Fast Parallel Algorithms for Euclidean Minimum Spanning Tree and Hierarchical Spatial Clustering

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Abstract
This paper presents new parallel algorithms for generating Euclidean minimum spanning trees and spatial clustering hierarchies (known as HDBSCAN∗). Our approach is based on generating a well-separated pair decomposition followed by using Kruskal’s minimum spanning tree algorithm and bichromatic closest pair computations. We introduce a new notion of well-separation to reduce the work and space of our algorithm for HDBSCAN∗. We also present a parallel approximate algorithm for OPTICS based on a recent sequential algorithm by Gan and Tao. Finally, we give a new parallel divide-and-conquer algorithm for computing the dendrogram and reachability plots, which are used in visualizing clusters of different scale that arise for both EMST and HDBSCAN∗. We show that our algorithms are theoretically efficient: they have work (number of operations) matching their sequential counterparts, and polylogarithmic depth (parallel time).

We implement our algorithms and propose a memory optimization that requires only a subset of well-separated pairs to be computed and materialized, leading to savings in both space (up to 10x) and time (up to 8x). Our experiments on large real-world and synthetic data sets using a 48-core machine show that our fastest algorithms outperform the best serial algorithms for the problems by 11.13–55.89x, and existing parallel algorithms by at least an order of magnitude.

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1 Introduction
This paper studies the two related geometric problems of Euclidean minimum spanning tree (EMST) and hierarchical density-based spatial clustering with added noise [16]. The problems take as input a set of \( n \) points in a \( d \)-dimensional space. EMST computes a minimum spanning tree on a complete graph formed among the \( n \) points with edges between two points having the weight equal to their Euclidean distance. EMST has many applications, including in single-linkage clustering [31], network placement optimization [60], and approximating the Euclidean traveling salesman problem [59].

Hierarchical density-based spatial clustering of applications with noise (HDBSCAN∗) is a popular hierarchical clustering algorithm [16]. The goal of density-based spatial clustering is to cluster points that are in dense regions and close together in proximity. One of the most widely-used density-based spatial clustering methods is the density-based spatial clustering of applications with noise (DBSCAN) method by Ester et al. [23]. DBSCAN requires two parameters, \( \epsilon \) and \( \text{minPts} \), which determine what is considered “close” and “dense”, respectively. In practice, \( \text{minPts} \) is usually fixed to a small constant, but many different values of \( \epsilon \) need to be explored in order to find high-quality clusters. Many efficient DBSCAN algorithms have been designed both for the sequential [18, 22, 27, 34] and the parallel context (both shared memory and distributed memory) [30, 36, 42, 50, 58, 61]. To avoid repeatedly executing DBSCAN for different values of \( \epsilon \), the OPTICS [7] and HDBSCAN∗ [16] algorithms have been proposed for constructing DBSCAN clustering hierarchies, from which clusters from different values of \( \epsilon \) can be generated. These algorithms are known to be robust to outliers in the data set. The algorithms are based on generating a minimum spanning tree on the input points, where a subset of the edge weights are determined by Euclidean distance and the remaining edge weights are determined by a DBSCAN-specific metric known as the core distance (to be defined in Section 2). Thus, the algorithms bear some similarity to EMST algorithms.

There has been a significant amount of theoretical work on designing fast sequential EMST algorithms (e.g., [6, 8, 14, 55, 63]). There have also been some practical implementations of EMST [10, 17, 43, 47], although most of them are sequential (part of the algorithm by Chatterjee et al. [17] is parallel). The state-of-the-art EMST implementations are either based on generating a well-separated pair decomposition (WSPD) [15] and applying Kruskal’s minimum spanning tree (MST) algorithm on edges produced by the WSPD [17, 47], or dual-tree traversals on \( k \)-d trees integrated into Boruvka’s MST algorithm [43]. Much less work has been proposed for parallel HDBSCAN∗ and OPTICS [51, 54]. In this paper, we design new algorithms for EMST, which can also be leveraged to design a fast parallel HDBSCAN∗ algorithm.

This paper presents practical parallel in-memory algorithms for EMST and HDBSCAN∗, and proves that the theoretical work (number of operations) of our implementations matches their state-of-the-art counterparts (\( O(n^2) \)), while having polylogarithmic depth.1 Our algorithms are based on finding the WSPD and then running Kruskal’s algorithm on the WSPD edges. For our HDBSCAN∗ algorithm, we propose a new notion of well-separation to include the

1The work is the total number of operations and depth (parallel time) is the length of the longest sequential dependence.
notion of core distances, which enables us to improve the space usage and work of our algorithm. The rest of the paper is organized as follows. Section 2 introduces some definitions. Section 3 presents our parallel well-separated

2 Preliminaries

2.1 Problem Definitions

EMST. The Euclidean Minimum Spanning Tree (EMST) problem takes \( n \) points \( P = \{p_1, \ldots, p_n\} \) and returns a minimum spanning tree (MST) of the complete undirected Euclidean graph of \( P \).

HDBSCAN*. The HDBSCAN* (hierarchical density-based spatial clustering of applications with noise) problem takes the same input as DBSCAN*, but without the \( \varepsilon \) parameter, and computes a hierarchy of DBSCAN* clusters for all possible values of \( \varepsilon \). We first introduce some definitions, and then describe how the hierarchy is computed and represented. The core distance of a point \( p \), \( \text{cd}(p) \), is the distance from \( p \) to its \( \text{minPts} \)-nearest neighbor (including \( p \) itself). The mutual reachability distance between two points \( p \) and \( q \) is defined to be \( \text{d}_{\text{m}}(p,q) = \max \{ \text{cd}(p), \text{cd}(q), d(p,q) \} \). The mutual reachability graph \( G_{\text{MR}} \) is a complete undirected graph, where the vertices are the points in \( P \), and the edges are weighted by the mutual reachability distances.

The HDBSCAN* hierarchy is sequentially computed in two steps [16]. The first step computes an MST of \( G_{\text{MR}} \) and then adds a self-edge to each vertex weighted by its core distance. An example MST is shown in Figure 1a. We note that the HDBSCAN* MST with \( \text{minPts} = 1 \) is equivalent to the EMST, since the mutual reachability distance at \( \text{minPts} = 1 \) is equivalent to the Euclidean distance. We further elaborate on the relationship between HDBSCAN* and EMST in Appendix D. A dendrogram representing clusters at different values of \( \varepsilon \) is computed by removing edges from the MST plus self-edges graph in decreasing order of weight. The root of the dendrogram is a cluster containing all points. Each non-self-edge removal splits a cluster into two, which become the two children of the cluster in the dendrogram. The height of the split cluster in the dendrogram is equal to the weight of the removed edge. If the removed edge is a self-edge, we mark the component (point) as a noise point. An example of a dendrogram is shown in Figure 1b. If we want to return the clusters for a particular value of \( \varepsilon \), we can horizontally cut the dendrogram at that value of \( \varepsilon \) and return the

1The original DBSCAN definition includes the notion of border points, which are non-core points that are within a distance of \( \varepsilon \) to core points [23]. DBSCAN* chooses to omit this to be more consistent with a statistical interpretation of clusters [16].

2The related OPTICS problem also generates a hierarchy of clusters but with a definition of reachability distance that is asymmetric, leading to a directed graph [7].
representation of the tree and returns a directed circuit that traverses every edge of the tree exactly once. *List ranking* takes a linked list with values on each node and returns for each node the sum of values from the node to the end of the list. All of the above primitives can be implemented in \(O(n)\) work and \(O(\log n)\) depth [38]. *Semisort* [32] takes as input \(n\) items, each with a key, and groups the items with the same key together, without any guarantee on the ordering of items with different keys. This algorithm takes \(O(n)\) expected work and \(O(\log n)\) depth with high probability. A parallel *hash table* supports \(n\) inserts, deletes, and finds in \(O(n)\) work and \(O(\log n)\) depth with high probability [29]. *WRITEMIN* is a priority concurrent write that takes as input two arguments, where the first argument is the location to write to and the second argument is the value to write; on concurrent writes, the smallest value is written [57].

### 2.3 Relevant Techniques

#### k-NN Query

A *k-nearest neighbor (k-NN) query* takes a point data set \(\mathcal{P}\) and a distance function, and returns for each point in \(\mathcal{P}\) its \(k\) nearest neighbors (including itself). Callahan and Kosaraju [13] show that k-NN queries in Euclidean space for all points can be solved in parallel in \(O(n\log n)\) work and \(O(\log n)\) depth.

#### kd-tree

A *kd-tree* is a commonly used data structure for k-NN queries [25]. It is a binary tree that is constructed recursively: each node in the tree represents a set of points, which are partitioned between its two children by splitting along one of the dimensions; this process is recursively applied on each of its two children until a leaf node is reached (a leaf node is one that contains at most \(c\) points, for a predetermined constant \(c\)). It can be constructed in parallel by processing each child in parallel. A \(k\)-NN query can be answered by traversing nodes in the tree that are close to the input point, and pruning nodes further away that cannot possibly contain the \(k\) nearest neighbors.

#### BCCP and BCCP*.

Existing algorithms, as well as some of our new algorithms, use subroutines for solving the *bichromatic closest pair (BCCP)* problem, which takes as input two sets of points, \(A\) and \(B\), and returns the pair of points \(p_1\) and \(p_2\) with minimum distance between them, where \(p_1 \in A\) and \(p_2 \in B\). We also define a variant, the *BCCP* problem, that finds the pair of points with the minimum mutual reachability distance, as defined for HDBSCAN*.

