

The Tree Inclusion Problem: In Linear Space and Faster

PHILIP BILLE and INGE LI GØRTZ, Technical University of Denmark

Given two rooted, ordered, and labeled trees P and T the tree inclusion problem is to determine if P can be obtained from T by deleting nodes in T . This problem has recently been recognized as an important query primitive in XML databases. Kilpeläinen and Mannila [1995] presented the first polynomial-time algorithm using quadratic time and space. Since then several improved results have been obtained for special cases when P and T have a small number of leaves or small depth. However, in the worst case these algorithms still use quadratic time and space. Let n_S , l_S , and d_S denote the number of nodes, the number of leaves, and the depth of a tree $S \in \{P, T\}$. In this article we show that the tree inclusion problem can be solved in space $O(n_T)$ and time:

$$O\left(\min\left\{\begin{array}{l} l_P n_T \\ l_P l_T \log \log n_T + n_T \\ \frac{n_P n_T}{\log n_T} + n_T \log n_T \end{array}\right\}\right).$$

This improves or matches the best known time complexities while using only linear space instead of quadratic. This is particularly important in practical applications, such as XML databases, where the space is likely to be a bottleneck.

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1. INTRODUCTION

Let T be a rooted tree. We say that T is *labeled* if each node is assigned a character from an alphabet Σ and we say that T is *ordered* if a left-to-right order among siblings in T is given. All trees in this article are rooted, ordered, and labeled. A tree P is *included* in T , denoted $P \subseteq T$, if P can be obtained from T by deleting nodes of T . Deleting a node v in T means making the children of v children of the parent of v and then removing v . The children are inserted in the place of v in the left-to-right order

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Authors' addresses: P. Bille and I. L. Gørtz (corresponding author), Department of Informatics and Mathematical Modelling, Technical University of Denmark; email: ilg@imm.dtu.dk.

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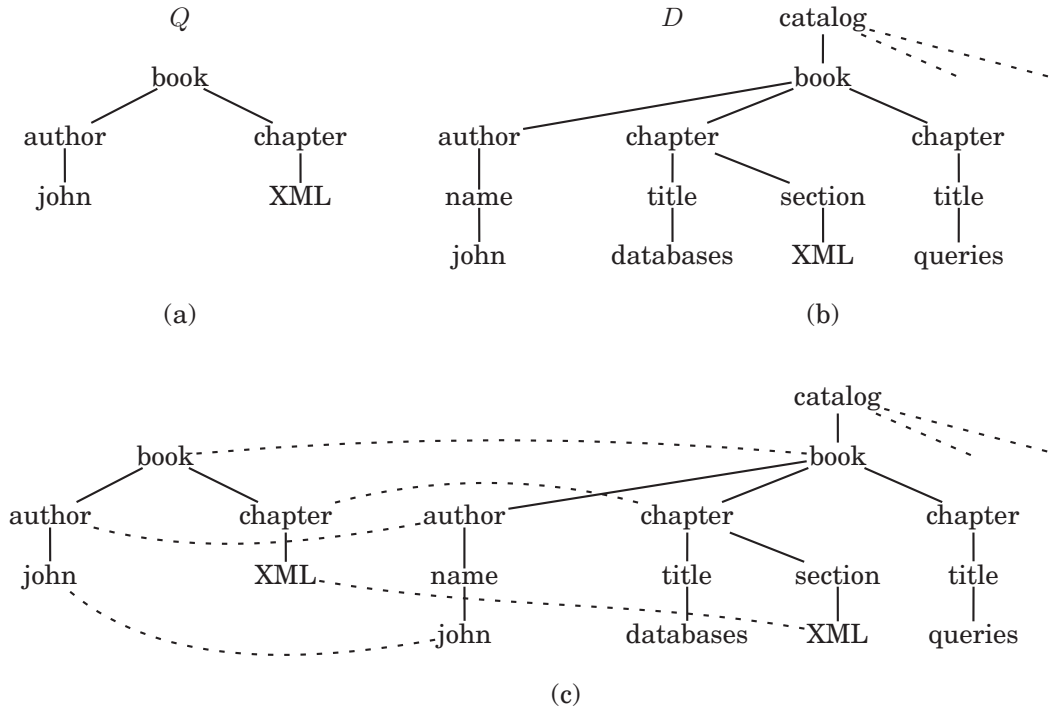


Fig. 1. (a) The tree Q corresponding to the query. (b) A fragment of the tree D . Can the tree Q be included in the tree D ? It can and an embedding is given in (c).

among the siblings of v . The *tree inclusion problem* is to determine if P can be included in T and if so report all subtrees of T that include P .

Recently, the problem has been recognized as an important query primitive for XML data and has received considerable attention, see, for example, Schlieder and Meuss [2002], [Yang et al. 2003, 2004], Zezula et al. [2003], Schlieder and Naumann [2000], and Termier et al. [2002]. The key idea is that an XML document can be viewed as a tree and queries on the document correspond to a tree inclusion problem. As an example consider Figure 1. Suppose that we want to maintain a catalog of books for a bookstore. A fragment of the tree, denoted D , corresponding to the catalog is shown in (b). In addition to supporting full-text queries, such as find all documents containing the word “John”, we can also utilize the tree structure of the catalog to ask more specific queries, such as “find all books written by John with a chapter that has something to do with XML”. We can model this query by constructing the tree, denoted Q , shown in (a) and solve the tree inclusion problem: is $Q \sqsubseteq D$? The answer is yes and a possible way to include Q in D is indicated by the dashed lines in (c). If we delete all the nodes in D not touched by dashed lines the trees Q and D become isomorphic. Such a mapping of the nodes from Q to D given by the dashed lines is called an *embedding* (formally defined in Section 3). We note that the ordering of the XML document, and hence the left-to-right order of siblings, is important in many cases. For instance, in the preceding example, the relative order of contents of the chapters is most likely important. Also, in biological databases, order is of critical importance. Consequently, standard XML query languages, such as XPath [Clark and DeRose 1999] and XQuery [Boag et al. 2001], require the output of queries to be ordered.

The tree inclusion problem was initially introduced by Knuth [1969, exercise 2.3.2-22] who gave a sufficient condition for testing inclusion. Motivated by applications in structured databases [Kilpeläinen and Mannila 1993; Mannila and Rähä 1990] Kilpeläinen and Mannila [1995] presented the first polynomial-time algorithm using $O(n_P n_T)$ time and space, where n_P and n_T is the number of nodes in P and T , respectively. During the last decade several improvements of the original algorithm of Kilpeläinen and Mannila [1995] have been suggested [Kilpeläinen 1992; Alonso and Schott 2001; Richter 1997; Chen 1998]. The previously best known bound is due to Chen [1998] who presented an algorithm using $O(l_P n_T)$ time and $O(l_P \cdot \min\{d_T, l_T\})$ space. Here, l_S and d_S denote the number of leaves and the depth of a tree S , respectively. This algorithm is based on an algorithm of Kilpeläinen [1992]. Note that the time and space is still $\Theta(n_P n_T)$ for worst-case input trees.

In this article we present three algorithms which combined improve all of the previously known time and space bounds. To avoid trivial cases we always assume that $1 \leq n_P \leq n_T$. We show the following theorem.

THEOREM 1.1. *For trees P and T the tree inclusion problem can be solved in $O(n_T)$ space with the following running time.*

$$O\left(\min\left\{\begin{array}{l} l_P n_T \\ l_P l_T \log \log n_T + n_T \\ \frac{n_P n_T}{\log n_T} + n_T \log n_T \end{array}\right\}\right)$$

Hence, when P has few leaves we obtain a fast algorithm and even faster if both P and T have few leaves. When both trees have many leaves and $n_P = \Omega(\log^2 n_T)$, we instead improve the previous quadratic time bound by a logarithmic factor. Most importantly, the space used is linear. In the context of XML databases this will likely make it possible to query larger trees and speed up the query time since more of the computation can be kept in main memory.

The extended abstract of this article [Bille and Gørtz 2005] contained an error. The algorithms in the article [Bille and Gørtz 2005] did not use linear space. The problem was due to a recursive traversal of P which stored too many sets of nodes leading to a worst-case space complexity of $\Omega(d_P l_T)$. In this article we fix this problem by recursively visiting the nodes such that the child with the largest number of descendant leaves is visited first, and by showing that the size of the resulting stored node sets exponentially decrease. With these ideas we show that all of our algorithms use $O(n_T)$ space. Additionally, our improved analysis of the sizes of the stored node sets also leads to an improvement in the running time of the algorithm in the second case given before. In the previous paper the running time was $O(n_P l_T \log \log n_T + n_T)$.

1.1. Techniques

Most of the previous algorithms, including the best one [Chen 1998], are essentially based on a simple dynamic programming approach from the original algorithm of Kilpeläinen and Mannila [1995]. The main idea behind this algorithm is the following: Let v be a node in P with children v_1, \dots, v_i and let w be a node in T . Consider the subtrees rooted at v and w , denoted by $P(v)$ and $T(w)$. To decide if $P(v)$ can be included in $T(w)$ we try to find a sequence w_1, \dots, w_i of left-to-right ordered descendants of w such that $P(v_k) \subseteq T(w_k)$ for all k , $1 \leq k \leq i$. The sequence is computed greedily from left-to-right in $T(w)$ effectively finding the *leftmost inclusion* of $P(v)$ in $T(w)$. Applying this approach in a bottom-up fashion we can determine, if $P(v) \subseteq T(w)$, for all pairs of nodes v in P and w in T .

In this article we take a different approach. The main idea is to construct a data structure on T supporting a small number of procedures, called the *set procedures*, on

subsets of nodes of T . We show that any such data structure implies an algorithm for the tree inclusion problem. We consider various implementations of this data structure which all use linear space. The first simple implementation gives an algorithm with $O(l_P n_T)$ running time. As it turns out, the running time depends on a well-studied problem known as the *tree color problem*. We show a direct connection between a data structure for the tree color problem and the tree inclusion problem. Plugging in a data structure of Dietz [1989] we obtain an algorithm with $O(l_P l_T \log \log n_T + n_T)$ running time.

Based on the simple algorithms given earlier we show how to improve the worst-case running time of the set procedures by a logarithmic factor. The general idea used to achieve this is to divide T into small trees called *clusters* of logarithmic size which overlap with other clusters in at most 2 nodes. Each cluster is represented by a constant number of nodes in a *macro tree*. The nodes in the macro tree are then connected according to the overlap of the cluster they represent. We show how to efficiently preprocess the clusters and the macro tree such that the set procedures use constant time for each cluster. Hence, the worst-case quadratic running time is improved by a logarithmic factor.

Our algorithms recursively traverse P top-down. For each node $v \in V(P)$ we compute a set of nodes representing all of the subtrees in T that include $P(v)$. To avoid storing too many of these node sets the traversal of P visits the child with the largest number of descendant leaves first. For the first two algorithms this immediately implies a space complexity of $O(l_T \log l_P)$, however, by carefully analyzing the sizes of stored node sets we are able to show that they decrease exponentially leading to the linear space bound. In the last algorithm the node sets are compactly encoded in $O(n_T / \log n_T)$ space and therefore our recursive traversal alone implies a space bound of $O(n_T / \log n_T \cdot \log l_P) = O(n_T)$.

Throughout the article we assume a unit-cost RAM model of computation with word size $\Theta(\log n_T)$ and a standard instruction set including bitwise boolean operations, shifts, addition, and multiplication. All space complexities refer to the number of words used by the algorithm.

1.2. Related Work

For some applications considering *unordered* trees is more natural. However, in Matoušek and Thomas [1992] and Kilpeläinen and Mannila [1995] this problem was proved to be NP-complete. The tree inclusion problem is closely related to the *tree pattern matching problem* [Hoffmann and O'Donnell 1982; Kosaraju 1989; Dubiner et al. 1990; Cole et al. 1999]. The goal is here to find an injective mapping f from the nodes of P to the nodes of T such that for every node v in P the i th child of v is mapped to the i th child of $f(v)$. The tree pattern matching problem can be solved in $(n_P + n_T) \log^{O(1)}(n_P + n_T)$ time. Another similar problem is the *subtree isomorphism problem* [Chung 1987; Shamir and Tsur 1999], which is to determine if T has a subgraph isomorphic to P . The subtree isomorphism problem can be solved efficiently for ordered and unordered trees. The best algorithms for this problem use $O\left(\frac{n_P^{1.5} n_T}{\log n_P} + n_T\right)$ time for unordered trees and $O\left(\frac{n_P n_T}{\log n_P} + n_T\right)$ time for ordered trees [Chung 1987; Shamir and Tsur 1999]. Both use $O(n_P n_T)$ space. The tree inclusion problem can be considered a special case of the *tree edit distance problem* [Tai 1979; Zhang and Shasha 1989; Klein 1998; Demaine et al. 2007]. Here one wants to find the minimum sequence of insert, delete, and relabel operations needed to transform P into T . Currently the best algorithm for this problem uses $O(n_T n_P^2 (1 + \log \frac{n_T}{n_P}))$ time [Demaine et al. 2007]. For more details and references see the survey [Bille 2005].

1.3. Outline

In Section 2 we give notation and definitions used throughout the article. In Section 3 a common framework for our tree inclusion algorithms is given. Section 4 presents two simple algorithms and then, based on these results, we show how to get a faster algorithm in Section 5.

2. NOTATION AND DEFINITIONS

In this section we define the notation and definitions we will use throughout the article. For a graph G we denote the set of nodes and edges by $V(G)$ and $E(G)$, respectively. Let T be a rooted tree. The root of T is denoted by $\text{root}(T)$. The *size* of T , denoted by n_T , is $|V(T)|$. The *depth* of a node $v \in V(T)$, $\text{depth}(v)$, is the number of edges on the path from v to $\text{root}(T)$ and the depth of T , denoted d_T , is the maximum depth of any node in T . The parent of v is denoted $\text{parent}(v)$ and the set of children of v is denoted $\text{child}(v)$. We define $\text{parent}(\text{root}(T)) = \perp$, where $\perp \notin V(T)$ is a special *null node*. A node with no children is a leaf and otherwise an internal node. The set of leaves of T is denoted $L(T)$ and we define $l_T = |L(T)|$. We say that T is *labeled* if each node v is assigned a character, denoted $\text{label}(v)$, from an alphabet Σ and we say that T is *ordered* if a left-to-right order among siblings in T is given. Note that we do not require that the size of the alphabet is bounded by a constant. All trees in this article are rooted, ordered, and labeled.

Ancestors and Descendants. Let $T(v)$ denote the subtree of T rooted at a node $v \in V(T)$. If $w \in V(T(v))$ then v is an ancestor of w , denoted $v \preceq w$, and if $w \in V(T(v)) \setminus \{v\}$ then v is a proper ancestor of w , denoted $v < w$. If v is a (proper) ancestor of w then w is a (proper) descendant of v . A node z is a common ancestor of v and w if it is an ancestor of both v and w . The nearest common ancestor of v and w , $\text{nca}(v, w)$, is the common ancestor of v and w of greatest depth. The *first ancestor of w labeled α* , denoted $\text{fl}(w, \alpha)$, is the node v such that $v \preceq w$, $\text{label}(v) = \alpha$, and no node on the path between v and w is labeled α . If no such node exists then $\text{fl}(w, \alpha) = \perp$.

Traversals and Orderings. Let T be a tree with root v and let v_1, \dots, v_k be the children of v from left-to-right. The *preorder traversal* of T is obtained by visiting v and then recursively visiting $T(v_i)$, $1 \leq i \leq k$, in order. Similarly, the *postorder traversal* is obtained by first visiting $T(v_i)$, $1 \leq i \leq k$, in order and then v . The *preorder number* and *postorder number* of a node $w \in T(v)$, denoted by $\text{pre}(w)$ and $\text{post}(w)$, are the number of nodes preceding w in the preorder and postorder traversal of T , respectively. The nodes to the left of w in T is the set of nodes $u \in V(T)$ such that $\text{pre}(u) < \text{pre}(w)$ and $\text{post}(u) < \text{post}(w)$. If u is to the left of w , denoted by $u \triangleleft w$, then w is to the right of u . If $u \triangleleft w$ or $u \preceq w$ or $w < u$ we write $u \trianglelefteq w$. The null node \perp is not in the ordering, that is, $\perp \not\triangleleft v$ for all nodes v .

Minimum Ordered Pairs. A set of nodes $X \subseteq V(T)$ is *deep* if no node in X is a proper ancestor of another node in X . For k deep sets of nodes X_1, \dots, X_k let $\Phi(X_1, \dots, X_k) \subseteq (X_1 \times \dots \times X_k)$, be the set of tuples such that $(x_1, \dots, x_k) \in \Phi(X_1, \dots, X_k)$ iff $x_1 \triangleleft \dots \triangleleft x_k$. If $(x_1, \dots, x_k) \in \Phi(X_1, \dots, X_k)$ and there is no $(x'_1, \dots, x'_k) \in \Phi(X_1, \dots, X_k)$, where either $x_1 \triangleleft x'_1 \triangleleft x'_k \trianglelefteq x_k$ or $x_1 \trianglelefteq x'_1 \triangleleft x'_k \triangleleft x_k$ then the pair (x_1, x_k) is a *minimum ordered pair*. Intuitively, (x_1, x_k) is a closest pair of nodes from X_1 and X_k in the left-to-right order for which we can find x_2, \dots, x_{k-1} such that $x_1 \triangleleft \dots \triangleleft x_k$. The set of minimum ordered pairs for X_1, \dots, X_k is denoted by $\text{mop}(X_1, \dots, X_k)$. Figure 2 illustrates these concepts on a small example.

For any set of pairs Y , let $Y|_1$ and $Y|_2$ denote the *projection* of Y to the first and second coordinate, that is, if $(y_1, y_2) \in Y$ then $y_1 \in Y|_1$ and $y_2 \in Y|_2$. We say that Y is *deep* if $Y|_1$ and $Y|_2$ are deep. The following lemma shows that given deep sets

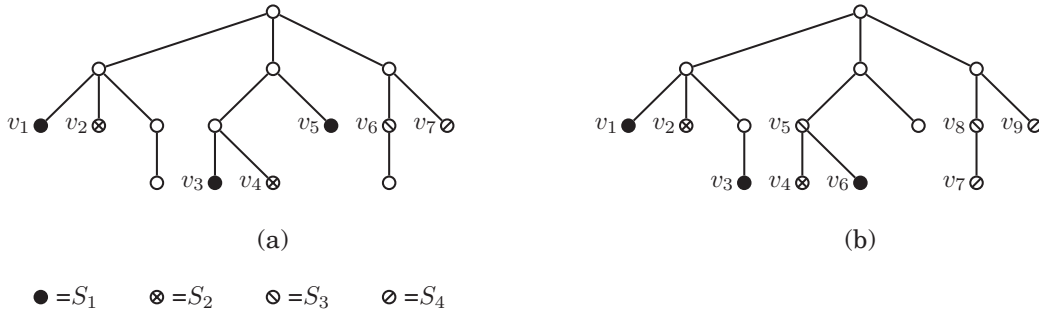


Fig. 2. In (a) we have $\{(v_1, v_2, v_3, v_6, v_7), (v_1, v_2, v_5, v_6, v_7), (v_1, v_4, v_5, v_6, v_7), (v_3, v_4, v_5, v_6, v_7)\} = \Phi(S_1, S_2, S_1, S_3, S_4)$ and thus $\text{mop}(S_1, S_2, S_1, S_3, S_4) = \{(v_3, v_7)\}$. In (b) we have $\Phi(S_1, S_2, S_1, S_3, S_4) = \{(v_1, v_2, v_3, v_5, v_7), (v_1, v_2, v_6, v_8, v_9), (v_1, v_2, v_3, v_8, v_9), (v_1, v_2, v_3, v_5, v_9), (v_1, v_4, v_6, v_8, v_9), (v_3, v_4, v_6, v_8, v_9)\}$ and thus $\text{mop}(S_1, S_2, S_1, S_3, S_4) = \{(v_1, v_7), (v_3, v_9)\}$.

X_1, \dots, X_k we can compute $\text{mop}(X_1, \dots, X_k)$ iteratively by first computing $\text{mop}(X_1, X_2)$ and then $\text{mop}(\text{mop}(X_1, X_2)|_2, X_3)$ and so on.

LEMMA 2.1. *For any deep sets of nodes X_1, \dots, X_k , $k > 2$, we have, $(x_1, x_k) \in \text{mop}(X_1, \dots, X_k)$ iff there exists a node x_{k-1} such that $(x_1, x_{k-1}) \in \text{mop}(X_1, \dots, X_{k-1})$ and $(x_{k-1}, x_k) \in \text{mop}(\text{mop}(X_1, \dots, X_{k-1})|_2, X_k)$.*

PROOF. We start by showing that if $(x_1, x_k) \in \text{mop}(X_1, \dots, X_k)$ then there exists a node x_{k-1} such that $(x_1, x_{k-1}) \in \text{mop}(X_1, \dots, X_{k-1})$ and $(x_{k-1}, x_k) \in \text{mop}(\text{mop}(X_1, \dots, X_{k-1})|_2, X_k)$.

First note that $(z_1, \dots, z_k) \in \Phi(X_1, \dots, X_k)$ implies $(z_1, \dots, z_{k-1}) \in \Phi(X_1, \dots, X_{k-1})$. Since $(x_1, x_k) \in \text{mop}(X_1, \dots, X_k)$ there must be a minimum node x_{k-1} such that the tuple (x_1, \dots, x_{k-1}) is in $\Phi(X_1, \dots, X_{k-1})$. We have $(x_1, x_{k-1}) \in \text{mop}(X_1, \dots, X_{k-1})$. We need to show that $(x_{k-1}, x_k) \in \text{mop}(\text{mop}(X_1, \dots, X_{k-1})|_2, X_k)$. Since $(x_1, x_k) \in \text{mop}(X_1, \dots, X_k)$ there exists no node $z \in X_k$ such that $x_{k-1} \triangleleft z \triangleleft x_k$. If such a z existed we would have $(x_1, \dots, x_{k-1}, z) \in \Phi(X_1, \dots, X_k)$, contradicting that $(x_1, x_k) \in \text{mop}(X_1, \dots, X_k)$. Assume there exists a node $z \in \text{mop}(X_1, \dots, X_{k-1})|_2$ such that $x_{k-1} \triangleleft z \triangleleft x_k$. Since $(x_1, x_{k-1}) \in \text{mop}(X_1, \dots, X_{k-1})$ this implies that there is a node $z' \triangleright x_1$ such that $(z', z) \in \text{mop}(X_1, \dots, X_{k-1})$. But this implies that the tuple (z', \dots, z, x_k) is in $\Phi(X_1, \dots, X_k)$ contradicting that $(x_1, x_k) \in \text{mop}(X_1, \dots, X_k)$.

We will now show that if there exists a node x_{k-1} such that $(x_1, x_{k-1}) \in \text{mop}(X_1, \dots, X_{k-1})$ and $(x_{k-1}, x_k) \in \text{mop}(\text{mop}(X_1, \dots, X_{k-1})|_2, X_k)$ then the pair $(x_1, x_k) \in \text{mop}(X_1, \dots, X_k)$. Clearly, there exists a tuple $(x_1, \dots, x_{k-1}, x_k) \in \Phi(X_1, \dots, X_k)$. Assume that there exists a tuple $(z_1, \dots, z_k) \in \Phi(X_1, \dots, X_k)$ such that $x_1 \triangleleft z_1 \triangleleft z_k \triangleleft x_k$. Among the tuples satisfying these constraints let $(y_1, \dots, y_{k-1}, y_k)$ be the one with maximum y_1 , minimum y_{k-1} , and maximum y_k . It follows that $(y_1, y_{k-1}) \in \text{mop}(X_1, \dots, X_{k-1})$. Since $(x_1, x_{k-1}) \in \text{mop}(X_1, \dots, X_{k-1})$ we must have $x_{k-1} \triangleleft y_{k-1}$. But this contradicts $(x_{k-1}, x_k) \in \text{mop}(\text{mop}(X_1, \dots, X_{k-1})|_2, X_k)$, since node $y_{k-1} \in \text{mop}(X_1, \dots, X_{k-1})|_2$.

