A Faster Algorithm for Constructing the Frequency Difference Consensus Tree

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Abstract

A consensus tree is a phylogenetic tree that summarizes the evolutionary relationships inferred from a collection of phylogenetic trees with the same set of leaf labels. Among the many types of consensus trees that have been proposed in the last 50 years, the frequency difference consensus tree is one of the more finely resolved types that retains a large amount of information. This paper presents a new deterministic algorithm for constructing the frequency difference consensus tree. Given \( k \) phylogenetic trees with identical sets of \( n \) leaf labels, it runs in \( O(kn \log n) \) time, improving the best previously known solution.

2012 ACM Subject Classification
Theory of computation → Graph algorithms analysis; Applied computing → Bioinformatics

Keywords and phrases
phylogenetic tree, frequency difference consensus tree, tree algorithm, centroid path decomposition, max-Manhattan Skyline Problem

Digital Object Identifier 10.4230/LIPIcs.STACS.2024.43

Supplementary Material
Software: https://github.com/tswddd2/FDCT_new
archived at swh:1:dir:7cb120cbc61221f740e9e824e93bce0b0f164270a

Funding
This work was partially funded by JSPS KAKENHI grant 22H03550 and NSERC Discovery Grants.

Acknowledgements
The authors would like to thank Varun Gupta for some ideas employed in the procedure Fast_Label_Trees.

1 Introduction

In phylogenetic analysis, variations in datasets, algorithms, and models of evolution typically yield different phylogenetic trees. Hence, researchers often need to analyze a collection of phylogenetic trees with the same set of leaf labels but different branching structures, and to this end, they use consensus trees. A consensus tree is a single phylogenetic tree that represents a collection of phylogenetic trees, aiming to highlight the commonly agreed-upon parts of the evolutionary history. Consensus trees have applications across various fields of science, including biology, evolutionary studies, epidemiology, and ecology. Many alternative consensus trees, each with its strengths and limitations, have been proposed; see, e.g., [7].

The frequency difference consensus tree (FDCT) [16] has garnered interest among researchers in recent years [15, 17, 20]. Given \( k \) phylogenetic trees with identical sets of \( n \) leaf labels, the FDCT is a phylogenetic tree consisting of each cluster that occurs more frequently
in the input trees than any single cluster incompatible with it. In this context, a cluster refers to any nonempty subset of the leaf label set and is said to occur in a phylogenetic tree iff it corresponds to the set of all leaf labels descending from a single node of the tree. Furthermore, two clusters are deemed incompatible if they cannot simultaneously occur in the same phylogenetic tree. The advantage of the FDCT compared to some other popular types of consensus trees, such as the strict consensus tree [30] and the majority rule consensus tree [25], is that it captures more of the shared branching information and has more clusters.

It is evident that $\Omega(kn)$ serves as a lower bound for the running time of any algorithm aiming to build the FDCT, given that it corresponds to the input size. Unlike certain other types of consensus trees such as the strict consensus tree and the majority rule consensus tree, there has been no algorithm proposed to construct the FDCT that can achieve a running time matching this lower bound. Before this paper, the $O(kn \log^2 n)$-time algorithm by Gawrychowski et al. [15] was the asymptotically fastest algorithm for constructing the FDCT. In this paper, we present an $O(kn \log n)$-time algorithm for constructing the FDCT, thus reducing the gap between the upper and lower bounds for the running time of the fastest algorithm to solve this problem.

The overarching structure of our new algorithm follows the framework proposed by Jansson et al. [20] for computing the FDCT. By improving the methods for solving two subproblems in [20], our algorithm achieves a running time of $O(kn \log n)$. First, our algorithm incorporates a novel divide-and-conquer solution that runs in $O(kn \log n)$ time for the weighting step, where the number of phylogenetic trees in which each cluster occurs is calculated. We remark that algorithms for computing other types of consensus trees such as the greedy consensus tree [7, 13] involve the same weighting step [15, 21, 32] and may derive advantages from our improved method. Second, the running time of the procedure Filter_Clusters is improved to $O(n \log n)$ by solving instances of the Max-Manhattan Skyline Problem [9] to identify the clusters that should be removed at each recursive stage of the algorithm (refer to Sections 3 and 5 for the detailed explanation).

1.1 Definitions and Notation

A phylogenetic tree is a rooted tree that represents the evolutionary relationships among different organisms. Every internal node of a phylogenetic tree has at least two unordered children and every leaf has a distinct label. The term trees will be employed as a shorthand for phylogenetic trees in the remainder of this paper. Let $T$ be some tree. The set of nodes of $T$ is denoted by $V(T)$. Let $\Lambda(T)$ be the set of leaf labels of $T$. Non-empty subsets of $\Lambda(T)$ are called clusters. Clusters with cardinality 1 or $|\Lambda(T)|$ are trivial clusters. For any node $u \in V(T)$, $T[u]$ is the subtree of $T$ rooted at $u$ and $\Lambda(T[u])$ is the set of leaf labels of $T[u]$, called the cluster associated with $u$. The cluster collection of $T$, denoted by $C(T)$, is the set $\bigcup_{u \in V(T)} \{\Lambda(T[u])\}$. Any cluster $C \subseteq \Lambda(T)$ occurs in $T$ iff $C \in C(T)$. For any nodes $u, v \in V(T)$, we denote the lowest common ancestor of $u$ and $v$ in $T$ by $\text{lca}^T(u, v)$. Further, for any non-empty set of nodes $U \subseteq V(T)$, we refer to the lowest common ancestor of all these nodes in $T$ by $\text{lca}^T(U)$.

Any two clusters $C_1, C_2 \subseteq \Lambda(T)$ are said to be compatible, written as $C_1 \sim C_2$, iff $C_1 \subseteq C_2, C_2 \subseteq C_1$, or $C_1 \cap C_2 = \emptyset$. If $C_1$ and $C_2$ satisfy none of the preceding properties, then they are incompatible, denoted as $C_1 \not\sim C_2$. Similarly, given trees $T_1$ and $T_2$ with identical leaf label sets, and nodes $u \in V(T_1)$ and $v \in V(T_2)$, we say $u$ is compatible with $v$, denoted as $u \sim v$, if the clusters associated with $u$ and $v$ are compatible. We now extend the notion of compatibility to trees. A cluster $C \subseteq \Lambda(T)$ is compatible with $T$ (denoted as $C \sim T$) iff for every $C' \subseteq C(T)$, we have $C \sim C'$. Further, two trees $T_1$ and $T_2$ with
identical leaf label sets are compatible (denoted as $T_1 \sim T_2$) iff for every $C \in C(T_1)$, $C \sim T_2$, i.e. iff every cluster in $T_1$ is compatible with $T_2$. This also means that every cluster in $T_2$ is compatible with $T_1$.