#### Well-Separated Pair Decomposition

We use the same definitions and notations as in Callahan and Kosaraju [15]. Two sets of points, \(A\) and \(B\), are *well-separated* if \(A\) and \(B\) can each be contained in spheres of radius \(r\), and the minimum distance between the two spheres is at least \(sr\), for a *separation constant* \(s\) (we use \(s = 2\) throughout the paper). An *interaction product* of point sets \(A\) and \(B\) is defined to be \(A \otimes B = \{(p, p') : p \in A, p' \in B, p \neq p'\}\) if: (1) \(A_i \subseteq A\) and \(B_i \subseteq B\) for all \(i = 1, \ldots, k\); (2) \(A_i \cap B_j = \emptyset\) for all \(i = 1, \ldots, k\); (3) \((A_i \otimes B_j) \cap (A_i \otimes B_k) = \emptyset\) for all \(i, j, k\) where \(1 \leq i < j \leq k\); (4) \(A \otimes B = \bigcup_{i=1}^{k} A_i \otimes B_i\); (5) \(A_i \) and \(B_i\) are well-separated for all \(i = 1, \ldots, k\).

For a point set \(\mathcal{P}\), a *well-separated pair decomposition (WSPD)* is a well-separated realization of \(\mathcal{P} \otimes \mathcal{P}\). We discuss how to construct a WSPD using a kd-tree in Section 3.

**Notation.** Table 1 shows notation frequently used in the paper.
3 Parallel EMST and HDBSCAN

In this section, we present our new parallel algorithms for EMST and HDBSCAN. We also introduce our new memory optimization to improve space usage and performance in practice.

3.1 EMST

To solve EMST, Callahan and Kosaraju present an algorithm for constructing a WSPD that creates an edge between the BCCP of each pair in the WSPD with weight equal to their distance, and then runs an MST algorithm on these edges. They show that their algorithm takes $O(T_d(n,n) \log n)$ work [14], where $T_d(n,n)$ refers to the work of computing BCCP on two sets each of size $n$.

For our parallel EMST algorithm, we parallelize WSPD construction algorithm, and then develop a parallel variant of Kruskal’s MST algorithm that runs on the edges formed by the pairs in the WSPD. We also propose a non-trivial optimization to make the implementation fast and memory-efficient.

3.1.1 Constructing a WSPD in Parallel

We introduce the basic parallel WSPD in Algorithm 1. Prior to calling WSPD, we construct a spatial median $kd$-tree $T$ in parallel with each leaf containing one point. Then, we call the procedure WSPD on Line 1 and make the root node of $T$ its input. In WSPD, we make parallel calls to FINDPAIR on the two children of all non-leaf nodes by recursively calling WSPD. The procedure FINDPAIR on Line 7 takes as input a pair $(P, P')$ of nodes in $T$, and checks whether $P$ and $P'$ are well-separated. If they are well-separated, then the algorithm records them as a well-separated pair on Line 10; otherwise, the algorithm splits the set with the larger bounding sphere into its two children and makes two recursive calls in parallel (Lines 13–14). This process is applied recursively until the input pairs are well-separated. The major difference of Algorithm 1 from the serial version is the parallel thread-splawning on Lines 3–5 and 12–14. This procedure generates a WSPD with $O(n)$ pairs [14].

3.1.2 Parallel GFK Algorithm for EMST

The original algorithm by Callahan and Kosaraju [14] computes the BCCP between each pair in the WSPD to generate a graph from which an MST can be computed to obtain the EMST. However, it is not necessary to compute the BCCP for all pairs, as observed by Chatterjee et al. [17]. Our implementation only computes the BCCP between a pair if their points are not yet connected in the spanning forest generated so far. This optimization reduces the total number of BCCP calls. Furthermore, we propose a memory optimization that avoids materializing all of the pairs in the WSPD. We will first describe how we obtain the EMST from the WSPD, and then give details of our memory optimization.

The original Kruskal’s algorithm is an MST algorithm that takes input edges sorted by non-decreasing weight, and processes the edges in order, using a union-find data structure to join components for edges with endpoints in different components. Our implementation is inspired by a variant of Kruskal’s algorithm, GeoFilterKruskal (GFK). This algorithm was used for sequential EMST by Chatterjee et al. [17], and for MST in general graphs by Osipov et al. [49]. It improves Kruskal’s algorithm by avoiding the BCCP computation between pairs unless needed, and prioritizing BCCPs between pairs with smaller cardinalities, which are cheaper, with the goal of pruning more expensive BCCP computations.

We propose a parallel GFK algorithm as shown in Algorithm 2. It uses Kruskal’s MST algorithm as a subroutine by passing it batches of edges, where each batch has edges with weights no less than those

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### Algorithm 1 Well-Separated Pair Decomposition

```plaintext
1: procedure WSPD(A)
2: if |A| > 1 then
3: do in parallel
4: WSPD(Aleft) \quad \triangleright \text{parallel call on the left child of } A
5: WSPD(Aright) \quad \triangleright \text{parallel call on the right child of } A
6: \text{FINDPAIR}(Aleft, Aright)
7: procedure FINDPAIR(P, P')
8: if $P_{\text{left}} < P_{\text{right}}$ then
9: SWAP(P, P')
10: if WELLSEPARATED(P, P') then RECORD(P, P')
11: else
12: do in parallel
13: FINDPAIR(Pleft, P') \quad \triangleright \text{Pleft is the left child of } P
14: FINDPAIR(Pright, P') \quad \triangleright \text{Pright is the right child of } P
```

### Table 1: Summary of Notation

| Notation          | Definition                                      |
|-------------------|-------------------------------------------------|
| $d(p, q)$         | Euclidean distance between points $p$ and $q$.   |
| $d(A, B)$         | Minimum distance between the bounding spheres of |
|                   | points in tree node $A$ and points in tree node $B$. |
| $w(u, v)$         | Weight of edge $(u, v)$.                        |
| $\gamma_A$       | Diameter of the bounding sphere of points in tree node $A$. |
| $\Gamma_{\min}(A)$ | Minimum core distance of points in tree node $A$.  |
| $\Gamma_{\max}(A)$ | Maximum core distance of points in tree node $A$.  |

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### Algorithm 2 Parallel GeoFilterKruskal

1: procedure PARALLELGFK(WSPD: S, Edges: $E_{\text{diff}}$, UnionFind: $U$)
2: $\beta = 2$
3: while $|E_{\text{diff}}| < (n - 1)$ do
4: $(S_i, S_k) = \text{SORT}(S, f_{\text{diff}})$ \quad \triangleright \text{For a pair (A, B), $f_{\text{diff}}$ checks if |A| + |B| \leq \beta}
5: $\rho_{\text{diff}} = \min_{(A, B) \in S} d(A, B)$
6: $(S_1, S_2) = \text{SORT}(S, f_{\text{diff}})$ \quad \triangleright \text{For a pair (A, B), $f_{\text{diff}}$ checks if BCCP(A, B) \leq \rho_{\text{diff}}}
7: $E_{\text{diff}} = \text{GETEDGES}(S_2)$ \quad \triangleright \text{Retrieves edges associated with pairs in } S_1
8: $\text{PARALLELKRUSKAL}(E_{\text{diff}}, U, \beta)$
9: $S = \text{FILTER}(S_1 \cup S_{\text{diff}}, f_{\text{diff}})$ \quad \triangleright \text{For a pair (A, B), $f_{\text{diff}}$ checks points in } A
10: $\beta = \beta \times 2$

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Figure 2: The is an example for both GFK (Algorithm 2) and Mem-
O-GFK (Algorithm 3) for EMST corresponding to the data set shown in
Figure 1. The red lines linking tree nodes and the boxes drawn below
represent well-separated pairs, and the boxes also show the cardinality
and BCCP value of the pair. Their correspondence with the symbols
$(S_1, S_2, S_k)$ in the pseudocode are color-coded. The pairs that generate
$\rho_{\text{diff}}$ are bold-squared, and the pairs filtered out have a red cross. Using
our MemO-GFK optimization, only the pairs in $S_1$ needs to be material-
ized, in contrast to needing to materialize all of the pairs in GFK.

