Decomposing arrangements of hyperplanes: VC-dimension, combinatorial dimension, and point location*

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Abstract

This work is motivated by several basic problems and techniques that rely on space decomposition of arrangements of hyperplanes in high-dimensional spaces, most notably Meiser's 1993 algorithm for point location in such arrangements. A standard approach to these problems is via random sampling, in which one draws a random sample of the hyperplanes, constructs a suitable decomposition of its arrangement, and recurses within each cell of the decomposition with the subset of hyperplanes that cross the cell. The efficiency of the resulting algorithm depends on the quality of the sample, which is controlled by various parameters.

One of these parameters is the classical *VC-dimension*, and its associated *primal shatter dimension*, of a suitably defined corresponding range space. Another parameter, which we refer to here as the *combinatorial dimension*, is the maximum number of hyperplanes that are needed to define a cell that can arise in the decomposition of some sample of the input hyperplanes; this parameter arises in Clarkson's (and later Clarkson and Shor's) random sampling technique.

We re-examine these parameters for the two main space decomposition techniques— $bottom-vertex\ triangulation$, and $vertical\ decomposition$, including their explicit dependence on the dimension d, and discover several unexpected phenomena, which show that, in both techniques, there are large gaps between the VC-dimension (and primal shatter dimension), and the combinatorial dimension.

For vertical decomposition, the combinatorial dimension is only 2d, the primal shatter dimension is at most d(d+1), and the VC-dimension is at least 1+d(d+1)/2 and at most $O(d^3)$. For bottom-vertex triangulation, both the primal shatter dimension and the combinatorial dimension are $\Theta(d^2)$,

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but there seems to be a significant gap between them, as the combinatorial dimension is $\frac{1}{2}d(d+3)$, whereas the primal shatter dimension is at most d(d+1), and the VC-dimension is between d(d+1) and $5d^2 \log d$ (for $d \ge 9$).

Our main application is to point location in an arrangement of n hyperplanes is \mathbb{R}^d , in which we show that the query cost in Meiser's algorithm can be improved if one uses vertical decomposition instead of bottom-vertex triangulation, at the cost of some increase in the preprocessing cost and storage. The best query time that we can obtain is $O(d^3 \log n)$, instead of $O(d^4 \log d \log n)$ in Meiser's algorithm. For these bounds to hold, the preprocessing and storage are rather large (superexponential in d). We discuss the tradeoff between query cost and storage (in both approaches, the one using bottom-vertex trinagulation and the one using vertical decomposition).

Our improved bounds rely on establishing several new structural properties and improved complexity bounds for vertical decomposition, which are of independent interest, and which we expect to find additional applications.

The point-location methodology presented in this paper can be adapted to work in the *linear decision-tree model*, where we are only concerned about the cost of a query, and measure it by the number of point-hyperplane sign tests that it performs. This adaptation is presented in the companion paper [ES17], where it yields an improved bound for the linear decision-tree complexity of k-SUM. A very recent breakthrough by Kane et al. [KLM17] further improves the bound, but only for special, "low-complexity" classes of hyperplanes. We show here how their approach can be extended to yield an efficient and improved point-location structure in the RAM model for such collections of hyperplanes.

1 Introduction

Point location. This work is motivated by several basic problems and techniques that rely on space decomposition of arrangements of hyperplanes in high-dimensional spaces, most notably (i) Meiser's 1993 algorithm for point location in such arrangements [Mei93], and (ii) the linear decision tree complexity of k-SUM, Subsetsum, Knapsack, and related problems.

Let H be a set of n hyperplanes in \mathbb{R}^d , and let $\mathcal{A}(H)$ denote the arrangement of H. The point-location problem in $\mathcal{A}(H)$ is to preprocess H into a data structure that supports efficient point-location queries, each of which specifies a point $q \in \mathbb{R}^d$ and asks for the (not necessarily full-dimensional) cell of $\mathcal{A}(H)$ that contains q. We represent the output cell C by its sign pattern with respect to the hyperplanes in H, where the sign of C with respect to a hyperplanes $h \in H$ is 0 if h contains h0, h1 if h2 is in the positive side of h3 and h4 and h5 is in the negative side of h5. A simpler variant, known as vertical ray-shooting, which does not seem to make the problem substantially simpler, is to ask for the hyperplane of h5 that lies directly above h6, namely, the first hyperplane that an upward h6 vertical ray emanating from h6 will hit (it is possible that the ray terminates right away, when h6 lies on one or several such hyperplanes).

Linear decision tree complexity of k-SUM and related problems. The k-SUM problem is to determine, for a given set A of n real numbers and a parameter k, whether there exist k (say, distinct) elements of A that sum up to 0. A simple transformation turns this into a point location problem: Let H be the set of all hyperplanes in \mathbb{R}^n of the form $x_{i_1} + x_{i_2} + \cdots + x_{i_k} = 0$, over all the $\binom{n}{k}$ k-tuples $1 \leq i_1 < i_2 < \cdots < i_k \leq n$. Map the given set $A = \{a_1, a_2, \ldots, a_n\}$ to the point $q_A = (a_1, a_2, \ldots, a_n) \in \mathbb{R}^n$. The k-SUM problem is then reduced to the problem of determining whether q_A lies on a hyperplane of H, an instance of point location amid hyperplanes in a high-simensional space.

We analyze the complexity of this problem in the *linear decision tree* model, where we only count linear sign tests involving the elements of A (and no other operation is allowed to access the actual values

of these elements). This problem is studied in the companion paper [ES17], where a full treatment and analysis are provided.

The challenge. In the context studied in this paper (as well as in Meiser's work), d is not assumed to be a constant, so the dependence of the bounds that we will derive on d is crucial for calibrating the quality of our solutions. This is a departure from classical approaches to this problem in computational geometry, in which d is assumed to be a small constant, and constants that depends solely on d (sometimes exponentially or worse) are ignored (i.e., hidden in the O-notation). In particular, we cannot use off-the-shelf results, in which the dependency on d is not made explicit, as a black box.

Time-space tradeoff. As is typical with problems of this kind, there is a trade-off between the cost of a query and the storage (and preprocessing time) required by the structure. We are interested here in solutions in which the query time is polynomial in d and (poly)logarithmic in n. The only known algorithm that achieves this goal is an old algorithm from 1993, due to Meiser [Mei93] (see also the related work [MadH84] under the decision-tree model). We review Meiser's algorithm in Section 5.1, add a few called-for enhancements, and show that it can achieve query time of $O(d^4 \log n)$, and that the storage, for this query $\cos t$, is $O(n^{2d \log d + O(d)})$. The storage has been tightened (in terms of its dependence on n, but not on d) to $O(d^{O(d^3)}n^d)$ in a follow-up work by Liu [Liu04].

Canonical decompositions. A standard approach to these problems is via random sampling, in which one draws a random sample of the hyperplanes, constructs a suitable decomposition of its arrangement, and recurses within each cell of the decomposition. The efficiency of the resulting algorithm depends on the quality of the sample, which is controlled by various parameters, discussed shortly.

Before discussing the random sampling methodologies that turn this intuition into rigorous theory, we briefly review the two basic techniques for decomposing an arrangement of hyperplanes into subcells of "constant" description complexity (here the qualifier "constant" is misleading, because it depends on d, which is not assumed to be constant, but this is how the standard terminology goes). These are bottom-vertex triangulation and vertical decomposition.

In the bottom-vertex triangulation approach (BVT for short; see [Mat02]), we triangulate (recursively) each facet in the arrangement (within the hyperplane containing it), and then triangulate d-space, by picking the lowest vertex w in each full-dimensional cell C, and by connecting w to each of the (d-1)-simplices in the triangulations of the facets of C that are not adjacent to w (some care is needed when triangulating the unbounded cells of $\mathcal{A}(H)$); see Section 3 for more details.

The other scheme, vertical decomposition (VD for short; see [CEGS91, SA95]), is an extension to higher dimensions of the standard two-dimensional vertical decomposition of arrangements of lines or curves (see, e.g., [AS00, dBCvKO08, SA95]). It is constructed by a careful and somewhat involved recursion on the dimension, and decomposes $\mathcal{A}(H)$ into box-like vertical prisms of some special structure; see [SA95] and Section 4 for full details.

Cuttings and random sampling. The key tool for fast point location is to construct a canonical decomposition of \mathbb{R}^d into cells, such that, for a given parameter 1 < r < n, the following properties hold.

(a) Each cell in the decomposition is "simple", and, in particular, it is relatively easy (and efficient, when r is small) to find the cell containing the query point.

¹This large dependence of the storage on d was missed in the analysis in [Mei93]; it can be reduced by increasing the query time—see Section 5.1 for full details.

- (b) The total number of cells in the decomposition is small (in particular, it only depends on r).
- (c) For each cell σ , the set of hyperplanes of H that cross σ , called the *conflict list* of σ , and denoted $K(\sigma)$, is of size at most n/r.

Such a decomposition is called a (1/r)-cutting. See [Cha05, CF90, dBS95, Har00] and references therein for more information about cuttings.

The point location algorithm then recursively constructs the same data structure for each cell σ , on the set $K(\sigma)$ of hyperplanes, and the overall tree-like structure allows us to locate a query point q in $\mathcal{A}(H)$ efficiently. Meiser's point location algorithm, as well as many other point location algorithms, follow this standard approach.

The main general-purpose tool for constructing a cutting is to take a random sample R of H of a suitable size (that depends on r), and argue that a canonical decomposition Ξ of $\mathcal{A}(R)$ (namely, either the BVT or the VD of R) is a (1/r)-cutting of $\mathcal{A}(H)$, with sufficiently large probability.

There are two basic techniques for estimating the size of the sample that is required to guarantee this property. They are based, respectively, on the ε -net theorem [HW87], and on the Clarkson-Shor random sampling theory [CS89]. We devote Section 2 for the analysis of these sampling methods. We first briefly review the first approach, and then spend most of the section on a careful analysis of various aspects of the Clarkson-Shor theory. Although we present it in more generality, we are mainly interested in its specialization to the case of hyperplanes in high-dimensional spaces.

Range spaces and growth functions. A key concept in the analysis around the ε -net theorem is the notion of a range space. In general, this is a pair (H, \mathcal{R}) , where H is some ground set (in our case, a set of hyperplanes in \mathbb{R}^d), and \mathcal{R} is a family of subsets of H, called ranges. In our settings, a range is the subset of all hyperplanes of H that cross some region that "looks like" a cell of the decomposition; that is, an arbitrary simplex for bottom-vertex triangulation, and an arbitrary vertical prism (with some constraints on its structure, discussed in Section 4) for vertical decomposition.

These range spaces are hereditary in nature, in the sense that each subset $H' \subseteq H$ defines an induced (or projected) range space (H', \mathcal{R}') , where $\mathcal{R}' = \mathcal{R}_{|H'} = \{\mathbf{r} \cap H' \mid \mathbf{r} \in \mathcal{R}\}$. Of key interest is the dependence of (an upper bound on) the number of ranges in this range space on the size of H'. Formally, we define the (global) growth function of (H, \mathcal{R}) to be $g_{\mathcal{R}}(m) = \max_{H' \subseteq H, |H'| = m} |\mathcal{R}_{|H'}|$.

We say that a growth function is (α, β) -growing, for a real parameter α and an integer parameter $\beta \geq 1$, if $g_{\mathcal{R}}(m) \leq 2^{\alpha} m^{\beta}$ (either for all m, or for all m larger than some constant threshold). As will be reviewed below, the growth function of a range space is a key tool in obtaining estimates on the size of a random sample R that guarantees that the corresponding decomposition of $\mathcal{A}(R)$ is a (1/r)-cutting. We note that in most previous studies, the parameter α is ignored, since it is considered to be a constant, and as such has little effect on the analysis. Here, in contrast, α will depend on d, which is not a constant, and this will lead to some "nonstandard" estimates on the performance of random sampling.

VC-dimension and primal shatter dimension. The VC-dimension of a range space (H, \mathcal{R}) is the size of the largest subset H' of H that can be *shattered* by \mathcal{R} ; that is, each of the $2^{|H'|}$ subsets of H' is a range in the restriction of \mathcal{R} to H'. In general, by the Sauer-Shelah lemma (see, e.g., [PA95, Har11]), if (H, \mathcal{R}) has finite VC-dimension δ (namely, a value independent of |H|, which is the case in the special instances considered here), then the growth function satisfies

$$g_{\mathcal{R}}(m) \le \sum_{j=0}^{\delta} {m \choose j} \le 2\left(\frac{me}{\delta}\right)^{\delta},$$
 (1.1)

where the right inequality holds for $m \geq \delta$. The primal shatter dimension δ_0 of (H, \mathcal{R}) is the smallest integer β for which there exists an $\alpha \geq 0$ such that $g_{\mathcal{R}}$ is (α, β) -growing. Informally, δ_0 is obtained (a) by obtaining the best upper bound on $g_{\mathcal{R}}(m)$, in terms of m, and then (b) by stripping away the dependence of $g_{\mathcal{R}}$ on the corresponding parameter α . In our contexts, α may be large (but it does not depend on m), so this simplified notation makes more sense as m gets larger. Clearly, (1.1) implies that $\delta_0 \leq \delta$, and in general they need not be equal. For example, for the range space in which the ground set consists of points in the plane and the ranges are (subsets obtained by intersecting the ground set with) unit disks, the VC-dimension is 3 but the primal shatter dimension is only 2. We also note that reducing δ_0 (down from δ , when possible) might incur an increase in α .

 ε -nets. These notions of dimension are used to control the quality of the decomposition, via the theory of ε -nets. For a general range space (H, \mathcal{R}) and a prespecified parameter $\varepsilon \in (0, 1)$, a subset $N \subseteq H$ is an ε -net if every "heavy" range $R \in \mathcal{R}$, of size at least $\varepsilon |H|$, contains an element of N. Equivalently, every range that is disjoint from N is of size smaller than $\varepsilon |H|$. The celebrated theorem of Haussler and Welzl [HW87], or rather its enhancement by Blumer et al. [BEHW89] (stated as Theorem 2.2 below) asserts that, if (H, \mathcal{R}) is a range space of finite VC-dimension δ , then a random sample of $\frac{c\delta}{\varepsilon} \log \frac{1}{\varepsilon}$ elements of H, for some suitable absolute constant c, is an ε -net with constant probability. As follows from the proof of this theorem, a similar assertion holds (more or less) when we replace δ by the (potentially smaller) primal shatter dimension δ_0 , except that the required sample size is now $\frac{c\delta_0}{\varepsilon} \log \frac{\delta_0}{\varepsilon}$, so the dimension also appears inside the logarithm.

In our context, if the sample R is of size $c\delta r \log r$ (resp., $c\delta_0 r \log(\delta_0 r)$), where δ (resp., δ_0) is the VC-dimension (resp., primal shatter dimension) of the corresponding range space (where ranges are defined by simplices or by vertical prisms), then, with constant probability, (the interior of) each cell in the decomposition of $\mathcal{A}(R)$, which, by construction, is not crossed by any hyperplane of R, is crossed by fewer than n/r hyperplanes of H, so the decomposition is a (1/r)-cutting of $\mathcal{A}(H)$. In particular, choosing r = 2, say, we guarantee, with constant probability, that if we choose R to be of size $2c\delta$ (resp., $2c\delta_0\log(2\delta_0)$), then (with constant probability) the conflict list of each of the cells of the decomposition is of size at most n/2.

In the point location application, presented in Section 5, this choice of |R|, namely, the one that guarantees (with constant probability), that the size of each conflict list goes down by a factor of at least 2, leads to the best bound for the cost of a query that this method yields, but it results in a rather large bound on the storage size. To decrease storage, we need to use significantly larger values of r, that is, larger samples. Loosely speaking, a larger sample size better controls the size of the recursive subproblems, and leads to smaller storage size, but one pays for these properties in having to spend more time to locate the query point in the canonical decomposition of the sample. See Section 5 for more details.

The Clarkson-Shor theory and combinatorial dimension. In contrast with the general approach based on range spaces, Clarkson [Cla87] (and later Clarkson and Shor [CS89]) developed an alternative theory, which, in the context considered here, focuses only on simplices or vertical prisms (referred to by the common term 'cell' in what follows, not to be confused with the undecomposed cells of the arrangement) that can arise in the actual canonical space decomposition of the arrangement of some sample R of H. Each such cell σ has, in addition to its conflict list $K(\sigma)$, defined as above, also a defining set $D(\sigma)$, which is the smallest subset H' of H (or a smallest subset, in case of degeneracies), for which σ is a cell in the decomposition of A(H'). We refer to the cells that arise in this manner as definable cells. Clearly, each definable cell determines a range in the corresponding range space (H, \mathcal{R}) , but, as

will follow from our analysis, not necessarily vice versa.

Define the *combinatorial dimension*, associated with the decomposition technique, to be the maximum size of the defining set of a cell. (This too is a much more widely applicable notion, within the Clarkson-Shor sampling theory, but, again, we only consider it here in the context of decomposing arrangements of hyperplanes.)

When we analyze the behavior of random sampling under the Clarkson-Shor theory, we replace the global growth function, as introduced earlier, by a *local* growth function u, so that u(m) is the maximum number of cells (simplices or vertical prisms) in the corresponding canonical decomposition of $\mathcal{A}(R)$, for a sample R of size m.

Exponential decay. The ε -net theory, as well as the alternative approach of Clarkson and Shor, are concerned with the "worst-case" behavior of a random sample, in the sense that, for a sample R, the quality of the decomposition associated with R is measured by the largest size of a conflict list of a cell in the decomposition, whereas the average size of such a list is in general smaller (typically, by a logarithmic factor). The analysis of Clarkson and Shor [CS89] shows that the average size of a conflict list for a sample of size O(br) (where b is the combinatorial dimension), raised to any fixed power c is $O((n/r)^c)$, suggesting that the number of cells whose conflict list is significantly larger must be very small. This has been substantiated by Chazelle and Friedman [CF90], who showed that the number of cells in a canonical decomposition of the sample, having a conflict list whose size is at least t times larger than n/r, is exponentially decreasing as a function of t. This is known as the exponential decay lemma. Various extensions and variants of the lemma have been considered in the literature; see, e.g., [AMS98, CMS93].

Back to our context. Our main motivation for this study was to (analyze more precisely, and) improve Meiser's data structure for point location in high-dimensional arrangements of hyperplanes. A first (and crucial) step towards this goal is to gain better understanding of the exact values of the above parameters (VC-dimension, primal shatter dimension, and combinatorial dimension), in particular of the way they depend on the dimension d.

Our results: The sampling parameters. We first re-examine the sampling parameters, namely, the VC-dimension, growth function (and primal shatter dimension), and combinatorial dimension, for the two canonical space decomposition techniques, bottom-vertex triangulation and vertical decomposition. We discover several unexpected phenomena, which show that (i) the parameters of the two techniques are quite different, and (ii) within each technique, there are large gaps between the VC-dimension, the primal shatter dimension, and the combinatorial dimension. Some of these gaps reflect our present inability to tighten the bounds on the corresponding parameters, but most of them are "genuine", and we provide lower bounds that establish the gaps.

For vertical decomposition, the combinatorial dimension is only 2d, as easily follows from the definition. We prove that the global growth function is at most $2^{O(d^3)}n^{d(d+1)}$, so the primal shatter dimension is at most d(d+1), and that the VC-dimension is at least $1+\frac{1}{2}d(d+1)$ and at most $O(d^3)$ (the constants of proportionality are absolute and rather small). Although we do not believe that the gap between the lower and upper bounds on the VC-dimension is really so large, we were unable to obtain a tighter upper bound on the VC-dimension, and do not know what is the true asymptotic growth of this parameter (in terms of its dependence on d). The local growth function is only $O(4^dn^{2d}/d^{7/2})$.

For bottom-vertex triangulation, both the primal shatter dimension and the combinatorial dimension are $\Theta(d^2)$, but there is still a significant gap between them: The combinatorial dimension is $\frac{1}{2}d(d+3)$,

whereas (i) the primal shatter dimension is at most d(d+1), and (ii) the VC-dimension is at least d(d+1); we do not know whether these two quantities are equal, and in fact do not even know whether the VC-dimension is $O(d^2)$ (here standard arguments imply that it is $O(d^2 \log d)$). We also bound the local growth function by n^d .

The bound on the local growth function for vertical decomposition is new. The bound for vertical decomposition is a drastic improvement from the earlier bounds (such as in [CEGS91]), in terms of its dependence on d, and we regard it as one of the significant contributions of this work. It is obtained using several fairly simple yet crucial observations concerning the structure of the vertical decomposition in an arrangement of hyperplanes. We regard this part of the paper as being of independent interest, and believe that it will find applications in further studies of the structure and complexity of vertical decompositions and their applications.

Our results: Point location. These findings have implications for the quality of random sampling for decompositions of arrangements of hyperplanes. That is, in view of our current state of knowledge, the best approach (with some caveats) is to use vertical decomposition, and analyze it via the Clarkson–Shor technique, in the sense that we can then ensure the desired sampling quality while choosing a much smaller random sample.

This will be significant in our main application, to point location in an arrangement of n hyperplanes in \mathbb{R}^d . We show that the (fastest) query cost in Meiser's algorithm can be improved, from $O(d^4 \log n)$ to $O(d^3 \log n)$, if one uses vertical decomposition instead of bottom-vertex triangulation (which is the one used in [Mei93]), and only wants to ensure that the problem size goes down by (at least) a factor of 2 in each recursive step (which is the best choice for obtaining fast query time).

In addition, we give a detailed and rigorous analysis of the tradeoff between the query time and the storage size (and preprocessing cost), both in the context of Meiser's algorithm (which, as noted, uses bottom-vertex triangulation), and ours (which uses vertical decomposition). Meiser's study does not provide such an analysis, and, as follows from our analysis in Section 5, the storage bound asserted in [Mei93] (for the query time mentioned above) appears to be incorrect. The storage bound has been improved, in a follow-up study of Liu [Liu04], to $O(n^d)$, but the constant of proportionality is $d^{O(d^3)}$.

We do not discuss here the second application of our analysis, namely to the decision complexity of k-SUM, as it is presented in a separate companion paper [ES17], and in the more recent work by Kane et al. [KLM17] (where the latter work is applicable only in certain restricted scenarios).

As far as we can tell, the existing literature lacks precise details of the preprocessing stage, including a sharp analysis of the storage and preprocessing costs. (For example, Meiser's work [Mei93] completely skips this analysis, and consequently misses the correct trade-off between query and storage costs.) One feature of our analysis is a careful and detailed description of (one possible simple version of) this preprocessing stage. We regard this too as an independent (and in our opinion, significant) contribution of this work.

The improvement that we obtain by using vertical decomposition (instead of bottom vertex triangulation) is a consequence of the ability to use a sample of smaller size (and still guarantee the desired quality). It comes with a cost, though, since (the currently best known upper bound on) the complexity of vertical decomposition is larger than the bound on the complexity of bottom-vertex triangulation. Specifically, focusing only on the dependence on n, the complexity of bottom-vertex triangulation is $O(n^d)$, but the best known upper bound on the complexity of vertical decomposition is $O(n^{2d-4})$ [Kol04].

Degeneracies. Another feature of our work is that it handles arrangements that are not in general position. This requires some care in certain parts of the analysis, as detailed throughout the paper. One

motivation for handling degeneracies is the companion study [ES17] of the k-SUM problem, in which the hyperplanes that arise are very much not in general position.

