Improved Representation of Sequence Bloom Trees

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Abstract. Algorithmic solutions to index and search biological databases are a fundamental part of bioinformatics, providing underlying components to many end-user tools. Inexpensive next generation sequencing has filled publicly available databases such as the Sequence Read Archive beyond the capacity of traditional indexing methods. Recently, the Sequence Bloom Tree (SBT) and its derivatives were proposed as a way to efficiently index such data for queries about transcript presence. We build on the SBT framework to construct the HowDe-SBT data structure, which uses a novel partitioning of information to reduce the construction and query time as well as the size of the index. We evaluate HowDe-SBT by both proving theoretical bounds on its performance and using real RNA-seq data. Compared to previous SBT methods, HowDe-SBT can construct the index in less than half the time, and with less than 32% of the space, and can answer small-batch queries nine times faster. HowDe-SBT is available as a free open source program on https://github.com/medvedevgroup/HowDeSBT.

Keywords: sequence Bloom trees, Bloom filters, RNA-seq, data structures, compression, bioinformatics

1 Introduction

Public read databases such as the Sequence Read Archive (SRA) contain a treasure trove of biological information and have the potential to become a ubiquitous community resource by enabling broad exploratory analyses. For example, given a long nucleotide sequence, which experiments in the database contain reads matching it? More concretely, which human RNA-seq experiments from the SRA contain a transcript of interest? Unfortunately, there does not exist a way for today's biologist to answer such a question in a reasonable amount of time. Tapping into the potential of these databases is hampered by scalability challenges and will require novel approaches from the algorithm community.

The computational problem falls into the widely-studied category of string alignment problems [6, 8]. However, it differs in several regards. The strings to be matched are rarely present in the database in their entirety. Instead, sequencers produce many highly fragmented copies of the desired string, each subjected to potential sequencing error. Furthermore, the scale of the databases makes traditional sequence alignment methods, such as SRA-BLAST [4], inadequate [16].

The seminal paper of Solomon and Kingsford [16] demonstrated that the above transcript question can be simplified to a question of approximate k-mer membership. Each experiment can be viewed as a collection of its constituent k-mers, and the biological question can be answered by finding all experiments which contain a high percentage of the k-mers in the query transcript. They demonstrated that this approach, even if only done approximately, is a good proxy for the answer to the transcript question. It also lends itself to answering a more broad range of questions, such as SNP presence, viral contamination, or gene fusion [3]. Their work has opened the door to a slew of data structures implementing various k-mer indices, roughly falling into two categories.

The first category of approaches are based on the Bloofi [5] data structure. Each experiment's k-mers are first stored in a Bloom filter [2], an efficient but lossy data structure for storing sets. The experiments are then grouped into a hierarchical structure (i.e. tree) based on their similarity, where each leaf corresponds to the k-mers in an experiment. Each internal node represents the union of the k-mers in its descendants. The tree allows an efficient search for experiments matching a given k-mer profile by pruning non-promising branches. Bloofi was first adapted to the sequencing context by the Sequence Bloom Tree (SBT) data structure [16], and further work improved the representation of the internal nodes [18, 17] and the clustering of the tree topology [18].

The SBT approaches aggregate k-mer information at the level of an experiment. The second category of approaches aggregate experiment information at the level of the k-mers. In such an approach, each query k-mer is independently looked up in an index to retrieve information about which experiments contain the k-mer [7, 11, 1, 12, 13, 19, 3]. In this context, experiments are referred to as colors, and such a data structure is sometimes called a colored de Bruijn graph. These approaches are complementary to the SBT and the best choice depends on the particular properties of the queries and the dataset, such as the sharedness of k-mers between experiments.

In this paper, we introduce HowDe-SBT, an improvement to the way bitvectors are represented in a SBT. We also propose a culling technique for allowing the tree to be non-binary, something that was explored in the original Bloofi paper but was not supported by subsequent SBT approaches [16, 18, 17]. We prove theoretical bounds on the performance of HowDe-SBT and also demonstrate its performance advantages on real data by comparing it to the previous SBT methods and to MANTIS, a representative from the second category of indexing methods.

2 Preliminaries

Let x and y be two bitvectors of the same length. A bitvector can be viewed as a set of the positions that are set to 1, and in this view, the set union (intersection, respectively) of x and y is equivalent to bitwise OR (AND, respectively). We write the bitwise AND between x and y as $x \cap y$, and the bitwise OR as $x \cup y$. The bitwise NOT operation on x is written as $\overline{x}$. The set difference of x and y is written as $x \backslash y$ and can be defined as $x \backslash y = x \cap \overline{y}$. The empty set is represented as a bitvector of zeros. The universal set, denoted by $\mathscr{E}$, is represented as a bitvector of ones. Given that the percentage of 1s in x is p, the *empirical entropy* of x is defined as $H(p) = -(p \log_2 p + (1-p)\log_2(1-p))$ [10].

A *Bloom filter* (BF) is a bitvector of length b, together with q hash functions, $h_1, \ldots, h_q$, where b and q are parameters. Each hash function maps a k-mer to an integer between 0 and $b-1$. To add a k-mer x to the set, we set the position $h_i(x)$ to 1, for all i. To check if a k-mer x is in the set, we check that the position $h_i(x)$ is 1, for all i. In this paper, we assume that the number of hash functions is 1.

Next, consider a rooted tree T where every non-leaf has at least two children. The parent of a non-root node u is denoted as $parent(u)$, and the set of all the leaves of the subtree rooted at a node u is denoted by $leaves(u)$. Let $children(u)$ refer to the child nodes of a non-leaf node u. Define $ancestors(u)$ as $\emptyset$ if node u is a root, and $parent(u) \cup ancestors(parent(u))$ otherwise. That is, $ancestors(u)$ are all the nodes on the path from u to the root, except u itself.