Assume that there exists a tuple $(z_1, \dots, z_k) \in \Phi(X_1, \dots, X_k)$ such that $x_1 \triangleleft z_1 \triangleleft z_k \triangleleft x_k$. Since $(x_1, x_{k-1}) \in \text{mop}(X_1, \dots, X_{k-1})$ we have $x_{k-1} \triangleleft z_{k-1}$ and thus $x_{k-1} \triangleleft z_k \triangleleft x_k$ contradicting $(x_{k-1}, x_k) \in \text{mop}(\text{mop}(X_1, \dots, X_{k-1})|_2, X_k)$. \square

The following lemma is the reverse of the previous lemma and shows that given deep sets X_1, \dots, X_k we also can compute $\text{mop}(X_1, \dots, X_k)$ iteratively from right-to-left. The proof is similar to the proof of Lemma 2.1.

LEMMA 2.2. *For any deep sets of nodes X_1, \dots, X_k , $k > 2$, we have, $(x_1, x_k) \in \text{mop}(X_1, \dots, X_k)$ iff there exists a node x_2 such that $(x_2, x_k) \in \text{mop}(X_2, \dots, X_k)$ and $(x_1, x_2) \in \text{mop}(X_1, \text{mop}(X_2, \dots, X_k)|_1)$.*

Heavy Leaf Path Decomposition. We construct a *heavy leaf path decomposition* of P as follows. We classify each node as *heavy* or *light*. The root is light. For each internal node v we pick a child v_j of v with maximum $l_{P(v_j)}$ and classify it as heavy. The remaining children of v are light. An edge to a light node is a *light edge*, and an edge to a heavy node is a *heavy edge*. The heavy child of a node v is denoted $\text{heavy}(v)$. Let $\text{ldepth}(v)$ denote the number of light edges on the path from v to $\text{root}(P)$.

Note that a heavy leaf path decomposition is the same as the classical *heavy path decomposition* [Harel and Tarjan 1984] except that the heavy child is defined as the child with largest number of the descendant leaves and not the child with the largest number of descendants. This distinction is essential for achieving the linear space bound of our algorithms. Note that heavy path decompositions have previously been used in algorithms for the related tree edit distance problem [Klein 1998].

LEMMA 2.3. *For any tree P and node $v \in V(P)$,*

$$l_{P(v)} \leq \frac{l_P}{2^{\text{ldepth}(v)}}.$$

PROOF. By induction on $\text{ldepth}(v)$. For $\text{ldepth}(v) = 0$ it is trivially true. Let $\text{ldepth}(v) = \ell$. Assume without loss of generality that v is light. Let w be the unique light ancestor of v with $\text{ldepth}(w) = \ell - 1$. By the induction hypothesis $l_{P(w)} \leq l_P/2^{\ell-1}$. Now v has a sibling $\text{heavy}(\text{parent}(v))$ and thus at most half of the leaves in $P(\text{parent}(v))$ can be in the subtree rooted at v . Therefore, $l_{P(v)} \leq l_{P(w)}/2 \leq l_P/2^\ell$. \square

COROLLARY 2.4. *For any tree P and node $v \in V(P)$, $\text{ldepth}(v) \leq \log l_P$.*

Notation. When we want to specify which tree we mean in the preceding relations we add a subscript. For instance, $v <_T w$ indicates that v is an ancestor of w in T .

3. COMPUTING DEEP EMBEDDINGS

In this section we present a general framework for answering tree inclusion queries. As in Kilpeläinen and Mannila [1995] we solve the equivalent *tree embedding problem*. Let P and T be rooted labeled trees. An *embedding* of P in T is an injective function $f : V(P) \rightarrow V(T)$ such that for all nodes $v, u \in V(P)$:

- (i) $\text{label}(v) = \text{label}(f(v))$. (label preservation condition)
- (ii) $v < u$ iff $f(v) < f(u)$. (ancestor condition)
- (iii) $v \triangleleft u$ iff $f(v) \triangleleft f(u)$. (order condition)

An example of an embedding is given in Figure 1(c).

LEMMA 3.1. [KILPELÄINEN AND MANNILA 1995]. *For any trees P and T , $P \sqsubseteq T$ iff there exists an embedding of P in T .*

We say that the embedding f is *deep* if there is no embedding g such that $f(\text{root}(P)) \triangleleft g(\text{root}(P))$. The deep occurrences of P in T , denoted $\text{emb}(P, T)$ is the set of nodes

$$\text{emb}(P, T) = \{f(\text{root}(P)) \mid f \text{ is a deep embedding of } P \text{ in } T\}.$$

By definition the set of ancestors of nodes in $\text{emb}(P, T)$ is exactly the set of nodes $\{u \mid P \sqsubseteq T(u)\}$. Hence, to solve the tree inclusion problem it is sufficient to compute $\text{emb}(P, T)$ and then, using additional $O(n_T)$ time, report all ancestors of this set. We note that Kilpeläinen and Mannila [1995] used the similar concept of *left embeddings*

in their algorithms. A left embedding of P in T is an embedding such that the root of P is mapped to the node in T with the smallest postorder number, that is, the deepest node among the nodes furthest to the left. Our definition of $\text{emb}(P, T)$ only requires that the root is mapped to a deepest node.

In the following we show how to compute deep embeddings. The key idea is to build a data structure for T allowing a fast implementation of the following procedures. For all $X \subseteq V(T)$, $Y \subseteq V(T) \times V(T)$, and $\alpha \in \Sigma$ define:

PARENT(X): Return the set $\{\text{parent}(x) \mid x \in X\}$.
NCA(Y): Return the set $\{\text{nca}(y_1, y_2) \mid (y_1, y_2) \in Y\}$.
DEEP(X): Return the set $\{x \in X \mid \text{there is no } z \in X \text{ such that } x < z\}$.
MOPRIGHT(Y, X): Return the set of pairs R such that for any pair $(y_1, y_2) \in Y$, $(y_1, x) \in R$ iff $(y_2, x) \in \text{mop}(Y|_2, X)$.
MOPLEFT(X, Y): Return the set of pairs R such that for any pair $(y_1, y_2) \in Y$, $(x, y_2) \in R$ iff $(x, y_1) \in \text{mop}(X, Y|_1)$.
FL(X, α): Return the set $\text{DEEP}(\{\text{fl}(x, \alpha) \mid x \in X\})$.

Collectively we call these procedures the *set procedures*. The procedures **PARENT** and **NCA** are self-explanatory. **DEEP**(X) returns the set of all nodes in X that have no descendants in X . Hence, the returned set is always deep. **MOPRIGHT** and **MOPLEFT** are used to iteratively compute minimum ordered pairs. **FL**(X, α) returns the deep set of first ancestors with label α of all nodes in X . If we want to specify that a procedure applies to a certain tree T we add the subscript T . With the set procedures we can compute deep embeddings. The following procedure **EMB**(v), $v \in V(P)$, recursively computes the set of deep occurrences of $P(v)$ in T . Figure 3 illustrates how **EMB** works on a small example.

Procedure **EMB**(v)

```

1 Let  $v_1, \dots, v_k$  be the sequence of children of  $v$  ordered from left-to-right. There are three
  cases:
2 case 1.  $k = 0$  //  $v$  is a leaf
3 | Compute  $R := \text{FL}(L(T), \text{label}(v))$ .
4 case 2.  $k = 1$ 
5 | Recursively compute  $R_1 := \text{EMB}(v_1)$ .
6 | Compute  $R := \text{FL}(\text{DEEP}(\text{PARENT}(R_1)), \text{label}(v))$ .
7 case 3.  $k > 1$ 
8 | Let  $v_j$  be the heavy child of  $v$ .
9 | Recursively compute  $R_j := \text{EMB}(v_j)$  and set  $U_j := \{(r, r) \mid r \in R_j\}$ .
10 | for  $i := j + 1$  to  $k$  do
11 | | Recursively compute  $R_i := \text{EMB}(v_i)$  and set  $U_i := \text{MOPRIGHT}(U_{i-1}, R_i)$ .
12 | end
13 | Set  $U_j := U_k$ .
14 | for  $i := j - 1$  downto  $1$  do
15 | | Recursively compute  $R_i := \text{EMB}(v_i)$  and set  $U_i := \text{MOPLEFT}(R_i, U_{i+1})$ .
16 | end
17 | Compute  $R := \text{FL}(\text{DEEP}(\text{NCA}(U_1)), \text{label}(v))$ .
18 if  $R = \emptyset$  then
19 | stop and report that there is no deep embedding of  $P(v)$  in  $T$ .
20 else
21 | Return  $R$ .
22
```

To prove the correctness of the **EMB** procedure we need the following two propositions. The first proposition characterizes for node $v \in V(P)$ the set $\text{emb}(P(v), T)$ using **mop**,

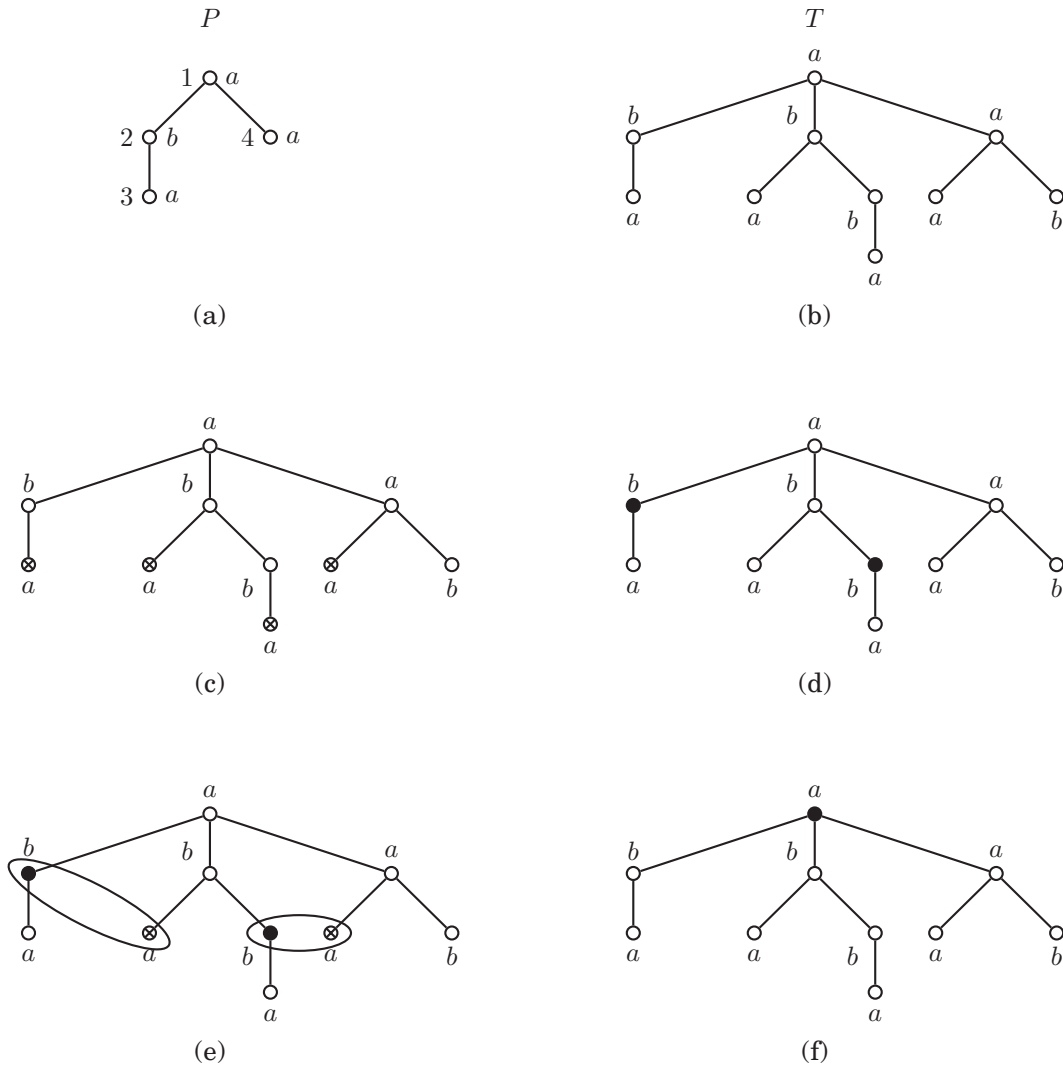


Fig. 3. Computing the deep occurrences of P into T depicted in (a) and (b) respectively. The nodes in P are numbered 1–4 for easy reference. (c) Case 1 of EMB: The crossed nodes are the nodes in the set $\text{EMB}(3)$. Since 3 and 4 are leaves and $\text{label}(3) = \text{label}(4)$ we have $\text{EMB}(3) = \text{EMB}(4)$. (d) Case 2 of EMB: The black nodes are the nodes in the set $\text{EMB}(2)$. Note that the middle child of the root of T is not in the set since it is not a deep occurrence. (e) and (f) illustrate the computation of $\text{EMB}(1)$ and case 3 of EMB: (e) The two minimal ordered pairs of the sets from (d) and (c). In the procedure R_1 is the set from (d) and R_2 is the set from (c). The set $U_1 = \{(v, v) \mid v \in R_1\}$ and the set $U_2 = \text{MOPRIGHT}(U_1, R_2)$ which corresponds to the pairs shown in (e). The black nodes in the pairs are the nodes from R_1 and the crossed nodes are the nodes from R_2 . Since $k = 2$ we set $U_1 = U_2$. (f) The nearest common ancestors of both pairs shown in (e) is the root node of T which is the only (deep) occurrence of P .

nca , and fl . The second proposition shows that the set U_1 computed in case 3 of the EMB procedure is the set $\text{mop}(\text{EMB}(v_1), \dots, \text{EMB}(v_k))$.

PROPOSITION 3.2. *Let v be a node in P and let v_1, \dots, v_k be the sequence of children of v ordered from left-to-right, where $k \geq 2$. For any node $w \in \text{emb}(P(v), T)$, there*

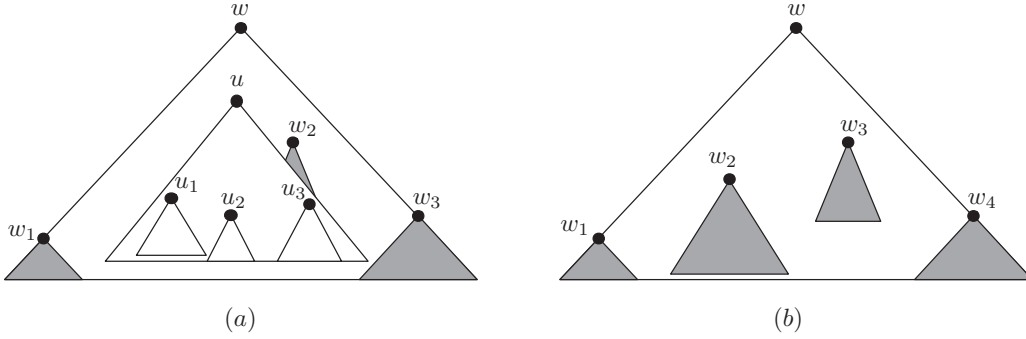


Fig. 4. (a) For all i , w_i and u_i are roots of occurrences of $P(v_i)$ in T , and w and u is the nearest common ancestor of (w_1, w_3) and (u_1, u_3) , respectively. Since $w_1 \triangleleft u_1$ and $u_3 \triangleleft w_3$ we cannot have $u < w$. (b) For all i , w_i is an embedding of $P(v_i)$ in T , (w_1, w_4) is a minimum ordered pair, and w is the nearest common ancestor of all the w_i 's. The number of leaves in $T(w)$ is at least $\sum_{i=1}^4 l_{T(w_i)} \geq \sum_{i=1}^4 l_{P(v_i)}$.

exists a pair of nodes $(w_1, w_k) \in \text{mop}(\text{emb}(P(v_1), T), \dots, \text{emb}(P(v_k), T))$ such that $w = \text{fl}(\text{nca}(w_1, w_k), \text{label}(v))$.

PROOF. Since w is the root of an occurrence of $P(v)$ in T there must exist a set of disjoint occurrences of $P(v_1), \dots, P(v_k)$ in $T(w)$ with roots $w_1 \triangleleft \dots \triangleleft w_k$, such that w is an ancestor of w_1, \dots, w_k . Since the w_i 's are ordered w must be an ancestor of $\text{nca}(w_1, w_k)$. Since w is the root of a *deep* occurrence of $P(v)$ in T it follows that $w = \text{fl}(\text{nca}(w_1, w_k), \text{label}(v))$.

It remains to show that we can assume $(w_1, w_k) \in \text{mop}(\text{emb}(P(v_1), T), \dots, \text{emb}(P(v_k), T))$. It follows from the previous discussion that $(w_1, \dots, w_k) \in \Phi(\text{emb}(P(v_1), T), \dots, \text{emb}(P(v_k), T))$. Assume for the sake of contradiction that (w_1, w_k) is *not* a minimum ordered pair. Then there exists a set of disjoint occurrences of $P(v_1), \dots, P(v_k)$ in $T(w)$ with roots $u_1 \triangleleft \dots \triangleleft u_k$, such that either $w_1 \triangleleft u_1 \triangleleft u_k \triangleleft w_k$ or $w_1 \triangleleft u_1 \triangleleft u_k \triangleleft w_k$, and $(u_1, u_k) \in \text{mop}(\text{emb}(P(v_1), T), \dots, \text{emb}(P(v_k), T))$. Therefore $u = \text{fl}(\text{nca}(u_1, u_k), \text{label}(v))$ is an embedding of $P(v)$ in T . Now either $w < u$ contradicting the assumption that w is a deep embedding or $w = u$ in which case (u_1, u_k) satisfies the properties of the lemma (see also Figure 4(a)). \square

PROPOSITION 3.3. For $j + 1 \leq l \leq k$,

$$U_l = \text{mop}(\text{EMB}(v_j), \dots, \text{EMB}(v_l)), \quad (1)$$

For $1 \leq l \leq j - 1$,

$$U_l = \text{mop}(\text{EMB}(v_l), \dots, \text{EMB}(v_k)). \quad (2)$$

PROOF. We first show Eq. (1) by induction on l . For $l = j + 1$ it follows from the definition of MOPRIGHT that U_l is the set of minimum ordered pairs of $\text{EMB}(v_j)$ and $\text{EMB}(v_{j+1})$, that is, $U_l = \text{mop}(\text{EMB}(v_j), \text{EMB}(v_{j+1}))$. Hence, assume that $l > j + 1$. By the induction hypothesis we have

$$U_l = \text{MOPRIGHT}(U_{l-1}, \text{EMB}(v_l)) = \text{MOPRIGHT}(\text{mop}(\text{EMB}(v_j), \dots, \text{EMB}(v_{l-1})), R_l).$$

By definition of MOPRIGHT , U_l is the set of pairs such that for any pair $(r_j, r_{l-1}) \in \text{mop}(\text{EMB}(v_j), \dots, \text{EMB}(v_{l-1}))$, $(r_j, r_l) \in U_l$ iff $(r_{l-1}, r_l) \in \text{mop}(\text{mop}(\text{EMB}(v_j), \dots, \text{EMB}(v_{l-1}))|_2, R_l)$. By Lemma 2.1 it follows that $(r_j, r_l) \in U_l$ iff $(r_j, r_l) \in \text{mop}(\text{EMB}(v_j), \dots, \text{EMB}(v_l))$.

We can now similarly show Equation (2) by induction on $j' = j - l$. By Equation (1) we have $U_j = \text{mop}(\text{EMB}(v_j), \dots, \text{EMB}(v_k))$ when we begin computing U_{j-1} . For $j' = 1$ ($l = j - 1$) it follows from the definition of `MOPLEFT` that $U_{j-1} = \text{mop}(\text{EMB}(v_{j-1}), \text{EMB}(v_j))$. Hence, assume that $j' > 1$. Using Lemma 2.2 the Equation follows similarly to the proof of Equation (1). \square

By Proposition 3.3, $U_1 = \text{mop}(\text{EMB}(v_1), \dots, \text{EMB}(v_k))$. We can now show the correctness of procedure `EMB`.

LEMMA 3.4. *For trees P and T and node $v \in V(P)$, `EMB`(v) computes the set of deep occurrences of $P(v)$ in T .*

PROOF. By induction on the size of the subtree $P(v)$. If v is a leaf, $\text{emb}(v, T)$ is the deep set of nodes in T with label $\text{label}(v)$. It immediately follows that $\text{emb}(v, T) = \text{FL}(L(T), \text{label}(v))$ and thus case 1 follows.

Suppose that v is an internal node with $k \geq 1$ children v_1, \dots, v_k . We show that $\text{emb}(P(v), T) = \text{EMB}(v)$. Consider cases 2 and 3 of the algorithm.

For $k = 1$ we have that $w \in \text{EMB}(v)$ implies that $\text{label}(w) = \text{label}(v)$ and there is a node $w_1 \in \text{EMB}(v_1)$ such that $\text{fl}(\text{parent}(w_1), \text{label}(v)) = w$, that is, no node on the path between w_1 and w is labeled $\text{label}(v)$. By induction $\text{EMB}(v_1) = \text{emb}(P(v_1), T)$ and therefore w is the root of an embedding of $P(v)$ in T . Since $\text{EMB}(v)$ is the deep set of all such nodes it follows that $w \in \text{emb}(P(v), T)$. Conversely, if $w \in \text{emb}(P(v), T)$ then $\text{label}(w) = \text{label}(v)$, there is a node $w_1 \in \text{emb}(P(v_1), T)$ such that $w < w_1$, and no node on the path between w and w_1 is labeled $\text{label}(v)$, that is, $\text{fl}(w_1, \text{label}(v)) = w$. Hence, $w \in \text{EMB}(v)$.

Next consider the case $k > 1$. By Proposition 3.3 and the induction hypothesis

$$U_1 = \text{mop}(\text{emb}(P(v_1), T), \dots, \text{emb}(P(v_k), T)).$$

We first show that $w \in \text{emb}(P(v), T)$ implies that $w \in \text{EMB}(v)$. By Proposition 3.2 there exists a pair of nodes $(w_1, w_k) \in \text{mop}(\text{emb}(P(v_1), T), \dots, \text{emb}(P(v_k), T))$ such that $w = \text{fl}(\text{nca}(w_1, w_k), \text{label}(v))$. We have $(w_1, w_k) \in U_1$ and it follows directly from the implementation that $w \in \text{EMB}(v)$. To see that we do not lose w by taking `DEEP` of `NCA`(U_1) assume that $w' = \text{nca}(w_1, w_k)$ is removed from the set in this step. This means there is a node u in `NCA`(U_1) which is a descendant of w' and which is still in the set. Since w is the root of a deep occurrence we must have $w = \text{fl}(w', \text{label}(v)) = \text{fl}(u, \text{label}(v))$.

Let $w \in \text{EMB}(v)$. Then w is the first ancestor with label $\text{label}(v)$ of a nearest common ancestor of a pair in U_1 . That is, $\text{label}(w) = \text{label}(v)$ and there exists nodes $(w_1, w_k) \in \text{mop}(\text{emb}(P(v_1), T), \dots, \text{emb}(P(v_k), T))$ such that $w = \text{fl}(\text{nca}(w_1, w_k), \text{label}(v))$. Clearly, w is the root of an embedding of $P(v)$ in T . Assume for contradiction that w is not a deep embedding, that is, $w < u$ for some node $u \in \text{emb}(P(v), T)$. We have just shown that this implies $u \in \text{EMB}(v)$. Since $\text{EMB}(v)$ is a deep set this contradicts $w \in \text{EMB}(v)$. \square

The set $L(T)$ is deep and in all three cases of `EMB`(V) the returned set is also deep. By induction it follows that the input to `PARENT`, `FL`, `NCA`, and `MOPRIGHT` is always deep. We will use this fact to our advantage in the following algorithms.

