for the trapezoidal decomposition of $\mathcal{A}(S_b)$. The leaves of the secondary history graph correspond to trapezoids in the trapezoidation of $\mathcal{A}(S_b)$, which, in turn, correspond to the new boxes in the three-dimensional vertical decomposition. In general, the union of the bottom faces of the boxes in B_b will not be the entire triangle s_r, since parts of s_r can lie outside the current single cell. The leaves that correspond to trapezoids lying outside this union are of no interest to us, so we color them red. Finally, we link all the boxes in B_b to the root of the secondary history graph. Note that the number of out-going arcs for every node is bounded by a constant.

[2] Some faces of the boxes in B_b can be contained in a portion of a primary wall that we must remove.

Now consider a later step in our algorithm, where we insert a triangle s_j, $j > r$. We have to determine the boxes in the current decomposition which are intersected by s_j. This we can still do by traversing the history graph, as follows.

The search in the history graph proceeds in the normal way as long as we do not encounter any secondary history graphs. Now suppose that we reach a node v in the primary history graph that has an out-going arc to the root of a secondary history graph. Assume that this secondary history graph was constructed when we inserted triangle s_r, and assume that $\Delta(v)$ is a box in B_b. (The set B_b is defined with respect to the triangle s_r, as above.) We compute a point $q \in s_j \cap \Delta(v)$, project this point onto s_r, and continue the search in the secondary history graph with the projected point $\bar{q}$. This way to find in $O(\log n)$ time the trapezoid in the trapezoidation of $\mathscr{A}(S_b)$ that contains $\bar{q}$. We now switch to the adjacency graph of the trapezoidation of $\mathscr{A}(S_b)$. Using a graph traversal we determine all the trapezoids that are in the single cell of $\mathscr{A}(S_b)$ defined by $\bar{q}$ and whose corresponding boxes are intersected by s_j. These boxes correspond to nodes in the primary history graph from which we continue our search.

Observe that s_j can intersect several of the boxes in B_b. For each of these boxes we compute a point to search with in the secondary history graph. Hence, we may visit trapezoids in $\mathscr{A}(S_b)$ more than once. To avoid traversing the same part of the adjacency graph too often, we mark every trapezoid when we visit it. When we reach this trapezoid again while handling s_j, we know that we already visited it and we do not start a graph traversal.

This finishes the description of the search in the secondary history graph. However, what about the correctness of the search, and what about the extra time we spend?

Lemma 7. *The searches in the secondary history graph for $\mathscr{A}(S_b)$ give us exactly those trapezoids whose corresponding box is intersected by s_j.*

Proof. We explicitly test boxes for intersection when we traverse the adjacency graph, so it remains to prove that we find all intersected boxes. Let Δ_1 be an intersected box corresponding to a trapezoid in $\mathscr{A}(S_b)$, and let q_1 be a point in $\Delta_1 \cap s_j$. Let Δ_2 be the box in B_b that contains q_1. The box Δ_2 intersects s_j, so we have generated some point $q_2 \in \Delta_2 \cap s_j$ to search in the history graph. It is not necessarily true that $\overline{q_2}$ and $\overline{q_1}$ are in the same trapezoid of $\mathscr{A}(S_b)$: some new secondary walls that arose when we constructed the trapezoidation for $\mathscr{A}(S_b)$ may prevent this. However, we claim that the two trapezoids containing $\overline{q_1}$ and $\overline{q_2}$ are connected in the adjacency graph of $\mathscr{A}(S_b)$. To see this, note that q_1q_2, the line segment connecting q_1 and q_2, is contained in Δ_2 and does not intersect any primary walls. When constructing the secondary history graph for $\mathscr{A}(S_b)$ we only add secondary walls. Hence, the segment $\overline{q_1q_2}$ does not intersect primary walls either, and the trapezoids containing $\overline{q_1}$ and $\overline{q_2}$ are connected in the adjacency graph. Moreover, the box corresponding to a trapezoid intersected by $\overline{q_1q_2}$ is intersected by q_1q_2 and, hence, by s_j. We conclude that we will report the box Δ_1 during a traversal of the adjacency graph. □

The time it takes to go down the secondary history graph with some point $\bar{q}$ is bounded by the depth of the secondary history graph, which is expected to be $O(\log n)$. We charge this extra time to the node v of the primary history graph that generated the point q. The time for traversing the adjacency graph is linear in the number of nodes in the primary history graph that we discover; we charge the time to these nodes. In total, every node in the primary history graph gets charged an extra $O(\log n)$ each time it is visited.