Suppose that there is a Bloom filter associated with each leaf of T. Then, define $B_\cup(u)$ for a leaf node u as its associated BF and $B_\cup(u)$ for an internal node as $\bigcup_{i \in leaves(u)} B_\cup(i)$. Note that $B_\cup(u)$ of an internal node u can be equivalently defined as $B_\cup(u) = \bigcup_{i \in children(u)} B_\cup(i)$. Define the intersection of leaf BFs in the subtree rooted at a node u as $B_\cap(u) = \bigcap_{i \in leaves(u)} B_\cup(i)$. Equivalently, $B_\cap(u) = \bigcap_{i \in children(u)} B_\cup(i)$.

In this paper, we solve the following problem:

Database input: A database $D = \{D_1, \ldots, D_n\}$, where each D_i is a BF of size b.
Query input: A multi-set of k-mers Q (called the query), and a threshold $0 < \theta \leq 1$.
Query output: The set of experiments that contain at least a fraction θ of the query k-mers, i.e. $\{i \ : \ |\{x \in Q \ : \ x \text{ exists in } D_i\}| \geq \theta \cdot |Q|\}$

Note that in this formulation, we assume that D (along with parameter b) is already given to us. How to choose b and construct D from raw reads was already described in [16].

3 Representation and querying

Let us assume we are given a forest T and a bijection between the leaves and the experiment BFs in our database. We refer to this as a *topology*, to underscore that the internal nodes are not yet assigned any bitvectors. We now show how to assign these bitvectors — B_{det} and B_{how}— and how they can be used to answer a query.

Conceptually, each node u represents the set of experiment BFs corresponding to $leaves(u)$. We observe that some positions are *determined* in u: they are set to the same value in each of $leaves(u)$. Moreover, for the positions that are determined, we know exactly *how* they are determined. Formally, we define

$$B_{\text{det}}(u) \triangleq B_\cap(u) \cup \overline{B_\cup(u)} \qquad\qquad B_{\text{how}}(u) \triangleq B_\cap(u) \tag{1}$$

Note that B_{how} is intended to only be informative for those positions that are in B_{det}.

Having B_{det} and B_{how} at each node can enable the following efficient query search; it is essentially the same strategy as in [18, 17], but adapted to the HowDe-SBT tree. When we receive the set of query k-mers Q, we hash each one to determine the list of BF positions corresponding to Q. We call this list the *unresolved* positions. We also maintain two counters: the number of positions that have been determined to be 1 (*present*), and the number of positions determined to be 0 (*absent*). These counters are both initially 0. We then proceed in a recursive manner, starting at the root of the tree. When comparing Q against a node u, each unresolved position that is 1 in $B_{\text{det}}(u)$ is removed from the unresolved list, and the corresponding bit in $B_{\text{how}}(u)$ determines which counter, present or absent, is incremented. If the present counter is at least $\theta|Q|$, we add $leaves(u)$ to the list of matches and terminate the search of u's subtree. If the absent counter exceeds $(1-\theta)|Q|$, Q cannot match any of the descendant leaves so we terminate the search of u's subtree. If neither of these holds, we recursively pass the two counters and the list of unresolved positions down to u's children. When we reach a leaf, the query unresolved list will become empty because B_{det} is all ones at a leaf, and the algorithm will necessarily terminate. Figure 1 shows an example of a tree and a query execution.

We observe that some bit positions will never be looked at during a search, as follows. First, if a position is determined at a node v, it will be removed from the query unresolved list (if it was even there) after node v is processed. We say that this position is inactive in v's descendents, since a search will never query that position. Formally, a position is *active in* $B_{det}(u)$ if it is not determined at its parent (equivalently, at any of its ancestors). Second, the only positions that are queried in $B_{\text{how}}(u)$ are those that are active and set to one in $B_{\text{det}}(u)$. We say these positions are *active in* $B_{how}(u)$.

Bits that are inactive are wasteful, since they take space to store but are never queried. We remove these bits from the bitvectors, as in [17]. Formally, let $B^{\text{sqz}}_{\text{det}}(u)$ be $B_{\text{det}}(u)$ with all the inactive bits removed, and we let $B^{\text{sqz}}_{\text{how}}(u)$ be $B_{\text{how}}(u)$ with all the inactive bits removed. $B^{\text{sqz}}_{\text{det}}$ and $B^{\text{sqz}}_{\text{how}}$ are further compressed with the general purpose RRR compression algorithm [15], and these compressed bitvectors are what, in the end, constitute our index. We note that since the removal of inactive bits changes the indices into the bitvectors, the query algorithm has to be modified accordingly by using rank and select. Since this is done in essentially the same way as in [17], we omit the details here.

4 Construction algorithm

HowDe-SBT is constructed from D in a two step process. In the first step, we construct a forest topology. We observed that tree topologies of previous SBT approaches, which were binary, resulted in some nodes which were unlikely to resolve many positions or prune any searches; the most notable example being the root of the tree. Instead, HowDe-SBT constructs a non-binary forest topology, which can allow the flexibility for avoiding such nodes and thereby potentially save query time.

First, we determine a baseline binary tree topology using the clustering algorithm of [18] as a black-box. This algorithm attempts to group together similar experiments close together in the tree. Second, for a node u, let $saturation(u)$ be the number of bits set to one and active in $B_{\text{det}}(u)$ divided by the number of bits that are active in $B_{\text{det}}(u)$. For example, in Figure 1, the left child of the root has saturation of 9/15. Since at this stage B_{det} and B_{how} are not yet computed, we estimate the saturation through a sub-sampling technique presented in [18]. Third, we identify the *culling*