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of edges in previous batches, and the union-find structure is shared across multiple invocations of Kruskal’s algorithm. PARALLELGFK takes as input the WSPD pairs $S$, an array $E_{out}$ to store the MST edges, and a union-find structure $UF$. On each round, given a constant $\beta$, we only consider node pairs in the WSPD with cardinality (sum of sizes) at most $\beta$ because it is cheaper to compute their BCCPs. To do so, the set of pairs $S$ is partitioned into $S_l$, containing pairs with cardinality at most $\beta$, and $S_u$, containing the remaining pairs (Line 4). However, it is only correct to consider pairs in $S_l$ that produce edges lighter than any of the pairs in $S_u$. On Line 5, we compute an upper bound $\rho_{hi}$ for the edges in $S_l$ by setting $\rho_{hi}$ equal to the minimum $d(A, B)$ for all $(A, B) \in S_u$ (this is a lower bound on the edges weights formed by these pairs). In the example shown in Figure 2, in the first round, with $\beta = 2$, the set $S_l$ contains $(a, d), (b, c), (f, g)$, and $(e, h)$, and the set $S_u$ contains $(h, Q_7), (e, Q_7), (e, Q_2), (Q_4, Q_5), (Q_3, Q_6)$, and $(Q_1, i)$. $\rho_{hi}$ corresponds to $(e, Q_7)$ on Line 5. Then, we compute the BCCP of all elements of set $S_l$, and split it into $S_{l1}$ and $S_{l2}$, where $S_{l1}$ has edges with weight at most $\rho_{lo}$ (Line 6). On Line 6, $S_{l1}$ contains $(a, d), (b, c)$ and $(f, g)$, as their BCCP distances are smaller than $\rho_{hi} = d(e, Q_7)$, and $S_{l2}$ contains $(e, h).$ After that, $E_{l1}$, the edges corresponding to $S_{l1}$, are passed to Kruskal’s algorithm (Lines 7–8). The remaining pairs $S_{l2} \cup S_u$ are then filtered based on the result of Kruskal’s algorithm (Line 9)—in particular, pairs that are connected in the union-find structure of Kruskal’s algorithm can be discarded, and for many of these pairs we never have to compute their BCCP. In Figure 2, the second round processes $(e, h), (h, Q_7), (e, Q_7), (e, Q_2), (Q_4, Q_5), (Q_3, Q_6),$ and $(Q_1, i)$, and works similarly to Round 1. However, $(Q_2, Q_8)$ gets filtered out during the second round, and we never have to compute its BCCP, leading to less work compared to a naive algorithm. Finally, the subsequent rounds process a single pair $(Q_1, i)$. At the end of each round, we double the value of $\beta$ to ensure that there are logarithmic number of rounds and hence better depth (in contrast, the sequential algorithm of Chatterjee et al. [17] increases $\beta$ by 1 every round). Throughout the algorithm, we cache the BCCP results of pairs to avoid repeated computations. Overall, the main difference between Algorithm 2 and sequential algorithm is the use of parallel primitives on nearly every line of the pseudocode, and the exponentially increasing value of $\beta$ on Line 11, which is crucial for achieving a low depth bound.

The following theorem summarizes the bounds of our algorithm.

**Theorem 3.1.** We can compute the EMST on a set of $n$ points in constant dimensions in $O(n^2)$ work and $O((\log n)^2)$ depth.

*Proof.* Callahan [13] shows that a WSPD with $O(n)$ well-separated pairs can be computed in $O(n \log n)$ work and $O(\log n)$ depth, which we use for our analysis. Our parallel GeoFilterKruskal algorithm for EMST proceeds in rounds, and processes the well-separated pairs in an increasing order of cardinality. Since $\beta$ doubles on each round, there can be at most $O(\log n)$ rounds since the largest pair can contain $n$ points. Within each round, the SPiLT on Line 4 and FILTER on Line 9 both take $O(n)$ work and $O(\log n)$ depth. We can compute the BCCP for each pair on Line 6 by computing all possible point distances between the pair, and using WRITE MIN to obtain the minimum distance. Since the BCCP of each pair will only be computed once and is cached, the total work of BCCP on Line 6 is $\sum_{A,B \in S} |A| |B| = O(n^2)$ work since the WSPD is an exact set cover for all distinct pairs. Therefore, Line 6 takes $O(n^2)$ work across all rounds and $O(1)$ depth for each round. Given $n$ edges, the MST computation on Line 8 can be done in $O(n \log n)$ work and $O(n \log n)$ depth using existing parallel algorithms [38]. Therefore, the overall work is $O(n^2)$. Since each round takes $O(n \log n)$ depth, and there are $O(\log n)$ rounds, the overall depth is $O((\log n)^2)$. ⊓⊔

We note that there exist subquadratic work BCCP algorithms [6], which result in a subquadratic work EMST algorithm. Although the algorithm is impractical and no implementations exist, for theoretical interest we give a work-efficient parallel algorithm with polylogarithmic depth in Section B of the Appendix.

We implemented our own sequential and parallel versions of the GFK algorithm as a baseline on Algorithm 2, which we found to be faster than the implementation of Chatterjee et al. [17] in our experiments. In addition, because the original GFK algorithm requires materializing the full WSPD, its memory consumption can be excessive, limiting the algorithm’s practicality. This issue worsens as the dimensionality of the data set increases, as the number of pairs in the WSPD increases exponentially with the dimension. While Chatterjee et al. [17] show that their GFK algorithm is efficient, they consider much smaller data sets than the ones in this paper.

### 3.1.3 The MemoGFK Optimization

To tackle the memory consumption issue, we propose an optimization to the GFK algorithm, which reduces its space usage and improves its running time in practice. We call the resulting algorithm MemoGFK (memory-optimized GFK). The basic idea is that, rather than materializing the full WSPD at the beginning, we partially traverse the $kd$-tree on each round and retrieve only the pairs that are needed. The pseudocode for our algorithm is shown in Algorithm 3, where PARALLELMEMOGEN takes in the root $R$ of a $kd$-tree, an array $E_{out}$ to store the MST edges, and a union-find structure $UF$.

The algorithm proceeds in rounds similar to parallel GeoFilterKruskal, and maintains lower and upper bounds ($\rho_{lo}$ and $\rho_{hi}$) on the weight of edges to be considered each round. On each round, it first computes $\rho_{hi}$ based on $\beta$ by a single $kd$-tree traversal, which will be elaborated below (Line 4). Then, together with $\rho_{lo}$ from the previous round ($\rho_{lo} = 0$ on the first round), the algorithm retrieves pairs with BCCP distance in the range $[\rho_{lo}, \rho_{hi}]$ via a second $kd$-tree traversal on Line 5. The edges corresponding to these pairs are then passed to Kruskal’s algorithm on Line 7. An example of the first round of the algorithm with MemoGFK is illustrated in Figure 2. Without the optimization, the GFK algorithm needs to first materialize all of the pairs in Round 1. With MemoGFK, $\rho_{hi} = d(e, Q_7)$ is computed via a tree traversal on Line 4, after which only the pairs in the set $S_1 = \{(a, d), (b, c), (f, g)\}$ are retrieved and materialized on Line 5 via a second tree traversal. Retrievin pairs only as needed reduces memory usage and improves performance. The correctness of the algorithm follows from the fact that each round considers
We represent pair \((A,B)\) as a line segment, based on the values of its \(d(A,B)\) and \(d_{\max}(A,B)\), which serve as the lower and upper bounds, respectively, for their BCCP and the BCCP of their descendants. The “\(\times\)”s on the line marks the value of the BCCP. (b) shows a conceptual example of tree node pairs encountered during a pruned tree traversal on Line 5 of Algorithm 3, where the pairs are represented the same way as in (a). The pairs in solid green lines, if well-separated, will be retrieved and materialized because their BCCPs are within the \(\rho_{lo} - \rho_{hi}\) range, whereas those in solid black lines will not as their BCCPs are out of range (although their BCCPs will still be computed, since their lower and upper bounds do not immediately put them out of range). The traversal will be pruned when encountering a pair represented by dotted lines as their BCCP and the BCCP of their descendants will be out of range.

non-overlapping ranges of edge weights in increasing order until all edges are considered, or when MST is completed.

Now we discuss the implementation details of the two-pass tree traversal on Line 4–5. The GETRHO subroutine, which computes \(\rho_{hi}\), does so by finding the lower bound on the minimum separation of pairs whose cardinality is greater than \(\beta\) and are not yet connected in the MST. We traverse the \(kd\)-tree starting at the root, in a similar way as when computing the WSPD in Algorithm 1. During the process, we update a global copy of \(\rho_{hi}\) using WRITEMIN whenever we encounter a well-separated pair in FINDPAIR, with cardinality greater than \(\beta\). We can prune the traversal once \(|A| + |B| \leq \beta\), as all pairs that originate from \((A,B)\) will have cardinality at most \(\beta\). We also prune the traversal when the two children of a tree node are already connected in the union-find structure, as these edges will not need to be considered by Kruskal’s algorithm. In addition, we prune the traversal when the distance between the bounding spheres of \(A\) and \(B\), \(d(A,B)\), is larger than \(\rho_{hi}\), as its descendants cannot produce a smaller distance.

The GETPAIRS subroutine then retrieves all pairs whose points are not yet connected in the union-find structure and have BCCP distances in the range \(\rho_{lo} - \rho_{hi}\). It does so also via a pruned traversal on the \(kd\)-tree starting from the root, similarly to Algorithm 1, but only retrieves the useful pairs. For a pair of nodes encountered in the FINDPAIR subroutine, we estimate the minimum and maximum possible BCCP between the pair using bounding sphere calculations, an example of which is shown in Figure 3a. We prune the traversal when \(d_{\max}(A,B) < \rho_{lo}\), or when \(d(A,B) \geq \rho_{hi}\), in which case BCCP\((A,B)\) (as well as those of its recursive calls on descendant nodes) will be outside of the range. An example is shown in Figure 3b. In addition, we also prune the traversal if \(A\) and \(B\) are already connected in the MST, as an edge between \(A\) and \(B\) will not be part of the MST.

We evaluate MemoGFK in Section 5. We also use the memory optimization for HDBSCAN∗, which will be described next.

### 3.2 HDBSCAN∗

#### 3.2.1 Baseline

Inspired by a previous sequential approximate algorithm to solve the OPTICS problem by Gan and Tao [28], we modified and parallelized their algorithm to compute the exact HDBSCAN∗ as our baseline. First, we perform \(k\)-NN queries using Euclidean distance with \(k = \min\text{Pts}\) to compute the core distances. Gan and Tao’s original algorithm creates a mutual reachability graph of size \(O(n \cdot \min\text{Pts}^2)\), using an approximate notion of BCCP between each WSPD pair, and then computes its MST using Prim’s algorithm. Our exact algorithm parallelizes their algorithm, and instead uses the exact BCCP∗ computations based on the mutual reachability distance to form the mutual reachability graph. In addition, we also compute the MST on the generated edges using the MemoGFK optimization described in Section 3.1.3. Summed across all well-separated pairs, the BCCP computations take quadratic work and constant depth. Therefore, our baseline algorithm takes \(O(n^2)\) work and \(O(\log n)\) depth, and computes the exact HDBSCAN∗. In Section C of the Appendix, we also describe a work-efficient parallel approximate algorithm based on [28].

