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On the Linear-Cost Subtree-Transfer Distance between Phylogenetic Trees[1]

B. DasGupta,[2] X. He,[3] T. Jiang,[4] M. Li,[5] and J. Tromp[6]

Abstract. Different phylogenetic trees for the same group of species are often produced either by procedures that use diverse optimality criteria [16] or from different genes [12] in the study of molecular evolution. Comparing these trees to find their *similarities* and *dissimilarities* (i.e., *distance*) is thus an important issue in computational molecular biology. Several distance metrics including the *nearest neighbor interchange* (nni) distance and the *subtree-transfer* distance have been proposed and extensively studied in the literature. This article considers a natural extension of the subtree-transfer distance, called the *linear-cost* subtree-transfer distance, and studies the complexity and efficient approximation algorithms for this distance as well as its relationship to the nni distance. The linear-cost subtree-transfer model seems more suitable than the (unit-cost) subtree-transfer model in some applications. The following is a list of our results:

1. The linear-cost subtree-transfer distance is in fact *identical* to the nni distance on unweighted phylogenies.
2. There is an algorithm to compute an optimal linear-cost subtree-transfer sequence between unweighted phylogenies in $O(n \cdot 2^{O(d)})$ time, where d denotes the linear-cost subtree-transfer distance. Such an algorithm is useful when d is small.
3. Computing the linear-cost subtree-transfer distance between two weighted phylogenetic trees is NP-hard, provided we allow multiple leaves of a tree to share the same label (i.e., the trees are not necessarily uniquely labeled).
4. There is an efficient approximation algorithm for computing the linear-cost subtree-transfer distance between weighted phylogenies with performance ratio 2.

Key Words. Evolutionary trees, Approximation algorithms, Lower bounds.

1. Introduction.

The evolution history of organisms is often conveniently represented by trees, called *phylogenetic trees* or simply *phylogenies*. Such a tree has uniquely labeled

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[2] Department of Computer Science, Rutgers University, Camden, NJ 08102, USA. bhaskar@crab.rutgers.edu.

[3] Department of Computer Science, SUNY-Buffalo, Buffalo, NY 14260, USA. xinhe@cs.buffalo.edu.

[4] Department of Computer Science, McMaster University, Hamilton, Ontario, Canada L8S 4K1. jiang@maccs.mcmaster.ca.

[5] Department of Computer Science, University of Waterloo, Waterloo, Ontario, Canada N2L 3G1. mli@math.uwaterloo.ca.

[6] CWI, P.O. Box 94079, 1090 GB Amsterdam, The Netherlands. tromp@cwi.nl.

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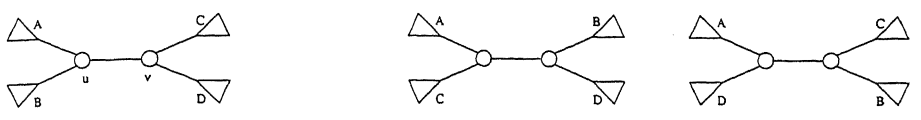

Fig. 1. The two possible nni operations on an internal edge (u, v): exchange $B \leftrightarrow C$ or $B \leftrightarrow D$.

leaves and unlabeled internal nodes, can be *unrooted* or *rooted* if the evolutionary origin is known, and usually has internal nodes of degree 3. Over the past few decades, many different objective criteria and algorithms for reconstructing phylogenies have been developed, including (not exhaustively) parsimony [6], [9], [22], compatibility [17], distance [10], [21], and maximum likelihood [6], [7], [1]. The outcomes of these methods usually depend on the data and the amount of computational resources applied. As a result, in practice they often lead to different trees on the same set of species [16]. It is thus of interest to compare phylogenies produced by different methods, or by the same method on different data, for similarity and discrepancy. The comparison of phylogenies is also routinely performed in simulation studies where people analyze reconstructed phylogenies against the true ones.

Several metrics for measuring the distance between phylogenies have been proposed in the literature. Among these measures, the *nearest neighbor interchange* (nni) distance [19], [20], [25] has perhaps received the most attention. An nni operation swaps two subtrees that are separated by an internal edge (u, v), as shown in Figure 1. The nni operation is said to *operate* or *perform* on this internal edge. The nni distance, $D_{\text{nni}}(T_1, T_2)$, between two trees T_1 and T_2 is defined as the minimum number of nni operations required to transform one tree into the other. The computational complexity of computing the nni distance has puzzled the research community for nearly 25 years until recently. It is shown in [3] that the nni distance is NP-hard to compute. Some efficient logarithmic-ratio approximation algorithms for the nni distance have also been proposed in [3] and [18].

The problem of computing distance between phylogenies also arises in a different context. When the data is in the form of some molecular sequences of organisms and the sequences have been subject to events such as *recombination* or *gene conversion* during the course of evolution, the evolutionary history of the sequences cannot be adequately described by a single tree. In an attempt to solve this problem, more general evolutionary models have been proposed including the network model [24] and a model using a list of phylogenetic trees [12], [13]. In the latter, every tree corresponds to a specific region of the sequences, and each tree can be obtained from the preceding tree on the list by transferring some subtrees from one place to another. Figure 2 shows a recombination event between two sequences and Figure 3 shows a *subtree-transfer* operation and its corresponding recombination event. The parsimony model in [12] and [13] requires the computation of the subtree-transfer distance between two trees, i.e., the minimum number of subtrees we need to move to transform one tree into the other. In [15] the authors show that computing the subtree-transfer distance is NP-complete and give a simple approximation algorithm with approximation ratio 3.

It is relevant in practice to discriminate among subtree-transfer operations as they occur with different frequencies. For example, it is reasonable to assume that sequences that have only diverged recently give rise to more recombinations than sequences that

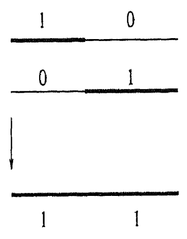

Fig. 2. Recombination event between two sequences. The genetic material (thick lines), that is in one sequence after recombination, was in two sequences just before the recombination.

diverged many generations ago [13], [14]. In this case we can charge each subtree-transfer operation a cost equal to the distance (number of nodes passed) that the subtree has moved in the current tree. The *linear-cost* subtree-transfer distance, $D_{st}(T_1, T_2)$, between two trees T_1 and T_2 is then the minimum total cost required to transform T_1 into T_2 by subtree-transfer operations. Clearly, both subtree-transfer and linear-cost subtree-transfer models can also be used as alternative measures for comparing phylogenies generated by different phylogeny reconstruction methods.

A phylogeny may also have *weights* on its edges, where an edge weight (more popu-

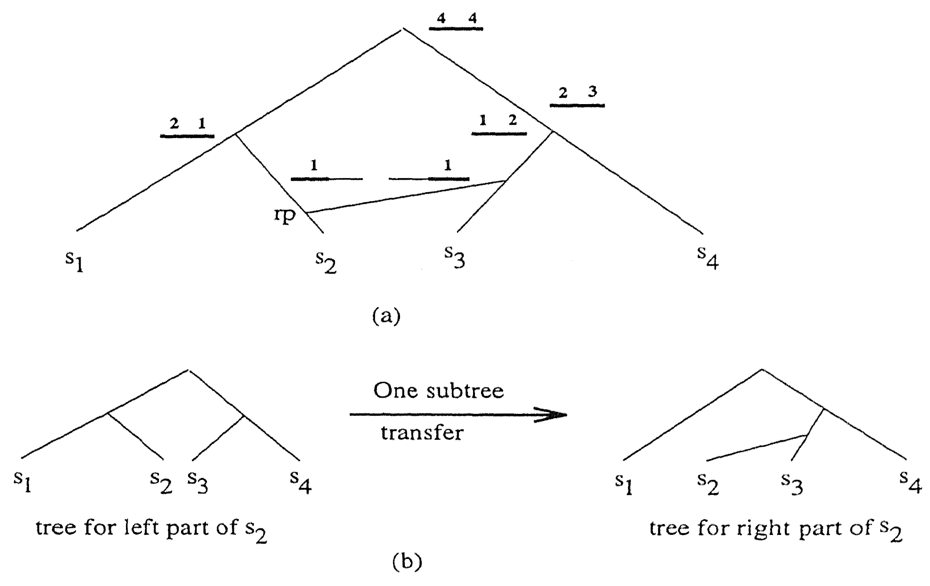

Fig. 3. [13] Recombination event at point rp in (a) corresponds to transferring subtree s_2 in (b). The genetic material (thick lines), that is in one sequence after recombination, was in two sequences just before the recombination. The two sets of numbers (on the thick lines) correspond to the two evolutionary histories (as shown in (b)) of two parts of the sequences. For example, in the evolutionary tree for the second parts of the sequences (rightmost tree in (b)), a common ancestor of s_2, s_3, s_4 is found going back in time; hence the second number of the thick line in the second row is 3.

larly known as *branch length* in genetics) could represent the evolutionary distance along the edge. Many phylogeny reconstruction methods, including the distance and maximum likelihood methods, actually produce weighted phylogenies. Comparison of weighted phylogenies has recently been studied in [16]. The distance measure adopted is based on the difference in the partitions of the leaves induced by the edges in both trees, and has the drawback of being somewhat insensitive to the tree topologies [8]. Just like the nni model [4], the linear-cost subtree-transfer model can be naturally extended to weighted phylogenies: a moving subtree is charged for the weighted distance it travels. Intuitively this measure is more sensitive to the tree topologies than the one in [16].

