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On the Maximum Parsimony Distance Between Phylogenetic Trees

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Abstract. Within the field of phylogenetics there is great interest in distance measures to quantify the dissimilarity of two trees. Here, based on an idea of Bruen and Bryant, we propose and analyze a new distance measure: the Maximum Parsimony (MP) distance. This is based on the difference of the parsimony scores of a single character on both trees under consideration, and the goal is to find the character which maximizes this difference. In this article we show that this new distance is a metric and provides a lower bound to the well-known Subtree Prune and Regraft (SPR) distance. We also show that to compute the MP distance it is sufficient to consider only characters that are convex on one of the trees, and prove several additional structural properties of the distance. On the complexity side, we prove that calculating the MP distance is in general NP-hard, and identify an interesting island of tractability in which the distance can be calculated in polynomial time.

Keywords: maximum parsimony, tree metric, subtree prune and regraft (SPR)

1. Introduction

Finding the optimal tree explaining a given dataset, e.g., a DNA alignment, is one of the biggest challenges in modern phylogenetics. One challenge is that for most optimization criteria finding the best tree is NP-hard (cf. [12, 17, 23]). For this reason heuristics based on local neighborhood search are often used. A second challenge concerns the fact that, for mathematical and/or biological reasons, many distinct tree solutions may be generated, and some way of determining their relative similarity is required. Both problems can be addressed using SPR (Subtree-Prune-and-Regraft). A single SPR move involves moving to a neighboring tree by detaching a branch and re-attaching it elsewhere. The SPR distance is the minimum number of SPR

moves required to transform one tree into another. Unfortunately, computing the SPR distance is hard [5, 6]. Moreover, for SPR it makes a big difference whether rooted or unrooted trees are considered [5]. Other metrics, which can be calculated in polynomial time, have been proposed, e.g., the so-called Robinson-Foulds metric [22], but are also sometimes criticized for lack of biological plausibility [20].

In this paper, we propose a new metric, namely, the Maximum Parsimony (MP) distance, which is biologically feasible in the parsimony sense. Our metric basically requires the search for a character which has a low parsimony score on one of the trees involved and a high score on the other one. As the parsimony score is independent of the root position, our metric applies both to rooted and unrooted trees — however, the rooted case requires a minor technical modification, which we explain in the context of Theorem 3.2. We analyze a number of structural properties of the metric, and explore its computational complexity. Indeed, this research was initially inspired by a question posed by Bruen and Bryant: is the MP distance efficiently computable, and could it act as a tractable approximation of the SPR distance? We show that there is a link, at least in one direction, between the two measures: the MP distance provides a lower bound on the SPR metric. Moreover, we show that finding the character maximizing the difference in parsimony performance on two trees can be achieved by considering only characters which are convex on one of the trees. Relatedly, we provide combinatorial bounds on the MP distance and observe that to compute this distance it is not sufficient to restrict our search to characters with a fixed number of states.

Despite the possibility of restricting the problem to convex characters, we prove that calculating the MP distance is, unfortunately, NP-hard. This hardness result also holds when characters with at most two states are considered; interestingly neither hardness result is directly implied by the other. On the positive side we show, by exploiting a classical result from the tree partitioning literature, that the MP distance can be computed in polynomial time when one of the trees is a so-called star tree.

2. Preliminaries and Notation

We need to introduce some notation before presenting our results.

Recall that an *unrooted phylogenetic X-tree* is a tree $\mathcal{T} = (V(\mathcal{T}), E(\mathcal{T}))$ on a leaf set $X = \{1, \ldots, m\} \subset V(\mathcal{T})$. Such a tree is named *binary* if it has only vertices of degree 1 (leaves) or 3 (internal vertices). A *rooted phylogenetic X-tree* additionally has one vertex specified as the *root*, and such a rooted tree is named *binary* if the root has degree 2 and all other vertices are of degree 1 (leaves) or 3 (internal vertices). We often denote trees in the well-known Newick format [3], which uses nested parentheses to group species together according to their degree of relatedness. For instance, $((1, 2), (3, 4))$ is a tree with two so-called cherries $(1, 2)$ and $(3, 4)$ and a root between the two. Unrooted trees have more than two groups of parentheses at the uppermost level.

Furthermore, recall that a *character* f is a function $f \colon X \to \mathcal{C}$ for some set $\mathcal{C} := \{c_1, c_2, c_3, \ldots, c_k\}$ of k *character states* ($k \in \mathbb{N}$). Often, k is assumed to equal 4 in order for $\mathcal{C}$ to represent the DNA alphabet $\{A, C, G, T\}$, but in the present paper k is not restricted this way but can be any natural number. Note that in the special cases

where $|f(X)| = 2$, $|f(X)| = 3$, or $|f(X)| = 4$, we also refer to f as a binary, ternary, or quaternary character, respectively. In general, when $|f(X)| = r$, f is called an *r-state character*. In order to shorten the notation, it is customary to write for instance $f = AACC$ instead of $f(1) = A$, $f(2) = A$, $f(3) = C$, and $f(4) = C$. Note that each r-state character f on taxon set X partitions X into r non-empty and non-overlapping subsets X_i, $i = 1, \ldots, r$, where $x_j, x_k \in X_i$ if and only if $f(x_j) = f(x_k)$. When $r = 2$, the resulting bipartition of X into the non-empty and disjoint sets X_1 and X_2 is called X-*split* and denoted by $X_1|X_2$. Note that the branches of a tree $\mathcal{T}$ induce a collection of X-splits: each edge separates some leaves from the others. Thus, labelling the leaves on one side of the branch with, say, A, and the others, say, with C, gives a binary character. The collection of all splits induced by $\mathcal{T}$ this way will be referred to as $\Sigma(\mathcal{T})$. A tree $\mathcal{T}_1$ is called a *refinement* of another tree $\mathcal{T}_2$, if $\Sigma(\mathcal{T}_2) \subseteq \Sigma(\mathcal{T}_1)$. The *star tree* is a tree $\mathcal{T}$ which has only one internal node with which all leaves are directly connected via a pendant edge, i.e., all splits induced by $\mathcal{T}$ are of the kind $x|X \setminus \{x\}$. Note that all phylogenetic X-trees are refinements of the star tree.

A *refinement* of an r-state character f on X is an $\hat{r}$-state character $\hat{f}$ on X with $r \leq \hat{r}$ such that the partitioning induced by $\hat{f}$ refines that given by f. This means that if f induces the partitioning $X_1|X_2|\cdots|X_r$ and $\hat{f}$ induces the partitioning $Y_1|Y_2|\cdots|Y_{\hat{r}}$, where X_i, Y_j are subsets of X for all $i = 1, \ldots, r$, $j = 1, \ldots, \hat{r}$, then for all $j = 1, \ldots, \hat{r}$ there exists an $i \in \{1, \ldots, r\}$ such that $Y_j \subseteq X_i$.

An *extension* of f to $V(\mathcal{T})$ is a map $g : V(\mathcal{T}) \to \mathcal{C}$ such that $g(i) = f(i)$ for all i in X. For such an extension g of f, we denote by $l_g(\mathcal{T})$ the number of edges $e = \{u, v\}$ in $\mathcal{T}$ on which a *substitution* occurs, i.e., where $g(u) \neq g(v)$. Such substitutions are also often referred to as *mutations* or *changes*. The *parsimony score* or *parsimony length* of a character f on $\mathcal{T}$, denoted by $l_f(\mathcal{T})$, is obtained by minimizing $l_g(\mathcal{T})$ over all possible extensions g of f. The parsimony score of a character f on a phylogenetic tree $\mathcal{T}$ can easily be calculated with the Fitch algorithm [16] if $\mathcal{T}$ is binary. Moreover, the Fitch algorithm was generalized by Hartigan [18] to apply also to non-binary trees. In order to simplify the notation, we will refer to both algorithms as the Fitch algorithm rather than the Fitch-Hartigan or generalized Fitch algorithm. (The only significant difference between the two algorithms is that in the non-binary algorithm, during the bottom-up phase, a parent is allocated all states that occur *most frequently* amongst its children. Letting m denote the number of times a most frequent state occurs amongst the children, the number of mutations incurred is equal to the number of children minus m. This generalizes the intersection/union operations used by the binary algorithm.)

Note that the Fitch algorithm can be applied both to rooted *and* unrooted trees — in the latter case, the tree can be rooted by placing an extra root node on an arbitrary edge of the tree. This implies that the parsimony score does not depend on the root position and that for the parsimony concept it does not matter if we discuss rooted or unrooted trees. This is the reason why the MP distance, which we define shortly, is unaffected by the presence, or location, of a root.

A character f is said to be *convex* or *homoplasy-free* on a tree $\mathcal{T}$ if $l_f(\mathcal{T}) = |f| - 1 = r - 1$, where $|f| = r$ denotes the number of character states employed by f. Note that if a character is convex on a certain tree, this tree minimizes its parsimony score and is therefore most parsimonious for this character. Moreover, recall that two

characters are *compatible* if there exists a phylogenetic X-tree on which both of them are convex, and two splits are said to be compatible if there is a phylogenetic X-tree which contains both branches corresponding to the splits.

Recall that a character f on a leaf set X is said to be *informative* (with respect to parsimony) if at least two distinct character states occur more than once on X. Otherwise f is called *non-informative*. Note that for a non-informative character f, $l_f(\mathcal{T}_i) = l_f(\mathcal{T}_j)$ for all trees $\mathcal{T}_i$, $\mathcal{T}_j$ on the same set X of leaves.

In this paper, we refer to a character always with its underlying taxon *set partition* in mind, i.e., for instance, we do not distinguish between *AACC*, *CCAA*, and *CCGG*, and so on. Moreover, when there is no ambiguity and when the stated result holds for both rooted and unrooted trees, we often just write 'tree' or 'phylogenetic tree' when referring to a phylogenetic X-tree.

Recall that a *subtree prune and regraft* (*SPR*) *move* on a phylogenetic tree $\mathcal{T}$ is defined for unrooted trees according to, e.g., [2, 8], and for rooted trees according to, e.g., [21], as cutting any edge and thereby pruning a subtree, $\tilde{\mathcal{T}}$, and then regrafting the subtree by the same cut edge to a new vertex obtained by subdividing a pre-existing edge in $\mathcal{T} \setminus \tilde{\mathcal{T}}$. If $\mathcal{T}$ is binary, one can suppress degree-2 vertices in order for the resulting tree to be binary, too. We define the *SPR distance* d_{SPR} of two unrooted phylogenetic trees $\mathcal{T}_1$, $\mathcal{T}_2$ as in [8] as the minimum number of SPR moves needed to change $\mathcal{T}_1$ into $\mathcal{T}_2$. Note that for SPR, it does make a difference whether the trees under consideration are rooted or not. When two trees have a different root position but are otherwise identical, d_{SPR} is 0, but their rooted SPR distance is greater than 0. If we refer to the rooted SPR distance as defined in [21], we therefore explicitly write d_{rSPR}.