#### 3.2.2 Improved Algorithm

Here, we present a more space-efficient algorithm that is also faster in practice. The idea is to use a different definition of well-separation for the WSPD in HDBSCAN∗. We denote the maximum and minimum core distances of the points in node \(A\) as \(cd_{\max}(A)\) and \(cd_{\min}(A)\), respectively. Consider a pair \((A,B)\) in the WSPD. We define \(A\) and \(B\) to be geometrically-separated if \(d(A,B) \geq \max\{Ad_{\text{diam}}, Bd_{\text{diam}}\}\) and mutually-unreachable if max \(d(A,B), cd_{\text{diam}}(A), cd_{\text{diam}}(B)\) \geq \max\{Ad_{\text{diam}}, Bd_{\text{diam}}, cd_{\max}(A), cd_{\max}(B)\}. We consider \(A\) and \(B\) to be well-separated if they are geometrically-separated, mutually-unreachable, or both. Note that the original definition of well-separation with only includes the first condition.

This leads to space savings because in Algorithm 1, recursive calls to procedure FINDPAIR\((A,B)\) on Line 7 will not terminate until \(A\) and \(B\) are well-separated. Since our new definition is a disjunction between mutual-unreachability and geometric-separation, the calls to FINDPAIR can terminate earlier, leading to fewer pairs generated. When constructing the mutual reachability subgraph to pass to MST, we add only a single edge between the BCCP∗ (BCCP with respect to mutual reachability distance) of each well-separated pair. With our new definition, the total number of edges generated is upper bounded by the size of the WSPD, which is \(O(n)\) [15]. In contrast, Gan and Tao’s approach generates \(O(n \cdot \min\text{Pts}^2)\) edges.

**Theorem 3.2.** Under the new definition of well-separation, our algorithm computes an MST of the mutual reachability graph.

**Proof.** Under our new definition, well-separated is defined as the disjunction between being geometrically-separated and mutually-unreachable. We connect an edge between each well-separated pair \((A,B)\) with the mutual-reachability distance \(\max\{d(u', v'), cd(u'), cd(v')\}\) as the edge weight, where \(u' \in A, v' \in B,\) and \((u', v')\) is the BCCP∗ of \((A,B)\). We overload the notation BCCP∗\((A,B)\) to also denote the mutual-reachability distance of \((u', v')\).

Consider the point set \(P_{\text{root}}\), which is contained in the root node of the tree associated with its WSPD. Let \(T\) be the MST of the full mutual reachability graph \(G_{\text{MRS}}\). Let \(T'\) be the MST of the mutual reachability subgraph \(G'_{\text{MRS}}\), computed by connecting the BCCP∗ of each well-separated pair. To ensure that \(T'\) produces the correct
Our algorithm achieves the following bounds.

**Theorem 3.3.** Given a set of \(n\) points, we can compute the MST on the mutual reachability graph in \(O(n^2)\) work, \(O(\log^2 n)\) depth, and \(O(n \cdot \text{minPts})\) space.

**Proof.** Compared to the cost of GFK for EMST, GFK for HDBSCAN* has the additional cost of computing the core distances, which takes \(O(\text{minPts} \cdot n \cdot \log n)\) work and \(O(\log n)\) depth using \(k\)-NN [13]. With our new definition of well-separation, the WSPD computation will only terminate earlier than in the original definition, and so the bounds that we showed for EMST above still hold. The new WSPD definition also gives an \(O(n)\) space bound for the well-separated pairs. The space usage of the \(k\)-NN computation is \(O(n \cdot \text{minPts})\), which dominates the space usage. Overall, this gives \(O(n^2)\) work, \(O(\log^2 n)\) depth, and \(O(n \cdot \text{minPts})\) space.

Our algorithm gives a clear improvement in space usage over the naive approach of computing an MST from the mutual reachability graph, which takes \(O(n^2)\) space, and our parallelization of the exact version of Gan and Tao’s algorithm, which takes \(O(n \cdot \text{minPts}^2)\) space. We will also see that the smaller memory footprint of this algorithm leads to better performance in practice.

3.2.3 **Implementation** We implement three algorithms for HDBSCAN*:

- a parallel version of the approximate algorithm based on Gan and Tao [28], a parallel exact algorithm based on Gan and Tao, and our space-efficient algorithm from Section 3.2.2. Our implementations all use Kruskal’s algorithm for MST and use the memory optimization introduced for MemoGFK in Section 3.1.3. For our space-efficient algorithm, we modify the WSPD and MemoGFK algorithm to use our new definition of well-separation.
4 Dendrogram and Reachability Plot

We present a new parallel algorithm for generating a dendrogram and reachability plot, given an unrooted tree with edge weights. Our algorithm can be used for single-linkage clustering [31] by passing the EMST as input, as well as for generating the HDBSCAN* dendrogram and reachability plot (refer to Section 2 for definitions). In addition, our dendrogram algorithm can be used in efficiently generating hierarchical clusters using other linkage criteria (e.g., [48, 62, 64]).

Sequentially, the dendrogram can be generated in a bottom-up (agglomerative) fashion by sorting the edges by weight and processing the edges in increasing order of weight [22, 31, 35, 44, 46]. Initially, all points are assigned their own clusters. Each edge merges the clusters of its two endpoints, if they are in different clusters, using a union-find data structure. The order of the merges forms a tree structure, which is the dendrogram. This takes $O(n \log n)$ work, but has little parallelism since the edges need to be processed one at a time. For HDBSCAN*, we can generate the reachability plot directly from the input tree by running Prim’s algorithm on the tree edges starting from an arbitrary vertex [7]. This approach takes $O(n \log n)$ work and is also hard to parallelize efficiently, since Prim’s algorithm is inherently sequential.

Our new parallel algorithm uses a top-down approach to generate the dendrogram and reachability plot given a weighted tree. Our algorithm takes $O(n \log n)$ expected work and $O(\log^* n \log n)$ depth with high probability, and hence is work-efficient.

4.1 Ordered Dendrogram

We discuss the relationship between the dendrogram and reachability plot, which are both used in HDBSCAN*. It is known [53] that a reachability plot can be converted into a dendrogram using a linear-work algorithm for Cartesian tree construction [26], which can be parallelized [56]. However, converting in the other direction, which is what we need, is more challenging because the children in dendrogram nodes are unordered, and can correspond to many possible sequences, only one of which corresponds to the traversal order in Prim’s algorithm that defines the reachability plot.

Therefore, for a specific starting point $s$, we define the ordered dendrogram of $s$, which is a dendrogram where its in-order traversal corresponds to the reachability plot starting at point $s$. With this definition, there is a one-to-one correspondence between a ordered dendrogram and a reachability plot, and there are a total of $n$ possible ordered dendrograms and reachability plots for an input of size $n$. Then, a reachability plot is just the in-order traversal of the leaves of an ordered dendrogram, and an ordered dendrogram is the corresponding Cartesian tree for the reachability plot.

4.2 A Novel Top-Down Algorithm

We introduce a novel work-efficient parallel algorithm to compute a dendrogram, which can be modified to compute an ordered dendrogram and its corresponding reachability plot.

Warm-up. As a warm-up, we first propose a simple top-down algorithm for constructing the dendrogram, which does not give us the desired work and depth bounds. We first generate an Euler tour on the input tree [38]. Then, we delete the heaviest edge, which can be found in linear work and $O(1)$ depth by checking all edges. By definition, this edge will be the root of the dendrogram, and removing this edge partitions the tree into two subtrees corresponding to the two children of the root. We then convert our original Euler tour into two Euler tours, one for each subtree, which can be done in constant work and depth by updating a few pointers. Next, we partition our list of edges into two lists, one for each subproblem. This can be done by applying list ranking on each Euler tour to determine appropriate offsets for each edge in a new array associated with its subproblem. This step takes linear work and has $O(\log n)$ depth [38]. Finally, we solve the two subproblems recursively.

Although the algorithm is simple, there is no guarantee that the subproblems are of equal size. In the worst case, one of the subproblems could contain all but one edges (e.g., if the tree is a path with edge weights in increasing order), and the algorithm would require $O(n)$ levels of recursion. The total work would then be $O(n^2)$ and depth would be $O(n \log n)$, which is clearly undesirable.

An algorithm with $O(\log n)$ levels of recursion. We now describe a top-down approach that guarantees $O(\log n)$ levels of recursion. We define the heavy edges of a tree with $n$ edges to be the $n/2$ (or any constant fraction of $n$) heaviest edges and the light edges of a tree to be the remaining edges. Rather than using a single edge to partition the tree, we use the $n/2$ heaviest edges to partition the tree. The heavy edges correspond to the part of the dendrogram closer to the root, which we refer to as the top part of the dendrogram, and the light edges correspond to subtrees of the top part of the dendrogram. Therefore, we can recursively construct the dendrogram on the heavy edges and the dendrograms on the light edges in parallel. Then, we insert the roots of the dendrograms for the light edges into the leaf nodes of the heavy-edge dendrogram. The base case is when there is a single edge, from which we can trivially generate a dendrogram.