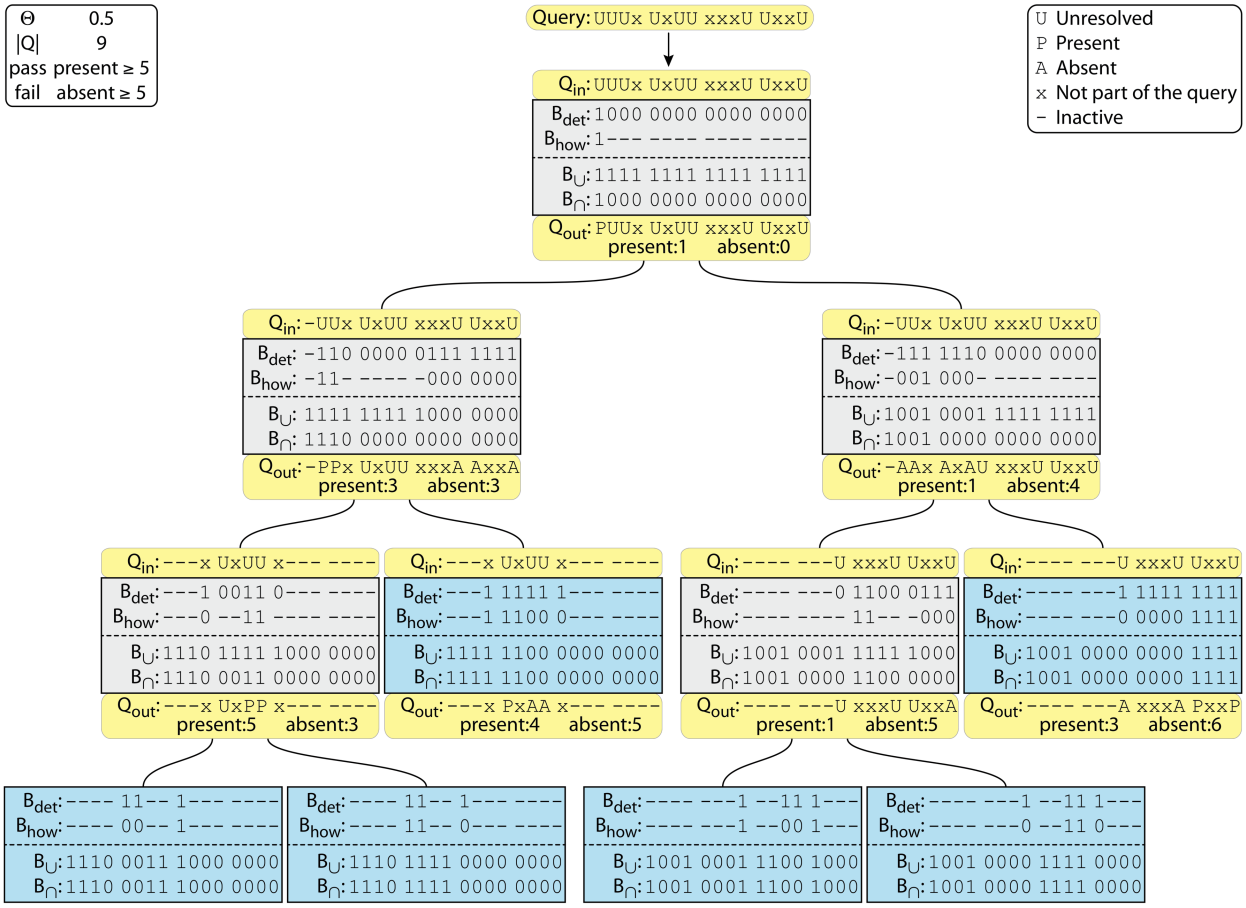


Fig. 1. Example HowDe-SBT on $D = \{1110\,0011\,1000\,0000,\ 1110\,1111\,0000\,0000,\ 1111\,1100\,0000\,0000,\ 1001\,0001\,1100\,1000,\ 1001\,0000\,1111\,0000,\ 1001\,0000\,0000\,1111\}$. Each box represents a node of the tree, with leaves shown in blue and internal nodes in gray. For conciseness, the boxes show B_{det}, B_{how}, $B_{\cup}$, and $B_{\cap}$, but do not show $B^{\text{sqz}}_{\text{det}}$ and $B^{\text{sqz}}_{\text{how}}$. The yellow boxes demonstrate the processing of an example nine k-mer query with $\theta = 0.5$. The initial query is shown at the top, with the bits corresponding to the query k-mers shown with a U. The query flows down the tree. The query state presented to a node is Q_{in} and the result from the node is Q_{out}. Some bits are resolved as either present (P) or absent (A) across the subtree. Such bits are counted in the corresponding totals and removed from further processing (hyphen) in descendants. Processing along a branch halts if either total reaches the threshold needed to determine the outcome — which in this case is 5. In this example, Q matches the first two experiments.

threshold as two standard deviations below the mean of the saturation value in the internal nodes. Fourth, we scan the baseline topology to identify internal nodes u for which $saturation(u)$ is below the threshold. These nodes are then removed from the topology, with their children reassigned as children of the removed node's parent; if no parent exists, these nodes become roots of a new tree in the forest. We call this process *culling*.

The second step of HowDe-SBT construction is to build $B^{\text{sqz}}_{\text{det}}$ and $B^{\text{sqz}}_{\text{how}}$ from the topology. Note that simply applying the definitions in Section 3 would be very inefficient. Instead, we use a two pass algorithm; in the first pass, we compute B_{det} and B_{how} in a bottom-up manner; in the second pass, we use B_{det} and B_{how} to compute $B^{\text{sqz}}_{\text{det}}$ and $B^{\text{sqz}}_{\text{how}}$ in a top-down manner.

