The Log-Interleave Bound: Towards a Unification of Sorting and the BST Model

Guy E. Blelloch
Carnegie Mellon University
guyb@cs.cmu.edu

Magdalen Dobson
Carnegie Mellon University
mrdobson@cs.cmu.edu

Abstract

We study the connections between sorting and the binary search tree model, with an aim towards showing that the fields are connected more deeply than is currently known. The main vehicle of our study is the log-interleave bound, a measure of the information-theoretic complexity of a permutation $\pi$. When viewed through the lens of adaptive sorting—the study of lists which are nearly sorted according to some measure of disorder—the log-interleave bound is comparable to the most powerful known measure of disorder. Many of these measures of disorder are themselves virtually identical to well-known upper bounds in the BST model, such as the working set bound or the dynamic finger bound, suggesting a connection between BSTs and sorting. We present three results about the log-interleave bound which solidify the aforementioned connections. The first is a proof that the log-interleave bound is always within a $\log \log n$ multiplicative factor of a known lower bound in the BST model, meaning that an online BST algorithm matching the log-interleave bound would perform within the same bounds as the state-of-the-art $\log \log n$-competitive BST. The second result is an offline algorithm in the BST model which uses $O(\log \log \pi)$ accesses to search for any permutation $\pi$. The technique used to design this algorithm also serves as a general way to show whether a sorting algorithm can be transformed into an offline BST algorithm. The final result is a mergesort algorithm which performs work within the log-interleave bound of a permutation $\pi$. This mergesort also happens to be highly parallel, adding to a line of work in parallel BST operations.

1 Introduction

Many different areas of theoretical computer science are concerned with quantifying the complexity of a permutation $\pi$, ranging widely from circuit lower bounds to data compression to Kolmogorov complexity. Two such areas are adaptive sorting—that is, the design of sorting algorithms which perform faster on data which is closer to sorted by some measure—and the design of binary search trees with short query times.

Adaptive Sorting. An adaptive sorting algorithm typically pairs a measure of disorder for a list $L$ with an algorithm which is optimal for this measure. Here, optimal roughly means that sorting $L$ only requires the number of comparisons needed to distinguish it from all other lists which are more presorted than $L$ [34]. An example of such a measure is the number $I$ of inverted pairs in an unsorted list, along with an algorithm which uses $\Theta(n \log \frac{1}{n})$ comparisons for a list of length $n$ [15]. An accompanying notion is that a measure of disorder may be superior to another measure—that is, always requires fewer comparisons for any given permutation. Mannila first formalized these ideas in [31]. During the 80s and 90s, many researchers devised new measures of disorder and searched for optimal algorithms for them [15, 22, 25, 27, 28, 29, 33]; furthermore, there was also interest in work-optimal parallel versions of optimal sorting algorithms [10, 12, 30]. Culminating this line of work, Petersson and Moffat in [34] give a complete hierarchy of all known measures of disorder, along with a new measure, $Reg$, which is superior to all known measures.

A concurrent line of work in adaptive sorting initiated by McIlroy concerns itself with the information-theoretic properties of a measure of disorder rather than its strict comparison with other measures [32].

Binary Search Trees. Most work on binary search trees (BSTs) and their associated cost model, the BST model, stems from the famous dynamic optimality conjecture of Sleator and Tarjan [35], which states that there exists a binary search tree whose performance on any online sequence of searches is constant factor competitive with the best offline algorithm. In the same paper, they present the splay tree, a BST which they conjecture to be dynamically optimal.

The pursuit of dynamic optimality led to a string of work in both upper and lower bounds on the cost of a sequence of searches on a BST. Three important upper bounds in the literature are the dynamic finger bound [8, 11, 13, 14, 23, 35], the working set bound [35], and the unified bound [4, 18], which respectively state that accessing an element is fast if its key is close to the key of the previous search, if it has been searched recently, and a combination of the two. There has
also been significant work in lower bounding the cost an access sequence in the BST model. Two such lower bounds, the \textit{interleave bound} and the \textit{funnel bound}, were introduced by Wilber in [36]; a recent work by Lecomte and Weinstein [26] affirmatively settled the 30-year open question of whether the funnel bound was tighter than the interleave bound, proving a \( \lg \lg n \) multiplicative separation in some cases. Another lower bound, the rectangle bound, was introduced by Demaine et al in [16].

The BST that comes closest to dynamic optimality is the \textit{tango tree} of Demaine et al [17], which has a competitive ratio of \( O(\lg \lg n) \) with respect to the best offline algorithm. Interestingly, Wilber’s interleave bound was vital in the analysis of the competitive ratio, since the authors showed that on any access sequence \( x \), the tango tree takes time \( O(\lg \lg n \ \text{IB}(x)) \), where \( \text{IB}(x) \) represents the interleave bound of the sequence.

**Commonalities Between Sorting and BSTs.** Sorting and the BST model share commonalities beyond the obvious one that every BST can be used to sort. Notably, the dynamic finger bound, the working set bound, and the unified bound are virtually identical to measures which Petersson and Moffat place near the top of their hierarchy: Loc, Hist and Reg, respectively. The commonalities between open problems in both sorting and BSTs also extend to McIlroy’s perspective on sorting, based on whether a sorting algorithm has certain information-theoretic properties. For example, one of McIlroy’s desirable properties of a sorting algorithm was that it sorted a permutation \( \pi \) and its inverse \( \pi^{-1} \) in the same number of comparisons. Similarly, in their pursuit of lower bounds in the BST model, Demaine et al noted in [16] that it was difficult to believe Wilber’s interleave bound was tight unless they could show it required the same number of accesses on a permutation and its inverse (the interleave bound was later shown not to be tight, as noted above, without settling the question of whether it performs optimally over inverse permutations).

Although BSTs can be used for sorting and hence an efficient BST algorithm on an input sequence gives an efficient sort for that input, this limits sorting to insertion sort and importantly seems to say nothing about efficient parallel sorting. Furthermore there seems to be little work that relates sorting costs back to the BST model. In this paper we are interested in better understanding the relationship between BSTs and sorting. We focus on sequences of unique keys since almost all the interesting results for sorting and BSTs pertain to the unique key setting. In this setting both BSTs and sorting are related to the question of the “complexity” of permutations. In particular, we are interested in the case of “low” complexity, where we can add fewer than \( O(n \log n) \) points, and correspondingly fewer than \( O(n \log n) \) comparisons for sorting and less than \( O(n \log n) \) cost in the BST model.

**Arborally Satisfied Point Sets and Sorting.** One of our most important tools in connecting BSTs and sorting is the geometric interpretation of BSTs [16, 19] and apply it to the sorting problem. In this interpretation an access sequence of \( n \) keys is represented as an \( n \times n \) grid with time order (input order) on one axis (here the \( x \) axis) and key order (output order) on the other axis. Points are added to the grid to account for all keys that must be visited when searching (or inserting) the keys one at a time from left to right. Demaine et al. [16], and Derryberry, Sleator, and Wang [19] show that for any BST algorithm, the accesses plotted in the plane must satisfy the property that for every pair of points \( p, q \) (both original and added points) there is a monotonic path from \( p \) to \( q \) consisting of horizontal and vertical segments with a point at each corner. Demaine et al refer such a set of points as being \textit{arborally satisfied}, and show that any such set of size \( m \) implies the sequence of \( n \) keys can be searched (or inserted) in cost \( O(m) \) in the BST model. The geometric interpretation is convenient for sorting since it does not directly enforce an order of insertion.

As some evidence of the utility of the geometric approach, consider two standard sorting algorithms, quicksort and mergesort, and how they can be used to create arborally satisfied sets of points. In quicksort, start by taking the pivot, and adding a point across the whole row containing the pivot. Now recurse on the top and bottom halves. For each half, pick a pivot and add a point at all locations in the row that has a key in its part. Continue to the base case. This will add a point for each comparison in quicksort and hence \( O(n \log n) \) points in expectation if pivots are picked randomly. It is not hard to verify the points added in this way are arborally satisfied—clearly any point \( p \) in the bottom half can reach any point \( q \) in the top half in a monotone path by going up to the pivot row, across (left or right) to the column of \( q \) and then up to \( q \). Similarly, mergesort would add points across the middle column representing the final merge, and then for the left and right, add points along their middle columns for all points in those halves, corresponding to those merges. Recursing to the base case again gives an arborally satisfied set, and the points added correspond precisely to the comparisons made by mergesort. We can therefore interpret these two sorting algorithms as algorithms for adding points to arborally satisfy the input points.

**1.1 Our Results.** In this paper we present specific results relating sorting and BSTs using arborally satisfied sets. We introduce the \textit{log-interleave bound}, a measure of the information-theoretic complexity of a permutation \( \pi \), which is as an upper bound on the number of bits needed to encode \( \pi \). Similarly to the bounds discussed earlier, the log-interleave bound can be understood as both a measure of disorder and an upper bound in the BST model. In Section 3, we define the
log-interleave bound and show that it is comparable to Reg, the most powerful known measure of disorder. We also note that the log-interleave bound has most of the information-theoretic properties that researchers look for in sorting algorithms.

Our main results on the log-interleave bound illustrate the connections between adaptive sorting and the BST model. In the statements of these results, we use the notation LIB(\(\pi\)) to refer to the log-interleave bound of a permutation \(\pi\). This will be defined formally in Section 3.

The first result is a proof that the log-interleave bound performs within a \(\lg \lg n\) multiplicative factor of the optimal offline BST algorithm on any permutation. Somewhat similarly to Demaine et al.’s proof of the closeness to optimality of tango trees [17], our proof shows closeness to optimality by comparing the log-interleave bound with the interpolate bound, a lower bound in the BST model.

**Theorem 3.1.** For any permutation \(\pi\), \(\text{LIB}(\pi) = O(\lg \lg n \text{IB}(\pi))\).

The second result is a concrete step towards unification of sorting and the BST model: we introduce an offline algorithm in the BST model which performs accesses within \(O(\text{LIB}(\pi))\) for any access sequence \(\pi\).

**Theorem 4.1.** There exists an offline algorithm in the BST model which searches for a sequence \(\pi\) using \(O(\text{LIB}(\pi))\) accesses.

The technique used to prove Theorem 4.1 comes from a paper by Demaine et al [16] on the geometric interpretation of binary search trees, which was discussed earlier in the section.

The final result is a parallel mergesort featuring a merge step which combines recent work on parallel split and join of BSTs [5] with a BST from [24] and a novel analysis which shows that with this new merge step, the merge sort is optimal for the log-interleave bound.