When discussing the relationship between MP distance and SPR we shall restrict our analysis to binary trees. This is because d_{rSPR} on non-binary trees is a relatively unknown measure (although see [13, 24, 27]) and is usually defined such that refinements of the original trees are permitted. These refinements lead to major technicalities and can be shown to severely weaken the relationship between MP distance and d_{rSPR}. Moreover, in the unrooted context, there are no major results available on d_{SPR} on non-binary trees. Thus, the present paper focusses on *SPR on binary trees*.

3. Structural Properties of MP Distance

3.1. The Maximum Parsimony Distance Between Phylogenetic Trees

3.1.1. Definition and Basic Properties

We are now in a position to introduce the concept of measuring the distance between phylogenetic trees as follows.

Definition 3.1. *Let $\mathcal{T}_1$, $\mathcal{T}_2$ be two (rooted or unrooted) phylogenetic trees on a set X of taxa with $|X| = n$. Then,*

$$d_{MP}(\mathcal{T}_1, \mathcal{T}_2) := \max_f \left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right|$$

describes the Maximum Parsimony distance or MP distance between $\mathcal{T}_1$ and $\mathcal{T}_2$, where the maximum is taken over all characters f on taxon set X.

   Where it is unambiguous from the context we will say that a character f is *optimal* for $\mathcal{T}_1, \mathcal{T}_2$ if $\left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right| = d_{MP}(\mathcal{T}_1, \mathcal{T}_2)$.

   Before we continue with some properties of d_{MP}, we note that the absolute value in the definition of d_{MP} is necessary in order to achieve symmetry: consider $\mathcal{T}_1 = (((1,3),(2,5)),(((4,7),6),8))$ and $\mathcal{T}_2 = ((((2,6),(3,5)),(1,4)),(7,8))$. These two trees are depicted by Figure 1. In this case, the character $f = ACAGCGGA$ gives a difference of $l_f(\mathcal{T}_2) - l_f(\mathcal{T}_1) = 5 - 2 = 3$. An exhaustive search through all characters on 8 taxa reveals that this is maximum; however, it also shows that there is no character $\tilde{f}$ such that $l_{\tilde{f}}(\mathcal{T}_1) - l_{\tilde{f}}(\mathcal{T}_2) = 3$, as all characters on 8 taxa give at most a difference of 2. Thus, the roles of $\mathcal{T}_1$ and $\mathcal{T}_2$ cannot simply be swapped, which is why the absolute value in the definition of d_{MP} is required.

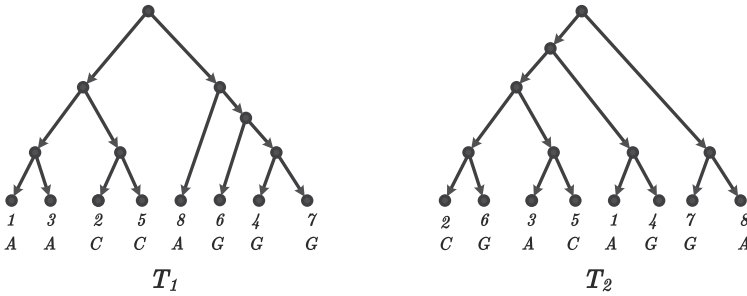Figure 1: Two rooted binary phylogenetic X-trees on the same set of eight taxa, for which the character $f = ACAGCGGA$ gives a difference of $l_f(\mathcal{T}_2) - l_f(\mathcal{T}_1) = 5 - 2 = 3$, but for which there is no character $\tilde{f}$ such that $l_{\tilde{f}}(\mathcal{T}_1) - l_{\tilde{f}}(\mathcal{T}_2) = 3$.

   We now formally state that the definition of d_{MP} is indeed a metric. Note that there is a slight technicality pertaining to rooted trees. For two distinct rooted trees $\mathcal{T}_1, \mathcal{T}_2$ which are identical when the root is suppressed, i.e., when they are regarded as unrooted, we have $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = 0$ even though $\mathcal{T}_1 \neq \mathcal{T}_2$. This is due to the fact that the parsimony score is not influenced by the root position. Thus, when regarding rooted trees, in order for d_{MP} to be a metric, we need to modify the trees such that an additional leaf is pending on the root. This is a standard assumption often made in phylogenetics when transforming rooted trees to unrooted ones.

Theorem 3.2. *The MP distance as defined in Definition 3.1 is a metric for unrooted trees as well as for rooted trees with the assumption of an additional leaf, say x, attached to the root, i.e., it fulfills the following properties*:

(1) $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) \geq 0$ *for all phylogenetic trees* $\mathcal{T}_1, \mathcal{T}_2$,
(2) $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = 0$ *if and only if* $\mathcal{T}_1 = \mathcal{T}_2$,
(3) $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = d_{MP}(\mathcal{T}_2, \mathcal{T}_1)$ *for all phylogenetic trees* $\mathcal{T}_1, \mathcal{T}_2$,
(4) $d_{MP}(\mathcal{T}_1, \mathcal{T}_3) \leq d_{MP}(\mathcal{T}_1, \mathcal{T}_2) + d_{MP}(\mathcal{T}_2, \mathcal{T}_3)$ *for all phylogenetic trees* $\mathcal{T}_1, \mathcal{T}_2, \mathcal{T}_3$.

   Before we can prove Theorem 3.2, we recall the following theorem from [25, Theorem 3.1.4], which goes back to [10]:

Theorem 3.3. (Splits Equivalence Theorem) *Let* Σ *be a collection of X-splits. Then, there is an X-tree* $\mathcal{T}$ *such that* $\Sigma(\mathcal{T}) = \Sigma$ *if and only if the splits in* Σ *are pairwise compatible. Moreover, if such an X-tree exists, then, up to isomorphism,* $\mathcal{T}$ *is unique.*

We are now in a position to prove Theorem 3.2.

Proof of Theorem 3.2. Properties (1) and (3) are clear by the usage of the absolute value in the definition of d_{MP}.

Now consider Property (2). Let $\mathcal{T}_1$, $\mathcal{T}_2$ be two phylogenetic X-trees with $|X| = n$. If $\mathcal{T}_1 = \mathcal{T}_2$, then for all characters f on X we have $l_f(\mathcal{T}_1) = l_f(\mathcal{T}_2)$ and therefore $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = 0$. This completes the first direction. If, on the other hand, $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = 0$, this implies, by the definition of d_{MP} and by Property (1), that $l_f(\mathcal{T}_1) = l_f(\mathcal{T}_2)$ for all characters f on X. In particular, all splits induced by $\mathcal{T}_1$ and their corresponding characters give the same parsimony score, namely 1, on $\mathcal{T}_2$. Thus, all binary characters induced by the branches of $\mathcal{T}_1$ are convex on $\mathcal{T}_2$ and thus are compatible with the binary characters induced by the splits of $\mathcal{T}_2$ and vice versa. So the entire collection of splits induced by both $\mathcal{T}_1$ and $\mathcal{T}_2$ is convex on both $\mathcal{T}_1$ and $\mathcal{T}_2$ and the splits are therefore in particular pairwise compatible. However, by Theorem 3.3, this implies $\mathcal{T}_1 = \mathcal{T}_2$.

Next we prove the triangle inequality stated by Property (4). Let $\mathcal{T}_1, \mathcal{T}_2, \mathcal{T}_3$ be phylogenetic X-trees. Let $\hat{f} := \arg\max_f \left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_3) \right|$, i.e., $\hat{f}$ is a character which gives $d_{MP}(\mathcal{T}_1, \mathcal{T}_3)$. Without loss of generality, assume $l_{\hat{f}}(\mathcal{T}_1) \geq l_{\hat{f}}(\mathcal{T}_3)$, which implies $d_{MP}(\mathcal{T}_1, \mathcal{T}_3) = l_{\hat{f}}(\mathcal{T}_1) - l_{\hat{f}}(\mathcal{T}_3)$. Now consider $\mathcal{T}_2$:

$$
\begin{aligned}
d_{MP}(\mathcal{T}_1, \mathcal{T}_2) + d_{MP}(\mathcal{T}_2, \mathcal{T}_3) &= \max_f \left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right| + \max_f \left| l_f(\mathcal{T}_2) - l_f(\mathcal{T}_3) \right| \\
&\geq \left(l_{\hat{f}}(\mathcal{T}_1) - l_{\hat{f}}(\mathcal{T}_2) \right) + \left(l_{\hat{f}}(\mathcal{T}_2) - l_{\hat{f}}(\mathcal{T}_3) \right) \\
&= l_{\hat{f}}(\mathcal{T}_1) - l_{\hat{f}}(\mathcal{T}_3) \\
&= d_{MP}(\mathcal{T}_1, \mathcal{T}_3).
\end{aligned}
$$

Here, the inequality is due to the definition of d_{MP} with the absolute value and the maximum, i.e., the inequality holds for any character on X and thus in particular for $\hat{f}$. This completes the proof. ∎

3.1.2. The Relationship of the MP Distance and the SPR Distance

The idea of introducing a new distance measure on the tree space was motivated by the search for bounds on the SPR distance. The fact that our MP distance indeed provides a lower bound for the (unrooted) SPR distance can be concluded by building on:

Theorem 3.4. (Bruen and Bryant, [8, Theorem 1]) *Let* f *be a character with r states on a taxon set X and let* $\mathcal{T}$ *be an unrooted binary phylogenetic X-tree. It takes exactly* $l_f(\mathcal{T}) - (r-1)$ *SPR moves to transform* $\mathcal{T}$ *into a tree on which* f *is convex.*

Before we can use Theorem 3.4 to prove that our new metric is a lower bound for the SPR distance, we first introduce a general observation on refinements of characters, which subsequently helps us to simplify the search for the character that maximizes the MP distance between any two trees.