An example is shown in Figure 5. We first construct the Euler tour of the input tree (Figure 5a). Then, we find the median edge based on edge weight, separate the heavy and light edges and compact them into a heavy-edge subproblem and multiple light-edge subproblems. For the subproblems, we construct their Euler tours by adjusting pointers, and mark the position of each light-edge subproblem in the heavy-edge subproblem where it is detached. Then, recursively and in parallel, we compute the dendrograms for each subproblem (Figure 5b). After that, we insert the roots of the light-edge dendrograms to the appropriate leaf nodes in the heavy-edge dendrogram, as marked earlier (Figure 5c).

Figure 5 shows how this algorithm applies to the input in Figure 1 with source vertex $a$. The four heaviest edges $(b, c), (d, e), (f, h),$ and $(h, i)$ divide the tree into two light subproblems, consisting of $\{(a, d), (d, b)\}$ and $\{(e, g), (g, f)\}$. The heavy edges form another.
subproblem. We mark vertices $b$ and $e$, where the light subproblems are detached. After constructing the dendrogram for the three subproblems, we insert the light dendrograms at leaf nodes $b$ and $e$, as shown in Figure 5b. It forms the correct dendrogram in Figure 5c.

We now describe the details of the steps to separate the subproblems and re-insert them into the final dendrogram.

**Subproblem Finding.** To find the position in the heavy-edge dendrogram to insert a light-edge dendrogram at, every light-edge subproblem will be associated with a unique heavy edge. The dendrogram of the light-edge subproblem will eventually connect to the corresponding leaf node in the heavy-edge dendrogram associated with it. We first explain how to separate the heavy-edge subproblem and the light-edge subproblems.

First, we compute the unweighted distance from every point to the starting point $s$ in the tree, and we refer to them as the vertex distances. For the ordered dendrogram, $s$ is the starting point of the reachability plot, whereas $s$ can be an arbitrary vertex if the ordering property is not needed. We compute the vertex distances by performing list ranking on the tree’s Euler tour rooted at $s$. These distances can be computed by labeling each downward edge (away from $s$) in the tree with a value of $1$ and each upward edge (towards $s$) in the tree with a value of $-1$, and running list ranking on the edges. The vertex distances are computed only once.

We then identify the light-edge subproblems in parallel by using the vertex distances. For each light edge $(u, v)$, we find an adjacent edge $(w, u)$ such that $w$ has smaller vertex distance than both $u$ and $v$. We call $(w, u)$ the predecessor edge of $(u, v)$. Each edge can only have one predecessor edge (an edge adjacent to $s$ will choose itself as the predecessor). In a light-edge subproblem not containing the starting vertex $s$, the predecessor of each light edge will either be a light edge in the same light-edge subproblem, or a heavy edge. The edges in each light-edge subproblem will form a subtree based on the pointers to predecessor edges. We can obtain the Euler tour of each light-edge subproblem by adjusting pointers of the original Euler tour. The next step is to run list ranking to propagate a unique label (the root’s label of the subproblem subtree) of each light-edge subproblem to all edges in the same subproblem. To create the Euler tour for the heavy subproblem, we contract the subtrees for the light-edge subproblems: for each light-edge subproblem, we map its leaves to its root using a parallel hash table. Now each heavy edge adjacent to a light-edge subproblem leaf can connect to the heavy edge adjacent to the light-edge subproblem root by looking it up in the hash table. The Euler tour for the heavy-edge subproblem can now be constructed by adjusting pointers. We assign the label of the heavy-edge subproblem root to all of the heavy edges in parallel. Then, we semisort the labeled edges to group edges of the same light-edge subproblems and the heavy-edge subproblem. Finally, we recursively compute the dendrograms on the light-edge subproblems and the heavy-edge subproblem. In the end, we connect the light-edge dendrogram for each subproblem to the heavy-edge dendrogram leaf node corresponding to the shared endpoint between the light-edge subproblem and its unique heavy predecessor edge. For the light-edge subproblem containing the starting point $s$, we simply insert its light-edge dendrogram into the left-most leaf node of the heavy-edge dendrogram.

Consider the example in Figure 5a. The heavy-edge subproblem contains edges $\{(b, c), (d, e), (f, h), (h, i)\}$, and its dendrogram is shown in Figure 5b. For the light-edge subproblem $\{(e, g), (g, f)\}$, $(e, g)$ has heavy predecessor edge $(d, e)$, and $(g, f)$ has light predecessor edge $(e, g)$. The unique heavy edge associated with the light-edge subproblem is hence $(d, e)$, with which it shares vertex $e$. Hence, we insert the light-edge dendrogram for the subproblem into leaf node $e$ in the heavy-edge dendrogram, as shown in Figure 5b. The light-edge subproblem containing $\{(a, d), (d, b)\}$ contains the starting point $s = a$, and so we insert its dendrogram into the leftmost leaf node $b$ of the heavy-edge dendrogram, as shown in Figure 5b.

We first show that our algorithm correctly computes a dendrogram, and analyze its cost bounds (Theorem 4.1). Then, we describe and analyze additional steps needed to generate an ordered dendrogram and obtain a reachability plot from it (Theorem 4.2).

**Theorem 4.1.** Given a weighted spanning tree with $n$ vertices, we can compute a dendrogram in $O(n \log n)$ expected work and $O((\log^2 n \log \log n) \log n)$ depth with high probability.

**Proof.** We first prove that our algorithm correctly produces a dendrogram. In the base case, we have one edge $(u, v)$, and the algorithm produces a tree with a root representing $(u, v)$, and with $u$ and $v$ as children of the root, which is trivially a dendrogram. We now inductively hypothesize that recursive calls to our algorithm correctly produce dendrograms. The heavy subproblem recursively computes a top dendrogram consisting of all of the heavy edges, and the light subproblems form dendrograms consisting of light edges. We replace the leaf vertices in the top dendrogram associated with light subproblems by the roots of the dendrograms on light edges. Since the edges in the heavy subproblem are heavier than all edges in light subproblems, and are also ancestors of the light edges in the resulting tree, this gives a valid dendrogram.

We now analyze the cost of the algorithm. To generate the Euler tour at the beginning, we first sort the edges and create an adjacency list representation, which takes $O(n \log n)$ work and $O(\log n)$ depth [19]. Next, we root the tree, which can be done by list ranking on the Euler tour of the tree. Then, we compute the vertex distances to $s$ using another round of list ranking based on the rooted tree.

There are $O(\log n)$ recursive levels since the subproblem sizes are at most half of the original problem. We now show that each recursive level takes linear expected work and polylogarithmic depth with high probability. Note that we cannot afford to sort the edges on every recursive level, since that would take $O(n \log n)$ work per level. However, we only need to know which edges are heavy and which are light, and so we can use parallel selection [38] to find the median and partition the edges into two sets. This takes $O(n)$ work and $O(\log n \log \log n)$ depth. Identifying predecessor edges takes a total of $O(n)$ work and $O(1)$ depth: first, we find and record for each vertex its edge where the other endpoint has a smaller vertex distance than it (using WRITEMIN); then, the predecessor of each edge can be found by checking the recorded edge for its endpoint with smaller vertex distance. We then use list ranking to assign labels to each subproblem, which takes $O(n)$ work and $O(\log n)$ depth [38]. The hash table operations to contract and look up the light-edge subproblems contribute $O(n)$ work and $O(\log n)$ depth with high probability. The semisort to group the subproblems takes $O(n)$ expected work and $O(\log n)$ depth with high probability. Attaching the light-edge
Theorem 4.1. We prove by contradiction that this cannot happen. Without loss of generality, let \( u \) be a smaller vertex distance than \( v \), our algorithm puts the result of the subproblem attached to \( u \) in the left subtree, and that of \( v \) in the right subtree. This additional comparison does not increase the work and depth of our algorithm.

Our algorithm recursively builds ordered dendrograms on the heavy-edge subproblem and on each of the light-edge subproblems, which we assume to be correct by induction. The base case is a single edge \( (u, v) \), and without loss of generality let \( u \) have a smaller vertex distance than \( v \). Then, the dendrogram will contain a root node representing edge \( (u, v) \), with \( u \) as its left child and \( v \) as its right child. Prim’s algorithm would visit \( u \) before \( v \), and the in-order traversal of the dendrogram does as well, so this is an ordered dendrogram. We now argue that the way that light-edge dendrograms are attached to the leaves of the heavy-edge dendrogram correctly produces an ordered dendrogram. First, consider a light-edge subproblem that contains the source vertex \( x \). In this case, its dendrogram is attached as the leftmost leaf of the heavy-edge dendrogram, and will be the first to be traversed in the in-order traversal. The vertices in the light-edge subproblem form a connected component \( A \). They will be traversed before any other vertices in Prim’s algorithm because all incident edges that leave \( A \) are heavy edges, and thus are heavier than any edge in \( A \). Therefore, vertices outside of \( A \) can only be visited after all vertices in \( A \) have been visited, which correctly corresponds to the in-order traversal.

Next, we consider the case where the light-edge subproblem does not contain \( x \). Let \( (u, v) \) be the predecessor edge of the light-edge subproblem, and let \( A \) be the component containing the edges in the light-edge subproblem \((v \text{ is a vertex in } A)\). Now, consider a different light-edge subproblem that does not contain \( x \), whose predecessor edge is \((x, y)\), and let \( B \) be the component containing the edges in this subproblem \((y \text{ is a vertex in } B)\). By construction, we know that \( A \) is in the right subtree of the dendrogram node corresponding to edge \((u, v)\) and \( B \) is in the right subtree of node corresponding to \((x, y)\). The ordering between \( A \) and \( B \) is correct as long as they are on different sides of either node \((u, v)\) or node \((x, y)\). For example, if \( B \) is in the left subtree of node \((u, v)\), then its vertices appear before \( A \) in the in-order traversal of the dendrogram. By the inductive hypothesis on the heavy-edge subproblem, in Prim’s order, \( B \) will be traversed before \((u, v)\) and \((u, v)\) is traversed before \( A \). We can apply a similar argument to all other cases where \( A \) and \( B \) are on different sides of either node \((u, v)\) or node \((x, y)\).