The frequency difference consensus tree (FDCT) is defined as follows. Let $S$ be a set of $k$ trees with identical sets of $n$ leaf labels, i.e. $S = \{T_1, T_2, \ldots, T_k\}$ and $\Lambda(T_1) = \Lambda(T_2) = \ldots = \Lambda(T_k) = L$ (where $|L| = n$). For any cluster $C \subseteq L$, let the weight of $C$, denoted as $w(C)$, be $|\{T : T \in S \text{ and } C \in C(T)\}|$, i.e., the number of trees in $S$ in which $C$ occurs. For any tree $T \in S$ and any node $u \in V(T)$, we define the weight of node $u$ as $w(u) = w(\Lambda[T[u]])$. Then, the FDCT of $S$ is the tree $T_{FD}$, where $C(T_{FD}) = \{C : C \subseteq L \text{ and } w(C) > \max\{w(C') : C' \subseteq L \text{ and } C \not\sim C'\}\}$. Thus, $T_{FD}$ contains every cluster that occurs more frequently than any cluster incompatible with it (we refer to such clusters as frequency difference clusters). By Proposition 3 in [31], this tree always exists and is unique for a given $S$. Figure 1 illustrates the FDCT for a collection of four phylogenetic trees.

**Figure 1** Let $S = \{T_1, T_2, T_3, T_4\}$. $T_{FD}$ is the FDCT of $S$. In each $T_i$, the number beside each non-root internal node $u$ indicates the weight $w(u)$. In this example, $T_{FD}$ does not contain the clusters $\{a, b\}$ and $\{b, c\}$ with weight 2 because they are incompatible with each other. On the other hand, $T_{FD}$ contains the cluster $\{d, e\}$ with weight 1. Furthermore, $T_{FD}$ contains the cluster $\{a, b, c\}$ with weight 2, even though that cluster is incompatible with two input trees.

### 1.2 Previous Work

A variety of types of consensus trees have been developed over the last half-century, starting with the Adams consensus tree [2] in 1972. Some of these consensus trees are summarized in [7]. Here, we describe two well-studied types of consensus trees: the strict consensus tree [30] and the majority-rule consensus tree [25]. The strict consensus tree keeps only the clusters that occur in all input trees and is easily computed in optimal $O(kn)$ running time [10]. However, some potentially important clusters might be discarded from this consensus tree, if one of the input trees does not contain them. The majority-rule consensus tree is a generalization of the previous consensus tree and contains all clusters that occur in more than half of the trees. The majority-rule consensus tree can also be computed in optimal $O(kn)$ time [21].
The frequency difference consensus tree (FDCT) was introduced by Goloboff et al. [16] as a more informative alternative that contains not only the clusters that occur in the majority of trees but also the other frequency difference clusters. Dong et al. [11] provided a comparison of the FDCT and a few other types of consensus trees. Barrett et al. [3] employed the idea of using the frequency difference metric while analyzing angiosperm phylogeny. Steel and Velasco [31] investigated a generalization of the FDCT to supertrees, i.e. consensus trees built from input trees that do not necessarily have the same leaf label sets. They showed that, unlike some other commonly used definitions, the FDCT easily generalizes to a viable supertree definition. Moreover, the FDCT has been utilized in various other studies over the years [14, 18, 19, 23, 24, 26, 27, 28, 29].

Several research works have focused on computing the FDCT of a set of \(k\) trees, each labeled by the same set of \(n\) leaf labels. An implementation of the FDCT can be found in the free software package TNT [17]; however, the algorithm employed by TNT and its complexity remain undisclosed. Jansson et al. [20] gave a deterministic \(\min\{O(kn^2), O(kn(k + \log^2 n))\}\)-time algorithm for constructing the FDCT. This algorithm was implemented in the open-source FACT package [21] and experimentally shown [20] to be significantly faster than TNT’s implementation. Subsequently, Gawrychowski et al. [15] developed a faster method for the weighting step in [20], yielding an improved running time of \(O(kn \log^2 n)\) for constructing the FDCT.

1.3 Organization of the Article

This paper is organized as follows. Section 2 contains some results from previous works that are utilized later in this paper. Section 3 gives the framework of the \(O(kn \log n)\)-time algorithm for computing the FDCT. Sections 4 and 5 present algorithms for solving the subproblems of the FDCT construction. Finally, Section 6 provides the concluding remarks.

2 Preliminaries

2.1 The delete Operation

The delete operation on a non-root internal node \(u\) in a tree \(T\) makes all children of \(u\) become children of \(u\)’s parent and then removes \(u\) along with all edges connected to it. After applying this operation on \(u\), the cluster \(\Lambda(T[u])\) is removed from the cluster collection of \(T\). If \(c\) denotes the number of \(u\)’s children, then the delete operation on \(u\) takes \(O(c)\) time.

2.2 The Lowest Common Ancestor

We restate the following lemma outlining the lowest common ancestor (lca) operation from [4]:

▶ Lemma 1. Given any tree \(T\), the lca data structure can be constructed in \(O(n)\) time, where \(n = |V(T)|\). Then, for any nodes \(u, v \in V(T)\), the query \(\text{lca}^T(u, v)\) can be answered in constant time.

2.3 Restriction of Trees

For any tree \(T\) and any cluster \(C \subseteq \Lambda(T)\), we define \(T|C\) (called \(T\) restricted to \(C\)) as the tree \(T’\) with \(V(T’) = \{\text{lca}^T(u, v) : u, v \in C\}\) such that \(\text{lca}^T(C') = \text{lca}^{T'}(C')\) for all \(C' \subseteq C\). Intuitively, \(T’\) has the leaf label set \(C\) and consists of all nodes in \(T\) that are lca’s of the leaves in \(C\), and the ancestral relationships between the nodes in \(T’\) are the same as they were in \(T\). Figure 2 provides an example of restricting a tree to different clusters.
2.4 Expanded Restriction of Trees

Recall that every node in the tree $T$ is associated with a weight. For any subset $C \subseteq L$, when we compute the restricted tree $T|C$, some nodes in $T$ are deleted. This leads to losing information about the weights of the clusters associated with these nodes. To address this, we extend the concept of restricted trees following the definition given in [20] and allow some nodes to be marked as spoiled (see below for details). For any $C \subseteq \Lambda(T)$, we obtain the weighted tree $T||C$ (called the expanded restriction of $T$ to $C$) as follows:

1. Let $T' = T|C$.
2. For every node $u$ in $T'$, set the weight of $u$ equal to its weight in $T$ and mark $u$ as spoiled if $\Lambda(T'[u]) \neq \Lambda(T[u])$ or if $u$ is a spoiled node in $T$.
3. For every edge $(u,v)$ in $T'$, let $P$ be the path in $T$ between $u$ and $v$, excluding $u$ and $v$. If $P$ contains at least one node, then create a new node $z$ in $T'$ (referred to as a path node), replace the edge $(u,v)$ with the two edges $(u,z)$ and $(z,v)$, assign the weight of $z$ to the highest weight among all nodes in $P$, and mark $z$ as spoiled.
4. Let $T||C = T'$.