Optimistic sampling. We also consider situations in which we do not insist that the entire decomposition of the arrangement of a random sample be a (1/r)-cutting, but only require that the cell of the decomposition that contain a prespecified point q have conflict list of size at most n/r. This allows us to use a slightly smaller sample size (smaller by a logarithmic factor), which leads to a small improvement in the cost of a point-location query. It comes with a cost, of some increase in the storage of the structure. We provide full analysis of this approach in Section 5.

The recent work of Kane et al. Very recently, in a dramatic breakthrough, Kane et al. [KLM17] presented a new approach to point location in arrangements of hyperplanes in higher dimensions, based on tools from active learning. Although not stated explicitly in their work, they essentially propose a new cell decomposition technique for such arrangements, which is significantly simpler than the two techniques studied here (bottom-vertex triangulation and vertical decomposition), and which, when applied to a suitable random sample of the input hyperplanes, has (with constant probability) the cutting property (having conflict lists of small size). However, their approach only works for "low-complexity" hyperplanes, namely hyperplanes that have integer coefficients whose tuple has small L₁-norm.² Moreover, the analysis in [KLM17] only caters to the linear decision tree model that we have already mentioned earlier. Nevertheless, when the input hyperplanes do have low complexity, the machinery in [KLM17] can be adapted to yield a complete solution in the RAM model, for point location in such arrangements. We present this extension in Section 5, using a suitable adaptation of our general point-location machinery.

Paper organization. We begin in Section 2 with the analysis of random sampling, focusing mainly on the Clarkson-Shor approach. We then study bottom-vertex triangulation in Section 3, including its representation and complexity, and the various associated sampling parameters. An analogous treatment of vertical decomposition is given in Section 4. Finally, in Section 5, we present the point location algorithms, for both decomposition methods considered here, including the improvement that cen be obtained from optimistic sampling, and the variant for low-complexity hyperplanes.

2 Random sampling

In this section we review various basic techniques for analyzing the quality of a random sample, focusing (albeit not exclusively) on the context of decompositions of arrangements of hyperplanes. We also add a few partially novel ingredients to the cauldron.

As mentioned in the introduction, there are two main analysis techniques for random sampling, one based on the VC-dimension or the primal shatter dimension of a suitably defined range space, and one that focuses only on definable ranges, namely those that arise in a canonical decomposition associated with some subset of the input. In this section we only briefly review the first approach, and then spend most of the section on a careful analysis of the second one. This latter technique, known as the Clarkson-Shor sampling technique (originally introduced in Clarkson [Cla87] and further developed in

²Kane et al. use a more general notion of "low inference dimension", and show that low-complexity hyperplanes do have low inference dimension.

Clarkson and Shor [CS89]), has been thoroughly studied in the past (it is about 30 years old by now), but the analysis presented here still has some novel features:

- (A) It aims to calibrate in a precise manner the dependence of the various performance bounds on the dimension d of the ambient space (in most of the earlier works, some aspects of this dependence were swept under the rug, and were hidden in the $O(\cdot)$ notation).
- (B) It offers an alternative proof technique that is based on *double sampling*. This method has been used in the work of Vapnik and Chervonenkis [VC71, VC13] and the proof of Haussler and Welzl [HW87] of the ε -net theorem. It is also (implicitly) used in the work of Chazelle and Friedman [CF90] in the context of the Clarkson-Shor framework.
- (C) We also study the scenario where we do not care about the quality of the sample in terms of how small are the conflict lists of all the cells of the decomposition, but only of the cell that contains some fixed pre-specified point. This allows us to use smaller sample size, and thereby further improve the performance bounds. As in the introduction, we refer to this approach as *optimistic sampling*.

2.1 Sampling, VC-dimension and ε -nets

We use the following sampling model, which is the one used in the classical works on random sampling, e.g., in Haussler and Welzl [HW87].

Definition 2.1. Let H be a finite set of objects. For a target size ρ , a ρ -sample is a random sample $R \subseteq H$, obtained by ρ independent draws (with repetition) of elements from H.

In this model, since we allow repetitions, the size of R is not fixed (as it was in the original analysis in [Cla87, CS89]); it is a random variable whose value is at most ρ .

The oldest approach for guaranteeing high-quality sampling is based on the following celebrated result of Haussler and Welzl. In its original formulation, the bound on the sample size is slightly larger; the improved dependence on the VC-dimension comes from Blumer et al. [BEHW89] (see [JK92] for a matching lower bound, and see also [PA95]).

Theorem 2.2 (ε -net theorem, Haussler and Welzl [HW87]). Let (H, \mathcal{R}) be a range space of VC-dimension δ , and let $0 < \varepsilon \le 1$ and $0 < \varphi < 1$ be given parameters. Let N be an m-sample, where

$$m \ge \max\left(\frac{4}{\varepsilon}\log\frac{4}{\varphi}, \frac{8\delta}{\varepsilon}\log\frac{16}{\varepsilon}\right).$$

Then N is an ε -net for H with probability at least $1-\varphi$.

Remark 2.3. A variant of the ε -net theorem also holds for spaces with primal shattering dimension δ_0 , except that the sample size has to be slightly larger. Specifically, for the assertion of Theorem 2.2 to hold, the required sample size is $\Theta(\frac{1}{\varepsilon}\log\frac{1}{\varphi}+\frac{\delta_0}{\varepsilon}\log\frac{\delta_0}{\varepsilon})$. That is, δ_0 also appears in the second logarithmic factor. See [Har11] for details.

2.2 The Clarkson-Shor framework

We present the framework in a more general and abstract setting than what we really need, in the hope that some of the partially novel features of the analysis will find applications in other related problems.

Let H be a set of m objects, which are embedded in some space E. We consider here a general setup where each subset $I \subseteq H$ defines a decomposition of E into a set ΞI of canonical *cells*, such that the following properties hold.

- (a) There exists an integer b > 0 such that, for each $I \subseteq H$ and for each cell $\sigma \in \Xi I$, there exists a subset $J \subseteq I$ of size at most b such that $\sigma \in \Xi J$. A smallest such set J is called a *defining set* of σ , and is denoted as $\mathsf{D}(\sigma)$. Note that in degenerate situations $\mathsf{D}(\sigma)$ may not be uniquely defined, but it is uniquely defined if we assume general position. In this paper we allow degeneracies, and when $\mathsf{D}(\sigma)$ is not unique, any of the possible defining sets can be used. The minimum value of b satisfying this property is called the *combinatorial dimension* of the decomposition.
- (b) For any $I \subseteq H$ and any cell $\sigma \in \Xi I$, an object $f \in H$ conflicts with σ , if σ is not a cell of $\Xi D(\sigma) \cup \{f\}$; that is, the presence of f prevents the creation of σ in the decomposition corresponding to the augmented set. The set of objects in H that conflict with σ is called the *conflict list* of σ , and is denoted by $K(\sigma)$. We always have $D(\sigma) \cap K(\sigma) = \emptyset$ for every defining set $D(\sigma)$ of σ .

Example 2.4. Consider the case where H is a set of m lines in the plane, and the plane decomposition that a subset $I \subseteq H$ induces is the standard *vertical decomposition* of $\mathcal{A}(I)$, as discussed in the introduction. Each cell in ΞH is a *vertical trapezoid*, defined by a subset of at most b=4 input lines. See Figure 2.1. The conflict list $\mathsf{K}(\sigma)$ of a vertical trapezoid σ is the set of lines in H that intersect the interior of σ . In degenerate situations, we may have additional lines that pass through vertices of σ without crossing its interior. Such lines are not included in $\mathsf{K}(\sigma)$, but may be part of an alternative defining set of σ , see Figure 2.1 (D).

We assume that the decomposition satisfies the following two conditions, sometimes referred to as the *axioms* of the framework.

- (i) For any $R \subseteq H$ and for any $\sigma \in \Xi R$, we have $\mathsf{D}(\sigma) \subseteq R$, for some defining set $\mathsf{D}(\sigma)$ of σ , and $\mathsf{K}(\sigma) \cap R = \emptyset$.
- (ii) For any $R \subseteq H$, if $\mathsf{D}(\sigma) \subseteq R$, for some defining set $\mathsf{D}(\sigma)$ of σ , and $\mathsf{K}(\sigma) \cap R = \emptyset$, then $\sigma \in \Xi R$.

When these conditions hold, the decomposition scheme *complies* with the analysis technique (or the framework) of Clarkson and Shor [CS89] (see also [Har11, Chapter 8]). These conditions do hold for the two decomposition schemes considered in this paper, where the objects of H are hyperplanes in $E = \mathbb{R}^d$, and the decomposition is either bottom-vertex triangulation or vertical decomposition.

2.3 Double sampling, exponential decay, and cuttings

2.3.1 Double sampling

One of the key ideas in our analysis is *double sampling*. This technique has already been used in the original analysis of Vapnik and Chervonenkis from 1968 (see the translated and republished version

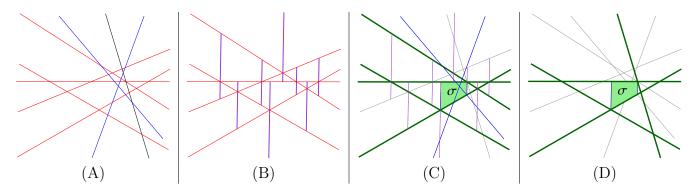


Figure 2.1: (A) Lines. (B) Vertical decomposition of the red lines. (C) Defining set for a vertical trapezoid σ , and its conflict list (the blue lines). (D) An alternative defining set for σ .

[VC13]) in the context of VC-dimension. In the context of the Clarkson-Shor framework it was used implicitly by Chazelle and Friedman [CF90]. The technique is based on the intuition that two independent random samples from the same universe (and of the same target size) should look similar, in the specific sense that the sizes of their intersections with any subset of the universe, of a suitable size, should not differ much from one another.

We need the following simple technical lemma.

Lemma 2.5. Let R_1 and R_2 be two independent ρ -samples from the same universe H, and consider the merged sample $R = R_1 \cup R_2$. Let $B \subseteq H$ be a subset of m elements. If $\rho \ge 2m$ then

$$\mathbf{Pr}\Big[B\subseteq R_1\mid B\subseteq R\Big]\geq \frac{1}{3^m}.$$

Proof: Let A denote the event $B \subseteq R$. Each point π in our probability space is an ordered sequence of 2ρ draws: the ρ draws of R_1 followed by the ρ draws of R_2 . The point π is in A if every member of B appears at least once in π . We define two sequences of 2ρ draws to be equivalent if one is a permutation of the other, and partition A into the equivalence classes of this relation, so that each class consists of all the $(2\rho)!$ shuffles of (the indices of) some fixed sequence. In each class, each member of B appears in R some fixed number (≥ 1) of times. Fix one such class A_1 . We estimate the conditional probability $\Pr[B \subseteq R_1 \mid A_1]$ from below, by deriving a lower bound for the number of shuffles in which every member of B appears at least once in R_1 . To do so, pick an arbitrary sequence σ in A_1 , and choose m (distinct) indices i_1, i_2, \ldots, i_m such that σ_{i_k} is the k-th element of B. (In general, this choice is not necessarily unique, in which case we arbitrarily pick one of these choices.) If the shuffle brings all these indices into R_1 (the first ρ indices) then the event $B \subseteq R_1$ holds. The number of such shuffles is $\binom{\rho}{m} m!(2\rho - m)!$. That is,

$$\mathbf{Pr}\Big[B \subseteq R_1 \mid A_1\Big] \ge \frac{\binom{\rho}{m}m!(2\rho - m)!}{(2\rho)!} \\
= \frac{\rho!}{(\rho - m)!} \cdot \frac{(2\rho - m)!}{(2\rho)!} \\
= \frac{\rho}{2\rho} \cdot \frac{\rho - 1}{2\rho - 1} \cdot \cdot \cdot \cdot \frac{\rho - m + 1}{2\rho - m + 1} \\
\ge \left(\frac{\rho - m + 1}{2\rho - m + 1}\right)^m \ge \frac{1}{3^m},$$

where the last inequality follows from our assumption that $\rho \geq 2m$. Since this inequality holds for every class A_1 within A, it also holds for A; that is,

$$\mathbf{Pr}\Big[B\subseteq R_1\mid A\Big]\geq \frac{1}{3^m},$$

as claimed.

Remark 2.6. The lower bound in Lemma 2.5 holds also if instead of conditioning on the event $A = B \subseteq R$ we condition on an event $A' \subseteq A$, where A' is closed under shuffles of the draws. That is, if some sequence π of 2ρ draws is in A' then every permutation of π should also be in A'. We use this observation in the proof of Lemma 2.7 below.

2.3.2 The exponential decay lemma

For an input set H of size n, and for parameters ρ and $t \ge 1$, we say that a cell σ , in the decomposition of a ρ -sample from H, is ℓ -heavy if the size of its conflict list is at least $\ell n/\rho$. (Note that ℓ -heaviness depends on ρ too; we will apply this notation in contexts where ρ has been fixed.)

Lemma 2.7 below is a version of the exponential decay lemma, which gives an upper bound on the expected number of ℓ -heavy cells in the decomposition of a ρ -sample from H. The original proof of the lemma was given by Chazelle and Friedman [CF90]; our proof follows the one in Har-Peled [Har16]. Other instances and variants of the exponential decay lemma can be found, e.g., in [AMS98, CMS93].

Before proceeding, recall the definition of the global growth function, which bounds the number of (definable or non-definable) ranges in any subset of H of a given size. In the rest of this section, we replace it by a "local" version, which provides, for each integer m, an upper bound on the number of cells in the decomposition of any subset I of at most m elements of H. We denote this function as u(m); it is simply

$$u(m) = \max_{I \subseteq H, |I| = m} |\Xi I|.$$

Lemma 2.7 (Exponential decay lemma). Let H be a set of n objects with an associated decomposition scheme of combinatorial dimension b that complies with the Clarkson-Shor framework, and with local growth function $u(m) \leq 2^{\alpha}m^{\beta}$, for some parameters α and $\beta \geq 1$. Let R be a ρ -sample, for some $\rho \geq 4b$, let $\ell > 1$ be arbitrary, and let $\Xi_{>\ell}(R)$ be the set of all ℓ -heavy cells of ΞR . Then

$$\mathbf{E}[|\Xi_{\geq \ell}(R)|] \le 3^b 2^{\alpha-\beta} \rho^{\beta} e^{-\ell/2}.$$

Proof: Consider R as the union of two independent $(\rho/2)$ -samples R_1 and R_2 . Let σ be a cell in ΞR . By the axioms of the Clarkson-Shor framework, R contains at least one defining set $D = \mathsf{D}(\sigma)$, and $K \cap R = \emptyset$ where $K = \mathsf{K}(\sigma)$. Let D_1, \ldots, D_y be all the possible defining sets of σ , and let A_i , for $i = 1, \ldots, y$, be the event that $D_i \subseteq R$ but $D_j \not\subseteq R$ for j < i. Then we have

$$\mathbf{Pr}\left[\sigma \in \Xi R_{1} \mid \sigma \in \Xi R\right] = \frac{\mathbf{Pr}\left[\sigma \in \Xi R_{1} \land \sigma \in \Xi R\right]}{\mathbf{Pr}\left[\sigma \in \Xi R\right]} \\
= \frac{\sum_{i=1}^{y} \mathbf{Pr}\left[\sigma \in \Xi R_{1} \land A_{i} \land (K \cap R = \emptyset)\right]}{\mathbf{Pr}\left[\sigma \in \Xi R\right]} \\
= \frac{\sum_{i=1}^{y} \mathbf{Pr}\left[\sigma \in \Xi R_{1} \mid A_{i} \land (K \cap R = \emptyset)\right] \mathbf{Pr}\left[A_{i} \land (K \cap R = \emptyset)\right]}{\mathbf{Pr}\left[\sigma \in \Xi R\right]} \\
= \sum_{i=1}^{y} \mathbf{Pr}\left[\sigma \in \Xi R_{1} \mid A_{i} \land (K \cap R = \emptyset)\right] \mathbf{Pr}\left[A_{i} \mid \sigma \in \Xi R\right] \\
\geq \sum_{i=1}^{y} \mathbf{Pr}\left[D_{i} \subseteq R_{1} \mid A_{i} \land (K \cap R = \emptyset)\right] \mathbf{Pr}\left[A_{i} \mid \sigma \in \Xi R\right].$$

We can now apply Lemma 2.5 and the following Remark 2.6; they apply since (i) each conditioning event $(D_i \subseteq R) \land (\forall_{j < i} (D_j \not\subseteq R)) \land (K \cap R = \emptyset)$ is contained in the corresponding event $D_i \subseteq R$, and is invariant under permutations of the draws, and (ii) $|R_1| = \rho/2 \ge 2b \ge 2|D|$. They imply that

$$\Pr[D_i \subseteq R_1 \mid A_i \land (K \cap R = \emptyset)] \ge 1/3^b,$$

for i = 1, ..., y. Furthermore, $\sum_{i=1}^{y} \mathbf{Pr}[A_i \mid \sigma \in \Xi R] = 1$, as is easily checked, so we have shown that

$$\Pr\left[\sigma \in \Xi R_1 \mid \sigma \in \Xi R\right] \ge 1/3^b.$$

Expanding this conditional probability and rearranging, we get

$$\mathbf{Pr}[\sigma \in \Xi R] \leq 3^b \mathbf{Pr}[\sigma \in \Xi R_1 \land \sigma \in \Xi R]$$
.

Now, if σ is ℓ -heavy with respect to R (i.e., $\kappa := |\mathsf{K}(\sigma)| \ge \ell n/\rho$), then

$$\mathbf{Pr}\left[\sigma \in \Xi R \mid \sigma \in \Xi R_1\right] = \mathbf{Pr}\left[\mathsf{K}(\sigma) \cap R_2 = \emptyset\right] = (1 - \kappa/n)^{\rho/2} \le e^{-\kappa\rho/(2n)} \le e^{-\ell/2}. \tag{2.1}$$

Let \mathcal{F} denote the set of all possible cells that arise in the decomposition of some sample of H, and let $\mathcal{F}_{>\ell} \subseteq \mathcal{F}$ be the set of all cells with $|K(\sigma)| \ge \ell n/\rho$. We have

$$\mathbf{E}[|\Xi_{\geq \ell}(R)|] = \sum_{\sigma \in \mathcal{F}_{\geq \ell}} \mathbf{Pr}[\sigma \in \Xi R] \leq \sum_{\sigma \in \mathcal{F}_{\geq \ell}} 3^{b} \mathbf{Pr}[\sigma \in \Xi R_{1} \land \sigma \in \Xi R]$$

$$= 3^{b} \sum_{\sigma \in \mathcal{F}_{\geq \ell}} \mathbf{Pr}[\sigma \in \Xi R \mid \sigma \in \Xi R_{1}] \mathbf{Pr}[\sigma \in \Xi R_{1}] \leq 3^{b} e^{-\ell/2} \sum_{\sigma \in \mathcal{F}_{\geq \ell}} \mathbf{Pr}[\sigma \in \Xi R_{1}]$$

$$\leq 3^{b} e^{-\ell/2} \sum_{\sigma \in \mathcal{F}} \mathbf{Pr}[\sigma \in \Xi R_{1}] = 3^{b} e^{-\ell/2} \mathbf{E}[|\Xi R_{1}|] \leq 3^{b} e^{-\ell/2} u(|R_{1}|)$$

$$\leq 3^{b} e^{-\ell/2} 2^{\alpha} (\rho/2)^{\beta} \leq 3^{b} 2^{\alpha-\beta} \rho^{\beta} e^{-\ell/2},$$

as asserted.

2.3.3 Cuttings from exponential decay

The following central lemma provides a lower bound on the (expected) size of a sample R that guarantes, with controllable probability, that the associated space decomposition is a (1/r)-cutting. In the general setting in which we analyze the Clarkson-Shor framework, this simply means that each cell of ΞR has conflict list of size at most n/r.

Lemma 2.8. Let H be a set of n objects with an associated decomposition scheme of combinatorial dimension b that complies with the Clarkson–Shor framework, with local growth function $u(m) \leq 2^{\alpha} m^{\beta}$, for some parameters α and $\beta \geq 1$. Let $\varphi \in (0,1)$ be some confidence parameter. Then, for

$$\rho \ge \max\left(4r\left(b\ln 3 + (\alpha - \beta)\ln 2 + \ln\frac{1}{\varphi}\right), 8r\beta\ln(4r\beta)\right),$$

a ρ -sample induces a decomposition ΞR that is a (1/r)-cutting with probability $\geq 1 - \varphi$.

Proof: By Lemma 2.7 (which we can apply since $\rho \geq 4r \left(b \ln 3 + (\alpha - \beta) \ln 2 + \ln \frac{1}{\varphi}\right) \geq 4b$), the expected number of cells in ΞR that are ℓ -heavy is $\mathbf{E}\left[|\Xi_{\geq \ell}(R)|\right] \leq 3^b 2^{\alpha-\beta} \rho^\beta e^{-\ell/2}$. We now require that $\ell n/\rho \leq n/r$, and that the probability to obtain at least one heavy cell be smaller than φ . We satisfy the first constraint by taking $\ell = \rho/r$, and we satisfy the second by making the expected number of heavy cells be smaller than φ . Solving for this latter constraint, we get

$$3^{b}2^{\alpha-\beta}\rho^{\beta}e^{-\rho/(2r)} \leq \varphi \iff b\ln 3 + (\alpha-\beta)\ln 2 + \beta\ln\rho - \frac{\rho}{2r} \leq \ln\varphi$$

$$\iff \rho \geq 2r\left(b\ln 3 + (\alpha-\beta)\ln 2 + \beta\ln\rho + \ln\frac{1}{\varphi}\right).$$

We assume that ρ satisfies the conditions in the lemma. If the term $\beta \ln \rho$ is smaller than the sum of the other terms (in the parenthesis), then the inequality holds since $\rho \geq 4r \left(b \ln 3 + (\alpha - \beta) \ln 2 + \ln \frac{1}{\varphi}\right)$. Otherwise, the inequality holds since $\rho \geq 8r\beta \ln(4r\beta)$, and for such values of ρ we have $\rho \geq 4r\beta \ln \rho$, as is easily checked.³

It follows that, with this choice of ρ , the probability of any heavy cell to exist in ΞR is at most φ (by Markov's inequality), and the claim follows.

2.3.4 Optimistic sampling

In this final variant of random sampling, we focus only on the cell in the decomposition that contains some prespecified point, and show that we can ensure that this cell is "light" (with high probability) by using a smaller sample size. Note that here, as can be expected, the local growth function plays no role.

Lemma 2.9. Let H be a set of n objects with an associated decomposition scheme of combinatorial dimension b that complies with the Clarkson-Shor framework, and let R be a ρ -sample from H. Then, for any fixed point q and any $\ell > 1$, we have

$$\Pr[|K(\sigma(q,R))| \ge \ell n/\rho] \le 3^b e^{-\ell/2},$$

where $\sigma = \sigma(q, R)$ is the cell in ΞR that contains q.