**Theorem 5.1.** There exists a parallel mergesort which for any permutation \(\pi\) performs \(O(\text{LIB}(\pi))\) work with polylogarithmic span.

**Model of Computation.** Our results for the parallel algorithms are given for the binary-fork-join model [6]. In this model a process can fork two child processes, which work in parallel and when both complete, the parent process continues. Costs are measured in terms of the work (total number of instructions across all processes) and span (longest dependence path among processes). Any algorithm in the binary forking model with \(W\) work and \(S\) span can be implemented on a CRCW PRAM with \(P\) processors in \(O(W/P + S)\) time with high probability [2, 7], so the results here are also valid on the PRAM, maintaining work efficiency.

**A Note on Independent Work.** McIlroy’s paper on information-theoretic properties of sorting algorithms [32] proposes a sequential sorting algorithm called mergesort with exponential search, which performs the same number of comparisons as our adaptive merge sort. However, since his algorithm uses a merge step which takes \(O(n)\) time, the overall cost of his algorithm is still \(O(n \lg n)\). McIlroy is also aware that this merge sort is at least a factor of \(O(\lg \lg n)\) away from optimal, but the proof that we present in Section 3 is to our knowledge the first to show that the log-interleave bound is no more than \(O(\lg \lg n)\)-competitive.

### 1.2 Related Work

**Adaptive Sorting in Practice.** Adaptive sorting algorithms are widely adopted in practice; surely the most widely adopted such algorithm is *timsort*, which is implemented as a built-in library for Python, Java, Swift, and Rust, among other languages [3]. The prevalence of the algorithm in libraries indicates that in practice input sequences often do have some order to them. Timsort is adaptive with respect to Runs—roughly, consecutive monotonic sequences in an unsorted list. Optimal algorithms for Inv—the number of inverted pairs in a list—are also commonly implemented in practice [20, 21]. Both Runs and Inv are theoretically weak measures, but algorithms which are optimal for stronger measures have not received much attention from the practical community.

**Parallel BST Operations.** A third line of work which influences our algorithm design is that of parallel split, join, and merge algorithms for binary search trees. Our primary tools in this work are the work-optimal parallel split and join algorithms of Blelloch et al [5], which are themselves parallel versions of the join-based BST algorithms of Adams [1]. These are also related to Brown and Tarjan’s sequential, work-optimal algorithms for union, intersection, and difference on red-black trees [9].
1.3 Open Problems. This work takes steps towards a goal of unifying adaptive sorting and the BST model by transforming sorting algorithms into offline algorithms in the BST model. We have suggested a technique—offline arboreal satisfaction algorithms—that can settle the question of whether a sorting algorithm can be transformed into a BST algorithm. A future goal would be to tightly characterize which sorting algorithms can be transformed into offline BST algorithms, or perhaps even online BST algorithms. Obviously, not all comparison-based sorting algorithms would fit such a claim; for example, an algorithm which simply guesses and checks for the correct permutation would not. However, it may be possible to arrive at such a tight characterization by restricting the model to avoid cases like this, perhaps by restricting operations to some kind of pointer machine.

There are also open problems about the log-interleave bound that are left unresolved. One question concerning information-theoretic properties is whether the log-interleave bound sorts a permutation and its inverse in the same number of comparisons. Perhaps the most obvious problem is creating an online BST algorithm which performs within the log-interleave bound on any query sequence, or proving that an existing BST, such as the splay tree or Demaine et al’s Greedy algorithm [16], satisfies the log-interleave bound.

2 Preliminaries

We begin with some preliminaries. The preliminaries stated here are those which are strictly necessary to understand the

\[ \pi \]

where each segment is a monotonically increasing or decreasing sequence, then optimality over runs requires \( M \) comparisons when \( x \) seeks optimality for the overall region of elements recently inserted in time and space. Let \( \alpha \) refer to optimal with respect to \( \pi \) or \( \beta \) refer to \( \pi \) as the number of comparisons performed by \( \pi \) by \( \beta \) on a permutation \( \pi \).

DEFINITION 1. Let \( M \) be a measure of disorder. Then, for any permutation \( \pi \) over \( n \) elements, let \( \text{below}_M(n, \pi) \) denote all permutations \( \sigma \) over \( n \) elements such that \( M(\sigma) \leq M(\pi) \).

DEFINITION 2. Let \( M \) be a measure of disorder and let \( \mathcal{A} \) be a comparison-based sorting algorithm. Algorithm \( \mathcal{A} \) is optimal with respect to \( M \) if for any permutation \( \pi \) over \( n \) elements, \( \mathcal{A} \) performs \( O(n + \log |\text{below}_M(n, \pi)|) \) comparisons. We refer to \( \mathcal{A}(\pi) \) as the number of comparisons performed by \( \mathcal{A} \) on a permutation \( \pi \).

DEFINITION 3. Let \( M \) and \( N \) be two measures of disorder, with optimal algorithms \( \mathcal{A}_M \) and \( \mathcal{A}_N \), respectively. \( M \) is superior to \( N \) if for all permutations \( \pi \) over \( n \) elements, \( \mathcal{A}_M(\pi) = O(\mathcal{A}_N(\pi)) \). Furthermore, \( M \) is strictly superior to \( N \) if \( M \) is superior to \( N \) and \( N \) is not superior to \( M \).

Note that the notions of superiority are measured in terms of comparisons rather than total runtime; in some cases, the total runtime of an algorithm may be greater due to the required data structures.

Measures of Disorder. Next, we will discuss some measures of disorder which are most relevant to this paper.

Inv. One of the measures of disorder commonly used in practical applications, Inv is defined as the number of inverted pairs present in a list—that is, the number of pairs \( x_i, x_j \) such that \( x_j \) comes before \( x_i \) in the list, but \( x_j \) is smaller than \( x_i \). An algorithm that is optimal for Inv sorts a permutation \( \pi \) with \( I \) inverted pairs in \( O(n \log I/n) \) comparisons.

Runs. Runs is another measure of disorder used in practice. If a permutation \( \pi \) consists of \( k \) segments of length \( N_i \), where each segment is a monotonically increasing or decreasing sequence, then optimality over runs requires \( \pi \) to be sorted using \( O(n + \sum_{i=1}^{k} N_i \log \frac{N_i}{n_i}) \) comparisons.

Reg. Readers who are unfamiliar with Reg or the unified bound may wish to read over the definitions of Loc and Hist in Section 6 before proceeding. The final measure presented here is based on the idea that an element should be cheap to insert if it is close in time or keyspace to a recently inserted element. The corresponding measure is known as Reg, since it seeks optimality for the overall region of elements recently inserted in time and space. Let \( x_i \) denote the element inserted...
in the $i$th place of a permutation $\pi$. Let $d_{i,j}$ measure that number of elements between $x_i$ and $x_{i-j}$ in keyspace. This enables us to define a measure which takes advantage of closeness in keyspace or time; for insertion of an element $x_i$, let $r_i = \min_{1 \leq t \leq i} |t + d_{i-t}| + 1$ and

$$\text{Reg}(\pi) = \prod_{i=2}^{n} r_i.$$  

There is a non-BST data structure proposed by Badoiu et al in [4] which sorts a list in $O(n + \lg \text{Reg}(\pi))$ comparisons. Furthermore, Derryberry’s cache tree [18] is a BST which, when used in an insertion sort, uses $O(n + \lg \text{Reg}(\pi))$ comparisons.

**McIlroy’s Properties.** Our work is also influenced by McIlroy’s perspective on the desirable properties of an adaptive sorting algorithm. He proposes seven desirable properties, such as that a sorting algorithm should sort a permutation and its inverse permutation in the same number of comparisons. These properties are discussed in detail in Section 6.

### 2.2 Binary Search Tree Preliminaries.

We begin with a more explicit definition of the BST model. The BST model is a cost model for binary search trees with rotations. Typically when discussing algorithms and bounds in the BST model, it is assumed that the BST already contains the keys which will be queried (assume there are $n$ such keys), and the subject of interest is the amount of time it takes to access a sequence of $m$ keys, which may be repeated. In the BST model, accessing an element incurs unit cost for every node searched along the path to accessing it, plus unit cost per rotation. An algorithm for querying keys in a BST may be offline, meaning it can use knowledge of the whole access sequence, or online.

**Wilber’s interleave bound.** Next, we define Wilber’s interleave bound, a lower bound on the cost of accessing any sequence in the BST model. Given an access sequence $\pi$ consisting of the keys $x_1, x_2, \ldots, x_n$, fix a static tree $P$ (meaning it will not be rotated) with the keys in $\pi$ at the bottom in the order they appear in $\pi$, as shown in Figure 1. Calculate the interleave bound of $\pi$ as follows: query the keys in $\pi$ in sorted order. For each vertex $v_j$, label each element $i$ of the sequence with $R$ or $L$, depending on whether accessing $i$ in $P$ goes through the right or the left subtree of $v_j$, respectively (if $i$ is in neither subtree, give it no label). The interleave bound of $v_j$, denoted $\text{IB}(v_j)$, is the number of switches between $R$ and $L$ in the labels of the access sequence. The interleave bound of the entire access sequence $\pi$ is calculated as follows:

$$\text{IB}(\pi) = \sum_{v \in P} \text{IB}(v_j).$$

See Figure 1 for an example calculation.

**Arborally Satisfied Sets.** In [16], Demaine et al formalize a connection between binary search trees and points in the plane satisfying a certain property. One of Wilber’s lower bounds in the BST model [36] is formulated using the following geometric description of a search sequence: plot the search sequence on points in a plane where one axis represents key values and the other axis represents the ordering of the search sequence (that is, time). In the context of sorting, these axes can also be referred to as input order and output order. In this work, we use the horizontal axis for time and the vertical access for keyspace.

In addition to plotting the search sequence on the plane, one can also plot the key values of the nodes which a BST algorithm accesses (for search or rotations) while searching for a node. When searching for an element $x_i$ which is inserted at time $i$, the values of the nodes in the search path are plotted on the same vertical. Demaine et al proved that such a plot satisfies the following property:

**Definition 2.1.** Given a set $P$ of points in the plane, $P$ is **arborally satisfied** if for every two points $x,y \in P$ that are not on the same vertical or horizontal, the rectangle defined by $x$ and $y$ contains at least one point on an edge adjacent to $x$ and at least one point on an edge adjacent to $y$.

See Figure 4 for an example of an arboreally satisfied set consisting of a search sequence and further accesses which arborally satisfy the set.