We are concerned with the case where \( A \) and \( B \) are both in the right subtrees of the nodes representing their predecessor edges. We prove by contradiction that this cannot happen. Without loss of generality, suppose node \((x, y)\) is in the right subtree of node \((u, v)\), and let both \( A \) and \( B \) be in the right subtree of \((x, y)\). There exists a lowest common ancestor (LCA) node \((x', y')\) of \( A \) and \( B \). \((x', y')\) must be a heavy edge in the right subtree of \((x, y)\). By properties of the LCA, \( A \) and \( B \) are in different subtrees of node \((x', y')\). Without loss of generality, let \( A \) be in the left subtree. Now consider edge \((x', y')\) in the tree. By the inductive hypothesis on the heavy-edge dendrogram, in Prim’s traversal order, we must first visit the leaf that \( A \) attaches to (and hence \( B \)) before visiting \((x', y')\), which must be visited before the leaf that \( B \) attaches to (and hence \( B \)). On the other hand, edge \((x, y)\) is also along the same path since it is the predecessor of \( B \). Thus, we must either have \((x', y')\) in \((x, y)\)’s left subtree or \((x, y)\) in \((x', y')\)’s right subtree, which is a contradiction to \((x', y')\) being in the right subtree of \((x, y)\).

We have shown that given any two light-edge subproblems, their relative ordering after being attached to the heavy-edge dendrogram is correct. Since the heavy-edge dendrogram is an ordered dendrogram by induction, the order in which the light-edge subproblems are traversed is correct. Furthermore, each light-edge subproblem generates an ordered dendrogram by induction. Therefore, the overall dendrogram is an ordered dendrogram.

Once the ordered dendrogram is computed, we can use list ranking to perform an in-order traversal on the Euler tour of the dendrogram to give each node a rank, and write them out in order. We then filter out the non-leaf nodes to obtain the reachability plot. Both list ranking and filtering take \( O(n) \) work and \( O(\log n) \) depth.

Implementation. In our implementation, we simplify the process of finding the subproblems by using a sequential procedure rather than performing parallel list ranking, because in most cases parallelizing over the different subproblems already provides sufficient parallelism. We set the number of heavy edges to \( n/10 \), which we found to give better performance in practice, and also preserves the theoretical bounds. We switch to the sequential dendrogram construction algorithm when the problem size falls below \( n/2 \).

5 Experiments

Environment. We perform experiments on an Amazon EC2 instance with 2 × Intel Xeon Platinum 8275CLK (3.00GHz) CPUs for a total of 48 cores with two-way hyper-threading, and 192 GB of RAM. By default, we use all cores with hyper-threading. We use the g++ compiler (version 7.4) with the -O3 flag, and use Cilk for parallelism [41]. We do not report times for tests that exceed 3 hours.

We test the following implementations for EMST (note that the EMST problem does not include dendrogram generation):

- **EMST-Naive**: The method of creating a graph with the BCCP edges from all well-separated pairs and then running MST on it.
- **EMST-GFK**: The parallel GeoFilterKruskal algorithm described in Section 3.1.2 (Algorithm 2).
- **EMST-MemoGFK**: The parallel GeoFilterKruskal algorithm with the memory optimization described in Section 3.1.3 (Algorithm 3).
- **EMST-Delaunay**: The method of creating an MST on a Delaunay triangulation for 2D data sets described in Appendix A.1.

We test the following implementations for HDBSCAN*:

- **HDBSCAN*-GanTao**: The modified algorithm of Gan and Tao for exact HDBSCAN* described in Section 3.2.1.
- **HDBSCAN*-MemoGFK**: The HDBSCAN* algorithm using our new definition of well-separation described in Section 3.2.2.

Both HDBSCAN*-GanTao and HDBSCAN*-MemoGFK use the memory optimization described in Section 3.1.3. All HDBSCAN*
running times include constructing an MST of the mutual reachability graph and computing the ordered dendrogram. We use a default value of minPts = 10 (unless specified otherwise), which is also adopted in previous work [16, 28, 44].

Our algorithms are designed for multicore, as we found that multicore are able to process the largest data sets in the literature for these problems (machines with several terabytes of RAM can be rented at reasonable costs on the cloud). Our multicore implementations achieve significant speedups over existing implementations in both the multicore and distributed memory contexts.

Data Sets. We use the synthetic seed spreader data sets produced by the generator in [27]. It produces points generated by a random walk in a local neighborhood (SS-varden). We also use UniformFill that contains points distributed uniformly at random inside a bounding hypergrid with side length \( \sqrt{n} \) where \( n \) is the total number of points. We generated the synthetic data sets with 10 million points (unless specified otherwise) for dimensions \( d = 2, 3, 5, 7 \).

We use the following real-world data sets. GeoLife [2, 65] is a 3-dimensional data set with 24,876,978 data points. This data set contains user location data (longitude, latitude, and altitude), and is extremely skewed. Household [3, 5] is a 7-dimensional data set with 2,049,280 points representing electricity consumption measurements in households. HT [4, 37] is a 10-dimensional data set with 928,991 data points containing home sensor data. CHEM [1, 24] is a 16-dimensional data set with 4,208,261 data points containing chemical sensor data. All of the data sets fit in the RAM of our machine.

Comparison with Previous Implementations. For EMST, we tested the sequential Dual-Tree Boruvka algorithm of March et al. [43] (part of mlpack), and our single-threaded EMST-MemoGFK times are 0.89–4.17 (2.44 on average) times faster. Raw running times for mlpack are presented in Table 3. We also tested McInnes and Healy’s sequential HDBSCAN* implementation which is based on Dual-Tree Boruvka [44]. We were unable to run their code on our data sets with 10 million points in a reasonable amount of time. On a smaller data set with 1 million points (2D-SS-varden-1M), their code takes around 90 seconds to compute the MST and dendrogram, whereas EMST-MemoGFK does not get good speedup, and is slower than EMST-Naive by up to 17.69x and 8.63x, respectively, due to its memory optimization, which reduces memory traffic. We note that EMST-GFK does not get good speedup, and is slower than EMST-Naive in all subplots of Figure 6. This is because for a small data set, the total work done is small and the parallelization overhead becomes prominent.

EMST-MemoGFK significantly outperforms EMST-GFK and EMST-Naive by up to 17.69x and 8.63x, respectively, due to its memory optimization, which reduces memory traffic. We note that EMST-GFK does not get good speedup, and is slower than EMST-Naive in all subplots of Figure 6. This is because for a small data set, the total work done is small and the parallelization overhead becomes prominent.

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In Figure 7, we see that our HDBSCAN*-MemoGFK method achieves good speedups over the best sequential times, ranging from 11.13–46.69x on 48 cores. Similar to EMST, we observe a similar lower speedup for 10D-HT-0.93M due to its

| Method                  | Speedup over Best Sequential | Self-relative Speedup |
|-------------------------|------------------------------|-----------------------|
| EMST-Naive              | 3.51–10.69x                  | 6.90x                 |
| EMST-GFK                | 1.52–7.01x                   | 3.60x                 |
| EMST-MemoGFK            | 14.61–55.89x                 | 31.31x                |
| Delaunay                | 14.12–16.64x                 | 15.38x                |
| HDBSCAN* MemoGFK        | 12.13–46.69x                 | 26.29x                |
| HDBSCAN* GanTao         | 4.29–35.14x                  | 13.76x                |

Table 2: Speedup over the best sequential algorithm as well as the self-relative speedup on 48 cores.
Figure 6: Speedup of EMST implementations over the best serial baselines vs. thread count. The best serial baseline and its running time for each data set is shown on the y-axis label. “48h” on the x-axis refers to 48 cores with hyper-threading.

Figure 7: Speedup of implementations for HDBSCAN’ MST generation over the best serial baselines vs. thread count using minPts = 10. The best serial baseline and its running time for each data set is shown on the y-axis label. “48h” on the x-axis refers to 48 cores with hyper-threading.

Figure 8: Decomposition of running times for constructing the EMST and HDBSCAN’ MST on various data sets using all 48 cores with hyper-threading, minPts = 10 for HDBSCAN’. In the legend, “dendrogram” refers to computing the ordered dendrogram; “delaunay” refers to computing the Delaunay triangulation; ”kruskal” refers to Kruskal’s MST algorithm; ”wspd” refers to computing the WSPD decomposition, or the sum of WSPD tree traversal times across rounds; ”core-dist” refers to computing core distances of all points; and ”build-tree” refers to building a k-d-tree on all points.
small size, and observe higher speedups for larger data sets. The dendrogram construction takes at least 50% of the total time for Figures 7a, b, and e–h, and hence has a large impact on the overall scalability. We discuss the dendrogram scalability separately.

We find that HDBSCAN*-MemoGFK consistently outperforms HDBSCAN*-GanTao due to having a fewer number of well-separated pairs (2.5–10.29x fewer) using the new definition of well-separation. This is also evident in Figure 8, where we see that HDBSCAN*-MemoGFK spends much less time than HDBSCAN*-GanTao in WSPD computation.

