Rotation Distance is Fixed-Parameter Tractable

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Abstract

Rotation distance between trees measures the number of simple operations it takes to transform one tree into another. There are no known polynomial-time algorithms for computing rotation distance. In the case of ordered rooted trees, we show that the rotation distance between two ordered trees is fixed-parameter tractable, in the parameter, k, the rotation distance. The proof relies on the kernalization of the initial trees to trees with size bounded by 7k.

1 Introduction

Balancing binary search trees is an important task to ensure good performance for searches. Rotations are simple transformations that can be used to dynamically adjust trees in an effort to keep them reasonably balanced. A left or right rotation at a node, shown in Figure 1, promotes one grandchild, demotes one child, and switches one grandchild to a different parent node. Sequences of rotations suffice to transform a tree to any other tree with the same number of nodes. The rotation distance between two trees is the minimum number of such rotations needed to transform one to the other. There has been a great deal of work on estimating, bounding and computing this distance. Culik and Wood [10] gave an immediate upper bound of 2n - 2 for the distance between two trees with n nodes, and in remarkable work using methods of hyperbolic volume, Sleator, Tarjan, and Thurston [17] showed not only that 2n - 6 is an upper bound, but furthermore that for all large n, that bound is realized. There are no known polynomial-time algorithms for computing rotation distance, though there are estimation algorithms of Pallo [15], Pallo and Baril [2], and Rogers [16]. The NP-hardness of this problem remains open.

We make progress on the computational complexity of rotation distance by showing that it is fixed-parameter tractable. We show the fixed-parameter tractability by reducing (or "kernalizing") the common structures in the trees being compared. The technique of

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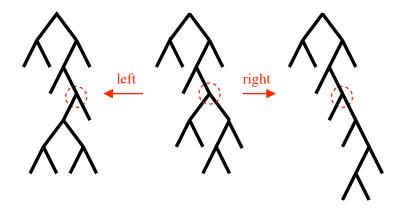


Figure 1: A right rotation at a node consists of rotating the right child of the left child of the node to the left child of the right child of the node. A left rotation is defined similarly by moving the left child of the right child of the node to the left child of the node. The circled node in the middle tree has been rotated right to yield the tree on the right, and similarly rotated right to yield the tree on the left.

kernalizing problem instances has been very successful in showing the tractability of a wide range of problems [12, 13]. For reduction rules, we use the "subtree reduction" where identical subtrees are reduced in both, which arises in several settings (including the study of tree pairs through Thompson's group F [8, 7, 9]) to produce "reduced tree pairs" which have the same rotation distance as the original tree pair, as shown in Figure 2. This subtree reduction rule also preserves biologically interesting distances for phylogenetic trees (roughly, leaf-labeled, unordered trees). Allen and Steel [1] showed that the biologically motivated "tree-bisectionand-reconnection" (TBR) distance is preserved under the subtree reduction rule, as well as a reduction rule that shrinks common chains, illustrated in Figure 3. They further show that the reduced trees have O(k) size, where k is the TBR distance between the trees. This reduces the question of calculating the TBR distance to comparing trees whose size is dependent only on k, which is used to prove that TBR distance is fixed-parameter tractable. Other distance calculations have also been shown to be fixed-parameter tractable via similar reductions [3, 5, 6].

To show that rotation distance is fixed-parameter tractable, we follow a similar strategy to those used for phylogenetic tree distances: we show that the subtree and chain reductions preserve distance and then show that the resulting reduced trees have size bounded by 7k, where k is the rotation distance. The reductions can be done in linear time [4]. The reduced trees can be checked in f(k) time to see if their distance is less than or equal to k. While this check could take exponential time, it depends only on k, yielding the fixed-parameter tractability of computing rotation distance.

2 Background

Rotation Distance

We consider ordered, leaf-labelled, rooted binary trees with n interior nodes and where each interior node has 2 children. Such trees are commonly called *extended binary trees* [14] or *full binary trees*. In the following, 'tree' refers to such a tree with an ordering on the leaves, 'node' refers to an interior node, and 'leaf' refers to a non-interior node. Our trees will have n interior nodes and n + 1 leaves numbered in left-to-right order from 0 to n.

Right rotation at a node of a rooted binary tree is defined as as a simple change to T and is illustrated in Figure 1, taking the middle tree to the right-hand one. Left rotation at a node is the natural inverse operation. The rotation distance $d_R(T_1, T_2)$ between two rooted binary trees T_1 and T_2 with the same number of leaves is the minimum number of rotations needed to transform T_1 to T_2 .