4. A SIMPLE TREE INCLUSION ALGORITHM

In this section we present a simple implementation of the set procedures which leads to an efficient tree inclusion algorithm. Subsequently, we modify one of the procedures to obtain a family of tree inclusion algorithms where the complexities depend on the solution to a well-studied problem known as the *tree color problem*.

4.1. Preprocessing

To compute deep embeddings we require a data structure for T which allows us, for any $v, w \in V(T)$, to compute $\text{nca}_T(v, w)$ and determine if $v < w$ or $v \triangleleft w$. In linear

time we can compute $\text{pre}(v)$ and $\text{post}(v)$ for all nodes $v \in V(T)$, and with these it is straightforward to test the two conditions. Furthermore, we have the next lemma.

LEMMA 4.1. [HAREL AND TARJAN 1984]. *For any tree T there is a data structure using $O(n_T)$ space and preprocessing time which supports nearest common ancestor queries in $O(1)$ time.*

Hence, our data structure uses linear preprocessing time and space (see also Bender and Farach-Colton [2000] and Alstrup et al. [2004] for more recent nearest common ancestor data structures).

4.2. Implementation of the Set Procedures

To answer tree inclusion queries we give an efficient implementation of the set procedures. The idea is to represent sets of nodes and sets of pairs of nodes in a left-to-right order using linked lists. For this purpose we introduce some helpful notation. Let $X = [x_1, \dots, x_k]$ be a linked list of nodes. The *length* of X , denoted $|X|$, is the number of elements in X and the list with no elements is written $[\]$. The i th node of X , denoted $X[i]$, is x_i . Given any node y the list obtained by *appending* y to X , is the list $X \circ y = [x_1, \dots, x_k, y]$. If for all i , $1 \leq i \leq |X| - 1$, $X[i] \triangleleft X[i + 1]$ then X is *ordered* and if $X[i] \trianglelefteq X[i + 1]$ then X is *semiordered*. Recall that $X[i] \trianglelefteq X[i + 1]$ means that we can have $X[i] \triangleleft X[i + 1]$ or either of the nodes can be an ancestor of the other ($X[i] \triangleleft X[i + 1]$ or $X[i] \leq X[i + 1]$ or $X[i] \geq X[i + 1]$). A list $Y = [(x_1, z_k), \dots, (x_k, z_k)]$ is a *node pair list*. By analogy, we define length, append, etc., for Y . For a pair $Y[i] = (x_i, z_i)$ define $Y[i]_1 = x_i$ and $Y[i]_2 = z_i$. If the lists $[Y[1]_1, \dots, Y[k]_1]$ and $[Y[1]_2, \dots, Y[k]_2]$ are both ordered or semiordered then Y is *ordered* or *semiordered*, respectively.

The set procedures are implemented using node lists. All lists used in the procedures are either ordered or semiordered. As noted in Section 3 we may assume that the inputs to all of the procedures, except DEEP, represent deep sets, that is, the corresponding node list or node pair list is ordered. We assume that the input list given to DEEP is semiordered and the output, of course, is ordered. Hence, the output of all the other set procedures must be semiordered. In the following let X be a node list, Y a node pair list, and α a character in Σ . The detailed implementation of the set procedures is given next. We show the correctness in Section 4.3 and discuss the complexity in Section 4.4.

Procedure PARENT(X)

1 Return the list $[\text{parent}(X[1]), \dots, \text{parent}(X[|X|])]$.

Procedure NCA(Y)

1 Return the list $[\text{nca}(Y[1]), \dots, \text{nca}(Y[|Y|])]$.

Procedure DEEP(X)

1 Initially, set $x := X[1]$ and $R := [\]$.
 2 **for** $i := 2$ to $|X|$ **do**
 3 Compare x and $X[i]$. There are three cases:
 4 **case 1.** $x \triangleleft X[i]$
 5 Set $R := R \circ x$ and $x := X[i]$.
 6 **case 2.** $x < X[i]$
 7 Set $x := X[i]$.
 8 **case 3.** $X[i] \leq x$
 9 Do nothing.
 10
 11 **end**
 12 Return $R \circ x$.

The implementation of procedure `DEEP` takes advantage of the fact that the input list is semiordered. In case 1 the node $X[i]$ is to the right of our “potential output node” x . Since any node that is a descendant of x must also be to the left of $X[i]$ it cannot appear later in the list X than $X[i]$. We can thus safely add x to R at this point. In case 2 the node x is an ancestor of $X[i]$ and thus x cannot be in $\text{DEEP}(X)$. In case 3 the node $X[i]$ is an ancestor of x and can therefore not be in $\text{DEEP}(X)$.

Procedure `MOPRIGHT`(Y, X)

```

1 Initially, set  $R := []$ .
2 Find the smallest  $j$  such that  $Y[1]_2 \triangleleft X[j]$  and set  $y := Y[1]_1$ ,  $x := X[j]$ . If no such  $j$  exists
  stop and return  $R$ .
3 for  $i := 2$  to  $|Y|$  do
4   until  $Y[i]_2 \triangleleft X[j]$  or  $j > |X|$  do
5     set  $j := j + 1$ .
6   if  $j > |X|$  then
7     stop and return  $R := R \circ (y, x)$ .
8   else
9     Compare  $X[j]$  and  $x$ . There are two cases:
10    case 1.  $x \triangleleft X[j]$ 
11      set  $R := R \circ (y, x)$ ,  $y := Y[i]_1$ , and  $x := X[j]$ .
12    case 2. If  $x = X[j]$ 
13      set  $y := Y[i]_1$ .
14
15
16 end
17 Return  $R := R \circ (y, x)$ .
```

In procedure `MOPRIGHT` we have a “potential pair” (y, x) where $y = Y[i']_1$ for some $i' < i$ and $Y[i']_2 \triangleleft x$. In case 1 we have $x \triangleleft X[j]$ and also $Y[i']_2 \triangleleft Y[i]_2$ since the input lists are ordered and $i' < i$ (see Figure 5(a)). Therefore, (y, x) is inserted into R . In case 2 we have $x = X[j]$, that is, $Y[i]_2 \triangleleft x$, and as before $Y[i']_2 \triangleleft Y[i]_2$ (see Figure 5(b)). Therefore (y, x) cannot be in `MOPRIGHT`(Y, X), and we set $(Y[i]_1, x)$ to be the new potential pair.

We can implement `MOPLEFT`(X, Y) similarly to `MOPRIGHT` replacing smallest by largest, \triangleleft by \triangleright , and traversing the lists backwards.

Procedure `MOPLEFT`(X, Y)

```

1 Initially, set  $R := []$ .
2 Find the largest  $j$  such that  $Y[|Y|]_1 \triangleright X[j]$  and set  $y := Y[|Y|]_2$  and  $x := X[j]$ . If no such  $j$ 
  exists stop and return  $R$ .
3 for  $i := |Y| - 1$  to 1 do
4   until  $Y[i]_1 \triangleright X[j]$  or  $j < 1$  do
5     set  $j := j - 1$ .
6   if  $j < 1$  then
7     stop and return  $R := (x, y) \circ R$ .
8   else
9     compare  $X[j]$  and  $x$ . There are two cases:
10    case 1.  $x \triangleright X[j]$ 
11      set  $R := (x, y) \circ R$ ,  $y := Y[i]_2$ , and  $x := X[j]$ .
12
13    case 2.  $x = X[j]$ 
14      set  $y := Y[i]_2$ .
15
16   end
17 end
18 Return  $R := (x, y) \circ R$ .
```

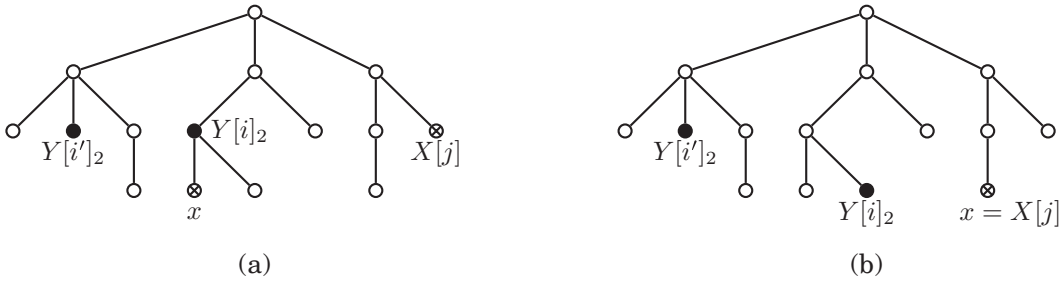


Fig. 5. Case 1 and 2 from the implementation of MOPRIGHT. (a) We have $x \triangleleft X[j]$ and therefore $Y[i]_2 \not\triangleleft x$. So (y, x) is inserted in R . (b) We have $Y[i']_2 \triangleleft Y[i]_2 \triangleleft x = X[j]$.

Procedure $\text{FL}(X, \alpha)$

```

1 Initially, set  $L := X, Z := L$ .
2 while  $Z \neq []$  do
3   for  $i := 1$  to  $|Z|$  do
4     case 1.  $\text{label}(Z[i]) = \alpha$ 
5       | Delete  $Z[i]$  from  $Z$  (but keep it in  $L$ ).
6     case 2.  $\text{label}(Z[i]) \neq \alpha$  and  $\text{parent}(Z[i]) \neq \perp$ 
7       | Replace  $Z[i]$  with  $\text{parent}(Z[i])$  in both  $Z$  and  $L$ .
8     case 3.  $\text{label}(Z[i]) \neq \alpha$  and  $\text{parent}(Z[i]) = \perp$ 
9       | Delete  $Z[i]$  from both  $Z$  and  $L$ .
10
11   end
12   Set  $(Z, L) := \text{DEEP}^*(Z, L)$ .
13 end
14 Return  $L$ .

```

The procedure FL computes the set $\text{DEEP}(\{\text{fl}(x, \alpha) \mid x \in X\})$ bottom-up. The list Z contains ancestors of the elements of X for which we have not yet found an ancestor with label α . In each step it considers each node z in the list Z . If it has the right label then $x \in \text{FL}(X, \alpha)$ and we remove it from Z but keep it in L . Otherwise we replace it with its parent (unless it is the root). Thus L contains both the elements in Z and the part of $\text{FL}(X, \alpha)$ found until now.

To keep the running time down we wish to maintain the invariant that L is deep at the beginning of each iteration of the outer loop. To do this procedure FL calls an auxiliary procedure $\text{DEEP}^*(Z, L)$ which takes two ordered lists Z and L , where $Z \subseteq L$, and returns two ordered lists representing the set $\text{DEEP}(L) \cap Z$ and $\text{DEEP}(L)$, that is, $\text{DEEP}^*(Z, L) = ([z \in Z \mid \nexists x \in L : z < x], \text{DEEP}(L))$. If we use the procedure DEEP to calculate DEEP^* it takes time $O(|Z| + |L|) = O(|L|)$. Instead we will show how to calculate it in time $O(|Z|)$ using a linked list representation for Z and L . We will need this in the proof of Lemma 4.9, which shows that the total running time of *all* calls to FL from EMB takes time $O(n_T)$. Next we describe in more detail how to implement FL together with the auxiliary procedures.

We use a doubly linked list to represent L and extra pointers in this list to represent Z . Each element in the list has pointers Succ_L and Pred_L pointing to its predecessor and successor in L . Similarly, each element in Z has pointers Succ_Z and Pred_Z pointing to its predecessor and successor in Z (right after the initialization these are equal to Succ_L and Pred_L). In the for loop we use the Succ_Z pointers to find the next element in Z . To delete $Z[i]$ from Z in case 1 we set $\text{Succ}_Z(\text{Pred}_Z(Z[i])) = \text{Succ}_Z(Z[i])$ and

$\text{Pred}_Z(\text{Succ}_Z(Z[i])) = \text{Pred}_Z(Z[i])$. The L pointers stay the same. In case 2 we simply replace $Z[i]$ with its parent in the linked list. The Succ and Pred pointers stay the same. To delete $Z[i]$ from both Z and L in case 3 we set $\text{Succ}_j(\text{Pred}_j(Z[i])) = \text{Succ}_j(Z[i])$ and $\text{Pred}_j(\text{Succ}_j(Z[i])) = \text{Pred}_j(Z[i])$ for $j \in \{Z, L\}$. Finally, to compute $\text{DEEP}^*(Z, L)$ walk through Z following the Succ_Z pointers. At each node z compare $\text{Pred}_L(z)$ and $\text{Succ}_L(z)$ with z . If one of them is a descendant of z remove z from the doubly linked list Z and L as in case 3. Note that instead of calling $\text{DEEP}^*(Z, L)$ this comparison can also be done directly in step 2, which is the only place where we insert nodes that might be an ancestor of another node in L . We will show in the next section that it is enough to compare z to its neighbors in the list L .

4.3. Correctness of the Set Procedures

Clearly, PARENT and NCA are correct. The following lemmas show that DEEP , FL , and MOPRIGHT are also correctly implemented. For notational convenience we write $x \in X$, for a list X , if $x = X[i]$ for some i , $1 \leq i \leq |X|$.

LEMMA 4.2. *Procedure $\text{DEEP}(X)$ is correct.*

PROOF. Let x be the variable in the procedure. We will first prove the following invariant on x .

INVARIANT. *At the beginning of each iteration of the for loop in line 2 we have $x \not\prec X[j]$ for any $1 \leq j \leq i - 1$.*

PROOF. We prove the invariant by induction on i . The invariant obviously holds for the base case $i = 2$.

For the induction step let $i \geq 3$. Let iteration k denote the iteration of the for loop when $i = k$. By the induction hypothesis we have $x \not\prec X[j]$ for any $1 \leq j \leq i - 2$ at the beginning of iteration $i - 1$.

Let x' denote the value of the variable x at the beginning of iteration $i - 1$. Consider the value of variable x at the beginning of the iteration i . There are two cases.

- (1) If $x = x'$ then by the induction hypothesis $x = x' \not\prec X[j]$ for any $1 \leq j \leq i - 2$. Since x was not changed in iteration $i - 1$ we have $X[i - 1] \leq x$ (case 3 of the procedure) and thus $x \not\prec X[j]$ for any $1 \leq j \leq i - 1$.
- (2) If $x \neq x'$ then x was set in either case 1 ($x' \triangleleft x$) or case 2 ($x' \prec x$) in iteration $i - 1$. Therefore, $x = X[i - 1]$ and by the induction hypothesis $x' \not\prec X[j]$ for any $1 \leq j \leq i - 2$. There are two subcases.
 - (a) If $x' \prec x$ it follows immediately from the induction hypothesis that $x \not\prec X[j]$ for any $1 \leq j \leq i - 1$, since all descendants of x also are descendants of x' .
 - (b) If $x' \triangleleft x$ we note that x is the first node to the left of x' occurring after x' in X (otherwise x would have been reset in case 1 of the procedure in an earlier iteration, contradicting that x' is the value of variable x at the beginning of iteration $i - 1$). Since X is semiordered no node $X[j]$ with smaller index in X than x' can be to the right of x' . Thus no node $X[j]$, $1 \leq j < i - 2$, can be to the right of x' . Since all descendants of x must be to the right of x' we have $x \not\prec X[j]$ for any $1 \leq j \leq i - 1$.

We are now ready to prove that $y \in \text{DEEP}(X)$ iff there exists no $z \in X$ such that $y \prec z$. We first argue that if $y \in \text{DEEP}(X)$ then $\nexists z \in X$ such that $y \prec z$. Let y be an element in $\text{DEEP}(X)$. Only elements that have been assigned to x during the procedure are in the output. Consider the iteration where $x = y$ is appended to R . This only happens in case 1 of the procedure and thus $y = x \triangleleft X[i]$. Since X is semiordered this implies that $x \triangleleft X[j]$ for $i \leq j \leq |X|$, and therefore $y = x \not\prec X[j]$ for $i \leq j \leq |X|$. By the preceding

invariant it follows that $y = x \not\prec X[j]$ for $1 \leq j \leq i - 1$. Thus if $y \in \text{DEEP}(X)$ then $\nexists z \in X$ such that $y \prec z$.

Let $y \in X$ be an element such that $X \cap V(T(y)) = \{y\}$. Let j be the smallest index such that $X[j] = y$. When comparing y and x during the iteration where $i = j$ we are in case 1 or 2, since j is the smallest index such that $X[j] = y$ (implying $x \neq y$) and $X \cap V(T(y)) = \{y\}$ (implying $y \not\prec x$). In either case x is set to y . Since there are no descendants of y in X , the variable x remains equal to y until added to R . If y occurs several times in X we will have $x = y$ each time we meet a copy of y (except the first) and it follows from the implementation that y will occur exactly once in R . \square

To show that the implementation of `MOPRIGHT` is correct we will use the following proposition.

PROPOSITION 4.3. *Before the first iteration of the for loop in line 3 of `MOPRIGHT` we have $y = Y[1]_1$, $x = X[j]$ and either $X[j - 1] \triangleleft Y[1]_2 \triangleleft X[j]$ (if $j > 1$) or $Y[1]_2 \triangleleft X[j]$ if ($j = 1$).*

At the end of each iteration of the for loop then, unless $Y[i]_2 \not\triangleleft X[|X|]$, we have $y = Y[i]_1$, $x = X[j]$ and either $X[j - 1] \triangleleft Y[i]_2 \triangleleft X[j]$ (if $j > 1$) or $Y[i]_2 \triangleleft X[j]$ if ($j = 1$).

PROOF. The first statement ($y = Y[1]_1$, $x = X[j]$ and either $X[j - 1] \triangleleft Y[1]_2 \triangleleft X[j]$ (if $j > 1$) or $Y[1]_2 \triangleleft X[j]$ if ($j = 1$)) follows immediately from the implementation of the procedure line 2 and the fact that the input lists are ordered.

We prove the second statement by induction on i . Base case $i = 2$. By the first statement we have $y = Y[1]_1$, $x = X[j]$ and either $X[j - 1] \triangleleft Y[1]_2 \triangleleft X[j]$ (if $j > 1$) or $Y[1]_2 \triangleleft X[j]$ if ($j = 1$) before this iteration. Let j' be the value of j before this iteration. It follows immediately from the implementation that $y = Y[2]_1$ since y is set to this in both case 1 and 2. If $Y[2]_2 \triangleleft X[j']$ then $j = j'$. Since Y is ordered it follows that $X[j - 1] \triangleleft Y[1]_2 \triangleleft Y[2]_2 \triangleleft X[j]$ (if $j > 1$) or $Y[2]_2 \triangleleft X[j]$ if ($j = 1$). If $Y[2]_2 \not\triangleleft X[j']$ then j is increased until $Y[2]_2 \triangleleft X[j]$ implying $X[j - 1] \triangleleft Y[2]_2 \triangleleft X[j]$ unless $j > |X|$, since X is ordered.

Induction step $i > 2$. It follows immediately from the implementation that $y = Y[i]_1$ since y is set to this in both case 1 and 2. By the induction hypothesis we have $y = Y[i]_1$, $x = X[j]$ and $Y[i]_2 \triangleleft X[j]$ right before this iteration. Let j' be the value of j before this iteration. If $Y[i]_2 \triangleleft X[j']$ then $j = j'$. Since Y is ordered it follows that $X[j - 1] \triangleleft Y[i - 1]_2 \triangleleft Y[i]_2 \triangleleft X[j]$ (if $j > 1$) or $Y[i]_2 \triangleleft X[j]$ if ($j = 1$). If $Y[i]_2 \not\triangleleft X[j']$ then j is increased until $Y[i]_2 \triangleleft X[j]$ implying $X[j - 1] \triangleleft Y[i]_2 \triangleleft X[j]$ unless $j > |X|$. \square

LEMMA 4.4. *Procedure `MOPRIGHT(Y, X)` is correct.*

PROOF. We want to show that for any $1 \leq i' \leq |Y|$, $1 \leq j' \leq |X|$:

$$(Y[i']_1, X[j']) \in R \iff (Y[i']_2, X[j']) \in \text{mop}(Y|_2, X).$$

Since $Y|_2$ and X are ordered lists we have $(Y[i']_2, X[j']) \in \text{mop}(Y|_2, X)$ if and only if:

- (1) $\arg \min_j Y[i']_2 \triangleleft X[j] = j'$
- (2) $\arg \max_i Y[i]_2 \triangleleft X[j'] = i'$.

We will first show that (1) and (2) implies $(Y[i']_2, X[j']) \in R$. We start by showing that when i is about to be incremented to $i' + 1$ then $y = Y[i']_1$ and $x = X[j']$. There are two cases to consider.

- $i' = 1$. After line 2 is executed, y is set to $Y[1]_1$, j is set to j' and x is set to $X[j']$.
- $i' > 1$. Consider the step in the iteration when $i = i'$. At the beginning of this iteration, $y = Y[i' - 1]_1$ and j is the minimal index such that $Y[i' - 1] \triangleleft X[j]$. By (1) this implies that $j \leq j'$, and that after line 4 and 5 are executed, j is set to j' . At the

end of the iteration $y = Y[i']$ (y is assigned to $Y[i']$ in both cases) and $x = X[j']$. If $j = j'$ then x set to $X[j']$ in case 1, otherwise we had $j = j'$ (case 2) and then x was set to $X[j']$ already).

We have established that when i is about to be incremented to $i' + 1$ then $y = Y[i']_1$ and $x = X[j']$. To show that $(Y[i']_2, X[j']) \in R$ we consider the following two cases.

— $i' < |Y|$. Consider the $(i' + 1)^{th}$ iteration. By condition (2) $X[j'] \triangleleft Y[i' + 1]_2$ and therefore j is increased in line 5. So now $j > j'$. If $j > |X|$ then $(y, x) = (Y[i']_2, X[j'])$ is added to R in line 7. Otherwise, since X is ordered, $x = X[j'] \triangleleft X[j]$. We are therefore in case 1 and $(y, x) = (Y[i']_2, X[j'])$ is added to R .

— $i' = |Y|$. Then $(y, x) = (Y[i']_2, X[j'])$ is added to R in line 15.

We will now show that $(Y[i']_1, X[j']) \in R$ implies (1) and (2). Since $(Y[i']_1, X[j']) \in R$ we had $(y, x) = (Y[i']_1, X[j'])$ at some point during the execution. The pair (y, x) can be added to R only in the for loop before changing the values of y and x or at the execution of the last line of the procedure. Therefore $(y, x) = (Y[i']_1, X[j'])$ at the beginning of some execution of the for loop, or after the last iteration ($i = |Y|$). It follows by Proposition 4.3 that $X[j - 1] \triangleleft Y[i]_2 \triangleleft X[j]$ if $j > 1$ or $Y[i]_2 \triangleleft X[j]$ if $j = 1$. It remains to show that $X[j'] \triangleleft Y[i' + 1]_2$ for $i' < |Y|$. It follows from the implementation that (y, x) only is added to R inside the for loop if j is increased. Thus j was increased in the next iteration ($i = i' + 1$) implying $X[j'] \triangleleft Y[i' + 1]_2$. \square

LEMMA 4.5. *Procedure MOPLEFT(X, Y) is correct.*

PROOF. Similar to the proof of Lemma 4.4. \square

To show that FL is correct we need the following proposition.

PROPOSITION 4.6. *Let X be an ordered list and let x be an ancestor of $X[i]$ for some $i \in \{1, \dots, k\}$. If x is an ancestor of some node in X other than $X[i]$ then x is an ancestor of $X[i - 1]$ or $X[i + 1]$.*

PROOF. Recall that $u \triangleleft v$ iff $\text{pre}(u) < \text{pre}(v)$ and $\text{post}(u) < \text{post}(v)$. Since $x \triangleleft X[i]$ we have $\text{pre}(x) < \text{pre}(X[i])$ and $\text{post}(X[i]) < \text{post}(x)$. Assume there exists a descendant $X[j]$ of x such that $j \notin \{i - 1, i, i + 1\}$. If $j < i - 1$ we have

$$\text{pre}(x) \leq \text{pre}(X[j]) < \text{pre}(X[i - 1]),$$

where the first inequality follows from $x \triangleleft X[j]$ and the second from X being ordered. And

$$\text{post}(X[i - 1]) < \text{post}(X[i]) \leq \text{post}(x),$$

where the first inequality follows from X being ordered and the second from $x \triangleleft X[i]$. Thus $x \triangleleft X[i - 1]$.