Intuitively, a node $u$ in $T|C$ that was not already spoiled in $T$ becomes spoiled in $T||C$ if at least one leaf label in $\Lambda(T[u])$ is not in $C$. It follows that if a node becomes spoiled in $T||C$, then all of its ancestors become spoiled. Furthermore, every path node is a spoiled node (but not vice versa). The purpose of the path nodes in $T||C$ is to compactly represent the weights of the clusters that were lost when building the restriction of $T$ to $C$ and that may conflict with clusters that are subsets of $C$. Figure 3 shows an example of the expanded restriction of trees.
We extend the definition of compatibility to spoiled nodes. Suppose that $C_1, C_2 \subseteq \Lambda(T)$ and that $u$ is a spoiled node in $T[|C_1|$. We have $C_2 \sim u$ iff $C_2$ and $\Lambda(T[|C_1|)[u])$ are disjoint or $C_2 \subseteq \Lambda(T[|C_1|)[u])$. Observe that if $\Lambda((T[|C_1|)[u]) \subseteq C_2$, then $C_2 \not\sim u$, i.e., the set inclusion relations in the definition of compatibility are asymmetric for spoiled nodes.

The expanded restrictions can be computed efficiently according to the following lemma:

**Lemma 2.** Let $T$ be a weighted phylogenetic tree with $n$ leaves. After $O(n \log n)$ time preprocessing, for any partition $C_1, C_2, \ldots, C_q$ of $\Lambda(T)$, the trees $T[|C_i|$ for all $i \in \{1, 2, \ldots, q\}$ can be constructed in a total of $O(n)$ time.

**Proof.** By Lemma 5.2 of [12], the trees $T[|C_i|$ for all $i \in \{1, 2, \ldots, q\}$ can be constructed in a total of $O(n)$ time. By Theorem 2 of [22], after an $O(n \log n)$-time preprocessing of $T$, the maximum weight of all nodes along the path between any two nodes $u$ and $v$ in $T$ can be found in $O(1)$ time. Furthermore, after an $O(n)$-time preprocessing of $T$, the second node on the path from any node $u$ in $T$ to any other node $v$ in $T$ can be found in $O(1)$ time. Consequently, $T[|C_i|$ can be constructed in $O(\lambda(|C_i|))$ time from $T[|C_i|$ for any $i \in \{1, 2, \ldots, q\}$, which completes the proof.

### 2.5 Merging Trees

Given two trees $T_1$ and $T_2$ where $\Lambda(T_1) = \Lambda(T_2) = L$ and $T_1 \sim T_2$, `Merge_Trees(T_1, T_2)` returns a tree $T$ such that $\Lambda(T) = L$ and $C(T) = C(T_1) \cup C(T_2)$. Jansson et al. [21] showed that `Merge_Trees` can be computed in $O(|L|)$ time. Figure 4 gives an example for `Merge_Trees`.

![Figure 4](image-url) Illustration of merging trees where $T = \text{Merge_Trees}(T_1, T_2)$.

### 2.6 The Max-Manhattan Skyline Problem

Given a set $S$ of $O(n)$ subintervals of $[1, n - 1]$ with positive integer heights of size $O(n)$, the MAX-MANHATTAN SKYLINE PROBLEM asks for a table $f$ such that for $t \in [1, n - 1]$, $f[t] = \max\{\text{height}([i, j]) : t \in [i, j], [i, j] \in S\}$. Crochemore et al. [9] gave an $O(n)$-time algorithm for the MIN-MANHATTAN SKYLINE PROBLEM, defined in a similar way as the MAX-MANHATTAN SKYLINE PROBLEM, except that it seeks the minimum height instead of the maximum in the definition of the output table $f$. Their algorithm first sorts the intervals according to their heights in non-decreasing order. Then, for each interval $[i, j]$ in this order, it sets the values of $f[t]$ for all positions $t \in [i, j]$ that have not yet been assigned a value to $\text{height}([i, j])$. By modifying Crochemore et al.’s algorithm [9] to sort the intervals in non-increasing order, we immediately have:

**Lemma 3.** The MAX-MANHATTAN SKYLINE PROBLEM can be solved in $O(n)$ time.
2.7 Centroid Paths and Side Trees

A centroid path \([8]\) of a tree \(T\) is a path of the form \(\pi = \langle p_\alpha, p_{\alpha-1}, \ldots, p_1 \rangle\), where \(p_\alpha\) is any node in \(T\), the node \(p_{i-1}\) for every \(i \in \{2, \ldots, \alpha\}\) is any child of \(p_i\) with the maximum number of leaf descendants (ties are broken arbitrarily), and \(p_1\) is a leaf. Suppose that \(\pi\) is a centroid path of \(T\). For any \(u \in V(T)\) such that \(u\) does not belong to \(\pi\) but the parent of \(u\) does, \(T[u]\) is called a side tree of \(\pi\). From these definitions, we can derive the following lemma:

\[\text{Lemma 4.} \text{ Let } T \text{ be a tree and } \tau \text{ a side tree of a centroid path that starts at the root of } T. \text{ Then } |\Lambda(\tau)| \leq |\Lambda(T)|/2.\]

By computing a centroid path \(\pi\) starting at the root of \(T\) and recursively applying this procedure to the side trees of \(\pi\), we obtain a centroid path decomposition of \(T\). It follows from Lemma 4 that the number of recursion levels needed to complete such a decomposition is \(O(\log |\Lambda(T)|)\).