The specific instance of the rotation distance problem we address is:

ROTATION DISTANCE

INPUT: Two rooted ordered trees, T_1 and T_2 on n leaves and parameter k, QUESTION: Is the rotation distance between them, $d_R(T_1, T_2) \leq k$?

There are no known polynomial time algorithms to compute rotation distance, though there are polynomial time algorithms of Rogers [16], Pallo[15] and Pallo and Baril [2] to estimate it. The general difficulty of computing rotation distance comes from the lower bound. Finding a sequence of rotations which accomplish the transformation gives only an upper bound.

Edge-Flipping Distance

Rooted binary trees correspond naturally to triangulations of polygons via a standard equivalence, described in [17]. A basic move of changing a triangulation is to choose two adjacent triangles forming a quadrilateral in the polygon, and replace it with two triangles where the resulting quadrilateral has the opposite diagonal. This edge-flipping move is exactly equivalent to performing a single rotation on the corresponding rooted trees. We define *edge-flipping distance* between two triangulations P_1 and P_2 of an *n*-gon to be the minimal number of such edge-flipping moves to transform P_1 to P_2 . In Lemma 3b, Sleator, Tarjan and Thurston [17] show that if two subdivisions P_1 and P_2 share a common diagonal, then the diagonal flip distance between P_1 and P_2 is equal to the sum of the distances between the polygonal subdivisions obtained by the subpolygons cut off before and after the common diagonal. The edge-flipping distance between P_1 and P_2 will be exactly the rotation distance of their corresponding trees.

Fixed-Parameter Tractability

Roughly, the ability to efficiently calculate instances that are small, with respect to some parameter, is called fixed-parameter tractability. In our case, the parameter is the distance,

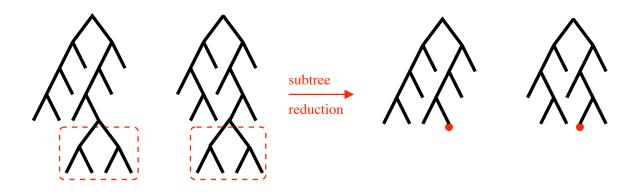


Figure 2: The subtree reduction rule replaces common subtrees, in the pair of ordered trees on the same number of leaves, by a placeholder of a single node. A necessary condition is that the leaves of subtree be labelled (numbered) identically in each of the initial trees. Note that the subtree enclosed by the dotted line is on the sixth through eighth leaves in the ordering in both trees. These subtrees are replaced by a single node, indicated by a circle in the right hand pair of trees. The new reduced trees, like the initial trees, are on the same number of leaves.

k, between the trees. We show that the rotation distance can be solved in time polynomial in the size of the input (that is, the number of leaves or nodes) but exponential in the size of a fixed-parameter, k the distance. See Downey and Fellows [11] for more details. More formally:

Definition 1 A problem Φ is fixed-parameter tractable in a parameter k, if there exists some constant c (independent of k) and a function f such Φ accepts $\langle x, k \rangle$ in time $O(f(k)|x|^c)$.

3 Reduction Rules

We use two reduction rules, to reduce the size of the problem. The first rule, as mentioned above, replaces common subtrees with a single node. The second rule replaces common chains with a sequence of 3 nodes, as done by Allen and Steel [1]. We will show in the next section that these reduced trees have distance bounded by f(k) for k the rotation distance and f a function that depends only on k, not n.

Subtree Reduction: This straightforward reduction eliminates a common subtree and replaces it with a single placeholder leaf. This reduction is a natural one: Sleator, Tarjan and Thurston [17] use it in rotation distance, interpreted there as diagonal-flip distance between triangulations of polygons. It arises naturally in connection with the tree pair diagrams representing elements of Thompson's group F [7]. And it also has been used in the comparison of phylogenetic trees [1]. More formally:

Definition 2 Given ordered trees T_1 and T_2 on n leaves, if there exists a subtree S that occurs in both T_1 and T_2 , an application of the subtree reduction rule consists of replacing S in both trees by a new leaf s and call the new trees T'_1 and T'_2 . See Figure 2.

In the context of triangulations of polygons, common subtrees give common diagonals between the triangulations. Lemma 3b of [17] is that if two triangulations share a common diagonal, then any shortest part realizing the rotation distance will not change that diagonal. Thus, in terms of the dual trees, the rotation distance is preserved under by the subtree reduction rule- there will be no rotations which change the common subtrees. Thus, $d_R(T_1, T_2) = d_R(T'_1, T'_2)$ if T'_1 and T'_2 are the result of applying the subtree rule to T_1 and T_2 , which gives the following lemma:

Lemma 1 [17] The subtree reduction rule preserves rotation distance.