Proof: We regard R as the union of two independent random $(\rho/2)$ -samples R_1 , R_2 , as in the proof of Lemma 2.7, where it is shown that, for cells σ that are ℓ -heavy, we have

$$\mathbf{Pr}\left[\sigma \in \Xi R\right] \leq 3^b \, \mathbf{Pr}\left[\sigma \in \Xi R_1 \, \wedge \, \sigma \in \Xi R\right] \leq 3^b e^{-\ell/2} \, \mathbf{Pr}\left[\sigma \in \Xi R_1\right].$$

Let $\mathcal{F}_{\geq \ell}(q)$ be the set of all possible canonical cells that are defined by subsets of H, contain q, and are ℓ -heavy (for the fixed choice of ρ). We have

$$\begin{split} \mathbf{Pr}\big[\big|\mathsf{K}(\sigma(q,R))\big| &\geq \ell n/\rho\big] = \sum_{\sigma \in \mathcal{T}_{\geq \ell}(q)} \mathbf{Pr}\big[\sigma \in \Xi R\big] \\ &\leq 3^b e^{-\ell/2} \sum_{\sigma \in \mathcal{T}_{\geq \ell}(q)} \mathbf{Pr}[\sigma \in \Xi R_1] \leq 3^b e^{-\ell/2}, \end{split}$$

since the events in the last summation are pairwise disjoint (only one cell in $\mathcal{F}_{\geq \ell}(q)$ can show up in ΞR_1).

Corollary 2.10. Let H be a set of n objects with an associated decomposition scheme of combinatorial dimension b that complies with the Clarkson-Shor framework, and let $\varphi \in (0,1)$ be a confidence parameter. Let R be a ρ -sample from H, for $\rho \geq 2r(b \ln 3 + \ln \frac{1}{\varphi})$. For any prespecified query point q, we have $\Pr[|K(\sigma(q,R))| > n/r] \leq \varphi$, where $\sigma = \sigma(q,R)$ is the canonical cell in ΞR that contains q.

Proof: Put $\ell = \rho/r \ge 2(b \ln 3 + \frac{1}{\varphi})$. By Lemma 2.9, we have $\Pr[|K(\sigma(q,R))| > n/r] \le 3^b e^{-\ell/2} \le \varphi$, as claimed.

Remark 2.11. The significance of Corollary 2.10 is that it requires a sample size of O(br), instead of $\Theta(br \log(br))$, if we are willing to consider only the single cell σ that contains q, rather than all cells in ΞR . We will use this result in Section 5 to obtain a slightly improved point-location algorithm.

The results of this section are summarized in the table in Figure 2.2.

³The general statement is that if $\rho \ge 2x \ln x$ then $\rho \ge x \ln \rho$. We will use this property again, in the proof of Lemma 3.7.

Technique	Sample size	parameters	
$\varepsilon\text{-net}$	$O(\delta r \log r)$	δ: VC-dim.	
Shatter dim.	$O(\delta_0 r \log(\delta_0 r))$	δ_0 : Shatter dim.	
Combinatorial dim.	$O(r(b + \alpha + \beta \log(\beta r)))$ Lemma 2.8	b: combinatorial dim. Number of cells in the decomposition is (α, β) -growing.	
Optimistic sampling	O(rb) Corollary 2.10	Relevant cell has conflict list of size $\leq n/r$ w.h.p.	

Figure 2.2: The different sizes of a sample that are needed to guarantee (with some fixed probability) that the associated decomposition is a (1/r)-cutting. The top two results and the third result are in different settings. In particular, the guarantee of the first two results is much stronger—any canonical (definable or non-definable) cell that avoids the sample is "light", while the third result only guarantees that the cells in the generated canonical decomposition of the sample are light. The fourth result caters only to the single cell that contains a specified point.

3 Bottom-vertex triangulation

We now apply the machinery developed in the preceding section to the first of the two canonical decomposition schemes, namely, to bottom-vertex triangulations, or BVT, for short.

3.1 Construction and number of simplices

Let H be a set of n hyperplanes in \mathbb{R}^d with a suitably defined generic coordinate frame. For simplicity, we describe the decomposition for the entire set H. Let C be a bounded cell of $\mathcal{A}(H)$ (unbounded cells are discussed later on). We decompose C into pairwise openly disjoint simplices in the following recursive manner. Let w be the bottom vertex of C, that is, the point of C with the smallest x_d -coordinate (we assume that there are no ties as we use a generic coordinate frame). We take each facet C' of C that is not incident to w, and recursively construct its bottom-vertex triangulation. To do so, we regard the hyperplane h' containing C' as a copy of \mathbb{R}^{d-1} , and recursively triangulate $\mathcal{A}(H')$ within h', where $H' = \{h \cap h' \mid h \in H \setminus \{h'\}\}$. We complete the construction by taking each (d-1)-simplex σ' in the resulting triangulation of C' (which is part of the triangulation of $\mathcal{A}(H')$ within h'), and by connecting it to w (i.e., forming the d-simplex $\operatorname{conv}(\sigma' \cup \{w\})$). Repeating this step over all facets of C not incident to w, and then repeating the whole process within each (bounded) cell of $\mathcal{A}(H)$, we obtain the bottom-vertex triangulation of $\mathcal{A}(H)$. The recursion terminates when d=1, in which case $\mathcal{A}(H)$ is just a partition of the line into intervals and points, which serves, as is, as the desired bottom-vertex decomposition. We denote the overall resulting triangulation as $\mathsf{BVT}(H)$. See [Cla88, Mat02] for more details. The resulting BVT is a simplicial complex [Spa66].

To handle unbounded cells, we first add two hyperplanes π_d^- , π_d^+ orthogonal to the x_d -axis, so that all vertices of $\mathcal{A}(H)$ lie below π_d^+ and above π_d^- . For each original hyperplane h', we recursively triangulate $\mathcal{A}(H')$ within h', where $H' = \{h \cap h' \mid h \in H \setminus \{h'\}\}$, and we also recursively triangulate $\mathcal{A}(H^+)$ within π_d^+ , where $H^+ = \{h \cap \pi_d^+ \mid h \in H\}$. This triangulation is done in exactly the same manner, by adding artificial (d-2)-flats, and all its simplices are either bounded or "artificially-bounded" (i.e., contained in an artificial bounding flat). We complete the construction by triangulating the d-dimensional cells in the arrangement of $H \cup \{\pi_d^-, \pi_d^+\}$. The addition of π_d^- guarantees that each such cell C has a bottom

vertex w. (Technically, since we want to ensure that each cell has a unique bottom vertex, we slightly tilt π_d^- , to make it non-horizontal, thereby ensuring this property, and causing no loss of generality.) We triangulate C by generating a d-simplex $\operatorname{conv}(\sigma' \cup \{w\})$ for each (d-1)-simplex σ' in the recursive triangulation of the facets on ∂C which are not incident to w (none of these facets lies on π_d^- , but some might lie on π_d^+). In the arrangement defined by the original hyperplanes of H only, the unbounded simplices in this triangulation correspond to simplices that contain features of the artificial hyperplanes added at various stages of the recursive construction.

Number of simplices. We count the number of d-simplices in the BVT in a recursive manner, by charging each d-simplex σ to the unique (d-1)-simplex on its boundary that is not adjacent to the bottom vertex of σ .

Lemma 3.1. For any hyperplane $h \in H \cup \{\pi_d^+\}$, each (d-1)-simplex ψ that is recursively constructed within h gets charged at most once by the above scheme.

Proof: Consider the cell C' of $\mathcal{A}(H \cup \{\pi_d^+\} \setminus \{h\})$ that contains ψ in its interior, and let p be the lowest vertex of C'. Assume first that h does not pass through p. The hyperplane h splits C' into two cells C_1, C_2 of $\mathcal{A}(H)$. One of these cells, say C_1 , has p as its bottom vertex. The bottom vertex of the other cell C_2 must lie on h. In other words, ψ gets charged by a full-dimensional simplex within C_1 but not within C_2 . If h passes through p, ψ cannot be charged at all.

Note that the proof also holds in degenerate situations, where p is incident to more than d hyperplanes of H.

The (d-1)-simplices that are being charged lie on original hyperplanes or on π_d^+ . This implies the following lemma.

Lemma 3.2. (a) The number of d-simplices in BVT(R), for any set R of ρ hyperplanes in d dimensions, is at most ρ^d .

(b) The total number of simplices of all dimensions in $\mathsf{BVT}(R)$ is at most $e\rho^d$.

Proof: (a) The analysis given above implies that the number of d-simplices in BVT(R) is at most the overall number of (d-1)-simplices in the bottom-vertex triangulations within the hyperplanes of R, plus the number of (d-1)-simplices in the bottom-vertex triangulations within π_d^+ . Hence, if we denote by $BV_d(\rho)$ the maximum number of d-simplices in a bottom-vertex triangulation of a set of ρ hyperplanes in \mathbb{R}^d , we get the recurrence $B_d(\rho) \leq (\rho+1)B_{d-1}(\rho-1)$, and $B_1(\rho) = \rho+1$. The solution of this recurrence is

$$B_d(\rho) \le (\rho+1)\rho(\rho-1)\cdots(\rho-d+3)B_1(\rho-d+1)$$

$$= (\rho+1)\rho(\rho-1)\cdots(\rho-d+3)(\rho-d+2)$$

$$= \rho^d \cdot \left(1 + \frac{1}{\rho}\right) \cdot 1\left(1 - \frac{1}{\rho}\right)\cdots\left(1 - \frac{d-2}{\rho}\right) \le \rho^d.$$

(b) The number of j-flats of $\mathcal{A}(R)$ is $\binom{\rho}{d-j}$, and each j-simplex belongs to the triangulation within some j-flat of $\mathcal{A}(R)$. It follows from (a) that the number of j-simplices in $\mathsf{BVT}(R)$ is at most $\binom{\rho}{d-j}\rho^j$. Summing over all j we get that the total number of simplices in $\mathsf{BVT}(R)$ is bounded by

$$\sum_{j=0}^{d} \binom{\rho}{d-j} \rho^j \le \sum_{j=0}^{d} \frac{\rho^d}{(d-j)!} \le e\rho^d.$$

In particular, the local growth function for bottom vertex triangulation satisfies

$$u(m) \le em^d = 2^{\log e} m^d ;$$

that is, it is (α, β) -growing, where the corresponding parameters are $\alpha = \log e$ and $\beta = d$.

Remark 3.3. The combinatorial dimension of bottom-vertex triangulation is $\frac{1}{2}d(d+3)$ [Mat02]. Indeed, if C(d) denotes the combinatorial dimension of bottom-vertex triangulation in d dimensions, then C(d) = d+1+C(d-1), where the non-recursive term d+1 comes from the d hyperplanes needed to specify the bottom vertex of the simplex, plus the hyperplane h' on which the recursive (d-1)-dimensional construction takes place. This recurrence, combined with C(1) = 2, yields the asserted value. Simplices in unbounded cells require fewer hyperplanes from H to define them.

Plugging the parameters $b = \frac{1}{2}d(d+3)$, $\alpha = O(1)$, $\beta = d$ into Lemma 2.8, we obtain:

Corollary 3.4. Let H be a set of n hyperplanes in \mathbb{R}^d and let $\varphi \in (0,1)$ be some confidence parameter. Then, for $\rho \geq cr(d^2 + d \log r + \ln \frac{1}{\varphi})$, for a suitable absolute constant c, the bottom-vertex triangulation of a ρ -sample is a (1/r)-cutting with probability $\geq 1 - \varphi$.

3.2 The primal shatter dimension and VC-dimension

Let H be a set of n hyperplanes in \mathbb{R}^d . The range space associated with the bottom-vertex triangulation technique is (H, Σ) , where each range in Σ is associated with some (arbitrary, open) d-simplex σ , and is the subset of H consisting of the hyperplanes that cross σ . Clearly, the same range will arise for infinitely many simplices, as long as they have the same set of hyperplanes of H that cross them.

Lemma 3.5 (See [AS00]). (a) The number of full dimensional cells in an arrangement of n hyperplanes in \mathbb{R}^d is at most $\sum_{i=0}^d \binom{n}{i} \leq 2\left(\frac{ne}{d}\right)^d$, where the inequality holds for $n \geq d$.

(b) The number of cells of all dimensions is at most $\sum_{i=0}^{d} {n \choose i} 2^i \leq 2 \left(\frac{2ne}{d}\right)^d$; again, the inequality holds for $n \geq d$.

Proof: See [AS00] for (a). For (b), as in the proof of Lemma 3.2(b), we apply the bound in (a) within each flat formed by the intersection of some subset of the hyperplanes. Since there are at most $\binom{n}{d-j}$ j-dimensional such flats, and at most n-d+j hyperplanes form the corresponding arrangement within

a j-flat, we get a total of at most

$$\begin{split} \sum_{j=0}^{d} \binom{n}{d-j} \sum_{i=0}^{j} \binom{n-d+j}{i} &= \sum_{j=0}^{d} \sum_{i=0}^{j} \frac{n!}{(d-j)!i!(n-d+j-i)!} \\ &= \sum_{j=0}^{d} \sum_{k=0}^{j} \frac{n!}{(d-j)!(j-k)!(n-d+k)!} \\ &= \sum_{j=0}^{d} \sum_{k=0}^{j} \frac{n!(d-k)!}{(d-j)!(j-k)!(n-d+k)!(d-k)!} \\ &= \sum_{j=0}^{d} \sum_{k=0}^{j} \binom{n}{d-k} \binom{d-k}{d-j} \\ &= \sum_{k=0}^{d} \binom{n}{d-k} \sum_{j=k}^{d} \binom{d-k}{d-j} \\ &= \sum_{k=0}^{d} \binom{n}{d-k} 2^{d-k} = \sum_{i=0}^{d} \binom{n}{i} 2^{i} \end{split}$$

cells of all dimensions. The asserted upper bound on this sum is an immediate consequence of (a).

Lemma 3.6. The global growth function $g_d(n)$ of the range space of hyperplanes and simplices in \mathbb{R}^d satisfies $g_d(n) \leq 2^{d+2} \left(\frac{e}{d}\right)^{(d+1)^2} n^{d(d+1)}$. Consequently, the primal shatter dimension of this range space is at most d(d+1).

We can write this bound as $g_d(n) \leq 2^{\alpha} n^{\beta}$, for $\beta = d(d+1)$ and $\alpha = d+2-(d+1)^2 \log(d/e)$ (α is negative when d is large).

Proof: Let σ be a d-simplex, and let C_1, \ldots, C_{d+1} denote the cells of $\mathcal{A}(H)$ that contain the d+1 vertices of σ ; in general, some of these cells may be lower-dimensional, and they need not be distinct. Moreover, the order of the cells is immaterial for our analysis. As is easily seen, the range associated with σ does not change when we vary each vertex of σ within its containing cell. Moreover, since crossing a simplex means intersecting its interior, we may assume, without loss of generality, that all the cells C_i are full-dimensional. It follows that the number of possible ranges is bounded by the number of (unordered) tuples of at most d+1 full-dimensional cells of $\mathcal{A}(H)$. The number of such cells in $\mathcal{A}(H)$ is $T \leq 2\left(\frac{ne}{d}\right)^d$, by Lemma 3.5(a). Hence, using the inequality again, in the present, different context, the number of distinct ranges is

$$\sum_{i=0}^{d+1} {T \choose i} \le 2 \left(\frac{Te}{d+1}\right)^{d+1} \le 2 \left(\frac{2\left(\frac{ne}{d}\right)^d e}{d+1}\right)^{d+1}$$

$$= 2 \left(\frac{2e}{d+1}\right)^{d+1} \left(\frac{e}{d}\right)^{d(d+1)} n^{d(d+1)} \le 2^{d+2} \left(\frac{e}{d}\right)^{(d+1)^2} n^{d(d+1)}.$$

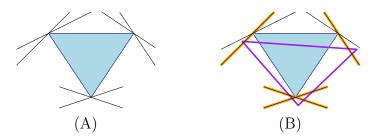


Figure 3.1: Illustration of the proof of Lemma 3.7. (A) The construction. (B) Turning a subset into a simplex range.

3.2.1 Bounds on the VC-dimension

Lemma 3.7. The VC-dimension of the range space of hyperplanes and simplices in \mathbb{R}^d is at least d(d+1) and at most $5d^2 \log d$, for $d \geq 9$.

Proof: Using the bound of Lemma 3.6 on the growth function, we have that if a set of size k is shattered by simplicial ranges then $2^k \leq g_d(k) \leq 2^{d+2} \left(\frac{e}{d}\right)^{(d+1)^2} k^{d(d+1)} \leq k^{d(d+1)}$, for $d \geq 2e$. This in turn is equivalent to $\frac{k}{\ln k} \leq \frac{d(d+1)}{\ln 2}$. Using the easily verified property, already used in the proof of Lemma 2.8, that $x/\ln x \leq u \implies x \leq 2u \ln u$, we conclude that $k \leq 2\frac{d(d+1)}{\ln 2} \ln \left(\frac{d(d+1)}{\ln 2}\right) \leq 5d^2 \log_2 d$, for $d \geq 9$, as can easily (albeit tediously) be verified.

For the lower bound, let σ_0 denote some fixed regular simplex, and denote its vertices as $v_1, v_2, \ldots, v_{d+1}$. For each v_i , choose a set H_i of d hyperplanes that are incident to v_i , so that (i) none of these hyperplanes crosses σ_0 , (ii) they are all nearly parallel to some 'ground hyperplane' $h^{(i)}$ that supports σ_0 at v_i , and the angles that $h^{(i)}$ forms with the vectors $v_i \vec{v}_j$, for $j \neq i$, are all at least some positive constant α (that depends on d but is bounded away from 0), and (iii) the hyperplanes of H_i are otherwise in generic position (except for being concurrent at v_i). The set $H := \bigcup_j H_j$ consists of d(d+1) hyperplanes, and we claim that H can be shattered by simplices.

Indeed, let c_0 denote the center of mass of σ_0 . In a suitable small neighborhood of v_i , the hyperplanes of H_i partition space into 2^d "orthants" (all of which are tiny, flattened slivers, except for the one containing σ_0 and its antipodal orthant), and for each subset H'_i of H_i there is a unique orthant $W(H'_i)$, such that for any point $q \in W(H'_i)$, the segment c_0q crosses all the hyperplanes of H'_i , and no hyperplane of $H_i \setminus H'_i$, see Figure 3.1. It is easily seen that the same property also holds in the following more general context. Perturb σ_0 by moving each of its vertices v_i to a point q_i , sufficiently close to v_i , in any one of the orthants incident to v_i . Then, assuming that the hyperplanes of each H_i are sufficiently 'flattened' near the ground hyperplane $h^{(i)}$, the perturbed simplex $\sigma = \text{conv}(\{q_1, \ldots, q_{d+1}\})$ is such that, for each i, a hyperplane of H_i crosses σ if and only if it crosses the segment c_0q_i .

All these considerations easily imply the desired property. That is, let H' be any subset of H, and put $H'_i := H' \cap H_i$. For each i, choose a point q_i near v_i in the incident orthant that corresponds to H'_i . Then H' is precisely the subset of the hyperplanes of H that are crossed by the simplex whose vertices are q_1, \ldots, q_{d+1} , showing that H is indeed shattered by simplices.

In particular, we have established a fairly large gap between the combinatorial dimension $\frac{1}{2}d(d+3)$ and the VC-dimension (which is at least d(d+1)). The gap exists for any $d \geq 2$, and increases as d grows—for large d the combinatorial dimension is about half the VC-dimension.

4 Vertical decomposition

In this section we study the combinatorial dimension, primal shatter dimension, and VC-dimension of vertical decomposition. In doing so, we gain new insights into the structure of vertical decomposition, and refine the combinatorial bounds on its complexity; these insights are needed for our analysis, but they are of independent interest, and seem promising for further applications.

4.1 The construction

Let H be a set of n hyperplanes in \mathbb{R}^d . The construction of the vertical decomposition (VD for short) of $\mathcal{A}(H)$ works by recursion on the dimension, and is somewhat more involved than the bottom-vertex triangulation. Its main merit is that it also applies to decomposing arrangements of more general (constant-degree algebraic) surfaces, and is in fact the only known general-purpose technique for this generalized task (although we consider it here only in the context of decomposing arrangements of hyperplanes). Moreover, as the analysis in this paper shows, this technique is the "winner" in obtaining faster point-location query time (with a few caveats, noted later).

Let H be a collection of n hyperplanes in \mathbb{R}^d with a suitably defined generic coordinate frame. We can therefore assume, in particular, that there are no vertical hyperplanes in H, and, more generally, that no flat of intersection of any subset of hyperplanes is parallel to any coordinate axis. The vertical decomposition VD(H) of the arrangement $\mathcal{A}(H)$ is defined in the following recursive manner (see [CEGS91, SA95] for the general setup, and [GHMS95, Kol04] for the case of hyperplanes in four dimensions, as well as the companion paper [ES17]). Let the coordinate system be x_1, x_2, \ldots, x_d , and let C be a d-dimensional cell in $\mathcal{A}(H)$. For each (d-2)-face g on ∂C , we erect a (d-1)-dimensional vertical wall passing through g and confined to C; this is the union of all the maximal x_d -vertical line-segments that have one endpoint on g and are contained in C. The walls extend downwards (resp., upwards) from faces q on the top boundary (resp., bottom boundary) of C (faces on the "equator" of C, i.e., faces that have a vertical supporting hyperplane, have no wall erected from them within C). This collection of walls subdivides C into convex vertical prisms, each of which is bounded by (potentially many) vertical walls, and by two hyperplanes of H, one appearing on the bottom portion and one on the top portion of ∂C , referred to as the floor and the ceiling of the prism, respectively; in case C is unbounded, a prism may be bounded by just a single (floor or ceiling) hyperplane of H. More formally (or, rather, in an alternative, equivalent formulation), this step is accomplished by projecting the bottom and the top portions of ∂C onto the hyperplane $x_d = 0$, and by constructing the overlay of these two convex subdivisions (of the projection of C). Each full-dimensional (i.e., (d-1)-dimensional) cell in the overlay, when lifted back to \mathbb{R}^d and intersected with C, becomes one of the above prisms.

Note that after this step, the two bases (or the single base, in case the prism is unbounded) of a prism may have arbitrarily large complexity, or, more precisely, be bounded by arbitrarily many hyperplanes (of dimension d-2). The common projection of the two bases is a convex polyhedron in \mathbb{R}^{d-1} , bounded by at most 2n-1 hyperplanes,⁴ where each such hyperplane is the vertical projection of either an intersection of the floor hyperplane h^- with another original hyperplane h, or an intersection of the ceiling hyperplane h^+ with some other h; this collection might also include $h^- \cap h^+$.

In what follows we refer to these prisms as first-stage prisms. Our goal is to decimate the dependence of the complexity of the prisms on n, and to construct a decomposition so that each of its prisms is bounded by no more than 2d hyperplanes. To do so, we recurse with the construction at the common projection of the bases onto $x_d = 0$. Each recursive subproblem is now (d-1)-dimensional.

⁴We will shortly argue that the actual number of hyperplanes is only at most n-1.

Specifically, after the first decomposition step described above, we project each prism just obtained onto the hyperplane $x_d = 0$, obtaining a (d-1)-dimensional convex polyhedron C', which we vertically decompose using the same procedure described above, only in one lower dimension. That is, we now erect vertical walls within C' from each (d-3)-face of $\partial C'$, in the x_{d-1} -direction. These walls subdivide C' into x_{d-1} -vertical prisms, each of which is bounded by (at most) two facets of C', which form its floor and ceiling (in the x_{d-1} -direction), and by some of the vertical walls. We keep projecting these prisms onto coordinate hyperplanes of lower dimensions, and produce the appropriate vertical walls. We stop the recursion as soon as we reach a one-dimensional instance, in which case all prisms projected from previous steps become line-segments, requiring no further decomposition. We now backtrack, and lift the vertical walls (constructed in lower dimensions, over all iterations), one dimension at a time, ending up with (d-1)-dimensional walls within the original cell C; that is, a (d-i)-dimensional wall is "stretched" in directions x_{d-i+2}, \ldots, x_d (applied in that order), for every $i=2,\ldots,d-1$. See Figure 4.1 for an illustration of the construction.