In this paper we study the computational complexity and approximation algorithms for linear-cost subtree-transfer distance on both unweighted and weighted phylogenies. The rest of the paper is organized as follows. In Section 1.1 we show that the linear-cost subtree-transfer distance is in fact *identical* to the nni distance on unweighted phylogenies. As a result, the complexity and approximation results for the nni distance reported in [3] and [4] directly apply to the linear-cost subtree-transfer distance on unweighted phylogenies too. Section 2 presents an algorithm to compute an optimal linear-cost subtree-transfer sequence on unweighted phylogenies in time $O(n \cdot 2^{O(d)})$, where d stands for the linear-cost subtree-transfer distance between the trees involved. In Section 3 we formalize the extension of the linear-cost subtree-transfer distance on weighted phylogenies and prove the following results:

- We show that computing the linear-cost subtree-transfer distance between two weighted trees is NP-hard, provided we allow multiple leaves of a tree to share the same label (i.e., the trees are not necessarily uniquely labeled).
- We devise an approximation algorithm for the linear-cost subtree-transfer distance between weighted trees with performance ratio 2.

The results presented in this paper form a part of the results in [3]. The remaining results in [3] deal with the proof of NP-hardness of computing the nni distance for (uniquely) labeled trees, as well as extending the nni distance for weighted phylogenies, and will be published separately [4].

Unless otherwise mentioned explicitly, the following definitions are used uniformly throughout the rest of the paper. All the trees in this paper are trees with *internal nodes* of degree 3 and with *unique* labels on leaves. We will mention it explicitly if a tree has nonuniquely labeled leaves or unlabeled leaves. An edge of a tree is *external* if it is incident on a leaf, otherwise it is *internal*. Finally, two weighted trees are considered equal iff there is an isomorphism between them preserving topology and edge weights (and leaf labels, if they are labeled).

1.1. *Nni and Subtree-Transfer on Unweighted Phylogenies.*

Surprisingly, although they are studied in parallel for very different reasons, we demonstrate here that the linear-cost subtree-transfer distance and the nni distance are very closely related for unweighted phylogenies.

LEMMA 1. *The linear-cost subtree-transfer distance is* identical *to the nni distance on unweighted phylogenies.*

PROOF. Observe that an nni move is just a restricted subtree-transfer where a subtree is only moved across a single edge. (In Figure 1 the first exchange can alternatively be seen as moving node v together with subtree C past node u toward subtree A, or vice versa.) On the other hand, when all internal nodes have degree 3, a subtree-transfer over a distance d can always be simulated by a series of d nni moves. Hence the linear-cost subtree-transfer distance is in fact *identical* to the nni distance on unweighted phylogenies. □

As a result, all the results on computing the nni distance reported in [3] and [4] directly apply to the linear-cost subtree-transfer problem on unweighted phylogenies also. In particular, this means that, for any two unweighted phylogenies T_1 and T_2:

- Computing $D_{st}(T_1, T_2)$ is NP-hard.
- $D_{st}(T_1, T_2)$ can be approximated within a logarithmic factor in polynomial time.

2. An Efficient Exact Algorithm for Small Subtree-Transfer Distance.

The result in this section concerns computing $D_{st}(T_1, T_2)$ exactly, where T_1 and T_2 are unweighted phylogenies. In practice, the trees to be compared usually have small subtree-transfer distances between them and it is of interest to devise efficient algorithms for computing an optimal subtree-transfer sequence when the $D_{st}(T_1, T_2)$ is small, say at most d. An $n^{O(d)}$ algorithm for this problem is trivial. With careful inspection, one can derive an algorithm that runs in $O(n^{O(1)} \cdot d^{O(d^2)})$ time. It turns out that by using the results in [23] and [18], we can improve this asymptotically to $O(n \cdot 2^{21d/2})$ time.

DEFINITION 1. Let T_1 and T_2 be the two trees being compared. An edge $e_1 \in T_1$ is *good* if there is another edge $e_2 \in T_2$ such that e_1 and e_2 partition the leaf labels of T_1 and T_2 identically; e_1 is *bad* otherwise.

The proof of the following lemma can be found in [5] which deals with computing strict consesus trees.

LEMMA 2. [5] *Let T_1 and T_2 be two trees, each with n leaves. Then the set of good edges of T_1 (with respect to T_2) can be enumerated in $O(n)$ time.*

We also need the following rather straightforward observation.

OBSERVATION 3. Let e and e' be two edges of a binary tree T which are not adjacent to each other. Then performing an nni operation σ across e followed by an nni operation σ' across e' is the same as performing the nni operation σ' across e' followed by the nni operation σ across e.

See Figure 4 for an illustration of the Observation 3.

THEOREM 4. *Suppose that $D_{st}(T_1, T_2) \leq d$. An optimal sequence of subtree-transfer operations transforming T_1 into T_2 can be computed in $O(n \cdot 2^{21d/2})$ time.*

PROOF. Since the linear-cost subtree-transfer distance is identical to the nni distance on unweighted trees, we choose, for convenience of understanding, to describe how to

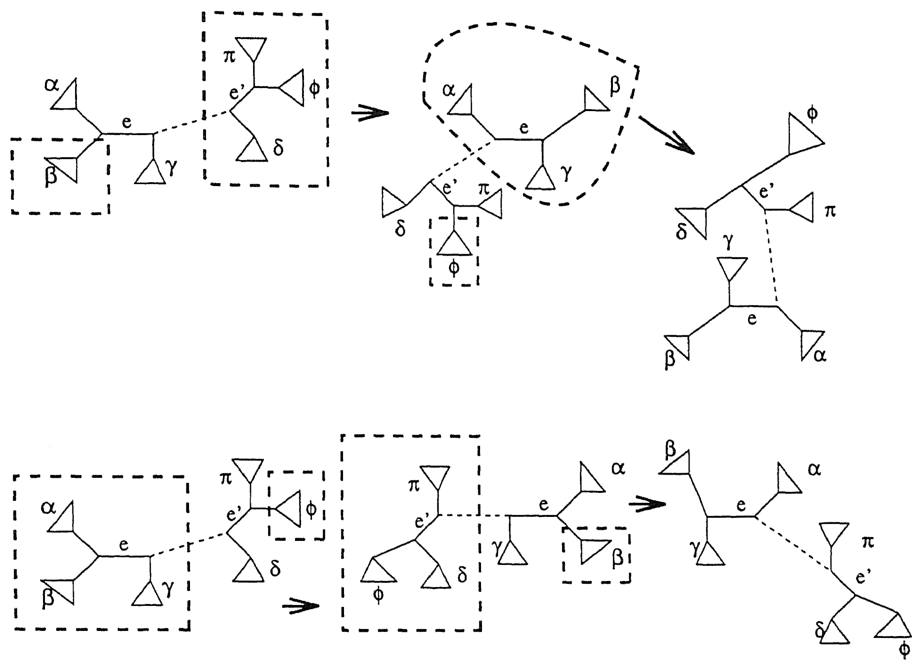

Fig. 4. Illustration of Observation 3. The subtrees swapped in each nni operation are shown by thick dashed rectangles. The final trees in the two nni sequences are the same. α, β, γ, δ, π and φ are subtrees. The portion of the tree connecting e to e' is shown by a dashed line.

find an optimal nni sequence (which is in fact an optimal subtree-transfer sequence). We know that T_1 contains at least one (and at most d) bad edge. Moreover, assume that these bad edges form t connected components $B_1, \ldots, B_t$ ($1 \le t \le d$). As observed in [18], for an optimal nni transformation, sometimes one or more nni operations are needed across a good internal edge of T_1. Consider the set of at most $d-1$ good edges in T_1 across which at least one nni operation is performed in an optimal nni sequence. This set of good edges forms at most $d-1$ connected components in T_1. Consider any one such connected component S. Since good edges in T_1 and T_2 partition the trees in a similar manner, it is very easy to see that there must be at least one connected component B_i sharing a vertex with S.