3 Algorithm Fast_Frequency_Difference

The pseudocode of our new algorithm, named Fast_Frequency_Difference, is shown in Algorithm 1. Its overall structure follows the framework developed in [20] for constructing the FDCT, which we review next.

\[\text{Algorithm 1} \text{ The algorithm Fast_Frequency_Difference for constructing the FDCT, which maintains the overall structure established by the algorithm Frequency_Difference in [20].}\]

Suppose that the input is \(S = \{T_1, T_2, \ldots, T_k\}\). The basic idea of the algorithm in [20] is to initially let \(T\) be a copy of \(T_1\) and then consider the other trees one by one while updating the clusters of \(T\) accordingly. More precisely, when considering any such tree \(T_j\), the algorithm deletes every cluster in \(T\) that is incompatible with a cluster in \(T_j\) of equal or higher weight, and also inserts every cluster from \(T_j\) into \(T\) that could potentially be a frequency cluster but is not already in \(T\). This strategy produces a tree \(T\) whose set of clusters is a superset of the set of the frequency difference clusters, so the algorithm applies a final postprocessing step to delete all non-frequency difference clusters from \(T\).
To update $T$ in each iteration, the procedure $\text{Merge_Trees}$, described in Section 2.5, and a procedure called $\text{Filter_Clusters}$ are used. The latter takes as input two trees $T_A$ and $T_B$ with identical leaf label sets and outputs a copy of $T_A$ from which every cluster that is incompatible with a cluster in $T_B$ of equal or higher weight has been deleted.

Our new algorithm $\text{Fast_Frequency_Difference}$ improves the time complexity of the previous algorithm from [20] by replacing the preprocessing step for computing the weights of all clusters occurring in $S$ (Step 1) and the procedure $\text{Filter_Clusters}$ (used in Steps 3 and 4) by more efficient solutions, referred to as $\text{Fast_Compute_Weights}$ and $\text{Fast_Filter_Clusters}$ below.

In Section 4, we will prove the following theorem concerning the correctness and time complexity of the procedure $\text{Fast_Compute_Weights}$:

> **Theorem 5.** Given a set $S = \{T_1, T_2, \ldots, T_k\}$ of trees with identical sets of $n$ leaf labels, the procedure $\text{Fast_Compute_Weights}(S)$ calculates the weights of all clusters occurring in $S$ in $O(kn \log n)$ time.

Moreover, Section 5 contains the proof for the following theorem regarding the correctness and time complexity of the procedure $\text{Fast_Filter_Clusters}$:

> **Theorem 6.** Given two weighted trees $T_A$ and $T_B$ with identical sets of $n$ leaf labels, the procedure $\text{Fast_Filter_Clusters}(T_A, T_B)$ filters out clusters as needed in $O(n \log n)$ time.

On the grounds of the two theorems stated above, we can prove the main theorem of this paper:

> **Theorem 7.** Given a set $S = \{T_1, T_2, \ldots, T_k\}$ of trees with identical sets of $n$ leaf labels, the algorithm $\text{Fast_Frequency_Difference}(S)$ constructs the FDCT of $S$ in $O(kn \log n)$ time.

**Proof.** Assuming that the improved procedures function as intended, the correctness of $\text{Fast_Frequency_Difference}$ follows from that of $\text{Frequency_Difference}$ proved by [20].

Now, we analyze the time complexity of the algorithm. Step 1 makes a call to the procedure $\text{Fast_Compute_Weights}$, which takes $O(kn \log n)$ time, according to Theorem 5. Furthermore, Steps 3 and 4 make $O(k)$ calls to the procedures $\text{Fast_Filter_Clusters}$ and $\text{Merge_Trees}$. By Theorem 6, each call to the procedure $\text{Fast_Filter_Clusters}$ takes $O(n \log n)$ time. Furthermore, the procedure $\text{Merge_Trees}$ runs in $O(n)$ time [21]. Hence, Steps 3 and 4 take $O(kn \log n)$ time. Consequently, the running time of the algorithm is $O(kn \log n)$.

4 Procedure $\text{Fast_Compute_Weights}$

We break down the improved procedure $\text{Fast_Compute_Weights}$ into two phases called labeling and counting, similar to the strategy used in [15]. The procedure $\text{Fast_Label_Trees}$ is responsible for the labeling phase. This procedure assigns an integer label to each node $u$ in every tree in $S$, denoted by $id(u)$, such that $id(u) \in \{1, \ldots, 2kn\}$ and that for any other node $u'$ in any tree in $S$, $id(u) = id(u')$ iff the clusters associated with $u$ and $u'$ are the same. Next, during the counting phase, the labels are sorted using counting sort, the count of each distinct label is determined, and the weight of each cluster is obtained from the count of the label of its associated node. Algorithm 2 presents the pseudocode for the procedure $\text{Fast_Compute_Weights}$. 


Label each node

Output:

Compute the weight of each cluster in which C occurs.

/* Labeling phase */
1 Fast_Label_Trees(S)

/* Counting phase */
2 Sort the obtained labels using counting sort.
3 Determine the count of each distinct label.
4 Set the weight of each cluster to the count of the label of its associated node.

End Fast_Compute_Weights

The procedure Fast_Label_Trees uses a divide-and-conquer approach to carry out the labeling phase. Let $L'$ and $L''$ form a partition of $L$ such that the difference between $|L'|$ and $|L''|$ is at most one. Fast_Label_Trees($\{T_1, \ldots, T_k\}$) recursively calls Fast_Label_Trees($\{T_1|L'|, \ldots, T_k|L'|\}$) and Fast_Label_Trees($\{T_1|L'', \ldots, T_k|L''\}$) to obtain the labels for all nodes in $T_i|L'$ and $T_i|L''$ for all $i \in \{1, 2, \ldots, k\}$. Then, for each node $u$ in any tree $T_i \in S$, the pair $(id(\varphi^C_u), id(\varphi^C_u'))$ is assigned to $u$, where $\varphi_u^C$ for any $C \subseteq L$ denotes the node in $T_i|C$ that corresponds to $u$ (if such node does not exist in $T_i|C$, then $\varphi_u^C$ is set to $\varnothing$, a special node with $id(\varnothing) = 0$). Next, all pairs are sorted using radix sort, and a positive integer rank is assigned to each unique pair. Finally, for each node $u$ in any tree $T_i \in S$, $id(u)$ is set to the rank of the pair $(id(\varphi^L_u), id(\varphi^L_u'))$. The pseudocode for the procedure Fast_Label_Trees is given in Algorithm 3. Moreover, Figure 5 illustrates one iteration of Fast_Label_Trees.

Algorithm 2 The procedure Fast_Compute_Weights.