Each of the final cells is a "box-like" prism, bounded by at most 2d hyperplanes. Of these, two are original hyperplanes (its floor and ceiling in \mathbb{R}^d), two are hyperplanes supporting two x_d -vertical walls erected from some (d-2)-faces, two are hyperplanes supporting two $x_{d-1}x_d$ -vertical walls erected from some (d-3)-faces (within the appropriate lower-dimensional subspaces), and so on.

We apply this recursive decomposition for each d-dimensional cell C of $\mathcal{A}(H)$, and we apply an analogous decomposition also to each lower dimensional cell C' of $\mathcal{A}(H)$, where the appropriate k-flat that supports C' is treated as \mathbb{R}^k , with a suitable generic choice of coordinates. The union of the resulting decompositions is the vertical decomposition $\mathsf{VD}(H)$.

Lemma 4.1. Consider the prisms in the vertical decomposition of a d-dimensional cell C of $\mathcal{A}(H)$. Then (i) Each final prism σ is defined by at most 2d hyperplanes of H. That is, there exists a subset $\mathsf{D}(\sigma) \subseteq H$ of size at most 2d, such that σ is a prism of $\mathsf{VD}(\mathsf{D}(\sigma))$.

(ii) $\mathsf{D}(\sigma)$ can be enumerated as $(h_1^-, h_1^+, h_2^-, h_2^+, \dots, h_d^-, h_d^+)$ (where some of these hyperplanes may be absent), such that, for each $j = d, d-1, \dots, 1$, the floor (resp., ceiling) of the projection of σ processed at dimension j is defined by a sequence of intersections and projections that involve only the hyperplanes $(h_1^-, h_1^+, h_2^-, h_2^+, \dots, h_{d-j}^-, h_{d-j}^+)$ and h_{d-j+1}^- (resp., h_{d-j+1}^+).

Proof: We first establish property (ii) using backward induction on the dimension of the recursive instance. For each dimension j = d, d - 1, ..., 1, we prove that when we are at dimension j, we already have a set D_j of (at most) 2(d-j) original defining hyperplanes (namely, original hyperplanes defining the walls erected so far, in the manner asserted in part (ii)), and that each (lower-dimensional) hyperplane in the current collection H_j of (j-1)-hyperplanes is obtained by an interleaved sequence of

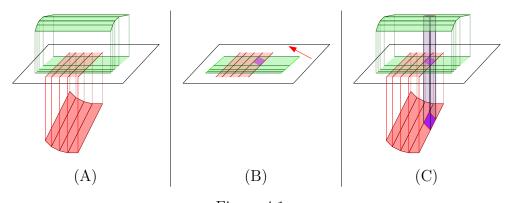


Figure 4.1:

intersections and projections, which are expressed in terms of some subset of the defining hyperplanes and (at most) one additional original hyperplane. This holds trivially initially, for j = d. For j = d - 1we have two defining hyperplanes h_1^- , h_1^+ in D_{d-1} , which contain the floor and ceiling of the prism, respectively. The collection H_{d-1} is obtained by intersecting h_1^- and h_1^+ with the remaining hyperplanes of H (including the intersection $h_1^- \cap h_1^+$), and by projecting all these intersections onto the (d-1)hyperplane $x_d = 0$. Then a new pair of hyperplanes h_2^- and h_2^+ (with shortest vertical distance) are chosen, and thus the floor (resp., ceiling) of the projection of σ is defined is defined by a sequence of intersections and projections that involve $h_1^-, h_1^+, h_2^-, h_2^+$. So the inductive property holds for j = d - 1. In general, when we move from dimension j to dimension j-1 we choose a new floor g_{j+1}^- and a new ceiling g_{i+1}^+ from among the hyperplanes in H_j , gaining two new (original) defining hyperplanes $h_{i+1}^$ and h_{j+1}^+ . We add these new defining hyperplanes to D_j to form D_{j-1} , and intersect each of the floor g_{i+1}^- and ceiling g_{i+1}^+ with the other hyperplanes in H_j , and project all the resulting (j-2)-intersections onto the (j-1)-hyperplane $x_j = 0$, to obtain a new collection H_{j-1} of (j-2)-hyperplanes. Clearly, the inductive properties that we assume carry over to the new sets D_{i-1} and H_{i-1} , so this holds for the final setup in d=1 dimensions. Since each step adds at most two new defining hyperplanes, one for defining the floor and one for defining the ceiling, the claim in (ii) follows. Property (i) follows too because the above construction will produce σ when the input consists of just the hyperplanes of $D(\sigma)$.

An analogous lemma holds for the vertical decomposition of lower dimensional cells of $\mathcal{A}(H)$, except that if the cell C' lies in a (d-k)-flat, we have to replace the original hyperplanes by the intersection of the k hyperplanes defining the flat with all other hyperplanes, and start the recursion in dimension d-k. The following corollary is an immediate consequence.

Corollary 4.2. The combinatorial dimension of the vertical prisms in the vertical decomposition of hyperplanes in \mathbb{R}^d is b = 2d.

Remark 4.3. Although this is marginal in our analysis, it is instructive to note that, even though it only takes at most 2d hyperplanes to define a prism, expressing how the prism is constructed in terms of these hyperplanes is considerably more space consuming, as it has to reflect the sequence of intersections and projections that create each hyperplane that bounds the prism (each of the 2d bounding hyperplanes carries a "history" of the way it was formed, of size O(d)). A naive representation of this kind would require $O(d^2)$ storage per prism. We will bypass this issue when handling point-location queries in Section 5.

4.2 The complexity of vertical decomposition

Our first step is to obtain an upper bound on the complexity of the vertical decomposition, that is, on the number of its prisms. This will also determine the local growth function in the associated Clarkson–Shor framework. Following the presentation in the introduction, we analyze the complexity within a single cell of $\mathcal{A}(H)$, and then derive a global bound for the entire arrangement. As it turns out, this is crucial to obtain a good dependence on d. In contrast, the traditional global analysis, as applied in [CEGS91, SA95], yields a significantly larger coefficient, which in fact is too large for the purpose of the analysis of the point-location mechanism introduced in this paper.

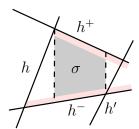
4.2.1 The analysis of a single cell

Let C be a fixed d-dimensional cell of $\mathcal{A}(H)$. With a slight abuse of notation, denote by n the number of its facets (that is, the number of hyperplanes of H that support these facets), and consider the

procedure of constructing its vertical decomposition, as described in Section 4.1. As we recall, the first stage produces vertical prisms, each having a fixed floor and a fixed ceiling. We take each such prism, whose ceiling and floor are contained in two respective hyperplanes h^+ , h^- of H, project it onto the hyperplane $x_d = 0$, and decompose the projection C_{d-1} recursively.

The (d-2)-hyperplanes that bound C_{d-1} are projections of intersections of the form $h \cap h^+$, $h \cap h^-$, for $h \in H \setminus \{h^+, h^-\}$, including also $h^+ \cap h^-$, if it arises. In principle, the number of such hyperplanes is at most 2n-1, but, as shown in the following lemma, the actual number is smaller.

Lemma 4.4. Let σ be a first-stage prism, whose ceiling and floor are contained in two respective hyperplanes h^+ , h^- . Then, for each hyperplane $h \in H$, $h \neq h^+, h^-$, then only one of $g^+ := h^+ \cap h$ or $g^- := h^- \cap h$ can appear on $\partial \sigma$. It is g^+ if C lies below h, and g^- if C lies above h. As a result, the projection C_{d-1} of σ onto $x_d = 0$ has at most n-1 facets.



Proof: Let σ^+ (resp., σ^-) denote the ceiling (resp., floor) of σ . Let f^+ (resp., f^-) denote the facet of C that contains σ^+ (resp., σ^-). By construction, the vertical projection of σ (onto $x_d=0$) is the intersection of the projections of f^+ and f^- . By construction, for each (d-2)-face of f^+ , the (d-2)-flat that supports it is either an intersection of h^+ with another hyperplane that lies above C, or the intersection $h^+ \cap h^-$. Symmetric properties hold for the floor f^- . See Figure Figure 4.2.1 for an illustration. This observation is easily seen to imply the assertions of the first part of the lemma.

Regarding the second part of the lemma, since for a hyperplane h, only one of $g^+ := h^+ \cap h$ or $g^- := h^- \cap h$, $h \neq h^+, h^-$, can appear on $\partial \sigma$, this contributes at most n-2 facets to C_{d-1} . Together with the possible facet obtained from $h^+ \cap h^-$, we get the asserted bound n-1.

Using Lemma 4.4, we derive a recurrence relation for bounding the complexity of the vertical decomposition of a single full-dimensional cell C, as follows.

Lemma 4.5. Let K(d,n) denote the maximum number of (final) prisms in the vertical decomposition of a convex polyhedron in \mathbb{R}^d with at most n facets. Then

$$K(d,n) \le \frac{1}{4^{d-2}} \left(\frac{n!}{(n-d+2)!}\right)^2 (n-d+2) \le \frac{n^{2d-3}}{4^{d-2}}.$$
 (4.1)

Proof: We first note that the number of pairs (h^-, h^+) that can generate the floor and ceiling of a first-stage prism is at most n^-n^+ , where n^- (resp., n^+) is the number of facets on the lower (resp., upper) boundary of C. Since the maximum value of n^-n^+ is $n^2/4$, we obtain, by Lemma 4.4,

$$K(d,n) \le \frac{n^2}{4}K(d-1,n-1),$$
 (4.2)

and (as is easily checked) $K(2,n) \leq n$. Solving the recurrence, we get

$$K(d,n) \le \frac{1}{4^{d-2}} \left(\frac{n!}{(n-d+2)!}\right)^2 (n-d+2),$$

which is bounded by $\frac{n^{2d-3}}{4^{d-2}}$.

4.2.2 Vertical decomposition of the entire arrangement

Next we prove the following theorem using Lemma 4.5. Note that here we consider prisms of the vertical decomposition of every cell of $\mathcal{A}(H)$, of any dimension.

Theorem 4.6. For $n \ge 2d$, the complexity of the vertical decomposition of an arrangement of n hyperplanes in \mathbb{R}^d is $O\left(\frac{4^d}{d^{7/2}}n^{2d}\right)$, with an absolute, d-independent constant of proportionality.

Proof: Let H be a set of n hyperplanes in \mathbb{R}^d , and let $\mathsf{VD}(H)$ denote the vertical decomposition of the entire arrangement $\mathcal{A}(H)$. The explicit construction of $\mathsf{VD}(H)$ is in fact equivalent to taking each cell C of $\mathcal{A}(H)$ and applying to it the vertical decomposition procedure outlined above. A naive implementation of this reasoning gives a somewhat inferior bound on the overall number of prisms (in terms of its dependence on d; see the remark following the proof), so we use instead the following somewhat indirect argument.

We first count the number of d-dimensional prisms in VD(H). Following Corollary 4.2, each such prism in VD(H) is defined in terms of $b \leq 2d$ hyperplanes of H. In addition, it is easily verified that the vertical decomposition scheme complies with the Clarkson–Shor framework (see Section 2.2). In particular, a prism σ that is defined by a subset H_0 of $b \leq 2d$ hyperplanes will appear as a prism of $VD(H_0)$. By (4.1), the overall number of d-dimensional prisms in the vertical decomposition of a single d-dimensional cell of $\mathcal{A}(H_0)$ is at most

$$O\left(\frac{d+2}{4^d}\left(\frac{(2d)!}{(d+2)!}\right)^2\right),\,$$

with an absolute constant of proportionality, independent of d. Multiplying this by the number of d-dimensional cells of $\mathcal{A}(H_0)$, which is $\sum_{j=0}^{d} {b \choose j} \leq 2^b$ (see Lemma 3.5(a)), we get a total of

$$O\left(2^b\left(\frac{d+2}{4^d}\right)\left(\frac{(2d)!}{(d+2)!}\right)^2\right)$$

prisms. Finally, multiplying this bound by the number $\binom{n}{b}$ of subsets of H of size b, and summing over $b = 0, \ldots, 2d$, we get a total of

$$O\left(\left(\sum_{b=0}^{2d} \binom{n}{b} 2^b\right) \cdot \frac{d+2}{4^d} \left(\frac{(2d)!}{(d+2)!}\right)^2\right)$$

prisms. As is easily checked, for $n \ge 4d$, the sum $\sum_{b=0}^{2d} {n \choose b} 2^b$ is proportional to its last element, i.e., it is

$$O\left(\binom{n}{2d}4^d\right) = O\left(\frac{n^{2d}}{(2d)!}4^d\right) = O\left(\sqrt{d}\left(\frac{2e}{2d}\right)^{2d}n^{2d}\right),\,$$

using Stirling's approximation. When $2d \le n < 4n$ we proceed as follows. We first observe that by the Multinomial Theorem it follows that

$$\sum_{b=0}^{2d} \binom{n}{b} 2^b = \sum_{b=0}^{2d} \binom{n}{b} \left(\sum_{i=1}^b \binom{b}{i} \right) = 3^n.$$

We claim that $3^n \leq \sqrt{d} \left(\frac{2e}{2d}\right)^{2d} n^{2d} \approx \frac{n^{2d}}{(2d)!}$ for $2d \leq n \leq 4d$. Indeed, putting x = n/(2d), this is equivalent to asserting that $\frac{3^x}{x} \leq d^{1/(4d)}2e$ for $1 \leq x \leq 2$, which does indeed hold. Hence, the overall number of prisms is

$$O\left(\frac{n^{2d}}{(2d)!}4^d \cdot \frac{d+2}{4^d} \left(\frac{(2d)!}{(d+2)!}\right)^2\right) = O\left(\frac{n^{2d}}{d^3} \cdot \binom{2d}{d}\right) = O\left(\frac{4^d}{d^{7/2}}n^{2d}\right).$$

So far we have accounted only for full-dimensional prisms, in the decomposition of full-dimensional cells of $\mathcal{A}(H)$. The number of prisms of all dimensions in $\mathsf{VD}(H)$, where prisms of dimension j arise in the vertical decomposition within some j-flat formed by the intersection of a corresponding subset of d-j hyperplanes of H, is easily seen to be bounded by:

$$O\left(\sum_{j=0}^{d} \binom{n}{d-j} \cdot \frac{4^{j}}{j^{7/2}} n^{2j}\right) = O\left(\sum_{j=0}^{d} \frac{n^{d-j}}{(d-j)!} \cdot \frac{4^{j}}{j^{7/2}} n^{2j}\right)$$
$$= O\left(\sum_{j=0}^{d} \frac{n^{d+j}}{(d-j)!} \cdot \frac{4^{j}}{j^{7/2}}\right) = O\left(\frac{4^{d}}{d^{7/2}} n^{2d}\right).$$

As a matter of fact, the preceding proof also implies the following stronger statement.

Corollary 4.7. Let H be a set of $n \geq 2d$ hyperplanes in \mathbb{R}^d . The overall number of prisms that can arise in the vertical decomposition of the arrangement of any subset of H is $O\left(\frac{4^d}{d^{7/2}}n^{2d}\right)$, with an absolute, d-independent constant of proportionality.

Remark 4.8. The bound in Theorem 4.6 is a significant improvement over the previous upper bound of [CEGS91] in terms of the dependence of its coefficient on d, from $2^{O(d^2)}$ to less than 4^d . We emphasize, however, that we pay a small price in terms of the dependence on n, which is n^{2d} in the new bound, instead of n^{2d-4} in [Kol04] (and only $O(n^d)$ if one uses instead bottom-vertex triangulation, by Lemma 3.2). The previous analysis of the complexity of the vertical decomposition in [CEGS91] is global (unlike ours, which is local in each cell), and yields a recurrence relation for the entire number of prisms in the vertical decomposition of n hyperplanes in d dimensions. Denoting this function by V(n,d), it is shown in [CEGS91] that $V(n,d) \leq n^2V(2n,d-1)$, which has the solution $V(n,d) \leq 2 \cdot 2^{d(d-1)}n^{2d-1}$ (when we stop at d=1, in which case $V(n,d) \leq n+1 \leq 2n$). The dependence of this bound on n can be reduced to n^{2d-4} (by a refined, and rather complicated, analysis in four dimensions, and using it as the base case for this recurrence, see [Kol04]) but not the dependence on d. In contrast, the coefficient in our bound is only singly exponential in d. As will follow later, this is a crucial property for improving the query cost in Meiser's point location algorithm. We pay a small cost (it is small when d is large) in that the power of n is larger by a small constant. It would be interesting to establish a bound that is both singly exponential in d and has the smaller power 2d-4 of n.

We also note that it is an open problem whether the complexity of $\mathsf{VD}(H)$ is really asymptotically larger than $O(n^d)$. If it were not, the preceding discussion would become vacuous.

Theorem 4.6 implies that the local growth function of VD satisfies $u(m) \leq 2^{\alpha} m^{\beta}$, with $\alpha = 2d$ and $\beta = 2d$. That is, we have $\alpha, \beta, b = 2d$. Substituting these values into Lemma 2.8, we obtain the following result.

Corollary 4.9. Let H be a set of n hyperplanes in \mathbb{R}^d and let $\varphi \in (0,1)$ be some confidence parameter. Then, for $\rho \geq cr(d\log(rd) + \ln\frac{1}{\varphi})$, for some suitable absolute constant c, the vertical decomposition of a ρ -sample is a (1/r)-cutting with probability $\geq 1 - \varphi$.

4.3 The shatter dimension and VC-dimension of prisms

So far we have only considered "definable" prisms that arise in the vertical decompositions of samples from H. In this subsection we extend them to arbitrary "similarly looking" vertical prisms, a notion to be formally defined momentarily, use these prisms to define a natural range space on H, and analyze the VC-dimension and the primal shatter dimension of this space.

Parameterizing a prism. Let σ be a vertical prism that arises in the vertical decomposition of a set of hyperplanes in \mathbb{R}^d , such that it is defined by exactly 2d of these hyperplanes; the case of fewer defining hyperplanes is discussed later on. It easily follows from the construction that σ can be represented as the intersection region of 2d halfspaces of the form

$$b_{1}^{-} \leq x_{1} \leq b_{1}^{+}$$

$$a_{2,1}^{-}x_{1} + b_{2}^{-} \leq x_{2} \leq a_{2,1}^{+}x_{1} + b_{2}^{+}$$

$$a_{3,1}^{-}x_{1} + a_{3,2}^{-}x_{2} + b_{3}^{-} \leq x_{3} \leq a_{3,1}^{+}x_{1} + a_{3,2}^{+}x_{2} + b_{3}^{+}$$

$$\vdots$$

$$a_{d,1}^{-}x_{1} + \dots + a_{d,d-1}^{-}x_{d-1} + b_{d}^{-} \leq x_{d} \leq a_{d,1}^{+}x_{1} + \dots + a_{d,d-1}^{+}x_{d-1} + b_{d}^{+},$$

$$(4.3)$$

for suitable parameter $a_{i,j}^{\pm}$ and b_j^{\pm} . The construction produces these inequalities in reverse order: the last pair of inequalities define the floor and ceiling of σ , and each preceding pair of inequalities define the floor and ceiling in the corresponding lower-dimensional projection of σ . When the number of hyperplanes defining σ is smaller than 2d, some of these inequalities are absent.

Let Σ denote the set of all prisms of the form (4.3) (including those prisms defined by fewer than 2d inequalities). We define the range space (H, Σ) on H, so that, for each $\sigma \in \Sigma$, the range associated with σ is the set of hyperplanes of H that cross (the interior of) σ .

Note that the (maximum) overall number of parameters that define a prism $\sigma \in \Sigma$ is D = d(d+1). We can therefore represent a vertical prism as a point in \mathbb{R}^D (or, rather, in the portion of \mathbb{R}^D consisting of points that represent nonempty prisms). Let h be a fixed hyperplane in \mathbb{R}^d . Let K_h denote the region in \mathbb{R}^D consisting of all (valid) points that represent prisms that are crossed by h. The boundary S_h of K_h is the locus of all (points representing) prisms for which h is a supporting hyperplane.

Consider a vertical prism $\sigma \in \Sigma$. In general, σ has 2^d vertices, each of which is obtained by choosing one inequality (the left or the right) out of each of the d pairs in (4.3), turning each chosen inequality into an equality, and solving the resulting linear system. We *label* each vertex q of σ by the sign sequence $(\varepsilon_1, \ldots, \varepsilon_d)$, where, for each i, ε_i is -1 (resp., +1) if the left (resp., right) inequality of the ith pair is the one involved in the construction of q.

The following analysis fixes h, with its normal vector v (actually two oppositely directed vectors), and constructs K_h in two stages. It first constructs a partition of \mathbb{R}^D into cells, so that, for a fixed cell, and for all the prisms σ whose representing points lie in the cell, the two vertices of σ supported by hyperplanes parallel to h have fixed labels. These cells are independent of the coordinates that represent the free coefficients b_j^{\pm} . In the second stage, we take each of these "cylindrical" cells, and extract from it the portion that represents prisms that are crossed by h (these are prisms for which h lies in between

the two hyperplanes that are parallel to h and support σ at the two vertices just mentioned). The union of these regions is the desired K_h .

Partitioning by the labels of the supported vertices. As already said, in what follows, the hyperplane h, and its pair of normal directions v and -v, are fixed, and the prism σ is regarded as a parameter.

Let q be the vertex of σ with label λ . We express algebraically the property that q is the contact vertex of a supporting hyperplane of σ with outward normal direction v, as follows. Let f_1, \ldots, f_d be the d facets of σ incident to v. The corresponding d (not necessarily normalized) outward normal directions w_1, \ldots, w_d of the hyperplanes of (4.3) that support these facets are given by

$$w_1 = \pm (1, 0, \dots, 0)$$

$$w_2 = \pm (-a_{2,1}^{\pm}, 1, 0, \dots, 0)$$

$$w_3 = \pm (-a_{3,1}^{\pm}, -a_{3,2}^{\pm}, 1, 0, \dots, 0)$$

$$\vdots$$

$$w_d = \pm (-a_{d,1}^{\pm}, \dots, -a_{d,d-1}^{\pm}, 1),$$

where, for each j, the sign of w_j (and the corresponding set of coefficients $a_{j,i}^{\pm}$) is the sign of the corresponding component of λ .

The vertex q is the contact vertex of a supporting hyperplane of σ with outward normal direction v if and only if v is in the convex cone generated by w_1, \ldots, w_d . The algebraic characterization of the latter condition is that v can be expressed as a nonnegative linear combination $v = \sum_{j=1}^{d} \beta_j w_j$ of w_1, \ldots, w_d (i.e., such that $\beta_j \geq 0$ for each j). The triangular structure of the coefficients of the w_j 's makes it easy to express the β_j 's in terms of the parameters $a_{j,i}^{\pm}$. It is simplest to reason by using Cramer's rule for solving the resulting system, noting that the determinant in the denominator is ± 1 (since the resulting matrix is triangular with ± 1 on the diagonal). The condition that all the β_j 's be nonnegative is therefore a system of d algebraic inequalities in the parameters $a_{i,j}^{\pm}$, each of which involves a polynomial (namely, the determinant in the corresponding numerator) of degree strictly smaller than d. Let $T_q(v)$ denote the "feasible region", which is the solution of these inequalities in $\mathbb{R}^{D'}$, for D' = d(d-1)/2, which is the subspace of the parameter space \mathbb{R}^D that is spanned by the coordinates $a_{j,i}^{\pm}$ that participate in the (in)equalities that define q.