The Clean-Up Step. We identify the connected component of $\mathcal{G}$ containing the node whose trapezoid contains the origin by a graph traversal. The nodes of $\mathcal{G}$ which are not in this component are deleted from $\mathcal{G}$ and the corresponding leaves of the history graph are colored red.

5.3. *Analysis of the Single-Cell Algorithm*

The analysis combines the analysis of Boissonnat and Dobrindt [3] with the results of Section 4.1. We distinguish *principal* nodes of the history graph, corresponding to boxes that have been created during the incremental construction, and *secondary* nodes, which are inner nodes of the secondary history graphs. We express the main results using the function $\psi(n)$, which denotes the maximum number of boxes in the vertical decomposition of a single cell in an arrangement of n triangles. We proceed as in Section 4.2. S is the given set of triangles, $\mathcal{F}$ is the set of all boxes (each defined by at most six triangles), $\mathcal{T}(R)$ is the set of boxes in the vertical decomposition of a subset $R \subseteq S$, and $\mathcal{M}(R)$ is the set of boxes in $\mathcal{F}$ contained in the single cell of $\mathcal{A}(R)$ containing the origin. It follows that $\mathcal{C}_r = \mathcal{T}(S_r) \cap \mathcal{M}(S_p)$, where p is the largest power of two that is less than r, is exactly the set of boxes present at stage r of our algorithm.

As in Section 4.2, we use Theorem 6 to bound the expected size of the structure we maintain. We prove that

$$E\left[|\mathcal{C}(S_t, S_q)|\right] = O(\psi(t)), \tag{9}$$

for $q < t \leq r \leq 4q$, which implies that $\tau(r, q) = O(\psi(r))$ for $q \leq r \leq 4q$.

In Section 4.2 we used the number of vertices of the planar arrangement $\mathcal{A}(S_t)$ lying in a single face of $\mathcal{A}(S_q)$ as an asymptotic bound on the complexity of the structure that we maintained. The number of such vertices was then bounded using (8). The complexity of the structure that we maintain in the three-dimensional setting can be analyzed in a similar way. In particular, to prove (9) it is sufficient to bound the expected number of vertices of $\mathcal{A}(S_t)$ that lie in that cell or on its boundary plus the expected number of intersections between two primary walls erected from edges of $\mathcal{A}(S_t)$ that lie in that cell or on its boundary. To bound the first number we have to add a term $\omega(\Delta)^3$ in (8). To bound the second number we note that the expected number of edges in a box $\Delta \in \mathcal{C}(S_q, S_q)$ is $\omega(\Delta)^2$; hence, the expected number of intersections between two primary walls erected from them adds a term $\omega(\Delta)^4$ in (8). By Theorem 5, this implies that the expected complexity of $\mathcal{C}_r$

is only $O(\psi(r))$. Again, the structure we are maintaining is asymptotically not larger than the single cell itself.

We now bound the expected size of the history graph constructed by the algorithm. The expected number of principal nodes can be bounded as

$$\sum_{r=1}^{n} E[|\mathscr{C}_r \setminus \mathscr{C}_{r-1}|] = \sum_{r=1}^{n} O\left(\frac{1}{r}\psi(r)\right) = O(\psi(n)),$$

since $\psi(n)$ is at least linear. Next we bound the number of secondary nodes created by the algorithm. Recall that the secondary history graphs are constructed on a set of nonintersecting line segments. This implies that the total number of trapezoids that are created for the secondary history graphs is linear in the number of line segments [2]. It remains to observe that this number is linear in the number of boxes of the vertical decomposition that are destroyed. Since a destroyed box has to be created first, the total number of secondary nodes is bounded by $O(\psi(n))$.