Using this observation, we can devise the following algorithm:

Algorithm NNI-d

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For every choice of integers $k_1, \ldots, k_t \ge 0$, $1 \le \sum_{i=1}^{t} k_i \le d$ do
    For every choice of connected subgraphs $A_1, \ldots, A_t$ of $T_1$ such that $A_i$
    has at most $k_i$ internal edges[7] and contains the component $B_i$ do
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[7] Nni operations cannot obviously be performed across external edges.

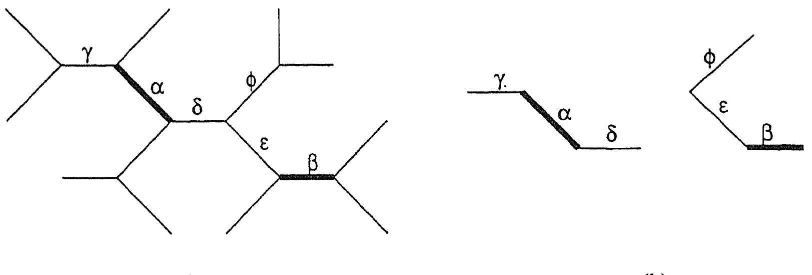

Fig. 5. Illustration of how Algorithm NNI-d works ($d = 6, k_1 = k_2 = 3, t = 2$).

Examine all sequences of nni transformations across edges of all A_i's such that no more than k_i nni operations are performed across the edges of A_i Among all sequences examined, select the one of shortest length that transforms T_1 into T_2

Figure 5 illustrates how the algorithm works. Figure 5(a) shows two bad edges α, β in T_1 (shown by thick lines) forming two connected components ($t = 2$). In Figure 5(b) we show one choice of two connected subgraphs containing k_1 and k_2 edges, and including the edges α and β, respectively. For each connected subgraph, Algorithm NNI-d computes all possible nni sequences such that at most three nni are performed across edges of each connected subgraph.

Now we analyze the running time of the above algorithm. The following countings are crucial for the analysis.

- There are at most

$$\sum_{i=1}^{d} \binom{i+t-1}{i} \le \sum_{i=1}^{d} \binom{i+d-1}{i} \le \sum_{i=1}^{d} 2^{i+d-1} < 2^{2d}$$

choices for the integers $k_1, \dots, k_t$.
- Note that any connected subgraph of k edges including a fixed edge ($k > 1$) can be represented by a rooted binary tree on $k + 2$ nodes (the root corresponding to the middle of the fixed edge), hence there are at most $C_{k+2} = (1/(k+3))\binom{2k+4}{k+2} < 2^{2k}$ such subgraphs [2, page 262]. For $k = 1$, there is exactly $1 < 2^{2k}$ such subgraph. Hence, it follows that the total number of choices for the subgraphs $A_1, \dots, A_t$ (for any particular value of $k_1, \dots, k_t$) is at most $2^{\sum_{i=1}^{t}(2k_i)} \le 2^{2d}$.

Consider a particular choice of subgraphs $A_1, A_2, \dots, A_t$ (with $k_1, k_2, \dots, k_t$ edges, respectively). Let $M_1, M_2, \dots, M_s$ be the s connected components of $A_1 \cup A_2 \cup \dots \cup A_t$. Assume that M_i has ℓ_i edges ($\sum_{i=1}^{s} \ell_i = \sum_{i=1}^{t} k_i \le d$). Notice that we are required to perform at most ℓ_i nni operations across the edges of M_i. Let $m_i \le \ell_i$ be the number of nni operations performed across the edges of M_i. Extend each M_i to M_i' by adding edges from T such that every degree 1 or degree 2 node of M_i (that is not a leaf of T) is of degree 3 in M_i'. Notice that M_i' has at most $\ell_i + 3$ leaves. Lemma 1 of [18] states that the number of trees within an nni distance of $m > 1$ from any given tree with n leaves is at most $3^{n-2}2^{4m}$ (for $m = 1$, the number of such trees is obviously at most $n - 3$). Hence, the total number of distinct nni operations we will need to consider for each connected subgraph M_i is at most $3^{(\ell_i+3)-2}2^{4\ell_i} = 3^{\ell_i+1}2^{4\ell_i} < 2^{13\ell_i/2}$ if $1 < m_i \leq \ell_i$, and at most $\ell_i < 2^{13\ell_i/2}$ if $m_i = 1$. By Observation 3, nni operations across the edges in M_i can be performed independently of the nni operations across the edges of M_j for $i \neq j$. Hence, the total number of nni operations across the edges of all M_i's is at most $2^{(13/2)\sum_{i=1}^{s}\ell_i} \leq 2^{13d/2}$. Combining everything, the total number of nni operations we will need to consider is at most

$$\begin{array}{l} \text{Number of choices for the} \\ \text{integers } k_1, k_2, \ldots, k_t \end{array} \times \begin{array}{l} \text{Number of choices of} \\ A_1, A_2, \ldots, A_t \text{ for each} \\ \text{choice of } k_1, k_2, \ldots, k_t \end{array} \times \begin{array}{l} \text{Number of nni op-} \\ \text{erations across the} \\ \text{edges of } M_1, M_2, \ldots, M_s \end{array}$$

which is at most $2^{2d} \times 2^{2d} \times 2^{13d/2} = 2^{21d/2}$.

The set of all good edges of T_1 can be found in $O(n)$ time using Lemma 2, and this time bound is also sufficient to find the connected components of good edges. Using the adjacency-list representation of trees, updating a tree during a single nni operation can be easily done in $O(1)$ time, and whether two trees are isomorphic can be easily checked in $O(n)$ time. Hence, this algorithm finds an optimal nni sequence in $O(n \cdot 2^{21d/2})$ time. □

3. Linear-Cost Subtree-Transfer Distance on Weighted Phylogenies. In this section we investigate the linear-cost subtree-transfer model on weighted phylogenies. Recall that the linear-cost subtree-transfer distance is identical to the nni distance on unweighted phylogenies. Below we formalize the linear-cost subtree-transfer model on weighted phylogenies.

Consider (unrooted) trees in which each edge e has a weight $w(e) \geq 0$. To ensure feasibility of transforming a tree into another, we require the total weight of all edges to equal one. A subtree-transfer is defined as follows. Select a subtree S of T at a given node u and select an edge $e_4 \not\in S$. Split the edge e_4 into two edges e_6 and e_7 with weights $w(e_6)$ and $w(e_7)$ ($w(e_6), w(e_7) \geq 0$, $w(e_6) + w(e_7) = w(e_4)$), and move S to the common endpoint of e_6 and e_7. Finally, merge the two remaining edges e_1 and e_2 adjacent to u into one edge e_5 with weight $w(e_5) = w(e_1) + w(e_2)$. The cost of this subtree-transfer is the total weight of all the edges over which S is moved. Figure 6 gives an example. The subtree S is transferred to split the edge e_4 to e_6 and e_7 such that $w(e_6), w(e_7) \geq 0$ and $w(e_6) + w(e_7) = w(e_4)$; finally, the two edges e_1 and e_2 are merged to e_5 such that $w(e_5) = w(e_1) + w(e_2)$. The cost of transferring S is $w(e_2) + w(e_3) + w(e_6)$.

3.1. *Some Definitions and a Useful Lower Bound.* In this section we introduce some notations and a lower bound on the subtree-transfer distance which will be useful in subsequent proofs. For any tree T, let $E(T)$ (resp. $V(T)$) denote the edge set (resp. node set) of T and let $L(T)$ denote the set of leaf nodes of T. An external edge of T incident on a leaf node a is denoted by $e_T(a)$. Let $E_{\text{int}}(T)$ and $E_{\text{ext}}(T)$ denote the set of internal and

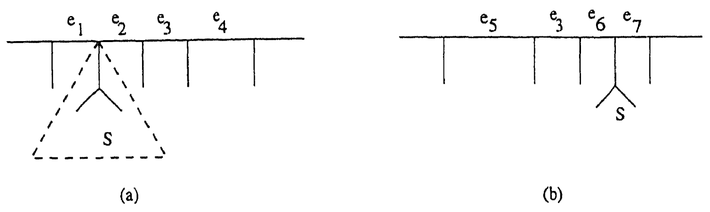

Fig. 6. Subtree-transfer on weighted phylogenies. Tree (b) is obtained from tree (a) with one subtree-transfer.

external edges of T, respectively. For a subset $E' \subseteq E(T)$, define $w(E') = \sum_{e \in E'} w(e)$. Define $W_{\text{int}}(T) = w(E_{\text{int}}(T))$ and $W_{\text{ext}}(T) = w(E_{\text{ext}}(T))$.