Algorithm Fast_Compute_Weights
Input: A set $S = \{T_1, T_2, \ldots, T_k\}$ of trees with $\Lambda(T_1) = \Lambda(T_2) = \ldots = \Lambda(T_k) = L$.
Output: Compute the weight of each cluster $C$ occurring in $S$, i.e., the number of trees in $S$ in which $C$ occurs.
/* Labeling phase */
1 Fast_Label_Trees(S)

/* Counting phase */
2 Sort the obtained labels using counting sort.
3 Determine the count of each distinct label.
4 Set the weight of each cluster to the count of the label of its associated node.

End Fast_Compute_Weights

Algorithm 3 The procedure Fast_Label_Trees.

Algorithm Fast_Label_Trees
Input: A set $S = \{T_1, T_2, \ldots, T_k\}$ of trees with $\Lambda(T_1) = \Lambda(T_2) = \ldots = \Lambda(T_k) = L$.
Output: Label each node $u$ in a tree in $S$ with $id(u) \in \{1, \ldots, 2k|L|\}$ such that two nodes in different trees receive the same label iff the clusters associated with them are the same.

1 if $|L| = 1$ then
   /* Base case (each tree has only one node) */
   For each node $u$ in any tree in $S$, set $id(u) = 1$.
   return
endif
2 Partition $L$ into $L'$ and $L''$, such that the difference between $|L'|$ and $|L''|$ is at most one.
3 For all $i \in \{1 \ldots k\}$, let $T_i' = T_i|L'|$ and $T_i'' = T_i|L''$.
4 Fast_Label_Trees($\{T_1', T_2', \ldots, T_k'\}$).
5 Fast_Label_Trees($\{T_1'', T_2'', \ldots, T_k''\}$).
6 For each node $u$ in any tree $T_i \in S$, assign the pair $(id(\varphi^L_u'), id(\varphi^L_u''))$ to $u$.
7 Sort all the obtained pairs using radix sort, remove duplicates, and assign a rank to each unique pair.
8 For each node $u$ in any tree $T_i \in S$, set $id(u)$ to the rank of the pair $(id(\varphi^L_u'), id(\varphi^L_u''))$.

End Fast_Label_Trees
The following lemma proves the correctness of the procedure \texttt{Fast_Label_Trees}:

\begin{lemma}
Given a set $S = \{T_1, T_2, \ldots, T_k\}$ of trees with identical sets of $n$ leaf labels, the following statements hold after running the procedure \texttt{Fast_Label_Trees}(S):
\begin{enumerate}
  \item For any node $u \in V(T_i)$ where $T_i \in S$, we have $\text{id}(u) \in \{1, \ldots, 2k|L|\}.$
  \item For any two nodes $u \in V(T_i)$ and $v \in V(T_j)$ where $T_i, T_j \in S$, we have $\text{id}(u) = \text{id}(v)$ iff $\Lambda(T_i[u]) = \Lambda(T_j[v]).$
\end{enumerate}
\end{lemma}

\textbf{Proof.} We start by showing that the first statement holds. It can be easily seen that $|V(T_i)| < 2|L|$ for any $T_i \in S.$ Thus, the total number of nodes in all trees is less than $2k|L|.$ Consequently, the label of each node is in $\{1, \ldots, 2k|L|\}.$

To prove the second statement, we use induction on $|L|.$ The base case of $|L| = 1$ holds because all nodes have the same cluster associated with them and receive the same label. The induction hypothesis states that if $|L| \leq k$ for some $k \geq 1$, then we have $\text{id}(u) = \text{id}(v)$ iff $\Lambda^T(u) = \Lambda^T(v).$ Now, we want to prove the statement for $|L| = k + 1.$

If $\Lambda(T_i[u]) = \Lambda(T_j[v]),$ we have $\Lambda((T_i|L'|)[\varphi^L_u]) = \Lambda((T_j|L'|)[\varphi^L_v])$ and $\Lambda((T_i|L'')[\varphi^L_u]) = \Lambda((T_j|L'')[\varphi^L_v]).$ Hence, considering that $|L'| \leq k$ and $|L''| \leq k,$ we can apply the induction hypothesis to state that $\text{id}(\varphi^L_u) = \text{id}(\varphi^L_v)$ and $\text{id}(\varphi^L_u) = \text{id}(\varphi^L_v).$ Consequently, we have $\text{id}(\varphi^L_u), \text{id}(\varphi^L_v), \text{id}(\varphi^L_u)$ and thereby, $\text{id}(u) = \text{id}(v).$

On the other hand, if $\text{id}(u) = \text{id}(v),$ we have $(\text{id}(\varphi^L_u), \text{id}(\varphi^L_u)) = (\text{id}(\varphi^L_v), \text{id}(\varphi^L_v)).$ As a result, we have $\text{id}(\varphi^L_u) = \text{id}(\varphi^L_v)$ and $\text{id}(\varphi^L_u) = \text{id}(\varphi^L_v).$ Therefore, considering that $|L'| \leq k$ and $|L''| \leq k,$ we can use the induction hypothesis to deduce that $\Lambda((T_i|L')[\varphi^L_u]) = \Lambda((T_j|L')[\varphi^L_u])$ and $\Lambda((T_i|L'')[\varphi^L_u]) = \Lambda((T_j|L'')[\varphi^L_u])$. Thus, we have $\Lambda(T_i[u]) = \Lambda(T_j[v]).$

Next, we analyze the time complexity of the procedure \texttt{Fast_Label_Trees}:

\begin{lemma}
Given a set $S = \{T_1, T_2, \ldots, T_k\}$ of trees with identical sets of $n$ leaf labels, the procedure \texttt{Fast_Label_Trees}(S) runs in $O(kn \log n)$ time.
\end{lemma}
Proof. Let $T(n)$ be the running time of $\text{Fast\_Label\_Trees}(S)$. By Lemma 5.2 of [12], the construction of $T_i'$ and $T_i''$ takes $O(n)$ time for each $T_i \in S$, and thereby, a total of $O(kn)$ time for all of the trees. Computing $\text{id}(\varphi_u')$ and $\text{id}(\varphi_u'')$ for each node $u$ in some tree $T_i \in S$ can be done by a bottom up traversal of $T_i$, along with $T_i'$ and $T_i''$, in a total of $O(kn)$ time. The number of obtained pairs is $O(n)$. Furthermore, we can deduce from Lemma 8 that all values in the pairs are in $\{0, 1, \ldots, O(kn)\}$. Thus, sorting these pairs using radix sort and assigning labels to the nodes take $O(kn)$ time. Therefore, we have $T(n) = 2T(n/2) + O(kn)$, and consequently, $T(n) = O(kn \log n)$.