Lemma 3.5. *Let $\mathcal{T}$ be a phylogenetic X-tree, let f be a character on $\mathcal{T}$ and $\tilde{f}$ a refinement of f. Then, $l_f(\mathcal{T}) \leq l_{\tilde{f}}(\mathcal{T})$.*

Proof. If $f = \tilde{f}$, there is nothing to show. Now let the partitioning induced by f be $X_1|X_2|\cdots|X_r$ and the partitioning induced by $\tilde{f}$ be $Y_1|Y_2|\cdots|Y_{\tilde{r}}$ with $\tilde{r} > r$, i.e., $\tilde{f}$ is a strict refinement of f. By definition of a refinement, every Y_j is contained in an X_i for some i. Now as $\tilde{f}$ strictly refines f, we can assume, without loss of generality, that X_1 contains Y_1 and Y_2. Now let $\tilde{g}_f$ be a most parsimonious extension of $\tilde{f}$ on $\mathcal{T}$. Consider all edges of $\mathcal{T}$ which, according to $\tilde{g}_f$, require a change.

We now construct an extension of f on $\mathcal{T}$ as follows: all nodes which are labelled Y_1 or Y_2 by $\tilde{g}_f$ are instead labelled X_1, including the leaves. We do this analogously for all other Y_j and X_i, i.e., we replace all Y_j labels by the X_i label such that $Y_j \subseteq X_i$. Thus, the leaves are now labelled by f and the number of edges on which changes are required may be unchanged or smaller (in case that $\tilde{g}_f$ requires a change from, say, Y_1 to Y_2, as in this case this edge would now start and end both in X_1). As this procedure does not introduce any new changes to edges, the score of the resulting extension g_f is at least as good as that of $\tilde{g}_f$. As every MP extension of f will again be at least as good as g_f, we altogether have $l_f(\mathcal{T}) \leq l_{\tilde{f}}(\mathcal{T})$. This completes the proof. ∎

Next, we simplify our metric by showing that the search for a character $\tilde{f}$ which maximizes $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = \max_f |l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2)|$ can be restricted to characters which are convex on either $\mathcal{T}_1$ or $\mathcal{T}_2$. Our proof provides an explicit algorithm which, for each character f with a given value of $|l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2)|$, returns a character $\hat{f}$ which is convex on one of the trees and for which we have $|l_{\hat{f}}(\mathcal{T}_1) - l_{\hat{f}}(\mathcal{T}_2)| \geq |l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2)|$. Note that $\hat{f}$ as we construct it is a refinement of f. In particular, it is possible that $\hat{f}$ employs strictly more character states than f.

Theorem 3.6. *Let $\mathcal{T}_1, \mathcal{T}_2$ be two phylogenetic trees on the same set X of n taxa. Then, there is a character $\tilde{f}$ such that $|l_{\tilde{f}}(\mathcal{T}_1) - l_{\tilde{f}}(\mathcal{T}_2)| = d_{MP}(\mathcal{T}_1, \mathcal{T}_2)$ and $\tilde{f}$ is convex on either $\mathcal{T}_1$ or $\mathcal{T}_2$.*

Proof. Let $\mathcal{T}_1, \mathcal{T}_2$ be two phylogenetic trees on the same set X of n taxa and let f be an r-state character with $l_f(\mathcal{T}_i) > r - 1$, i.e., f is not convex on $\mathcal{T}_i$ for $i \in \{1, 2\}$. We first show that there exists an $\hat{r}$-state character $\hat{f}$ with $|l_{\hat{f}}(\mathcal{T}_1) - l_{\hat{f}}(\mathcal{T}_2)| \geq |l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2)|$ and $l_{\hat{f}}(\mathcal{T}_2) = \hat{r} - 1$ for some $\hat{r} \geq r$, i.e., $\hat{f}$ is convex on $\mathcal{T}_2$ and its induced parsimony distance is at least as good as the one induced by f.

Without loss of generality, we assume that $l_f(\mathcal{T}_1) \geq l_f(\mathcal{T}_2)$. We consider a most parsimonious extension g_f of f on $\mathcal{T}_2$. Let k denote the number of changes required by g_f. We delete all k edges which require a state change according to g_f. Now $\mathcal{T}_2$ is split into $k + 1$ connected components. Assume that there is a component which does not contain a leaf. This means that all edges leading to this component were edges which need a change, but this implies that g_f cannot be most parsimonious:

modifying g_f such that all nodes in this leafless component get the same state as one of the components connected to it would reduce k by at least 1. This is a contradiction and thus all components contain at least one leaf. Thus, we can consider the components labelled by the state assigned to this leaf (and note that all leaves in one component are in the same state, because all edges which require a change have been deleted). But as f is not convex on $\mathcal{T}_2$ by assumption, $k > r - 1$. We now re-label all components, i.e., we introduce $k + 1$ new states and assign each component its own unique state, i.e., we label each node in this component with this state (including the leaves). This leads to a $(k+1)$-state character $\hat{f}$ and an extension $g_{\hat{f}}$ requiring exactly k changes (as changes still only occur only the edges between the components once they are re-introduced to $\mathcal{T}_2$). Now we set $\hat{r} := k + 1$. Then, $\hat{f}$ employs $\hat{r}$ states, and $l_{\hat{f}}(\mathcal{T}_2) = \hat{r} - 1$, i.e., $\hat{f}$ is convex on $\mathcal{T}_2$.

Thus, on the one hand the number of changes needed by $\hat{f}$ equals the number of changes needed by f on $\mathcal{T}_2$. On the other hand, $\hat{f}$ is by construction a refinement of f and thus by Lemma 3.5, this procedure cannot decrease the parsimony score on $\mathcal{T}_1$, i.e., $l_f(\mathcal{T}_1) \leq l_{\hat{f}}(\mathcal{T}_1)$. So altogether, we have $\left| l_{\hat{f}}(\mathcal{T}_1) - l_{\hat{f}}(\mathcal{T}_2) \right| \geq \left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right|$.

Last, assume we have a character f which maximizes $\left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right|$, i.e., we have $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2)$. Then, if f not convex on $\mathcal{T}_2$, we can apply the explained procedure to obtain $\tilde{f}$ such that $\tilde{f}$ is convex on $\mathcal{T}_2$ and $\left| l_{\tilde{f}}(\mathcal{T}_1) - l_{\tilde{f}}(\mathcal{T}_2) \right| = l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) = d_{MP}(\mathcal{T}_1, \mathcal{T}_2)$. This completes the proof. ∎

Note that in order to find a character f that maximizes $\left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right|$ for two given trees $\mathcal{T}_1, \mathcal{T}_2$, by Theorem 3.6, we can restrict our search on convex characters, but this potentially requires that the number of character states employed is not fixed. On the other hand, if we fix the number of states, the optimal character might not be convex on either of the two trees (and this is why Theorem 3.6 does not imply that MP distance is polynomial-time solveable for a fixed number of states). We elaborate this in the following lemma.

Lemma 3.7. *There exist trees $\mathcal{T}_1, \mathcal{T}_2$ and a fixed number r of character states, such that for all characters f maximizing $\left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right|$ under the restriction of employing only r character states, f is not convex on either $\mathcal{T}_1$ or $\mathcal{T}_2$.*

Proof. We give an explicit example, taking $r = 2$. Consider the two trees shown in Figure 2. The set of informative binary characters that are convex on $\mathcal{T}_2$ is $C_2 :=$ $\{ACACCCCC, CACACCCC, CCCCACAC, CCCCCACA, AAAACCCC\}$. All characters in C_2 refer to splits induced by $\mathcal{T}_2$ and thus have a parsimony score of 1 on $\mathcal{T}_2$. All of the characters featuring only two taxa, i.e., characters in which two taxa are in one state and all other taxa are in another state, can at most have a parsimony score of 2 on $\mathcal{T}_1$. The character $AAAACCCC$, however, has a score of 1 on $\mathcal{T}_2$ as well as on $\mathcal{T}_1$. Thus, $\left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right| \leq 1$ for all convex binary characters $f \in C_2$.

For C_1, which we define to be the set of all informative binary characters that are convex on $\mathcal{T}_1$, i.e., $C_1 := \{AACCCCCC, AAACCCCC, AAAACCCC, AAAAACCC, AAAAAACC\}$, we get the same result: $\left| l_{\tilde{f}}(\mathcal{T}_1) - l_{\tilde{f}}(\mathcal{T}_2) \right| \leq 1$ for all convex binary characters $\tilde{f} \in C_1$. So the maximum value of the MP difference $\left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right|$ is 1 for any binary character f which is convex on either $\mathcal{T}_1$ or $\mathcal{T}_2$.

On the other hand, for the character $\hat{f} := ACACACAC$, which is not convex on either of the trees $\mathcal{T}_1, \mathcal{T}_2$, we have $\left| l_{\hat{f}}(\mathcal{T}_1) - l_{\hat{f}}(\mathcal{T}_2) \right| = 4 - 2 = 2$. This completes the proof. ∎
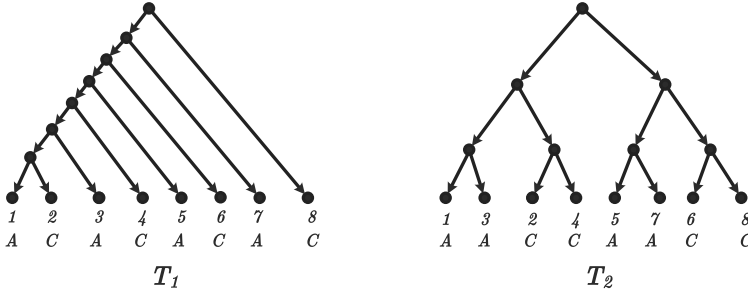

Figure 2: Two rooted binary phylogenetic X-trees on the same set of eight taxa and the performance of the character $ACACACAC$ on these trees. The corresponding parsimony scores are 4 and 2, respectively.

As Lemma 3.7 shows, Theorem 3.6 does not hold if we bound the number of character states.

We are now in a position to state and prove the following theorem, which shows that the SPR and MP distances are related.