Consider the transformation of tree T_1 to tree T_2 (hence $L(T_1) = L(T_2)$). We partition $E_{\text{ext}}(T_1)$ into three subsets as follows:

$$\begin{aligned} E_{\text{ext},T_1>T_2}(T_1) &= \{e_{T_1}(a) \mid w(e_{T_1}(a)) > w(e_{T_2}(a))\}, \\ E_{\text{ext},T_1=T_2}(T_1) &= \{e_{T_1}(a) \mid w(e_{T_1}(a)) = w(e_{T_2}(a))\}, \\ E_{\text{ext},T_1<T_2}(T_1) &= \{e_{T_1}(a) \mid w(e_{T_1}(a)) < w(e_{T_2}(a))\}, \\ W_{\text{ext},T_1>T_2}(T_1) &= \sum_{e_{T_1}(a) \in E_{\text{ext},T_1>T_2}(T_1)} w(e_{T_1}(a)) - w(e_{T_2}(a)). \end{aligned}$$

Similarly, $E_{\text{ext}}(T_2)$ can be partitioned into $E_{\text{ext},T_1>T_2}(T_2)$, $E_{\text{ext},T_1=T_2}(T_2)$, and $E_{\text{ext},T_1<T_2}(T_2)$. $W_{\text{ext},T_1<T_2}(T_2)$ is defined analogously.

LEMMA 5. $W_{\text{int}}(T_1) + W_{\text{ext},T_1>T_2}(T_1) = W_{\text{int}}(T_2) + W_{\text{ext},T_1<T_2}(T_2)$.

PROOF. Since $w(E_{\text{ext},T_1>T_2}(T_1)) = w(E_{\text{ext},T_1>T_2}(T_2)) + W_{\text{ext},T_1>T_2}(T_1)$, we have

$$\begin{aligned} W_{\text{int}}(T_1) &+ w(E_{\text{ext},T_1=T_2}(T_1)) + w(E_{\text{ext},T_1<T_2}(T_1)) \\ &+ w(E_{\text{ext},T_1>T_2}(T_2)) + W_{\text{ext},T_1>T_2}(T_1) = w(T_1) = 1. \end{aligned}$$

Similarly, we have

$$\begin{aligned} W_{\text{int}}(T_2) &+ w(E_{\text{ext},T_1=T_2}(T_2)) + w(E_{\text{ext},T_1>T_2}(T_2)) \\ &+ w(E_{\text{ext},T_1<T_2}(T_1)) + W_{\text{ext},T_1<T_2}(T_2) = w(T_2) = 1. \end{aligned}$$

Since $w(E_{\text{ext},T_1=T_2}(T_1)) = w(E_{\text{ext},T_1=T_2}(T_2))$, the lemma follows from the above two equations. □

We next define the notion of good edge pairs in the following:

DEFINITION 2. Let $e_1 \in E_{\text{int}}(T_1)$ and $e_2 \in E_{\text{int}}(T_2)$. Let T_1' and T_1'' be the two subtrees of T_1 partitioned by e_1. Let T_2' and T_2'' be the two subtrees of T_2 partitioned by e_2. The edges e_1 and e_2 are called a *good edge pair* of T_1 and T_2 iff the following two conditions hold:

1. $L(T_1') = L(T_2')$ and $L(T_1'') = L(T_2'')$.

2. One of the following two conditions holds:
   (a) $w(E(T_1')) \le w(E(T_2')) < w(E(T_1')) + w(e_1)$; or
   (b) $w(E(T_2')) \le w(E(T_1')) < w(E(T_2')) + w(e_2)$.

The following lemma provides a lower bound on $D_{\mathrm{st}}(T_1, T_2)$ when T_1 and T_2 do not share good edge pairs.

LEMMA 6. *If T_1 and T_2 share no good edge pairs, then*:

(1) $D_{\mathrm{st}}(T_1, T_2) \ge W_{\mathrm{int}}(T_1) + W_{\mathrm{ext,T_1>T_2}}(T_1)$.
(2) $D_{\mathrm{st}}(T_1, T_2) \ge W_{\mathrm{int}}(T_2) + W_{\mathrm{ext,T_1<T_2}}(T_2)$.

PROOF. We only prove (1). The proof of (2) follows from (1) and Lemma 5. For each edge $e \in E(T_1)$, we determine the minimum portion of e over which some subtrees of T_1 must be transferred in order to transform T_1 to T_2. First consider an edge $e_1 \in E_{\mathrm{int}}(T_1)$. By the assumption of the lemma, there is no edge e_2 in T_2 such that e_1 and e_2 are a good pair. There are two cases:

Case 1. The partition of $L(T_1)$ induced by e_1 is different from the partition of $L(T_2)$ induced by any edge in T_2. Then, in order to transform T_1 to T_2, some leaf nodes of T_1 must be transferred across the entire length of e_1.

Case 2. The partition of $L(T_1)$ induced by e_1 is the same as the partition of $L(T_2)$ induced by an edge e_2 in T_2. Let T_1' and T_1'' be the two subtrees of T_1 partitioned by e_1. Let T_2' and T_2'' be the two subtrees of T_2 partitioned by e_2, where $L(T_1') = L(T_2')$ and $L(T_1'') = L(T_2'')$.

Case 2.1. $w(E(T_2')) \ge w(E(T_1')) + w(e_1)$. In this case, in order to transform T_1' to T_2', some subtree in T_1' must be transferred across the entire length of e_1.

Case 2.2. $w(E(T_1')) \ge w(E(T_2')) + w(e_2)$. This implies $w(E(T_1'')) + w(e_1) \le w(E(T_2''))$. In order to transform T_1'' to T_2'', some subtree in T_1'' must be transferred across the entire length of e_1.

In either case, some subtree of T_1 must be transferred across the entire length of e_1 with cost $w(e_1)$.

Next consider an edge $e_{T_1}(a) \in E_{\mathrm{ext,T_1>T_2}}(T_1)$. In order to transform $e_{T_1}(a)$ to $e_{T_2}(a)$, a subtree of T_1 must be transferred across a portion of $e_{T_1}(a)$ of length $w(e_{T_1}(a)) - w(e_{T_2}(a))$. Thus:
$D_{\mathrm{st}}(T_1, T_2) \ge \sum_{e \in E_{\mathrm{int}}(T_1)} w(e) + \sum_{e \in E_{\mathrm{ext,T_1>T_2}}(T_1)} [w(e_{T_1}(a)) - w(e_{T_2}(a))] = W_{\mathrm{int}}(T_1) + W_{\mathrm{ext,T_1>T_2}}(T_1)$ □

REMARK. Assume that the given trees T_1 and T_2 are not uniquely labeled (i.e., a label may appear in more than one leaf). Extend the definition of good edge pairs by treating $L(T)$ as the multiset of leaves for a tree T and considering the conditions $L(T_1') = L(T_2')$ or $L(T_1'') = L(T_2'')$ to hold if the corresponding multisets are identical. Assume that all the leaves are incident on *zero-weight* edges (i.e., $W_{\mathrm{int}}(T_1) = W_{\mathrm{int}}(T_2)$ and $W_{\mathrm{ext}}(T_1) = W_{\mathrm{ext}}(T_2) = 0$), and that T_1 and T_2 share no good edge pairs. Then, in a manner very similar

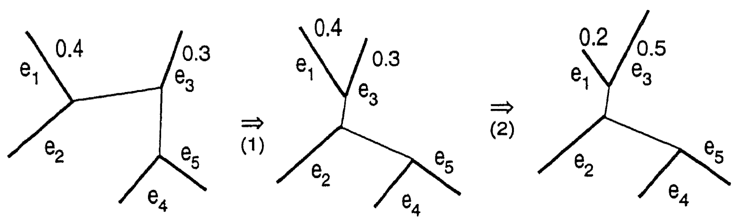

Fig. 7. The operation $move(e_1, 0.2, e_3)$. (1) e_2, e_4, e_5 are assembled into a tree S; (2) S is moved along e_1 by a length of 0.2.

to the proof of Lemma 6, one can show that $D_{\mathrm{st}}(T_1, T_2) \geq W_{\mathrm{int}}(T_1)$ (and that some subtree is transfered over every internal edge of T_1 to transform T_1 to T_2).