Instead of using a BST to arborally satisfy an access sequence, one can also use an algorithm that directly places points in the plane to produce an arboreally satisfied set.

**Definition 2.2.** Given a set of points in the plane corresponding to an access sequence $\pi$, an **offline arboreal satisfaction algorithm** adds points to the plane to make an arboreally satisfied set. An **online arboreal satisfaction algorithm** also adds points in the plane to form an arboreally satisfied set, but it cannot use knowledge of future accesses.
Demaine et al show that a BST algorithm is equivalent to an arboral satisfaction algorithm, but they also show a more surprising result: an arboral satisfaction algorithm is equivalent to a BST algorithm. Specifically, they show that an offline arboral satisfaction algorithm which requires \( f(\pi) \) accesses to arborally satisfy a search sequence \( \pi \) can be transformed to an offline BST algorithm which requires \( O(f(\pi)) \) accesses to search for the elements of a sequence \( \pi \). They also showed the analogous statement for offline BST algorithms.

3 The Log-Interleave Bound

In this section, we define the log-interleave bound and prove some of its desirable properties. Then, we go on to show that the log-interleave bound is within a \( \lg \lg n \) multiplicative factor of a known lower bound in the BST model.

**Defining the log-interleave bound.** The tools for calculating the log-interleave bound are similar to the interleave bound. Given an access sequence \( \pi \), fix a static tree \( P \), and for each vertex \( v_j \), label the elements of the sorted sequence according to whether they access the left or right subtree of \( v_j \). Then let \( L_{v_j}(\pi) \) be the labeled sequence. Let \( D(L_{v_j}(\pi)) \) refer to the decomposition of \( L_{v_j}(\pi) \) into the smallest possible number of runs of consecutive Rs or Ls, where an element of \( D \) refers to a run and has a size corresponding to the number of elements in that run. Then the log-interleave bound of \( v_j \) is calculated as follows,

\[
\text{LIB}(v_j) = \sum_{r \in D(L_{v_j}(\pi_j))} \log(|r| + 1),
\]

and the log-interleave bound of \( \pi \) is calculated similarly to the interleave bound:

\[
\text{LIB}(\pi) = \sum_{v_j \in P} \text{LIB}(v_j).
\]

See Figure 1 for an example calculation of the log-interleave bound, and to see how it differs from the interleave bound.

### 3.1 Properties of the log-interleave bound

**Encoding.** We first show that the log-interleave bound upper bounds on the number of bits to encode a permutation, meaning it is also an upper bound on the information content of permutations.

**Lemma 3.1.** A permutation \( \pi \) can be encoded in \( O(\text{LIB}(\pi)) \) bits.

**Proof.** The proof is by induction on the subtrees. Assume inductively that a permutation \( \pi \) can be encoded in \( k \times \text{LIB}(\pi) \) bits for some constant \( k \). Clearly this is true for the leaves, which contain a single element. For an internal node, we need to encode the permutation defined by each of its two children, and how the two permutations are interleaved. The costs of encoding the two children are accounted for in the \( k \times \text{LIB}(\pi_i) \) bits for each child subtree \( \pi_i \) inductively. To encode the interleaving we can use a code such as the gamma code to encode the length of each run. Such a code requires \( k \log i \) bits to encode \( i \), and hence can be charged to the log-interleave bound for that node. We might want to encode the overall size \( n \), which can be done easily in \( k' \log n \) bits and is subsumed by other terms by choosing large enough \( k \).
Both terms are dominated by the last term of the sum, which is $O(\pi)$ elements permuted according to the bit-reversal sequence—that is, $1, 1 + \sqrt{n}, 1 + 2\sqrt{n}, \ldots, 1 + (\sqrt{n} - 1)\sqrt{n}, 2, 2 + \sqrt{n}, \ldots, 2 + (\sqrt{n} - 1)\sqrt{n}, \ldots, n$.

The log-interleave bound of this permutation is calculated as follows: letting the root of the tree be depth 0, note that for every balanced tree node of depth $i \geq \lg \sqrt{n}$, the input is sorted, so there will simply be two runs one on the left and one on the right, each of size $n/2^i$. Now consider the levels above $\lg \sqrt{n}$. The number of nodes at each level is $2^i$. Furthermore, the number of runs within each node is $2\sqrt{n}$, and the size of each run is $\sqrt{n}/2^i$ (i.e., the number of elements covered by the node, $n/2^i$, divided by the number of runs, $\sqrt{n}$), as illustrated in Figure 2. This gives a total log-interleave bound cost for the permutation $\pi$ across levels of

$$\text{LIB}(\pi) = \sum_{i=0}^{(\lg \sqrt{n})-1} 2 \cdot 2^i \sqrt{n} \lg \left(\frac{\sqrt{n}}{2^i}\right) + \sum_{i=\lg \sqrt{n}}^{(\lg n)-1} 2 \cdot 2^i \lg \left(\frac{n}{2^i}\right)$$

Both terms are dominated by the last term of the sum, which is $O(n)$, so the total cost is $O(n)$.

To show that $\text{Reg}(\pi) = \theta(n \log n)$, consider calculating $r_i$ for any element such that $i > n/2$. Consider inserting element $i + j\sqrt{n}$ and searching for the element which minimizes $r_i$. The closest inserted element to it in keyspace is $(i - 1) + j\sqrt{n}$; it has $d = 0$ and $t = \sqrt{n}$. Choosing an element further back in time will only increase $t$ and $d$, so only elements inserted after $(i - 1) + j\sqrt{n}$ are possible minimizers.

Consider increasing the previous candidate by 2 to $(i - 1) + (j + 1)\sqrt{n}$—then, $d$ must increase by 1 since $(i - 1) + (j + 1)\sqrt{n}$ is now in between the current element and the minimizer. Increasing $j$ by 1 until $j$ hits $\sqrt{n} - 1$ increases $d$ by at least 1 each time.

Now, examine the situation where the minimizer is some $i + (j - k)\sqrt{n}$. If $k = 1$, then every element $m + (j - 1)\sqrt{n}$ is in between the target element and the minimizer, and there are $\sqrt{n}/2$ such elements by our assumption that the first $n/2$ elements have already been inserted. Decreasing $k$ towards 1 only increases $d$ and $t$, since now the set of in between elements includes, for example, $i + (j - 1)\sqrt{n}$.

Thus we have shown that after the first $\frac{n}{2}$ elements are inserted, each remaining element has a cost of $O(\log n)$ to insert, so a Reg-optimal algorithm would perform $\theta(n \log n)$ comparisons.

**Bit-reversal permutation.** For the next lemma, we will need to define a particularly useful permutation. The bit-reversal permutation on $n = 2^k$ keys is generated by beginning with the sorted list $[0, 1, \ldots, n]$, writing each key in binary, then reversing the bits of each key. For example, the bit-reversal permutation on 8 keys is $[0, 4, 2, 6, 1, 5, 3, 7]$. Wilber showed in [36] that any BST algorithm takes $\theta(n \log n)$ time to query the bit-reversal permutation.

The bit-reversal permutation can also be constructed using the following algorithm: start with a sorted list of keys. Let $m = 2$, and place all keys $k$ such that $k \mod m$ is odd in the second half, and all other keys in the first half. Recursively repeat this routine on each half, multiplying $m$ by two each time. This construction illustrates that if we fix a static tree $P$ with keys of the bit-reversal permutation at the bottom, at each vertex $v$ of $P$, querying the keys in sorted order will switch between left and right subtrees of $v$ on each query.

**Lemma 3.3.** The log-interleave bound is not superior to Reg.

**Proof.** Consider the permutation $\pi$ obtained by splitting the sorted list into $n/\log n$ segments of equal size, and then permuting those $n/\log n$ segments according to the bit-reversal permutation.

Due to the properties of the bit-reversal sequence, the interleave bound of $\pi$ will be the same as for a list with $n/\log n$ elements permuted according to the bit-reversal sequence—that is, $(n/\log n) \log(n/\log n) = O(n)$. In $\pi$, every block is of size $\log n$, so to calculate the log-interleave bound, we multiply by $\log \log n$ on all but the bottom $\log \log n$ levels. Thus, the log-interleave bound of $\pi$ is $\theta(n \log \log n)$.
Since all but \( n/\lg n \) elements are next to their adjacent element, \( r_i = 2 \) for all but these elements. In the worst case, \( r_i = n \) at each of these elements. Then, letting \( \mathcal{A}_{\text{Reg}}(\pi) \) be the cost of a Reg-optimal algorithm on \( \pi \),

\[
\mathcal{A}_{\text{Reg}}(\pi) = O\left(n + \lg \left(\prod_{i=1}^{\lfloor \log n \rfloor} n \right)\right)
= O\left(n + \frac{n}{\lg n} \lg n \right) = O(n)
\]

\[\Box\]

**Other properties of the log-interleave bound.** As noted in Section 1, McIlroy invented an algorithm which he calls \( \text{Reg} \)-sort with exponential search, which performs the same number of comparisons (but in \( \theta(n \lg n) \) total time) as an algorithm optimal for the log-interleave bound. He shows that this \( \text{Reg} \)-sort is optimal over reversal, weak composition, weak segmentation, riffle shuffles, and runs, fulfilling all but one of his criteria. Strong segmentation fails due to the example described in the previous paragraph. Refer to Section 6 for a longer discussion of these properties.

**Relation to Practical Measures of Disorder.** As noted in Section 1, the two measures of disorder that are most widely used in practical adaptive sorting are Runs and Inv. As mentioned in the previous paragraph, McIlroy’s work shows that the log-interleave bound is optimal over Runs; here, we show that the log-interleave bound shares the same superiority relation with Inv that it does with \( \text{Reg} \): it is neither superior to Reg, nor is Reg superior to it.

First, note that for an algorithm to be optimal for Inv, it must sort a permutation \( \pi \) in \( \sum_{i=1}^{n} \lg |i - \pi(i) + 1| \) comparisons [34].

**Lemma 3.4.** The measure Inv is not superior to the log-interleave bound.

**Proof.** This follows from the fact that Reg is superior to Inv (Lemma 3.2), and Reg is not superior to the log-interleave bound. \[\Box\]

**Lemma 3.5.** The log-interleave bound is not superior to Inv.

**Proof.** Consider the permutation \( \pi \) constructed by breaking the sorted list into \( n/\lg n \) sorted segments of size \( \lg n \) and then taking the last element of each segment and permuting these elements among each other according to the bit-reversal sequence, as illustrated in Figure 3.