Now, we can prove Theorem 5, regarding the correctness and time complexity of the procedure $\text{Fast\_Compute\_Weights}$:

$\begin{align*}
\textbf{Theorem 5.} \text{ Given a set } S = \{T_1, T_2, \ldots, T_k\} \text{ of trees with identical sets of } n \text{ leaf labels, the procedure } \text{Fast\_Compute\_Weights}(S) \text{ calculates the weights of all clusters occurring in } S \text{ in } O(kn \log n) \text{ time.}
\end{align*}$

Proof. We start by proving that the procedure $\text{Fast\_Compute\_Weights}$ works correctly. The correctness of Step 1, making a call to the procedure $\text{Fast\_Label\_Trees}$, follows from Lemma 8. In the following steps, the weight of each cluster is set to the count of the label of its associated node, indicating the number of trees in $S$ in which that cluster occurs.

Now, we analyze the time complexity. As shown in Lemma 9, assigning labels to each node in Step 1 takes $O(kn \log n)$ time. Considering that there are $O(kn)$ labels in total and each label is in $[1, \ldots, 2kn]$, Step 2 (counting sort) takes $O(kn)$ time. Furthermore, it is easy to see that Steps 3 and 4 take $O(kn)$ time each. Therefore, the running time of the procedure is $O(kn \log n)$.

$\begin{align*}
\textbf{Procedure Fast\_Filter\_Clusters}
\end{align*}$

On a high level, our new procedure $\text{Fast\_Filter\_Clusters}$, with an improved running time of $O(n \log n)$, follows a similar approach as the $O(n \log^2 n)$-time procedure $\text{Filter\_Clusters}$ in [20]. The objective is to build a tree $T$ whose cluster collection is $\mathcal{C}(T) = \{\Lambda(T_A[u]) : u \in V(T_A) \text{ and } \omega(u) > \omega(v) \text{ for every } v \in V(T_B) \text{ with } \Lambda(T_A[u]) \neq \Lambda(T_B[v])\}$, i.e., to delete every cluster $u$ in $T_A$ that conflicts with at least one cluster in $T_B$ with a weight greater than or equal to that of $u$. To do this, both procedures apply the centroid path decomposition technique to divide $T_A$ into a centroid path $\pi = \{p_0, p_0 - 1, \ldots, p_1\}$, where $p_0$ is the root of $T_A$, and the set $\sigma(\pi)$ of side trees of $\pi$. Since each cluster in $T_A$ is either located inside a side tree of $\pi$ or associated with a node belonging to $\pi$, the cluster collection $\mathcal{C}(T_A)$ may be expressed recursively as:

$$\mathcal{C}(T_A) = \bigcup_{\tau \in \sigma(\pi)} \mathcal{C}(\tau) \cup \bigcup_{p_i \in \pi} \{\Lambda(T_A[p_i])\}. \quad (1)$$

Following this key observation, to check all clusters of $T_A$ in order to decide which ones to delete, the procedures handle the side trees of $\pi$ recursively and the clusters associated with $\pi$ directly.

The main difference between $\text{Filter\_Clusters}$ from [20] and $\text{Fast\_Filter\_Clusters}$ presented here is how they handle the clusters $\bigcup_{p_i \in \pi} \{\Lambda(T_A[p_i])\}$. The former uses a dynamic data structure to keep track of the currently conflicting nodes from $T_B$ while traversing $\pi$ upwards and retrieving the heaviest conflicting cluster at each step, taking $O(n \log n)$ time to process all the clusters associated with $\pi$. In addition, the time taken to set up the recursive calls to the side trees is $O(n)$. Since the total time spent on each recursion level is $O(n \log n)$ and there are $O(\log n)$ recursion levels, the time complexity of $\text{Filter\_Clusters}$ is
$O(n \log^2 n)$. In contrast, \texttt{Fast\_Filter\_Clusters} detects conflicts between clusters associated with $\pi$ and clusters in $T_B$ by representing clusters as suitably defined integer intervals. It then solves an instance of the \textsc{Max-Manhattan Skyline Problem} to identify the heaviest conflicting clusters. We will show that this method requires $O(n)$ time to handle all of the clusters associated with $\pi$. Thus, each recursion level takes $O(n)$ time, and the total running time becomes $O(n \log n)$.

The pseudocode of \texttt{Fast\_Filter\_Clusters} is presented in Algorithm 4.

\textbf{Algorithm 4} The procedure \texttt{Fast\_Filter\_Clusters}.