Similarly, for $j > i + 1$, we have $\text{pre}(x) \leq \text{pre}(X[i]) < \text{pre}(X[i + 1])$ and $\text{post}(X[i + 1]) < \text{post}(X[j]) \leq \text{post}(x)$ implying that $x \triangleleft X[i + 1]$. \square

Proposition 4.6 shows that the doubly linked list implementation of DEEP* is correct. Since all changes to the list are either deletions or insertions of a parent in the place of its child, the list L (and thus also Z) is ordered at the beginning of each iteration of the outer loop.

LEMMA 4.7. *Procedure FL(X, α) is correct.*

PROOF. Let $F = \{\text{fl}(x, \alpha) \mid x \in X\}$. We first show that $\text{FL}(X, \alpha) \subseteq F$. Consider a node $x \in \text{FL}(X, \alpha)$. Since x is in L after the final iteration, x was deleted from Z during some iteration. Thus $\text{label}(x) = \alpha$. For any $y \in X$ we follow the path from y to the root and

stop the first time we meet a node with label α or even earlier since we keep the list deep. Thus $x \in F$.

The set $\text{FL}(X, \alpha)$ is a deep set, and therefore $\text{DEEP}(F) \subseteq \text{FL}(X, \alpha) \subseteq F \Rightarrow \text{DEEP}(F) = \text{FL}(X, \alpha)$. Hence, it remains to show that $\text{DEEP}(F) \subseteq \text{FL}(X, \alpha)$. Let x be a node in $\text{DEEP}(F)$, let $z \in X$ be a node such that $x = \text{fl}(z, \alpha)$, and let $z = x_1, x_2, \dots, x_k = x$ be the nodes on the path from z to x . We will argue that after each iteration of the algorithm we have $x_i \in L$ for some i . Since $\text{label}(x_i) \neq \alpha$ for $i < k$ this is the same as $x_i \in Z$ for $i < k$. Before the first iteration we have $x_1 \in X = Z$. As long as $i < k$ we replace x_i with x_{i+1} in case 2 of the for loop, since $\text{label}(x_i) \neq \alpha$. When $i = k$ we remove x_k from Z but keep it in L . It remains to show that we do not delete x_i in the computation of $\text{DEEP}^*(Z, L)$ in any iteration. If x_i is removed then there is a node $y \in L$ that is a descendant of x_i and thus also a descendant of x . We argued earlier that $L \setminus Z \subseteq F$ and thus $y \in Z$ since $x \in \text{DEEP}(F)$. But since $x \in \text{DEEP}(F)$ no node on the path from y to x can have label α and therefore x_i will eventually be reinserted in Z . \square

4.4. Complexity of the Set Procedures

For the running time of the node list implementation observe that, given the data structure described in Section 4.1, all set procedures, except FL , perform a single pass over the input using constant time at each step. Hence we have the next lemma.

LEMMA 4.8. *For any tree T there is a data structure using $O(n_T)$ space and preprocessing which supports each of the procedures PARENT , DEEP , MOPRIGHT , MOPLEFT , and NCA in linear time (in the size of their input).*

The running time of a single call to FL might take time $O(n_T)$. Instead we will divide the calls to FL into groups and analyze the total time used on such a group of calls. The intuition behind the division is that for a path in P the calls made to FL by EMB are done bottom-up on disjoint lists of nodes in T .

LEMMA 4.9. *For disjoint ordered node lists X_1, \dots, X_k and labels $\alpha_1, \dots, \alpha_k$, such that any node in X_{i+1} is an ancestor of some node in $\text{FL}_T(X_i, \alpha_i)$, $1 \leq i < k$, all of $\text{FL}_T(X_1, \alpha_1), \dots, \text{FL}_T(X_k, \alpha_k)$ can be computed in $O(n_T)$ time.*

PROOF. Let Z and L be as in the implementation of the procedure. Since DEEP^* takes time $O(|Z|)$ and each of the steps in the for loop takes constant time, we only need to show that the total length of the lists Z —summed over all the calls—is $O(n_T)$ to analyze the total time usage. We will show that any node in T can be in Z at the beginning of the while loop at most twice during all calls to FL . The size of Z cannot increase in the iterations of the for loop (line 3–10), and thus the size of Z when DEEP^* is called (line 11) is at most the size of Z at the beginning of this iteration of the while loop.

Consider a single call to FL . Except for the first iteration, a node can be in Z only if one of its children were in Z in the last iteration. Note that Z is ordered at the beginning of each for loop. Thus if a node is in Z at the beginning of the while loop none of its children is in Z and thus in one call to FL a node can be in Z only once.

Look at a node z the first time it appears in Z at the beginning of an execution of the while loop. Assume that this is in the call $\text{FL}(X_i, \alpha_i)$.

- If $z \in X_i$ then z cannot be in Z in any later calls, since no node in X_j where $j > i$ can be a descendant of a node in X_i .
- If $\text{label}(z) \neq \alpha_i$ then z is removed from Z in case 2 or case 3 of the procedure and cannot be in Z in any of the later calls. To see this consider the time when z is removed from Z (case 2 or case 3). Since the set L is deep at the beginning of the while loop and $Z \subseteq L$, no descendant of z will appear in Z later in this call to FL , and no node in the output from $\text{FL}(X_i, \alpha_i)$ can be a descendant of z . Since any node in X_j , $j > i$, is an

- ancestor of some node in $\text{FL}(X_i, \alpha_i)$ neither z or any descendant of z can be in any X_j , $j > i$. Thus z cannot appear in Z in any later calls to FL .
- Now if $\text{label}(z) = \alpha_i$ then we might have $z \in X_{i+1}$. In that case, z will appear in Z in the first iteration of the procedure call $\text{FL}(X_{i+1}, \alpha_i)$, but not in any later calls since the lists are disjoint, and since no node in X_j where $j > i + 1$ can be a descendant of a node in X_{i+1} . If $\text{label}(z) = \alpha_i$ and $z \notin X_{i+1}$ then clearly z cannot appear in Z in any later call.

Thus a node in T is in Z at the beginning of an execution of the while loop at most twice during all the calls. \square

4.5. Complexity of the Tree Inclusion Algorithm

Using the node list implementation of the set procedures we get the following.

LEMMA 4.10. *For trees P and T the tree inclusion problem can be solved in $O(l_P n_T)$ time.*

PROOF. By Lemma 4.8 we can preprocess T in $O(n_T)$ time and space. Let $g(n)$ denote the time used by FL on a list of length n . Consider the time used by $\text{EMB}(\text{root}(P))$. We bound the contribution for each node $v \in V(P)$. If v is a leaf we are in case 1 of EMB . The cost of computing $\text{FL}(L(T), \text{label}(v))$ is $O(g(l_T))$, and by Lemma 4.9 (with $k = 1$) we get $O(g(l_T)) = O(n_T)$. Hence, the total cost of all leaves is $O(l_P n_T)$. If v has a single child w we are in case 2 of EMB , and by Lemma 4.8 the cost is $O(g(|\text{EMB}(w)|))$. If v has more than one child the cost of MOPRIGHT , NCA , and DEEP is bounded by $\sum_{w \in \text{child}(v)} O(|\text{EMB}(w)|)$. Furthermore, since the length of the output of MOPRIGHT (and thus NCA) is at most $z = \min_{w \in \text{child}(v)} |\text{EMB}(w)|$ the cost of FL is $O(g(z))$. Hence, the total cost for internal nodes is

$$\sum_{v \in V(P) \setminus L(P)} O\left(g\left(\min_{w \in \text{child}(v)} |\text{EMB}(w)|\right) + \sum_{w \in \text{child}(v)} |\text{EMB}(w)|\right) = \sum_{v \in V(P)} O(g(|\text{EMB}(v)|)). \quad (3)$$

Next we bound (3). For any $w \in \text{child}(v)$ we have that $\text{EMB}(w)$ and $\text{EMB}(v)$ are disjoint ordered lists. Furthermore we have that any node in $\text{EMB}(v)$ must be an ancestor of some node in $\text{FL}(\text{EMB}(w), \text{label}(v))$. Hence, by Lemma 4.9, for any leaf-to-root path $\delta = v_1, \dots, v_k$ in P , we have that $\sum_{u \in \delta} g(|\text{EMB}(u)|) = O(n_T)$. Let Δ denote the set of all root-to-leaf paths in P . It follows that

$$\sum_{v \in V(T)} g(|\text{EMB}(v)|) \leq \sum_{p \in \Delta} \sum_{u \in p} g(|\text{EMB}(u)|) = O(l_P n_T).$$

Since this time is the same as the time spent at the leaves the time bound follows. \square

To analyze the space used by the algorithm we first bound the size of $\text{EMB}(v)$ for each node $v \in V(P)$. We then use this to bound the total the size of embeddings stored in the recursion stack in the computation of $\text{EMB}(\text{root}(P))$, that is, the total size of embeddings stored by recursive calls during the computation.

LEMMA 4.11. *For any tree P we have $\forall v \in V(P)$:*

$$|\text{EMB}_T(v)| \leq \frac{l_T}{l_{P(v)}}.$$

PROOF. By Lemma 3.4 $\text{EMB}(v)$ is the set of deep occurrences of $P(v)$ in T . By the definition of deep the occurrences are disjoint and no node in one occurrence can be an ancestor of a node in another occurrence. Each occurrence has at least $l_{P(v)}$ descendant

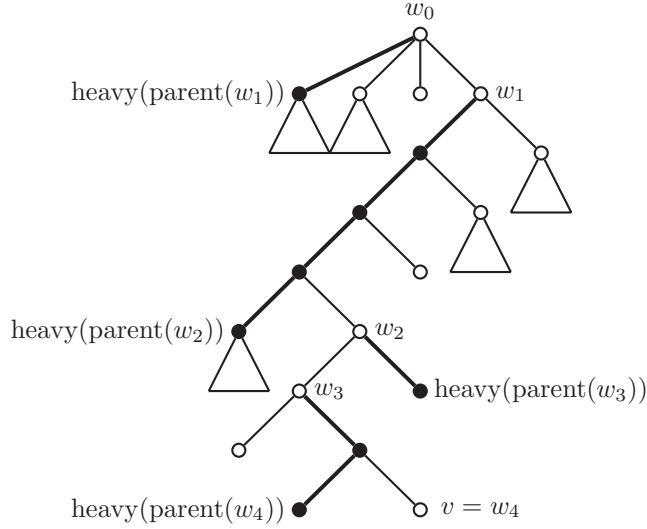


Fig. 6. Path from root to v . The heavy nodes are black and the light nodes are white. The heavy edges are the thick edges and the light edges are thin.

leaves and each of these leaves is an ancestor of at least one distinct leaf in T (see also Figure 4(b)). Thus the number of occurrences is bounded by $l_T/l_{P(v)}$. \square

LEMMA 4.12. *The total size of saved embeddings on the recursion stack at any time during the computation of $\text{EMB}(\text{root}(P))$ is at most $O(l_T)$.*

PROOF. Let node v be the node for which we are currently computing EMB . Let p be the path from the root to v and let w_0, \dots, w_ℓ be the light nodes on this path. Let $\ell = \text{ldepth}(v)$. There is one embedding on the stack for each light node on the path (see Figure 6): For the heavy nodes on the path there can be no saved embeddings in the recursion as the algorithm always recurses on the heavy child first. For each light node w_i on the path p except the root w_0 the stack will contain either $\text{EMB}(\text{heavy}(\text{parent}(w_i)))$, or $U_j = \text{MOPRIGHT}(U_{j-1}, R_j)$, where v_j is w_i 's left sibling, or $U_j = \text{MOPLEFT}(U_{j-1}, R_j)$, where v_j is w_i 's right sibling. The computation of U_j is a series of MOPRIGHT (or MOPLEFT) computations that started with the pair of node lists $(\text{EMB}(\text{heavy}(\text{parent}(w_i))), \text{EMB}(\text{heavy}(\text{parent}(w_i))))$ as the first argument to MOPRIGHT (or MOPLEFT). As the output of MOPRIGHT (or MOPLEFT) can be no larger than the input to the procedure we have $|U_j| = O(|\text{EMB}(\text{heavy}(\text{parent}(w_i)))|)$ and thus the total space used at any time during the recursion is

$$O\left(\sum_{i=1}^{\text{ldepth}(v)} |\text{EMB}(\text{heavy}(\text{parent}(w_i)))|\right).$$

By Lemma 4.11 we have

$$|\text{EMB}(\text{heavy}(\text{parent}(w_i)))| \leq \frac{l_T}{l_{P(\text{heavy}(\text{parent}(w_i)))}},$$

and thus

$$\sum_{i=1}^{\text{ldepth}(v)} |\text{EMB}(\text{heavy}(\text{parent}(w_i)))| \leq l_T \sum_{i=1}^{\text{ldepth}(v)} \frac{1}{l_{P(\text{heavy}(\text{parent}(w_i)))}}. \quad (4)$$

By the definition of heavy the node $\text{heavy}(\text{parent}(w_i))$ has more leaves in its subtree than w_i , that is,

$$l_{P(w_i)} \leq l_{P(\text{heavy}(\text{parent}(w_i)))}. \quad (5)$$

Obviously, $\text{heavy}(\text{parent}(w_i))$ has no more leaves in its subtree than its parent, that is,

$$l_{P(\text{heavy}(\text{parent}(w_i)))} \leq l_{P(\text{parent}(w_i))}. \quad (6)$$

Since w_i is light it has at most half the number of leaves in its subtree as its parent, that is

$$l_{P(w_i)} \leq l_{P(\text{parent}(w_i))}/2. \quad (7)$$

Combining this with the fact that w_i is an ancestor of w_{i+1} and $\text{heavy}(\text{parent}(w_{i+1}))$ we get

$$\begin{aligned} l_{P(\text{heavy}(\text{parent}(w_j)))} &\leq l_{P(\text{parent}(w_j))} && \text{by (6)} \\ &\leq l_{P(w_{j-1})} && \text{since } w_{j-1} \text{ is an ancestor of } w_j \\ &\leq l_{P(\text{parent}(w_{j-1}))}/2 && \text{by (7)} \\ &\leq l_{P(w_{j-2})}/2 && \text{since } w_{j-2} \text{ is an ancestor of } \text{parent}(w_{j-1}) \\ &\leq l_{P(\text{heavy}(\text{parent}(w_{j-2})))}/2, && \text{by (5)} \end{aligned}$$

for any $2 < j \leq \text{ldepth}(v)$. Let $l_i = l_{P(\text{heavy}(\text{parent}(w_i)))}$ for all i . To bound the sum in (4) we will use that $l_i \leq l_{i-2}/2$, $l_i < l_{i-1}$, and $l_{\text{ldepth}(v)} \geq 1$. We have

$$\sum_{i=1}^{\text{ldepth}(v)} \frac{1}{l_i} \leq 2 \sum_{i=2, i \text{ odd}}^{\text{ldepth}(v)} \frac{1}{l_i} \leq 2 \cdot 2 = 4,$$

since the l_i 's in the last sum are decreasing with a factor of 2. Combining this with Eq. (4) we get

$$\sum_{i=1}^{\text{ldepth}(v)} |\text{EMB}(\text{heavy}(\text{parent}(w_i)))| \leq l_T \sum_{i=1}^{\text{ldepth}(v)} \frac{1}{l_{P(\text{heavy}(\text{parent}(w_i)))}} \leq 4l_T. \quad \square$$

THEOREM 4.13. *For trees P and T the tree inclusion problem can be solved in $O(l_{PT})$ time and $O(n_T)$ space.*

PROOF. The time bound follows from Lemma 4.10. Next consider the space used by $\text{EMB}(\text{root}(P))$. The preprocessing of Section 4.1 uses only $O(n_T)$ space. By Lemma 4.12 the space used for the saved embeddings is $O(l_T) = O(n_T)$. \square

4.6. An Alternative Algorithm

In this section we present an alternative algorithm. Since the time complexity of the algorithm in the previous section is dominated by the time used by FL, we present an implementation of this procedure which leads to a different complexity. Define a *firstlabel data structure* as a data structure supporting queries of the form $\text{fl}(v, \alpha)$, $v \in V(T)$, $\alpha \in \Sigma$. Maintaining such a data structure is known as the *tree color problem*. This is a well-studied problem; see for example, Dietz [1989], Muthukrishnan and Müller [1996], Ferragina and Muthukrishnan [1996], and Alstrup et al. [1998]. With such a data structure available we can compute FL as follows.

$\text{FL}(X, \alpha)$: Return the list $\text{DEEP}([\text{fl}(X[1], \alpha), \dots, \text{fl}(X[|X|], \alpha)])$.

THEOREM 4.14. *Let P and T be trees. Given a firstlabel data structure using $s(n_T)$ space, $p(n_T)$ preprocessing time, and $q(n_T)$ time for queries, the tree inclusion problem can be solved in $O(p(n_T) + l_p l_T \cdot q(n_T))$ time and $O(s(n_T) + n_T)$ space.*

PROOF. Constructing the firstlabel data structures uses $O(s(n_T))$ space and $O(p(n_T))$ time. The total cost of the leaves is bounded by $O(l_p l_T \cdot q(n_T))$, since the cost of a single leaf is $O(l_T \cdot q(n_T))$. As in the proof of Theorem 4.13 we have that the total time used by the internal nodes is bounded by $\sum_{v \in V(P)} g(|\text{EMB}(v)|)$, where $g(n)$ is the time used by FL on a list of length n , that is, $g(n) \leq n \cdot q(n_T)$. By Lemma 4.8 and Lemma 4.12 for any leaf-to-root path $\delta = v_1, \dots, v_k$ in P , we have that $\sum_{u \in \delta} |\text{EMB}(u)| \leq O(l_T)$. Let Δ denote the set of all root-to-leaf paths in P . It follows that

$$\sum_{v \in V(P)} g(|\text{EMB}(v)|) \leq \sum_{p \in \Delta} \sum_{u \in p} g(|\text{EMB}(u)|) \leq \sum_{p \in \Delta} O(l_T \cdot q(n_T)) \leq O(l_p l_T \cdot q(n_T)).$$

Since this time is the same as the time spent at the leaves the time bound follows. \square

Several firstlabel data structures are available, for instance, if we want to maintain linear space we have the next lemma.

LEMMA 4.15. [DIETZ 1989]. *For any tree T there is a data structure using $O(n_T)$ space, $O(n_T)$ expected preprocessing time which supports firstlabel queries in $O(\log \log n_T)$ time.*

The expectation in the preprocessing time is due to perfect hashing. Since our data structure does not need to support efficient updates we can remove the expectation by using the deterministic dictionary of Hagerup et al. [2001]. This gives a worst-case preprocessing time of $O(n_T \log n_T)$. However, using a simple two-level approach this can be reduced to $O(n_T)$ (see, e.g., Thorup [2003]). Plugging in this data structure we obtain the next corollary.

COROLLARY 4.16. *For trees P and T the tree inclusion problem can be solved in $O(l_p l_T \log \log n_T + n_T)$ time and $O(n_T)$ space.*

5. A FASTER TREE INCLUSION ALGORITHM

In this section we present a new tree inclusion algorithm which has a worst-case subquadratic running time. As discussed in the Introduction, the general idea is to divide T into clusters of logarithmic size which we can efficiently preprocess and then use this to speed up the computation with a logarithmic factor.

5.1. Clustering

In this section we describe how to divide T into clusters and how the macro tree is created. For simplicity in the presentation we assume that T is a binary tree. If this is not the case it is straightforward to construct a binary tree B , where $n_B \leq 2n_T$, and a mapping $g : V(T) \rightarrow V(B)$ such that for any pair of nodes $v, w \in V(T)$, $\text{label}(v) = \text{label}(g(v))$, $v < w$ iff $g(v) < g(w)$, and $v \triangleleft w$ iff $g(v) \triangleleft g(w)$. The nodes in the set $U = V(B) \setminus \{g(v) \mid v \in V(T)\}$ are assigned a special label $\beta \notin \Sigma$. It follows that for any tree P , $P \sqsubseteq T$ iff $P \sqsubseteq B$.

Let C be a connected subgraph of T . A node in $V(C)$ adjacent to a node in $V(T) \setminus V(C)$ is a *boundary* node. The boundary nodes of C are denoted by δC . We have $\text{root}(T) \in \delta C$ if $\text{root}(T) \in V(C)$. A *cluster* of C is a connected subgraph of C with at most two boundary nodes. A set of clusters CS is a *cluster partition* of T iff $V(T) = \cup_{C \in CS} V(C)$, $E(T) = \cup_{C \in CS} E(C)$, and for any $C_1, C_2 \in CS$, $E(C_1) \cap E(C_2) = \emptyset$, $|E(C_1)| \geq 1$. If $|\delta C| = 1$ we call C a *leaf cluster* and otherwise an *internal cluster*.

We use the following recursive procedure $\text{CLUSTER}_T(v, s)$, adopted from Alstrup and Rauhe [2002], which creates a cluster partition CS of the tree $T(v)$ with the property that $|CS| = O(s)$ and $|V(C)| \leq \lceil n_T/s \rceil$ for each $C \in CS$. A similar cluster partitioning achieving the same result follows from Alstrup et al. [2000, 1997] and Frederickson [1997].

$\text{CLUSTER}_T(v, s)$: For each child u of v there are two cases.

- (1) $|V(T(u))| + 1 \leq \lceil n_T/s \rceil$. Let the nodes $\{v\} \cup V(T(u))$ be a leaf cluster with boundary node v .
- (2) $|V(T(u))| \geq \lceil n_T/s \rceil$. Pick a node $w \in V(T(u))$ of maximum depth such that $|V(T(u))| + 2 - |V(T(w))| \leq \lceil n_T/s \rceil$. Let the nodes $V(T(u)) \setminus V(T(w)) \cup \{v, w\}$ be an internal cluster with boundary nodes v and w . Recursively, compute $\text{CLUSTER}_T(w, s)$.

LEMMA 5.1. *Given a tree T with $n_T > 1$ nodes, and a parameter s , where $\lceil n_T/s \rceil \geq 2$, we can build a cluster partition CS in $O(n_T)$ time, such that $|CS| = O(s)$ and $|V(C)| \leq \lceil n_T/s \rceil$ for any $C \in CS$.*

PROOF. The procedure $\text{CLUSTER}_T(\text{root}(T), s)$ clearly creates a cluster partition of T and it is straightforward to implement in $O(n_T)$ time. Consider the size of the clusters created. There are two cases for u . In case 1, $|V(T(u))| + 1 \leq \lceil n_T/s \rceil$ and hence the cluster $C = \{v\} \cup V(T(u))$ has size $|V(C)| \leq \lceil n_T/s \rceil$. In case 2, $|V(T(u))| + 2 - |V(T(w))| \leq \lceil n_T/s \rceil$ and hence the cluster $C = V(T(u)) \setminus V(T(w)) \cup \{v, w\}$ has size $|V(C)| \leq \lceil n_T/s \rceil$.

Next consider the size of the cluster partition. Let $c = \lceil n_T/s \rceil$. We say that a cluster C is *bad* if $|V(C)| \leq c/2$ and *good* otherwise. We will show that at least a constant fraction of the clusters in the cluster partition are good. It is easy to verify that the cluster partition created by procedure CLUSTER has the following properties.

- (i) Let C be a bad internal cluster with boundary nodes v and w ($v < w$). Then w has two children with at least $c/2$ descendants each.
- (ii) Let C be a bad leaf cluster with boundary node v . Then the boundary node v is contained in a good cluster.