First, we calculate the cost of sorting under \( \mathcal{A}_{\text{Inv}} \)—that is, an algorithm optimal for Inv. A rough upper bound suffices: note that each element that is in its sorted position incurs only unit cost. Upper-bounding the out-of-order elements with cost \( \log n \) gives an upper bound of \( O(n) \) for sorting the sequence.

Now, to calculate the log-interleave bound, refer to Figure 3 for an illustration of one merge step; similarly to the proof of Lemma 3.3, due to the properties of the bit-reversal sequence, every merge step at a level of the tree above which the data is not perfectly sorted will have cost \( O(\log \log n) \cdot \frac{n}{\lg n} \). Thus the overall cost under the log-interleave bound is \( \theta(n \log \log n) \). \[\Box\]

### 3.2 Comparing the Log-Interleave Bound with Wilber’s Interleave Bound

A natural question one might ask about a BST algorithm or an adaptive sorting algorithm is how far, in the worst case, is the cost of this algorithm from any known lower bounds? Or, in other words, how close is this algorithm to optimal? In this section, we will settle this question for the log-interleave bound in the BST model. Lemma 3.3 contains an example showing that on one particular sequence, the log-interleave bound is an \( O(\log \log n) \) multiplicative factor slower than another measure of disorder. Here, we will show that this separation from optimality is tight, culminating in the following theorem:

**Theorem 3.1.** For any permutation \( \pi \), \( \text{LIB}(\pi) = O(\log \log n \cdot \text{IB}(\pi)) \).

As mentioned earlier, \( \text{IB}(\pi) \) refers to Wilber’s interleave bound.

The proof will proceed by first characterizing the situation where the log-interleave bound and the interleave bound differ the most from each other, and then proving that that difference is no more than \( O(\log \log n) \), multiplicatively.

**Lemma 3.6.** For a permutation \( \pi \), let \( v \) be a vertex of the corresponding static tree \( P \) such that \( \text{IB}(v) = S \). Then \( \text{LIB}(v) \) will differ from \( \text{IB}(v) \) by the greatest amount when each “run” of \( L \) or \( R \) in the labeled sequence \( L_v(\pi) \) is the same size.

**Proof.** Let \( r_i \) be the size of each run of \( L \) or \( R \) in the labeled sequence, then \( \sum_{i=1}^{\ell} \lg r_i \) is maximized when each \( r_i = r_j \) due to the concavity of the logarithm. \[\Box\]
LEMMA 3.7. For a permutation π, let v be a vertex of the corresponding static tree P such that IB(v) = S. Furthermore, let the number of leaves below vertex v be n. Then for any \(\frac{n}{\lg n} \leq \alpha \leq n\) and some constant c,
\[
c \lg (\alpha + 1) \left( S + \frac{n}{\lg n} \right) \geq 5 \lg \left( \frac{n}{S} + 1 \right).
\]

Before the proof, note that the expression on the right-hand side captures the log-interleave bound of an access sequence whose runs of L and R are all the same size. The left-hand side is an expression which we will show is bounded by \(\lg \lg n\) times the interleave bound.

**Proof.** Begin by assuming \(\alpha = \lg n\), the lower end of its range. Then the expression we are proving reads:
\[
c \lg(\lg n + 1) \left( S + \frac{n}{\lg n} \right) \geq 5 \lg \left( \frac{n}{S} + 1 \right).
\]
Now, examine the cases where the two added terms on the left may each be smaller than the term on the right. If the first term is smaller:
\[
\lg(\lg n + 1)S < S \lg \left( \frac{n}{S} + 1 \right) \implies \lg(\lg n + 1) < \lg \left( \frac{n}{S} + 1 \right) \implies \lg n < \frac{n}{S} \implies S < \frac{n}{\lg n}.
\]
This shows that when \(S \geq \frac{n}{\lg n}\), the inequality is true. Now, when \(S < \frac{n}{\lg n}\), the second term in the sum dominates. When the second term dominates, the expression reads
\[
c \lg(\lg n + 1) \cdot \frac{n}{\lg n} \geq \frac{n}{\lg n} \lg(\lg n + 1)
\]
which is self-evidently true for all \(c \geq 1\).

So far, we have shown that our inequality holds when \(\alpha\) is at its smallest, so we must examine the expression for other \(\alpha\). To do this, examine the derivative of the right-hand expression with respect to \(\alpha\); here, the +1s in the logarithm are omitted since they do not affect whether the derivative increases or decreases:
\[
\frac{d}{d\alpha} \text{(RHS)} = \frac{S}{\alpha \ln(2)} + \frac{1 - \ln(\alpha)}{\alpha^2 \ln(2)}.
\]
As \(\alpha\) increases from \(\lg n\) to \(n\), the derivative begins positive, then decreases to zero, then continues decreasing. Hence, the two smallest points of the expression are at the endpoints, \(\alpha = \lg n\) and \(\alpha = n\). The case where \(\alpha = \lg n\) is already covered above, so it remains to check when \(\alpha = n\):
\[
\lg(n + 1)(S + 1) \geq S \lg \left( \frac{n}{S} + 1 \right)
\]
which is clearly true. □

Now, these two lemmas are put together to prove Theorem 3.1.

**Proof.** [Proof of Theorem 3.1] Let \(P\) be the static tree corresponding to \(\pi\), and for each vertex \(v_i\) of \(P\), let \(S_i = \text{IB}(v_i)\). By Lemma 3.6, we can assume that if the number of leaves below \(v_i\) is \(n_i\), then \(\text{LIB}(v_i) = S_i \lg \left( \frac{n_i}{S_i} + 1 \right)\). Then \(\text{IB}(\pi) = \sum_{i=1}^{n-1} S_i\).
Next, we can use the upper bound on \(\text{LIB}(v_i)\) from Lemma 3.7 to upper bound \(\text{LIB}(\pi)\):
\[
\text{LIB}(\pi) \geq \sum_{i=1}^{n-1} c \lg \lg \left( S + \frac{|v_i|}{\lg n} \right) = c \lg \lg \left( \text{IB}(\pi) + \frac{\lg n}{\lg n} \sum_{i=1}^{n-1} 2^i \frac{n}{2^i} \right) = c \lg \lg n (\text{IB}(\pi) + n) = O(\text{IB}(\pi) \lg \lg n).
\]
□
4 Offline BST Algorithm

In this section, we present an offline BST algorithm that uses $O(\text{LIB}(\pi))$ accesses for any permutation $\pi$. This algorithm makes use of a transformation devised by Demaine et al in [16] from points in the plane satisfying a certain property to an offline algorithm in the BST model. The transformation completes the proof of the following theorem:

**Theorem 4.1.** There exists an offline algorithm in the BST model which searches for a sequence $\pi$ using $O(\text{LIB}(\pi))$ accesses.

The offline arboral satisfaction algorithm can be found in Algorithm 1. We named this algorithm *arboral mergesort*, since it works by recursively dividing the input in half, arborally satisfying each half, and then combining the two halves by satisfying any unsatisfied rectangles between points in one half and points in the other. The merge routine, found in Algorithm 3 and named *arboral merge*, merges two arborally satisfied sets $A_L, A_R$ by using the keys of $A_L$ to split $A_R$ into “blocks” of keys in $A_R$ that remained consecutive after the merge and vice versa; then, it combines these blocks into one arborally satisfied set.

The arboral merge works as follows: let $A_L$ contain $h$ keys and $A_R$ contain $n - h$ keys. For a block in $A_L$ whose leftmost element was inserted at time $t$, the algorithm adds accesses of the first and last element (in keyspace) of the block at time $h$—that is, on the first vertical line in $A_R$—and at the vertical line corresponding to time $t$. It then adds any additional accesses needed on those lines to make the set arborally satisfied. Furthermore, it adds accesses of the first and last element at time 0 and time $n - 1$.

A rough intuition behind this algorithm is that the purpose of the points added down the middle of the merge of $A_L \cdot A_R$ is to join the two sets together, and the points added at the ends of the merged set serve to “rebalance” the set so that future merges retain its desired query times.

An example of this algorithm can be found in Figure 5.  

**Proof Overview.** Now we build up to the proof of Theorem 4.1. First, we show that the arboral mergesort returns an arborally satisfied set. Then, as a warmup, we prove that any split of a set that has been satisfied using the arboral mergesort requires at most $O(\lg n)$ additional access to remain arborally satisfied. Next, we show via example that as initially written, the algorithm does NOT have all the properties needed to prove that it only requires $O(\text{LIB}(\pi))$ accesses for any permutation $\pi$. Finally, we give a construction to amend the arboral mergesort so that it has the desired property.

First, we show correctness of Algorithm 1.

**Lemma 4.1.** Algorithm 1 is correct; that is, it outputs an arborally satisfied set containing the access sequence $\pi$.

**Proof.** It is sufficient to show that Algorithm 3 always returns an arborally satisfied set if its inputs are themselves arborally satisfied. Assume that two inputs $A_L, A_R$ are arborally satisfied. Without loss of generality, we will show that in the combined grid, $A_L$ remains arborally satisfied after the merge step. We will consider an arbitrary “block”, i.e. a horizontal section of the grid that is arborally satisfied by Algorithm 2 during the merge step. In either case, the block itself is arborally satisfied by the definition of Algorithm 2. Now we consider any other unsatisfied rectangles that may be created by the additional
Case 1: the block contains points only in $A_R$. In this case there will be points placed on the left and right (horizontal) boundaries of $A_L$. The points will correspond to the largest and smallest element in the block; since the blocks above and below will also have points on the left and right boundaries placed at their largest and smallest element, any rectangle between a point in $A_L$ and a point in the block we consider must contain one of the aforementioned boundary points of the slices above and below. Thus it cannot create any unsatisfied rectangles in $A_L$.

Case 2: the block contains points only in $A_L$. Since $A_L$ is arborally satisfied, we need only consider unsatisfied rectangles created by the additional accesses we added. However, similarly to Case 2, due to the fact that each block has accesses at its boundary, all rectangles are arborally satisfied. □

---

Algorithm 1: $\text{arboralMergesort}(A)$

**Input**: A point set $A$ representing the access sequence, with time on the horizontal axis and key values on the vertical axis.