Theorem 3.8. *Let $\mathcal{T}_1$, $\mathcal{T}_2$ be two binary phylogenetic X-trees. Then, $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) \leq d_{SPR}(\mathcal{T}_1, \mathcal{T}_2)$.*

Proof. Let $\tilde{f} := \arg\max_f \left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right|$, i.e., $\tilde{f}$ defines $d_{MP}(\mathcal{T}_1, \mathcal{T}_2)$. Let $r = \left| \tilde{f} \right|$. By Theorem 3.6 we may assume that $\tilde{f}$ is convex on one of the trees. So without loss of generality, we assume that $\tilde{f}$ is convex on $\mathcal{T}_2$, i.e., $l_{\tilde{f}}(\mathcal{T}_2) = r - 1$. If $\mathcal{T}_1 = \mathcal{T}_2$, there is nothing to show as both the SPR and MP distances are then equal to 0. Now if $\mathcal{T}_1 \neq \mathcal{T}_2$ and $\tilde{f}$ is convex on $\mathcal{T}_2$, we have $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = l_{\tilde{f}}(\mathcal{T}_1) - (r - 1)$. By Theorem 3.4, this is equal to $d_{SPR}(\mathcal{T}_1, \tilde{\mathcal{T}})$, where $\tilde{\mathcal{T}}$ is the tree which minimizes $\min_{\mathcal{T}} d_{SPR}(\mathcal{T}_1, \mathcal{T})$ such that $\tilde{f}$ is convex on $\mathcal{T}$. So $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = d_{SPR}(\mathcal{T}_1, \tilde{\mathcal{T}}) \leq d_{SPR}(\mathcal{T}_1, \mathcal{T}_2)$, which completes the proof. ∎

Theorem 3.8 states that the MP distance provides a lower bound to the SPR distance. It does not, however, prove that the two distance measures are actually different. But this becomes apparent when we consider the two unrooted trees $\mathcal{T}_1 = (1, (3, 4), (2, (5, 6)))$ and $\mathcal{T}_2 = (3, (1, 4), (5, (6, 2)))$ as depicted in Figure 3. The SPR distance between these two trees is 2, as can be seen when considering all 9 edges of, say, $\mathcal{T}_1$: no matter which one we prune and regraft to another place, we cannot generate $\mathcal{T}_2$. If we, on the other hand, first cut leaf 1 and attach it next to leaf 4, and then cut leaf 2 and attach it next to leaf 6, and suppress all resulting vertices of degree 2, we obtain tree $\mathcal{T}_2$. So the SPR distance from $\mathcal{T}_1$ to $\mathcal{T}_2$ is 2, but an exhaustive search through all possible informative characters on 6 taxa shows that the MP distance in this case is 1. It is, for instance, achieved by character $AACCAA$, which has a

score of 1 on T_1 and 2 on T_2. So in this case, the MP distance is strictly smaller than the SPR distance.
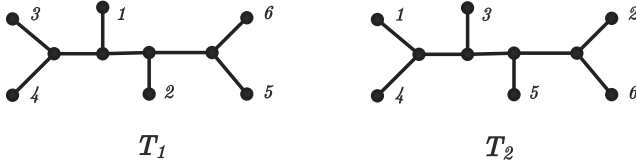

Figure 3: The MP distance of these two trees is 1, but their SPR distance is 2.

Note that by [6, Proposition 5.1], the rooted SPR distance d_{rSPR} and the (unrooted) SPR distance d_{SPR} are closely related. We present this proposition in the following lemmas and subsequently combine them in order to match our purposes. This way, we justify the fact that we only consider the (unrooted) SPR distance in the following, as any lower bound for the latter also provides a lower bound for the rooted SPR distance.

Lemma 3.9. (Bordewich and Semple [6, Proposition 5.1]) *Let T_1 and T_2 be two rooted binary phylogenetic X-trees. Let T_1' and T_2' be the (unrooted) binary phylogenetic $X \cup \{r\}$-trees obtained by attaching a pendant leaf r to the root of T_1 and T_2, respectively, and then regarding the resulting trees as unrooted. Then, $d_{SPR}(T_1', T_2') \leq d_{rSPR}(T_1, T_2)$.*

Note that Lemma 3.9 is not directly applicable to our setting, because trees T_1' and T_2' as mentioned in this lemma have $n + 1$ leaves, where $n = |X|$, whereas what we want is to relate a rooted binary tree to the same tree regarded as unrooted by suppressing the root node, i.e., by deleting the degree-2 node and its incident edges and reconnecting the then unconnected components with a new edge. We achieve this in the following lemma.

Lemma 3.10. *Let T_1 and T_2 be two rooted binary phylogenetic X-trees. Let $\tilde{T}_1$ and $\tilde{T}_2$ be the unrooted binary phylogenetic X-trees derived from T_1 and T_2, respectively, by suppressing the root. Let T_1' and T_2' be the (unrooted) binary phylogenetic $X \cup \{r\}$-trees obtained by attaching a pendant leaf r to the root of T_1 and T_2, respectively, and then regarding the resulting trees as unrooted. Then, $d_{SPR}(\tilde{T}_1, \tilde{T}_2) \leq d_{SPR}(T_1', T_2') \leq d_{SPR}(\tilde{T}_1, \tilde{T}_2) + 1$.*

Proof. First, note that $\tilde{T}_1$ is a subtree of T_1' and $\tilde{T}_2$ is a subtree of T_2'. Assume $d_{SPR}(\tilde{T}_1, \tilde{T}_2) = 1$, i.e., one SPR move is needed to get from $\tilde{T}_1$ to $\tilde{T}_2$. Then also at least one SPR move is needed to get from T_1' to T_2' to get the correct arrangement of the subtree $\tilde{T}_1$ or $\tilde{T}_2$, respectively (and possibly one more if the position of r also has to be modified). So in this case, $d_{SPR}(\tilde{T}_1, \tilde{T}_2) \leq d_{SPR}(T_1', T_2')$. However, if more SPR moves are needed to get from $\tilde{T}_1$ to $\tilde{T}_2$, we consider a shortest path of single SPR moves $\tilde{T}_1, T_a, T_b, \ldots, \tilde{T}_2$ from $\tilde{T}_1$ to $\tilde{T}_2$. Each such required move enforces the same move from T_1' to T_2'. In the end, possibly an adjustment of the position of leaf

r has to be made, but this can be made in a single move cutting leaf r and attaching it at the appropriate position. So iteratively, we get $d_{SPR}(\tilde{T}_1, \tilde{T}_2) \leq d_{SPR}(T_1', T_2') \leq d_{SPR}(\tilde{T}_1, \tilde{T}_2) + 1$. ∎

Now we are finally in a position to show the required relation between d_{MP}, d_{SPR}, and d_{rSPR}.

Theorem 3.11. *Let T_1 and T_2 be two rooted binary phylogenetic X-trees. Let $\tilde{T}_1$ and $\tilde{T}_2$ be the unrooted binary phylogenetic X-trees derived from T_1 and T_2, respectively, by suppressing the root. Then, $d_{MP}(T_1, T_2) = d_{MP}(\tilde{T}_1, \tilde{T}_2) \leq d_{SPR}(\tilde{T}_1, \tilde{T}_2) \leq d_{rSPR}(T_1, T_2)$.*

Proof. The equality follows from the fact that for parsimony there is no difference between rooted and unrooted trees. The first inequality follows from Theorem 3.8. It remains to show that $d_{SPR}(\tilde{T}_1, \tilde{T}_2) \leq d_{rSPR}(T_1, T_2)$. Let T_1' and T_2' be the two $X \cup \{r\}$-trees as defined in Lemma 3.9. Then Lemma 3.10 gives $d_{SPR}(\tilde{T}_1, \tilde{T}_2) \leq d_{SPR}(T_1', T_2')$ and Lemma 3.9 leads to $d_{SPR}(T_1', T_2') \leq d_{rSPR}(T_1, T_2)$. So altogether we have $d_{SPR}(\tilde{T}_1, \tilde{T}_2) \leq d_{rSPR}(T_1, T_2)$. This completes the proof. ∎

So Theorem 3.11 shows that the Maximum Parsimony distance is a lower bound both for the rooted and the unrooted SPR distances, but also that the unrooted SPR distance itself is a lower bound for the rooted SPR distance, which is why analyzing the relationship of d_{MP} to d_{SPR} is sufficient.

We finish this section by noting that each character provides a lower bound for the SPR distance.

Corollary 3.12. *Let T_1, T_2 be two binary phylogenetic X-trees and let f be any character on X. Then, $\left| l_f(T_1) - l_f(T_2) \right| \leq d_{SPR}(T_1, T_2)$.*

Proof. This follows from Theorem 3.8 and the fact that $d_{MP}(T_1, T_2) \geq \left| l_f(T_1) - l_f(T_2) \right|$ by definition of $d_{MP}(T_1, T_2)$. ∎

3.1.3. Bounds on the MP Distance

In this section, we want to provide an upper bound for the MP distance. We start with the following lemma.

Lemma 3.13. *The MP score of an r-state character on taxon set X on any phylogenetic X-tree is at most $\left\lfloor (r-1) \cdot \frac{n}{r} \right\rfloor$, where $|X| = n$.*

Proof. It is easy to see that the parsimony score of the star tree is never better than that of any refinement, as in the star tree one state will be the root state and all leaves which are not in this state require exactly one change (note that one can construct binary trees with this property, too, but for simplicity we now consider the star tree). Now let us consider a character $\tilde{f}$ using the states $c_1, \dots, c_r$ and let n_i denote the number of leaves assigned state c_i, for $i = 1, \dots, r$. Note that $\sum_{i=1}^{r} n_i = n$. Without loss of generality, assume $n_1 \geq n_i$ for all $i = 2, \dots, r$. As parsimony seeks to minimize the number of changes needed, it will choose the state which occurs most often as root state, so the root will be in state c_1. In the extreme case of a star tree, the number of changes needed by any most parsimonious extension is $\sum_{i=2}^{r} n_i$, which is maximized

when $n_1 = n_i$ for all $i = 2, \ldots, r$. Note that this choice is only possible if $n = r \cdot n_1$, in which case the MP score will be exactly $(r-1) \cdot \frac{n}{r}$. In the case that n is not a multiple of r, taking $n_1 = \lceil \frac{n}{r} \rceil$ yields a maximum MP score of $n - \lceil \frac{n}{r} \rceil$, which is $\lfloor (r-1) \cdot \frac{n}{r} \rfloor$, completing the proof. ∎

We now use Lemma 3.13 to state the following lemma, which in turn will then provide the desired bound on the MP distance.

Lemma 3.14. *Let $\mathcal{T}_1$, $\mathcal{T}_2$ be two (rooted or unrooted) phylogenetic X-trees with $|X| = n$. Let f be any r-state character on X for some $r \leq n$. Then, $\left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right| \leq \left\lfloor (r-1)(\frac{n}{r} - 1) \right\rfloor$.*

Proof. Without loss of generality, we assume $l_f(\mathcal{T}_2) \leq l_f(\mathcal{T}_1)$. First we note that the parsimony score of f on any tree, and thus particularly on $\mathcal{T}_2$, is at least $r-1$, because only one of the states employed by f can be the root state, and to all other states there has to be at least one change (and in the optimal case, when the score on some tree equals exactly $r-1$, f is convex on this tree). Then by Lemma 3.13, the score of f on $\mathcal{T}_1$ cannot exceed $\lfloor (r-1)\frac{n}{r} \rfloor$. So altogether, $\left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right| \leq \lfloor (r-1)\frac{n}{r} \rfloor - (r-1) = \lfloor (r-1)\frac{n}{r} \rfloor - \lfloor r-1 \rfloor \leq \lfloor (r-1)\frac{n}{r} - (r-1) \rfloor = \lfloor (r-1)(\frac{n}{r} - 1) \rfloor$. The latter inequality is due to $r \in \mathbb{N}$. This completes the proof. ∎

We now derive an upper bound on the MP distance between two phylogenetic trees using Lemma 3.14.