By (ii) the number of bad leaf clusters is at most twice the number of good internal clusters and by (i) each bad internal cluster has two child clusters. Therefore, the number of bad internal clusters is bounded by the number of leaf clusters. Let b_i and g_i denote the number of bad and good internal clusters, respectively, and let b_l and g_l denote the number of bad and good leaf clusters, respectively. We have

$$b_i \leq b_l + g_l \leq 2g_i + g_l,$$

and therefore the number of bad clusters is bounded by

$$b_l + b_i \leq 2g_i + g_l + 2g_i = 4g_i + g_l.$$

Thus the number of bad clusters is at most 4 times the number of good clusters, and therefore at most a constant fraction of the total number of clusters. Since a good cluster is of size more than $c/2$, there can be at most $2s$ good clusters and thus $|CS| = O(s)$. \square

Let $C \in CS$ be an internal cluster with $v, w \in \delta C$. The *spine path* of C is the path between v, w excluding v and w . A node on the spine path is a *spine node*. A node to the left and right of v or of any node on the spine path is a *left node* and *right node*, respectively. If C is a leaf cluster with $v \in \delta C$ then any proper descendant of v is a *leaf node*.

Let CS be a cluster partition of T as described in Lemma 5.1. We define an ordered *macro tree* M . Our definition of M may be viewed as an “ordered” version

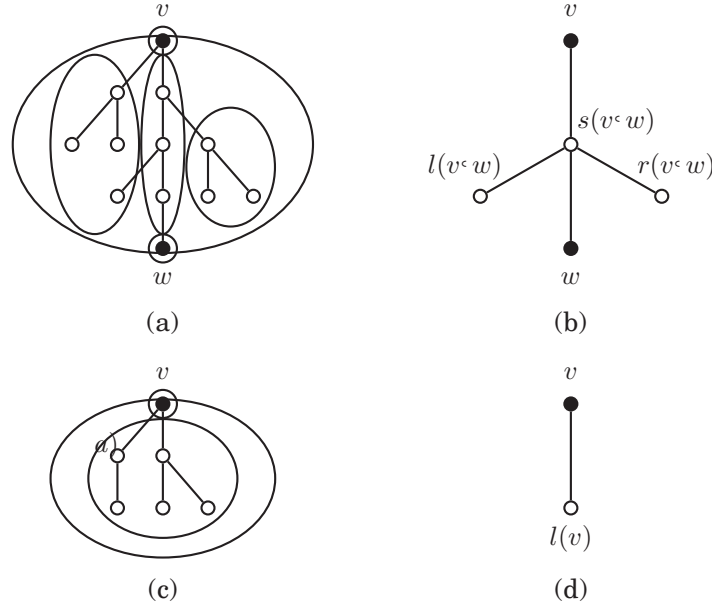


Fig. 7. The clustering and the macro tree. (a) An internal cluster. The black nodes are the boundary nodes and the internal ellipses correspond to the boundary nodes, the right and left nodes, and spine path. (b) The macro tree corresponding to the cluster in (a). (c) A leaf cluster. The internal ellipses are the boundary node and the leaf nodes. (d) The macro tree corresponding to the cluster in (c).

of the macro tree defined in Alstrup and Rauhe [2002]. The node set $V(M)$ consists of the boundary nodes in CS . Additionally, for each internal cluster $C \in CS$ with $v, w \in \delta C$, $v < w$, we have the nodes $s(v, w)$, $l(v, w)$ and $r(v, w)$ and edges $(v, s(v, w))$, $(s(v, w), l(v, w))$, $(s(v, w), w)$, and $(s(v, w), r(v, w))$. That is, the nodes $l(v, w)$, $r(v, w)$ and w are all children of $s(v, w)$. The nodes are ordered so that $l(v, w) < w < r(v, w)$. For each leaf cluster C , $v \in \delta C$, we have the node $l(v)$ and edge $(v, l(v))$. Since $\text{root}(T)$ is a boundary node, M is rooted at $\text{root}(T)$. Figure 7 illustrates these definitions.

With each node $v \in V(T)$ we associate a unique macro node denoted $c(v)$. Let $u \in V(C)$, where $C \in CS$.

$$c(u) = \begin{cases} u & \text{if } u \text{ is boundary node,} \\ l(v) & \text{if } u \text{ is a leaf node and } v \in \delta C, \\ s(v, w) & \text{if } u \text{ is a spine node, } v, w \in \delta C, \text{ and } v < w, \\ l(v, w) & \text{if } u \text{ is a left node, } v, w \in \delta C, \text{ and } v < w, \\ r(v, w) & \text{if } u \text{ is a right node, } v, w \in \delta C, \text{ and } v < w. \end{cases}$$

Conversely, for any macro node $i \in V(M)$ define the *micro forest*, denoted $C(i)$, as the induced subgraph of T of the set of nodes $\{v \mid v \in V(T), i = c(v)\}$. We also assign a *set* of labels to i given by $\text{label}(i) = \{\text{label}(v) \mid v \in V(C(i))\}$. If i is a spine node or a boundary node the unique node in $V(C(i))$ of greatest depth is denoted by $\text{first}(i)$. Finally, for any set of nodes $\{i_1, \dots, i_k\} \subseteq V(M)$ we define $C(i_1, \dots, i_k)$ as the induced subgraph of the set of nodes $V(C(i_1)) \cup \dots \cup V(C(i_k))$.

The following propositions state useful properties of ancestors, nearest common ancestor, and the left-to-right ordering in the micro forests and in T . The propositions follow directly from the definition of the clustering. See also Figure 8.

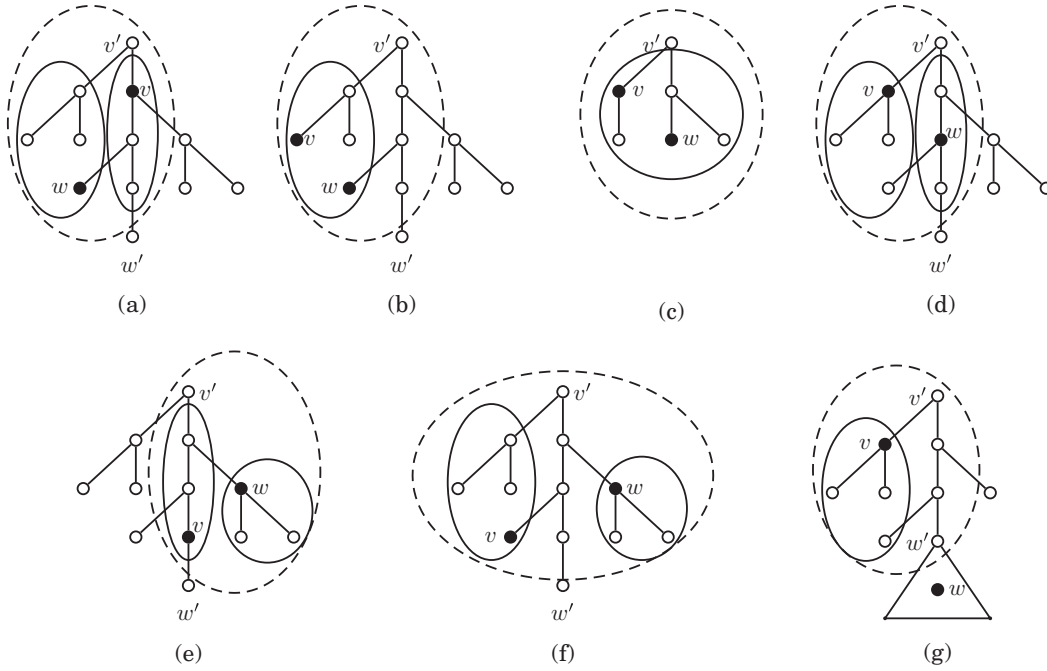


Fig. 8. Examples from the propositions. In all cases v' and w' are top and bottom boundary nodes of the cluster, respectively. (a) Proposition 5.2(ii). Here $c(v) = s(v', w')$ and $c(w) = l(v', w')$ (solid ellipses). The dashed ellipse corresponds to $C(c(w), s(v', w'), v')$. (b) Proposition 5.3(i) and 5.4(ii). Here $c(v) = c(w) = l(v', w')$ (solid ellipse). The dashed ellipse corresponds to $C(c(w), s(v', w'), v')$. (c) Proposition 5.3(ii) and 5.4(i). Here $c(v) = c(w) = l(v')$ (solid ellipse). The dashed ellipse corresponds to $C(c(v), v')$. (d) Proposition 5.3(iii). Here $c(v) = l(v', w')$ and $c(w) = s(v', w')$ (solid ellipses). The dashed ellipse corresponds to $C(c(v), c(w), v')$. (e) Proposition 5.3(iv). Here $c(v) = s(v', w')$ and $c(w) = r(v', w')$ (solid ellipses). The dashed ellipse corresponds to $C(c(v), c(w), v')$. (f) Proposition 5.4(iv). Here $c(v) = l(v', w')$ and $c(w) = r(v', w')$ (solid ellipses). The dashed ellipse corresponds to $C(c(v), c(w), s(v', w'), v')$. (g) Proposition 5.4(v). Here $c(v) = l(v', w')$ (solid ellipse) and $w' \preceq_M c(w)$. The dashed ellipse corresponds to $C(c(v), s(v', w'), v', w')$.

PROPOSITION 5.2 (ANCESTOR RELATIONS). *For any pair of nodes $v, w \in V(T)$, the following hold:*

- (i) *If $c(v) = c(w)$ then $v <_T w$ iff $v <_{C(c(v))} w$.*
- (ii) *If $c(v) \neq c(w)$, and for some boundary nodes v', w' we have $c(v) = s(v', w')$, and $c(w) \in \{l(v', w'), r(v', w')\}$, then $v <_T w$ iff $v <_{C(c(w), s(v', w'), v')} w$.*
- (iii) *In all other cases, $v <_T w$ iff $c(v) <_M c(w)$.*

Case (i) says that if v and w belong to the same macro node then v is an ancestor of w iff v is an ancestor of w in the micro forest for that macro node. Case (ii) says that if v is a spine node and w is a left or right node in the same cluster then v is an ancestor of w iff v is an ancestor of w in the micro tree induced by that cluster (Figure 8(a)). Case (iii) says that in all other cases v is an ancestor of w iff the macro node v belongs to is an ancestor of the macro node w belongs to in the macro tree.

PROPOSITION 5.3 (LEFT-OF RELATIONS). *For any pair of nodes $v, w \in V(T)$, the following hold:*

- (i) *If $c(v) = c(w) \in \{r(v', w'), l(v', w')\}$ for some boundary nodes v', w' , then $v \triangleleft w$ iff $v \triangleleft_{C(c(v), v', s(v', w'))} w$.*
- (ii) *If $c(v) = c(w) = l(v')$ for some boundary node v' , then $v \triangleleft w$ iff $v \triangleleft_{C(c(v), v')} w$.*

- (iii) If $c(v) = l(v', w')$ and $c(w) = s(v', w')$ for some boundary nodes v', w' , then $v \triangleleft w$ iff $v \triangleleft_{C(c(v), c(w), v')} w$.
- (iv) If $c(v) = s(v', w')$ and $c(w) = r(v', w')$ for some boundary nodes v', w' , then $v \triangleleft w$ iff $v \triangleleft_{C(c(v), c(w), v')} w$.
- (v) In all other cases, $v \triangleleft w$ iff $c(v) \triangleleft_{MC} c(w)$.

Case (i) says that if v and w are both either left or right nodes in the same cluster then v is to the left of w iff v is to the left of w in the micro tree induced by their macro node together with the spine and top boundary node of the cluster (Figure 8(b)). Case (ii) says that if v and w are both leaf nodes in the same cluster then v is to the left of w iff v is to the left of w in the micro tree induced by that leaf cluster (Figure 8(c)). Case (iii) says that if v is a left node and w is a spine node in the same cluster then v is to the left of w iff v is to the left of w in the micro tree induced by their two macro nodes and the top boundary node of the cluster (Figure 8(d)). Case (iv) says that if v is a spine node and w is a right node in the same cluster then v is to the left of w iff v is to the left of w in the micro tree induced by their two macro nodes and the top boundary node of the cluster (Figure 8(e)). In all other cases v is to the left of w if the macro node v belongs to is to the left of the macro node of w in the macro tree (Case (v)).

PROPOSITION 5.4 (NCA RELATIONS). *For any pair of nodes $v, w \in V(T)$, the following hold:*

- (i) If $c(v) = c(w) = l(v')$ for some boundary node v' , then $\text{nca}_T(v, w) = \text{nca}_{C(c(v), v)}(v, w)$.
- (ii) If $c(v) = c(w) \in \{l(v', w'), r(v', w')\}$ for some boundary nodes v', w' , then $\text{nca}_T(v, w) = \text{nca}_{C(c(v), s(v', w'), v)}(v, w)$.
- (iii) If $c(v) = c(w) = s(v', w')$ for some boundary nodes v', w' , then $\text{nca}_T(v, w) = \text{nca}_{C(c(v))}(v, w)$.
- (iv) If $c(v) \neq c(w)$ and $c(v), c(w) \in \{l(v', w'), r(v', w'), s(v', w')\}$ for some boundary nodes v', w' , then $\text{nca}_T(v, w) = \text{nca}_{C(c(v), c(w), s(v', w'), v)}(v, w)$.
- (v) If $c(v) \neq c(w)$, $c(v) \in \{l(v', w'), r(v', w'), s(v', w')\}$, and $w' \preceq_M c(w)$ for some boundary nodes v', w' , then $\text{nca}_T(v, w) = \text{nca}_{C(c(v), s(v', w'), v, w')}(v, w')$.
- (vi) In all other cases, $\text{nca}_T(v, w) = \text{nca}_M(c(v), c(w))$.

Case (i) says that if v and w are leaf nodes in the same cluster then the nearest common ancestor of v and w is the nearest common ancestor of v and w in the micro tree induced by that leaf cluster (Figure 8(c)). Case (ii) says that if v and w are both either left nodes or right nodes then the nearest common ancestor of v and w is the nearest common ancestor in the micro tree induced by their macro node together with the spine and top boundary node of the cluster (Figure 8(b)). Case (iii) says that if v and w are both spine nodes in the same cluster then the nearest common ancestor of v and w is the nearest common ancestor of v and w in the micro tree induced by their macro node. Case (iv) says that if v and w are in different macro nodes but are right, left, or spine nodes in the same cluster then the nearest common ancestor of v and w is the nearest common ancestor of v and w in the micro tree induced by that cluster (we can omit the bottom boundary node) (Figure 8(f)). Case (v) says that if v is a left, right, or spine node, and the bottom boundary node w' of v 's cluster is an ancestor in the macro tree of the macro node containing w , then the nearest common ancestor of v and w is the nearest common ancestor of v and w' in the micro tree induced by the macro node of v , the spine node, and the top and bottom boundary nodes of v 's cluster (Figure 8(g)). In all other cases the nearest common ancestor of v and w is the nearest common ancestor of their macro nodes in the macro tree (Case (vi)).

5.2. Preprocessing

In this section we describe how to preprocess T . First build a cluster partition CS of the tree T with clusters of size s , to be fixed later, and the corresponding macro tree M in $O(n_T)$ time. The macro tree is preprocessed as in Section 4.1. However, since nodes in M contain a set of labels, we now store a dictionary for $\text{label}(v)$ for each node $v \in V(M)$. Using the deterministic dictionary of Hagerup et al. [2001] all these dictionaries can be constructed in $O(n_T \log n_T)$ time and $O(n_T)$ space. Furthermore, we extend the definition of fl such that $\text{fl}_M(v, \alpha)$ is the nearest ancestor w of v such that $\alpha \in \text{label}(w)$.

Next we show how to preprocess the micro forests. For any cluster $C \in CS$, deep sets $X, Y, Z \subseteq V(C)$, $i \in \mathbb{N}$, and $\alpha \in \Sigma$ define the following procedures.

SIZE(X): Return the number of nodes in X .
LEFT(i, X): Return the leftmost i nodes in X .
RIGHT(i, X): Return the rightmost i nodes in X .
LEFTOF(X, Y): Return all nodes of X to the left of the leftmost node in Y .
RIGHTOF(X, Y): Return all nodes of X to the right of the rightmost node in Y .
MATCH(X, Y, Z), where $X = \{m_1 \triangleleft \dots \triangleleft m_k\}$, $Y = \{v_1 \triangleleft \dots \triangleleft v_k\}$, and $Z \subseteq Y$. Return $R := \{m_j \mid v_j \in Z\}$.
MOP(X, Y) Return the pair (R_1, R_2) , where $R_1 = \text{mop}(X, Y)|_1$ and $R_2 = \text{mop}(X, Y)|_2$.

If we want to specify that a procedure applies to a certain cluster C we add the subscript C . In addition to these procedures we also define the set procedures on clusters, that is, **PARENT**, **NCA**, **DEEP**, and **FL**, as in Section 3. Collectively, we will call these the *cluster procedures*. We represent the input and output sets in the procedures as bit strings indexed by preorder numbers. Specifically, a subset X in a cluster C is given by a bit string $b_1 \dots b_s$, such that $b_i = 1$ iff the i th node in a preorder traversal of C is in X . If C contains fewer than s nodes we set the remaining bits to 0.

The procedure **SIZE(X)** is the number of ones in the bit string. The procedure **LEFT(i, X)** corresponds to setting all bits in X larger than the i th set bit to zero. Similarly, **RIGHT(i, X)** corresponds to setting all bits smaller than the i th largest set bit to zero. Similarly, the procedures **LEFTOF(X, Y)**, **RIGHTOF(X, Y)**, **MOP(X, Y)**, and **MATCH(X, Y, Z)** only depend on the preorder of the nodes and thus only on the bit string and not any other information about the cluster.

Next we show how to implement the cluster procedures efficiently. We precompute the value of all procedures, except **FL**, for all possible inputs and clusters. By definition, these procedures do not depend on any specific labeling of the nodes in the cluster. Hence, it suffices to precompute the value for all rooted, ordered trees with at most s nodes. The total number of these is less than 2^{2s} (consider, e.g., an encoding using balanced parenthesis). Furthermore, the number of possible input sets is at most 2^s . Since at most 3 sets are given as input to a cluster procedure, it follows that we can tabulate all solutions using less than $2^{3s} \cdot 2^{2s} = 2^{5s}$ bits of memory. Hence, choosing $s \leq 1/10 \log n$ we use $O(2^{\frac{1}{2} \log n}) = O(\sqrt{n})$ bits. Using standard bitwise operations each solution is easily implemented in $O(s)$ time giving a total time of $O(\sqrt{n} \log n)$.

Since the procedure **FL** depends on the alphabet, which may be of size n_T , we cannot efficiently apply the same trick as before. Instead define for any cluster $C \in CS$, $X \subseteq V(C)$, and $\alpha \in \Sigma$:

ANCESTOR(X): Return the set $\{x \mid x \text{ is an ancestor of a node in } X\}$.
EQC(α): Return the set $\{x \mid x \in V(C), \text{label}(x) = \alpha\}$.

Clearly, ANCESTOR can be implemented as done earlier. For EQ_C note that the total number of distinct labels in C is at most s . Hence, EQ_C can be stored in a dictionary with at most s entries each of which is a bit string of length s . Thus, (using again the result of Hagerup et al. [2001]) the total time to build all such dictionaries is $O(n_T \log n_T)$.

By the definition of FL we have that

$$\text{FL}_C(X, \alpha) = \text{DEEP}_C(\text{ANCESTOR}_C(X) \cap \text{EQ}_C(\alpha)).$$

Since intersection can be implemented using a binary *and*-operation, $\text{FL}_C(X, \alpha)$ can be computed in constant time. Later, we will also need to compute union of sets represented as bit strings and we note that this can be done using a binary *or*-operation.

To implement the set procedures in the following section we often need to “restrict” the cluster procedures to work on a subtree of a cluster. Specifically, for any set of macro nodes $\{i_1, \dots, i_k\}$ in the *same* cluster C (hence, $k \leq 5$), we will replace the subscript C with $C(i_1, \dots, i_k)$. For instance, $\text{PARENT}_{C(s(v,w), l(v,w))}(X) = \{\text{parent}(x) \mid x \in X \cap V(C(s(v,w), l(v,w))) \cap V(C(s(v,w), l(v,w)))\}$. To implement all restricted versions of the cluster procedures, we compute for each cluster $C \in CS$ a bit string representing the set of nodes in each micro forest. Clearly, this can be done in $O(n_T)$ time. Since there are at most 5 micro forests in each cluster it follows that we can compute any restricted version using an additional constant number of and-operations.

Note that the total preprocessing time and space is dominated by the construction of deterministic dictionaries which use $O(n_T \log n_T)$ time and $O(n_T)$ space.

5.3. Implementation of the Set Procedures

Using the preprocessing from the previous section we show how to implement the set procedures in sublinear time. First we define a compact representation of node sets. Let T be a tree with macro tree M . For simplicity, we identify nodes in M with a number almost equal to their preorder number, which we denote their *macro tree number*: All nodes nodes except spine and left nodes are identified with their preorder number. Spine nodes are identified with their preorder number +1 if they have a left node as a child and with their preorder number otherwise, and left nodes are identified with their preorder number -1. Hence, we swap the order of left and spine nodes in the macro tree numbering. We will explain the reason for using macro tree numbers shortly. Note that the macro tree numbers are the same as the preorder numbers would be if we had let $l(v, w)$ and $r(v, w)$ be children of v instead of children of $s(v, w)$ in the definition of the macro tree.

Let $S \subseteq V(T)$ be any subset of nodes of T . A *micro-macro node array* (abbreviated node array) X representing S is an array of size n_M . The i th entry, denoted $X[i]$, represents the subset of nodes in $C(i)$, that is, $X[i] = V(C(i)) \cap S$. The set $X[i]$ is encoded using the same bit representation as in Section 5.2. By our choice of parameter in the clustering the space used for this representation is $O(n_T / \log n_T)$.

We can now explain the reason for using macro tree numbers to identify the nodes instead of preorder numbers. Consider a node array representing a deep set. If a left node and the corresponding spine node are both nonempty, then all nodes in the left node are to the left of the node in the spine node. Formally, we have the next proposition.

PROPOSITION 5.5. *Consider a node array X representing a deep set \mathcal{X} . For any pair of nodes $v, w \in \mathcal{X}$, such that $v \in X[i]$ and $w \in X[j]$, $i \neq j$, we have*

$$v \triangleleft w \Leftrightarrow i < j.$$

PROOF. By Proposition 5.3(v) the claim is true for $i \triangleleft j$. The remaining cases are $i = l(v', w')$ and $j = s(v', w')$ (Proposition 5.3 (iii)) and $i = s(v', w')$ and $j = r(v', w')$

(Proposition 5.3(iv)). In both cases $i < j$ and it follows immediately that $v \triangleleft w \Rightarrow i < j$. For the other direction, it follows from the structure of the macro tree that in both cases either $v \triangleleft w$ or $w \triangleleft v$. But \mathcal{X} is deep and thus $v \triangleleft w$. \square

Thus, by using macro tree numbers we encounter the nodes in X according to their preorder number in the original tree T . This simplifies the implementation of all the procedures except DEEP, since they all get deep sets as input.

We now present the detailed implementation of the set procedures on node arrays. As in Section 4 we assume that the input to all of the procedures, except DEEP, represent a deep set. Let X be a node array.

Implementation of PARENT. Procedure PARENT takes a node array X representing a deep set as input.