We tried varying minPts over a range from 10 to 50 for our HDBSCAN* implementations and found just a moderate increase in the running time for increasing minPts.

**MemoGFK Memory Usage.** Overall, the MemoGFK method for both EMST and HDBSCAN* reduces memory usage by up to 10x compared to materializing all WSPD pairs in a naive implementation.

**Dendrogram Results.** We separately report the performance of our parallel dendrogram algorithm in Figure 9, which shows the speedups and running times on all of our data sets. We see that the parallel speedup ranges from 5.69–49.74x (with an average of 17.93x) for the HDBSCAN* MST with minPts =10, and 5.35–52.58x (with an average 20.64x) for single-linkage clustering, which is solved by generating a dendrogram on the EMST. Dendrogram construction for single-linkage clustering shows higher scalability because the heavy edges are more uniformly distributed in space, which creates a larger number of light-edge subproblems and increases parallelism. In contrast, for HDBSCAN*, which has a higher value of minPts, the sparse regions in the space tend to have clusters of edges with large weights even if some of them have small Euclidean distances, since these edges have high mutual reachability distances. Therefore, these heavy edges are less likely to divide up the edges into a uniform distribution of subproblems in the space, leading to lower parallelism. On the other hand, we observe that across all data sets, the dendrogram for single-linkage clustering takes an average of 16.44 seconds, whereas the dendrogram for HDBSCAN* takes an average of 9.27 seconds. This is because the single-linkage clustering generates more light-edge subproblems and hence requires more work. While it is possible to tune the fraction of heavy edges for different values of minPts, we found that using \( n/10 \) heavy edges works reasonably well in all cases.

6 Conclusion

We presented practical and theoretically-efficient parallel algorithms of EMST and HDBSCAN*. We also presented a work-efficient parallel algorithm for computing an ordered dendrogram and reachability plot. Finally, we showed that our optimized implementations achieve good scalability and outperform state-of-the-art implementations for EMST and HDBSCAN*.

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![Figure 9: Self-relative speedups and times for ordered dendrogram computation for single-linkage clustering and HDBSCAN* (minPts = 10). The x-axis indicates the self-relative speedup on 48 cores with hyper-threading. The speedup and time is shown at the end of each bar.](image)

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A Parallel EMST and HDBSCAN’ in 2D

A.1 Parallel EMST in 2D

The Delaunay triangulation on a set of points in 2D contains triangles among every triple of points $p_1$, $p_2$, and $p_3$ such that there are no other points inside the circumcircle defined by $p_1$, $p_2$, and $p_3$ [21].

In two dimensions, Shamos and Hoey [55] show that the EMST can be computed by computing an MST on the Delaunay triangulation of the points. Parallel Delaunay triangulation can be computed in $O(n \log n)$ work and $O(n \log^3 n)$ depth [52], and has $O(n)$ edges, and so the MST computation requires the same work and depth. We provide an implementation of this algorithm using the parallel Delaunay triangulation and parallel implementation of Kruskal’s algorithm from the Problem Based Benchmark Suite [11].

A.2 Parallel HDBSCAN’ in 2D

The ordinary Voronoi diagram is a planar subdivision of a space where points in each cell share the same nearest neighbor. The k-order Voronoi Diagram is a generalization of the ordinary Voronoi diagram, where points in each cell share the same k-nearest neighbors [9]. A k-order edge is a closely related concept, and defined to be an edge where there exists a circle through the two edge endpoints, such that there are at most k points inside the circle [33].

De Berg et al. [22] show that in two dimensions, the MST on the mutual reachability graph can be computed in $O(n \log n)$ work. Their algorithm computes an MST on a graph containing the k-order edges, where $k = \min\text{Pts} - 3$, and where the edges are weighted by the mutual reachability distances between the two endpoints. They prove that the MST returned is an MST on the mutual reachability graph. In this section, we extend their result to the parallel setting.

To parallelize the algorithm, we need to compute the k-order edges of the points in parallel. This can be done by first computing the $(k + 1)$-order Voronoi diagram, and then converting the edges in the Voronoi diagram to k-order edges, as shown by Gudmundsson et al. [33]. Specifically, we convert each Voronoi edge into a k-order edge by connecting the two points that induce the two cells sharing the Voronoi edge.

Meyerhenke [45] shows that the family of the order-j Voronoi diagrams for all $1 \leq j \leq k$ can be computed in $O(k^2 n \log n)$ work and $O(k \log^2 n)$ depth. The algorithm works by first computing the ordinary Voronoi diagram on the input points. Then for each Voronoi cell, it computes the ordinary Voronoi diagram again on the points that induce the neighboring cells. This ordinary Voronoi diagram divides the Voronoi cell into multiple subcells, each of which corresponds to a cell in the Voronoi diagram of one higher order. This process is repeated until obtaining the order-k Voronoi diagram. Lee [40] proves that the number of k-order edges is $O(nk)$, and so we can run parallel MST on these edges in $O(nk \log n)$ work and $O(\log n)$ depth. This gives us the following theorem.

Theorem A.1. Given a set of n points in two dimensions, we can compute the MST on the mutual reachability graph in $O(\min\text{Pts}^2 \cdot n \log n)$ work and $O(\min\text{Pts} \cdot \log^2 n)$ depth.

For computing the ordinary Voronoi diagrams on each step of Meyerhenke’s algorithm, we use the parallel Delaunay triangulation implementation from the Problem Based Benchmark Suite [11] and take the dual of the resulting triangulation. However, we found it to be significantly slower than our other methods due to high work of the Voronoi diagram computations.

B Subquadratic-work Parallel EMST

Callahan and Kosaraju’s algorithm [14] first constructs a fair-split tree $T$ and its associated WSPD in $O(n \log n)$ work and $O(\log n)$ depth [13], which is improved from a previous version with $O(n \log n)$ work and $O(\log^2 n)$ depth [15]. Then, the algorithm runs Boruvka’s steps for $\lfloor \log_2 n \rfloor$ rounds. In particular, in each round, the algorithm finds the lightest outgoing edges only for the components with size at most $2^{k+1}$ and merges the components connected by these edges. To do so, the algorithm constructs for every component a set of candidate points that contains the nearest point outside the component. The algorithm searches for the candidates top-down on $T$, and maintains for each node in the tree, a list of all the component s that can have candidates in the subtree of that node. They ensure the size of each list is $O(1)$ using the WSPD in a manner identical to the all-nearest-neighbors algorithm of [15]. In this process, they push the lists down to the leaves of $T$, so that the candidates corresponding to a component will be the leaves that contain that component in their lists.

Let $P_j$ be the set of candidates for the $j$th component. $P_j$ is split into $\lfloor |P_j|/2^{k+1} \rfloor$ subsets of size at most $2^{k+1}$ each, and the BCCP is found between each subset and the $j$th component. At round $i$, there are $n/2^i$ components, and the BCCP routine is invoked $\sum_{j=1}^{n/2^i} |P_j|/2^{i+1} = O(n/2^i)$ times, each with size at most $2^{i+1}$. Therefore, the work for BCCP on each round is $O((n/2^i)T_d(2^{i+1}, 2^{i+1}))$. Since $T_d$ is at least linear, this dominates the work for each phase. The total work for BCCP computations is $O(T_d(n, n) \log n)$. In our parallel algorithm, on each round, we perform both the candidate listing step and BCCP computations in parallel. Listing candidates for all components can be computed in parallel given a WSPD. In particular, this uses the top-down computation used for the all-nearest-neighbor search, parallelized using rake and compress operations [15], and takes logarithmic depth. Wang et al. [61] show that BCCP can be computed in parallel in $O(n^{2−2/((\log^2 d)+\log s)})$ expected work and $O(\log^2 n \log^2 n)$ depth w.h.p. Both the work and depth at each round is therefore dominated by computing the BCCPs. With $O(\log n)$ rounds, this results in $O(T_d(n, n) \log n)$ expected work and $O(\log^2 n \log^2 n)$ depth w.h.p, where $T_d(n, n) = O(n^{2−2/((\log^2 d)+\log s)})$. This is also the work and depth of the overall EMST algorithm, as WSPD construction only contributes lower-order terms to the complexity.

Theorem B.1. We can compute the EMST on a set of $n$ points in $d$ dimensions in $O(n^{2−2/((\log^2 d)+\log s)} \log n)$ expected work and polylogarithmic depth w.h.p.

C Parallel Approximate OPTICS

Parallel Algorithm. Gan and Tao [28] propose a sequential algorithm to solve the approximate OPTICS problem, defined in Lemma 4.2 of their paper [28] (this also gives an approximation to HDBSCAN’). The algorithm takes in an additional parameter $\rho \geq 0$, which is related to the approximation factor. The algorithm makes use of the WSPD and uses $O(n \cdot \min\text{Pts}^2)$ space, with the separation constant $s = \sqrt{8/\rho}$. They construct a base graph by adding
we call OPTICS-GanTaoApprox. It uses the MemoGFK optimization described in Section 3.1.3. We found that when run with a reasonable parameter of $\rho$ that leads to good clusters, OPTICS-GanTaoApprox is usually slower than our exact version of the algorithm (HDBSCAN*-GanTao, described in Section 3.2.1). The primary reason is that a reasonable $\rho$ value requires a high separation constant in the WSPD, which produces a very large number of well-separated pairs, leading to poor performance. In contrast, in the exact algorithm, a small separation constant ($s = 2$) is sufficient for correctness, Figure 10 shows the speedups on two data sets for OPTICS-GanTaoApprox with $\rho = 0.125$ (corresponding to a separation constant of 8) compared with other methods. Across all of the data sets, we found OPTICS-GanTaoApprox to be slower than HDBSCAN*-GanTao by a factor of 1.00–1.96x, and slower than HDBSCAN*-MemoGFK by a factor of 1.72–7.48x.