Theorem 3.15. *Let $\mathcal{T}_1$, $\mathcal{T}_2$ be two phylogenetic X-trees with $|X| = n$. Then,*

$$d_{MP}(\mathcal{T}_1, \mathcal{T}_2) \leq n - 2\sqrt{n} + 1.$$

Proof. We define the function $f(r, n) := (r-1)\left(\frac{n}{r} - 1\right)$. By considering the first and second derivative with respect to r, one can see that $f(r, n)$ is maximized at $r = \sqrt{n}$. Let $\tilde{f}$ be the character which maximizes $\left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right|$ and thus provides $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = \left| l_{\tilde{f}}(\mathcal{T}_1) - l_{\tilde{f}}(\mathcal{T}_2) \right|$. Let $\tilde{r}$ be the number of states employed by $\tilde{f}$. Then by Lemma 3.14, we conclude $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = \left| l_{\tilde{f}}(\mathcal{T}_1) - l_{\tilde{f}}(\mathcal{T}_2) \right| \leq \lfloor (\tilde{r} - 1)(\frac{n}{\tilde{r}} - 1) \rfloor \leq (\tilde{r} - 1)\left(\frac{n}{\tilde{r}} - 1\right) = f(\tilde{r}, n) \leq f(\sqrt{n}, n) = (\sqrt{n} - 1)^2 = n - 2\sqrt{n} + 1$. This completes the proof. ∎

Theorem 3.15 is useful in the sense that it provides an upper bound on d_{MP}, which is in fact a tight bound as can be seen in Figure 4: there, the trees $\mathcal{T}_1 = ((((1,2), 3), (4, (5,6))), (7, (8,9)))$ and $\mathcal{T}_2 = ((((1,4), 7), (2, (5,8))), (3, (6,9)))$ are depicted together with the character $f = ACGACGACG$. The parsimony score of f on $\mathcal{T}_1$ and $\mathcal{T}_2$ can be easily calculated with the Fitch algorithm [16] to be $l_f(\mathcal{T}_1) = 6$ and $l_f(\mathcal{T}_2) = 2$. In particular, f is convex on $\mathcal{T}_2$. By Theorem 3.15, the upper bound of the MP distance two 9-taxon trees is $n - 2\sqrt{n} + 1 = 9 - 2 \cdot 3 + 1 = 4$. As $l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) = 4$, this implies that f provides the MP distance and that the optimum is indeed achieved. Note that this theoretical bound is achieved here even though both trees under consideration are binary — but examples for multifurcating trees can be constructed in a similar way. In fact, if we chose $\mathcal{T}_1$ to be the star tree, we would get the same result. We also note that Theorem 3.15 yields a stronger bound than that obtained by combining $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) \leq d_{SPR}(\mathcal{T}_1, \mathcal{T}_2)$ with the fact, proven in [15], that $d_{SPR}(\mathcal{T}_1, \mathcal{T}_2) \leq n - \frac{1}{2}\sqrt{n}$.
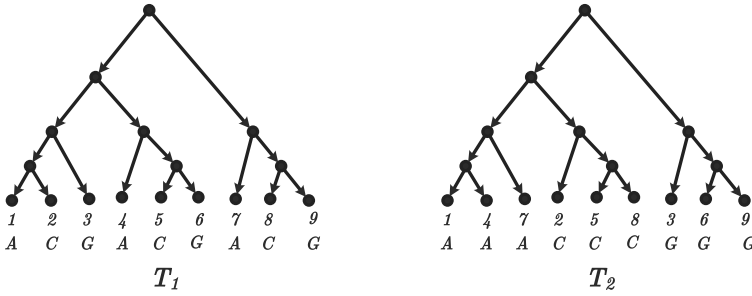
Figure 4: Two rooted binary phylogenetic X-trees $\mathcal{T}_1$ and $\mathcal{T}_2$ for $X = \{1, \ldots, 9\}$ and the performance of the character $f = ACGACGACG$ on these trees. The corresponding parsimony scores are $l_f(\mathcal{T}_1) = 6$ and $l_f(\mathcal{T}_2) = 2$, respectively. The MP distance $d_{MP}(\mathcal{T}_1, \mathcal{T}_2)$ can be shown to equal 4. It is achieved by f.

3.1.4. The Number of Character States Needed to Maximize the Parsimony Difference Between Two Trees

We continue by considering the obvious question whether or not the MP distance can be maximized by considering only characters with a fixed number of states. For instance, one could wonder if the optimum performance difference can always be reached by a binary character. The following theorem leads to the conclusion that this is unfortunately not the case.

Theorem 3.16. *Let $r > 1$. Then there exist two binary phylogenetic trees $\mathcal{T}_1$, $\mathcal{T}_2$ on a set of $n = (r+1)^2$ taxa and an $(r+1)$-state character f such that $\left| l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2) \right| > \left| l_{\hat{f}}(\mathcal{T}_1) - l_{\hat{f}}(\mathcal{T}_2) \right|$ for all r-state characters $\hat{f}$.*

Proof. We give an explicit construction of $\mathcal{T}_1$ and $\mathcal{T}_2$ as rooted binary trees, but for unrooted trees the root can later on be ignored. We draw a root node and continue by adding a subtree of size $r+1$ taxa to the right hand side of the root. This subtree may have any binary topology, for instance it can be chosen to be a so-called caterpillar. On the left hand side of the root, we draw an edge leading to a new node, which we regard the root of a new subtree. With this new root we continue just as before by adding another subtree of size $r+1$ to the right. We continue this procedure until there are r such subtrees to the right of their corresponding parental node. For the last such node we create another subtree of size $r+1$ taxa and add it to the left hand side of this node in a way that the entire tree remains binary. Altogether, there are now $r+1$ subtrees of $r+1$ taxa each.

Now for $\mathcal{T}_1$, label the leaves $1, 2, 3, \ldots, (r+1)^2$ from the left to the right. Thus, the leftmost subtree will have the labels $1, \ldots, r+1$, the second subtree $r+2, r+3, \ldots, 2(r+1)$, and so on. For $\mathcal{T}_2$, keep the same tree topology of $r+1$ subtrees, but use a different leaf labelling: label the leftmost subtree $1, (r+1)+1, 2(r+1)+1, \ldots, k(r+1)+1$, the second subtree $2, (r+1)+2, 2(r+1)+2, \ldots, k(r+1)+2$, and so on. The last subtree will be labelled $r+1, (r+1)+(r+1), 2(r+1)+(r+1), \ldots, r(r+1)+(r+1)$. For $r = 2$, this will lead to the trees shown in Figure 4.

Now introduce character

$$f := \underbrace{c_1, c_2, c_3, \ldots, c_{r+1}}_{(r+1)times} = c_1, c_2, c_3, \ldots, c_{r+1}, c_1, c_2, c_3, \ldots, c_{r+1}, \ldots,$$

for some distinct $r+1$ character states $c_1, \ldots, c_r, c_{r+1}$. Since in every pending $(r+1)$-taxon subtree of $\mathcal{T}_1$ all $r+1$ character states appear, the score of this character on each of these subtrees is r and the total MP score on $\mathcal{T}_1$ is $l_f(\mathcal{T}_1) = (r+1)r$. According to the labelling of $\mathcal{T}_2$, f is convex there as the first pending $(r+1)$-taxon subtree only contains taxa that are in state c_1, the second one only taxa of state c_2, and so on. Thus, by construction, the MP score on $\mathcal{T}_2$ is $l_f(\mathcal{T}_2) = (r+1) - 1 = r$. Altogether, the difference equals $|l_f(\mathcal{T}_1) - l_f(\mathcal{T}_2)| = (r+1)r - r = r^2$.

Next we show that for every r-state character $\hat{f}$, the difference $|l_{\hat{f}}(\mathcal{T}_1) - l_{\hat{f}}(\mathcal{T}_2)|$ is smaller than r^2. By Lemma 3.14, for $n = (r+1)^2$ we have $|l_{\hat{f}}(\mathcal{T}_1) - l_{\hat{f}}(\mathcal{T}_2)| \le \lfloor (r-1)(\frac{n}{r} - 1) \rfloor = \lfloor (r-1)(\frac{(r+1)^2}{r} - 1) \rfloor = \lfloor r^2 - \frac{1}{r} \rfloor = r^2 - 1 < r^2$. This completes the proof. ∎

Note that Figure 4 illustrates the construction described in the proof of Theorem 3.16 for the case where $r = 2$: the two trees depicted here have an MP distance of at least 4, which can be seen by considering the depicted 3-state character. However, by Lemma 3.14, for all binary characters $\hat{f}$ on nine taxa we obtain a difference $|l_{\hat{f}}(\mathcal{T}_1) - l_{\hat{f}}(\mathcal{T}_2)| \le \lfloor (2-1)(\frac{9}{2} - 1) \rfloor = 3$. This means that no binary character reaches a difference of 4 for those two trees.

So there exist two trees where more than two states can give a higher difference, and in general, by Theorem 3.16, no constant number of character states is sufficient as the described construction can be extended to more taxa. Thus, the optimal number of states to employ depends on the tree shapes of the trees under consideration. This can be seen when considering the theoretical bound of 3 for binary characters on nine taxa: for the two trees displayed in Figure 4, not even the bound of 3 can be reached, as an exhaustive search reveals that there is no binary character f such that $l_f(\mathcal{T}_1) = 4$ and at the same time $l_f(\mathcal{T}_2) = 1$ or vice versa (which is sufficient, because $l_f(\mathcal{T}) \le 4$ for any binary character on a tree with 9 taxa, so the difference of 3 could only be reached as the difference $4 - 1$).

All this already gives a hint to the complexity of the underlying problem, which we analyze further in the subsequent section.

4. On the Complexity of Calculating the MP Distance

In this section we show that computation of MP distance is NP-hard on non-binary trees, and that a fixed-state variant of the problem is also NP-hard. As we shall see the NP-hardness reductions do not, in their present form, work for binary trees. We address this issue further in Section 5.