Procedure PARENT(X)

```

1 Initialize an empty node array  $R$  of size  $n_M$  ( $R[i] := \emptyset$  for  $i = 1, \dots, n_M$ ) and set  $i := 1$ .
2 while  $i \leq n_M$  do
3   while  $X[i] = \emptyset$  do  $i := i + 1$ .
4   There are three cases depending on the type of  $i$ :
5   case 1.  $i \in \{l(v, w), r(v, w)\}$ 
6     Compute  $N := \text{PARENT}_{C(i, s(v, w), v)}(X[i])$ .
7     foreach  $j \in \{i, s(v, w), v\}$  do
8        $R[j] := R[j] \cup (N \cap V(C(j)))$ .
9     end
10
11  case 2.  $i = l(v)$ 
12    Compute  $N := \text{PARENT}_{C(i, v)}(X[i])$ .
13    foreach  $j \in \{i, v\}$  do
14       $R[j] := R[j] \cup (N \cap V(C(j)))$ .
15    end
16
17  case 3.  $i \notin \{l(v, w), r(v, w), l(v)\}$ 
18    Compute  $N := \text{PARENT}_{C(i)}(X[i])$ .
19    if  $N \neq \emptyset$  then
20      set  $R[i] := R[i] \cup N$ .
21    else if  $j := \text{parent}_M(i) \neq \perp$  then
22      set  $R[j] := R[j] \cup \{\text{first}(j)\}$ .
23    end
24  Set  $i := i + 1$ .
25 end
26 Return  $R$ .
```

Procedure PARENT has three cases. Case 1 handles the fact that left or right nodes may have a node on a spine or the top boundary node as parent. Since no left or right nodes can have their parent outside their cluster there is no need to compute parents in the macro tree. Case 2 handles the fact that a leaf node may have the boundary node as parent. Since no leaf node can have its parent outside its cluster there is no need to compute parents in the macro tree. Case 3 handles boundary and spine nodes. In this case there is either a parent within the micro forest or we can use the macro tree to compute the parent of the root of the micro tree. Since the input to PARENT is deep we only need to do one of the two things. If the computation of parent in the micro tree returns a nonempty set, this set is added to the output (line 18). Otherwise (the returned set is empty), we compute parent of i in the macro tree (line 19). If the computation of parent in the macro tree returns a node j , this will either be a spine

node or a boundary node. To take care of the case where j is a spine node, we add the lowest node ($\text{first}(j)$) in j to the output (line 20). If j is a boundary node this is just j itself.

Implementation of NCA. We now give the implementation of procedure NCA. The input to procedure NCA is two node arrays X and Y representing two subsets $\mathcal{X}, \mathcal{Y} \subseteq V(T)$, $|\mathcal{X}| = |\mathcal{Y}| = k$. The output is a node array R representing the set $\text{DEEP}(\{\text{nca}(\mathcal{X}_i, \mathcal{Y}_i) \mid 1 \leq i \leq k\})$, where \mathcal{X}_i and \mathcal{Y}_i is the i th element of \mathcal{X} and \mathcal{Y} , with respect to their preorder number in the tree, respectively. We also assume that we have $\mathcal{X}_i \triangleleft \mathcal{Y}_i$ for all i (since NCA is always called on a set of minimum ordered pairs). Note, that \mathcal{X}_i and \mathcal{Y}_i can belong to different clusters/nodes in the macro tree, that is, we might have $\mathcal{X}_i \in X[i]$ and $\mathcal{Y}_i \in Y[j]$ where $i \neq j$.

Procedure NCA(X, Y)

```

1 Initialize an empty node array  $R$  of size  $n_M$ , set  $i := 1$  and  $j := 1$ .
2 while  $i \leq n_M$  and  $j \leq n_M$  do
3   while  $X[i] = \emptyset$  do  $i := i + 1$ .
4   while  $Y[j] = \emptyset$  do  $j := j + 1$ .
5   Set  $n := \min(\text{SIZE}(X[i]), \text{SIZE}(Y[j]))$ ,  $X_i := \text{LEFT}(n, X[i])$ , and  $Y_j := \text{LEFT}(n, Y[j])$ .
6   Compare  $i$  and  $j$ . There are two cases:
7   case 1.  $i = j$ .
8     Set
          
$$S := \begin{cases} C(i, v), & \text{if } i = l(v), \\ C(i, s(v, w), v), & \text{if } i \in \{l(v, w), r(v, w)\}. \end{cases}$$

9     Compute  $N := \text{NCA}_S(X_i, Y_j)$ .
10    foreach macro node  $h = c(s)$  where  $s \in V(S)$  do
11      | set  $R[h] := R[h] \cup (N \cap V(C(h)))$ .
12    end
13
14  case 2.  $i \neq j$ .
15    Compute  $h := \text{NCA}_M(i, j)$ . There are two subcases:
16    case (a)  $h$  is a boundary node
17      | Set  $R[h] := 1$ .
18    case (b)  $h$  is a spine node  $s(v, w)$ 
19      | There are three subcases:
20      | case i.  $i \in \{l(v, w), s(v, w)\}$  and  $j \in \{s(v, w), r(v, w)\}$ 
21      | | Compute  $N := \text{NCA}_{C(i, j, s(v, w), v)}(X_i, Y_j)$ .
22      |
23      | case ii.  $i = l(v, w)$  and  $w \leq j$ 
24      | | Compute  $N := \text{NCA}_{C(i, s(v, w), v, w)}(\text{RIGHT}(1, X_i), w)$ .
25      | case iii.  $j = r(v, w)$  and  $w \leq i$ 
26      | | Compute  $N := \text{NCA}_{C(j, s(v, w), w, v)}(w, \text{LEFT}(1, Y_j))$ .
27      |
28      | Set  $R[h] := R[h] \cup (N \cap V(C(h)))$  and  $R[v] := R[v] \cup (N \cap V(C(v)))$ .
29
30    Set  $X[i] := X[i] \setminus X_i$  and  $Y[j] := Y[j] \setminus Y_j$ .
31 end
32 Return  $\text{DEEP}(R)$ .

```

In the main loop of procedure NCA (line 2–27) we first find the next nonempty entries in the node arrays $X[i]$ and $Y[j]$ (line 3 and 4). We then compare the sizes of $X[i]$ and $Y[j]$ and construct two sets of equal sizes X_i and Y_j consisting of the $\min(\text{SIZE}(X[i]), \text{SIZE}(Y[j]))$ leftmost nodes from $X[i]$ and $Y[j]$ (line 5). In Section 5.4 we

prove the following invariant on X_i and Y_j .

$$\text{LEFT}(1, X_i) = \mathcal{X}_l \text{ and } \text{LEFT}(1, Y_j) = \mathcal{Y}_l \text{ for some } l.$$

The procedure has two main cases.

- If $i = j$ (Case 1), then i is either a leaf, left, or right node due to the invariant and the assumption on the input that $\mathcal{X}_i \triangleleft \mathcal{Y}_i$ (for a formal proof see Section 5.4). If i is a leaf node the nearest common ancestors of all pairs in X_i and Y_j are in the leaf node or the boundary node. If i is a left or right node the nearest common ancestors of all the pairs are in i , on the spine, or in the top boundary node. In line 9 we compute NCA in the appropriate cluster depending on the type of i .
- If $i \neq j$ (Case 2), we first compute the nearest common ancestor h of i and j in the macro tree (line 14). Due to the structure of the macro tree h is either a spine node or a boundary node (left, right, and leaf nodes have no descendants). If h is a boundary node all pairs in X_i and Y_j have the same nearest common ancestor, namely h (Case 2(a)). If h is a spine node there are three cases depending on the types of i and j .

In Case 2(b)(i), we have $i = l(v, w)$ and $j \in \{s(v, w), r(v, w)\}$ (see Figure 8(d) and (f)), or $i = s(v, w)$ and $j = r(v, w)$ (see Figure 8(e)). In this case we compute NCA in the cluster containing $i, j, s(v, w), v$.

In Case 2(b)(ii), i is a left node $l(v, w)$ and j is a (not necessarily proper) descendant of w (see Figure 8(g)). In this case we compute NCA on the rightmost node in X_i and w in the cluster containing $i, v, w, s(v, w)$. We can restrict the computation to $\text{RIGHT}(1, X_i)$ because we always run DEEP on the output from NCA before using it in any other computation and all nearest common ancestors of the pairs in X_i and Y_j will be on the spine, and the deepest one will be the nearest common ancestor of the rightmost nodes in X_i and Y_j (see Section 5.4 for a formal proof).

Case 2(b)(iii) is similar to Case 2(b)(ii).

In the end of the iteration we have computed the nearest common ancestors of all the pairs in X_i and Y_j and the nodes from these pairs are removed from $X[i]$ and $Y[j]$.

Implementation of DEEP. The implementation of DEEP resembles the previous implementation, but takes advantage of the fact that the input list is in macro tree order.

The procedure DEEP has three cases. In case 1 node i is to the right of our “potential output node” j . Since any node l that is a descendant of j must be to the left of i ($l < i$) it cannot appear later in the list X than i . We can thus safely add $\text{DEEP}_S(X[j])$ to R at this point. To ensure that the cluster we compute DEEP on is a tree we include the top boundary node if j is a leaf node and the top and spine node if j is a left or right node. We add the result to R and set i to be our new potential output node.

In case 2 node j is an ancestor of i and therefore no node from $C(j)$ can be in the output list unless j is a spine node and i is the corresponding right node. If this is the case we compute DEEP of $X[j]$ and $X[i]$ in the cluster containing i and j and add the result for j to the output and set i to be our new potential output node.

In case 3 node i is an ancestor of j . This can only happen if j is a left node and i the corresponding spine node. We compute DEEP of $X[j]$ and $X[i]$ in the cluster containing i and j and add the result for j to the output. We restrict $X[i]$ to the nodes both in $X[i]$ and the result N of the DEEP computation, and let i be our potential output node. The results for $X[i]$ cannot be added directly to the input since there might be nodes later in the input that are descendants of i . Since a left node has no children we can safely add the result for j to the output.

After iterating through the whole node array X we add the last potential node j to the output after computing DEEP of it as in Case 1.

Procedure DEEP(X)

```

1 Initialize an empty node array  $R$  of size  $n_M$ .
2 Find the smallest  $j$  such that  $X[j] \neq \emptyset$ . If no such  $j$  exists stop. Set  $i := j + 1$ .
3 while  $i \leq n_M$  do
4   while  $X[i] = \emptyset$  do  $i := i + 1$ .
5   Compare  $j$  and  $i$ . There are three cases:
6   case 1.  $j < i$ .
7     Set
           
$$S := \begin{cases} C(j, v), & \text{if } j = l(v), \\ C(j, s(v, w), v), & \text{if } j \in \{l(v, w), r(v, w)\}, \\ C(j), & \text{otherwise.} \end{cases}$$

8     Set  $R[j] := \text{DEEP}_S(X[j])$ .
9   case 2.  $j < i$ .
10    if  $j = s(v, w)$  and  $i = r(v, w)$  then
11      compute  $N := \text{DEEP}_{C(r(v, w), s(v, w), v)}(X[i] \cup X[j])$ .
12      Set  $R[j] := X[j] \cap N$ .
13    end
14  case 3.  $i < j$  (can happen if  $i = s(v, w)$  and  $j = l(v, w)$ ).
15    Compute  $N := \text{DEEP}_{C(l(v, w), s(v, w), v)}(X[i] \cup X[j])$ .
16    Set  $R[j] := X[j] \cap N$ ,  $X[i] := X[i] \cap N$ .
17    Set  $j := i$  and  $i := i + 1$ .
18 end
19 Set  $R[j] := \text{DEEP}_S(X[j])$ , where  $S$  is set as in Case 1.
20 Return  $R$ .
```

Implementation of MOPRIGHT. We now give the implementation of procedure MOPRIGHT. Procedure MOPRIGHT takes a pair of node arrays (X, Y) and another node array Z as input. The pair (X, Y) represents a set of minimum ordered pairs, where the first coordinates are in X and the second coordinates are in Y . To simplify the implementation of procedure MOPRIGHT it calls two auxiliary procedures MOPSIM and MATCH defined shortly. Procedure MOPSIM computes mop of Y and Z , and procedure MATCH computes the first coordinates from X corresponding to the first coordinates from the minimum ordered pairs of Y and Z computed by MOPSIM.

Procedure MOPRIGHT($(X, Y), Z$)

```

1 Compute  $M := \text{MOPSIM}(Y, Z)$ .
2 Compute  $R := \text{MATCH}(X, Y, M|_1)$ .
3 Return  $(R, M|_2)$ .
```

Procedure MOPSIM takes two node arrays as input and computes mop of these.

Procedure MOPSIM is somewhat similar to the previous implementation of the procedure MOPRIGHT from Section 4.2. As in the previous implementation we have a “potential pair” $((r_1, r_2), (s_1, s_2))$, where r_1 and s_1 are macro nodes, $r_2 \subseteq X[r_1]$, $s_2 \subseteq Y[s_1]$, where $r_2 = \{r^1 \triangleleft \dots \triangleleft r^k\}$ and $s_2 = \{s^1 \triangleleft \dots \triangleleft s^k\}$ such that $r^l \triangleleft s^l$ for $l = 1, \dots, k$. Furthermore, for any l there exists no node $y \in Y[j]$, for $j < s_1$, such that $r^l \triangleleft y \triangleleft s^l$ and no node $x \in X[i]$, for $i < r_1$, such that $r^l \triangleleft x \triangleleft s^l$.

We have the following invariant at the beginning of each iteration.

$$\nexists x \in X[i], \text{ such that } x \triangleleft x', \text{ for any } x' \in r_2 \quad (8)$$

Procedure MOPSIM(X, Y)

```

1 Initialize two empty node arrays  $R$  and  $S$  of size  $n_M$ .
2 Set  $i := 1, j := 1, (r_1, r_2) := (0, \emptyset), (s_1, s_2) := (0, \emptyset)$ .
3 repeat
4   while  $X[i] = \emptyset$  do set  $i := i + 1$ .
5   There are four cases:
6   case I.  $i = l(v, w)$  for some  $v, w$ .
7     | Until  $Y[j] \neq \emptyset$  and either  $i \triangleleft j, i = j$ , or  $j = s(v, w)$  do set  $j := j + 1$ .
8   case II.  $i = s(v, w)$  for some  $v, w$ .
9     | Until  $Y[j] \neq \emptyset$  and either  $i \triangleleft j$  or  $j = r(v, w)$  do set  $j := j + 1$ .
10  case III.  $i \in \{r(v, w), l(v)\}$  for some  $v, w$ .
11    | Until  $Y[j] \neq \emptyset$  and either  $i \triangleleft j$  or  $i = j$  do set  $j := j + 1$ .
12  case IV.  $i$  is a boundary node.
13    | Until  $Y[j] \neq \emptyset$  and  $i \triangleleft j$  do set  $j := j + 1$ .
14
15  Compare  $i$  and  $j$ . There are two cases:
16  case 1.  $i \triangleleft j$ .
17    | if  $s_1 < j$  then
18      | set  $R[r_1] := R[r_1] \cup r_2, S[s_1] := S[s_1] \cup s_2$ , and  $(s_1, s_2) := (j, \text{LEFT}_{C(j)}(1, Y[j]))$ .
19    | end
20    | Set  $(r_1, r_2) := (i, \text{RIGHT}_{C(i)}(1, X[i]))$  and  $i = i + 1$ .
21
22  otherwise // case 2.
23    | Compute  $(r, s) := \text{MOP}_{C(i,j,v)}(X[i], Y[j])$ , where  $v$  is the top boundary node in the
24    | cluster  $i$  and  $j$  belong to.
25    | if  $r \neq \emptyset$  then
26      | if  $s_1 < j$  or if  $s_1 = j$  and  $\text{LEFT}_{C(i,j)}(X[i], s_2) = \emptyset$  then
27        | set  $R[r_1] := R[r_1] \cup r_2, S[s_1] := S[s_1] \cup s_2$ .
28      | end
29      | Set  $(r_1, r_2) := (i, r)$  and  $(s_1, s_2) := (j, s)$ .
30    | end
31    | There are two subcases:
32    | case (a)  $i = j$ , or  $i = l(v, w)$  and  $j = s(v, w)$ .
33    |   | Set  $X[i] := \text{RIGHT}_{C(i)}(1, \text{RIGHT}_{C(i)}(X[i], r))$  and  $j := j + 1$ .
34    | case (b)  $i = s(v, w)$  and  $j = r(v, w)$ .
35    |   | if  $r = \emptyset$  then set  $j := j + 1$  else set  $i := j$ .
36  endsw
37 until  $i > n_M$  or  $j > n_M$ ;
38 Set  $R[r_1] := R[r_1] \cup r_2$  and  $S[s_1] := S[s_1] \cup s_2$ .
39 Return  $(R, S)$ .
```

We first find the next nonempty macro node i . We then have 4 cases depending on which kind of node i is.

In Case I, i is a left node. Due to Proposition 5.3 we can have mop in i (case (i), see Figure 8(b)), in the spine (case (iii), see Figure 8(d)), or in a node to the right of i (case(v)).

In Case II, i is a spine node. Due to Proposition 5.3 we can have mop in the right node (case (iv), see Figure 8(e)) or in a node to the right of i (case(v)).

In Case III, i is a right node or a leaf node. Due to Proposition 5.3 we can have mop in i (case (i) and (ii), see Figure 8(b)–(c)) or in a node to the right of i (case(v)).

In Case IV, i must be a boundary node and mop must be in a node to the right of i .

We then compare i and j . The case where $i \triangleleft j$ is similar to the previous implementation of the procedure. We compare j with our potential pair (line 16). If $s_1 < j$ then $s_1 \triangleleft j$ since the input is deep, and we can insert r_2 and s_2 into our output node arrays R and S , respectively. We also set s_1 to j and s_2 to the leftmost node in $Y[j]$ (if $s_1 = j$ we already have $(s_1, s_2) = (j, \text{LEFT}_{C(j)}(1, Y[j]))$). Then—both if $s_1 \triangleleft j$ or $s_1 = j$ —we set r_1 to i and r_2 to the rightmost node in $X[i]$ (line 19). That we only need the rightmost node in $X[i]$ and the leftmost node in $Y[j]$ follows from the definition of `mop` and the structure of the macro tree.

Case 2 ($i \not\triangleleft j$) is more complicated. In this case we first compute `mop` in the cluster i and j belong to (line 21). If this results in any minimum ordered pairs ($r \neq \emptyset$) we must update our potential pair (line 22–27). Otherwise we leave the potential pair as it is and only update i and j . If $r \neq \emptyset$ we compare s_1 and j (line 23). As in Case 1 of the procedure we add our potential pair to the output and update the potential pair with r and s if $s_1 < j$, since this implies $s_1 \triangleleft j$. If $s_1 = j$ and no nodes in $X[i]$ are to the left of the leftmost node in s_2 we also add the potential pair to the output and update it. We show in the next section that in this case $|s_2| = 1$. Therefore we can safely add the potential pair to the output. In all other cases the pair $(r, s) \neq (\emptyset, \emptyset)$ shows a contradiction to our potential pair and we update the potential pair without adding anything to the output.

Finally, in Case 2, we update $X[i]$, i , and j (line 28–32). There are two cases depending on i and j . In Case (a) either $i = j$ or i is a left node and j is the corresponding spine node. In both cases we can have nodes in $X[i]$ that are not to the left of any node in $Y[j]$. These nodes could be in a minimum ordered pair with nodes from another macro node. We show in the next section that this can only be true for the rightmost node in $X[i]$. $X[i]$ is updated accordingly. After this update all nodes in $Y[j]$ are to the left of all nodes in $X[i]$ in the next iteration and therefore j is incremented. In Case (b) i is a spine node and j is the corresponding right node. Since the input lists are deep, there is only one node in $X[i]$. If $r = \emptyset$ then no node in $Y[j]$ is to the right of the single node in $X[i]$. Since the input arrays are deep, no node later in the array X can be to the left of any node in $Y[j]$ and we therefore increment j . If $r \neq \emptyset$ then $(r_1, r_2) = (i, X[i])$ and we update i . Instead of incrementing i by one we set $i := j$, this is correct since all macro nodes with macro node number between i and j are descendants of i , and thus contains no nodes from X , since X is deep.

When reaching the end of one of the arrays we add our potential pair to the output and return (line 35–36).

As in Section 4.2 we can implement `MOPLEFT` similarly to `MOPRIGHT`.

Recall that procedure `MOPRIGHT` calls `MATCH` to find the first coordinates from X corresponding to the first coordinates from the minimum ordered pairs computed by `MOPSIM`. Procedure `MATCH` takes three node arrays X , Y , and Y' representing deep sets \mathcal{X} , \mathcal{Y} , and \mathcal{Y}' , where $|\mathcal{X}| = |\mathcal{Y}|$, and $\mathcal{Y}' \subseteq \mathcal{Y}$. The output is a node array representing the set $\{\mathcal{X}_j \mid \mathcal{Y}_j \in \mathcal{Y}'\}$.

Procedure `MATCH` proceeds as follows. First we find the first nonempty entries in the two node arrays $X[i]$ and $Y[j]$ (line 4–5). We then compare $Y[j]$ and $Y'[j]$ (line 7).

If they are equal we keep all nodes in X with the same rank as the nodes in $Y[j]$ (case 1). We do this by splitting into three cases. If there are the same number of nodes $X[i]$ and $Y[j]$ we add all nodes in $X[i]$ to the output and increment i and j (case 1(a)). If there are more nodes in $Y[j]$ than in $X[i]$ we add all nodes in $X[i]$ to the output and update $Y[j]$ and $Y'[j]$ to contain only the $y - x$ leftmost nodes in $Y[j]$ (case 1(b)). We then increment i and iterate. If there are more nodes in $X[i]$ than in $Y[j]$ we add the first y nodes in $X[i]$ to the output, increment j , and update $X[i]$ to contain only the nodes we did not add to the output (case 1(c)).

If $Y[j] \neq Y'[j]$ we call the cluster procedure `MATCH` (case 2). Again we split into three cases depending on the number of nodes in $X[i]$ and $Y[j]$. If they have the same number

of nodes we can just call `MATCH` on $X[i]$, $Y[j]$, and $Y'[j]$ and increment i and j (case 2(a)). If $\text{SIZE}(Y[j]) > \text{SIZE}(X[i])$ we call `match` with $X[i]$ the leftmost $\text{SIZE}(X[i])$ nodes of $Y[j]$ and with the part of $Y'[j]$ that are a subset of these leftmost $\text{SIZE}(X[i])$ nodes of $Y[j]$ (case 2(b)). We then update $Y[j]$ and $Y'[j]$ to contain only the nodes we did not use in the call to `MATCH` and increment i . If $\text{SIZE}(Y[j]) < \text{SIZE}(X[i])$ we call `MATCH` with the leftmost $\text{SIZE}(Y[j])$ nodes of $X[i]$, $Y[j]$, and $Y'[j]$ (case 2(c)). We then update $X[i]$ to contain only the nodes we did not use in the call to `MATCH` and increment j .

Procedure `MATCH`(X, Y, Y')

```

1 Initialize an empty node array  $R$  of size  $n_M$ .
2 Set  $X_L := \emptyset, Y_L := \emptyset, Y'_L := \emptyset, x := 0, y := 0, i := 1$  and  $j := 1$ .
3 repeat
4   while  $X[i] = \emptyset$  do set  $i := i + 1$ .
5   while  $Y[j] = \emptyset$  do set  $j := j + 1$ .
6   Set  $x := \text{SIZE}(X[i])$  and  $y := \text{SIZE}(Y[j])$ .
7   Compare  $Y[j]$  and  $Y'[j]$ . There are two cases:
8   case 1.  $Y[j] = Y'[j]$ 
9     Compare  $x$  and  $y$ . There are three subcases:
10    case (a)  $x = y$ .
11      Set  $R[i] := R[i] \cup X[i], i := i + 1$ , and  $j := j + 1$ .
12
13    case (b)  $x < y$ .
14      Set  $R[i] := R[i] \cup X[i], Y[j] := \text{RIGHT}(y - x, Y[j]), Y'[j] := Y[j]$ , and  $i := i + 1$ .
15
16    case (c)  $x > y$ .
17      Set  $X_L := \text{LEFT}(y, X[i]), R[i] := R[i] \cup X_L, X[i] := X[i] \setminus X_L$ , and  $j := j + 1$ .
18
19  case 2.  $Y[j] \neq Y'[j]$ 
20    Compare  $x$  and  $y$ . There are three subcases:
21    case (a)  $x = y$ .
22      Set  $R[i] := R[i] \cup \text{MATCH}(X[i], Y[j], Y'[j]), i := i + 1$ , and  $j := j + 1$ .
23
24    case (b)  $x < y$ .
25      Set  $Y_L := \text{LEFT}(x, Y[j]), Y'_L := Y'[j] \cap Y_L, R[i] := R[i] \cup \text{MATCH}(X[i], Y_L, Y'_L)$ ,
26       $Y[j] := Y[j] \setminus Y_L, Y'[j] := Y'[j] \setminus Y'_L$ , and  $i := i + 1$ .
27
28    case (c)  $x > y$ .
29      Set  $X_L := \text{LEFT}(y, X[i]), R[i] := R[i] \cup \text{MATCH}(X_L, Y[j], Y'[j])$ ,
30       $X[i] := X[i] \setminus X_L$ , and  $j := j + 1$ .
31
32
33 until  $i > n_M$  or  $j > n_M$ ;
34 Return  $R$ .
```

Implementation of FL. Procedure `FL` takes as input a node array X representing a deep set and a label α .