We repeat the above analysis to each of the 2^d possible labels of vertices q of a prism, with the fixed direction v. Each label λ uses a different set of D' coordinates from among the $a_{j,i}^{\pm}$. Let $D_0 = 2D' = d(d-1)$ be the total number of coordinates $a_{j,i}^{\pm}$. Extend each region $T_q(v)$ in all the complementary, unused, D' coordinates into a suitable cylindrical region within \mathbb{R}^{D_0} .

Remark 4.10. Note that so far we only handle bounded prisms, namely those defined by exactly 2d inequalities (as in (4.3)). It is easy to extend the analysis to prisms that use fewer inequalities: There are 3^d subsets of inequalities, each of which corresponds to a different representation of σ (for each j, we take from the jth pair the left inequality, the right inequality, or neither of them), and we repeat the ongoing analysis to each of them, more or less verbatim, except that the dimension of the parametric space that represent prisms is smaller. Multiplying the bounds that we are going to get by 3^d will not affect the asymptotic nature of the analysis—see below.

We claim that the regions $T_q(v)$, over all possible vertices q, form a decomposition of \mathbb{R}^{D_0} into 2^d pairwise openly disjoint regions. It is indeed a cover because each point $\zeta \in \mathbb{R}^{D_0}$ is the projection (in

which the coordinates b_j^{\pm} are ignored) of infinitely many valid prisms σ ; this holds because there is always a solution to the system (4.3) if we choose b_j^{-} and b_j^{+} far apart from one another, for each j. Any such prism σ has at least one vertex q supported by a hyperplane with an outward normal direction v, and therefore ζ must belong to $T_q(v)$. Moreover, if these prisms have more than one such vertex, then it is easily seen that ζ cannot lie in the interior of any region $T_q(v)$.

Denote the resulting subdivision of \mathbb{R}^{D_0} as \mathcal{M}_h^+ .

To complete this part of the construction, we apply the same construction to the opposite normal vector -v, and obtain a second subdivision of \mathbb{R}^{D_0} , which we denote by \mathcal{M}_h^- . We then apply both steps to each hyperplane $h \in H$, and obtain a collection of 2n subdivisions $\{\mathcal{M}_h^+, \mathcal{M}_h^- \mid h \in H\}$ of \mathbb{R}^{D_0} .

Partitioning by the positions of the supporting hyperplanes. So far the analysis has only focused on the parameters $a_{j,i}^{\pm}$, and ignored the parameters b_i^{\pm} . This was sufficient in order to classify the family of prisms into subsets depending on the discrete nature of the two vertices supported by each input hyperplane. Now we want to bring the parameters b_i^{\pm} into the game, thereby further classifying the prisms by distinguishing, for each input hyperplane h, between those prisms crossed by h and those that h misses. This proceeds as follows.

Fix again a hyperplane $h \in H$, and its two directed normal vectors v^+ , $v^- = -v^+$, which give rise to the respective subdivisions \mathcal{M}_h^+ , \mathcal{M}_h^- . In the second stage of the construction, we construct the desired region K_h in \mathbb{R}^D , by "lifting" (and then overlaying) \mathcal{M}_h^+ and \mathcal{M}_h^- to \mathbb{R}^D , as follows.

Fix $v \in \{v^+, v^-\}$, and assume, without loss of generality, that $v = v^+$. We take each cell $T_q(v)$ of \mathcal{M}_h^+ , consider the cylinder $T_q^*(v)$ over $T_q(v)$ in the remaining 2d dimensions that encode the coordinates b_j^{\pm} (i.e., $T_q^*(v) = T_q(v) \times \mathbb{R}^{2d}$), and partition $T_q^*(v)$ by the surface $T_q^0(v)$, which is the locus of all (points encoding valid) prisms for which h passes through the vertex q. Concretely, recall that the label of q determines the d inequalities, one out of each pair in (4.3), which we turn into equalities, and solve the resulting linear system (a trivial step, using backward substitution), to obtain q itself (in terms of the D parameters defining σ). The equation defining $T_q^0(v)$ is then obtained by substituting this q into the linear equation defining h.

Write $T_q^0(v)$ as the zero set $F_{q,v} = 0$ of a suitable function $F_{q,v}$, which, by the triangular structure of (4.3), is a polynomial (in D/2 out of the D coordinates) of degree d. The surface $T_q^0(v)$ partitions $T_q^*(v)$ into two regions. In one of them, h passes above its parallel copy that supports the corresponding prism and has outward normal vector v, and in the other region h passes below that hyperplane.

We apply a similar construction for h and its opposite normal vector $v^- = -v$, and then repeat the whole procedure for all $h \in H$ (and for all labels of vertices q of the prism).

The resulting *D*-dimensional arrangement. In the final step of the construction, we form the overlay \mathcal{O} of the subdivisions \mathcal{M}_h^+ , \mathcal{M}_h^- , over all $h \in H$, and obtain a subdivision of \mathbb{R}^{D_0} into regions, so that each region Q has a fixed sequence of labels, $(\lambda_1^+, \lambda_1^-, \dots, \lambda_n^+, \lambda_n^-)$, so that, for each prism represented by a point in Q, and for each j, the two hyperplanes that support the prism and are parallel to the jth hyperplane h_j of H touch it at the two vertices with labels λ_j^+ , λ_j^- .

For each region Q, we draw the 2n surfaces $T_{\lambda_j^+}^0(v_j)$, $T_{\lambda_j^-}^0(-v_j)$, where v_j is the positive normal vector of h_j , and form their arrangement within the corresponding cylinder $Q^* = Q \times R^{2d}$. We take the union of these arrangements, over all the regions Q, and obtain a final subdivision Ξ of \mathbb{R}^D into cells, so that in each cell, the prisms represented by its points have a fixed conflict list of hyperplanes that cross them.

The complexity of the subdivision. We next bound the complexity of Ξ . Let us first bound the number of vertices of Ξ . Each such vertex is formed by the intersection of D surfaces, each of

which is either a vertical cylindrical surface obtained by lifting a boundary surface between two regions $T_q(v)$, $T_{q'}(v)$ (such a surface is obtained by turning an inequality $\beta_j \geq 0$ in the definition of $T_q(v)$ into an equality), or a surface of the form $T_q^0(v)$. That is, to obtain a vertex of Ξ , we need to choose (with repetitions) D hyperplanes from H, say h_1, h_2, \ldots, h_D , choose for each of them the corresponding outward normal direction v_1, v_2, \ldots, v_D (there are two choices for each v_i), associate with each of them a respective label of a vertex q_1, q_2, \ldots, q_D of the prism (again, possibly with repetitions), and, for each j, choose either one of the d surfaces defining $T_{q_j}^*(v_j)$ or the surface $T_{q_j}^0(v_j)$. The number of choices is thus

$$X = n^{D} \cdot 2^{D} \cdot (2^{d})^{D} \cdot (d+1)^{D} = 2^{(d+1+\log(d+1))D} n^{D}.$$
(4.4)

Finally, by Bézout's theorem, each such D-tuple of surfaces intersect in at most d^D vertices (recalling that the degree of each surface is at most d). Altogether, the overall number of vertices of Ξ is at most

$$Xd^D = X2^{D\log d} = 2^{(d+1+2\log(d+1))D}n^D = 2^{d(d+1)^2 + 2d(d+1)\log(d+1)}n^{d(d+1)} = 2^{O(d^3)}n^{d(d+1)}.$$

It is easy to see that this bound on the number of vertices also controls the number of cells of Ξ ; that is, the number of cells is also $2^{O(d^3)}n^{d(d+1)}$. This is therefore an upper bound on the number of subsets of H that can be crossed by a prism. That is, the global growth function of our range space (H, Σ) satisfies

$$g_{\Sigma}(n) = 2^{O(d^3)} n^{d(d+1)}$$
.

Hence, the primal shatter dimension is then at most d(d+1).

However, the only upper bound that we can get on the VC-dimension is $O(d^3)$. This follows from the standard reasoning, where we denote by x the largest cardinality of a set of hyperplanes that can be shattered by vertical prisms of Σ , and then use the inequality

$$2^x \le 2^{O(d^3)} x^{d(d+1)}, \quad \text{or} \quad x = O(d^3) + d(d+1) \log x = O(d^3).$$

We remark that the factor $2^{O(d^3)}$ that appears in the bound for $g_{\Sigma}(n)$ arises from the factor $(2^d)^D$ in (4.4). This raises a challenging open question, of whether all D-tuples of vertices of a prism can be the contact vertices of D given hyperplanes. This can also be stated as a question of whether the complexity of the overlay \mathcal{O} can really be so high. At the moment, we do not have any solid conjecture to offer.

Lower bound. We next show that the VC-dimension of hyperplanes and vertical prisms, that is, of the range space (H, Σ) , is at least 1 + d(d+1)/2. That is, we construct a set H of 1 + d(d+1)/2 hyperplanes in \mathbb{R}^d , and a set $C \subset \Sigma$ of $2^{1+d(d+1)/2}$ vertical prisms in \mathbb{R}^d , each having a representation as in (4.3), such that the prisms in C shatter H. That is, for every subset $S \subseteq H$ there is a prism $\tau(S) \in C$ for which S is the subset of the hyperplanes of H that intersect (the interior of) $\tau(S)$.

All the prisms in \mathcal{C} will be sufficiently small perturbations of the unit cube $U = [0, 1]^d$, and each hyperplane in H will be a supporting hyperplane of U, touching it at a unique corresponding vertex. To simplify and unify the construction, we will only specify the vertex v at which the hyperplane supports U, and the hyperplane itself, denoted as h_v , will be the hyperplane that passes through v and is perpendicular to the segment vo, connecting v with the center o = (1/2, 1/2, ..., 1/2) of U.

Constructing H. We begin with the construction of H, or rather of the set P of vertices of U that are supported by the hyperplanes in H, as just defined. Let e_i denote the unit vector in the x_i -direction, for i = 1, ..., d. The set P is the union of disjoint sets $P_1, ..., P_d$, where $P_1 = \{0, e_1\}$, where $\mathbf{0}$ is the origin, and for $i \geq 2$, $P_i = \{e_i\} \cup \{e_i + e_i \mid j < i\}$, that is, P_i consists of e_i and i - 1 vectors, which are

sums of pairs of the form $e_j + e_i$. Intuitively, except for P_1 , which is somewhat special, P_i lies in the (i-1)-dimensional flat $x_i = 1$, $x_{i+1} = x_{i+2} = \cdots = x_d = 0$, and consists of the (suitably shifted) origin and of the i-1 unit vectors within that subspace. Since $|P_1| = 2$ and $|P_i| = i$ for $i \geq 2$, it follows that |P| = 1 + d(d+1)/2. Note that P consists exactly of all the vertices of U with at most two nonzero coordinates. We denote by H_i the subset of H that corresponds to the vertices in P_i , for $i = 1, \ldots, d$.

Constructing C. We define a sequence of perturbation parameters $\varepsilon_1, \varepsilon_2, \ldots, \varepsilon_d$, such that $\varepsilon_i = \sqrt{2(d+1)}\varepsilon_{i-1}$, for $i=2,3,\ldots,d$, and ε_1 is chosen sufficiently small so as to guarantee that ε_d is also sufficiently small, say smaller than some prescribed $\varepsilon_0 \ll 1$. By definition, we have $\varepsilon_d < (2(d+1))^{d/2}\varepsilon_1$, so we choose $\varepsilon_1 = \frac{\varepsilon_0}{(2(d+1))^{d/2}}$, to obtain the desired property.

Now let S be an arbitrary subset of H. We will construct a vertical prism $\tau = \tau(S)$, such that $S = \{h \in H \mid h \cap \operatorname{int}(\tau) \neq \emptyset\}$. The construction of τ proceeds inductively on the dimension, and produces a sequence of prisms $\tau_1, \tau_2, \ldots, \tau_d = \tau$, such that, for each i, τ_i is of dimension i, in the sense that it is contained in the flat $\{x \in \mathbb{R}^d \mid x_j = 0 \text{ for all } i < j \leq d\}$. Specifically, τ_i is obtained from τ_{i-1} by

$$\tau_i = \left\{ (x_1, x_2, \dots, x_i, 0, \dots, 0) \mid (x_1, \dots, x_{i-1}, 0, \dots, 0) \in \tau_{i-1}, \text{ and } 0 \le x_i \le \sum_{j < i} a_{i,j}^+ x_j + b_i^+ \right\},\,$$

for suitable coefficients $a_{i,j}^+$ and b_i^+ . Clearly, the final prism τ_i has (a special form of) the representation given in (4.3).

Let $S_j = S \cap H_j$, for j = 1, ..., d. We will enforce, by induction, that for each i, the prism τ_i satisfies the following two conditions for every $j \leq i$.

- 1. Every vertex $p \in P_j$ is ε_j -close to some vertex of τ_i .
- 2. $S_j = \{h \in H_j \mid h \cap \operatorname{int}(\tau_i) \neq \emptyset\}$, where $\operatorname{int}(\tau_i)$ denotes the relative interior of the *i*-dimensional prism τ_i .

We begin the construction of τ by constructing τ_1 , which is simply $\pm \varepsilon_1 \leq x_1 \leq 1 \pm \varepsilon_1$, where the signs are chosen so that Condition (2) holds for j = i = 1 (Condition (1) obviously holds).

Suppose now that i > 1 and that we have already constructed τ_{i-1} , which satisfies Conditions 1 and 2. We construct τ_i as follows.

For each $q \in P_i$ let q' be the vertex obtained from q by replacing the 1 in its ith coordinate by 0. Clearly, $q' \in P_j$ for some j < i. Since τ_{i-1} satisfies Condition (1), there exists a (unique) vertex w of τ_{i-1} that lies at distance at most ε_j from q'. Let z denote the point at which the x_i -parallel line through w meets h_q . Write z as $w + (1+t)e_i$, where, as above, e_i is the unit vector in the x_i -direction and t is a real parameter, and note that the coordinates x_{i+1}, \ldots, x_d of z are all 0. Since $z \in h_q$, we have $(z-q) \cdot (q-o) = 0$. That is, we have

$$(w + (1+t)e_i - q' - e_i) \cdot (q - o) = ((w - q') + te_i) \cdot (q - o) = 0, \text{ or}$$
$$te_i \cdot (q - o) = (q' - w) \cdot (q - o).$$

We have $q - o = (\pm 1/2, \pm 1/2, \dots, \pm 1/2)$, so $te_i \cdot (q - o) = \pm t/2$. We thus get

$$|t|/2 = |(q'-w)\cdot(q-o)| \le ||q'-w|| \cdot ||q-o|| \le \frac{\sqrt{d}}{2}\varepsilon_{i-1}.$$

That is, $|t| \leq \sqrt{d\varepsilon_{i-1}}$. It thus follows that

$$||z-q|| = ||w+(1+t)e_i-q'-e_i|| \le ||w-q'|| + |t| \le (1+\sqrt{d})\varepsilon_{i-1}.$$

We now replace z by $z_q := z \pm se_i$, where

$$s = \left(\sqrt{2(d+1)} - (1+\sqrt{d})\right)\varepsilon_{i-1};$$

it is easily checked that s > 0 for $d \ge 2$. The sign of se_i is positive (resp., negative) if $h_q \in S_i$ (resp., $h_q \notin S_i$). Applying this procedure to each vertex in P_i , we get i points z_q , for $q \in P_i$, such that we have

$$||z_q - q|| \le (1 + \sqrt{d})\varepsilon_{i-1} + s$$
, or $||z_q - q|| \le \sqrt{2(d+1)}\varepsilon_{i-1} = \varepsilon_i$,

for each q.

Let π_i denote the hyperplane that passes through the *i* points z_q , for $q \in P_i$, and is parallel to all coordinates x_{i+1}, \ldots, x_d . Write its equation as $x_i = \sum_{j < i} a_{i,j}^+ x_j + b_i^+$ (it is easily checked that π_i is not x_i -parallel, assuming that the ε_j 's are sufficiently small). We then define τ_i to be the prism

$$\tau_i = \left\{ (x_1, x_2, \dots, x_i, 0, \dots, 0) \mid (x_1, \dots, x_{i-1}, 0, \dots, 0) \in \tau_{i-1}, \text{ and } 0 \le x_i \le \sum_{j \le i} a_{i,j}^+ x_j + b_i^+ \right\},\,$$

It is easy to verify that Conditions (1) and (2) hold for τ_i , assuming that the ε_j 's are sufficiently small. In conclusion, we obtain:

Theorem 4.11. The VC-dimension of the range space (H, Σ) of hyperplanes and vertical prisms in \mathbb{R}^d is at least 1 + d(d+1)/2 and at most $O(d^3)$.

An interesting open question is to tighten this gap. We conjecture that the VC-dimension is quadratic, or nearly quadratic in d.

5 Point location in an arrangement of hyperplanes

Let H be a set of n hyperplanes in \mathbb{R}^d . We wish to preprocess H into a data structure for point location in $\mathcal{A}(H)$. There are several variants that depend on how we want the output to a query to be. We consider here two variants. In the first one we return, for a query point q, the (possibly lower-dimensional) cell of $\mathcal{A}(H)$ that contains it, which we represent by the sign pattern of q with respect to the entire set H. In the second variant, referred to as vertical ray shooting, we return the first hyperplane that is hit by the upward-directed ray emanating from q (in the positive x_d -direction), including the case where q lies on one or several hyperplanes of H, in which case we return one of them. The goal is to make the query as efficient as possible, in its dependence on both n and d, at the cost of large (but not too large) storage and preprocessing time.

We begin in Section 5.1 by reviewing Meiser's algorithm [Mei93] (see also the introduction) in some detail, and by providing a rigorous analysis of the tradeoff between the query time and storage; the analysis of this tradeoff, as presented in [Mei93], is sketchy and suffers from several technical difficulties. We also discuss the improvement of Meiser's algorithm, due to Liu [Liu04], which reduces and tightens the dependence of the storage size on n (but not on d—this dependence is actually worse than what we

obtain here). In Section 5.1 we only consider the variant where we return the (sign pattern of the) cell of $\mathcal{A}(H)$ containing the query point.

We then improve the query time, in Section 5.2, by replacing bottom-vertex triangulation by vertical decomposition, using the Clarkson–Shor random sampling analysis (which is based on the combinatorial dimension), as presented in Section 2. This saves about a factor of d in the query time, and constitutes, in our opinion, one of the main contributions of this paper.

A second, smaller improvement, by a $\log d$ factor, is obtained by using the optimistic sampling technique, presented in Section 2.3.4, which makes do with a slightly smaller sample size. This leads to a slightly faster processing of a single recursive step (on the size of H) of the query. This refined approach is presented in Section 5.2.6.

Finally, in Section 5.3, we consider the case of low-complexity hyperplanes, and present a simpler variant of our data structures for this case. It has comparable bounds on the storage and preprocessing, but the query is faster by roughly a factor of d.

5.1 Meiser's algorithm, with an enhancement

Essentially, the only known algorithm for point location, in which the query time is *polynomial* in d and in $\log n$, is due to Meiser [Mei93] (it has been improved in a follow-up study by Liu [Liu04]).

Meiser's preprocessing stage constructs the following data structure. It draws a ρ -sample $R \subset H$, of actual size at most ρ , where the specific choices of ρ are discussed later, and constructs the bottom-vertex triangulation BVT(R), as described in Section 3.1. By its recursive nature, this construction also produces the bottom-vertex triangulation within every flat, of any dimension $1 \leq j \leq d-1$, that is the intersection of some d-j hyperplanes of R.

The construction identifies each cell of $\mathcal{A}(R)$, of any dimension, by its sign pattern with respect to R. We store the sign patterns, of all the cells of all dimensions, in a ternary trie, denoted by $T = T_R$, whose leaves correspond to the cells. We represent each cell C by a structure containing, among other features, its bottom vertex w_C , which is represented by the d hyperplanes that define it (or, in case of degeneracies, the d hyperplanes of smallest indices that define it). Each leaf ξ of T stores a pointer to the structure of its cell C_{ξ} .

Let $C = C_{\xi} \in \mathcal{A}(R)$ be the cell associated with a leaf ξ of the trie T. We store at ξ (or rather at the structure associated with C_{ξ} , which is accessible from ξ) a secondary tree Q_C that "encodes" the bottom vertex triangulation $\mathsf{BVT}(C)$ of the cell C, as follows. The root of Q_C corresponds to the cell C itself, and each internal node of Q_C corresponds to some (lower dimensional) cell on (i.e., a face of) ∂C . (There could be several nodes that correspond to the same subcell in Q_C .) A node v in Q_C , which corresponds to some j-dimensional face C'_v of C, has a child for each (j-1)-dimensional face on $\partial C'_v$ that does not contain $w_{C'_v}$. We index each child of v by the hyperplane that supports the corresponding (j-1)-dimensional face of C'_v (but does not support C'_v itself). In this manner, each leaf v of Q_C is associated with a vertex of ∂C . We store at v the simplex of $\mathsf{BVT}(C)$, which is spanned by the lowest vertices $w_{C'_v}$ of the cells associated with the nodes u on the path to v, including the vertex associated with v. It is easily verified that all simplices of $\mathsf{BVT}(C)$ (whose dimension is equal to that of C) are obtained in this manner (and only these simplices). Repeating this construction for every cell C of $\mathcal{A}(R)$, we obtain all the simplices of $\mathsf{BVT}(R)$.

The algorithm then constructs the conflict list $K(\sigma)$ for each simplex $\sigma \in BVT(R)$, in brute force, by checking for each hyperplane $h \in H$ whether it separates the vertices of σ . The actual procedure that implements this step is presented later.

We process each of these conflict lists recursively. That is, for each simplex σ , we draw a ρ -sample R' from $K(\sigma)$, compute BVT(R'), and construct the corresponding trie $T_{R'}$ and the trees Q_C for each

cell $C \in \mathcal{A}(R')$. We store R' and the data structures associated with it, at the leaf v_{σ} representing σ in the tree Q_C of the cell $C \in \mathcal{A}(R)$ containing σ . (We do not need to keep the conflict lists themselves in the final data structure, because the queries do not access them.)

At each recursive step, when we construct, for each simplex $\sigma \in \mathsf{BVT}(R)$, the conflict list $\mathsf{K}(\sigma)$, we also get the (fixed) sign pattern of all the points in σ with respect to all the hyperplanes that do not cross σ , and we temporarily store this subpattern at v_{σ} .

The recursion bottoms out when the conflict list of the current simplex σ is of size smaller than ρ . We call such a simplex σ a leaf-simplex (of the entire structure). A leaf-simplex does not have a recursive structure associated with it. We only construct the arrangement $\mathcal{A}(\mathsf{K}(\sigma))$ of the conflict list $\mathsf{K}(\sigma)$ of σ (whose size is at most ρ), and store at v_{σ} a trie structure $T_{\mathsf{K}(\sigma)}$ over the cells of $\mathcal{A}(\mathsf{K}(\sigma))$. We attach to each cell C (of any dimension) of $\mathcal{A}(\mathsf{K}(\sigma))$ its fixed sign pattern with respect to $\mathsf{K}(\sigma)$.

Finally, we extend the sign pattern of each cell C at the bottom of recursion to a sign pattern with respect to all hyperplanes in H, as follows. We iterate over all simplices along the path to the corresponding leaf-simplex σ in our overall hierarchical structure, retrieve the subpatterns stored at them, and merge them into a single sign pattern with respect to all of H. It is easy to verify that each hyperplane $h \in H$ appears exactly once in this collection of subpatterns (for a fixed "leaf-cell" C)—it either happens at the (unique) node at which h has stopped belonging to the corresponding conflict list (it could be one of the hyperplanes that define, and in particular touch, the present simplex), or else h is in $K(\sigma)$. We store the merged sign pattern at the leaf of $T_{K(\sigma)}$ corresponding to C. Alternatively, depending on the application at hand, we might only store a link to some data structure (or just data) associated with C. This storage is permanent, and is part of the output structure, whereas the sign patterns of intermediate simplices are discarded after their recursive processing terminates.