**Output**: An arborally satisfied set consisting of the original point set and additional accesses.

```plaintext
1 if $A == \emptyset$ || $\text{size}(A) == 1$ then
  2 return $A$;
else
  4 $n \leftarrow \text{width}(A)$;
  5 $L \leftarrow \text{verticalSlice}(A, 0, \frac{n}{2})$;
  6 $R \leftarrow \text{verticalSlice}(A, \frac{n}{2}, n)$;
  7 do in parallel
  8 $A_L \leftarrow \text{arboralMergesort}(L)$;
  9 $A_R \leftarrow \text{arboralMergesort}(R)$;
 10 $A \leftarrow \text{arboralMerge}(A_L, A_R)$;
11 return $A$;
```

Algorithm 2: $\text{arboralMerge}(A_L, A_R)$

The arboral satisfaction algorithm. The function $\text{verticalSlice}$ takes in a set $A$ and an element $k$ and returns the vertical slice of $A$ corresponding to all elements less than $k$ and the horizontal slice of $A$ corresponding to all elements greater than $k$.

**Input**: Two arborally satisfied sets $A_L, A_R$.

**Output**: An arborally satisfied set $A$ consisting of the concatenation of $A_L$ and $A_R$ as well as any additional accesses needed to arborally satisfy the concatenation.

```plaintext
1 if $A_L == \emptyset$ then
  2 return $A_R$;
if $A_R == \emptyset$ then
  4 return $A_L$;
else
  6 $A \leftarrow \emptyset$;
  7 $n_L \leftarrow \text{maxTime}(A_L)$;
  8 while $A_L != \emptyset$ && $A_R != \emptyset$ do
  9 $e_L \leftarrow \text{minKey}(A_L)$;
  10 $e_R \leftarrow \text{minKey}(A_R)$;
  11 if $e_L < e_R$ then
  12 $S, A_L \leftarrow \text{horizontalSplit}(A_L, e_L)$;
  13 $A_t \leftarrow \text{satisfy}(S, n_L, false)$;
  14 $A \leftarrow \text{horizontalConcat}(A, A_t)$;
  15 else
  16 $S, A_R \leftarrow \text{horizontalSplit}(A_R, e_R)$;
  17 $A_t \leftarrow \text{satisfy}(S, n_R, true)$;
  18 $A \leftarrow \text{horizontalConcat}(A, A_t)$;
19 return $A$;
```

---

As a warmup to the proof of the main theorem, we show that any insertion of a new key into an arborally satisfied set which has been satisfied using Algorithm 1 requires at most $O(\lg n)$ accesses to arborally satisfy. This lemma will use the following definition.
**Definition 4.1.** Given an arborally satisfied point set $A$ and a key $k$ placed to the right or left of $A$, the **envelope** of $k$ in $A$ is the set of all accesses $a$ in $k$ such that the rectangle between each and $k$ has no other points in it.

Note that this is slightly different from the rectangle being unsatisfied, since a satisfied rectangle must contain a point adjacent to both corners of the rectangle—in fact, another way to think of the definition of arboral satisfaction is that there is a path from each point to any other point that uses only vertical and horizontal lines. Using this explanation, it is easy to see that satisfying the rectangles formed between $k$ and the envelope is sufficient to arborally satisfy the set, since there is a path between each point in the envelope and every other point in the set.

The envelope’s name corresponds to its geometry: the envelope must be a convex funnel, with the points at the top of the funnel a strictly increasing sequence and the points at the bottom of the funnel a strictly decreasing sequence (these will be referred to as the upper and lower envelope, respectively). This will be shown in the proof of the following proposition, which provides a warmup and acquaints the reader more fully with the concept of the envelope.

**Proposition 4.1.** Given a set $A$ of size $n$ which has been arborally satisfied using Algorithm 1, an insertion of a key $k$ to the left or right of $A$ requires at most $O(\lg n)$ additional accesses to arborally satisfy.

**Proof.** Assume without loss of generality that $k$ is placed to the right of $A$. Consider the envelope of $k$ in $A$. On every vertical line, the envelope of $k$ in $A$ contains at most two points, since if it contained more than two, only the two closest to $A$ could form an empty rectangle. The first two points in the envelope (that is, the points closest to $k$) must be on the vertical adjacent to $k$ by our construction. Call these points $p_1, p_2$, and let the key of $p_1$ be greater than the key of $p_2$. Then since all points in $A$ are to the right of $p_1$ and $p_2$, every point with key greater than $p_1$ or less than $p_2$ must be arborally satisfied when accesses to $p_1, p_2$ are placed on $k$’s vertical. Thus the next two points on either side of the envelope must be less than $p_1$ and greater than $p_2$, respectively. This implies that when viewed from the leftmost point in the envelope, the upper envelope forms a strictly increasing sequence and the lower envelope forms strictly decreasing sequence.

Now, we will show that this envelope contains at most $O(\lg n)$ points. Consider when the leftmost element of the funnel was inserted as a singleton. There are at most $O(\lg n)$ merges that involve that element; merges to the left of the element cannot contribute to the funnel, and merges to the right of the funnel may add elements to the funnel. Since the set of points being merged is arborally satisfied within itself, only one element per block can be in a given funnel, and the bound follows.

Proposition 4.1 shows that any insertion requires at most $O(\lg n)$ accesses to arborally satisfy. However, to achieve the log-interleave bound, an insertion of two keys $k_1, k_2$ to the left or right of $A$ such that $k$ keys of $A$ are between $k_1$ and $k_2$ must require only $O(\lg k)$ accesses between $k_1$ and $k_2$ for arboral satisfaction.

The following example shows that thus far, the arboral mergesort does not have this property, and it gives the first clue to how one might modify the algorithm to achieve it.

**Example 4.1.** Consider an access sequence $\pi$ which is arborally satisfied using Algorithm 1. The sequence $\pi$ starts with two consecutive elements; then the next groups of $2, 4, 8, \ldots, n/2$ additional elements all contain one element larger than the first two elements, and the rest of their elements are smaller. Furthermore, these largest elements of each group form a strictly increasing sequence. These groups of elements correspond to the merges that Algorithm 1 would perform; each merge places one element above the first two elements and all the rest of its keys below.

Figure 6 shows the top $\lg n$ elements of this access sequence, where a split that separates the lowest and second-lowest keys requires $O(\lg n)$ accesses to arborally satisfy, since the funnel contains $O(\lg n)$ points.

The geometric properties of the envelope shown in the proof of Proposition 4.1 will be useful in developing a fix for this issue. We now provide the machinery necessary for this fix in the following lemmas.

**Lemma 4.2.** Given a set of points in the plane consisting of a strictly increasing or decreasing sequence $\pi$, this sequence can be arborally satisfied such that any insertion of keys $k_1, k_2$ to the right or left of the sequence, with $k$ keys from $\pi$ between them, requires at most $O(\lg k)$ accesses to arborally satisfy. If $\pi$ contains $n$ keys, then $O(n)$ additional accesses are required for this procedure.

**Proof.** This proof will only consider the case where the sequence is strictly increasing and a key is inserted to the right, since the rest of the cases are symmetric. The algorithm is simple: for the $0$th key, make no additional accesses. Then, for every $2^i$th key $c$, make $i + 1$ accesses below $c$. Make these accesses to the keys $c - 1, c - 2, c - 4, \ldots, c - 2^i$—that is, one element below $c$, two elements below $c$, and so on up to $2^i$ elements below $c$. This process is illustrated in Figure 4.
Arboreal Satisfaction. First, we confirm that this algorithm creates an arboreally satisfied set. Let \( c \) be a \( 2^i \)th key. The first access directly below \( c \) satisfies the unsatisfied rectangle created between key \( c \) and key \( c - 1 \). The remaining keys are at places \( 2, 4, \ldots, 2^i \) below \( c \). Out of the remaining keys, consider the key \( c_j \), \( 2^j \) elements below \( c \). The closest access on its horizontal line must be an access below a \( 2^{i-1} \)th key, since this is the largest key that has so far placed an access on that horizontal. Thus, every rectangle between \( c_j \) is either satisfied by this point, or the point on \( c \)'s vertical above \( c_j \).

Number of Accesses. Second, we show that if the sequence contains \( n \) points, the algorithm puts down only \( O(n) \) additional accesses. Assuming \( n \) is a power of two, this algorithm places \( \lg n \) accesses for one point (the halfway point), \( \lg n/2 \) accesses for two points (the two quarter-way points), and so on, with one access being placed for \( n/2 - 1 \) points (excluding the zeroth point). This leads to the following summation:

\[
\sum_{i=0}^{\lg n-1} 2^i \lg(n/2^{i+1}) - 1 = O(n).
\]

Insertion Property. Let \( k_1 < k_2 \) be two keys inserted to the right of the sequence, with \( k \) keys from the sequence in between them. Now we show that at most \( O(\lg k) \) accesses between \( k_1, k_2 \) are required to arboreally satisfy the set.

First, we define a subset of an envelope that we call a complete envelope. A complete envelope is a subset of an envelope where for each element in the upper envelope, there is an element in the lower envelope directly below it. For a sequence satisfied using the algorithm in the lemma, we can show that the distance between the two points on each vertical in a complete envelope must half (or decrease by more than half) each time we move closer to the end of the envelope. Furthermore, since the sequence is strictly increasing, once one point in an envelope is part of the complete envelope, all points to the left of it must also be. Recall that a vertical line below a \( 2^i \)th access \( c \) must place points \( 1, 2, 4, \ldots, 2^i \) elements below \( c \). Consider a gap between two points on a vertical, at places \( 2^i \) and \( 2^{i+1} \) below the \( 2^i \)th point. The access below \( c \) corresponding to place \( 2^i \) must be to the right of a \( 2^i \)th point \( d \), so \( d \) has a vertical line below it ending at the \( 2^{i+1} \)th point and following the same pattern. Since the largest gap in this line is at most \( 2^{i-1} \), the space between elements on vertical lines in the envelope must half every time.

Next, we note that since the sequence is strictly increasing, when a key \( k \) is inserted to the right of it, the rightmost element below \( k \) which forms an empty rectangle with \( k \) must be on the rightmost vertical in the complete envelope of \( k \). This is because the access above this rightmost element must be greater than \( k \)—otherwise, that access would be in the bottom of \( k \)'s envelope itself.

Now we give the final piece needed to show the split property. Let \( d \) be the key such that the first two elements of the complete envelope of \( k \) are directly below \( d \). Let \( d \) be a \( 2^i \)th element. Then at most \( 2^i \) elements of the initial sequence can exist above \( d \), since the \( 2^i \) + 1th element above \( d \) would trigger a vertical line covering all the elements from \( d - 2^i \) to \( d + 2^i \), contradicting our assumption. The worst case for number of elements of this nature in the envelope is when there are \( 2^i - 1 \) elements above \( d \) for some \( j < i \), since this is right before a vertical line would have covered all \( 2^i \) elements on the next insertion. In this case, there is one element in the envelope for the first \( 2^{i-1} \) elements above \( d \), another for the next \( 2^{i-2} \) elements, and so on. Hence, for any slice of \( k \) elements starting at \( d \) and ending above \( d \), at most \( \lg k \) elements can be in the envelope of a key inserted below \( d \).