The `FL` procedure is similar to `PARENT`. The cases 1, 2 and 3 compute `FL` on a micro forest. If the result is within the micro tree we add it to R and otherwise we store in a node list L the node in the macro tree which contains the parent of the root of the micro forest. Since we always call `DEEP` on the output from `FL`(X, α) there is no need to compute `FL` in the macro tree if N is nonempty. We then compute `FL` in the macro tree on the list L , store the results in a list S , and use this to compute the final result.

Consider the cases of procedure `FL`. In case 1 i is a left or right node. Due to Proposition 5.2 case (i) and (ii) fl of a node in i can be in i or on the spine or in the top boundary

node. If this is not the case it can be found by a computation of FL of the parent of the top boundary node of i 's cluster in the macro tree (Proposition 5.2 case (iii)). In case 2 i is a leaf node. Then fl of a node in i must either be in i , in the top boundary node, or can be found by a computation of FL of the parent of the top boundary node of i 's cluster in the macro tree. If i is a spine node or a boundary node (case 3), then fl of a node in i is either in i or can be found by a computation of FL of the parent of i in the macro tree.

Procedure $\text{FL}(X, \alpha)$

```

1  q Initialize an empty node array  $R$  of size  $n_M$  and two node lists  $L$  and  $S$ .
2  repeat
3    while  $X[i] = \emptyset$  do set  $i := i + 1$ .
4    There are three cases depending on the type of  $i$ :
5    case 1.  $i \in \{l(v, w), r(v, w)\}$ 
6      Compute  $N := \text{FL}_{C(i, s(v, w), v)}(X[i], \alpha)$ .
7      if  $N \neq \emptyset$  then
8        |   foreach  $j \in \{i, s(v, w), v\}$  do set  $R[j] = R[j] \cup (N \cap V(C(j)))$ .
9      else set  $L := L \circ \text{parent}_M(v)$ .
10   case 2.  $i = l(v)$ 
11     Compute  $N := \text{FL}_{C(i, v)}(X[i], \alpha)$ .
12     if  $N \neq \emptyset$  then
13       |   foreach  $j \in \{i, v\}$  do set  $R[j] := R[j] \cup (N \cap V(C(j)))$ .
14     else set  $L := L \circ \text{parent}_M(v)$ .
15   case 3.  $i \notin \{l(v, w), r(v, w), l(v)\}$ 
16     Compute  $N := \text{FL}_{C(i)}(X[i], \alpha)$ .
17     if  $N \neq \emptyset$  then
18       |   set  $R[i] := R[i] \cup N$ .
19     else set  $L := L \circ \text{parent}_M(i)$ .
20
21  until  $i > n_M$ ;
22  Compute the list  $S := \text{FL}_M(L, \alpha)$ .
23  foreach node  $i \in S$  do set  $R[i] := R[i] \cup \text{FL}_{C(i)}(\text{first}(i), \alpha)$ .
24  Return  $\text{DEEP}(R)$ .
```

5.4. Correctness of the Set Procedures

The following lemmas show that the set procedures are correctly implemented.

LEMMA 5.6. *Procedure PARENT is correctly implemented.*

PROOF. We will prove that in iteration i the procedure correctly computes the parents of all nodes in the macro node i . There are four cases depending on the type of i .

- Consider the case $i \in \{l(v, w), r(v, w)\}$, that is, i is a left or right node. For all nodes x in $C(i)$, $\text{parent}(x)$ is either in $C(i)$, on the spine $s(v, w)$, or is the top boundary node v . The parents of all input nodes in $C(i)$ is thus in N computed in Case 1 in the procedure. The last line in Case 1 (“For each $j \in \{i, s(v, w), v\}, \dots$ ”) adds the set of parents to the appropriate macro node in the output array.
- If i is a leaf node $l(v)$ then for any node $x \in C(i)$, $\text{parent}(x)$ is either in $C(i)$ or is the boundary node v . The parents of all input nodes in $C(i)$ is thus in N computed in Case 2 in the procedure. The last line in Case 2 (“For each $j \in \{i, v\}, \dots$ ”) adds the set of parents to the appropriate macro node in the output array.
- If i is a spine node $s(v, w)$ then the input contains at most one node in $C(i)$, since the input to the procedure is deep. For any $x \in C(i)$, $\text{parent}(x)$ is either a node on the spine or the top boundary node v . This is handled by Case 3 in the procedure. Let x be the node in $X[i]$. If $\text{parent}(x) = v$, then $N = \emptyset$, and we compute j , which is the parent

v of i in the macro tree, and add j to the output array (since $j = v$ is a boundary node $\text{first}(j) = v$). If $\text{parent}(x)$ is another node y on the spine, then $N = \{y\} \neq \emptyset$ and y is added to the output array.

- If i is a boundary node v , then $\text{parent}(v)$ is either another boundary node v' , the bottom node on a spine, or \perp if v is the root. This is handled by Case 3 in the procedure. In all three cases $N = \emptyset$ and we compute the parent j of i in the macro tree. If i is the root, then $j = \perp$ and we do nothing. Otherwise, we add $\text{first}(j)$ to the output. If $\text{parent}(v)$ is a boundary node then $\text{first}(j) = j$. If j is a spine node then $\text{first}(j)$ is the bottom node on j .

In each iteration of the procedure we might add nodes to the output, but we never delete anything written to the output in earlier iterations. Procedure PARENT thus correctly computes the parents of all nodes in X . \square

Before proving the correctness of procedure NCA we will prove the following invariant on the variables X_i and Y_j in the procedure.

LEMMA 5.7. *In procedure NCA we have the following invariant of X_i and Y_j :*

$$\text{LEFT}(1, X_i) = \mathcal{X}_l \text{ and } \text{LEFT}(1, Y_j) = \mathcal{Y}_l \text{ for some } l.$$

PROOF. The proof is by induction on the number of iterations of the outer loop. After the while loop on X in the first iteration (line 3), i is the smallest integer such that $X[i] \neq \emptyset$. Due to the macro tree order of the array X , $X[i]$ contains the first nodes from X with respect to the preorder of the original tree (Proposition 5.5). Similarly, $Y[j]$ contains the leftmost node in \mathcal{Y} . The invariant now follows immediately from the assignment of X_i and Y_j .

For the induction step consider iteration m and let i' and j' be the values of i and j after the while loops in the previous iteration, that is, after line 4. By the induction hypothesis $\text{LEFT}(1, X_{i'}) = \mathcal{X}_l$ and $\text{LEFT}(1, Y_{j'}) = \mathcal{Y}_l$ for some l . Let $n' = \min(\text{SIZE}(X[i']), \text{SIZE}(Y[j']))$. Then $X_{i'}$ contains $\mathcal{X}_l, \dots, \mathcal{X}_{l+n'}$ and $Y_{j'}$ contains $\mathcal{Y}_l, \dots, \mathcal{Y}_{l+n'}$. We will show that $\text{LEFT}(1, X_i) = \mathcal{X}_{l+n'+1}$. In the end of the previous iteration we removed $X_{i'}$ from $X[i']$ (line 26). There are two cases depending on whether $X[i']$ is empty or not at the beginning of iteration m .

- If $X[i'] \neq \emptyset$ then it clearly contains $\mathcal{X}_{l+n'+1}$ as its leftmost node. Since a spine node can only contain one node from \mathcal{X} , i' cannot be a spine node. Thus $i = i'$, when we get to line 5 in the current iteration it follows that $\text{LEFT}(1, X_i) = \mathcal{X}_{l+n'+1}$.
- $X[i'] = \emptyset$. It follows from the macro tree order of X that $X[i]$ contains $\mathcal{X}_{l+n'+1}$ as its leftmost node.

It follows by a similar argument that $\text{LEFT}(1, Y_j) = \mathcal{Y}_{l+n'+1}$. \square

LEMMA 5.8. *Let X and Y be two node arrays representing the deep sets \mathcal{X} and \mathcal{Y} , $|\mathcal{X}| = |\mathcal{Y}| = k$, and let \mathcal{X}_i and \mathcal{Y}_i denote the i th element of \mathcal{X} and \mathcal{Y} , with respect to their preorder number in the tree, respectively. For all $i = 1, \dots, k$, assume $\mathcal{X}_i \triangleleft \mathcal{Y}_i$. Procedure NCA(X, Y) correctly computes $\text{DEEP}(\{\text{nca}(\mathcal{X}_i, \mathcal{Y}_i) \mid 1 \leq i \leq k\})$.*

PROOF. We are now ready to show that the procedure correctly takes care of all possible cases from Proposition 5.4. The proof is split into two parts. First we will argue that some of the cases from the proposition cannot occur during an iteration of the outer loop of NCA. Afterwards we prove that the procedure takes care of all the cases that can occur.

Case (iii) cannot happen since if $i = j$ is a spine node then \mathcal{X}_i is either a descendant or an ancestor of \mathcal{Y}_i contradicting the assumption on the input that $\mathcal{X}_i \triangleleft \mathcal{Y}_i$. Case (vi) can only happen if $i \neq j$: If $i = j$ and we are in case (vi) then $i = j$ is a boundary node,

and this would imply that $C(i)$ only consists of one node, that is, $\mathcal{X}_i = X[i] = Y[j] = \mathcal{Y}_i$ contradicting the assumption on the input that $\mathcal{X}_i \triangleleft \mathcal{Y}_i$. Due to this assumption on the input we also have that in case (iv) of the proposition i is either a left node or a spine node and j is a spine node or a right node. For case (v) either i is a left node and j is a descendant of the bottom boundary node of i 's cluster or j is a right node and i is a descendant of the bottom boundary node of j 's cluster. All the other cases from case (v) would contradict the assumption that $\mathcal{X}_i \triangleleft \mathcal{Y}_i$.

The procedure first constructs two sets X_i and Y_j containing the elements $\mathcal{X}_l, \dots, \mathcal{X}_{l+n}$ and $\mathcal{Y}_l, \dots, \mathcal{Y}_{l+n}$ for some l , respectively, where $n = \min(\text{SIZE}(X[i]), \text{SIZE}(Y[j]))$. The procedure NCA has two main cases depending on whether $i = j$ or not. Case 1 ($i = j$) takes care of cases (i)–(ii) from Proposition 5.4. Case 2 ($i \neq j$) takes care of the remaining cases from Proposition 5.4 (iv)–(vi) that can occur.

First consider Case 1. We compute nearest common ancestors N of the n nodes in X_i and Y_j in a cluster S depending on what kind of node i is. We need to show that Case 1 handles Case (i) and (ii) from the Proposition correctly.

Case (i). $i = j$ is a leaf node. By the Proposition the nearest common ancestors of the pairs in $(\mathcal{X}_l, \mathcal{Y}_l), \dots, (\mathcal{X}_{l+n}, \mathcal{Y}_{l+n})$ from X_i and Y_j is either in $c(i)$ or in the boundary node, that is, in $C(i, v)$.

Case (ii). $i = j$ is a left or right node. By the Proposition the nearest common ancestors of the pairs in $\{(\mathcal{X}_l, \mathcal{Y}_l), \dots, (\mathcal{X}_{l+n}, \mathcal{Y}_{l+n})\}$ from X_i and Y_j is either in $c(i)$, on the spine, or in the top boundary node, that is, in $C(i, s(v, w), v)$.

Thus S is correctly set in both cases. After the computation of N in line 9 the output is then added to the entries in the output array R for each of the macro nodes belonging to nodes in $V(S)$ (line 10–12). Case 1 thus handles Case (i)–(ii) (and only these two cases) from Proposition 5.4.

Next consider Case 2 ($i \neq j$). We first compute the nearest common ancestor h of i and j in the macro tree. The macro node h is either a boundary node or a spine node due to the structure of the macro tree (see also Proposition 5.4). We will show that Case 2 takes care of the remaining cases.

Case (iv). From the previous discussion it follows that we have one of the three following cases. $i = l(v, w)$ and $j = s(v, w)$, $i = l(v, w)$ and $j = r(v, w)$, or $i = s(v, w)$ and $j = r(v, w)$. All three cases are handled in Case 2(b)(i) of the procedure. It follows from the proposition that NCA is computed in the correct cluster.

Case (v). It follows from the discussion preceding that either $i = l(v, w)$ and $w \leq j$, or $j = r(v, w)$ and $w \leq i$. These two cases are handled by Case 2(b)(ii) and 2(b)(iii) of the procedure. It follows from the Proposition that NCA is computed in the correct cluster. We need to argue that we can restrict the computation of NCA to the pair $(\text{RIGHT}(1, X_i), w)$ instead of computing NCA for all nodes in $\{\mathcal{X}_l, \dots, \mathcal{X}_{l+n}\}$. Consider the case where $i = l(v, w)$ and $w \leq j$ (Case 2(b)(ii) of the procedure). Since $w \leq \mathcal{Y}_r$ for all $r = l, \dots, l+n$, and $\mathcal{X}_l \triangleleft \mathcal{X}_{l+1} \triangleleft \dots \triangleleft \mathcal{X}_{l+n}$, then $\text{nca}(\mathcal{X}_r, \mathcal{Y}_r) \leq \text{nca}(\mathcal{X}_{l+n}, \mathcal{Y}_{l+n})$ for all $r = l, \dots, l+n$. Thus we do not need to compute $\text{nca}(\mathcal{X}_r, \mathcal{Y}_r)$ for $r \neq n+l$, since the output of the procedure is $\text{DEEP}(\{\text{nca}(\mathcal{X}_i, \mathcal{Y}_i) \mid 1 \leq i \leq k\})$. A similar argument shows that we can restrict the computation to $(w, \text{LEFT}(1, Y_j))$ in Case 2(b)(iii).

Case (vi). It follows from the preceding discussion and the proposition that $i \neq j$ and i and j are in different clusters, and we are not in any of the cases from (iv) and (v). Thus h must be a boundary node and all the pairs $\{(\mathcal{X}_l, \mathcal{Y}_l), \dots, (\mathcal{X}_{l+n}, \mathcal{Y}_{l+n})\}$ have the same nearest common ancestor, namely h . This is handled by Case 2(a).

We have now argued that the procedure correctly takes care of all possible cases from Proposition 5.4. It remains to show that all pairs from $\{\text{nca}(\mathcal{X}_i, \mathcal{Y}_i) \mid 1 \leq i \leq k\}$ are considered during the computation. It follows from the invariant that we only consider

pairs from the input. In the last lines we remove the nodes from the input that we have computed the ncas of in this iteration. It follows from the proof of the invariant that no entry in the input arrays is left nonempty. Thus all pairs are taken care of. \square

To prove that procedure DEEP is correctly implemented we will use the following fact about preorder and postorder numbers in the macro tree.

PROPOSITION 5.9. *Let i and j be nodes in the macro tree identified by their macro tree number such that $i < j$. For all $x \in C(i)$, $y \in C(j)$ we have:*

- (1) $\text{pre}(x) < \text{pre}(y)$ unless $i = l(v, w)$ and $j = s(v, w)$.
- (2) $\text{post}(y) > \text{post}(x)$ unless $i = s(v, w)$ and $j = r(v, w)$.

PROPOSITION 5.10. *Let x_1, \dots, x_n be nodes from the macro tree associated with their macro tree number such that $x_1 < x_2 < \dots < x_n$. If $x_i \triangleleft x_j$ for some i and j then $x_i \triangleleft x_k$ for all $x_k > x_j$.*

PROOF. From $x_i \triangleleft x_j$ we have $\text{pre}(x_i) < \text{pre}(x_j)$ and $\text{post}(x_i) < \text{post}(x_j)$. Since $x_k > x_j$ we have $\text{pre}(x_j) < \text{pre}(x_k)$ unless $x_k = s(v, w)$ and $x_j = l(v, w)$. In that case, $\text{pre}(x_k) + 1 = \text{pre}(x_j) > \text{pre}(x_i)$. Since $x_i \triangleleft x_j$ we have $x_i \neq x_j$ and thus $\text{pre}(x_k) > \text{pre}(x_i)$.

It remains to show that $\text{post}(x_i) < \text{post}(x_k)$. Assume for the sake of contradiction that $\text{post}(x_k) < \text{post}(x_i) < \text{post}(x_j)$. This implies $x_i < x_k$ and $x_j < x_k$ contradicting $x_i \triangleleft x_j$. \square

We will first prove the following invariants on i and j in procedure DEEP.

LEMMA 5.11. *In line 5 of procedure DEEP we have the following invariant on i and j : For all l such that $j < l < i$ we have $X[l] = \emptyset$.*

PROOF. Let i' be the value of i in line 5 of the previous iteration of the outer loop (line 3–18). Then i is the smallest index greater than i' such that the corresponding entry in X is nonempty. This is true since i was set to $i' + 1$ in the end of the previous iteration (line 17), and in line 4 of this iteration i was incremented until we found a nonempty entry. Since $j = i'$ (this was also set in line 17 of the previous iteration), i is the first nonempty entry greater than j and the claim follows. \square

LEMMA 5.12. *At the beginning of each iteration of the main loop of procedure DEEP (line 3) we have the following invariant on j : For all nodes $x \in X[j]$ and $y \in X[l]$, where $1 \leq l < j$, we have $x \not< y$.*

PROOF. Recall that $x < y \Leftrightarrow \text{pre}(x) < \text{pre}(y)$ and $\text{post}(y) < \text{post}(x)$. By Proposition 5.9 the only case where we can have $\text{pre}(x) < \text{pre}(y)$ is if $l = l(v, w)$ and $j = s(v, w)$ for some v, w . Assume this is the case. If $X[l] = \emptyset$ the claim follows trivially. Otherwise, let i' and j' be the values of i and j in the previous iteration, respectively (since $l < j$ and $X[l] \neq \emptyset$ there must be such an iteration). We have $j = l + 1$, $i' = j = s(v, w)$ and $j' = l = l(v, w)$. Thus in the previous iteration the procedure entered case 3, where $X[i']$ was set to $X[i'] \cap \text{DEEP}_{C(l(v,w),s(v,w),v)}(X[i'] \cup X[j'])$, and thus $X[j]$ contains no nodes that are ancestors of nodes in $X[j'] = X[l]$. \square

LEMMA 5.13. *Procedure DEEP is correctly implemented.*

PROOF. We will prove that $x \in \text{DEEP}(X)$ iff $x \in X$ and there exists no $y \in X$ such that $x < y$.

Assume $x \in \text{DEEP}(X)$. Consider the iteration when x is assigned to the output. There are three cases depending on which case we are in when x is added to the input. If $j \triangleleft i$ (Case 1 of the procedure) then $x \in \text{DEEP}_S(X[j])$ and it follows from the invariant on j (Lemma 5.12) that x has no descendants in any nodes $y \in X[l]$, $l < j$. For $j < l < i$ the claim follows directly from Lemma 5.11. It remains to show that x has no descendants

in $X[l]$ for $l \geq i$. By Proposition 5.10 we have $j \triangleleft l$ for all $l > i$ and the claim follows from Proposition 5.2.

If $j < i$ (Case 2 of the procedure) then j is a spine node $s(v, w)$ and i is the corresponding right node $r(v, w)$, and we compute $N := \text{DEEP}_{C(r(v,w),s(v,w),v)}(X[i] \cup X[j])$. Since $x \in \text{DEEP}(X)$ we have $x \in R[j] = X[j] \cap N$. It follows from the invariant (Lemma 5.12) and the computation of N that x has no descendants in $X[l]$ for any $l \leq j$. For $l > j$ it follows from the structure of the macro tree that for any $l > i$ we have $j \triangleleft l$. For $j < l < i$ the claim follows directly from Lemma 5.11. The claim follows from Proposition 5.2. For $j < l < i$ the claim follows directly from Lemma 5.11.

If $i < j$ (Case 3 of the procedure) then i is a spine node $s(v, w)$ and j is the corresponding left node $l(v, w)$, and we compute $N := \text{DEEP}_{C(l(v,w),s(v,w),v)}(X[i] \cup X[j])$. Since $x \in \text{DEEP}(X)$ we have $x \in R[j] = X[j] \cap N$. It follows from the computation of N that x has no descendants in $X[i] \cup X[j]$. Since $l(v, w)$ has no descendants in the macro tree it follows from Proposition 5.2 that x has no descendants in $X[l]$ for any $l \neq j$.

If x is assigned to the output in line 19 then it follows from the invariant on j (Lemma 5.12) and the computation of $\text{DEEP}_S(X[j])$ that x has no descendants in X .

For the other direction let $x \in X$ be a node such that $X \cap V(T(x)) = \{x\}$. Let l be the index such that $x \in X[l]$. All nonempty entries in X are i in line 5 at some iteration. Consider the iteration when $i = l$. Unless $i = l(v, w)$ and $j = s(v, w)$ (Case 3 of the procedure) $X[i]$ is not changed in this iteration. If we are in Case 3, then N is computed and $X[i]$ is set to $X[i] \cap N$. Since x has no descendants in X we have $x \in N$ and thus $x \in X[i]$ after the assignment. At the end of this iteration j is set to i . Consider the next iteration when $j = l$. If $j \triangleleft i$ or $i > n_M$ then $x \in \text{DEEP}_S(X[j]) = R[j]$. If $j < i$ we have $j = s(v, w)$ and $i = r(v, w)$ since x has no descendants in X . For the same reason we have $x \in N$ and thus $x \in X[j] \cap N = R[j]$. If $i < j$ we have $i = s(v, w)$ and $j = l(v, w)$. Again $x \in N$ and thus $x \in X[j] \cap N = R[j]$. \square

We now consider procedures `MOPSIM` and `MATCH`.

LEMMA 5.14. *Let $((r_1, r_2), (s_1, s_2))$ be as defined in procedure `MOPSIM`. Then r_1 and s_1 are macro nodes, $r_2 \subseteq X[r_1]$, $s_2 \subseteq Y[s_1]$, where $r_2 = \{r^1 \triangleleft \dots \triangleleft r^k\}$ and $s_2 = \{s^1 \triangleleft \dots \triangleleft s^k\}$. For any $l = 1, \dots, k$ we have:*

- (1) $r^l \triangleleft s^l$,
- (2) for all $j \leq s_1$ there exists no node $y \in Y[j]$ such that $r^l \triangleleft y \triangleleft s^l$,
- (3) for all $i \leq r_1$ there exists no node $x \in X[i]$ such that $r^l \triangleleft x \triangleleft s^l$.

PROOF. It follows immediately from the code that r_1 and s_1 are macro nodes and that $r_2 \subseteq X[r_1]$, $s_2 \subseteq Y[s_1]$, where $r_2 = \{r^1 \triangleleft \dots \triangleleft r^{k_1}\}$ and $s_2 = \{s^1 \triangleleft \dots \triangleleft s^{k_2}\}$. Due to the macro tree order of the tree and the fact that X represents a deep set, no node in $X[i]$ can be to the right of any node in $X[r_1]$ for $i < r_1$. To prove condition 3 it is thus enough to prove it for $i = r_1$. We proceed by induction on the number k of iterations of the outer loop (line 3–34). We consider the time right after the k th iteration of the loop, that is, right before the $(k + 1)$ th iteration. The base case ($k = 0$) is trivially satisfied.

For the induction step let i^* and j^* be the values of i and j at line 14 in iteration k . Let r'_i and s'_i for $i = 1, 2$ be the values of r_i and s_i , respectively, after the $(k - 1)$ th round. There are 3 cases.