In the first pass, we first take each leaf u and set $B_{\text{det}}(u) = \mathscr{E}$ and $B_{\text{how}}(u) = B_{\cup}(u)$. For an internal node u, we first construct $B_{\cap}(u)$ and $B_{\cup}(u)$ using the operations:

$$B_{\cap}(u) \leftarrow \bigcap_{c \in children(u)} B_{\text{how}}(c) \qquad\qquad B_{\cup}(u) \leftarrow \bigcup_{c \in children(u)} \left(\overline{B_{\text{det}}(c)} \cup B_{\text{how}}(c)\right)$$

Then, $B_{\text{det}}(u)$ and $B_{\text{how}}(u)$ are constructed by directly applying their definitions (Equation (1)). The B_{det} and B_{how} vectors can either be stored in memory for all the nodes in preparation for the second pass, or, in order to save memory, they can be written to disk and loaded to memory in the second pass only as needed. For the second pass, we start with all roots u and apply the following operations:

$$B^{\text{sqz}}_{\text{det}}(u) \leftarrow B_{\text{det}}(u) \qquad\qquad B^{\text{sqz}}_{\text{how}}(u) \leftarrow B_{\text{how}}(u) \cap B_{\text{det}}(u)$$

Then, for all non-leaf nodes u, we compute for each child c of u:

$$B^{\text{sqz}}_{\text{det}}(c) \leftarrow B_{\text{det}}(c) \cap \overline{B_{\text{det}}(u)} \qquad\qquad B^{\text{sqz}}_{\text{how}}(c) \leftarrow B_{\text{how}}(c) \cap B^{\text{sqz}}_{\text{det}}(c)$$

Finally, we scan through $B^{\text{sqz}}_{\text{det}}$ and $B^{\text{sqz}}_{\text{how}}$ to remove all the inactive bits. The result is then RRR compressed and written to disk.

Our bitvector construction algorithm visits each node twice — once on the way up, and once on the way down. At each visit, it performs a constant number of bitwise operations which each takes $\mathcal{O}(b)$ time. Similarly, the linear scan to remove inactive bits can be done in $\mathcal{O}(b)$ time by simply copying the active bits to a new vector. Furthermore, the operations our algorithm performs correctly compute $B^{\text{sqz}}_{\text{det}}$ and $B^{\text{sqz}}_{\text{how}}$, but we leave the proof for Appendix A.1. We have thus shown:

Theorem 1. *Given a database of n Bloom filters, each of size b, and a tree topology, our method constructs B^{sqz}_{det} and B^{sqz}_{how} for all nodes in $\mathcal{O}(nb)$ time.*

We note that the complexity of constructing the tree topology was not studied in [18], but the obvious implementation would take $\Omega(n^2)$ time. Though it takes negligible time on currently tested datasets, it may become the bottleneck in the future if n increases by several orders of magnitude.

5 Analysis of savings compared to previous work

In this section, we show the connection of our representation to previous approaches and analyze the improvements. The structuring of our bitvectors can be viewed as an extension of the approach in [17], which is called SSBT. The SSBT representation approach subsumes that of [18] (called AllSome-SBT), so we focus our comparison on SSBT. Briefly, SSBT uses the same approach of having a tree where the bitvectors at a node u represent, for each bit position x, whether x is 1 in all, none, or some of the $leaves(u)$. It also marks a bit position as inactive if it can never be reached during a query. The SSBT bitvectors are called u_{sim} and u_{rem}. If the SSBT is constructed using the same topology as HowDe-SBT, and HowDe-SBT is done without any culling, then the relationship of SSBT to HowDe-SBT can be summarized as a one-to-one relationship between all possible bitvector states, shown in Figure 2.

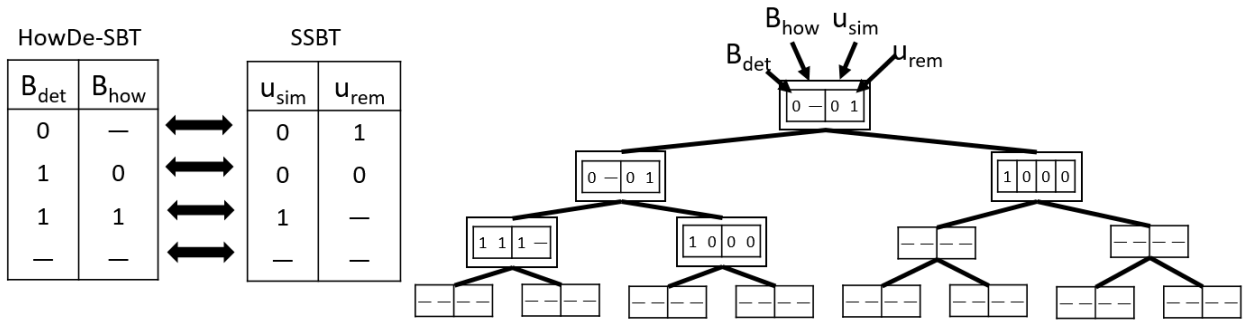


Fig. 2. The left tables show the correspondence between the possible states of SSBT and HowDe-SBT bitvectors. A dash represents an inactive bit. The tree is an example of a bit position x and its values in both representations. In this example, $n_x = 5$, $\ell_x = 3$, and $s_x = 1/3$. The nodes of T_x have a double border.

We used the SSBT representation as our starting point for HowDe-SBT, but we were guided by the intuition of 1) minimizing the number of active positions and 1 bits (to improve space), and 2) minimizing the number of bit lookups performed during a query (to improve speed). To try to theoretically quantify this improvement, we derive a savings rate per bit position x, in terms of 1) n_x, the number of nodes where x is active in B_{det}, and 2) s_x, the percentage of nodes where x is active in B_{how} that have a 1.