**D Relationship between EMST and HDBSCAN**

**MST**

We now show that for $\text{minPts} \leq 3$, the EMST is always an MST of the HDBSCAN* base graph by having the same set of edges, but for higher values of $\text{minPts}$ it is possible that this is not the case. For example, Figure 11 gives an example where EMST is not an MST of the HDBSCAN* base graph when $\text{minPts} = 4$.

**Theorem D.1.** An EMST is always an MST for the HDBSCAN* mutual reachability graph when $\text{minPts} \leq 3$.

**Proof.** For $\text{minPts} \leq 2$, all edges in the HDBSCAN* mutual reachability graph have edge weights defined by Euclidean distances, and so the edge weights are identical. We now discuss the case when $\text{minPts} = 3$.

Let $T$ be an EMST, and $T' \neq T$ be an MST in $G_{MR}$. We show that we can convert $T'$ to $T$ without changing the total weight. Consider any edge $(u, v) \in T$, but not in $T'$. If we add $(u, v)$ to $T'$, then we get a cycle $C$.

First, we show that $(u, v)$ cannot be the unique heaviest edge in $C$ under $d_m$. Recall that $cd(p)$ is the core distance of a point $p$ and $d_m(p, q) = \max\{cd(p), cd(q), d(p, q)\}$. Assume by contradiction that $(u, v)$ is the unique heaviest edge in $C$ under $d_m$.

If $d_m(u, v) = d(u, v)$, then $(u, v)$ is also the unique heaviest edge in $C$ in the Euclidean complete graph, and so it cannot be in $T$, which is the EMST. This is a contradiction.

Now we consider the case where $d_m(u, v) > d(u, v)$. Without loss of generality, suppose that $d_m(u, v) = cd(u)$. Then $v$ must be $u$'s unique nearest neighbor; otherwise, $d_m(u, v) = cd(u) = d(u, v)$ because we have $\text{minPts} = 3$. However, then all other points have larger distance to $u$ than $d(u, v)$, and $u$ must have an edge to one of these other points in the cycle $C$. Thus, $(u, v)$ cannot be the unique heaviest edge in $C$. This is a contradiction.

Now, given that $(u, v)$ is not the unique heaviest edge in $C$, we can replace one of the heaviest edges $e$ that is in $C$, but not in $T$, with $(u, v)$, and obtain another MST in $G_{MR}$ with the same weight.

Below we show that there is always such an edge $e$ in $C$. We first argue that there must be some heaviest edge in $C$ that has its Euclidean distance as its weight in $G_{MR}$. Consider a heaviest edge $(a, b)$ in $C$, and without loss of generality, suppose that $d_m(a, b) = cd(a)$.

If $(a, b)$ does not have its Euclidean distance as its edge weight, then...
Figure 11: An example where the EMST is not an MST of HDBSCAN\textsuperscript{*} base graph (call it MST\textsuperscript{*}), when minPts = 4. The blue values are core distances of the points. The yellow values are weights of edges according to their mutual reachability distances. The solid edges form MST\textsuperscript{*}. Both edge (f, g) and (e, f) are in the EMST, but cannot both be in MST\textsuperscript{*} because they are the heaviest edges in the g-b-c-d-e-f-g cycle.

b must be a’s unique nearest neighbor. Besides (a, b), a must be incident to another edge in C, which we denote as (a, c). \( d_m(a, c) \) must equal \( d_m(a, b) \): we have \( d_m(a, c) \geq \text{cd}(a) = d_m(a, b) \) because b is a’s unique nearest neighbor, but we also have \( d_m(a, c) \leq d_m(a, b) \) because (a, b) is a heaviest edge in C. Therefore, \( d_m(a, c) = d_m(a, b) \), and (a, c) is one of the heaviest edges in C under \( d_m \). Furthermore, \( d_m(a, c) = d(a, c) \) because \( d(a, c) \leq d_m(a, c) \) by definition and \( d(a, c) \geq \text{cd}(a) = d_m(a, b) = d_m(a, c) \) because minPts = 3 and \( b \neq c \) is a’s unique nearest neighbor. Thus, we have shown that (a, c) is a heaviest edge in C that has its Euclidean distance as its weight in \( G_{MR} \).

All heaviest edges that have the Euclidean distance as their weight must also be the heaviest edges in C in the Euclidean complete graph, and thus they cannot all be in the EMST \( T \). Therefore, there must exist some heaviest edge \( e \in C \) that is in \( T' \) but not in \( T \). We can always find such an edge in \( T' \) and swap it with the edge \((u, v)\) in \( T \) to make \( T' \) share more edges with \( T \), without changing the total weight of \( T' \) in \( G_{MR} \), as both edges are heaviest edges in \( C \) under \( d_m \). We can repeat this process until we obtain \( T \). Therefore, \( T \) is also an MST in \( G_{MR} \). □

E Additional Data from Experiments

Table 3 shows the running times for mlpack. Table 4 shows the running times of our implementations for EMST. Table 5 shows the running times of our implementations for HDBSCAN\textsuperscript{*}.

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Table 3: Table of running times in seconds for the sequential EMST implementation from mlpack.

|                | EMST-Naive 1 thread | EMST-Naive 48 cores | EMST-GFK 1 thread | EMST-GFK 48 cores | EMST-MemoGFK 1 thread | EMST-MemoGFK 48 cores | Delaunay 1 thread | Delaunay 48 cores |
|----------------|---------------------|---------------------|-------------------|-------------------|-----------------------|-----------------------|-------------------|------------------|
| 2D-UniformFill-10M | 62.51               | 3.64                | 57.93             | 6.11              | 31.54                 | 1.20                  | 65.46             | 1.90             |
| 3D-UniformFill-10M | 400.57              | 19.30               | 218.02            | 26.07             | 67.80                 | 2.24                  | –                 | –                |
| 5D-UniformFill-10M | –                   | –                   | –                 | –                 | 230.93                | 5.03                  | –                 | –                |
| 7D-UniformFill-10M | –                   | –                   | –                 | –                 | 1585.65               | 28.37                 | –                 | –                |
| 2D-SS-varden-10M  | 57.84               | 3.45                | 60.64             | 6.90              | 27.48                 | 1.60                  | 64.42             | 1.95             |
| 3D-SS-varden-10M  | 240.24              | 12.13               | 189.52            | 23.37             | 48.72                 | 1.85                  | –                 | –                |
| 5D-SS-varden-10M  | 478.40              | 19.41               | 278.10            | 31.19             | 96.19                 | 3.04                  | –                 | –                |
| 7D-SS-varden-10M  | 626.76              | 21.10               | 336.62            | 29.26             | 205.15                | 6.18                  | –                 | –                |
| 3D-GeoLife-10M    | 271.95              | 10.97               | 328.76            | 36.31             | 117.31                | 4.77                  | –                 | –                |
| 7D-Household-2.05M| 280.28              | 8.37                | 214.08            | 24.77             | 37.60                 | 1.40                  | –                 | –                |
| 10D-HT-0.93M      | 19.28               | 0.64                | 12.36             | 1.40              | 5.17                  | 0.35                  | –                 | –                |
| 16D-CHEM-4.2M     | –                   | –                   | –                 | –                 | 821.81                | 19.11                 | –                 | –                |

Table 4: Table of running times in seconds for EMST. The fastest parallel time for each data set is in bold. The tests that do not complete within 3 hours or that run out of memory are shown as “–”. The data sets with dimensionality greater than 2 are not applicable to Delaunay, and also shown as “–”.

|                | HDBSCAN∗-MemoGFK 1 thread | HDBSCAN∗-MemoGFK 48 cores | HDBSCAN∗-GanTao 1 thread | HDBSCAN∗-GanTao 48 cores |
|----------------|---------------------------|---------------------------|--------------------------|--------------------------|
| 2D-UniformFill-10M | 197.55                    | 10.34                     | 298.03                   | 18.71                    |
| 3D-UniformFill-10M | 321.97                    | 14.66                     | 517.71                   | 24.04                    |
| 5D-UniformFill-10M | 1217.87                   | 38.41                     | 2395.68                  | 68.54                    |
| 7D-UniformFill-10M | 7487.95                   | 289.27                    | –                        | –                        |
| 2D-SS-varden-10M  | 163.73                    | 6.07                      | 163.37                   | 15.66                    |
| 3D-SS-varden-10M  | 154.31                    | 7.56                      | 253.06                   | 15.44                    |
| 5D-SS-varden-10M  | 716.81                    | 22.20                     | 885.92                   | 34.51                    |
| 7D-SS-varden-10M  | 2253.38                   | 48.26                     | 2583.83                  | 64.13                    |
| 3D-GeoLife-10M    | 687.75                    | 22.70                     | 1320.13                  | 160.48                   |
| 7D-Household-2.05M| 93.23                     | 3.54                      | 204.75                   | 13.51                    |
| 10D-HT-0.93M      | 15.74                     | 1.41                      | 29.75                    | 3.21                     |
| 16D-CHEM-4.2M     | 1165.20                   | 35.77                     | 1820.61                  | 55.52                    |

Table 5: Table of running times in seconds for HDBSCAN∗ with minPts = 10. The fastest parallel time for each data set is in bold. The tests that do not complete within 3 hours, or that run out of memory are shown as “–”.

HDBSCAN∗ (minPts = 10)