As for the running time, we observe that the history search for a new triangle s_r visits only principal nodes ν of the current history graph with $s_r \in \mathscr{R}(\Delta(\nu))$. It follows that the expected number of principal nodes visited during all history searches can be bounded by

$$\sum_{r=1}^{n} E\left[\sum_{\Delta \in \mathscr{C}_r \setminus \mathscr{C}_{r-1}} \omega(\Delta)\right] = \sum_{r=1}^{n} O\left(\frac{n}{r^2}\psi(r)\right) = O(\psi(n)),$$

since $\psi(n) = \Omega(n^{1+\varepsilon})$ for a constant $\varepsilon > 0$. As argued above, the searches in the secondary history graphs can be charged to principal nodes in such a way that every principal node gets charged an extra $O(\log n)$ factor each time it is visited.

After we have identified the boxes of the current decomposition that are intersected by the new triangle, we perform the merging step as described before. Creating the secondary history graph takes $O(m \log m)$ time, where m is the number of boxes that are destroyed in this step. By the bound on the total number of boxes created by the algorithm, this results in an expected total update time of $O(\psi(n) \log n)$.

Finally, the total expected work for the clean-up steps is bounded by

$$\sum_{i=1}^{\lfloor \log n \rfloor} \psi(2^i) = O(\psi(n)).$$

This completes the analysis of the algorithm and yields the following theorem.

Theorem 8. *Given a set of n triangles in 3 space, the cell in the arrangement containing the origin can be computed in $O(\psi(n) \log n)$ expected time using $O(\psi(n))$ storage, where $\psi(m)$ denotes the maximum number of boxes in the vertical decomposition of a single cell in an arrangement of m triangles.*

By Theorem 6 we obtain the following corollary.

Corollary 9. *Given a set S of n triangles in 3 space, the cell in the arrangement containing the origin can be computed in $O(n^2 \log^3 n)$ expected time using $O(n^2 \log^2 n)$ storage.*

5.4. *Computing Zones in Arrangements of Hyperplanes*

Given a set S of n hyperplanes in d-dimensional space and a surface γ, the *zone of γ with respect to S* is the set of cells of $\mathscr{A}(S)$ intersected by γ. We assume that γ has constant description complexity.

Our algorithm follows the lazy incremental construction paradigm outlined in Section 3. Thus we add the hyperplanes of the set S in random order, meanwhile, maintaining the bottom-vertex decomposition of the arrangement $\mathscr{A}(S)$ (see for instance Mulmuley's book [16, Chapter 6.3] for a definition of the bottom-vertex triangulation). After inserting the hyperplane number 2^i, for $i = 1, \ldots, \lfloor \log n \rfloor$, we do a clean-up step and we discard all cells that are no longer in the zone. We depart from our previous scheme and describe this algorithm using a *conflict graph* instead of a history graph. Using conflict graphs turns out to be slightly simpler for this problem; if necessary, the algorithm can be modified to use a history graph. It also shows that the lazy paradigm is independent of the nature of the conflict search. So, for every simplex Δ of the bottom-vertex decomposition of $\mathscr{A}(S_r)$, we maintain the conflict list $\mathscr{K}(\Delta)$. For every s_j not yet added we maintain reverse pointers to all Δ with $s_j \in \mathscr{K}(\Delta)$. The update step and the clean-up step are performed as follows.

The Update Step. Using the reverse pointers to the conflict lists, we first collect the simplices in the current arrangement intersected by the new hyperplane s_r. This tells us which cells of the current arrangement have to be split and retriangulated. This can be done in time proportional to the total number of simplices intersected, since we are allowed to spend time proportional to the size of the subcell that does not contain the bottom-vertex of the cell. See again Mulmuley's book for details.

It remains to create the conflict lists for the newly created simplices. To this end we collect the hyperplanes in all conflict lists of all destroyed simplices of a given cell. For every such hyperplane s_j, $j > r$, we then determine the new simplices Δ intersected by s_j. For the simplices in each of the two new cells this can be done in the following way. First, we find one vertex of the cell that is on the opposite side of s_r than the bottom vertex of the cell. From that vertex we perform a graph search on the boundary of the cell. It is not difficult to show that the total time for this operation is proportional to the total length of the conflict lists of all destroyed and created simplices. Details can be found in [18].

The Clean-Up Step. First, we test every simplex of the current arrangement to find those intersected by the surface γ. Then we traverse the triangulation, starting from these simplices, to identify the cells in the zone of γ. All simplices not in the zone of γ are simply discarded.