\begin{algorithm}
\caption{The procedure \texttt{Fast\_Filter\_Clusters}.}
\begin{algorithmic}
\Input Two weighted trees $T_A$ and $T_B$ with $\Lambda(T_A) = \Lambda(T_B) = L$ such that every $u \in V(T_A) \cup V(T_B)$ has a positive integer weight $w(u)$, and that some nodes in $T_B$ may be spoiled.
\Output A tree $T$ with $\Lambda(T) = L$ and $C(T) = \{\Lambda(T_A[u]) : u \in V(T_A) \text{ and } w(u) > w(x) \text{ for every } x \in V(T_B) \text{ with } \Lambda(T_A[u]) \neq \Lambda(T_B[x])\}$.
\State Compute a centroid path $\pi = (p_a, p_{a-1}, \ldots, p_1)$ of $T_A$, where $p_a$ is the root of $T_A$ and $p_1$ is a leaf, and compute the set $\sigma(\pi)$ of side trees of $\pi$.
\State /* Handling the side trees */
\For {$\sigma$ each side tree $\tau$ of $\pi$}
\State Construct $T_B||\Lambda(\tau)$. Temporarily change the node weights in $\tau$ and $T_B||\Lambda(\tau)$ by sorting them in nondecreasing order and setting each node weight equal to its rank. Let $\tau' := \texttt{Fast\_Filter\_Clusters}(\tau, T_B||\Lambda(\tau))$.
\State Replace $\tau$ by $\tau'$ in $T_A$ and restore the node weights in $\tau'$.
\EndFor
\State /* Handling the centroid path */
\For {$i = 1$ to $\alpha$}
\State Compute $n_i := |\Lambda(T_A[p_i])|$.
\State Temporarily relabel the leaf labels in $L$ by the positive integers $\{1, 2, \ldots, n_\alpha\}$ in a way that makes $\pi$ become a stratifying path in $T_A$.
\State Compute and store, for every $v \in V(T_B)$, the values $m(v) = \min\{\Lambda(T_B[v])\}$ and $M(v) = \max\{\Lambda(T_B[v])\}$. For any $v \in V(T_B)$, if $v$ is a spoiled node, then set $M(v) = n_\alpha + 1$.
\State Compute and store, for every $v \in V(T_B)$, the value $\text{filled}(v)$ equivalent to the largest integer $x$ such that $\{1, 2, \ldots, x\} \subseteq \Lambda(T_B[v])$.
\State Create a set $I$ of weighted intervals over $\{1, 2, \ldots, n_\alpha + 1\}$ as follows:
\State For each $v \in V(T_B)$, make an interval $[v_L, v_U]$ with weight $w(v)$, where $v_L = 2 \cdot \max\{\text{filled}(v) + 1, m(v)\}$ and $v_U = 2 \cdot M(v)$. Insert the weighted interval into $I$.
\State Solve the \textsc{Max-Manhattan Skyline Problem} on $I$ and let $f$ be the solution.
\State /* $i = 1$ downto $\alpha$ */
\If {$w(p_i) \leq f[2 \cdot n_i + 1]$}
\State Apply a delete operation on $p_i$ in $T_A$.
\EndIf
\EndFor
\State Restore the leaf labels of $L$ to the values that they had before Step 4.
\State \Return $T_A$
\End
\end{algorithmic}
\end{algorithm}
Before describing the correctness of \texttt{Fast\textunderscore Filter\textunderscore Clusters}, we introduce a lemma that can be used to speed up the detection of conflicting clusters. Let $T$ be a phylogenetic tree such that $\Lambda(T)$ is a set of positive integers $\{1, 2, \ldots, n\}$. Moreover, let $\pi = \langle p_\alpha, p_{\alpha-1}, \ldots, p_1 \rangle$ denote a path in $T$, where $p_\alpha$ is the root of $T$ and $p_1$ is a leaf. For each $i \in \{1, 2, \ldots, \alpha\}$, define $n_i := |\Lambda(T[p_i])|$. Note that $n_1 = 1$ and $n_\alpha = n$. The path $\pi$ is called a stratifying path if $\Lambda(T[p_i]) = \{1, 2, \ldots, n_i\}$ for every $i \in \{1, 2, \ldots, \alpha\}$. Furthermore, for any $C \subseteq \Lambda(T)$, define $\text{filled}(C)$ as the largest integer $x$ such that $\{1, 2, \ldots, x\} \subseteq C$. In the following lemma, we determine whether a specified cluster $C$ and the cluster associated with a specified node $p_i$ on a stratifying path $\pi$ are compatible:

\begin{lemma}
Let $T$ be a phylogenetic tree with $\Lambda(T) = \{1, 2, \ldots, n\}$. Also, let $\pi = \langle p_\alpha, p_{\alpha-1}, \ldots, p_1 \rangle$ be a stratifying path in $T$. For any $C \subseteq \Lambda(T)$ and $i \in \{1, 2, \ldots, \alpha\}$, we have $C \not\prec \Lambda(T[p_i])$ if $\max\{\text{filled}(C) + 1, \min(C)\} < n_i + 0.5 < \max(C)$ holds, where $\Lambda(T[p_i]) = \{1, 2, \ldots, n_i\}$.
\end{lemma}

\begin{proof}
First suppose that $C \not\prec \Lambda(T[p_i])$. This means that there exist $x, y, z \in \Lambda(T)$ such that $x, y \in C$, $z \not\in C$, $x, z \in \Lambda(T[p_i])$, and $y \not\in \Lambda(T[p_i])$. Then:
- $x \in \Lambda(T[p_i])$ implies $x \leq n_i$. Since $x \in C$, we have $\min(C) < n_i + 0.5$.
- $y \not\in \Lambda(T[p_i])$ gives $y > n_i$. Since $y \in C$ is an integer, we deduce that $n_i + 0.5 < \min(C)$.
- $z \in \Lambda(T[p_i])$ implies $z \leq n_i$. Furthermore, $z \not\in C$ gives $z \geq \text{filled}(C) + 1$. Combining the two inequalities, we get $\text{filled}(C) + 1 < n_i + 0.5$.

On the other hand, suppose that $C \prec \Lambda(T[p_i])$. By the definition of cluster compatibility, at least one of the following three cases holds:
- $C \subseteq \Lambda(T[p_i])$: Then $x \leq n_i$ for all $x \in C$, i.e., $\max(C) \leq n_i$. Thus, the inequality $n_i + 0.5 < \max(C)$ is false.
- $\Lambda(T[p_i]) \subseteq C$: Then $\text{filled}(C) \geq n_i$, and hence $\text{filled}(C) + 1 < n_i + 0.5$ is false.
- $C \cap \Lambda(T[p_i]) = \emptyset$: Then $x > n_i$ for all $x \in C$, i.e., $\min(C) > n_i$. Thus, $\min(C) < n_i + 0.5$ is false.
\end{proof}

Figure 6 provides an illustration of Lemma 10.

\[\text{Figure 6 Illustration of Lemma 10.}\]

Let $T$ be the tree with a stratifying path $\langle p_\alpha, p_{\alpha-1}, \ldots, p_1 \rangle$ shown above. Consider the node $p_2$ and a cluster $C = \{5, 6, 8, 9\}$. Since $\min(C) = 5$, $\max(C) = 9$, $\text{filled}(C) = 0$, and $n_2 = 8$, Lemma 10 implies $C \not\prec \Lambda(T[p_2])$. Next, consider $p_2$ and $C' = \{1, 2, \ldots, 12\}$. Since $\min(C') = 1$, $\max(C') = 12$, $\text{filled}(C') = 13$, and $n_2 = 8$, the inequality in Lemma 10 does not hold. Thus, $C' \prec \Lambda(T[p_2])$.

Now, we prove the correctness of the procedure \texttt{Fast\textunderscore Filter\textunderscore Clusters}:
Lemma 11. Given two weighted trees $T_A$ and $T_B$ with identical sets of $n$ leaf labels, the procedure $\text{Fast\_Filter\_Clusters}(T_A, T_B)$ works correctly.

Proof. In Step 1, the procedure computes a centroid path $\pi = \langle p_0, p_0-1, \ldots, p_1 \rangle$, where $p_0$ is the root of $T_A$, and the set $\sigma(\pi)$ of side trees of $\pi$. According to Equation (1), any cluster $C$ in $T_A$ that should be removed is in either $\pi$ or one of its side trees. In the former case, $C$ will be removed in Steps 3–10, and in the latter case, $C$ will be removed during some recursive call in Step 2.