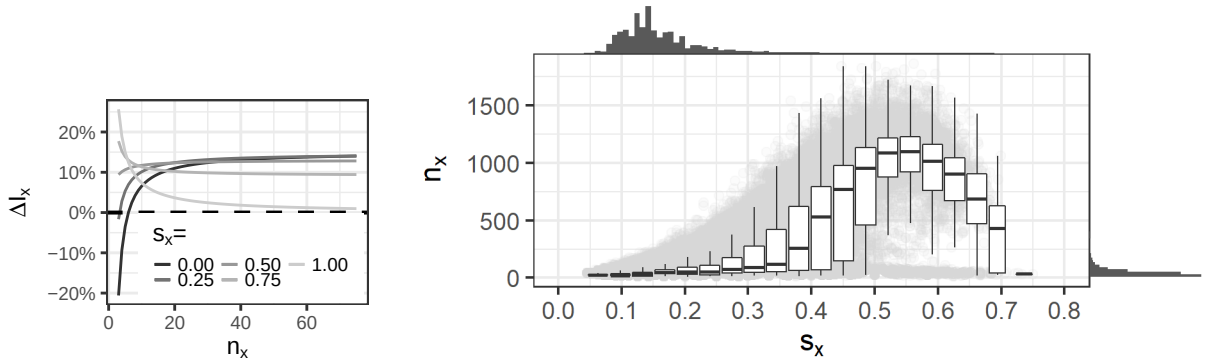
Let T be the non-culled tree topology. We are not able to directly derive the savings rate for T after RRR compression, but we instead rely on Shannon's information compression bound. For a bitvector a that is generated by a 0th order Markov model and that has a fraction p of 1s, the best that a lossless compression algorithm can achieve is $|a|H(p)$ bits. While in practice this bound might be beaten because our bitvectors are not generated by a 0th order Markov chain, we believe it is still a useful proxy for the compressability Let I_x^{howde} (respectively, I_x^{ssbt}) denote Shannon's information bound for storing all the bit values at x in T using HowDe-SBT's representation (respectively, SSBT's representation).

Theorem 2. *Let $0 \leq x < b$ be a bit position. Then,*

$$I_x^{howde} = \frac{3n_x + 1}{2} H\left(\frac{(n_x+1)(1+s_x)}{3n_x+1}\right) \quad \textit{and} \quad I_x^{ssbt} = \frac{n_x(4-s_x)+1}{2} H\left(\frac{n_x(1+s_x)+s_x-1}{n_x(4-s_x)+1}\right)$$

Proof. Let T_x be the subtree of T containing all nodes where x is active in B_{det}. Observe that T_x is indeed a subtree and it contains exactly the nodes where x is determined and their ancestors. The total number of nodes in T_x is n_x. Let ℓ_x be the number of leaves of T_x. Note that since every internal node of T has two children, $\ell_x = (n_x + 1)/2$, for all x. Note that the nodes at which the B_{how} bits are active are exactly the leaves of T_x, and s_x is the percentage of these that are 1.

Now, the nodes for which x is active in B_{det} are exactly the nodes of T_x, and thus x contributes n_x active B_{det} bits. The only time B_{how} is active at x is when B_{det} is set to 1, which is exactly at the leaves of T_x. Hence, the total number of active bits is $n_x + \ell_x = (3n_x + 1)/2$. Next, we count the number of active bits that are set to 1. The B_{det} bits set to one are exactly at the leaves of T_x. There are ℓ_x active B_{how} bits, of which a fraction s_x are set to one. Hence, the number of active bits set to one is $\ell_x(1 + s_x) = (n_x + 1)(1 + s_x)/2$.



(a) (b)

Fig. 3. (a) ΔI_x as a function of n_x, for various values of s_x. (b) The distributions of and dependencies between s_x and n_x on the real data. We use a random subsample of 1 mil bit positions for the plot, but omit those positions that are determined at a root (i.e. $n_x = 1$). These make up 15% of all values, and the all have $s_x = 0$. Each of the remaining positions are shown as a gray dot in the background. The s_x values are binned and the disribution of n_x within each bin is shown as a box plot. On the top (respectively, right) of the plot is the histogram of s_x (respectively, n_x).

To prove the statement about I_x^{ssbt}, we use the equivalences in Figure 2 as a guide. The number of active positions in the u_{sim} vectors is n_x and in the u_{rem} vectors is $n_x - s_x\ell_x$. In sum, the number of active positions is $2n_x - s_x\ell_x = \frac{n_x(4-s_x)+1}{2}$. The number of active bits in u_{sim} that are set to 1 is $\ell_x s_x$ and the number of active bits in u_{rem} that are set to 1 is $n_x - \ell_x$. Hence the number of 1 bits in S is $n_x - \ell_x(1 - s_x) = \frac{n_x(1+s_x)+s_x-1}{2}$. □

Theorem 3. *Suppose both the* SSBT *and* HowDe-SBT *are built from the same binary tree topology T. Then the number of bit lookups necessary to resolve a bit position x is $(3n_x + 1)/2$ in* HowDe-SBT*, and $(n_x(4 - s_x) - s_x)/2$ in* SSBT*.*

Proof. Consider HowDe-SBT. For every internal node of T_x, we only make one lookup to B_{det}, resulting in $n_x - \ell_x$ lookups. At the leaves of T_x, we must also look at B_{how}, resulting in $2\ell_x$ lookups. The total number of lookups is then $n_x + \ell_x = (3n_x + 1)/2$. For SSBT, we must always check both u_{sim} and u_{rem} at every node, with one exception: at a leaf of T_x, we do not need to check u_{rem} if u_{sim} is 1. Hence, the number of lookups is $2n_x - \ell_x s_x = (n_x(4 - s_x) - s_x)/2$. □

We can measure the percent improvement in the space bound as $\Delta I_x = (I_x^{\text{ssbt}} - I_x^{\text{howde}})/I_x^{\text{ssbt}}$, shown in Figure 3(a). The curves behave differently for different values of s_x, with a change in concavity between $s_x = 0.75$ and $s_x = 0.5$. In the limit, ΔI_x approaches between 9% and 14% for $s_x \leq 0.75$. The percentage improvement in the number of lookups is $1 - \frac{3n_x+1}{(4-s_x)n_x-s_x}$, which in the limit goes to $\frac{1-s_x}{4-s_x}$. The improvement in lookups is thus between 0 (for $s_x = 1$) and 25% (for $s_x = 0$); for $s_x = 0.5$, it is 14%.