Now, we can put all these pieces together. Recall that we assume \( k_2 \) is above \( k_1 \). For key \( k_2 \), we only pay for keys below \( k_2 \) in its envelope, so since the rightmost bottom element of the envelope must be between \( k_1 \) and \( k_2 \), and the space between elements of the complete envelope halves at each step, at most \( \lg k \) accesses are required to satisfy any unsatisfied rectangles created below \( k_2 \). For \( k_1 \), we similarly pay at most \( \lg k \) for the top part of its complete envelope, and then the result from the previous paragraph gives that at most \( \lg k \) accesses are required above the complete envelope to arboreally satisfy any unsatisfied rectangles created by \( k_1 \) that aren’t in the complete envelope. Hence at most \( 3 \lg k = O(\lg k) \) accesses are required between \( k_1 \) and \( k_2 \).

Keeping Example 4.1 in mind, Lemma 4.2 suggests a way that this difficult case could be fixed: if the upper and lower parts of an envelope could be satisfied using the procedure in the lemma, the cost of a split would be the logarithm of the number of points in the original funnel. Since the algorithm only requires \( O(n) \) points for a sequence of length \( n \), it seems plausible that adding these points could be charged to the accesses already added by the algorithm. The following lemma will help address an issue with this idea: what if a funnel that is “fixed” using this procedure is then split on a later merge? In particular, if we are charging these extra accesses to accesses that the algorithm has already added, how can we ensure that the split of a funnel would never result in double counting?

The statement of the lemma addresses only the increasing case for ease of exposition, but it also holds symmetrically for the decreasing case.
Lemma 4.3. Let \( \pi \) be a strictly increasing sequence which is arborally satisfied using the algorithm in Lemma 4.2, or the extension algorithm we are about to present. Let \( \pi_k \) be a contiguous subsequence of \( \pi \) of size \( k \). Imagine isolating \( \pi_k \) and then adding new points larger than the largest element in \( \pi_k \). Then there is a way to continue adding points to \( \pi_k \) such that the following properties are preserved:

1. The sequence is arborally satisfied.
2. Only \( O(n) \) points are added to a sequence of size \( n \).
3. Any insertion of keys \( k_1, k_2 \) to the right or left of the sequence with \( k \) keys of the sequence between them requires at most \( O(\lg k) \) accesses between \( k_1 \) and \( k_2 \) to arborally satisfy.

Proof. Like the proof of the previous lemma, we address only the increasing case without loss of generality. To begin with, the explicit instructions for how to continue \( \pi_k \) when more elements are added to it are as follows: in \( \pi_k \), identify the element \( c \) of the sequence which has the largest number of points below it. If there are two such elements, choose the one whose key is larger. Let that element have \( j + 1 \) such points below it. Then when more elements are added to \( \pi_k \), add them using the procedure in Lemma 4.2 as if element \( c - 2^j \) is the zeroth element.

Now, we examine what this sequence looks like after any number of insertions. There are at most \( 2^{j+1} - 1 \) elements below the new "zeroth" element, since otherwise this would contradict \( c \) being the element with the most accesses below it. As elements are added to \( \pi_k \), the subset of \( \pi_k \) from the new zeroth element onwards is identical to a sequence satisfied using Lemma 4.2. Below this subset, there is another such sequence of length up to \( 2^{j+1} - 1 \).

The cost of an insertion at a key greater than the new zeroth key would not change from Lemma 4.2, since the closest point in its lower envelope would be at or above the new zeroth key. The cost of an insertion below the zeroth key could increase beyond the costs in Lemma 4.2 by at most an additive factor of \( j + 1 \), since the subsequence below the new zeroth element will never be covered by another vertical line—an insertion at the very bottom of the sequence could incur an extra cost of \( j + 1 \), where it could have required only a single access in the case where the bottom subsequence is covered by a vertical line of accesses. \( \square \)

Before we can move on to the full fix of Algorithm 1, we need another definition that builds on the envelope concept. Since the goal is to prove an upper bound on the cost of arborally satisfying a set of insertions instead of a single insertion, it is useful to capture the set of all upper and lower envelopes in an arborally satisfied set \( A \). The only subtlety in such a definition is that some upper envelopes may be a strict subset of another upper envelope, and we wish to avoid double counting. The following definition treats only the upper envelopes and insertions to the right, but the remaining three cases are symmetric.

Definition 4.2. Given an arborally satisfied set \( A \) over \( n \) keys, the upper envelope set of \( A \) is a union of the upper envelopes of the \( n + 1 \) places where keys can be inserted to the right of \( A \), excluding upper envelopes whose keys are a strict subset of another upper envelope.

Lemma 4.4. Let \( A \) be a set arborally satisfied using Algorithm 1. Let keys \( k_1, k_2 \) be inserted to the left or right of \( A \) such that \( k \) keys of \( A \) are between \( k_1 \) and \( k_2 \). Then it is possible to modify the merge step of Algorithm 1 such that only \( O(\lg k) \) additional accesses between \( k_1 \) and \( k_2 \) are required to arborally satisfy the set.

Proof. This proof assumes that the keys are cutting the set from the right, but the left case is symmetric. In this proof, an upper or lower envelope refers only to an envelope in the envelope set to avoid the confusion of double-counting. It will use the procedure from Lemma 4.2 to modify Algorithm 1. As seen in Example 4.1, the obstacle to achieving the desired bound occurs when a narrow envelope contains too many points. However, since the two sides of an envelope form a monotonic sequence, Lemma 4.2 gives a procedure to "pad" each of the two monotonic sequences of the envelope such that any key inserted in between elements of the envelope requires costs only proportional to the logarithm of the number of points in the envelope.

If it were possible to add these additional accesses without increasing the overall cost of the algorithm, this would prove the lemma. To show this, consider two keys \( k_1, k_2 \) inserted beside a set \( A \) that is arborally satisfied using Algorithm 1. The keys \( k_1, k_2 \) fall into at most two distinct envelopes in the envelope set, and since only \( k \) keys are between \( k_1 \) and \( k_2 \), the envelopes whose keys fall in between \( k_1, k_2 \) have at most \( k \) points between them. If the first envelope has \( m_1 \) points above \( k_1 \) and the second has \( m_2 \) points below \( k_2 \), \( (m_1 + m_2 \leq k) \), our modification to the algorithm gives that the cost of satisfying any unsatisfied rectangles from keys between \( k_1, k_2 \) costs \( O(\lg m_1) + O(\lg m_2) = O(\lg k) \).


Now, if the set $A$ is frozen in time, it is clear that the cost of adding these “buffering” points can be charged to the accesses already added up to this point, since the number of extra points is linear in the number of points that form the envelopes in $A$. Arboreal satisfaction must also be addressed. Imagine doing the process in Lemma 4.2 to the upper and lower envelope. The points added at the top cannot create unsatisfied rectangles with any points above them, since they are placed below existing accesses; the equivalent statement is true of the bottom. To prevent any unsatisfied rectangles between the upper and lower envelope, all that is needed is to add a horizontal line of points along the “center” (that is, the point furthest from the key which creates the envelope) of each envelope, with one point per alternation in the envelope from top to bottom. This line can also be charged to the accesses already present.

To ensure that the charging bound remains valid, we must show that this routine never charges an access more than twice (once for it being the top part of a envelope, and once for it being the bottom part). Future merges may take one of three forms: (1) they may not insert anything either adjacent or within the envelope, (2) they may insert an element adjacent to the most recent accesses in the envelope (that is, to the bottom of the lower envelope and/or the top of the upper envelope), or (3) they may split the envelope. In the case of (1) it is clear that the statement holds. In the case of (2), the next merge adds elements to the envelope, which can continue the algorithm laid out in Lemma 4.2.

In the case of (3) where the accesses in the envelope are split, Lemma 4.3 comes to the rescue. A segment of the envelope that contains part of the increasing sequence AND part of the decreasing sequence will be able to continue the sequences with their original zeroth elements, and will just replace its rightmost elements with a new access further to the right of them. Its center line can also be added to as new accesses are added to the new envelope. A segment that only contains part of an increasing or decreasing sequence can be continued according to the modified process in Lemma 4.3. It will have no center line to begin with, since accesses on the center line are only necessary once there are alterations between the top and bottom of an envelope.

**Proof.** [Proof of Theorem 4.1] Through Lemmas 4.1, 4.2, and 4.4, we have shown that with a simple modification, Algorithm 1 produces an arboreal set with the property that an arbitrary cut of the set $A$ by keys $k_1, k_2$ with $k$ keys in $A$ between them requires at most $\log k$ accesses to reintroduce arboreal satisfaction.

This implies that when we use Algorithm 3 to merge together two sets that have been arboreally satisfied according to our algorithm, for each set, when we place additional points on both the inside and outside edge, the cost of the two additional columns is at most the sum of the logarithms of the block sizes. Thus each merge adds accesses proportional to the sum of the logarithms of the block sizes on a single merge, and when summed over all the merges amounts to a total cost of $O(\text{LIB}(\pi))$.

Finally, the theorem of Demaine et al in [16] provides a transformation from an offline arboreal satisfaction algorithm to an offline BST algorithm, completing the proof.

5 Adaptive Parallel Mergesort

Section 4 showed an offline algorithm in the BST model which used $O(\text{LIB}(\pi))$ accesses for any $\pi$. Here, we give a more traditional parallel sorting algorithm which sorts a permutation $\pi$ using $O(\text{LIB}(\pi))$ comparisons, and the same amount of work. We call this algorithm our **adaptive parallel mergesort**.

First we introduce a few basic terms and the data structure used in our mergesort. Given a BST $T$ and a key $k$, a **split** refers to returning two BSTs, one containing all keys from $T$ which are greater than $k$, and one containing all keys which are less than $k$. Given two BSTs $T_1, T_2$ such that any key in $T_1$ is greater than every key in $T_2$, **join** returns a single BST $T$ containing the union of the keys in $T_1$ and $T_2$. As previously stated, we assume keys are unique.