We note that an alternative approach, which saves on preprocessing, is to keep the intermediate partial sign patterns at their respective nodes, and concatenate the patterns along the search path of a query point q, during the query processing step, to obtain the complete sign pattern at q. In this approach the resulting sign pattern is given as a list rather than a vector, which is provided by the previous approach.

5.1.1 Answering a query

A point-location query with a point q is processed as follows. We retrieve the initial random sample R, and explicitly construct the simplex $\sigma = \sigma_q$ of $\mathsf{BVT}(R)$ that contains q. To do this, we first compute the sign pattern of the cell C_q of $\mathcal{A}(R)$ that contains q, namely, the side of each hyperplane $h \in H$ that contains q, including the case where q lies on h. (If q does lie on one or several hyperplanes of R then C_q is lower-dimensional.) It is straightforward to do this in $O(d\rho)$ time. We then search the trie T_R with this sign pattern, and identify C_q and its bottom vertex $w = w_{C_q}$.

We next perform ray shooting along the line wq, from q in the direction away from w, and find the first hyperplane h_1 of R hit by this ray. In case C_q is lower-dimensional, the hyperplane h_1 is the first new hyperplane that the ray hits, namely a hyperplane not containing q. We assume, for simplicity of presentation, that there are no ties, that is, there is a unique (new) hyperplanes first hit by \vec{wq} . This can be achieved, for example, by perturbing q slightly within C_q . Let q_1 denote the point at which h_1 is hit. Then we compute the sign pattern of q_1 with respect to R, and search T_R again with this pattern, to identify the cell C_{q_1} containing q_1 , and its bottom vertex $w_{C_{q_1}}$. We keep collecting the vertices of σ in this manner, one vertex per dimension. After d recursive steps (on the dimension), we obtain all the vertices of σ (and the cells of progressively decreasing dimension of which they are bottom vertices), in overall time $O(d \cdot d\rho) = O(d^2\rho)$. See Figure 5.1.

Note that the sequence of ray shootings, as just described, identifies the path in Q_{C_q} that leads to

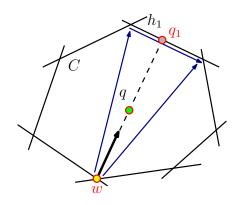


Figure 5.1: The recursive construction of the simplicial cell containing q.

Parameter / method	Value	Sample size	Using
VC-dim.	$O(d^2 \log d)$ Lemma 3.7	$O(rd^2\log r\log d)$	ε -net theorem (Theorem 2.2)
Shatter dim.	$O(d^2)$ Lemma 3.6	$O(rd^2\log(rd))$	Remark 2.3
Combinatorial dim.	$b = d(d+3)/2$ Remark 3.3 $\alpha = O(1),$ $\beta = d$ Lemma 3.2	$O(rd^2)$	Lemma 2.8
Optimistic sampling	As above	$O(rd^2)$	Corollary 2.10

Figure 5.2: The different sizes of the sample R, needed to ensure that the corresponding $\mathsf{BVT}(R)$ in \mathbb{R}^d is, with high probability, a (1/r)-cutting, according to the different tools at our disposal. The probability depends on the (absolute) constant parameters in the bounds.

the leaf v_{σ} associated with σ in Q_{C_q} . Indeed, the shootings identify the sequence of faces of C_q , of progressively decreasing dimensions $d-1, d-2, \ldots, 0$, which support the corresponding faces of σ , and this sequence of faces identifies the path in Q_{C_q} that we need to follow—at each visited node we go to the child associated with the new hyperplane that supports the next face in the sequence. At v_{σ} we find the recursive structure associated with σ and continue the query recursively in this structure. The recursion terminates when we reach a leaf-simplex σ . We then locate the cell of $\mathcal{A}(\mathsf{K}(\sigma))$ containing q, from its sign pattern with respect to $\mathsf{K}(\sigma)$, which we compute in brute force in $O(d\rho)$ time, and return the overall sign pattern that is stored at this leaf.

5.1.2 The cost of a query

Each step of the main recursion (on the size of the input) takes $O(d^2\rho)$ time. This bound has already been noted for the cost of the ray shootings, and it also dominates the cost of the search for the leaf representing the simplex of $\mathsf{BVT}(R)$ containing q. Thus the overall cost of a query is $O(d^2\rho)$ times the number of recursive steps in the main hierarchy.

Ignoring for the moment the issue of the storage and preprocessing costs (namely, their dependence on ρ), the main issue is how large should ρ be to make the query efficient. On one hand, we would like

to make ρ as small as possible, so that the cost $O(d^2\rho)$ of each recursive step is small, but we cannot take ρ to be too small, for then we lose control over the recursion depth, as the problem size might then not decrease sufficiently, or not at all. The different sample sizes that are needed to ensure (with high probability) that the resulting bottom-vertex triangulation is a (1/r)-cutting for $\mathcal{A}(H)$, according to the different sampling theories at our disposal, as reviewed and developed in Section 2, are summarized in the table in Figure 5.2. As the table shows, the various techniques for ensuring the sample quality do not really differ that much from one another. Still, the smallest sample size that ensures the (1/r)-cutting property is $\rho = O(rd^2)$, using Lemma 2.8 (or its optimistic sampling variant Corollary 2.10 which, in the present context, does not make a difference). If the sample does not yield a (1/r)-cutting, we simply take another sample and repeat the whole step. In an expected small number of steps we get a sample that satisfies this property.

Assuming that the (1/r)-cutting property does indeed hold throughout the hierarchical structure, the number of recursive steps used by the query is $\lceil \log_r(n/\rho) \rceil = \lceil \frac{\log(n/\rho)}{\log r} \rceil$, making the query cost

$$Q(n) = O\left(\frac{d^2 \rho \log(n/\rho)}{\log r}\right) = O\left(\frac{d^4 r \log n}{\log r}\right) = O\left(d^4 \log n\right),\tag{5.1}$$

if we take r=2 (the best choice for making the query fast).

Remark 5.1. In the original formulation of the algorithm, Meiser's analysis uses the VC-dimension, which is $O(d^2 \log d)$, instead of the combinatorial dimension, and thereby incurs an (unnecessary) extra factor of $\log d$ in the query cost. Another issue is that using the ε -net theorem (Theorem 2.2), instead of the combinatorial dimension approach, also requires an extra $\log r$ factor (this however does not arise if we use the primal shatter dimension instead). This is not an issue if we choose r = 2, as we just did, but it becomes an issue for larger values of r, which are needed when we want to reduce the storage required by the algorithm; see below for details.

5.1.3 Storage

Consider a sample R and the storage required for the trie T_R and the trees Q_C for each cell C in $\mathcal{A}(R)$, but excluding the storage required for the recursive (or leaf) substructures associated with the simplices of BVT(R). The space taken by T_R is $O(\rho K_d(\rho))$, where $K_d(\rho)$ is the maximum number of cells, of all dimensions, in an arrangement of ρ hyperplanes in \mathbb{R}^d , which is $O(\rho^d)$ by Lemma 3.5. That is T_R requires $O(\rho^{d+1})$ storage. The space taken by the trees Q_C is $O(dS_d(\rho))$, where $S_d(\rho)$ is the maximum number of simplices, of all dimensions, in the bottom vertex triangulation of an arrangement of ρ hyperplanes in \mathbb{R}^d , which is $O(\rho^d)$ by Lemma 3.2. It follows that the total space required for the data structures associated with R is $O(\rho^{d+1})$.

In addition, we do construct the conflict list $K(\sigma)$ of each simplex σ of BVT(R), and the sign pattern of σ with respect to the hyperplanes of $H \setminus K(\sigma)$, but we keep them only temporarily, while the recursive processing of σ takes place. Once this processing is over, we discard $K(\sigma)$, as the queries that reach σ make no use of it—they only access the random sample chosen from $K(\sigma)$ and its associated recursive data structure, which we do store at the leaf corresponding to σ . The sign pattern of σ with respect to the hyperplanes of $H \setminus K(\sigma)$ is integrated in the sign patterns of the cells of the arrangements of the leaf-simplices generated by the recursive processing of σ .

If σ is a leaf-simplex (of the whole structure) we store with it the trie $T_{\mathsf{K}(\sigma)}$ which we use to identify the cells in the arrangement $\mathcal{A}(\mathsf{K}(\sigma))$. At each leaf of $T_{\mathsf{K}(\sigma)}$ we store the sign pattern, with respect to H, of the cell of $\mathcal{A}(H)$ that contains all the query points in σ that reach this leaf. (As discussed earlier, this storage can be saved in applications that do not need explicit access to these sign patterns.)

	Query time	Storage
r	$O(\frac{d^4r}{\log r}\log n)$	$O(n^{d\log(crd^2)/\log r + \log e/\log r})$
2	$O(d^4 \log n)$	$O(n^{2d\log d + O(d)})$
d	$O\left(\frac{d^5}{\log d}\log n\right)$	$O(n^{(3+o_d(1))d})$
$d^{1/\varepsilon}$	$O\left(\frac{\varepsilon d^{4+1/\varepsilon}}{\log d}\log n\right)$	$O(n^{d+2\varepsilon d+o_d(1)})$
d^d	$O(\frac{d^{d+3}}{\log d}\log n)$	$O(n^{d+2+o_d(1)})$
$d^{2d/\varepsilon}$	$O(\frac{\varepsilon d^{2d/\varepsilon+3}}{\log d}\log n)$	$O(n^{d+\varepsilon+o_d(1)})$

Figure 5.3: Query time and storage for Meiser's data structure (using BVT). The notation $o_d(1)$ in the various exponents means a term that depends on d and tends to 0 as d increases.

Let $S_d(n)$ denote the maximum overall storage used by the algorithm for an instance involving n hyperplanes in d dimensions, ignoring the storage used for the sign patterns of the cells of the arrangements of the conflict lists of leaf-simplices. We take, as above, $\rho = crd^2$, for some suitable absolute constant c, and redo the sampling until the size of each recursive subproblem is at most n/r, and we get the following recurrence for $S_d(n)$.

$$S_d(n) \le \begin{cases} a\rho^{d+1} + e\rho^d S_d(n/r), & \text{for } n > \rho \\ a\rho^{d+1} & \text{for } n \le \rho, \end{cases}$$

where a is a suitable absolute constant (independent of d). Unfolding the recursion, we get

$$S_d(n) \le a\rho^{d+1} (1 + e\rho^d + \dots + e^j \rho^{jd}) \le a'\rho^{d+1} (e\rho^d)^j,$$

where a' is another absolute constant, and $j = \lceil \log_r(n/\rho) \rceil = \lceil \log(n/\rho)/\log r \rceil$ is the depth of the recurrence. Substituting this value of j (and neglecting the rounding), we get that

$$S_d(n) = O(\rho^{d+1}(e\rho^d)^{(\log(n/\rho))/\log r}) = O(\rho^{d+1}(n/\rho)^{(d\log\rho + \log e)/\log r}) = O(n^{(d\log\rho + \log e)/\log r}).$$
 (5.2)

In particular, for r=2 (so that $\rho=2cd^2$), we get the storage bound $O(n^{2d\log d+O(d)})$. The different bounds for storage and query time achievable according to this scheme are depicted in the table in Figure 5.3. Note that, to get the near-ultimate bound $O(n^{d+\varepsilon})$ for the storage (for $n\gg d$, ignoring the coefficient that depends on d), which is slightly larger but close to the bound $O(n^d)$ asserted (apparently wrongly) in Meiser [Mei93], and established in Liu [Liu04], the query time bound becomes super-exponential in d. As a matter of fact, even to get bounds like $n^{d+\kappa}$, for a controlled (constant) value of κ , we already get super-polynomial bounds for the query cost.

In addition, when the answer to a query is the sign pattern of the corresponding cell, we need to add O(n) storage at each leaf of the trie $T_{\mathsf{K}(\sigma)}$ of each leaf-simplex σ , for storing the sign pattern (with respect to H) that serves as the output to all queries that reach that leaf. This will increase the space by an additional factor of n. Technically, unless r is huge, this does not affect the asymptotic form of the bound in Equation (5.2).

We also mention the follow-up study by Liu [Liu04], which has improved the storage cost in terms of its dependence on n, using Chazelle's hierarchical cutting technique (see [Cha05]), to the optimal value $O(n^d)$, except that the constant of proportionality is still super-exponential in terms of d. Specifically,

catering only to the case of the best possible query time, Liu achieves query time⁵ of $\tilde{O}(d^5(\log n + d))$, but the constant hidden in the storage bound $O(n^d)$ is $d^{O(d^3)}$. Although our storage bounds are weaker than Liu's, in terms of their dependence on n, the dependence on d in the coefficient of proportionality is significantly smaller—it actually decreases to 0 as d increases.

5.1.4 Preprocessing

The nonrecursive preprocessing of a subproblem in the main recursion tree, with an associated ρ -sample R, consists of (i) computing $\mathcal{A}(R)$, storing the sign patterns of its cells in the trie T_R , and computing the bottom vertex of each cell, (ii) constructing $\mathsf{BVT}(R)$ and the corresponding trees Q_C for each cell C of $\mathcal{A}(R)$, and (iii) constructing the conflict list of each simplex (and the partial sign pattern for hyperplanes not crossing the simplex).

We perform step (i) using the following simple vertex-based approach. We iterate over the vertices of $\mathcal{A}(R)$. Fix a vertex v, and denote by $\delta(v) \geq d$ its degree, namely the number of hyperplanes of R incident to v. In general position, we have $\delta(v) = d$ and the procedure about to be described becomes much simpler. To handle the general case, we intersect the $\delta(v)$ hyperplanes incident to v with a hyperplane h_v parallel to the hyperplane $x_d = 0$ and passing slightly above v. We recursively compute the cells of the (d-1)-dimensional arrangement, within h_v , of these intersections. For a cell C incident to v, v is the bottom vertex of C if and only if $C \cap h_v$ is bounded. We thus collect all the bounded cells of the arrangement within h_v , of any dimension, and associate each such cell C' with the corresponding cell C of $\mathcal{A}(R)$ (which is one dimension higher). The portion of C between v and h_v is the pyramid conv $(C' \cup \{v\})$. The sign patterns of C' and of C, with respect to R, are identical. In fact, all the cells within h_v have the same sign pattern with respect to all the hyperplanes not incident to v, and they can differ only in their signs with respect to the incident hyperplanes.

By construction, each cell of $\mathcal{A}(R)$, of dimension at least 1, has a bottom vertex, either a real vertex of the original arrangement, or an artificial one, on the artificial plane π_d^- (see Section 3), so it will be detected exactly once by the procedure just presented. The only cells of $\mathcal{A}(R)$ that do not have an associated cell on some auxiliary hyperplane h_v , are the vertices themselves. We add each vertex v to the output, together with its sign pattern (which is 0 at each incident hyperplane).

Let $Z_d(\rho)$ be the maximum time it takes to perform this computation on an arrangement of ρ hyperplanes in d dimensions. It follows from the preceding discussion that the full problem is reduced to a collection of (d-1)-dimensional subproblems, one for each vertex of $\mathcal{A}(R)$. To prepare for these subproblems, we need to construct the vertices, find the hyperplanes incident to each vertex v, and prepare them for the recursive subproblem at v by intersecting them with the hyperplane h_v . To perform all these preparations, we iterate over the $\binom{\rho}{d}$ choices of d-tuples of hyperplanes, compute the intersection vertex of each such tuple, in $O(d^3)$ time, using Gaussian elimination, identify vertices that arise multiple times (and thereby obtain their degree), and then, for each vertex v, intersect each incident hyperplane with h_v , in O(d) time. With a suitable implementation, the pre-recursive overhead takes

$$O\left(d^3\binom{\rho}{d}+d\sum_v\delta(v)\right)$$

time. We have the following identity:

$$\sum_{v} \binom{\delta(v)}{d} \le \binom{\rho}{d},\tag{5.3}$$

⁵Here the notation \tilde{O} hides a polylogarithmic factor in d.

as the left-hand side counts the number of d-tuples of hyperplanes that have a singleton intersection (a vertex), while the right-hand side counts all d-tuples of hyperplanes. Using (5.3), the cost of the pre-recursive overhead is easily seen to be

$$O\left(d^3\binom{\rho}{d}\right)$$
.

In a post-recursive step, we need to compute the sign pattern of each cell with respect to the entire set of ρ hyperplanes. We do it by computing, for each vertex v, its sign pattern with respect to all the hyperplanes not incident to v, in $O(\rho d)$ time. We then pad up this sequence with the local sign pattern of each (bounded) cell constructed in the recursive call at v. To save on time (and storage), we do not copy the global sign pattern (involving the non-incident hyperplanes) into the pattern of each local cell. Instead we keep the global sign pattern as a separate entity, shared by all the local cells, and just form, and store separately, the local sign pattern for each cell. Only at the bottom of recursion we will construct the full sign pattern of each cell, as the union of the subpatterns, global and local, from each node along the path to the corresponding leaf.

With this approach, the post-recursive overhead at v, which can also be applied before the recursive call, only involves the computation of the global sign pattern. Hence the non-recursive overhead at v is

$$O\left((d^3 + \rho d) \binom{\rho}{d}\right).$$

Note that each cell of $\mathcal{A}(R)$ arises exactly once as a local cell above a vertex v, namely at the unique bottom vertex v of the cell.

We thus obtain the following recurrence for $Z_d(\rho)$.

$$Z_d(\rho) \le c_0 \left((d^3 + \rho d) \binom{\rho}{d} \right) + \max_{\delta} \sum_{v} Z_{d-1}(\delta(v)) , \qquad (5.4)$$

where c_0 is some absolute constant, and where the maximum is taken over all possible assignments of degrees to vertices (each such assignment must satisfy (5.3)).

We claim that $Z_d(\rho) \leq cd! \rho \binom{\rho}{d}$, for some absolute constant c. We will establish, by induction on d, the refined bound $Z_d(\rho) \leq c_d d! \rho \binom{\rho}{d}$, where the coefficients c_d form an increasing convergent sequence, from which the claim follows.

The case d=1 is easy, since there is no further recursion, and we only need to handle $O(\rho)$ vertices and edges, each taking $O(\rho)$ time (mainly to compute its sign pattern). For d>1, the induction hypothesis implies that

$$Z_{d}(\rho) \leq c_{0} \left((d^{3} + \rho d) \begin{pmatrix} \rho \\ d \end{pmatrix} \right) + \max_{\delta} \left(c_{d-1}(d-1)! \sum_{v} \delta(v) \begin{pmatrix} \delta(v) \\ d-1 \end{pmatrix} \right)$$

$$= c_{0} \left((d^{3} + \rho d) \begin{pmatrix} \rho \\ d \end{pmatrix} \right) + \max_{\delta} \left(c_{d-1}(d-1)! \sum_{v} \delta(v) \begin{pmatrix} \delta(v) \\ d \end{pmatrix} \right) \frac{d}{\delta(v) - d + 1}$$

$$\leq c_{0} \left((d^{3} + \rho d) \begin{pmatrix} \rho \\ d \end{pmatrix} \right) + \max_{\delta} \left(c_{d-1} d! \rho \sum_{v} \begin{pmatrix} \delta(v) \\ d \end{pmatrix} \right)$$

$$= c_{0} \left((d^{3} + \rho d) \begin{pmatrix} \rho \\ d \end{pmatrix} \right) + c_{d-1} d! \rho \begin{pmatrix} \rho \\ d \end{pmatrix}.$$

Hence, by putting

$$c_d := c_{d-1} + \frac{c_0(d^3 + d)}{d!} \ge c_{d-1} + \frac{c_0(d^3 + \rho d)}{d! \rho},$$

for all $\rho \geq 1$, we establish the induction step. Clearly, the coefficients c_d form an increasing convergent sequence, as claimed.

Once we have computed all the cells of $\mathcal{A}(R)$ and their sign patterns, it is straightforward to construct T_R in $O(\rho^{d+1})$ time.

We perform step (ii) by locating the children of each cell C' in brute force, as follows. (Note that C' may appear multiple times in each and all the trees Q_C , but we apply the following procedure only once for each such cell.) For each non-zero entry b in the sign pattern of C', we check whether setting b to 0 yields a valid cell C'' on the boundary of C'. More precisely, in case of degeneracies, it might be necessary to set more signs to 0 for the resulting cell C''. To handle this issue, we iterate over all choices of j hyperplanes of R, for $j = 2, \ldots, d$, form the intersection of these j hyperplanes, and collect all other hyperplanes that vanish identically on the resulting flat. Hence, after setting b = 0, we take all zero entries in the sign pattern of C' (including b) and find all the other hyperplanes whose sign should also be set to 0, along with that of b. It thus takes $O(\rho)$ time to form the children of a cell C' in any of the trees Q_C , which, by Lemma 3.5, takes a total of $O(\rho^{d+1})$ time for all cells. Once we know the children of every cell we can assemble the trees Q_C in time proportional to their size, which is $O(d\rho^d)$.

In step (iii), we compute, for each vertex y of $\mathcal{A}(R)$ and for each hyperplane h of H, the sign of y with respect to h. These signs then allow us to decide whether h is in $\mathsf{K}(\sigma)$ for each σ in $\mathsf{BVT}(R)$ by checking whether the sign of h is positive for some of the d+1 vertices of σ and negative for others. This costs $O(dn\rho^d)$ time and, as can be easily checked, constitutes the dominant part of the preprocessing. We separate between the hyperplanes in $K(\sigma)$ and those that do nor cross σ . We (temporarily) store the sign pattern of σ with respect to the second subset.

Let $T_d(n)$ denote the maximum expected overall preprocessing time of the algorithm for an instance involving n hyperplanes in d dimensions. If we take, as above, $\rho = crd^2$, for some suitable absolute constant c, then, with high probability, the size of each recursive subproblem is at most n/r. If this is not the case, we discard the structure (that we have constructed locally for R), take a new random sample, and construct the structure anew from scratch.

All these considerations lead to the following recurrence for $T_d(n)$.

$$T_d(n) \le \begin{cases} adn\rho^d + e\rho^d T_d(n/r) & \text{for } n > \rho \\ a\rho^{d+1} & \text{for } n \le \rho, \end{cases}$$

where a is an suitable absolute constant (independent of d). Unfolding the recurrence, we get

$$T_d(n) \le adn\rho^d \left(1 + \frac{e\rho^d}{r} + \left(\frac{e\rho^d}{r}\right)^2 + \dots + \left(\frac{e\rho^d}{r}\right)^{j-1}\right) + a\left(e\rho^d\right)^j \rho^{d+1},$$

for $j = \lceil \log(n/\rho)/\log r \rceil$. Ignoring the rounding, as before, it follows that

$$T_d(n) = O\left(d\rho^{d+1}(n/\rho)^{(d\log\rho + \log e)/\log r}\right) = O\left(n^{(d\log\rho + \log e)/\log r}\right),\,$$

which is the same as our asymptotic bound on $S_d(n)$. Note again that the coefficient of proportionality is independent of d, and in fact tends to 0 as d increases.

The number of distinct cells is only $O(\rho^d)$, but because of their possible repetitions in the trees Q_C , we simply multiply by d the number of leaves.