Chain Reduction: This reduction eliminates a (potentially long) chain common to both trees and replaces it with a short chain consisting of 3 pendant leaves. This is a useful reduction rule for phylogenetic trees since it does not change many of the common tree distances. Allen & Steel [1] showed that TBR distance is preserved when long common chains are replaced by chains of length 3. Variants of this rule have also been used to show that other biologically inspired calculations are fixed-parameter tractable [3, 5, 6]. Formally,

Definition 3 Given ordered trees T_1 and T_2 on n leaves, a common chain t_1, t_2, \ldots, t_m is a sequence of pendant subtrees that occur identically in T_1 and T_2 and for which in both T_1 and T_2 :

- For each j and k such that $1 \leq j < k \leq$, the path between the root and the subtree t_j is shorter than the path between the root and the subtree t_k .
- For each j = 1, ..., m 1, the parent of the subtree t_j is the grandparent of t_{j+1} , and
- For each j = 1, ..., m, t_j is the left child of its parent in T_1 if and only if t_j is the right child of its parent in T_2 .

the restrictions of

Definition 4 Given ordered trees T_1 and T_2 on n leaves, if there exists a common chain t_1, t_2, \ldots, t_m that occurs identically in both T_1 and T_2 , an application of the common chain reduction rule consists of replacing t_1, t_2, \ldots, t_m in both trees by a chain of pendant leaves a, b, c, ordered the same way and calling the new trees T'_1 and T'_2 . See Figure 3.

We note that the chain of pendant leaves, a, b, c serve as a placeholder in the reduction and can be oriented in any way, as long as they meet the definition of a chain.

4 Fixed-Parameter Tractability

To show that rotation distance is fixed-parameter tractable, we first show that the common chain rule reductions preserve rotation distance. This, combined with the straightforward fact that subtree rule reductions preserve distances (stated in [17]), gives reduced trees whose

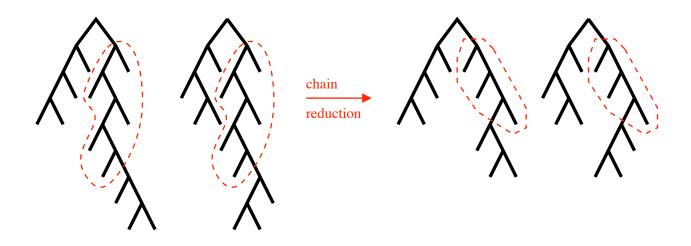


Figure 3: The common chain reduction rule replaces long common chains in ordered trees on the same number of leaves. Since the trees are ordered, we can assume that the leaves have increasing labels from 0 to 11. On the left, the common chain, enclosed by the dotted line, consists of the leaves, 11, 4, 10, 5, and 6, traversing the chain from top to bottom. We apply the chain reduction to this chain to yield the trees on the right. Note that the resulting trees are on the same number of leaves and the reduced chain contains leaves 4, 5, and 9, under the new labeling 0 to 9.

size is bounded only by a function of k. To check if the distance between original trees is at most k, if suffices to check the distance between the reduced trees. This can be done in O(f(k)) time, where f(k) does not depend on n, but is exponential in k.

Lemma 2 Let T_1 and T_2 be ordered rooted trees, and T'_1 and T'_2 the result of applying the chain rule reduction to these initial trees. Then $d_R(T'_1, T'_2) = d_R(T_1, T_2)$.

Proof: Let T_1 and T_2 be ordered, rooted trees with a common chain, l_1, l_2, \ldots, l_m , and let T'_1 and T'_2 the result of applying the chain rule reduction to these initial trees. We consider the dual polygonal subdivisions of the trees. In that case, having a common chain means having a sequence of adjacent shared diagonals. In Lemma 3b, Sleator, Tarjan and Thurston [17] show that if two subdivisions P_1 and P_2 share a common diagonal, then the diagonal flip distance between P_1 and P_2 is equal to the sum of the distances between the polygonal subdivisions obtained by the subpolygons cut off before and after the common diagonal. Since the sequence of common diagonals (i.e. the common chain) are contiguous, the distance equals the sum of the distances of the subpolygons above and below the sequence of diagonals. Shrinking the number of common diagonals does not change the distances. Thus, the distance between the original trees equals the distances between the reduced trees: $d_R(T_1, T_2) = d_R(T'_1, T'_2)$.

The proof of fixed-parameter tractability relies on bounding the size of the reduced trees, since as noted above, our algorithm consists of reducing the trees to ones with equivalent distance but size bounded by a function of k and then exhaustively trying all sequences of $\leq k$ moves to find the distance.