Step 2 handles the side trees in $\sigma(\pi)$ by recursively calling the procedure for each $\tau \in \sigma(\pi)$ and replacing $\tau$ in $T_A$ by the obtained tree $\tau'$. Before each recursive call, the procedure normalizes the weights of the nodes in $\tau$ and $T_B | \Lambda(\tau)$ to make them positive integers of size $O(|\Lambda(\tau)|)$. This is achieved by sorting the weights in non-decreasing order and then setting the weight of each node equal to its rank in this order, where equally ranked nodes get identical weights.

Steps 3–10 handle the centroid path $\pi$ as follows. After doing a bottom-up traversal of $T_A$ to compute $n_i := |\Lambda(T_A[p_i])|$ for all $p_i \in \pi$, the leaf labels are modified to make $\pi$ a stratifying path in $T_A$. As a consequence, for any node $p_i$ on the centroid path $\pi$, its associated cluster $\Lambda(T_A[p_i])$ makes an integer interval of the form $[1, n_i]$. According to Lemma 10, $\Lambda(T_A[p_i])$ and any cluster $C$ associated with a non-spoiled node in $T_B$ conflict with each other iff $\max\{\text{filled}(C) + 1, \min(C)\} < n_i + 0.5 < \max(C)$. Therefore, one can determine whether $\Lambda(T_A[p_i]) \neq C$ by constructing an interval whose left endpoint is $2 \cdot \max\{\text{filled}(C) + 1, \min(C)\}$ and whose right endpoint is $2 \cdot \max(C)$, and then checking if it contains the point $2 \cdot n_i + 1$. Otherwise, if $C$ is associated with a spoiled node in $T_B$, the condition for a conflict becomes $\max\{\text{filled}(C) + 1, \min(C)\} < n_i + 0.5$, and the corresponding interval’s right endpoint is set to $2 \cdot (n_i + 1)$. Steps 5–9 determine conflicts simultaneously between all clusters associated with $\pi$ and all clusters in $T_B$ by solving an instance of the Max-Manhattan Skyline Problem. By the above, its solution $f$ has the property that $f[2 \cdot n_i + 1]$ is the weight of the heaviest cluster in $T_B$ that conflicts with any cluster of the form $\Lambda(T_A[p_i])$. If this number is greater than or equal to $w(p_i)$, then the procedure deletes $p_i$ from $T_A$.

Next, we show that $\text{Fast\_Filter\_Clusters}$ runs in $O(n \log n)$ time:

Lemma 12. Given two weighted trees $T_A$ and $T_B$ with identical sets of $n$ leaf labels, the procedure $\text{Fast\_Filter\_Clusters}(T_A, T_B)$ runs in $O(n \log n)$ time.

Proof. Step 1 can be completed in $O(n)$ time [8]. Step 2 uses $O(n)$ time to construct the $T_B | \Lambda(\tau)$-trees according to Lemma 2 and by applying radix sort to normalize the node weights. Step 2 also makes a recursive call for each $\tau$. Next, bottom-up traversals of $T_A$ and $T_B$ are used to implement Steps 3–6, taking an additional $O(n)$ time. Creating the intervals that represent clusters in Step 7 takes $O(n)$ time. Also, solving the Max-Manhattan Skyline Problem in Step 8 takes $O(n)$ time, according to Lemma 3. This is because there are $O(n)$ intervals and their weights are positive integers of size $O(n)$. The necessary delete operations on $\pi$ are carried out in top-down order, which means that the parent of any node in $T_A$ is changed at most once and thereby, Step 9 takes $O(n)$ time in total. Finally, Step 10 restores the original leaf labels in $O(n)$ time.

The time complexity of $\text{Fast\_Filter\_Clusters}(T_A, T_B)$ is thus $g(n) + \sum_{\tau \in \sigma(\pi)} h(\tau)$, where $g(n)$ is the execution time, excluding any recursive calls, and $h(\tau)$ is the running time of $\text{Fast\_Filter\_Clusters}(\tau, T_B | \Lambda(\tau))$ for any side tree $\tau$ of $\pi$. According to the discussion above, $g(n) = O(n)$. For any recursion level $j$, let $\sigma_j$ denote the set of all side trees that are computed for all the centroid paths on this level. The total time taken on the recursion
level \(j + 1\) for the non-recursive parts is \(\sum_{\tau \in \sigma_j} g(|\Lambda(\tau)|)\), and since the trees in \(\sigma_j\) are disjoint, \(\sum_{\tau \in \sigma_j} g(|\Lambda(\tau)|) = g(n) = O(n)\). By Lemma 4, every \(\tau\) satisfies \(|\Lambda(\tau)| \leq n/2\), and hence there are \(O(\log n)\) recursion levels. Therefore, the total running time is \(O(n \log n)\).

Combining Lemmas 11 and 12 provides the proof of Theorem 6:

**Theorem 6.** Given two weighted trees \(T_A\) and \(T_B\) with identical sets of \(n\) leaf labels, the procedure \texttt{Fast\_Filter\_Clusters}(\(T_A, T_B\)) filters out clusters as needed in \(O(n \log n)\) time.

### 6 Concluding Remarks

In this paper, we introduced an \(O(kn \log n)\)-time algorithm for computing the FDCT, leading to an asymptotically faster approach compared to the best previously known algorithm (Gawrychowski et al. [15]). The improved procedure \texttt{Fast\_Compute\_Weights}, presented as part of our new algorithm, can also be employed in algorithms for building the greedy consensus tree [15, 21, 32], replacing the slower versions of the procedure. Closing the gap between the upper bound of \(O(kn \log n)\) and the lower bound of \(\Omega(kn)\) for the running time of the fastest FDCT construction algorithm remains an important open problem.

We implemented our \(O(kn \log n)\)-time algorithm for constructing the FDCT. The source code can be found at https://github.com/tswddd2/FDCT_new. We achieved this implementation by adding approximately 2000 lines of C++ code to the source code of the \(\min\{O(kn^2), O(kn(k + \log^2 n))\}\)-time algorithm [20] for the same problem, available at https://github.com/Mesh89/FACT2 and also included in the FACT package [21], which was previously the fastest implementation. To implement the new \(O(kn \log n)\) algorithm, we followed the descriptions in this article and used \texttt{dynamic\_bitset} from the Boost libraries [1]. Preliminary experiments to evaluate the performance of our new algorithm indicate that it is faster in practice than the \(O(kn^2)\)-time and \(O(kn(k + \log^2 n))\)-time algorithms from [20]. The detailed results will be reported in the journal version of this paper.

### References

A Faster Algorithm for Constructing the Frequency Difference Consensus Tree