5.2 Improved algorithm via vertical decomposition

In this subsection we improve upon Meiser's algorithm by using vertical decomposition instead of bottom-vertex triangulation. This allows us to use a smaller sample size, exploiting the smaller combinatorial dimension of vertical prisms, thereby making the query run faster. We pay for it (potentially)⁷ in the storage size, due to the discrepancy between the upper bounds on the complexities of bottom-vertex triangulation (given in Lemma 3.2) and of vertical decomposition (given in Theorem 4.6). Nevertheless, observing the data in Figure 5.3, the bounds on the storage size for BVT, at least for the case of reasonably fast queries, are already rather large, making the (possible additional) increase in the storage bound when using vertical decomposition relatively less significant. We will also use the enhancement suggested in the previous subsection, which is based on optimistic sampling (unlike the case for BVT, here using optimistic sampling does make a difference), to improve the query time further, by another factor of log d. This further enhancement faces certain additional technical issues, so we first present the standard approach, and only then discuss the improved one.

5.2.1 The data structure

The general strategy of the algorithm is similar to Meiser's: We draw a ρ -sample $R \subset H$, construct the arrangement $\mathcal{A}(R)$, compute the sign pattern of each cell (of any dimension) in $\mathcal{A}(R)$, and store the cells in a ternary trie $T = T_R$, indexed by their sign patterns, exactly as in the previous subsection. We then construct the vertical decomposition within each cell C of $\mathcal{A}(R)$ separately, a decomposition that we denote as $\mathsf{VD}(C)$, by recursing on the dimension, following the constructive definition of vertical decomposition given in Section 4.

Let $C = C_{\xi} \in \mathcal{A}(R)$ be the cell associated with the leaf ξ of the trie T. We store at ξ (or at the structure associated with C_{ξ} , which is accessible from ξ) a secondary tree Q_C that "encodes" the vertical decomposition $\mathsf{VD}(C)$ of the cell C (described in more detail below). Each leaf of Q_C corresponds to a prism $\sigma \in \mathsf{VD}(C)$.

Once all these structures have been constructed, we take each prism $\sigma \in VD(C)$, for every cell $C \in \mathcal{A}(R)$, compute its conflict list $K(\sigma)$ (in brute force, see below), and continue the main recursion (on the size of the input) on $K(\sigma)$. During the construction of $K(\sigma)$, we also obtain the partial sign pattern of all points in σ with respect to all the hyperplanes that do not cross σ , and store the resulting partial sign pattern temporarily at σ .

The recursion bottoms out when the conflict list is of size smaller than ρ . Exactly as in the structure in Section 5.1, at each such leaf-prism we compute the arrangement of the at most ρ remaining hyperplanes, and store with each cell C of this arrangement a pointer to the unique cell of $\mathcal{A}(H)$ whose sign pattern is the union of all partial sign patterns stored along the path to the leaf, including the sign pattern of C with respect to the hyperplanes of $K(\sigma)$. This sign pattern is the answer to all the queries that end up in C. The argument that justifies the last property is identical to the one given for bottom vertex triangulation.

We next describe in more detail the construction of VD(C) and the tree Q_C encoding it.

The sign pattern of C identifies the set R_0 of the hyperplanes of R that contain C (if any), the set R^+ of the hyperplanes of R that pass above C (and can only appear on its upper boundary), and the set R^- of the hyperplanes of R that pass below C (and can only appear on its lower boundary). For simplicity, we only consider the full-dimensional case (where $R_0 = \emptyset$); the lower-dimensional instances are handled in the same way, restricting everything to the flat $\bigcap R_0$ that supports C. We iterate over

⁷Since the bounds on the complexity of vertical decomposition are not known to be tight, it is conceivable that we do not pay anything extra for storage using this technique.

all pairs (h^-, h^+) of hyperplanes, such that $h^- \in R^-$ and $h^+ \in R^+$, and for each such pair, we check whether ∂C contains facets $f^- \subseteq h^-$ and $f^+ \subseteq h^+$ that are vertically visible within C. To do so, we construct the following set of halfspaces within the hyperplane $\pi_0: x_d = 0$. For each $h \in R^+$, take the halfspace in h^+ , bounded by $h^+ \cap h$, in which h^+ is below h (in the x_d -direction), and project it onto π_0 . Similarly, for each $h \in H^-$, take the projection onto π_0 of the halfspace in h^- , bounded by $h^- \cap h$, in which h^- is above h. Finally, take the projection of the halfspace in h^+ (or in h^-), bounded by $h^+ \cap h^-$, in which h^- is lower than h^+ . Denote the resulting set of halfspaces by G. See Figure Figure 5.4.

The proof of the following lemma is straightforward and hence omitted.

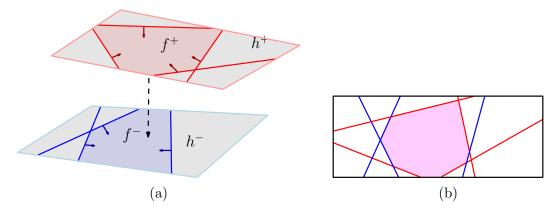


Figure 5.4: (a) The halfspaces on h^+ (resp. h^-) are depicted by the straight lines and the arrows (indicating their direction). (b) The resulting set of halfspaces projected onto the hyperplane π_0 : $x_d = 0$. Their intersection is depicted by the shaded polygon.

Lemma 5.2. There are facets $f^- \subseteq h^-$ and $f^+ \subseteq h^+$ on ∂C that are vertically visible within C if and only if the intersection of the halfspaces in G is nonempty.

To apply this lemma, we construct the halfspaces within π_0 , as prescribed in the lemma. Denote by R' the set of the (d-2)-hyperplanes (within π_0) that bound these halfspaces, and note that $|R'| \leq \rho - 1$. We then apply linear programming (LP for short) to determine whether the intersection of these halfspaces, denoted as C'_{h^-,h^+} , is nonempty. Assume that h^- and h^+ are indeed vertically visible within C. We then recurse on the convex polyhedron $C' = C'_{h^-,h^+}$. For this we need the sign pattern of C' with respect to hyperplanes in R' in the x_{d-1} -direction. We compute these signs in brute force, in $O(d\rho)$ time, with respect to a witness point within C', that the LP procedure does provide.

We have omitted in this description details concerning the handling of unbounded cells that do not have a lower or an upper boundary. Handling such cells is in fact simpler, because there is no need to pair up a facet from the top boundary with a facet on the bottom boundary. Assuming that the top boundary does not exist, we simply take each facet on the bottom boundary, intersect its hyperplane with all other hyperplanes of R (all lying below the cell), project, and recurse. We omit the further straightforward details.

We now construct the tree Q_C . Its root represents C and all the hyperplanes in R. The root has a child for each pair of hyperplanes h^- and h^+ that are vertically visible inside C. Each child v, with a corresponding pair h_v^- , h_v^+ of vertically visible hyperplanes, represents the polyhedron $C_v' = C_{h_v^-, h_v^+}'$ and the set R_v' of the (d-2)-hyperplanes in π_0 that surround C_v' , as specified in Lemma 5.2. The construction of Q_C proceeds recursively at each node v, with C_v' and R_v' as input. At level i, each node v represents a (d-i)-dimensional polyhedron C_v' within the subspace $x_d = 0, \ldots, x_{d-i+1} = 0$, and a corresponding set R_v' of fewer than ρ hyperplanes in this subspace. Each node v in Q_C has at most $\frac{1}{4}\rho^2$

children, where each child w is associated with a pair (h_w^-, h_w^+) of vertically visible hyperplanes of R'_v inside C'_v .

By Lemma 4.1, if v is a child of a node u that arises at dimension j, each of h_v^- , h_v^+ is defined by a sequence of intersections and projections of 2(d-j) original hyperplanes of R, and one additional respective original hyperplane \hat{h}_v^- , \hat{h}_v^+ . Since the other previous 2(d-j) hyperplanes are those that define u, v can be uniquely indexed from u by the pair $(\hat{h}_v^-, \hat{h}_v^+)$ of original hyperplanes. We therefore use these pairs to index the children of u. Using appropriate pointers, this takes only O(1) storage per child. The query will navigate through Q_C using these indexed links.

The recursion bottoms out at d=1, where the relevant cell C', which is equal to its trivial vertical decomposition, is just a (possibly unbounded) interval. Each leaf v_{σ} of Q_C corresponds to a prism σ in $\mathsf{VD}(C)$ which is defined by the pairs of hyperplanes associated with the nodes along the path of Q_C from the root to v.

It is noteworthy to compare this technique with the corresponding one used in Section 5.1 for bottom-vertex triangulation. The only significant difference is that here the parent-child links are indexed by a pair of hyperplanes, whereas there a single hyperplane was used.

Constructing the conflict lists. The construction continues recursively at each prism σ in the vertical decomposition of $\mathsf{VD}(R)$, with the conflict list of σ as input. To proceed, we construct, for each σ , the conflict list $\mathsf{K}(\sigma)$ of σ in brute force, by determining for each hyperplane $h \in H$, whether h crosses σ . This is done using linear programming, regarding σ as the feasible region defined by (at most) 2d linear inequalities, and regarding the normal direction \mathbf{n} of h as an objective function $\mathbf{x} \cdot \mathbf{n}$, for $\mathbf{x} \in \sigma$. By computing the minimum and the maximum values of this function over σ , we get two hyperplanes that are parallel to h and support σ . Then h crosses σ if and only if it lies (strictly) between these two supporting hyperplanes.

Note that constructing the conflict lists in the case of bottom-vertex triangulation was much simpler, since we only had to deal with the original vertices of $\mathcal{A}(R)$. Here, in contrast, the prisms have too many vertices, so constructing the conflict lists by checking which hyperplane separates the vertices of which prisms is too expensive, and one has to resort to the LP-based technique (which is different than the approach taken in [ES17]).

We do not store $K(\sigma)$ explicitly after the preprocessing is over, but only maintain it temporarily, as long as the recursive construction at σ is still going on. We only store (permanently) the random sample R_{σ} drawn from $K(\sigma)$ and its associated data structures (defined recursively). Similarly, we store the partial sign pattern with respect to the complement of the conflict list only temporarily and discard it once we have computed the complete sign patterns at the leaves.

5.2.2 Answering a query

The query with a point q follows a path in the main hierarchical tree structure, where at each step we have access to a random sample R, drawn from the conflict list of a parent prism, and we identify the prism of VD(R) that contains q. We recursively search through the structure in this manner until we reach a leaf, from which we retrieve, as in the case of BVT, the sign pattern of the cell of $\mathcal{A}(H)$ that contains q.

Consider a single step of this procedure. We compute the sign pattern of the cell C of $\mathcal{A}(R)$ containing q (with respect to the hyperplanes of the current random sample R); as before, this is straightforward to do in $O(d\rho)$ time. We then locate the leaf ξ of the top level trie that is associated with C (and the tree Q_C which encodes $\mathsf{VD}(C)$). This sign pattern also identifies (i) the set of hyperplanes that pass above C (and can contribute facets on its upper boundary), (ii) the set of hyperplanes that pass below

C (and can contribute facets on its lower boundary), and (iii) the set of hyperplanes that contain C (if C is lower-dimensional).

We then compute the hyperplane h^- (resp., h^+) that is first hit by the downward (resp., upward) x_d -vertical ray emanating from q; this too takes $O(d\rho)$ time. The pair (h^-, h^+) identifies the child v of the root of the search tree Q_C in which our search has to continue.

To continue the search from v, we apply the filtering procedure of Lemma 4.4. That is, we compute the intersection hyperplanes $h \cap h^-$, for the hyperplanes $h \in R \setminus \{h^-, h^+\}$ that pass below C, the intersection hyperplanes $h \cap h^+$, for the hyperplanes $h \in R \setminus \{h^-, h^+\}$ that pass above C, and also include the intersection $h^- \cap h^+$. We then project all these (d-2)-flats onto $x_d = 0$. This yields the set R'_v of at most $\rho - 1$ hyperplanes within $x_d = 0$. We also take the projection q' of q onto $x_d = 0$, and compute the sign pattern of q' with respect to the set R'_v and the x_{d-1} -direction. We continue the search with q' within the cell C'_v , within $x_d = 0$, that contains q' (that is, the cell that has the sign pattern that we have just computed).

In general, the search reaches node v of level i in Q_C when the query q projected into the (d-i)-dimensional subspace $x_d = 0, \ldots, x_{d-i+1} = 0$ is contained the polyhedron C'_v (also in this subspace) which is represented by v. To continue the search we find the hyperplanes h^- (resp., h^+) that is first hit by the downward (resp., upward) x_j -vertical ray emanating from q' in C'_v . The hyperplanes h^- and h^+ correspond to a pair of respective original hyperplanes (\hat{h}^-, \hat{h}^+) , that were intersected with previous floors and ceilings along the path to v so far and projected into the subspace $x_d = 0, \ldots, x_{d-i+1} = 0$. We continue the search with the child w of v in Q_C that is indexed by (\hat{h}^-, \hat{h}^+) ; w must exist by construction.

We trace the path in Q_C in this manner for the sole purpose of reaching its leaf w, which represents the prism σ in $\mathsf{VD}(R)$ containing q. This leaf stores the next random sample R_w and its associated data structures in which we continue the search.

When we reach a leaf-prism σ of the overall tree hierarchy (a prism whose conflict list is of size smaller than ρ), we compute the sign pattern of the query with respect to the at most ρ remaining hyperplanes stored at that leaf to identify the cell of the arrangement $\mathcal{A}(\mathsf{K}(\sigma))$ that contains q. We locate the leaf corresponding to σ in the trie associated with it and return the sign pattern (with respect to all of H) stored there.

Remark 5.3. Instead of answering point-location queries by returning the (sign pattern of the) cell of $\mathcal{A}(H)$ containing the query point q, as described above, and as in Meiser's algorithm, here it is somewhat more natural to return the lowest hyperplane of H (in the x_d -direction) that lies above the query point q (or a hyperplane that contains q). The ceiling of each prism containing q, along the search path in the main tree hierarchy, is a candidate for the answer, and we return the vertically closest hyperplane among these ceilings (and the hyperplanes in the leaf-subproblem). The correctness of this procedure is easy to establish, and we omit its details.

5.2.3 The cost of a query

As in Meiser's algorithm, each step of the main recursion (on the set of hyperplanes, passing from some parent subset H' to the conflict list of the vertical prism σ_q containing q in the vertical decomposition of a ρ -sample R from H') takes $O(d^2\rho)$ time. Indeed, the main operations performed in each dimension-reducing recursive step in the construction of σ_q are (i) computing the sign pattern of the query point q with respect to R, (ii) searching the trie T with the sign pattern to a leaf ξ associated with the cell C

 $^{^{8}}$ This (d-1)-dimensional sign pattern can also be computed and stored during preprocessing, but computing it on the fly, as we do here, does not affect the asymptotic cost of the query, and somewhat simplifies the preprocessing and storage.

Parameter	Value	Sample size	Using
VC-dim.	$O(d^3)$ Theorem 4.11	$O(rd^3 \log r)$	ε -net theorem (Theorem 2.2)
Shatter dim.	d(d+1) Theorem 4.11	$O(rd^2\log(dr))$	Remark 2.3
Combinatorial dim.	$b = 2d$ Corollary 4.2 $\alpha, \beta \le 2d$ Theorem 4.6	$O(rd\log(rd))$	Lemma 2.8
Optimistic sampling	$b = 2d$ $\alpha, \beta \le 2d$ Same references	O(rd)	Corollary 2.10

Figure 5.5: The different sizes of a sample R needed to ensure, with high probability, that VD(R) is a (1/r)-cutting for R, in \mathbb{R}^d , according to the different tools at our disposal. The probability increases with the constant of proportionality.

that contains q, and (iii) searching Q_C , by identifying, at each node v along this search path, the pair (\hat{h}^-, \hat{h}^+) of the original hyperplanes involved in the definition of the floor and ceiling of the corresponding projected cell. Steps (i) and (ii) take $O(d\rho)$ time, and step (iii) takes $O(d\rho)$ time at each node v, using vertical ray shootings, for a total of $O(d^2\rho)$ time. That is, the overall cost of a query is $O(d^2\rho)$ times the number of steps in the main recursion (on the size of the input).

It remains to determine how large should ρ be to make the decomposition efficient, that is, to make it be a (1/r)-cutting for a suitable parameter r. Here we do not want to use the VC-dimension or the primal shatter dimension, since they are both at least $\Omega(d^2)$. Instead, we use the smaller combinatorial dimension, via the Clarkson–Shor analysis technique. See the table in Figure 5.5 for a summary of the various bounds, as derived earlier in this paper.

The best option in Figure 5.5 (ignoring the issue of optimistic sampling, which will be discussed later in this section is the one based on the combinatorial dimension b = 2d (see Corollary 4.2), so we take

$$\rho = cbr\log(br) = 2cdr\log(2dr),\tag{5.5}$$

where c is some small absolute constant. This choice guarantees that, with constant probability (which can be made larger by increasing c), the conflict list of each prism in the vertical decomposition of $\mathcal{A}(R)$ is of size at most n/r. If we discover, during preprocessing, that this is not the case, we take, as in the case of bottom-vertex triangulation, another sample, and repeat the whole step. In an expected small number of steps we will get a sample that satisfies this property. By applying this approach at each recursive step where we draw a random sample, we may assume that this (1/r)-cutting property holds at all sampling steps, over the entire structure.

As before, this implies that the number of recursive steps is $\log_r(n/\rho) = \frac{\log(n/\rho)}{\log r}$, making the query time

$$Q(n) = O\left(\frac{d^2\rho \log(n/\rho)}{\log r}\right) = O\left(\frac{d^3r \log(dr) \log n}{\log r}\right) = O\left(d^3 \log n \cdot \frac{r \log(dr)}{\log r}\right). \tag{5.6}$$

This replaces one factor of d from the bound using bottom vertex triangulation in Eq. (5.1) by the factor $\log(dr)$. When we discuss optimistic sampling (see below) we show how to slightly improve this bound.

5.2.4 Storage

The storage required for the vertical decomposition of a ρ -sample R of some subset of the hyperplanes is estimated as follows. The trie T has a leaf for each cell of $\mathcal{A}(R)$, and the number of cells (of any dimension) is at most $e\rho^d$, by Lemma 3.5. Each cell has a sign pattern of length ρ , so the total size of the trie T is $O(\rho^{d+1})$.

By Theorem 4.6, the overall number of prisms of all dimensions (where prisms of dimension j arise in the vertical decomposition within some j-flat formed by the intersection of a corresponding subset of d-j hyperplanes of R) is at most $c'\frac{4^d}{d^{7/2}}\rho^{2d}$ for some absolute constant c'. Hence this also bounds the total number of leaves in the trees Q_C and the branching factor of our global hierarchical structure.

The depth of each leaf v of any tree Q_C that represents a j-dimensional prism is at most j, for j = 0, ..., d. Moreover, we store, at each internal node of each such tree, only the identifiers of two (original) hyperplanes. Finally, there are no unary nodes in Q_C , because no cell (or any dimension larger than 1) can have a single facet on its top boundary and a single facet on the bottom boundary. It therefore follows that the total size of the trees Q_C is at most $O(\frac{4^d}{d^{7/2}}\rho^{2d})$.

We conclude that the total storage required for VD(R) (the trie T and the associated trees Q_C of the cells C in $\mathcal{A}(R)$) is

$$O\left(\rho^{d+1} + \frac{4^d \rho^{2d}}{d^{7/2}}\right) \le c_0 \frac{4^d \rho^{2d}}{d^{7/2}},$$

for some absolute constant c_0 .

Let $S_d(n)$ denote the maximum overall storage used by the data structure for an instance involving n hyperplanes in d dimensions, ignoring the storage used for the sign patterns (with respect to the entire H) stored at the cells of the arrangements of the conflict lists of the bottommost leaf-prisms. We take, as above, $\rho = 2cdr \log(2dr)$, for some suitable absolute constant c, and repeat the sampling until the size of each recursive subproblem is n/r. This leads to the following recurrence for $S_d(n)$.

$$S_d(n) \le \begin{cases} c_0 \frac{4^d \rho^{2d}}{d^{7/2}} + c' \frac{4^d \rho^{2d}}{d^{7/2}} S_d(n/r), & \text{for } n > \rho \\ a \rho^{d+1} & \text{for } n \le \rho, \end{cases}$$

where c' is another absolute constant, and the bound at the bottom of recursion is the same as for bottom-vertex triangulation, with a suitable absolute constant a. Unfolding the recurrence, and upper bounding both factors $c_0/d^{7/2}$ and $c/d^{7/2}$ by 1, for simplicity (this holds when d is at least some sufficiently large constant), we get

$$S_d(n) \le 4^d \rho^{2d} (1 + 4^d \rho^{2d} + \dots + (4^d \rho^{2d})^j) \le c'' 4^d \rho^{2d} (4^d \rho^{2d})^j,$$

where c'' is another absolute constant (very close to 1), and $j = \lceil \log_r(n/\rho) \rceil = \lceil \log(n/\rho)/\log r \rceil$ is the depth of the recurrence. Substituting this value of j (and neglecting the rounding) we get that

$$S_d(n) = O\left(4^d \rho^{2d} (4^d \rho^{2d})^{\log(n/\rho)/\log r}\right) = O\left(4^d \rho^{2d} (n/\rho)^{\frac{2d+2d\log\rho}{\log r}}\right) = O\left(n^{\frac{2d+2d\log\rho}{\log r}}\right),\tag{5.7}$$

where $\rho = 2cdr \log(2dr)$. As is easily checked, the coefficient of proportionality is independent of d.

5.2.5 Preprocessing

We construct $\mathcal{A}(R)$, as in the case of bottom-vertex triangulation. That is, we compute the sign pattern of each vertex, and then of each cell of $\mathcal{A}(R)$ (with respect to R), and store these sign patterns in a trie $T = T_R$. This takes $O(\rho^{d+1})$ time by the procedure described in Section 5.1.4.

We next construct the trees Q_C . For each leaf ξ of T, we take the cell $C = C_{\xi}$ of $\mathcal{A}(R)$ associated with ξ , construct $\mathsf{VD}(C)$ and, in parallel, the tree Q_C , by the dimension-recursive construction described above. Specifically, for each projected subcell C', at any dimension $j \leq d$, with its associated set R' of at most ρ (j-1)-hyperplanes, we have $O(\rho^2)$ potential floor-ceiling pairs of hyperplanes in R'. For each such pair (h^-, h^+) , we determine whether h^- and h^+ are vertically visible within C', using the LP-based procedure described earlier. Using the best known randomized sub-exponential algorithm for linear programming, as presented in Gärtner and Welzl [GW96], we can solve a linear program with n constraints in d dimensions in

 $O\left(d^2n + e^{O(\sqrt{d\log d})}\right)$

expected time. It follows that the total expected time to perform the computation described above, for all $O(\rho^2)$ pairs (h^-, h^+) , is

$$O\left(\rho^2 \cdot \left(d\rho + \left(d^2\rho + e^{O(\sqrt{d\log d})}\right)\right)\right) = O\left(d^2\rho^3 + \rho^2 e^{O(\sqrt{d\log d})}\right).$$

As we already argued, the number of nodes in all trees Q_C is $O\left(\frac{4^d \rho^{2d}}{d^{7/2}}\right)$. Hence the overall cost of constructing the trees Q_C is

$$O\left(\frac{4^d \rho^{2d}}{d^{7/2}} \cdot \left(d^2 \rho^3 + \rho^2 e^{O(\sqrt{d \log d})}\right)\right). \tag{5.8}$$

Once all the leaves of Q_C (that is, prisms of VD(C)), over all cells C of $\mathcal{A}(R)$, have been constructed, we proceed to construct the conflict list of each of these prisms. Using linear programming once again, as described above, this takes $O\left(n\left(d^2\rho + e^{O(\sqrt{d\log d})}\right)\right)$ expected time per prism, for a total time of

$$O\left(\frac{4^d \rho^{2d}}{d^{7/2}} n\left(d^2 \rho + e^{O(\sqrt{d\log d})}\right)\right). \tag{5.9}$$

This step also yields the partial sign pattern of each prism, with respect to the hyperplanes not corssing it, so the bound in Equation 5.9 also bounds the cost of the preparation of these partial patterns.