We begin, however, with a positive result which introduces several key concepts used by the more involved hardness results.

Lemma 4.1. *Let $\mathcal{T}_1$ and $\mathcal{T}_2$ be two (not necessarily binary) phylogenetic X-trees*

with $|X| = n$, where at least one of the trees is a star tree. Then $d_{MP}(\mathcal{T}_1, \mathcal{T}_2)$ can be computed in polynomial time.

Proof. If $\mathcal{T}_1$ and $\mathcal{T}_2$ are identical then $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = 0$ and we are done, so let us assume that $\mathcal{T}_1$ is a star, $\mathcal{T}_2$ is not a star and $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) > 0$. Without loss of generality, we also assume that $\mathcal{T}_1$ and $\mathcal{T}_2$ are rooted. Clearly, $\mathcal{T}_2$ is a refinement of $\mathcal{T}_1$, so for any character f we have, by Lemma 3.5, $l_f(\mathcal{T}_1) \geq l_f(\mathcal{T}_2)$. If we combine this with Theorem 3.6 then we know that there exists a character $\tilde{f}$ such that $l_{\tilde{f}}(\mathcal{T}_1) - l_{\tilde{f}}(\mathcal{T}_2) = d_{MP}(\mathcal{T}_1, \mathcal{T}_2)$ and $\tilde{f}$ is convex for $\mathcal{T}_2$. Let $r(\tilde{f})$ be the number of states in $\tilde{f}$. The value $l_{\tilde{f}}(\mathcal{T}_1)$ is equal to $n - m(\tilde{f})$, where $m(\tilde{f})$ is the frequency of the most frequently used state in $\tilde{f}$. Hence, $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = (n - m(\tilde{f})) - (r(\tilde{f}) - 1) = (n+1) - (m(\tilde{f}) + r(\tilde{f}))$. To construct such an $\tilde{f}$, it is sufficient to construct a character f that is convex for $\mathcal{T}_2$ and such that $m(f) + r(f)$ is minimized. We can do this by exhaustively trying all possible pairs (m, r), where $1 \leq m, r \leq n$, and returning the minimum value of $m + r$ ranging over all "valid" pairs (m, r). A pair (m, r) is valid if there exists a character f that is convex for $\mathcal{T}_2$ such that $m(f) \leq m$ and $r(f) \leq r$. Due to minimality it is sufficient to consider (m, r) pairs in order of increasing $m + r$ and to stop as soon as a valid pair is encountered. The only task that remains is to determine validity in polynomial time. To do this we first observe that, if a character f has exactly r states and is convex for $\mathcal{T}_2$, then any optimal extension of f to the interior nodes of $\mathcal{T}_2$ naturally induces $r - 1$ edges upon which mutations between character states occur. If these $r - 1$ edges are removed, $\mathcal{T}_2$ is partitioned into exactly r components, and $m(f)$ is then equal to the maximum number of taxa in any of these components. Hence, for a given value m, determining the smallest value r such that (m, r) is valid is equivalent to the question: what is the smallest number of edge cuts I need to make to $\mathcal{T}_2$ to ensure that every resulting component contains at most m taxa? Fortunately, this problem can be solved in polynomial time by giving each taxon weight 1, each inner node weight 0, and using the polynomial-time "tree partitioning" algorithm in [19] to compute an optimal m-partition. ∎

Let $d_{MP}^i(\mathcal{T}_1, \mathcal{T}_2)$ denote the MP distance of two trees when restricted to characters with at most i states. Note that by similar arguments as used in the proof of Theorem 3.2, d_{MP}^i is also a metric. Moreover, note that, for constant i, there is no obvious relationship between the complexity of computing $d_{MP}^i(\mathcal{T}_1, \mathcal{T}_2)$ and $d_{MP}(\mathcal{T}_1, \mathcal{T}_2)$. However, as we will now show, both problems are NP-hard. We start with the hardness proof for $d_{MP}^2(\mathcal{T}_1, \mathcal{T}_2)$. The proof that $d_{MP}(\mathcal{T}_1, \mathcal{T}_2)$ is NP-hard will use similar, but somewhat more complex, techniques. First, we present some auxiliary results.

Observation 4.2. Let f be a character on X and $\mathcal{T}$ a tree on X. Let f' be any character obtained from f by changing the state of exactly one taxon. Then, $l_f(\mathcal{T}) - 1 \leq l_{f'}(\mathcal{T}) \leq l_f(\mathcal{T}) + 1$, i.e., the parsimony score can change by at most one.

Proof. Suppose $l_{f'}(\mathcal{T}) \leq l_f(\mathcal{T}) - 2$. Consider any extension of f' to the interior nodes of $\mathcal{T}$ that achieves $l_{f'}(\mathcal{T})$ mutations. Using the same extension but on f gives at most $l_{f'}(\mathcal{T}) + 1$ mutations, because only one taxon changed state. So $l_f(\mathcal{T}) \leq l_{f'}(\mathcal{T}) + 1 \leq l_f(\mathcal{T}) - 1$, which is a contradiction. In the other direction, take any optimal extension of f and apply it to f'. At most one extra mutation will be created, so $l_{f'}(\mathcal{T}) \leq l_f(\mathcal{T}) + 1$. ∎

Lemma 4.3. *Let f be an optimal character for two trees $\mathcal{T}_1$ and $\mathcal{T}_2$, i.e., $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) = \left| l_f(\mathcal{T}_2) - l_f(\mathcal{T}_1) \right|$. Without loss of generality, assume $l_f(\mathcal{T}_1) < l_f(\mathcal{T}_2)$. Then we can construct in polynomial time an optimal character f' with the following property: $l_{f'}(\mathcal{T}_1) < l_{f'}(\mathcal{T}_2)$ and for each vertex u of $\mathcal{T}_1$ such that all u's children are leaves, f' assigns all the children of u the same state.*

Proof. Consider a vertex u of $\mathcal{T}_1$ such that all its children are taxa, but such that f assigns the children two or more states. We calculate an optimal extension of f to the interior nodes of $\mathcal{T}_1$ by applying Fitch's algorithm. Fitch will allocate a most frequently occurring state amongst the children of u, to u. (If there is a unique such state then Fitch will choose it, otherwise it will break ties in the top-down phase of the algorithm). Let s be the state allocated to u. Choose a child of u that does not have state s and change its state to s. This yields a new character f^*. Clearly, $l_{f^*}(\mathcal{T}_1) < l_f(\mathcal{T}_1)$, simply by using the same extension that Fitch gave. Combining this with Observation 4.2 gives $l_{f^*}(\mathcal{T}_1) = l_f(\mathcal{T}_1) - 1$ and thus $l_{f^*}(\mathcal{T}_2) = l_f(\mathcal{T}_2) - 1$ (otherwise f could not have been optimal). Hence, f^* is also an optimal character, and $l_{f^*}(\mathcal{T}_1) < l_{f^*}(\mathcal{T}_2)$. This process can be iterated as long as necessary until all the children of u have the same state. (Note that in subsequent iterations Fitch will definitely assign state s to u, because s will have become the unique most frequently occurring state amongst the children of u.) Then we can iterate the process on other vertices u' whose children do not all have the same state, for as long as necessary. Polynomial time is guaranteed since the state of each taxon is changed at most once. ∎

Observation 4.4. Lemma 4.3 also holds for optimal characters under the $d_{MP}^i(\mathcal{T}_1, \mathcal{T}_2)$ model.

Proof. The transformation in the proof of Lemma 4.3 does not increase the number of states in the character. ∎

Lemma 4.5. *Computing $d_{MP}^2(\mathcal{T}_1, \mathcal{T}_2)$ is NP-hard.*

Proof. We reduce from the NP-hard (and APX-hard) problem CUBIC MAX CUT, see [1]. In this problem we are given an undirected 3-regular graph $G = (V, E)$. A *cut* is a bipartition of V and the size of the cut is the number of edges that cross the bipartition. The goal is to compute a cut of maximum-size. The restriction to 3-regular graphs is not strictly necessary but simplifies the proof somewhat. Clearly, $|E| = 3|V|/2$. Let $MAXCUT(G)$ be the size of the maximum cut in G; it is well known that $MAXCUT(G) \geq 2|E|/3 = |V|$ (by repeatedly moving nodes to the other side of the partition that have only one of their three incident edges in the cut). Let $\{0, 1\}$ be the two character states. During this proof we will write "any character" as shorthand for "any character with at most two states".

The high-level idea is to construct two trees $\mathcal{T}_1$ and $\mathcal{T}_2$, henceforth referred to as $\mathcal{T}_V$ and $\mathcal{T}_E$, where $\mathcal{T}_V$ encodes the vertices and $\mathcal{T}_E$ the edges of G. In $\mathcal{T}_V$ the character states $\{0, 1\}$ will be used to indicate whether a vertex is on the left or right side of the bipartition. The mutations induced in $\mathcal{T}_E$ will be used to count the number of edges crossing the bipartition. Intuitively, $d_{MP}^2(\mathcal{T}_V, \mathcal{T}_E)$ will be maximized by choosing a maximum-size cut.
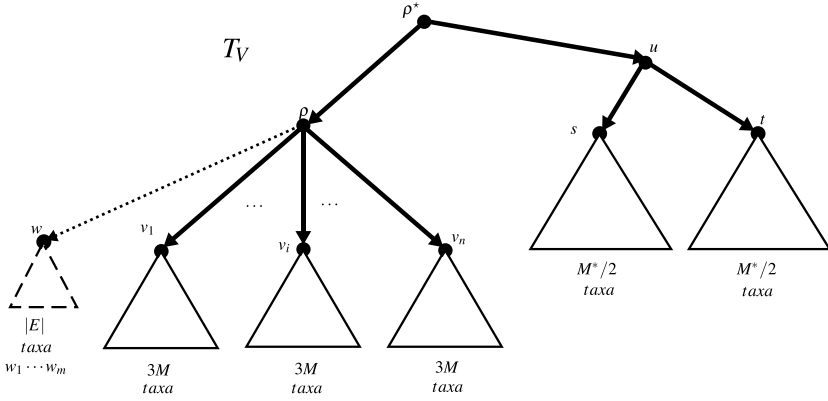
Figure 5: The tree $\mathcal{T}_V$ used in the proofs of Lemma 4.5 and Theorem 4.6. Note that the dotted parts are only used in the proof of Theorem 4.6.

Let $V = \{v_1, \ldots, v_n\}$ and $E = \{e_1, \ldots, e_m\}$. Throughout the reduction we will utilize two large numbers, M and an even number M^*, such that $n << M << M^*$ and both are still at most $poly(n)$. In due course we will explain how these numbers are calculated. Both trees will have $3|V|M + M^*$ taxa.