The BST used in our mergesort algorithm is a modified 2-3 tree proposed by Kaplan and Tarjan in [24], which we will refer to as a **KT-tree**. These trees have the useful property that a key $d$ in a KT-tree with $n$ elements can be accessed in time $O(\log(\min(d, n-d) + 1))$. This property allowed Kaplan and Tarjan to devise fast split and join algorithms for KT-trees; split runs in time $O(\log(\min(|T_1|, |T_2|) + 1))$—that is, the logarithm of the size of the smaller tree returned. Join similarly is bounded by $O(\log(\min(|T_1|, |T_2|) + 1))$—in this case, the size of the smaller of the two trees being joined together.

**Sequential Mergesort.** As a warmup, we present a sequential merge algorithm which, when used in as the merge step of a mergesort algorithm, sorts a permutation $\pi$ in $O(\text{LIB}(\pi))$ time. Refer to Algorithm 4 for the algorithm.

**Lemma 5.1.** Algorithm 4 is correct and, if it breaks $T_i$ into subtrees $t_1, \ldots, t_j$ and $T_j$ into subtrees $t_{j+1}, \ldots, t_k$, then it runs in time

$$O\left(\sum_{i=1}^{k} \log(|t_i| + 1)\right).$$
Figure 8: One round of our recursive merge algorithm. The nodes shown in red are the nodes used to split a tree; the small blue nodes denote merges.

Proof. The proof of the time bound is immediate, since a KT-tree has split and join cost $O(\lg(|t| + 1))$ for every subtree that it breaks off from $T_1$ and $T_2$.

Correctness will be shown via induction. The inductive hypothesis is that after each split and join of a new subtree, $T$ remains a valid BST, and each key of $T$ is smaller than every key in $T_1[\cap]T_2[\cup]T_3$.

The base case is when $T$ is empty. Assume without loss of generality that $k_1 > k_2$. Then split($T_2$, $k_1$) returns $T_2$ and $T$, where $t$ contains only keys which are smaller than all keys in $T_2$. They are also smaller than all keys in $T_1$, since $k_1$ was the minimum key in $T_1$ and $t$ contains only keys less than $k_1$. The operation join($T$, $t$) successfully returns the BST $t$ since $T = \emptyset$.

Now, assume that after any number of split/join actions that $T$ is a valid BST and contains only keys that are less than those in $T_1[\cup]T_2$. Similarly to the proof of the base case, assuming wlog that $k_1 > k_2$, we know that the split of $T_2$ returns a tree $t$ such that each key in $t$ is larger than any key in $T$, and such that each key in $t$ is smaller than any key in $T_1[\cup]T_2$. Furthermore, since $t$ contains only keys larger than those in $T$, join($T$, $t$) returns a valid BST.

Next, we show that the mergesort algorithm which uses Algorithm 4 as its merge routine is optimal for the log-interleave bound.

Lemma 5.2. When Algorithm 4 is used as the merge step in a mergesort algorithm, the mergesort will sort a sequence $\pi$ in time $O(LIB(\pi))$.

Proof. When merging two trees $T_1$, $T_2$, consider any permutation $\pi$ such that the keys of $T_1$ correspond to the keys in the first half of $\pi$, and the keys of $T_2$ correspond to the keys in the second half of $\pi$.

Consider the static tree $P_\pi$ used to calculate the log-interleave bound of $\pi$. The root vertex $v$ then contains all the keys in $T_1$ in its left subtree, and all the keys in $T_2$ in its right subtree. Thus

$$LIB(v) = \sum_{i=1}^{k} \lg(|t_i| + 1)$$

since the $t_i$’s correspond to switching between $T_1$ and $T_2$ when querying the keys in sorted order.

Finally, observe that each non-leaf vertex of $P_\pi$ corresponds to a merge that a mergesort algorithm would carry out, and the result follows.

Parallel Mergesort. The natural parallel equivalent of the merge presented in Algorithm 4 is as follows: starting with two trees, split each tree using the other tree’s root; then, recurse in parallel to merge the two left halves and the two right halves, respectively, joining the two at the end. This idea was presented by Blelloch et al in [5], and is shown here in Algorithm 5. This algorithm, however, does not meet the log-interleave bound even if we use KT trees for the split and join.
We therefore modify the algorithm as is shown in Algorithm 6 and illustrated in Figure 8, which follows the same idea with some small modifications. In addition to splitting the second tree $T_2$ into $L_2$ and $R_2$ based on the root of the first tree ($T_1$), it then splits $T_1$ by the maximum value of $L_2$ and the minimum value of $R_2$ to effectively break $T_1$ into three parts. The middle part need not be split recursively since it falls between two elements of $T_2$. This avoids redundant splits.

Algorithm 4: merge($T_1, T_2$).
---

**Input:** Two BSTs $T_1, T_2$ with disjoint keys.

**Output:** A BST containing the union of the keys of $T_1$ and $T_2$.

1. $T = \emptyset$;
2. while true do
   3. if $T_1 = \text{leaf}$ then
      4. return join($T, T_2$);
   5. else if $T_2 = \text{leaf}$ then
      6. return join($T, T_1$);
   7. else
      8. $k_1 = \text{min}(T_1)$;
      9. $k_2 = \text{min}(T_2)$;
     10. if $k_1 > k_2$ then
         11. $T_1, T_2 = \text{split}(T_2, k_1)$;
         12. $T = \text{join}(T, t)$;
     13. else
         14. $T, T_1 = \text{split}(T_1, k_2)$;
         15. $T = \text{join}(T, t)$;

Algorithm 5: union($T_1, T_2$).
---

Blelloch et al’s union algorithm. Here, the function expose refers to returning the root and its right and left subtrees; the symbol || refers to parallel calls.

**Input:** Two BSTs $T_1, T_2$ with disjoint keys.

**Output:** A BST containing the union of the keys of $T_1$ and $T_2$.

1. if $T_1 = \text{Leaf}$ then
   2. return $T_2$;
3. else if $T_2 = \text{Leaf}$ then
   4. return $T_1$;
5. else
   6. $L_1, k_2, R_1 = \text{expose}(T_1)$;
   7. $L_2, R_2 = \text{split}(T_2, k_2)$;
   8. $T_L = \text{union}(L_1, L_2) \ || \ T_R = \text{union}(R_1, R_2)$;
   9. return join($T_L, k_2, T_R$);

Algorithm 6: mergeKT($T_1, T_2$)
---

Pseudocode for the merge step of our mergesort. The properties of the KT-tree guarantee that retrieving the minimum and maximum element of a tree has $O(1)$ cost.

**Input:** Two BSTs $T_1, T_2$

**Output:** A BST containing the union of the keys of $T_1$ and $T_2$

1. if $T_1 = \text{Leaf}$ then
   2. return $T_2$;
3. else if $T_2 = \text{Leaf}$ then
   4. return $T_1$;
5. else
   6. $k = \text{root}(T_1)$;
   7. $L_2, R_2 = \text{split}(T_2, k)$;
   8. $k_1 = \text{max}(L_2)$;
   9. $k_2 = \text{min}(R_2)$;
10. $L_1, l = \text{split}(T_1, k_1)$;
11. $M, R_1 = \text{split}(l, k_2)$;
12. $T_L = \text{merge}(L_1, L_2) \ || \ T_R = \text{merge}(R_1, R_2)$;
13. return join(joined($T_L, M, T_R$));

Unlike the sequential algorithm, it is not immediate that even our modified algorithm’s work is bounded by the log-interleave bound, since it performs a different set of splits and joins than the sequential version. We will show that this different sequence of splits and joins also performs within the log-interleave bound, culminating in the following theorem:

**Theorem 5.1.** There exists a parallel mergesort which for any permutation $\pi$ performs $O(\text{LIB}(\pi))$ work with polylogarithmic span.

First, we introduce a useful lemma which shows that the work performed to split a KT-tree into $k$ smaller trees is independent of the order in which the splits are carried out.

**Lemma 5.3.** Let $T$ be a KT-tree and consider splitting $T$ into $k$ smaller trees $t_1, \ldots, t_k$. Then the work required to split $T$ is $O\left(\sum_{i=1}^{k} \log(|t_i| + 1)\right)$ regardless of the order in which the splits are performed.
Proof. The proof proceeds by induction on the size. Let \(|T| = n\), and make an inductive hypothesis that the total split work of \(T\) is
\[
\left(\sum_{i=1}^{k} \lg(|t_i| + 2)\right) - (\lg n + 2).
\]
Begin by verifying the base case: splitting a BST of size 1 should have a cost of zero:
\[
\lg(1) + 2 - (\lg(1) + 2) = 0.
\]
Now, for the inductive step, assume we are splitting \(T\) into two parts of size \(an\) and \((1 - \alpha)n\) for \(\alpha \in [0, 1]\), and that the first part consists of the smaller trees \(t_1, \ldots, t_j\) while the second part consists of the trees \(t_{j+1}, \ldots, t_k\). Then our inductive step requires that:
\[
\left(\sum_{i=1}^{j} \lg |t_i| - \lg(an) - 2\right) + \left(\sum_{i=j+1}^{k} \lg |t_i| - \lg((1 - \alpha)n) - 2\right) + \lg(\min(an, (1 - \alpha)n)) + 1 \leq \sum_{i=1}^{k} \lg |t_i| - \lg n - 2
\]
Assume without loss of generality that the size of the first subtree is smaller than the second, i.e. \(\alpha \in [0, \frac{1}{2}]\). Then canceling on both sides and substituting in the minimum value gives:
\[
- \lg(an) - \lg((1 - \alpha)n) - 4 + \lg an + 1 \leq -\lg n - 2
\]
Finally, since \(1 - \alpha \in [\frac{1}{2}, 1]\), in the case where the right-hand expression is smallest and \(\alpha = \frac{1}{2}\), \(\lg(\frac{1}{2}n) + 1 = \lg n\), so the inequality is both true and tight in the worst case.

This lemma allows us to show the correctness and the work bounds for Algorithm 6.

Lemma 5.4. Algorithm 6 is correct, and if merging \(T_1\) and \(T_2\) requires \(T_1\) and \(T_2\) to be split into \(k\) trees \(t_1, \ldots, t_k\) and \(j\) smaller trees \(t_1, \ldots, t_j\) respectively, then Algorithm 6 performs \(O(\sum_{i=1}^{k} \lg |t_i| + 1 + \sum_{i=1}^{j} \lg |t_i| + 1)\) work.

Proof. Correctness follows from the fact that by the assumptions on the input, the interval \(I\) contains all keys between those of \(L_1, L_2\) and \(R_1, R_2\), and from the correctness of Algorithm 5.