If any of the conflict lists is of size larger than n/r, we repeat the whole construction with a new sample. Taking ρ as in Eq. (5.5), the probability of such a failure is small, so this resampling approach increases the expected running time by at most some small constant factor.

Let $T_d(n)$ denote the maximum overall preprocessing time of the algorithm for an instance involving n hyperplanes in d dimensions. By Equations (5.8) and (5.9), we get the following recurrence for $T_d(n)$.

$$T_d(n) \le \begin{cases} a \frac{4^d \rho^{2d}}{d^{7/2}} (n + \rho^2) \left(d^2 \rho + e^{O(\sqrt{d \log d})} \right) + b \frac{4^d \rho^{2d}}{d^{7/2}} T_d(n/r) & \text{for } n > \rho \\ a \rho^{d+1} & \text{for } n \le \rho \end{cases}$$

where a and b are suitable absolute constants (independent of d). Unfolding the recurrence, and upper bounding $a/d^{1/2}$ and $b/d^{7/2}$ by 1, for simplicity, we get

$$T_d(n) \le a' 4^d \rho^{2d} n \left(\rho + e^{O(\sqrt{d \log d})} \right) \left(\frac{4^d \rho^{2d}}{r} \right)^j + a' 4^d \rho^{2d+2} \left(\rho + e^{O(\sqrt{d \log d})} \right) (4^d \rho^{2d})^j,$$

where a' is another absolute constant and $j = \lceil \log(n/\rho)/\log r \rceil$. Substituting this value of j (and neglecting the rounding) we get

$$T_d(n) = O\left(4^d \rho^{2d+2} \left(\rho + e^{O(\sqrt{d\log d})}\right) \left(n/\rho\right)^{\frac{2d+2d\log\rho}{\log r}}\right) = O\left(n^{\frac{2d+2d\log\rho}{\log r}}\right),\tag{5.10}$$

where $\rho = 2cdr \log(2dr)$.

We can therefore conclude with the following main result of this section.

Theorem 5.4. Given a set H of n hyperplanes in \mathbb{R}^d , and a parameter r > 1, one can construct a data-structure for point location (or vertical ray-shooting) in $\mathcal{A}(H)$ that answers a query in time $O\left(d^3\log n \cdot \frac{r\log(dr)}{\log r}\right)$. The bounds on the storage and expected preprocessing costs of the structure are given in (5.7) and (5.10), respectively, where $\rho = 2cdr\log(2dr)$.

The query and storage bounds of Theorem 5.4, according to the chosen value of r, are depicted in the table in Figure 5.6.

	Query time	Storage
r	$O\left(d^3 \log n \cdot \frac{r \log(dr)}{\log r}\right)$	$O\left(n^{(2d+2d\log\rho)/\log r}\right)$
2	$O(d^3 \log d \log n)$	$O\left(n^{2d(\log d + \log\log 2d + 2 + \log c)}\right)$
d	$O(d^4 \log n)$	$O(n^{4d(1+o_d(1))})$
$d^{1/\varepsilon}$	$O(d^{3+1/\varepsilon}\log n)$	$O(n^{2d+2d\varepsilon(1+o_d(1))})$
d^d	$O(d^{d+3}\log n)$	$O(n^{2d+4+o_d(1)})$
$d^{4d/\varepsilon}$	$O(d^{4d/\varepsilon+3}\log n)$	$O(n^{2d+\varepsilon(1+o_d(1))})$

Figure 5.6: Query and storage costs for our variant of Meiser's data structure, which uses vertical decomposition, with sample size $\rho = 2cdr \log(2dr)$.

5.2.6 Optimistic sampling

We can slightly improve the query time further, by using a slightly smaller random sample. Set $\varphi = 1/(2h)$, where $h = \frac{\log(n/\rho)}{\log r}$ is the maximum recursion depth. The strategy is to take a sample of size

$$\rho = O\left(r\left(b + \ln\frac{1}{\varphi}\right)\right) = O(dr + \log\log n).$$

	Query time	Storage
r	$O\left(d^3\log n \cdot \frac{r}{\log r}\right)$	$O\left(n^{(2d+2d\log\rho)/\log r}\right)$
2	$O(d^3 \log n)$	$O(n^{2d(\log d + 2 + \log c)})$
d	$O(\frac{d^4}{\log d}\log n)$	$O(n^{4d(1+o_d(1))})$
$d^{1/\varepsilon}$	$O\left(\frac{\varepsilon d^{3+1/\varepsilon}}{\log d}\log n\right)$	$O(n^{2d+2d\varepsilon(1+o_d(1))})$
d^d	$O(\frac{d^{d+2}}{\log d}\log n)$	$O(n^{2d+2+o_d(1)})$
$d^{2d/\varepsilon}$	$O\left(\frac{\varepsilon d^{2d/\varepsilon+2}}{\log d}\log n\right)$	$O(n^{2d+\varepsilon+o_d(1)})$

Figure 5.7: Query and storage costs for the optimistic version of the structure, with $\rho = O(dr + \log \log n)$. The table only depicts the resulting bounds when dr dominates $\log \log n$.

For a fixed query point q, Corollary 2.10 implies that, with probability at least $\geq 1 - \varphi$, the prism containing q in the vertical decomposition of the arrangement of the random sample has at most n/r elements in its conflict list.

We modify the construction of the data structure, so that the recursion continues into a prism only if its conflict list is sufficiently small (i.e., of size at most n/r), in which case we call the prism light. That is, we continue the construction only with the light prisms. In order to be able to answer queries that get stuck at a heavy prism, we build $u := \beta d^2 \log(2n)$ independent copies of the data-structure, for a suitable sufficiently large constant β . Clearly, for a query point q, there are at most h nodes in the search path of the main hierarchical structure in a single copy, and the probability that at least one of the prisms associated with these nodes is heavy is at most $h \cdot \varphi \leq 1/2$. If this happens, we say that the current copy of the data structure fails for q, and we move to the next copy, starting the query process from scratch at this copy. Clearly, the expected number of nodes that the query process visits, over all copies, is O(h), and the probability that the query, with a specific point q, succeeds in at least one copy is at least $1 - 1/2^u \geq 1 - 1/(2n)^{\beta d^2}$.

To continue the analysis, we need the following lemma. In its statement, two points q, q' are said to be *combinatorially equivalent* if, for any choice of random samples, at all nodes of the main recursion, if q and q' land at the same prism, at each node along their (common) search path.

Lemma 5.5. The number of combinatorially distinct queries, i.e., the number of classes in the combinatorial equivalence relation, is at most $(2n)^{2d^2}$.

Proof: To establish the lemma, we construct the collection of all possible hyperplanes that can bound a prism, in the decomposition of the arrangement of any subset of H. Since each prism is bounded by at most 2d hyperplanes, the desired number is at most 2d times the number of all possible such prisms. By Corollary 4.7, this number is

$$N := O\left(d \cdot O\left(\frac{4^d}{d^{7/2}}n^{2d}\right)\right) = O\left(\frac{4^d}{d^{5/2}}n^{2d}\right).$$

We now form the overlay of all these hyperplanes. It is clear from the construction that for each cell of the overlay, all its points are combinatorially equivalent, so the number of desired equivalence classes is at most the complexity of the overlay of N hyperplanes in \mathbb{R}^d , which, by Lemma 3.5, is

$$\sum_{i=0}^{d} \binom{N}{i} 2^{i} \le 2 \left(\frac{2Ne}{d}\right)^{d} \le (2n)^{2d^{2}},$$

as is easily checked.

Lemma 5.5 implies that, choosing $\beta > 2$, the resulting structure will answer correctly, with probability at least $1 - 1/(2n)^{(\beta-2)d^2}$, all possible queries.

The new expected query time is

$$Q(n) = O\left(\frac{d^2 \rho \log n}{\log r}\right) = O\left(\frac{d^2 (dr + \log \log n) \log n}{\log r}\right) = O\left(d^2 \log n \cdot \frac{dr + \log \log n}{\log r}\right).$$

This expected query time is $O(d^3r \log n / \log r)$ when $\log \log n = O(dr)$, which is an improvement by a $O(\log(dr))$ factor over the previous (deterministic) bound.

Storage and preprocessing. The preprocessing proceeds exactly as in the general treatment of vertical decomposition, in Section 5.2, except that (i) the sample size is smaller, by a logarithmic factor, and (ii) we need to construct $u = O(d^2 \log n)$ independent copies of the structure. Otherwise, the algorithm and its analysis are identical to those presented above. That is, the storage used by the structure is

$$S_d(n) = O\left(d^2 \log n \cdot n^{\frac{2d+2d \log \rho}{\log r}}\right),$$

and the preprocessing cost is

$$T_d(n) = O\left(d^2 \log n \cdot n^{\frac{2d+2d \log \rho}{\log r}}\right),$$

for $\rho = O(dr + \log \log n)$.

Discussion. The improvement achieved by optimistic sampling comes at a cost. First, the algorithm is Monte Carlo, that is, with some small probability, queries may fail. We do not know how to turn it into a Las Vegas algorithm; the resampling approach that we have used earlier in this section is too inefficient, because it requires that we test all possible combinatorially distinct queries for success,, and there are too many such points, by Lemma 5.5.

Second, we only have an expected time bound for a query. We do not know how to turn it into a high-probability bound without repeating the query $\Theta(\log(1/\varphi))$ times, if we want to ensure the bound with probability at least $1-\varphi$, which kills the improvement that we have for small values of φ .

Still, optimistic sampling is an interesting alternative to consider for the problems at hand.

5.3 Point location in arrangements of low-complexity hyperplanes

Let H be a set of n low complexity hyperplanes in \mathbb{R}^d . By this we mean that each $h \in H$ has integer coefficients, and the L_1 -norm of the sequence of its coefficients is at most some (small) parameter w; we refer to the L_1 -norm of h as its complexity. We also assume that all the hyperplanes of H pass through the origin. (This involves no real loss of generality, as we can identify \mathbb{R}^d with the hyperplane $x_{d+1} = 1$ in \mathbb{R}^{d+1} , and replace each input hyperplane h by the affine hull of $h \cup \{o\}$, where o is the origin in \mathbb{R}^{d+1} .)

Low-complexity hyperplanes have been studied in the recent groundbreaking work of Kane et al. [KLM17]. They have shown that the *inference dimension* of the set of all such hyperplanes (with integer coefficients and complexity at most w) is $\delta = O(d \log w)$. Without getting into the details of this somewhat technical notion (full details of which can be found in [KLM17]), this implies that a random sample R of 2δ hyperplanes of H has the following property.

Regard each $h \in H$ as a vector in \mathbb{R}^d (it should actually be a vector in projective d-space, but we stick to one concrete real representation).⁹ Let R - R denote the set $\{h - h' \mid h, h' \in R\}$. Let x be some point in \mathbb{R}^d , and let C(x) denote the relatively open cell (actually, a cone with apex at the origin), of the appropriate dimension, that contains x in the arrangement $\mathcal{A}(R \cup (R - R))$. Then the expected number of hyperplanes of H that cross C(x) is smaller than |H|/2.

Actually, Kane et al. [KLM17] also establish the stronger property, that a random sample of $\rho := O(\delta + d \log \delta) = O(d \log(dw))$ hyperplanes of H is such that, with constant probability, every $x \in \mathbb{R}^d$ has the property that C(x) is crossed by at most $\frac{7}{8}|H|$ hyperplanes of H.

Note that C(x) is uniquely determined by the subset $R^0(x)$ of hyperplanes of R that vanish at x, and by the sequences $R^-(x)$, $R^+(x)$, where $R^-(x)$ (resp., $R^+(x)$) consists of the hyperplanes of R that are negative (resp., positive) at x, so that each of these sequences is sorted by the values $\langle h, x \rangle$, for the

⁹These arbitrary choices of affine representations of projective quantities should give us some flexibility in the algorithm that follows. However, we do not see how to exploit this flexibility; neither does the machinery in [KLM17].

hyperplanes h in the respective sequence. Note also that if $h \in H$ does not cross C(x) then it has a fixed sign with respect to all the points in the cell.

Paraphrasing what has just been discussed, a random ρ -sample R from H has the property that the cell decomposition formed by $\mathcal{A}(R \cup (R - R))$ is a (7/8)-cutting of $\mathcal{A}(H)$, with constant probability.

Preprocessing. We now apply the point-location machinery developed so far in Section 5 using $\mathcal{A}(R \cup (R-R))$ as the cell decomposition. We go briefly over this machinery, highlighting mainly the new aspects that arise when dealing with this kind of cell decomposition.

We construct a hierarchical tree structure similar to the one in Section 5.1 and Section 5.2. Here the hierarchy consists only of tries, where each trie indexes cells of an arrangement $\mathcal{A}(R \cup (R-R))$ for some random sample R. The top trie is associated with a random sample R from the entire H. Each leaf ξ of this trie corresponds to a cell C_{ξ} of $\mathcal{A}(R \cup (R-R))$, and points to a trie associated with a random sample R_{ξ} from the corresponding conflict list $K(C_{\xi})$.

Each random sample R (we abuse the notation slightly and use H to denote some conflict list in the hierarchical structure and R the random sample from H) is of size $\rho = O(\delta + d \log \delta) = O(d \log(dw))$. Each cell C of $\mathcal{A}(R \cup (R-R))$ is identified by a compact sign pattern, which, for an arbitrary point $x \in C$, consists of the set $R^0(x)$ (sorted, say, by the indices of its hyperplanes) and of the two sequences $R^+(x)$, $R^-(x)$, sorted by the values $\langle h, x \rangle$ of their hyperplanes. Clearly, this compact sign pattern is independent of the choice of $x \in C$. The trie T_R , at the present node of the structure, stores the compact sign patterns of the cells in $\mathcal{A}(R \cup (R-R))$. That is, each parent-child link in T_R is associated with some hyperplane of R, and the hyperplanes associated with the edges on the path from the root of T_R to a leaf ξ , associated with cell C_{ξ} , appear in their order R^0, R^- , R^+ , appropriately delimited, in the compact sign pattern of C_{ξ} . It follows that each node of T_R may have up to ρ children, each corresponding to a different hypeplane in R.¹⁰

The construction of $\mathcal{A}(R \cup (R-R))$ is performed using the same vertex-based scheme presented in Section 5.1.4. (Here too we expect the arrangement to be degenerate, and we handle vertices of high degree exactly as before.) We store the compact sign patterns of the cells in T_R and compute the conflict list K(C) of each cell $C \in \mathcal{A}(R \cup (R-R))$, using linear programming as in Section 5.2.5. Specifically, to check, for a hyperplane $h \in H$, whether h crosses C, we observe that the compact sign pattern of C defines it as an intersection of at most ρ halfspaces and hyperplanes, where the hyperplanes are of the form h = 0, for $h \in R^0$, and the halfspaces are of the form $h_{i+1} - h_i \geq 0$, for all the pairs of consecutive elements h_i , h_{i+1} in R^+ and in R^- . We then determine whether h crosses C using the LP-based method of Section 5.2.5 with this set of linear inequalities.

By the aforementioned properties, as established in [KLM17], we have the property that, with constant probability, the size of K(C), for every cell C, is at most $\frac{7}{8}|H|$. As before, we can ensure this property with certainty by discarding samples that do not satisfy this property, and by resampling, at each node of the recursive structure, yielding, almost surely, a structure that satisfies that the size reduction property holds at each of its nodes. As before we keep each conflict list and the sign pattern of C with respect to each hypeplane in $R \setminus K(C)$, only temporarily and discard it once the recursive preprocessing terminates. We only store permanently the hierarchy of the tries.

The recursion bottoms out at each cell C for which K(C) is of size smaller than ρ . In each such leaf-cell C, we construct the arrangement $\mathcal{A}(K(C))$ (there is no need to consider K(C) - K(C) now), in the same vertex-based manner as before, where each cell is represented by its sign pattern with respect to K(C), and store at each cell $C' \in \mathcal{A}(K(C))$ a pointer to the sign pattern of (every point in) C' with

To traverse a compact sign pattern in T_R in constant time per hyperplane, we store the children of each node in T_R in a hash table.

respect to the full original set H. This sign pattern is simply the union of the partial sign patterns computed (and stored) at the nodes of the path from the root to v, including the sign pattern with respect to K(C), as just computed; see Section 5.1.4 for details.

We note that the structure here is simpler than its counterparts considered earlier, since each of its nodes only has to store a trie; there is no need for the "cell trees" Q_C that were attached to the leaves of the tries in the previous versions.

Answering a query. A query with a point x is processed by following a path in the hierarchical structure. At each level we take the sample R and compute the compact sign pattern of x with respect to the hyperplanes of $R \cup (R - R)$. That is, we compute the sign of each $h \in R$ at x, separate the hyperplanes into the sets $R^0(x)$, $R^+(x)$, $R^-(x)$, as defined above, and sort each of $R^+(x)$, $R^-(x)$, in increasing order of the values $\langle h, x \rangle$ and sort $R^0(x)$ with respect to the indices of the hyperplanes. We then search the trie T_R with this compact sign pattern to locate the leaf ξ representing the cell C_{ξ} of $\mathcal{A}(R \cup (R - R))$ that contains x. Then we continue the search recursively at the trie stored at ξ (which is associated with a random sample out of $K(C_{\xi})$). When we reach a leaf-cell C we search the trie associated with $\mathcal{A}(K(C))$ for the appropriate cell C' of this arrangement containing x, and return the sign pattern associated with C'.

We search $O(\log n)$ tries. At each recursive step, computing the compact sign pattern of x with respect to $R \cup (R - R)$ takes $O(\rho \log \rho)$ linear tests, each taking O(d) time, for a total of $O(\rho d \log \rho)$ time. Searching the trie T_R takes $O(\rho)$ time, so the cost of the query at each visited node is $O(\rho d \log \rho)$. With the choice $\rho = O(d \log(dw))$, the total cost of the query is

$$O(\rho d \log \rho \log n) = O(d^2 \log^2(dw) \log n).$$

Storage. Each trie of the main hierarchical structure indexes a random sample R, of size $\rho = cd \log(dw)$, for a suitable absolute constant c. The size of the trie T_R is at most ρ times the number of its leaves, namely, the number of cells, of all dimensions, in $\mathcal{A}(R \cup (R-R))$ which, by Lemma 3.5, is $O((2e\rho^2/d)^d)$. So the storage used by T_R is $O(\rho(2e\rho^2/d)^d)$.

We thus obtain the following recurrence for the maximum storage $S_d(n)$ needed for an input set of n hyperplanes in d dimensions.

$$S_d(n) \le a\rho \left(\frac{2e\rho^2}{d}\right)^d + b\left(\frac{2e\rho^2}{d}\right)^d \cdot S_d\left(\frac{7}{8}n\right),$$

where a and b are absolute constants. The cost of storage at a leaf node of the structure is only $O(\rho^d)$. The solution of this recurrence is easily seen to be

$$S_d(n) = O\left(\rho^d b^j \left(\frac{2e\rho^2}{d}\right)^{dj}\right),$$

for $j = \lceil \log(n/\rho)/\log(8/7) \rceil$. Ignoring rounding, we get

$$S_d(n) = O\left(\rho^d(n/\rho)^{(d\log(2e\rho^2/d) + \log b)/\log(8/7)}\right) = O\left(n^{(d\log(2e\rho^2/d) + \log b)/\log(8/7)}\right),\tag{5.11}$$

where the coefficient of proportionality tends to 0 as d increases.

The resulting bound, which is $n^{O(d \log d)}$, falls short off the ideal bound $O(n^d)$, but is reasonably close to it, and is comparable with the previous off-ideal bounds for r = 2, although the constant of proportionality in the exponent is slightly larger, (see Figure 5.6 and Figure 5.7), topped with the fact that the query cost here is faster (by roughly a factor of d) than the best previous query costs.

Preprocessing. At each step of the main structure, with its associated random sample R or size ρ , we perform the following steps: (i) Construct the arrangement $\mathcal{A}(R \cup (R-R))$. (ii) Compute the compact sign pattern of each cell. (iii) Construct the trie T_R . (iv) Construct the conflict list of each cell.

Step (i) is carried out as in Section 5.1.4, in $O(\rho^{2(d+1)})$ time. Creating the compact sign pattern of each of the $O((2e\rho^2/d)^d)$ cells of $\mathcal{A}(R \cup (R-R))$ takes $O(\rho \log \rho)$ time, for a total of $O((2e/d)^d \rho^{2d+1} \log \rho)$ time. It is also straightforward to create T_R within the same amount of time. Finally, we compute the conflict list of each cell by solving, for each hyperplane in H, a linear program with at most ρ constraints in d dimensions. This takes, as in Section 5.2.5, $O\left(n\left(d^2\rho + e^{O(\sqrt{d\log d})}\right)\right)$ expected time per cell of $\mathcal{A}(R \cup (R-R))$, for a total expected time of

$$O\left(\left(\frac{2e\rho^2}{d}\right)^d n\left(d^2\rho + e^{O(\sqrt{d\log d})}\right)\right).$$

Let $T_d(n)$ denote the maximum overall expected preprocessing time of the algorithm for an instance involving n hyperplanes in d dimensions. We get the following recurrence for $T_d(n)$.

$$T_d(n) \le \begin{cases} a \left(\frac{2e\rho^2}{d}\right)^d n \left(d^2\rho + e^{O(\sqrt{d\log d})}\right) + a\rho^{2(d+1)} + b \left(\frac{2e\rho^2}{d}\right)^d T_d\left(\frac{7}{8}n\right) & \text{for } n > \rho \\ a\rho^{2(d+1)} & \text{for } n \le \rho, \end{cases}$$

for some absolute constants a and b. Unfolding the recurrence, and noting that the overhead is dominated by the $a\rho^{2(d+1)}$ term, we get that

$$T_d(n) = O\left(\rho^{2(d+1)}b^j \left(\frac{2e\rho^2}{d}\right)^{jd}\right)$$

where $j = \lceil \log(n/\rho)/\log(8/7) \rceil$. Substituting this value of j (and neglecting the rounding), we get

$$T_d(n) = O\left(\rho^{2(d+1)} (n/\rho)^{(d\log(2e\rho^2/d) + \log b)/\log(8/7)}\right) = O\left(n^{(d\log(2e\rho^2/d) + \log b)/\log(8/7)}\right),\tag{5.12}$$

where the coefficient of proportionality tends to 0 as d increases. In summary we have the following result.

Theorem 5.6. Given a set H of n hyperplanes in \mathbb{R}^d with vectors of coefficient of L_1 -norm bounded by w, one can construct a data-structure for point location in $\mathcal{A}(H)$ that answers a query in $O(\rho d \log \rho \log n) = O(d^2 \log^2(dw) \log n)$ time. The bounds on the storage and expected preprocessing costs of the structure are given in (5.11) and (5.12), respectively, where $\rho = O(d \log(dw))$.

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