We say that nodes connected by zero-weight edges are equivalent and call the resulting equivalence classes *supernodes*. Let $e_1, \ldots, e_k$ be all positive weight edges incident to a supernode o. With zero cost, we can reconnect the edges $e_1, \ldots, e_k$ by any subtree, consisting of only zero-weight edges. In particular, the following observation will be useful in our subsequent descriptions.

OBSERVATION. Let o be a supernode of T. Let $e_1, \ldots, e_k$ be all positive weight edges incident on o. Pick any e_i and e_j. We can assemble $\{e_1, \ldots, e_k\} - \{e_i, e_j\}$ into a single subtree S with zero cost; and then transfer S along e_i by a distance $d \leq w(e_i)$. The effect of this operation is that the edges $e_1, \ldots, e_k$ are still incident on a supernode, and a portion of e_i of length d is *moved* into e_j. The total cost of this operation is d. We denote this operation by $move(e_i, d, e_j)$. This operation can be implemented in $O(k)$ time using the adjacency-list representation of the tree (where the weight of the edge is also stored in the adjacency list).

Figure 7 shows an example of this operation. In the figure the thin lines denote zero-weight edges and heavy lines denote positive-weight edges.

A tree T is called a *superstar* if all of its internal edges have zero weight. In other words, all external edges of a superstar T are incident to a single supernode.

3.2. *An NP-hardness Result.* It is open whether the linear-cost subtree-transfer problem is NP-hard for weighted phylogenies. However, we can show that the problem is NP-hard for weighted trees with nonuniquely labeled leaves.

THEOREM 7. *Let T_1 and T_2 be two weighted trees with (not necessarily uniquely) labeled leaves. Then computing $D_{\mathrm{st}}(T_1, T_2)$ is NP-hard.*

Our proof is by a reduction from the *Exact Cover by 3-Sets* (X3C) problem, which is defined as follows:

Instance: $S = \{s_1, \ldots, s_m\}$, where $m = 3q$, and $C_1, \ldots, C_n$, where $C_i = \{s_{i_1}, s_{i_2}, s_{i_3}\} \subseteq S$.

Question: Are there q disjoint sets $C_{i_1}, \ldots, C_{i_q}$ such that $\bigcup_{j=1}^{q} C_{i_j} = S$?

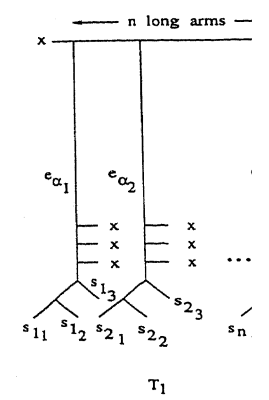

Fig. 8. Trees T_1 and T_2 use
leaves. The notations for s
weights are as follows: $w(e$
$w(e_{\gamma_1}) = w(e_{\gamma_2}) = \cdots =$

X3C is known to b
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PROOF OF THEOREM
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weighted *labeled* (bu
arms, $\alpha_1, \ldots, \alpha_n$. T_2
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Figure 8. For notatio
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long arm of T_2, there
leaves of T_2 is as foll

- At the bottom of t
- The remaining $3n$
  (in any order) wit
  short arms.

Note that $W_{\mathrm{int}}(T_1$
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LEMMA 8. $D_{\mathrm{st}}(T_1,$

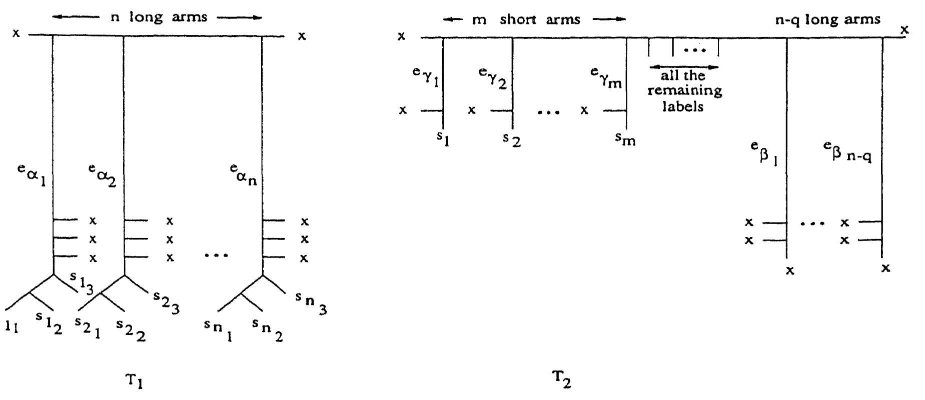
n long arms
x
x
e_{α_1}
e_{α_2}
e_{α_n}
s_{1_1} s_{1_2} s_{1_3} s_{2_1} s_{2_2} s_{2_3} s_{n_1} s_{n_2} s_{n_3}
T_1
m short arms
n-q long arms
e_{γ_1} e_{γ_2} e_{γ_m}
all the remaining labels
s_1 s_2 s_m
e_{β_1} $e_{\beta_{n-q}}$
T_2

Fig. 8. Trees T_1 and T_2 used in the proof of Theorem 7. The leaf labels are shown beside the corresponding leaves. The notations for some of the internal edges are shown beside the corresponding edges. The edge weights are as follows: $w(e_{\alpha_1}) = w(e_{\alpha_2}) = \cdots = w(e_{\alpha_n}) = w(e_{\beta_1}) = w(e_{\beta_2}) = \cdots = w(e_{\beta_{n-q}}) = 1/n$, $w(e_{\gamma_1}) = w(e_{\gamma_2}) = \cdots = w(e_{\gamma_m}) = 1/3n$, and all other edges have zero weights.

X3C is known to be NP-complete [11]. We will construct two trees T_1 and T_2 with leaf labels (not necessarily unique), such that transforming from T_1 into T_2 requires subtree-transfers of total cost exactly one iff an exact cover of S exists.

PROOF OF THEOREM 7. Assume that an instance, $S = \{s_1, s_2, \ldots, s_m\}$ (with $m = 3q$) and $C_1, C_2, \ldots, C_n$ (with $|C_i| = 3$), of the X3C problem is given. We construct two weighted *labeled* (but not uniquely labeled) trees as shown in Figure 8. T_1 has n long arms, $\alpha_1, \ldots, \alpha_n$. T_2 has $n - q$ long arms, $\beta_1, \ldots, \beta_{n-q}$, and m short arms, $\gamma_1, \ldots, \gamma_m$. Each long (resp. short) arm consists of an edge of weight $1/n$ (resp. $1/3n$), with three leaves (resp. one leaf) labeled by the same label x ($x \notin S$), connected to it as shown in Figure 8. For notational convenience, let e_{α_i} (resp. e_{β_i}, e_{γ_i}) denote the edge of nonzero weight in the long arm α_i (resp. in the long arm β_i, in the short arm γ_i). In T_1, at the bottom of the ith long arm α_i, we attach a subtree t_i consisting of three leaves, as shown in Figure 8, labeled by the three elements s_{i_1}, s_{i_2}, and s_{i_3} of C_i. At the bottom of each long arm of T_2, there are no additional subtrees attached. The labeling of the remaining leaves of T_2 is as follows:

- At the bottom of the ith short arm γ_i, we attach a leaf labeled by s_i.
- The remaining $3n - m$ leaf labels (each leaf label is an element of S) are associated (in any order) with the $3n - m$ leaves in the middle of T_2 between the long and the short arms.

Note that $W_{\text{int}}(T_1) = W_{\text{int}}(T_2) = 1$ and $W_{\text{ext}}(T_1) = W_{\text{ext}}(T_2) = 0$. Also, notice that the trees T_1 and T_2 are not uniquely labeled. The following lemma proves the correctness of the NP-hardness reduction.

LEMMA 8. *$D_{\text{st}}(T_1, T_2) = 1$ iff there is a solution of the X3C problem.*

The following lemma is needed in the proof of Lemma 8.