We caution, however, that our analysis does not automatically translate to total improvements when all the positions are considered jointly. The total data structure size depends a lot on the structure of the input. That is reflected by the distribution of n_x and s_x in the real data, whether or not they are correlated, the entropy of all the bits together, rather than separated by position,

and the higher-order entropy of the bitvectors. The above analysis also ignores the effect of culling on the tree. These effects can be analyzed using real data, which we do in the next section.

6 Results

6.1 Experimental setup

To evaluate HowDe-SBT, we compared it against three other tools. The first are its two predecessors, AllSome-SBT [18] and SSBT [17]. The third is mantis [13], a representative from the second category of approaches to k-mer indexing, which was previously shown to outperform SBT approaches in some cases [13]. We note that mantis, unlike the SBTs, solves the query problem exactly; i.e., the SBT approaches use BFs to represent the k-mers, which can result in false positives, while mantis uses an exact representation of the k-mers. There are therefore scenarios where mantis is a more appropriate tool than an SBT, making the two approaches complementary. All experiments were run on an Intel Xeon CPU with 512 GB of RAM and 64 cores (at 2.10 GHz). Our tool is open source and available for free through https://github.com/medvedevgroup/HowDeSBT. All details about how the tools were run, including parameters, together with datasets needed to reproduce our results, are available on https://github.com/medvedevgroup/HowDeSBT/reproduce.

We used the same data for evaluation as [16], except that we removed experiments that did not have reads longer than k. This contained 2,585 human RNA-seq runs from blood, brain, and breast tissues, compromising all relevant human RNA-seq datasets in the SRA at the time of [16]. For the SBT approaches, we first processed each read fastq file to build our database as in [16], i.e. the k-mers from each sequencing run were converted (using Jellyfish [9]) to a k-mer Bloom filter ($b = 2 \cdot 10^9$, $k = 20$). For mantis, we first converted the fastq files to Squeakr-exact files [14], using slot counts estimated as per section 4.1 of [13]. For both approaches, k-mers that occurred less than than a file-dependent threshold were filtered out during construction. We initially used the thresholds from [18], but mantis was not able to run for those thresholds. We therefore used the thresholds from [13].

To study query performance, we created four types of queries: a single transcript, a batch of ten transcripts, a batch of 100, and a batch of 1000. Transcripts were picked arbitrarily from Gencode (ver. 25) transcripts that are at least k nt long. We created 100, 10, 3, and 3 replicates for each type of query, respectively. We include batches of multiple transcripts in our tests because SBT performance is known to depend on batch size [16].

6.2 Performance comparison

Table 1 shows the time and space taken to construct the index. The index took less than half the time to create and was at least 32% smaller for HowDe-SBT than for all other approaches. One downside of mantis compared to SBT methods is that it requires 5x the intermediate space (> 3 TB) and is 50x longer (132 days) to process the fastq files.

Figure 4 shows the query speed for all tools. HowDe-SBT was faster than other SBT approaches, with a 9x speedup on single-transcript batches. HowDe-SBT is more than 8 times faster than mantis on single-transcript batches, but is slower for hundred-transcript and thousand-transcript batches, by 2x and 8x, respectively. Peak RAM usage was < 1.3 GiB for all batches for all SBT tools, while it was 38 GiB for mantis for all batches (Table 3 in Appendix). Warming the cache prior to querying had some effect on the performance, but the relative performance remained the same (Figure 5 in Appendix).

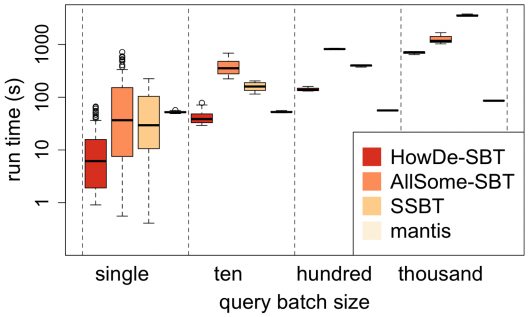


Fig. 4. Run times, shown in log-scale, comparing HowDe-SBT, AllSome-SBT, SSBT, and mantis, for single-transcript batches, ten-transcript batches, hundred-transcript batches, and thousand-transcript batches. We used 100, 10, 3, and 3 replicates, respectively. The cache was cleared prior to each run. A single thread was used.

Table 1. File sizes and build times. The intermediate space refers to the initial experiment Bloom filters for the SBT approaches and to the Squeakr files for mantis. The final index size is shown using two different sets of abundance thresholds; the rows below only show results for the thresholds from [13]. The fastq processing time is the time to convert the fastq files into either BFs or Squeakr files. The index construction time is the time to build the index from either the BFs or Squeakr files. All times shows are on one processor.

	HowDe-SBT	AllSome-SBT	SSBT	mantis
intermediate space	602 GiB	602 GiB	602 GiB	3,524 GiB
final index size (thresholds from [18])	28 GiB	176 GiB	41 GiB	N/A
final index size (thresholds from [13])	14 GiB	142 GiB	23 GiB	32 GiB
fastq processing time	63h	83h	83h	132 days
index construction time	9h	25h	57h	22h

6.3 Tree properties and culling effects

First, we investigate how many positions are active and how saturated the active bits are. The fraction of active B_{det} positions decreases going down the tree (by definition), with a median of .012 at internal nodes and 0.004 at leafs. The saturation of $B_{\text{det}}^{\text{sqz}}$ (i.e. the % of the active bits that are determined) is 100% at the leaves (by definition) and has a median of 40% at the internal nodes. The saturation of $B_{\text{how}}^{\text{sqz}}$ (i.e. the % of the active B_{how} bits that are 1) has a median of 51% at the leaves and 11% at the internal nodes. It decreases with the height of a node, meaning that at higher levels of the tree, the vast majority of positions that are determined are found to be absent rather than present. In terms of final space on disk, after RRR compression, the leaves account for only 18% of the total index size. Figure 6 in the Appendix shows the saturations in more detail.