- $r'_2 = r_2$ and $s'_2 = s_2$: the claim follows directly from the induction hypothesis.
- $r'_2 \neq r_2$ and $s'_2 = s_2$: condition 2 from the lemma follows directly from the induction hypothesis. Since s_2 and thus also s_1 were not changed, r_2 was set in case 1 of the procedure and $j^* = s_1$. Therefore, $i^* \triangleleft j^*$, $r_1 = i^*$, and $|r_2| = 1$. Let $r_2 = \{r^1\}$ and $s_2 = \{s^1\}$. We have $r_1 = i^* \triangleleft j^* = s_1$ and thus $r^1 \triangleleft s^1$ satisfying condition 1 from the lemma. To prove condition 3 is satisfied we only have to consider the case $i = r_1$.

Since r_2 was set in case 1 of the procedure, r^1 is the rightmost node in $X[r_1]$ and it follows immediately that there exists no node $x \in X[r_1]$ such that $r^1 \triangleleft x \triangleleft s^1$.

— $r'_2 \neq r_2$ and $s'_2 \neq s_2$: We first prove condition 1 and 3. If the potential pair was set in case 1 (line 15–19) of the procedure then $r_1 = i^* \triangleleft j^* = s_1$ and $|r_2| = 1$ implying $r^1 \triangleleft s^1$ (condition 1). The node r^1 is the rightmost node in $X[r_1]$ (line 19) and it follows that there exists no node $x \in X[r_1]$ such that $r^1 \triangleleft x \triangleleft s^1$ proving condition 3. If the potential pair was set in case 2 then both condition 1 and 3 follows from the correctness of the implementation of mop and the computation $(r, s) = \text{mop}_{C(i,j,v)}(X[i^*], Y[j^*]) = \text{mop}_{C(i,j,v)}(X[i^*], Y[s_1])$ in line 21.

Let $y \in Y[j]$, for $j \leq s_1$, be a node such that $y \notin s_2$. To prove condition 2 is satisfied we will show that r^l is not to the left of y . There are two cases

— $j = s_1$. Since $s'_2 \neq s_2$ there are two cases depending on which case of the procedure the potential pair was set in. If the potential pair was set in case 2 of the procedure the claim follows from the correctness of the implementation of mop and the computation $(r, s) = \text{mop}_{C(i,j,v)}(X[i^*], Y[j^*]) = \text{mop}_{C(i,j,v)}(X[i^*], Y[s_1])$ in line 21.

If the potential pair was set in case 1, then $r_1 = i^* \triangleleft j^* = s_1$. Since $s_2 \neq s'_2$, s_2 was changed in the k th iteration and is therefore the leftmost node in $Y[s_1]$ (line 17). The claim follows.

— $j < s_1$. We will use that we just proved the claim for $j = s_1$. Assume for the sake of contradiction that there exists a $y \in Y[j]$ such that $r^l \triangleleft y$. Since Y is representing a deep set and due to the macro tree order of Y this implies $r^l \triangleleft y \triangleleft y'$ for all $y' \in Y[s_1]$ contradicting that the claim is true for $j = s_1$. \square

LEMMA 5.15. *We have the following invariant at the beginning of each iteration of the main loop (line 3) of MOPSIM:*

$$\nexists x \in X[i], \text{ such that } x \triangleleft x', \text{ for any } x' \in r_2.$$

PROOF. By induction on the number of iterations of the outer loop. In the base case $r_2 = \emptyset$ and the condition is trivially satisfied. Note that X is representing a deep set and thus either $x \triangleleft x'$ or $x' \triangleleft x$ for all $x \in X[i]$. For the induction step let i' , j' , and r'_2 be the values of i , j , and r_2 respectively in the iteration before this. By the induction hypothesis $x' \triangleleft x$ for all $x \in X[i']$ and $x' \in r'_2$. Due to the macro tree order of X and the fact that X represents a deep set, all nodes in $X[i']$ are to the left of all nodes in $X[i]$. Thus, if $r_2 = r'_2$ it follows from the induction hypotheses that $x' \triangleleft x$ for all $x \in X[i]$ and $x' \in r'_2 = r_2$. For $r'_2 \neq r_2$ there are two cases: If $i' \triangleleft j'$ then $r_2 = \text{RIGHT}_{C(i')}(1, X[i'])$ and $i > i'$ and thus the condition is satisfied. Otherwise r_2 was set in case 2 of the procedure. Since $r_2 \neq r'_2$ we have $r_2 = r \subseteq X[i']$ and $r \neq \emptyset$. There are two subcases: If $i = j$ or $i = l(v, w)$ and $j = s(v, w)$ (Case 2(a) of the procedure) then $X[i]$ either contains a single node, which is the rightmost of the nodes in $X[i']$ that are to the right of all nodes in r_2 or if there are no such nodes $X[i] = \emptyset$. In both cases the condition is satisfied. If $i = s(v, w)$ and $j = r(v, w)$ then $i > i'$ and the condition is satisfied. \square

LEMMA 5.16. *Procedure MOPSIM is correctly implemented.*

PROOF. Let \mathcal{X} and \mathcal{Y} be the sets represented by X and Y , respectively. Let $R = \text{MOPSIM}(X, Y)|_1$ and $S = \text{MOPSIM}(X, Y)|_2$. For simplicity we will slightly abuse the notation and write $(x, y) \in \text{MOPSIM}(X, Y)$ iff there exists an i such that $x \in R[i]$ and $y \in S[i]$. We want to show that

$$(x, y) \in \text{MOPSIM}(X, Y) \Leftrightarrow (x, y) \in \text{mop}(\mathcal{X}, \mathcal{Y}).$$

Assume $(x, y) \in \text{MOPSIM}(X, Y)$. Consider the round where x and y were added to R and S , respectively. We have $x = r^l \in r_2$ and $y = s^l \in s_2$. We want to show that there is no node $x' \in X[i]$ for any i such that $x \triangleleft x' \triangleleft y$ and no node $y' \in Y[j]$ for any j such that $x \triangleleft y' \triangleleft y$. By Lemma 5.14 this is true for $i \leq r_1$ and $j \leq s_1$. By the macro tree order of Y we have that $y \triangleleft y'$ for any $y' \in Y[j]$ when $j > s_1$. Let i' be the value of i in the round where x and y is added to the output. We will show that no node in $X[i']$ is to the left of any node in s_2 . Due to the macro tree order of X this implies that no node in $X[i]$ is to the left of any node in s_2 for any $i \geq i'$. If $i' = r_1$ then it follows directly from Lemma 5.14. If $i' > r_1$ it follows from the implementation of the procedure that i' is the first nonempty entry in X greater than r_1 . Thus the claim follows for any j . We now return to show that no node in $X[i']$ is to the left of any node in s_2 . There are two cases depending on whether $j = s_1$ or $j > s_1$. If $j > s_1$ then j was changed either in one of the four cases I–IV, or in the previous iteration in case 2. If j was equal to s_1 at the beginning of this iteration then j was incremented in one of the four cases I–IV. Thus none of the cases applied to s_1 . By Proposition 5.3 no node in $X[i']$ can be to the left of a node in $X[s_1]$. Since $s_2 \subseteq X[s_1]$ the claim follows. If $j = s_1$ it follows from case 2 that $\text{LEFT}(X[i'], s_2) = \emptyset$ (otherwise the potential pairs would not have been added to the output in this iteration) and the claim follows immediately.

Now assume $(x, y) \in \text{mop}(\mathcal{X}, \mathcal{Y})$. We will deal with each of the cases from Proposition 5.3 separately.

- (1) Case (i): $c(x) = c(y) = r(v, w)$.
- (2) Case (i): $c(x) = c(y) = l(v, w)$.
- (3) Case (ii): $c(x) = c(y) = l(v)$.
- (4) Case (iii): $c(x) = l(v, w)$ and $c(y) = s(v, w)$.
- (5) Case (iv): $c(x) = s(v, w)$ and $c(y) = r(v, w)$.
- (6) Case (v): $c(x) = l(v, w)$ and $c(y) = r(v, w)$.
- (7) Case (v): $c(x) \triangleleft c(y)$ and $c(x)$ and $c(y)$ belong to different clusters.

Note that if $c(x) \triangleleft c(y)$ then x is the rightmost node in $X[c(x)]$ and y is the leftmost node in $Y[c(y)]$. We first show that in all cases we will have $x = r^l \in r_2$ and $y = s^l \in s_2$ for some l at some iteration. Consider the first iteration where either $x \in X[i]$ or $y \in Y[j]$. Let i' and j' be the values of i and j , respectively, in this iteration. There are three cases.

Case (a). $x \in X[i']$ and $y \in Y[j']$. For case 1–5 the procedure goes into case 2. From the correctness of MOP we get $x \in r$ and $y \in s$. Thus $r \neq \emptyset$ and we set $(r_1, r_2) = (i', r)$ and $(s_1, s_2) = (j', s)$ and the claim follows. For case 6–7 the procedure goes into case 1. Since this iteration is the first where $y \in Y[j']$ we have $j' > s_1$ and we set $(r_1, r_2) = (i', \text{RIGHT}_{C(i)}(1, X[i']))$ and $(s_1, s_2) = (j', \text{LEFT}_{C(j)}(1, Y[j']))$. Since x is the rightmost node in $X[i']$ and y is the leftmost node in $Y[c(j')]$ the claim follows.

Case (b). $x \in X[i']$ and $y \notin Y[j']$. Since $(x, y) \in \text{mop}(\mathcal{X}, \mathcal{Y})$ this implies $j' < c(y)$ and there exists no node $y' \in Y[j']$ such that $x \triangleleft y'$. Assume that there existed such a y' . Then $x \triangleleft y' \triangleleft y$ due to the macro tree order of Y contradicting $(x, y) \in \text{mop}(\mathcal{X}, \mathcal{Y})$. Thus $i' \not\triangleleft j'$. From case I–IV of the procedure it follows that either $i' = j'$, $i' = l(v, w)$ and $j' = s(v, w)$, or $i' = s(v, w)$ and $j' = r(v, w)$. From this and $j' < c(y)$ it follows that we are in case 4 or 7 from before.

The procedure enters case 2 in this iteration. If we are in case 4 then $i' = l(v, w) = j'$ and $c(y) = s(v, w)$. If $r = \emptyset$ then $i = i'$, $X[i']$ is unchanged, and $j = j' + 1 = s(v, w) = c(y)$ at the end of this iteration. If $r \neq \emptyset$ then x must be to the right of all nodes in $x' \in r$. Assume that there is a $x' \in r$ such that $x \triangleleft x'$. Since $x' \in r$ there exists a node $y' \in s$ such that $x' \triangleleft y' \triangleleft y$. That $y' \triangleleft y$ follows from $y' \in l(v, w)$ and $y \in s(v, w)$ and the assumption that \mathcal{Y} is deep. Thus $x \triangleleft x' \triangleleft y' \triangleleft y$ contradicting that $(x, y) \in \text{mop}(\mathcal{X}, \mathcal{Y})$. Therefore,

$i = i'$, $x \in X[i']$ and $j = j' + 1 = s(v, w) = c(y)$ at the end of this iteration. From case I of the procedure and the analysis of case (a) it follows that $x = r^l \in r_2$ and $y = s^l \in s_2$ for some l .

Now assume we are in case 7. By the same argument as before $i = i'$, $x \in X[i]$, and $j > j'$ at the end of this iteration. Unless $i' = l(v, w) = j'$ this implies that $i < j$ at line 14 (“Compare i and j ”) in the next iteration. If $i' = l(v, w) = j'$ then either $i < j$ after the first loop in the next iteration (line 7), and the claim follows as before, or $i = l(v, w)$ and $j = s(v, w)$. In the last case we get into case (b) again, but it follows from the analysis that in the iteration after the next we will have $i < j = c(y)$. The claim follows from the analysis of case (a).

Case (c). $x \notin X[i']$ and $y \in Y[j']$. It follows by inspection of the cases that unless we are in case 1 we have $i' < j'$. If we are in case 1 ($j' = c(x) = r(v, w) = c(y)$) we have either $i' < j'$ or $i' = s(v, w)$. First we consider the cases 2–7. Since $i' < j'$ the procedure enters case 1 in this iteration. Thus i is incremented and j stays the same. This happens until $i = c(x)$. Now consider case 1. If $i' < j'$ the procedure enters case 1 in this iteration. Thus i is incremented and j stays the same. In the next iteration either the same happens or $i' = s(v, w)$. If $i' = s(v, w)$ the procedure enters case 2. Since i' is a spine node and \mathcal{X} is deep, $X[i]$ contains only one node x' . By the structure of the macro tree and the assumption that \mathcal{X} is deep $x' < x$. Since $x < y \in Y[j']$ this implies $r \neq \emptyset$. It follows from case 2(b) of the procedure that i is incremented while j stays the same. At line 14 (“Compare i and j ”) in the next iteration we will have $j = i = r(v, w)$ since all entries in X between j' and $r(v, w)$ are empty due to the assumption that \mathcal{X} is deep. The claim follows from the analysis in case (a).

It remains to show that once $x = r^l \in r_2$ and $y = s^l \in s_2$ they will stay this way until added to the output. Consider the iteration where x and y are assigned to r_2 and s_2 . At the end of this iteration either i or j or both are incremented. Assume j is incremented while the potential pairs are still unchanged. Since j is incremented we have $s_1 < j$ until s_1 is changed. It follows from case 1 and 2 of the procedure that in this case (r_1, r_2) is only changed if at the same time (s_1, s_2) are changed and right before that (r_1, r_2) and (s_1, s_2) are added to the output.

Consider first case 1–3. If i is incremented then j is incremented in one the cases I–V in the next iteration since $i' = j'$. By the previous argument x and y are added to the output. For case 4 j is incremented (case 2(a) of the procedure) and the claim follows as before. For case 5–7 first note that r_2 and s_2 contain only one node each, that is, $x = r_2$ and $y = s_2$. For case 5 i is incremented (case 2(b) of the procedure). Since \mathcal{X} is deep we have $i \geq r(v, w) = j'$ at line 14 (“Compare i and j ”) in the next iteration. If $i > r(v, w)$ then $j > j'$ and the claim follows. If $i = r(v, w)$ the procedure enters case 2. If $r = \emptyset$ then j is incremented and the claim follows. If $r \neq \emptyset$ then $s_1 = j$ and $(x, y) \in \text{mop}(\mathcal{X}, \mathcal{Y})$ implies $\text{LEFT}_{C(i,j)}(X[i], s_2) = \text{LEFT}_{C(i,j)}(X[i], y) = \emptyset$. Thus (r_1, r_2) and (s_1, s_2) are added to the output. If we are in case 6 and 7, i is incremented. Consider case 6. Since $(x, y) \in \text{mop}(\mathcal{X}, \mathcal{Y})$ all entries in X between $l(v, w)$ and $r(v, w)$ are empty. Thus at line 14 (“Compare i and j ”) in the next iteration $i \geq r(v, w)$. The proof is equivalent to the one for case 5. Consider case 7. If j is a boundary node then all entries in X between $c(x)$ and j are empty. Thus j is incremented in the second loop of the next iteration. For all other cases for j the proof is similar to the proof of case 5. \square

LEMMA 5.17. *In procedure MATCH we have the following invariant of $X[i]$ and $Y[j]$ in line 6:*

$$\text{LEFT}(1, X[i]) = \mathcal{X}_l \text{ and } \text{LEFT}(1, Y[j]) = \mathcal{Y}_l \text{ for some } l.$$

PROOF. Induction on the number of iterations of the outer loop. Base case: In the first iteration $X[i]$ and $Y[j]$ are the first nonempty entries in X and Y and

thus $\text{LEFT}(1, X[i]) = \mathcal{X}_1$ and $\text{LEFT}(1, Y[j]) = \mathcal{Y}_1$. For the induction step let i' and j' be the values of i and j in the previous iteration. By the induction hypothesis $\text{LEFT}(1, X[i']) = \mathcal{X}_{i'}$ and $\text{LEFT}(1, Y[j']) = \mathcal{Y}_{j'}$. If $x = |X[i']| = |Y[j']|$ both i and j were incremented and $\text{LEFT}(1, X[i]) = \mathcal{X}_{i'+x}$ and $\text{LEFT}(1, Y[j]) = \mathcal{Y}_{j'+x}$. If $x = |X[i']| < |Y[j']|$ then i was incremented implying $\text{LEFT}(1, X[i]) = \mathcal{X}_{i'+x}$. In that case $j = j'$ and $Y[j] = \text{LEFT}(x, Y[j'])$ implying $\text{LEFT}(1, Y[j]) = \mathcal{Y}_{j'+x}$. Similarly, if $|X[i']| > |Y[j']| = y$ we have $\text{LEFT}(1, X[i]) = \mathcal{X}_{i'+y}$. In that case $j = j'$ and $\text{LEFT}(1, Y[j]) = \mathcal{Y}_{j'+y}$. \square

LEMMA 5.18. *Procedure MATCH is correctly implemented.*

PROOF. We need to show that for all $1 \leq k \leq |\mathcal{X}|$: $\mathcal{X}_k \in \text{MATCH}(X, Y, Y') \Leftrightarrow \mathcal{X}_k \in \{\mathcal{X}_j | \mathcal{Y}_j \in \mathcal{Y}\}$. Consider the iteration where $\mathcal{X}_k \in X[i]$ and $\mathcal{Y}_k \in Y[j]$. By Lemma 5.17 such an iteration exists. If $Y[j] = Y[j']$ then $\mathcal{Y}_k \in \mathcal{Y}'$ implying $\mathcal{X}_k \in \{\mathcal{X}_j | \mathcal{Y}_j \in \mathcal{Y}\}$. It follows from the implementation of case 1(a) and 1(b) that if $x \leq y$ all nodes in $X[i]$ are added to the output and thus $\mathcal{X}_k \in \text{MATCH}(X, Y, Y')$. If $x > y$ then $\mathcal{X}_k \in \text{LEFT}(y, X[i])$ since $\mathcal{Y}_k \in Y[j]$ and thus $\mathcal{X}_k \in \text{MATCH}(X, Y, Y')$.

If $Y[j] \neq Y[j']$ the procedure calls MATCH with some subset of $X[i]$, $Y[j]$, and $Y'[j]$ depending on the size of x and y . By Lemma 5.17 and the correctness of MATCH it follows that $\mathcal{X}_k \in \text{MATCH}(X, Y, Y') \Leftrightarrow \mathcal{X}_k \in \{\mathcal{X}_j | \mathcal{Y}_j \in \mathcal{Y}\}$. \square

LEMMA 5.19. *Procedure MOPRIGHT is correctly implemented.*

PROOF. Follows from the correctness of MOPSIM (Lemma 5.16) and MATCH (Lemma 5.18). \square

Finally, we consider correctness of the FL procedure.

LEMMA 5.20. *Procedure FL is correctly implemented.*

PROOF. Let \mathcal{X} denote the set represented by X and let $F = \{\text{fl}(x, \alpha) | x \in \mathcal{X}\}$. To show $\text{FL}(X, \alpha) \subseteq F$ we will first show that for any node x added to R during the computation $x \in F$. Consider a node $x \in R[i]$ for some i . Either x was added directly to R after a computation of N in one of the three cases of the procedure or it was added after the computation of S . In the first case $x \in F$ follows from the correctness of FL_C . If x was added after the computation of S it follows from the correctness of FL_M that $x \in C(i)$ for some $i \in S$. Due to the correctness of FL_C we have $x \in F$.

To show $\text{DEEP}(F) \subseteq \text{FL}(X, \alpha)$ we use Proposition 5.2. Let x be a node in $\text{DEEP}(F)$ and let x' be a node in X such that $\text{fl}(x', \alpha) = x$. We have $x' \in X[i]$ for some i . If i is a left or right node then according to Proposition 5.2 x can be in i (case (i)), on the spine (case (ii)), in the top boundary node (case (ii)), or in an ancestor of i in the macro tree (case (iii)). If x is in the same cluster as x' then it follows from the correctness of FL_C that $x \in N$. Thus x is added to R and due to the correctness of DEEP we have $x \in \text{FL}(X, \alpha)$. If $c(x)$ is in a different cluster than $c(x')$ then $c(x)$ is an ancestor of $c(x')$ in the macro tree due to Proposition 5.2. Since $x \in \text{DEEP}(F)$ we have $N = \emptyset$ and thus $\text{parent}(v) \prec_M c(x')$ is added to L . It follows from the correctness of FL_M that $c(x) \in S$. Due to the structure of the macro tree $c(x)$ is either a boundary node or a spine node and thus $x = \text{fl}_{C(c(x))}(\text{first}(c(x)), \alpha) = \text{FL}_{C(c(x))}(\text{first}(c(x)), \alpha)$. The last equality follows from the correctness of FL_C . That $x \in \text{FL}(X, \alpha)$ now follows from the preceding analysis showing that only nodes from F are added to R and the correctness of DEEP.

If i is a leaf node then x can be in i (case (i)), in the top boundary node (case (iii)), or in an ancestor of i in the macro tree (case (iii)). The correctness follows by an analysis similar to the one for the previous case. If i is a spine node or a boundary node, then x is either in i (case (i)) or in an ancestor of i in the macro tree (case (iii)). The correctness follows by an analysis similar to the one for the first case. \square

5.5. Complexity of the Tree Inclusion Algorithm

To analyze the complexity of the node array implementation we first bound the running time of the preceding implementation of the set procedures. All procedures scan the input from left-to-right while gradually producing the output. In addition to this procedure FL needs a call to a node list implementation of FL on the macro tree. Given the data structure described in Section 5.2 it is easy to check that each step in the scan can be performed in $O(1)$ time giving a total of $O(n_T / \log n_T)$ time. Since the number of nodes in the macro tree is $O(n_T / \log n_T)$, the call to the node list implementation of FL is easily done within the same time. Hence, we have the following lemma.

LEMMA 5.21. *For any tree T there is a data structure using $O(n_T)$ space and $O(n_T \log n_T)$ preprocessing time which supports all of the set procedures in $O(n_T / \log n_T)$ time.*

Next consider computing the deep occurrences of P in T using the procedure EMB of Section 3 and Lemma 5.21. The following lemma bounds the space usage.

LEMMA 5.22. *The total size of the saved embeddings at any time during the computation of $\text{EMB}(\text{root}(P))$ is $O(n_T)$.*

PROOF. Let v be the node for which we are currently computing EMB. Let p be the path from the root to v and let w_0, \dots, w_l be the light nodes on this path. We have $l = \text{ldepth}(v)$. As in the proof of Lemma 4.12 it suffices to bound $|\text{EMB}(\text{heavy}(\text{parent}(w_i)))|$ for all i . Assume that $l_P \leq l_T$ (otherwise we can check this in linear time and conclude that P cannot be included in T). Each of the node arrays use $O(n_T / \log n_T)$ space and therefore by Corollary 2.4 we have that $\sum_{i=1}^l |\text{EMB}(\text{heavy}(\text{parent}(w_i)))| = O(n / \log n_T \cdot \log l_P) = O(n_T)$. \square

For the time complexity note that during the computation of $\text{EMB}(\text{root}(P))$ each node $v \in V(P)$ contributes a constant number of calls to the set procedures. Hence, the total time used by the algorithm is $O(n_P n_T / \log n_T + n_T \log n_T)$. Thus we have shown the following.

THEOREM 5.23. *For trees P and T the tree inclusion problem can be solved in $O(n_P n_T / \log n_T + n_T \log n_T)$ time and $O(n_T)$ space.*

Combining the results in Theorems 4.13, 5.23 and Corollary 4.16 we have the main result of Theorem 1.1.

6. CONCLUSION

We have presented three algorithms for the tree inclusion problem, which match or improve the best known time complexities while using only linear space. We believe that some of the new ideas are likely to be of both practical and theoretical value in future work. From a practical perspective, space is a common bottleneck for processing large datasets and hence reducing the space can significantly improve performance in practice. From a theoretical perspective, we have introduced several non-trivial algorithms to manipulate sets of nodes in trees that may have applications to other problems. For instance, the NCA procedure from Section 5 computes multiple nearest common ancestor queries in time sublinear in the size of input sets.

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