LEMMA 9. $D_{\rm st}(T_1, T_2) \geq 1$. *Moreover, if* $D_{\rm st}(T_1, T_2) = 1$, *then, over any portion of any of the edges* e_{α_i}, *exactly one subtree-transfer takes place.*

PROOF. We first verify that every edge e_{α_i} of T_1 is not a good edge pair with *any* edge of T_2. Consider the edge e_{α_i} $(1 \leq i \leq n)$. This edge partitions T_1 into two trees T_1' and T_1'', where $L(T_1')$ consists of six leaves labeled with $s_{i_1}, s_{i_2}, s_{i_3}, x, x, x$ and $L(T_1'')$ consists of the remaining leaves of T_1. Also, note that $w(E(T_1')) = 0$ and $w(E(T_1'')) = 1 - 1/n$. Consider any edge $e \in T_2$ partitioning T_2 into two trees T_2' and T_2''. Since both the conditions $L(T_1') = L(T_2')$ and $L(T_1'') = L(T_2'')$ must be satisfied for e_{α_i} to be a good edge pair with e, the only possibility for the edge e is to be the zero-weight edge between e_{γ_3} and e_{γ_4}. However, in that case, $w(E(T_2')) = 1/n$ and $w(E(T_2'')) = 1 - 1/n$. Then, clearly both $w(E(T_2')) > w(E(T_1'))$ and $w(E(T_2')) = w(E(T_1')) + w(e_{\alpha_i})$ are true. Hence, e_{α_i} is not a good edge pair with e.

Hence, from the Remark following the proof of Lemma 6, some subtree is transferred over every internal edge e_{α_i} of T_1, and we get

$$D_{\rm st}(T_1, T_2) \geq \sum_{i=1}^{n} w(e_{\alpha_i}) = 1.$$

The remaining part of the lemma is now straightforward. Assume that over a portion γ of some e_{α_i}, more than one subtree is transfered $(0 < w(\gamma) \leq w(e_{\alpha_i}))$. Then $D_{\rm st}(T_1, T_2) \geq \sum_{i=1}^{n} w(e_{\alpha_i}) + w(\gamma) = 1 + w(\gamma) > 1$. □

PROOF OF LEMMA 8. Suppose that there is an exact cover of S, say (without loss of generality) $C_1, \ldots, C_q$. Then we transform T_1 to T_2 in the following manner:

- First we consider the corresponding long arms $\alpha_1, \ldots, \alpha_q$ in T_1 and move the leaves of each subtree t_j $(j = 1, \ldots, q)$ up in the following way as shown in Figure 9. Without loss of generality, we describe the procedure for α_1 only. Leave one of the three leaves, say s_{1_3}, with a leaf x at the bottom, and move the subtree containing the other two leaves s_{1_1} and s_{1_2} together with two leaves labeled x up by a distance $1/3n$ (remember that we can use zero-weight edges to assemble many subtrees at a given node into one subtree with *zero* cost). Now leave one of these two leaves, say s_{1_1}, with a leaf labeled x there, and move the subtree containing leaves s_{1_2} and s_{1_3} together with two leaves labeled x up by a distance $1/3n$. Finally, move the subtree containing the leaf s_{1_1} and a leaf labeled x and the subtree containing the leaf s_{1_3} and a leaf labeled x together up by a distance $1/3n$. After this, we have created all the short arms of T_2, but not necessarily in the correct order. After some rearrangements of the short arms of total cost *zero* (since we move subtrees across zero-weight edges), we can create the short arms of T_2 in the correct order.
- For each C_l not in the cover, we simply move the subtree containing the three leaves of the subtree t_l up by a distance $1/n$ (see Figure 10). This already creates the remaining long arms of T_2. Now, with some extra rearrangements of total cost *zero*, we can create, in correct order, the leaves in the middle part of T_2 between the long and the short arms.

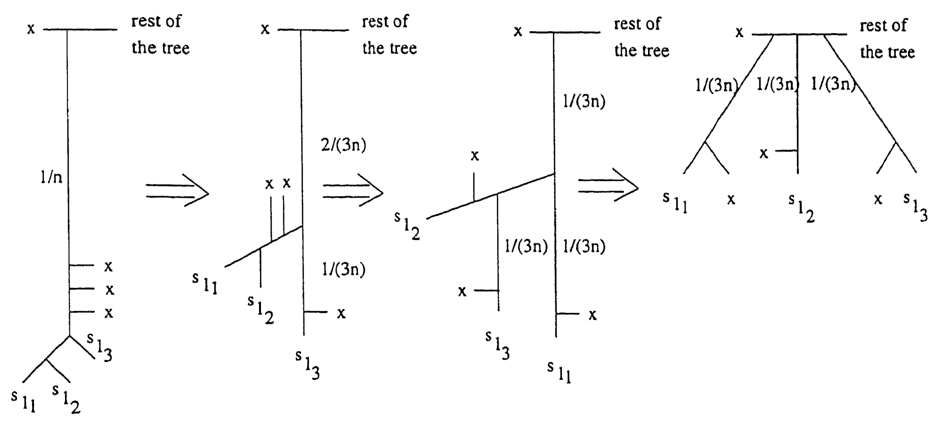

Fig. 9. Moving leaves of the long arm α_1.

Hence, our conversion of T_1 to T_2 is complete. The total cost of conversion is $q \cdot 1/n + (n-q) \cdot 1/n = 1$, as promised.

Conversely, assume that there is no exact cover of S. Then, by Lemma 9, if $D_{\mathrm{st}}(T_1, T_2) = 1$, then over any portion of any of the edges e_{α_i}, at most one subtree transfer takes place. However, in that case, the only possible way to create the m short arms of T_2 is to use exactly q long arms in T_1, which means there was an exact cover of S. □

REMARK. Since the X3C problem is NP-complete even if each element occurs in at most three sets [11], it follows that Theorem 7 holds even if every label, except only one label (label x in the proof), occurs in at most three leaves.

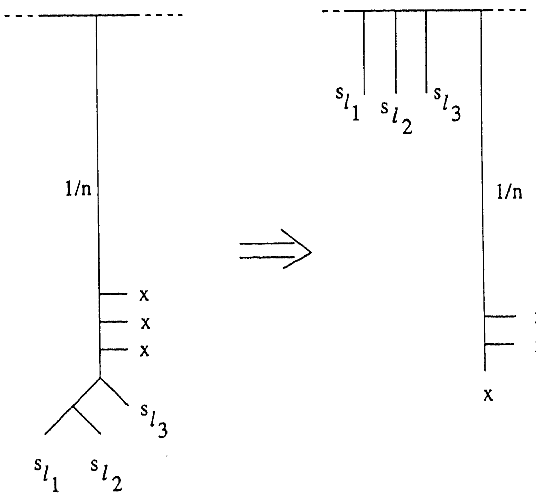

Fig. 10. Moving leaves of the long arm α_l for every C_l not in cover.

3.3. *An Approximation Algorithm.* In this section, we prove the following theorem.

THEOREM 10. *For any two (uniquely-labeled) weighted phylogenies T_1 and T_2, $D_{st}(T_1, T_2)$ can be approximated to within a factor of 2 in $O(n^2)$ time.*