In Section 5, we derived the reduction in space and query time for a bit position x in terms of the number of nodes where it is active in B_{det} (denoted by n_x) and the fraction of nodes where it is set to one in B_{how} (denoted by s_x). Figure 3(b) shows the distribution of these values on our tree. The median value for s_x is 0.14 and for n_x is 31, which corresponds to $\Delta I_x \approxeq 14\%$ in Figure 3(a). However, we also see a correlation between n_x and s_x (Pearson coefficient of $r = 0.63$). Any future extension of our theoretical analysis per bit position to one of all bit positions jointly should take this complexity into account. We note that the total reduction in index size of HowDe-SBT over SSBT on our data (38%) is due not only to the improved bit representation but also due to the

Table 2. The effect of culling on HowDe-SBT.

Culling threshold	total n. nodes	n. nodes culled	max depth	n. trees in forest	tree size (GiB)	median query time (s)			
						singles	tens	hundreds	thousands
0%	5169	0	26	1	14.3	5.4	45	171	720
10%	5157	12	25	1	14.3	5.1	43	170	713
20%	5056	113	23	2	14.3	6.1	39	137	712
30%	4679	490	19	8	14.9	7.7	44	155	636
40%	3997	1172	16	407	23.2	7.4	44	154	625

better tree topology that HowDe-SBT constructs; thus, a direct comparison to our theoretical predictions is challenging.

Finally, we investigate the effect of culling on the tree, as a function of the culling threshold (Table 2). At our chosen threshold of 20%, we remove about 4% of the nodes, with a negligible decrease in total index size. The query times fluctuate, showing a slight increase or decrease depending on the batch size. Overall, we conclude that culling did not have a substantial effect on the SBT. It is interesting to observe that when the threshold is high (40%), 45% of the nodes are removed but the index size actually increases by 62%. This is due to the fact that a single active bit in $B_{\text{det}}(u)$ is replaced by two active bits in u's children, if u is removed.

7 Conclusion

In this paper, we presented a novel approach for the representation of Sequence Bloom Trees and studied its performance from both a theoretical and experimental perspective. The main intuition behind our representation is that it reduces the number and entropy of the active bits. Compared to previous SBT approaches, HowDe-SBT is an improvement on all fronts; HowDe-SBT can construct the index in less than half the time, and with less than 32% of the space, and can answer small-batch queries nine times faster.

With the improvements in this paper, the SBT can already be deployed for small and mid-size databases, such as a private patient cohort or all the sequencing data in flybase.org or TCGA. Such a deployment will need to provide an automated way to update the database; while our method supports insertions in $\mathcal{O}(height \cdot b)$ time (we have omitted details due to space constraints), a quality assurance step will be necessary prior to automating database updates. It will also be necessary to provide a front-end interface (e.g. Galaxy or similar to [3]) for easy access. Such front-ends should also provide wrappers for more biologically-oriented queries (i.e. to convert "which sample has a SNP" into a k-mer query).

While HowDe-SBT already scales well enough for many databases, more algorithmic advances are needed before we are able to truly keep up with the ever-growing databases such as the SRA. This, in addition to deployment, are the next steps in the development of Sequence Bloom Trees.

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A Appendix

A.1 Proof of construction correctness

In this section, we prove the main correctness of Theorem 1. First, we need a lemma:

Lemma 1. *The following properties are true:*

$$B_{\cap}(u) = B_{\cup}(u) \qquad \textit{if } u \textit{ is a leaf} \tag{2}$$

$$B_{\cup}(u) = \overline{B_{det}(u)} \cup B_{how}(u) \tag{3}$$

Proof. Equation (2) trivially follows from the definition of $B_{\cap}$. For Equation (3), first observe that $B_{\cap}(u)$ and $\overline{B_{\cup}(u)}$ are disjoint (since $B_{\cap}(u) \subseteq B_{\cup}(u)$). Combine this with the definition of $B_{\text{det}}(u)$, and we get $\overline{B_{\cup}(u)} = B_{\text{det}}(u) \setminus B_{\cap}(u) = B_{\text{det}}(u) \cap \overline{B_{\cap}(u)}$. Negating both sides, we get $B_{\cup}(u) = \overline{B_{\text{det}}(u)} \cup B_{\cap}(u) = \overline{B_{\text{det}}(u)} \cup B_{\text{how}}(u)$ □

Theorem 1. *Given a database of n Bloom filters, each of size b, and a tree topology, our method constructs B^{sqz}_{det} and B^{sqz}_{how} for all nodes in $\mathcal{O}(nb)$ time.*

Proof. We argued about the running time in the main text and here it remains to show the correctness of the bitvector construction. Let $B^{active}_{det}(u)$ denote the active bits in $B_{\text{det}}(u)$, and $B^{active}_{how}(u)$ the active bits in $B_{\text{how}}(u)$. Recall that the active bits can be defined as:

$$B^{active}_{det}(u) \triangleq \begin{cases} \overline{B_{\text{det}}(parent(u))} & \text{if } u \text{ has a parent} \\ \mathscr{E} & \text{if } u \text{ is a root} \end{cases} \tag{4}$$

$$B^{active}_{how}(u) \triangleq B_{\text{det}}(u) \cap B^{active}_{det}(u) \tag{5}$$

We first show the correctness of the bottom-up phase in computing B_{det} and B_{how}. For a leaf u,

$$\begin{aligned} B_{\text{det}}(u) &= B_{\cap}(u) \cup \overline{B_{\cup}(u)} && \text{(by definition)} \\ &= B_{\cup}(u) \cup \overline{B_{\cup}(u)} && \text{(from Equation (2))} \\ &= \mathscr{E} \\ B_{\text{how}}(u) &= B_{\cap}(u) && \text{(by definition)} \\ &= B_{\cup}(u) && \text{(from Equation (2))} \end{aligned}$$

If u is an internal node, then it is enough to show that $B_{\cap}$ and $B_{\cup}$ are computed correctly.