5.5. *Analysis of the Zone Algorithm*

Let $\zeta_\gamma(n, d)$ denote the maximum complexity of the zone of γ in an arrangement of n hyperplanes in d-dimensional space. We want to bound the running time of our algorithm in terms of $\zeta_\gamma(n, d)$.

We employ our tools from Section 4.1 and define $\mathscr{F}$ as the set of all simplices defined by hyperplanes in S. For a box $\Delta \in \mathscr{F}$, $\mathscr{H}(\Delta)$ is the set of hyperplanes intersecting Δ. For $R \subseteq S$, we define $\mathscr{T}(R)$ as the set of simplices in the bottom-vertex triangulation of $\mathscr{A}(R)$, and $\mathscr{M}(R)$ as the set of all simplices in $\mathscr{F}$ that are contained in the zone of γ with respect to R. Then $\mathscr{C}_r$ as defined in Section 4.1 is the set of simplices present in our structure after inserting hyperplane s_r, but before any clean-up step.

We first want to bound the expected size of $\mathscr{C}(S_t, S_q)$, for $q < t \leq r \leq 4q$. It suffices to bound the number of vertices of $\mathscr{A}(S_t)$ within the zone of γ with respect to S_q. We can bound this using Theorem 3 as

$$E\big[|\mathscr{C}(S_t, S_q)|\big] = O(\zeta_\gamma(t, d)).$$

This implies that $\tau(r, q) = O(\zeta_\gamma(r, d))$, for $q > r/4$.

As observed before, the running time in step r is dominated by the total size of the conflict lists of all simplices that are created or destroyed. It follows that the total expected running time is bounded by

$$\sum_{r=1}^{n} E\left[\sum_{\Delta \in \mathscr{C}_r \setminus \mathscr{C}_{r-1}} \omega(\Delta)\right] = \sum_{r=1}^{n} O\left(\frac{n}{r^2}\zeta_\gamma(r, d)\right).$$

To bound the storage requirement of the algorithm, we have to bound the expected total size of all conflict lists at time r, which is

$$E\left[\sum_{\Delta \in \mathscr{C}_r} \omega(\Delta)\right].$$

The same proof technique used in Theorem 5 can be applied to show that this sum is bounded by $O((n/r)\zeta_\gamma(r, d))$. This is always bounded by $O(n + \zeta_\gamma(n, d))$. Thus, we obtain the following theorem.

Theorem 10. *Let $\zeta_\gamma(n, d)$ denote the maximum complexity of the zone of a surface γ in an arrangement of n hyperplanes in d-dimensional space. Then the zone of γ with respect to an arrangement $\mathscr{A}(S)$ of n hyperplanes in d-dimensional space can be computed in expected time*

$$\sum_{r=1}^{n} O\left(\frac{n}{r^2}\zeta_\gamma(r, d)\right)$$

and storage $O(n + \zeta_\gamma(n, d))$.

When γ is a hyperplane, then tight bounds are known on the maximum zone complexity: the famous Zone Theorem [10] states that in d-dimensional space the complexity is $O(n^{d-1})$. In this case we obtain an optimal algorithm.

Corollary 11. *The zone of a hyperplane in an arrangement of n hyperplanes in d-dimensional space can be computed in $O(n^{d-1} + n \log n)$ time using $O(n^{d-1})$ storage.*

6. Conclusion

We introduced a new type of randomized incremental algorithms, which is suited for computing structures that have a "nonlocal" definition. In order to analyze these lazy randomized algorithms we generalized the results of Clarkson and Shor on random sampling to such situations. Our technique yields efficient algorithms for computing single cells in arrangements of segments in the plane and in arrangements of triangles in 3-space, and for computing zones.

We believe that our technique can be useful for a number of other problems as well. For example, the best-known algorithm for computing all nonconvex cells in an arrangement of triangles in 3-space runs in $O(n^{8/3} \log^{14/3} n)$ time [1], although the total complexity of these cells is known to be $O(n^{7/3} \log n)$. If the maximum complexity of the vertical decomposition of m cells in an arrangement of n triangles is close to the maximum complexity of the cells themselves, which is $O(n^2 \log^2 n + nm^{2/3} \log n)$, then we immediately obtain an algorithm with a running time close to $O(n^{7/3})$.

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