Theorem 3 Given two ordered, rooted trees, T_1 and T_2 with the same number of leaves. Let T'_1 and T'_2 be the result of applying the two reductions rules exhaustively to the given trees. If $d(T_1, T_2) \leq k$, then $|T'_1| \leq 7k$.

Proof: Given two ordered, rooted trees, T_1 and T_2 with the same number of leaves. Assume that $d(T_1, T_2) \leq k$. We will show, by induction on k, that $|T'_1| \leq 7k$.

k = 1: Assume that T_1 and T_2 are not identical and that $d(T_1, T_2) = d(T'_1, T'_2) = 1$. Then, a single rotation, at some node N, transforms T'_1 into T'_2 . Since by the subtree reduction rule, identical subtrees have been reduced, the descendants of N are singletons. If N is not the root, the path from N to the root must be identical in both trees and can have at most three pendant leaves (since larger common chains and identical subtrees have been reduced). The other child of the root must be a singleton and identical in both, so, is a single leaf. Thus, the total number of leaves in T'_1 is no more than 7.

k > 1: Without loss of generality, we assume that $k = d(T_1, T_2) = d(T'_1, T'_2) > 1$. Then there exists trees, I, with the same number of leaves as T_1 , and I', with the same number of leaves as T'_1 , such that $d(T_1, I) = d(T'_1, I') = 1$ and $d(I, T_2) = d(I', T'_2) = k - 1$. T'_1 and I'differ by a single rotation, r.

First, assume that this first rotation at node N yields a subtree identical to that in T_2 (that is, the subtrees rooted at N are identical in I and T_2). Then, the trees I' and T'_2 are not reduced (since they have a common subtree rooted at N). Since their only difference with the tree pair T'_1 and T'_2 occurs at node N, a single subtree reduction will fully reduce I' and T'_2 . We now argue that the subtree rooted at N can have at most 7 leaves. Since the subtrees rooted at N are identical in I' and T'_2 , there are no rotations below N in the tree, and N has exactly 3 leaves below it. As in the base case, N could have a chain of at most 3 pendant leaves above it. If N is replaced by a single node in I' and T'_2 , yielding new trees I'' and T''_2 , then I'' and T''_2 have fewer than |I'| - 6 leaves. I'' and T''_2 satisfy the induction hypothesis with $d(I', T'_2) = d(I'', T''_2) = k - 1$, yielding $|I''| \leq 7(k - 1)$. Thus, $|T'_1| \leq |I''| + 6 \leq 7(k - 1) + 6 \leq 7k$.

Now, assume that this first rotation at node N yields a subtree that is not identical to that in T_2 . Then, the trees I' and T'_2 are fully reduced and have distance k - 1, and we can apply the induction hypothesis to them, yielding $|I'| \leq 7(k - 1)$. Since $|I'| = |T'_1|$, we have $|T'_1| = 7(k - 1) < 7k$.

From the kernalization of the problem, the fixed-parameter tractability easily follows:

Corollary 4 Rotation distance is fixed-parameter tractable in parameter, k, the distance.

Proof: Given two ordered, rooted trees, T_1 and T_2 on the same leaf set, and a parameter k. We define an algorithm for computing " $d_R(T_1, T_2) \leq k$ " as follows:

- 1. Let T'_1 and T'_2 be the result of applying the two reductions rules exhaustively to the given trees.
- 2. If $|T'_1| > 7k$, then output "NO."
- 3. Else, $|T'_1| \leq 7k$. Try all sequences of k or less rotations to transform T'_1 to T'_2 . If one such sequence is successful, ouput "YES."

4. Else, if no such sequence transforms T'_1 to T'_2 , then output "NO."

Step 1 takes time linear in the number of nodes n, and by Theorem 3 the distances between the given trees and the reduced trees are the same. Step 3 can take no more than $(7k)^k$ steps. Thus rotation distance is fixed-parameter tractable in the parameter k.

We note that the bound of $(7k)^k$ is crude and can be improved either by using any of the standard exhaustive methods for computing rotation distance which are exponential in 7k, or by precomputing the rotation distances for pairs of trees of size no more than 7k. The Catalan numbers C_{7k} count the number of trees of size 7k, and the number of tree pairs to consider is thus on the order of $(4^{7k})^2$.

5 Conclusion

We have shown that rotation distance of ordered trees is fixed-parameter tractable in parameter, k, the distance. Step 3 of the algorithm from Section 4 is exponential in the parameter k, the distance. An obvious remaining open question is "can rotation distance be calculated in polynomial time?"

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