$$\begin{aligned} B_{\cap}(u) &= \bigcap_{c \in children(u)} B_{\cap}(c) && \text{(by definition)} \\ &= \bigcap_{c \in children(u)} B_{\text{how}}(c) && \text{(from definition of } B_{\text{how}}) \\ B_{\cup}(u) &= \bigcup_{c \in children(u)} B_{\cup}(c) && \text{(by definition)} \\ &= \bigcup_{c \in children(u)} \left(\overline{B_{\text{det}}(c)} \cup B_{\text{how}}(c) \right) && \text{(from Equation (3))} \end{aligned}$$

For the top-down phase, we show the correctness in computing $B^{\text{sqz}}_{\text{det}}$ and $B^{\text{sqz}}_{\text{how}}$. For a root u,

$$\begin{aligned}
B^{\text{sqz}}_{\text{det}}(u) &= B_{\text{det}}(u) \cap B^{active}_{det}(u) && \text{(by definition)} \\
&= B_{\text{det}}(u) && \text{(from Equation (4) for root } u\text{)} \\
B^{\text{sqz}}_{\text{how}}(u) &= B_{\text{how}}(u) \cap B^{active}_{how}(u) && \text{(by definition)} \\
&= B_{\text{how}}(u) \cap (B_{\text{det}}(u) \cap B^{active}_{det}(u)) && \text{(from Equation (5))} \\
&= B_{\text{how}}(u) \cap B_{\text{det}}(u) && \text{(from Equation (4) for root } u\text{)}
\end{aligned}$$

Finally, consider a non-leaf node u and its child c. The algorithm first computes $B^{\text{sqz}}_{\text{det}}$ and $B^{\text{sqz}}_{\text{how}}$ with the active bits intact but set to zero. We show that this computation is correct. The final step of the algorithm, to remove inactive bits, preserves the correctness.

$$\begin{aligned}
B^{\text{sqz}}_{\text{det}}(c) &= B_{\text{det}}(c) \cap B^{active}_{det}(c) && \text{(by definition)} \\
&= B_{\text{det}}(c) \cap \overline{B_{\text{det}}(parent(c))} && \text{(from Equation (4) for non-root } c\text{)} \\
&= B_{\text{det}}(c) \cap \overline{B_{\text{det}}(u)} \\
B^{\text{sqz}}_{\text{how}}(c) &= B_{\text{how}}(c) \cap B^{active}_{how}(c) && \text{(by definition)} \\
&= B_{\text{how}}(c) \cap (B_{\text{det}}(c) \cap B^{active}_{det}(c)) && \text{(from Equation (5))} \\
&= B_{\text{how}}(c) \cap B^{\text{sqz}}_{\text{det}}(c) && \text{(from definition of } B^{\text{sqz}}_{\text{det}}\text{)}
\end{aligned}$$

This completes the proof. □

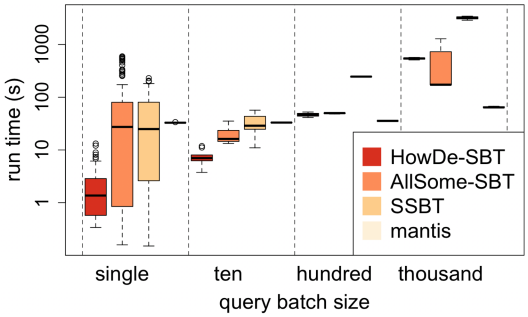

Fig. 5. Effect of warming the cache on run-times. The same experiments were run as in Figure 4. However, each batch was run two consecutive times and the reported run-times were from the second run.

Table 3. Peak resident RAM observed during queries. Values shown are the maximum over all the replicates.

	HowDe-SBT	AllSome-SBT	SSBT	mantis
single	0.7 GiB	0.3 GiB	1.3 GiB	38 GiB
ten	0.7 GiB	0.3 GiB	1.1 GiB	38 GiB
hundred	0.7 GiB	0.3 GiB	1.1 GiB	38 GiB
thousand	0.7 GiB	0.6 GiB	1.1 GiB	38 GiB

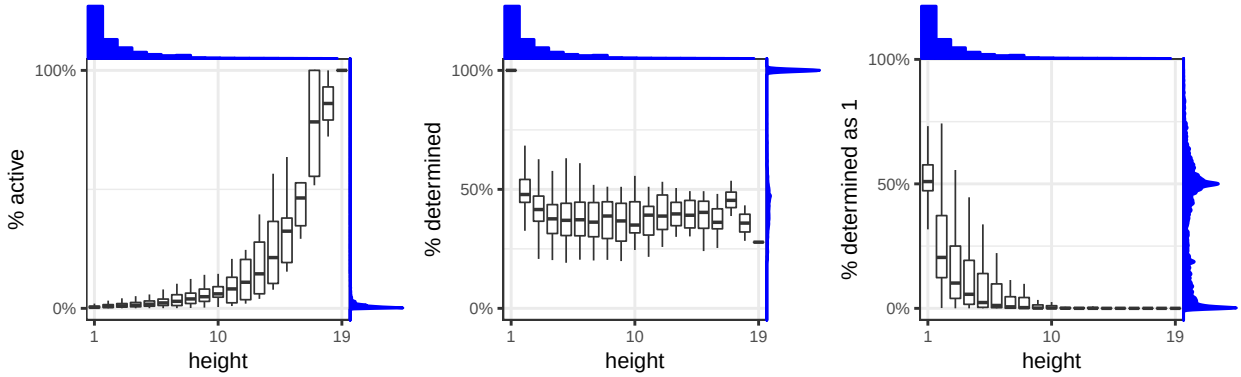

Fig. 6. The distribution of nodes' bitvector saturations, as a function of a node's height. The left panel shows barplots for the percentages of positions in the B_{det} vector that are active, the middle panel shows barplots for the percentages of those positions that are set to 1 (i.e. determined), and the right panel shows barplots for the percentage of active B_{how} positions that are set to 1. Above each plot is the histogram of height values, and to the right of each plot is the density plot of the percentages being measured in that plot.