To construct $\mathcal{T}_V$ we first introduce vertices ρ^*, ρ, s, t, u, and $\{v_1, \ldots, v_n\}$. We add edges $\{\rho^*, \rho\}$, $\{\rho^*, u\}$, $\{u, s\}$, $\{u, t\}$, and $\{\rho, v_i\}$ for $1 \le i \le n$. We connect each v_i to $3M$ taxa. We connect s to $M^*/2$ taxa and t to $M^*/2$ taxa. Figure 5 depicts the construction idea.

To construct $\mathcal{T}_E$ we introduce vertices ρ^*, ρ, u, and $\{e_1, \ldots, e_m\}$. We add edges $\{\rho^*, \rho\}$, $\{\rho^*, u\}$, and $\{\rho, e_i\}$ for $1 \le i \le m$. To u we connect the M^* taxa that were connected to s and t in $\mathcal{T}_V$. Next we introduce mM vertices $e_{i,j}$ for $i \in \{1, \ldots, m\}$ and $j \in \{1, \ldots, M\}$. We connect each vertex e_i to all the $e_{i,j}$, for $j \in \{1, \ldots, M\}$. To each $e_{i,j}$ we connect two taxa, representing the endpoints (of the jth copy) of edge e_i. To determine which two taxa these are, suppose in G the edge e_i is connected to vertices v_a and v_b. Then one of the two taxa is taken from the clade of taxa we connected to v_a in $\mathcal{T}_V$, and the other from the clade of taxa beneath v_b in $\mathcal{T}_V$. The exact mapping chosen does not matter. The construction is depicted by Figure 6. This completes the construction.

For $x \in \mathbb{R}$ let $round(x)$ be x rounded to the nearest integer. (By construction we will actually only use values of x that are at most $1/3$ above or below the nearest integer; this will become clearer later.) We shall prove the following:

$$MAXCUT(G) = round\left(\frac{d_{MP}^2(\mathcal{T}_V, \mathcal{T}_E) - M^*/2}{M}\right). \tag{4.1}$$

Moreover, we will show how any optimal character f can be transformed in polynomial-time into a maximum-size cut of G. From this the NP-hardness of com-
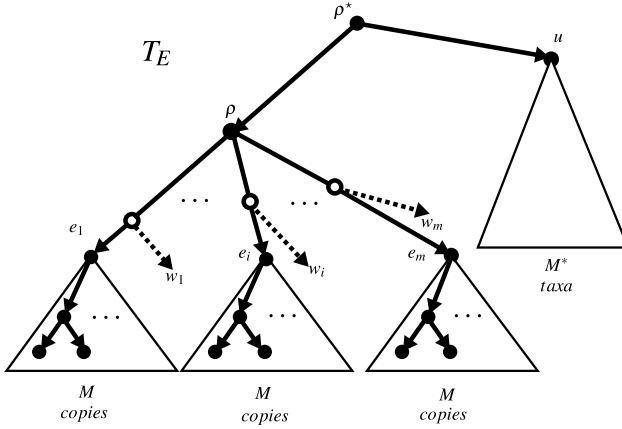
Figure 6: The tree $\mathcal{T}_E$ used in the proofs of Lemma 4.5 and Theorem 4.6. Note that the dotted parts and the unfilled vertices are only used in the proof of Theorem 4.6. Below each e_i vertex there are in total $2M$ taxa, organized in cherries. If e_i has endpoints v_a and v_b in G, then each cherry will have one taxon from the v_a clade in $\mathcal{T}_V$ and one taxon from the v_b clade.

puting $d^2_{MP}(\mathcal{T}_V, \mathcal{T}_E)$ will follow.

Note that in $\mathcal{T}_V$ the subtree rooted at u is a refinement of the subtree rooted at u in $\mathcal{T}_E$. This means that, for any character f, a (crude) upper bound on $l_f(\mathcal{T}_V) - l_f(\mathcal{T}_E)$ is $3|V|M$. To see this, observe that for any character the number of mutations incurred in $\mathcal{T}_V$ in the subtree rooted at u, is less than or equal to the number of mutations incurred in the corresponding subtree of $\mathcal{T}_E$. Therefore, mutations in this subtree can never contribute to an increase in $l_f(\mathcal{T}_V) - l_f(\mathcal{T}_E)$. Hence, an upper bound on $l_f(\mathcal{T}_V) - l_f(\mathcal{T}_E)$ can be achieved by maximizing the number of mutations that occur in $\mathcal{T}_V$ on edges that are not in this subtree, and minimizing the number of mutations that occur in $\mathcal{T}_E$ on edges that are not in this subtree. A (trivial) lower bound on the latter is 0, while a (trivial) upper bound on the former is $3|V|M$ (e.g., by assigning the same state to all internal nodes of $\mathcal{T}_V$).

On the other hand, consider a character f such that the $M^*/2$ taxa underneath s in $\mathcal{T}_V$ are allocated state 0, and all other taxa are allocated state 1. Then $l_f(\mathcal{T}_V) = 1$ and $l_f(\mathcal{T}_E) \geq M^*/2$. For this reason, we choose M^* such that

$$M^*/2 - 1 > 3|V|M.$$

After choosing M^* this way, we know that $d^2_{MP}(\mathcal{T}_V, \mathcal{T}_E) \geq (M^*/2) - 1$ and, more importantly, that for every optimal character f, $l_f(\mathcal{T}_V) < l_f(\mathcal{T}_E)$.

From Observation 4.4 we can therefore assume that, for each vertex of $\mathcal{T}_V$ in the set $\{s, t, v_1, \ldots, v_n\}$, all the taxa beneath the vertex are allocated the same state by f. (Note also that the state of the taxa in the s clade, and the state of the taxa in the t

clade, must be different, otherwise f could not possibly be optimal.)

Such a character naturally induces a cut, with a vertex v_i being on the left (right) side of the bipartition if the taxa in its clade are allocated state 0 (1). The core observation is that if an edge e_i is in the induced cut (i.e., crosses the bipartition) then f will induce at least M mutations in the subtree of $\mathcal{T}_E$ rooted at e_i. On the other hand, an edge e_i *not* in the cut will induce 0 mutations in the subtree rooted at e_i.

More formally, suppose f induces a cut of size k. The parameter k does not, in itself, give us enough information to *exactly* determine $l_f(\mathcal{T}_V)$ and $l_f(\mathcal{T}_E)$, but we can get close enough. Counting crudely,

$$0 \le l_f(\mathcal{T}_V) \le |V|,$$

where the upper bound of $|V|$ can be obtained by applying Fitch (and observing that, by the earlier assumption, the taxa in the s clade have a different state to the taxa in the t clade). Also,

$$M \cdot k + M^*/2 \le l_f(\mathcal{T}_E) \le M \cdot k + |E| + 2 + M^*/2.$$

(The $|E| + 2$ on the right-hand side of the above expression is an upper bound on the number of mutations incurred on the $|E|$ edges leaving ρ and the 2 edges leaving ρ^*.) From this, it follows that

$$M \cdot k + M^*/2 - |V| \le l_f(\mathcal{T}_E) - l_f(\mathcal{T}_V) \le M \cdot k + |E| + 2 + M^*/2.$$

Assuming M has been chosen such that $M > |V| + |E| + 2$, we observe that $l_f(\mathcal{T}_E) - l_f(\mathcal{T}_V)$ — and thus also $d_{MP}^2(\mathcal{T}_V, \mathcal{T}_E)$ — will be maximized by selecting k as large as possible, i.e., by selecting a maximum-size cut. So,

$$MAXCUT(G) - \frac{|V|}{M} \le \frac{d_{MP}^2(\mathcal{T}_V, \mathcal{T}_E) - M^*/2}{M} \le MAXCUT(G) + \frac{|E| + 2}{M}.$$

Taking $M > 3(|V| + |E| + 2)$ is therefore sufficient to yield Equation (4.1). This completes the reduction. ∎

In fact, we can show that computing $d_{MP}^i(\mathcal{T}_1, \mathcal{T}_2)$ is NP-hard for every fixed integer $i \ge 2$. This will be proven as a corollary of the following theorem, which is the main result of this section.

Theorem 4.6. *Computing $d_{MP}(\mathcal{T}_1, \mathcal{T}_2)$ is NP-hard.*

Proof. This time we reduce from CUBIC MAXIMUM INDEPENDENT SET. This is the problem of computing a maximum-size independent set (i.e., set of mutually non-adjacent vertices) of an undirected 3-regular graph $G = (V, E)$. The problem is NP-hard (and APX-hard), see again [1]. Again, the restriction to 3-regular graphs is not essential but simplifies the proof a little. Let $MIS(G)$ be the size of a maximum-size independent set. It is easy to show that $MIS(G) \ge |V|/4$ (by adding an arbitrary vertex to be in the independent set, deleting this vertex and its at most three neighbors, and then iterating this process). Let $V = \{v_1, \ldots, v_n\}$ and $E = \{e_1, \ldots, e_m\}$. For convenience, we assume $|V| \ge 8$, so $MIS(G) \ge 2$, and that G is not bipartite (because computing $MIS(G)$ on bipartite G can be done in polynomial time).

We construct the trees $\mathcal{T}_V$ and $\mathcal{T}_E$ as described in the previous reduction. We then change the trees slightly; the changes are shown as dotted lines in Figures 5 and 6. To $\mathcal{T}_V$ we add a new vertex w and we add the edge $\{\rho, w\}$. Then we add $|E|$ taxa directly beneath w. In $\mathcal{T}_E$, for each e_i, we subdivide the edge entering e_i, and attach one of the new taxa to the newly created node; we will call this taxon w_i. Each tree will have $3|V|M + |E| + M^*$ taxa.

As in the previous reduction we choose M^* sufficiently large such that, for all optimal characters f, $l_f(\mathcal{T}_V) < l_f(\mathcal{T}_E)$. Using the same refinement argument as before, this can be achieved simply by choosing M^* to be any even number such that

$$M^*/2 - 1 > 3|V|M + |E|.$$

Consider an optimal character f for $\mathcal{T}_V$ and $\mathcal{T}_E$. Due to our choice of M^* we know $l_f(\mathcal{T}_V) < l_f(\mathcal{T}_E)$. Hence, we can apply Lemma 4.3 to transform f, in polynomial time, such that for each vertex in $\{w, s, t, v_1, \ldots, v_n\}$, all the children of that vertex (in $\mathcal{T}_V$) have the same state. From now on we will refer to these states as *colors*. Indeed, f naturally induces a coloring of the vertices of G: vertex v_i of G is allocated the color of its children in $\mathcal{T}_V$. In fact, we argue that for appropriately large M, f must induce a *proper* coloring of G, i.e., a coloring such that every edge is bichromatic. To see why this is, suppose the induced coloring of G has at least one monochromatic edge. Then a (crude) upper bound on $l_f(\mathcal{T}_E)$, and thus also $l_f(\mathcal{T}_E) - l_f(\mathcal{T}_V)$, is

$$(|E| - 1)M + 3|E| + 2 + M^*/2.$$

(The $3|E| + 2$ term is obtained by assuming that on all edges entering the e_i and w_i nodes, on all edges leaving ρ, and on the two edges leaving ρ^*, incur mutations.)