The work bound comes from Lemma 5.3, which shows that it does not matter in what order the splits are performed, and therefore they are bounded by the sequential work. Since each join is the same cost as a split, the proof of Lemma 5.3 also suffices to show that the join work is bounded by the split work, so the work bound follows.

Note that the position of the “root” in the tree \(T_1\) as selected in line 6 does not matter for the purpose of the work bounds. Picking the first element, for example, would lead to an algorithm that is very similar to the sequential algorithm. However for the purpose of parallelism it is important that the root in near the middle—i.e., cuts off at least a constant fraction of \(T_1\)’s keys from each side. This could be achieved by finding the median element, and the cost would be within bounds.

Our last lemma concerns the span of the parallel mergesort algorithm.

Lemma 5.5. The span of the parallel adaptive mergesort is \(O(\lg^3 n)\).

Proof. Our merge has the same span as Blelloch et al’s union algorithm, which they proved in [5] to have span \(O(\lg^2 n)\) when merging two trees of size \(n\). Since parallel mergesort has span \(O(\lg n)\), the total span is \(O(\lg^3 n)\). We only require binary forking since the only parallel calls are the two recursive calls inside merge, and the two recursive calls inside mergesort.

Now, we can put all these results together to prove our theorem.

Proof. [Proof of Theorem 5.1] Lemma 5.3 shows that the merge step in our parallel mergesort performs the same amount of work as the mergestep in the sequential mergesort from Lemma 5.2; Lemma 5.4 shows correctness. Lemma 5.5 shows the span.
Figure 9: Petersson and Moffat’s hierarchy of measures of disorder. A downwards line connecting two measures indicates that the higher measure is strictly superior to the lower. The ≡ symbol indicates that two measures are each superior to the other.

6 Additional Background on Binary Search Trees and Measures of Disorder

This section describes in more detail the previous results on measures of disorder and BST upper bounds which will inform our understanding of the log-interleave bound.

Measures of Disorder. First, we give a more complete accounting of important measures of disorder, and show the entirety of Petersson and Moffat’s hierarchy.

Loc. This measure of disorder exploits the idea that inserting an element whose key is close to the most recently inserted element should be cheap. The corresponding algorithmic idea is an insertion sort where keys are inserted into a finger search tree, keeping a finger at the most recently inserted element. Let $x_i$ represent the most recently inserted element, and consider inserting $x_i$; the BST property then implies that if $d_i$ is the number of elements already in the tree whose keys are between that of $x_i$ and $x_{i-1}$, the cost of inserting $x_i$ must be $O(\log d_i)$. The measure of disorder corresponding to this algorithm is called Loc, standing for local insertion sort, and is defined as follows:

$$\text{Loc}(\pi) = \prod_{i=2}^{n} (d_i + 1)$$

and the insertion sort algorithm described above requires $O(n + \lg \text{Loc}(\pi))$ comparisons.

Hist. While Loc took advantage of closeness of elements in keyspace, the next measure of disorder takes advantage of closeness of elements in time—that is, if two adjacent elements are inserted close in time to each other, the second insertion should be cheap. The corresponding measure is called Hist, since it takes advantage of the history of the sequence. The precise definition of Hist is as follows: let $x_i$ be the element currently being inserted, and let $x_j$ be the closest already inserted element to $x_i$ in keyspace. Then let $t_i$ be $(i - j)$, and let

$$\text{Hist}(\pi) = \prod_{i=2}^{n} t_i.$$  

There exists a data structure which sorts a list in $O(n + \lg \text{Hist}(\pi))$ comparisons, but it is not a binary search tree. In an earlier paper [33], Petersson and Moffat propose a data structure which sorts a list in $O(n \lg \lg n + \lg \text{Hist}(\pi))$ time; in later, independent work, Badoiu et al [4] propose a data structure which would bring the total runtime down to $O(n + \lg \text{Hist}(\pi))$.

Full Hierarchy. The main results of Petersson and Moffat are the invention of the measure of disorder Reg and the organization of all existing known measures of disorder into a hierarchy based on superiority, which is shown in Figure 9. Measures not defined here can be found in [34].

McIlroy’s Properties Our work is also influenced by McIlroy’s perspective on the desirable properties of an adaptive sorting algorithm. Here we describe the six properties he proposes in his 1993 paper [32]. For a permutation $\pi$, let $C(\pi)$ denote the number of comparisons required to sort $\pi$. Since Runs was defined in Section 3, it is not defined here.

Reversal. A sorting algorithm should take the same number of comparisons sorting both a list and its reverse.

Inversion. A sorting algorithm that sorts $\pi$ in $C(\pi)$ comparisons should sort $\pi^{-1}$ in $O(C(\pi))$ comparisons.

Weak Segmentation. Imagine taking a sorted list and breaking it into $k$ sorted segments, then permuting the elements within each segment. For optimality over weak segmentation, this permutation $\pi$ should be sorted in $C(\pi) = O(n + \sum_{i=1}^{k} C_i)$, where $C_i$ represents the number of comparisons required to sort the $i$th segment.
Strong Segmentation. Strong segmentation is a similar idea to weak segmentation: break a sorted list into \( k \) segments, permute within the segments, and then permute the segments themselves. A sorting algorithm is optimal over strong segmentation if for a permutation \( \pi \), it sorts in \( C(\pi) = O(\sum_{i=1}^{k} C_{i} + k \log n) \) comparisons—that is, the comparisons required to sort each individual segment, plus the comparisons needed to sort the segments if they were individual elements of a list.

Riffle shuffles. This property takes its name from card shuffling, where a deck of cards is divided and two halves are interleaved randomly. A feature of this kind of shuffle is that two halves remain monotonic subsequences of the final sequence. This property can be generalized in a natural way to a \( k \)-way riffle, where \( k \) monotonically increasing subsequences are randomly interleaved. If a permutation \( \pi \) is a riffle shuffle of \( k \) sequences of length \( n_{i} \), then an algorithm which is optimal over riffles should have \( C(\pi) = O(n + \sum_{i=1}^{k} n_{i} \log \frac{n}{n_{i}}) \).

Composition. Given two permutations \( \sigma \) and \( \gamma \) such that \( \sigma \circ \gamma = \pi \), \( C(\pi) \) should be \( O(C(\sigma) + C(\gamma)) \). McIlroy shows that full optimality over comparisons is not possible, but a weaker version is attainable. If \( \sigma \) and \( \gamma \) require only optimality over inversion, runs, and weak segmentation in order to be sorted efficiently, then weak composition requires that \( C(\pi) = O(C(\gamma) + C(\sigma)) \).

Binary Search Trees Two BSTs are conjectured to be dynamically optimal—that is, on any online access sequence, they perform within \( O(1) \) of the best offline algorithm. They are Sleator and Tarjan’s splay trees [35] and Demaine et al’s greedy BST [16]. A common question that researchers try to answer in pursuit of dynamic optimality is whether a BST performs within certain upper bounds on any access sequence.

Here, we introduce three of the most well-known upper bounds in the BST model: the dynamic finger bound, the working set bound, and the unified bound. These bounds are very closely related to Loc, Hist, and Reg, providing more evidence of the connection between adaptive sorting and binary search trees.

Dynamic finger bound. The dynamic finger bound is almost identical to Loc. Given a BST containing \( n \) keys and an access sequence of \( m \) elements, let \( d_{i} \) be defined the same way as in the definition of Loc. Then a BST satisfies the dynamic finger bound if it accesses the query sequence in time \( O(n + m + \sum_{i=1}^{m} \log d_{i}) \).

In [13, 14], Cole shows that splay trees satisfy the dynamic finger bound. In [8], Bose et al propose a generalization of dynamic finger bound known as the lazy finger bound, where each search starts from the previous one on the best static tree. In [23], Iacono and Langerman show that the greedy BST satisfies this property, making the lazy finger bound the strongest known bound on any BST.

Working set bound. For each access \( i \) to element \( x_{j} \), let \( t_{i} \) designate the number of accesses since the previous access to element \( x_{i} \). Then a BST satisfies the working set bound if it accesses the query sequence in time \( O(n + m + \sum_{i=1}^{m} \log t_{i}) \). Notice that this is almost identical to the definition of Hist, but where time is measured by the time passed since the last access to the same element rather than its neighbor.

In their original paper introducing splay trees and the dynamic optimality conjecture, Sleator and Tarjan show that splay trees satisfy the working-set bound [35].

Unified bound. The unified bound combines the working-set bound and the dynamic finger bound in the same way Reg does. Let \( S \) consist of the set of elements already accessed, ordered by time, and let \( t_{j} \) denote the number of accesses since the most recent access of element \( j \). Let \( d_{i,j} \) be defined as in the definition of Reg. Then let \( u_{i} = \min_{j \in S_{i}}(t_{j} + d(i, j) + 2) \). A BST satisfies the unified bound if it accesses any query sequence in time \( O(n + m + \sum_{i=1}^{m} \log u_{i}) \).

In [4], Badoiu et al propose a data structure which satisfies the unified bound on any access sequence, but it is not strictly a BST as it consists of a forest of chronologically ordered trees as well as an additional reference tree. Furthermore, in [11], Chalermsook et al show that a BST with multiple fingers satisfies a weaker version of the unified bound. In his 2009 thesis, Derryberry presents the cache tree [18], a BST which satisfies the unified bound.

References

[1] S. Adams. Implementing sets efficiently in a functional language. Technical Report CSTR 92-10, University of Southampton, 1992.
[2] N. S. Arora, R. D. Blumofe, and C. G. Plaxton. Thread scheduling for multiprogrammed multiprocessors. Theory of Computing Systems (TOCS), 34(2), Apr 2001.
[3] N. Auger, V. Jugé, C. Nicaud, and C. Pivoteau. On the worst-case complexity of timsort. In 26th Annual European Symposium on Algorithms, ESA 2018, August 20-22, 2018, Helsinki, Finland, volume 112 of LIPIcs, pages 4:1–4:13. Schloss Dagstuhl - Leibniz-Zentrum für Informatik, 2018.
[4] M. Badoiu, R. Cole, E. D. Demaine, and J. Iacono. A unified access bound on comparison-based dynamic dictionaries. Theoretical Computer Science, 382(2):86–96, 2007.
[5] G. E. Blelloch, D. Ferizovic, and Y. Sun. Just join for parallel ordered sets. In ACM Symposium on Parallelism in Algorithms and Architectures (SPAA), 2016.