We are now ready to describe our algorithm. First we consider the special case when T_1 and T_2 do not have any good edge pairs. Algorithm DST, as described below, approximates $D_{st}(T_1, T_2)$ to within a factor of 2. The algorithm transforms T_1 into a superstar T_1' (by moving the weight of internal edges into external edges). Similarly, the algorithm transforms T_2 into a superstar T_2'. The transformations are chosen to make T_1' coincide with T_2'. To transform T_1 to T_2, we first transform T_1 to $T_1'(= T_2')$ and then transform this to T_2. Let T_1' (resp. T_2') denote the tree during the transformation of T_1 (resp. T_2). T_1' (resp. T_2') is initialized to be T_1 (resp. T_2).

```
Algorithm DST
Step 0. Initialize $T_1' = T_1$ and $T_2' = T_2$.
Step 1. While $T_1'$ is not a superstar yet and there is an external edge
    $e_{T_1'}(a) = (a, u)$ in $T_1'$ such that $w(e_{T_1'}(a)) < w(e_{T_2'}(a))$, do:
    • Let $e_1$ be any positive weight internal edge of $T_1'$ incident on the
      supernode containing $u$. Let $d = \min\{w(e_1), [w(e_{T_2'}(a)) - w(e_{T_1'}(a))]\}$.
    • Perform the operation $move(e_1, d, e_{T_1'}(a))$ in $T_1'$. (Note: after this
      move operation, either the entire length of $e_1$ is moved into $e_{T_1'}(a)$ or
      $w(e_{T_1'}(a)) = w(e_{T_2'}(a))$.)
      (Note: after the loop terminates, either $T_1'$ is a superstar or $w(e_{T_1'}(a)) \geq$
      $w(e_{T_2'}(a))$ for all leaf nodes $a$. Also we perform subtree-transfer only
      on internal edges of $T_1$.)
Step 2. Similar to Step 1, with the roles of $T_1'$ and $T_2'$ swapped.
Step 3. We transform $T_1'$ and $T_2'$ into two superstars such that $w(e_{T_1'}(a)) =$
    $w(e_{T_2'}(a))$ for all leaf nodes $a$. There are two possible cases as follows.
    Case 3.1. $w(e_{T_1'}(a)) = w(e_{T_2'}(a))$ for all leaf nodes $a$. Perform the
      following loop to transform both $T_1'$ and $T_2'$ into superstars. During the
      execution of the loop, we maintain the condition $w(e_{T_1'}(a)) =$
      $w(e_{T_2'}(a))$ for all leaf nodes $a$ (this condition implies that $T_1'$ is a
      superstar iff $T_2'$ is a superstar).
      Repeat
        Pick any edge $e_{T_1'}(a) = (a, u_1)$ in $T_1'$. Suppose that the corre-
        sponding edge $e_{T_2'}(a)$ in $T_2'$ is $(a, u_2)$. Let $e_1$ be any positive
        weight internal edge of $T_1'$ incident on the super-node containing
        $u_1$. Let $e_2$ be any positive weight internal edge of $T_2'$ inci-
        dent on the supernode containing $u_2$. Let $d = \min\{w(e_1),$
        $w(e_2)\}$. In $T_1'$ perform the operation $move(e_1, d, e_{T_1'}(a))$. In $T_2'$
        perform the operation $move(e_2, d, e_{T_2'}(a))$. (After this, we have
        moved the entire length of either $e_1$ or $e_2$ into external edges.)
      Until both $T_1'$ and $T_2'$ are superstars.
```

(Note: during this step we perform subtree-transfer only on internal edges of T_1 and T_2.)

Case 3.2. There exists a leaf node a such that $w(e_{T'_1}(a)) \neq w(e_{T'_2}(a))$. This can happen only if both T'_1 and T'_2 are superstars already. We need to make $w(e_{T'_1}(a)) = w(e_{T'_2}(a))$ for all leaf nodes a. This is done as follows. Partition $L(T'_1)$ into three subsets A, B, and C as follows: A (resp. B, C) is the set of leaf nodes a (resp. b, c) such that $w(e_{T'_1}(a)) = w(e_{T'_2}(a))$ (resp. $w(e_{T'_1}(b)) < w(e_{T'_2}(b))$, $w(e_{T'_1}(c)) > w(e_{T'_2}(c))$).

```
Repeat
    Pick any edge $e_{T'_1}(b)$ with $b \in B$ and $e_{T'_1}(c)$ with $c \in C$. Let
    $d = \min\{[w(e_{T'_1}(c)) - w(e_{T'_2}(c))], [w(e_{T'_2}(b)) - w(e_{T'_1}(b))]\}$. In
    $T'_1$, perform $move(e_{T'_1}(c), d, e_{T'_1}(b))$. Then:
    • If $d = w(e_{T'_2}(b)) - w(e_{T'_1}(b))$, remove $b$ from $B$ and put $b$ into $A$.
    • If $d = w(e_{T'_1}(c)) - w(e_{T'_2}(c))$, remove $c$ from $C$ and put $c$ into $A$.
    • If $d = w(e_{T'_1}(c)) - w(e_{T'_2}(c)) = w(e_{T'_2}(b)) - w(e_{T'_1}(b))$,
      remove $b$ from $B$; remove $c$ from $C$; put both $b$ and $c$ into $A$.
Until $B = C = \emptyset$.
```

Step 4. Now both T'_1 and T'_2 are superstars and $w(e_{T'_1}(a)) = w(e_{T'_1}(a))$ for all leaf nodes a. We adjust the topology of the supernodes of T'_1 and T'_2 so that T'_1 and T'_2 are identical.

LEMMA 11. *Assume that T_1 and T_2 do not share any good edge pairs. Then Algorithm DST approximates $D_{\mathrm{st}}(T_1, T_2)$ to within a factor of 2 in $O(n^2)$ time.*

PROOF. We analyze the cost and running time of each step of the algorithm. We use the adjacency-list representation of a tree. Steps 0 and 4 incur no costs and can be easily implemented in $O(n)$ time. During Steps 1, 2, and 3.1, we only transfer subtrees across internal edges of T_1 and T_2. Over any portion of such an edge e, at most one subtree-transfer operation occurs. So the total cost of these steps is bounded above by $W_{\mathrm{int}}(T_1) + W_{\mathrm{int}}(T_2)$. Moreover, it is easy to see that at most $O(n)$ moves are performed during Steps 1, 2, and 3.1, and since each move operation can be implemented in $O(n)$ time, the total time for all these steps is at most $O(n^2)$.

Next, consider Step 3.2. Before the repeat loop is entered, for any $c \in C$, we have:

- $w(e_{T'_1}(c)) = w(e_{T_1}(c))$. (This is because no additional weight is moved to the edge $e_{T'_1}(c)$ during Steps 1 and 2.)
- $w(e_{T'_2}(c)) \geq w(e_{T_2}(c))$.

During Step 3.2 we only transfer subtrees across the edges $e_{T'_1}(c)$ for $c \in C$. Fix such an edge. Note that any portion of $e_{T'_1}(c)$ is traversed at most once during Step 3.2. Once the length of $e_{T'_1}(c)$ is reduced to $w(e_{T'_2}(c))$, c is removed from C. So the portion of $e_{T'_1}(c)$ traversed during Step 3.2 is $w(e_{T'_1}(c)) - w(e_{T'_2}(c)) = w(e_{T_1}(c)) - w(e_{T'_2}(c)) \leq w(e_{T_1}(c)) - w(e_{T_2}(c))$. So the total cost of Step 3.2 is at most $\sum_{c \in C}[w(e_{T'_1}(c)) - w(e_{T'_2}(c))] \leq$

$\sum_{c \in C}[w(e_{T_1}(c)) - w(e_{T_2}(c))] \le W_{\mathrm{ext},T_1>T_2}(T_1)$. Also, we perform at most $O(n)$ move operations during Step 3.2, and hence this step can also be implemented in $O(n^2)$ time.

Thus the total cost of the algorithm is bounded above by $W_{\mathrm{int}}(T_1) + W_{\mathrm{int}}(T_2) + W_{\mathrm{ext},T_1>T_2}(T_1)$, which is at most $2D_{\mathrm{st}}(T_1, T_2)$ by Lemma 6. □

Next we consider the general case when T_1 and T_2 may share some good edge pairs. First we show how to find all good edge pairs efficiently.

LEMMA 12. *Let T_1 and T_2 be two trees, each with n leaves. Then the set of good edges of T_1 (with respect to T_2) can be enumerated in $O(n^2)$ time.*

PROOF. First we calculate, for every edge e of either T_1 or T_2, $w(E(T_{11}))$ and $w(E(T_{12}))$ where T_{11} and T_{12} are two subtrees at the two endpoints of e. This can be trivially done in $O(n^2)$ time. Next we ignore condition 2 of the definition of good edge pairs (Definition 2), and find all those edge pairs of T_1 and T_2 which satisfy only condition 1 of this definition. This can be done in $O(n)$ time by Lemma 12. Finally, for every such edge pair which satisfies condition 1 of this definition, we check if it satisfies condition 2 of the definition also. This takes $O(n^2)$ time. □

We now show how to apply Algorithm DST to achieve an approximation ratio of 2 when T_1 and T_2 may share some good edge pairs. Let K be the number of good edge pairs in T_1 and T_2. Our algorithm is by induction on K. If $K = 0$, Algorithm DST works by Lemma 11. Suppose $K > 0$. Let $e_1 = (u_1, v_1) \in E(T_1)$ and $e_2 = (u_2, v_2) \in E(T_2)$ be a good edge pair. Let T_1' and T_1'' be the two subtrees of T_1 partitioned by e_1. Let T_2' and T_2'' be the two subtrees of T_2 partitioned by e_2, where $L(T_1') = L(T_2')$ and $L(T_1'') = L(T_2'')$.

Assume $w(E(T_1')) \le w(E(T_2')) < w(E(T_1')) + w(e_1)$. (The other case can be handled in a similar way.) Add a new edge (u_1, x) to T_1' and assign $w((u_1, x)) = w(E(T_2')) - w(E(T_1'))$. Add a new edge (x, v_1) to T_1'' and assign $w((x, v_1)) = w(e_1) - w((u_1, x))$. Add a new edge (u_2, x) to T_2' and assign $w((u_2, x)) = 0$. Add a new edge (x, v_2) to T_2'' and assign $w((x, v_2)) = w(e_2)$. (See Figure 11). Note that the weights of all new edges are nonnegative.

Now we have $L(T_1') = L(T_2')$ and $w(T_1') = w(T_2')$. We can normalize the weights of T_1' and T_2' such that their sum is one. By induction hypothesis, we can transform T_1' to T_2' with cost at most $2D_{\mathrm{st}}(T_1', T_2')$. Similarly, we can transform T_1'' to T_2'' with cost at most

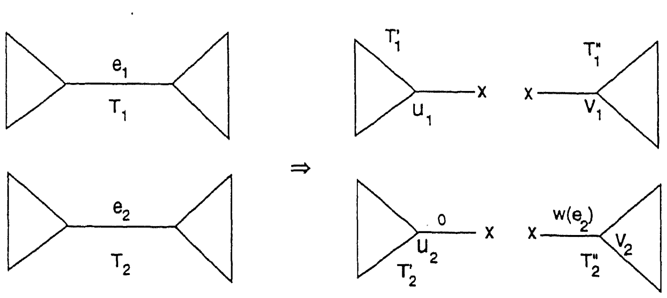

Fig. 11. Cut each of T_1 and T_2 into two smaller trees.

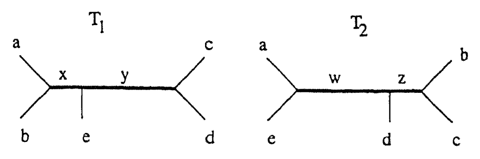

Fig. 12. A counterexample to the entangle conjecture.

$2D_{st}(T_1'', T_2'')$. Combining the two transfer sequences, we can transform T_1 to T_2 with cost at most $2D_{st}(T_1, T_2)$. The complete algorithm takes $O(n^2)$ time. This completes the proof of Theorem 10.

REMARK. Naturally, one may try to investigate if the performance ratio of 2 in Theorem 10 can be further improved. For this purpose, note that in some cases, the lower bounds of Lemma 6 are rather weak, for instance if two trees have four leaves each, differently partitioned over the single internal edge of weight one, with all four external edges having zero weight. The transformation cost in this case is two, whereas the above only shows a lower bound of one. The internal edges of these two trees could be said to be *entangled*, since they partition the leaves in sets none of which is contained in another. So one must bring the various leaves together first, and after repartitioning, move them apart again. This led us to the following conjecture: *Disjoint pairs of entangled edges contribute at least their sum of weights to the optimal cost.* However, the trees in Figure 12 provide a counterexample (external edges have zero weight), in that the edge pairs $\{x, w\}$ and $\{y, z\}$ are both entangling, yet the distance between T_1 and T_2 is less than the sum weight of these four edges.

4. Discussion and Open Problems.

These results have been obtained as a part of our larger project of building a comprehensive software package for comparing phylogenetic trees.

One may wonder why we could obtain a factor 2 approximation for the linear-cost subtree-transfer distance on weighted phylogenies, where we could get only a $\log n$ factor approximation for unweighted phylogenies. However, notice that all intermediate trees in the unweighted case are also binary trees, whereas in the weighted case, intermediate trees of high degree may be produced (e.g., by allowing zero length edges). In other words, in the weighted case, the topology of an intermediate tree may be considerably different from the given trees, and in fact, we do utilize this to get a factor 2 approximation. Consequently, the distance may vary considerably depending on whether we are considering unweighted or weighted phylogenies. For example, consider unweighted trees with n labeled leaves, and weighted trees with n labeled leaves where the weight of every internal edge is $1/(n-3)$ and the rest of the edges have zero weights. Assume also the two (unweighted or weighted) trees involved in the distance calculation share no good edge pairs (Definition 1 or 2, as appropriate). In the unweighted case, it is known that there are two trees which are at a distance of $\Omega(n \log n)$ [23]. However, in the weighted case, our factor 2 approximation algorithm and the lower bounds in Lemma 6 imply that any two trees are at a distance of at most $O(1)$.

Several open questions still remain and may be worth pursuing further:

1. Is the linear-cost subtree-transfer problem NP-hard when the trees are (uniquely) labeled **and** weighted?
2. Can we approximate the linear-cost subtree-transfer distance for weighted phylogenies with a ratio better than 2?

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References

[1] D. Barry and J. A. Hartigan, Statistical analysis of hominoid molecular evolution, *Statist. Sci.*, 2 (1987), 191–210.

[2] T. H. Cormen, C. E. Leiserson, and R. L. Rivest, *Introduction to Algorithms*, The MIT Press, Cambridge, MA, 1990.

[3] B. DasGupta, X. He, T. Jiang, M. Li, J. Tromp, and L. Zhang, On distances between phylogenetic trees, *Proc. 8th Annual ACM-SIAM Symposium on Discrete Algorithms*, 1997, pp. 427–436.

[4] B. DasGupta, X. He, T. Jiang, M. Li, J. Tromp, and L. Zhang, On computing the nearest neighbor interchange distance, Preprint, 1997.

[5] W. H. E. Day, Optimal algorithms for comparing trees with labeled leaves, *J. Classification*, 2 (1985), 7–28.

[6] A. W. F. Edwards and L. L. Cavalli-Sforza, The reconstruction of evolution, *Ann. Human Genetics*, 27 (1964), 105. (Also in *Heredity*, 18, 553.)

[7] J. Felsenstein, Evolutionary trees for DNA sequences: a maximum likelihood approach. *J. Mol. Evol.*, 17 (1981), 368–376.

[8] J. Felsenstein, Personal communication, 1996.

[9] W. M. Fitch, Toward defining the course of evolution: minimum change for a specified tree topology, *Syst. Zool.*, 20 (1971), 406–416.

[10] W. M. Fitch and E. Margoliash, Construction of phylogenetic trees, *Science*, 155 (1967), 279–284.

[11] M. R. Garey and D. S. Johnson, *Computers and Intractability: A Guide to the Theory of NP-Completeness*, Freeman, San Francisco, CA, 1979.

[12] J. Hein, Reconstructing evolution of sequences subject to recombination using parsimony, *Math. Biosci.*, 98 (1990), 185–200.

[13] J. Hein, A heuristic method to reconstruct the history of sequences subject to recombination, *J. Mol. Evol.*, 36 (1993), 396–405.

[14] J. Hein, Personal email communication, 1996.

[15] J. Hein, T. Jiang, L. Wang, and K. Zhang, On the complexity of comparing evolutionary trees, *Discrete Appl. Math.*, 71 (1996), 153–169.

[16] M. Kuhner and J. Felsenstein, A simulation comparison of phylogeny algorithms under equal and unequal evolutionary rates. *Mol. Biol. Evol.* 11(3) (1994), 459–468.

[17] W. J. Le Quesne, The uniquely evolved character concept and its cladistic application, *Syst. Zool.*, 23 (1974), 513–517.

[18] M. Li, J. Tromp, and L. Zhang, Some notes on the nearest neighbor interchange distance, *J. Theoret. Biol.*, 182 (1996), 463–467.

[19] G. W. Moore, M. Goodman, and J. Barnabas, An iterative approach from the standpoint of the additive hypothesis to the dendrogram problem posed by molecular data sets, *J. Theoret. Biol.*, 38 (1973), 423–457.

[20] D. F. Robinson, Comparison of labeled trees with valency three, *J. Combin. Theory Ser. B*, 11 (1971), 105–119.

[21] N. Saitou and M. Nei, The neighbor-joining method: a new method for reconstructing phylogenetic trees, *Mol. Biol. Evol.*, 4 (1987), 406-425.

[22] D. Sankoff, Minimal mutation trees of sequences, *SIAM J. Appl. Math.*, 28 (1975), 35–42.

[23] D. Sleator, R. Tarjan, and W. Thurston, Short encodings of evolving structures, *SIAM J. Discrete Math.*, 5 (1992), 428–450.

[24] A. von Haseler and G. A. Churchill, Network models for sequence evolution, *J. Mol. Evol.*, 37 (1993), 77–85.

[25] M. S. Waterman and T. F. Smith, On the similarity of dendrograms, *J. Theoret. Biol.*, 73 (1978), 789–800.