On the other hand, if the induced coloring is proper, a *lower* bound on $l_f(\mathcal{T}_E)$ is

$$|E|M + M^*/2,$$

and an upper bound on $l_f(\mathcal{T}_V)$ is $|V| + 3$. So, if the coloring is proper,

$$l_f(\mathcal{T}_E) - l_f(\mathcal{T}_V) \geq |E|M + M^*/2 - |V| - 3.$$

So to enforce that the induced coloring is proper we simply choose M such that

$$|E|M + M^*/2 - |V| - 3 > (|E| - 1)M + 3|E| + 2 + M^*/2.$$

A choice of $M > 3|E| + |V| + 5$ is adequate.

Henceforth, we can focus our attention on optimal characters f that have the Lemma 4.3 property and that induce proper colorings in G. Note that, if we apply Fitch to f on $\mathcal{T}_V$, each vertex in $\{w, s, t, v_1, \ldots, v_n\}$ will be allocated the same color as its children. The colors assigned to ρ, ρ^*, and u depend on the exact colors used for $\{w, s, t, v_1, \ldots, v_n\}$. Fitch will assign ρ a color that occurs most frequently on $\{w, v_1, \ldots, v_n\}$ and (as discussed earlier) will break any ties in the top-down phase of the algorithm. If the most frequent color on $\{w, v_1, \ldots, v_n\}$ occurs z times, there will be exactly $(n + 1) - z$ mutations incurred on the edges leaving ρ.

Let c be the color of w and its children in $\mathcal{T}_V$. By a very careful analysis of Fitch's algorithm on $\mathcal{T}_E$, we can see that Fitch will definitely assign color c to ρ in

$\mathcal{T}_E$. Specifically, note that in the bottom-up phase of Fitch, c will definitely be in the set of labels allocated to the parent of each w_i. Color c is thus a most frequently occurring color amongst the children of ρ. There can be no other most frequently occurring color c', because c' would then have to appear as an endpoint of every edge in the proper coloring, implying that G is bipartite, which we have apriori excluded as a possibility. Hence, c is already chosen by Fitch in its bottom-up phase to be the definite label of ρ.

Consequently, in its top-down phase the parents of the w_i in $\mathcal{T}_E$ will also be labelled c. This means that, for an edge e_i of G, there will be a mutation on the edge entering e_i (in $\mathcal{T}_E$) *if and only if* neither endpoint of e_i is colored c. Now, suppose that c is one of the colors used to color $\{v_1, \ldots, v_n\}$ in $\mathcal{T}_V$. Then there exists an edge e_i which has exactly one endpoint colored c, meaning that no mutation is incurred on the edge entering e_i in $\mathcal{T}_E$. If we relabel the $|E|$ taxa beneath w to a new color that does not appear elsewhere in f, then the parsimony score of $\mathcal{T}_V$ under f increases by at most one, while the parsimony score of $\mathcal{T}_E$ under f definitely increases by (at least) one. The latter increase occurs because Fitch will now ascribe mutations to *all* the edges entering the e_i vertices, without causing a reduction in the number of mutations on the edges $\{\rho^*, \rho\}$, $\{\rho^*, u\}$.

Hence, the new f is still optimal and still has the earlier derived properties, plus the new property that c, the color of w, can be assumed to be distinct from the colors used on $\{v_1, \ldots, v_n\}$.

Now, knowing that Fitch will definitely assign c to ρ in $\mathcal{T}_E$, we can argue, without loss of generality, that the colors assigned to s and t in $\mathcal{T}_V$ can also be distinct from c. To see this, suppose one of s and t is colored c, without loss of generality let this be s. (We note that s and t must have different colors, otherwise f cannot possibly be optimal.) Then Fitch will definitely color ρ^* and u with color c in $\mathcal{T}_E$ and there will be no mutation on edge $\{\rho^*, \rho\}$ or $\{\rho^*, u\}$ in $\mathcal{T}_E$. Recoloring the clade s with a new color d will cost at most one new mutation in $\mathcal{T}_V$, and at least one new mutation in $\mathcal{T}_E$ (on the edge $\{\rho^*, \rho\}$ or $\{\rho^*, u\}$), so the new f will still be optimal.

Hence, we can assume that in f neither s nor t has color c (where c is the color of w), and that c is not a color used on $\{v_1, \ldots, v_n\}$.

Now, consider the most frequently occurring colors on $\{w, v_1, \ldots, v_n\}$. Given that c is only used to color w, there must exist at least one most frequently occurring color distinct from c. Furthermore, one of these colors must be used to color s or t. To see why this is, let $c' \neq c$ be one of the most frequently occurring colors; if we relabel (say) clade s with c' we lower the parsimony score of $\mathcal{T}_V$, without lowering the parsimony score of $\mathcal{T}_E$, contradicting the optimality of the character.

We have thus reached the point that we can assume that in f neither s nor t has color c (where c is the color of w), that c is not a color on $\{v_1, \ldots, v_n\}$, and that either s or t has the same color as some most frequently occurring color on $\{v_1, \ldots, v_n\}$. All such f have the same parsimony score on $\mathcal{T}_E$. The only degree of freedom left is to minimize the parsimony score of $\mathcal{T}_V$. This can be achieved by choosing a proper coloring of G such that the frequency of the most frequently occurring color is maximized. This is essentially equivalent to constructing a maximum-size independent set of G: give all the vertices in the independent set the same color, and all the other vertices distinct colors. When this is done, $|V| - MIS(G)$ mutations will be incurred

in $\mathcal{T}_V$ on the edges feeding into the v_i nodes, 1 mutation will be incurred on the edge entering w, and in total 1 mutation will be incurred on the two edges leaving u. Hence, we finally arrive at the following conclusion:

$$d_{MP}(\mathcal{T}_V, \mathcal{T}_E) = M^*/2 + 1 + |E| + |E|M - ((|V| + 1) - MIS(G) + 1).$$

From this the value $MIS(G)$ can easily be computed, and the independent set itself can be obtained by applying Fitch to $\mathcal{T}_V$ (after having applied all the necessary transformations to the character) and returning all v_i that are labelled with the same color as ρ. This completes the reduction. ∎

The above theorem assists us in extending the result given in Lemma 4.5.

Corollary 4.7. *Computing $d^i_{MP}(\mathcal{T}_1, \mathcal{T}_2)$ is NP-hard for every fixed integer $i \geq 2$.*

Proof. The case $i = 2$ is proven in Lemma 4.5. The case $i = 3$ requires an ad-hoc extension of that lemma and we defer this to the appendix. Assume then that $i \geq 4$. In the above proof we argued that in f neither s nor t has color c (where c is the color of w), that c is not a color on $\{v_1, \ldots, v_n\}$, and that either s or t has the same color as some most frequently occurring color on $\{v_1, \ldots, v_n\}$. To achieve this, we are free to use some colors more than once. Now, observe that G has chromatic number 3. This follows from Brook's Theorem [7], because G has maximum degree 3, is not equal to K_4, and is not bipartite. Moreover, the results in [11] state that such a graph can be colored with 3 colors such that the most frequently occurring color induces a maximum independent set. Let *blue* be the color corresponding to the vertices of the maximum independent set, and let *red* and *green* be the remaining two colors. We use, without loss of generality, *blue* and *red* to color s and t, and introduce a new fourth color *yellow* to color w. Hence, at most 4 colors are needed to optimize $d_{MP}(\mathcal{T}_V, \mathcal{T}_E)$, even when more are available, from which the result follows. ∎

5. Discussion

In this article we have explored several properties of the MP distance measure. We have also proven that this new metric is NP-hard. A hardness result for the case of *binary* trees remains elusive, although we strongly believe that this is also NP-hard and shall elaborate upon this in a forthcoming publication. In any case, the NP-hardness of the metric is not, in itself, a reason to cease investigating it. Recent years have seen an explosion of academic interest in overcoming in practice the theoretical intractability of attractive measures such as SPR distance and hybridization number (see e.g., [26, 28]). A potentially attractive feature of MP distance is that (unlike, for example, the Robinson-Foulds metric) it is robust against SPR moves. That is, the difference between $d_{MP}(\mathcal{T}_1, \mathcal{T}_2)$ and $d_{MP}(\mathcal{T}_1, \mathcal{T}_2')$, where $\mathcal{T}_2'$ is obtained from $\mathcal{T}_2$ by applying a single SPR move, is at most 1. This is because (by the triangle inequality

and the fact that MP distance is a lower bound on the SPR distance),

$$d_{MP}\left(\mathcal{T}_1, \mathcal{T}_2'\right) \leq d_{MP}(\mathcal{T}_1, \mathcal{T}_2) + d_{MP}\left(\mathcal{T}_2, \mathcal{T}_2'\right)$$

$$\leq d_{MP}(\mathcal{T}_1, \mathcal{T}_2) + d_{SPR}\left(\mathcal{T}_2, \mathcal{T}_2'\right)$$

$$\leq d_{MP}(\mathcal{T}_1, \mathcal{T}_2) + 1.$$

Similarly, $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) \leq d_{MP}\left(\mathcal{T}_1, \mathcal{T}_2'\right) + 1$, from which the observation follows. Robustness to SPR moves is considered an important property when modelling horizontal gene transfer, which is one of the reasons for the prominence of SPR distance in that literature (see, e.g., [4]).

Indeed, one particularly important line of research will be to clarify the exact relationship between MP distance and SPR distance, both in theory and in practice. As far as practice is concerned, it is useful to recall Corollary 3.12, which observes that *every* character gives a lower bound on the MP distance, and thus also on the SPR distance. Perhaps randomized sampling of characters is a good way of heuristically maximizing MP distance in polynomial time, and perhaps this in turn gives good bounds on SPR distance. On the theoretical side, it is interesting to note that MP distance is also a lower bound on a different distance, d_{TBR}, which is the metric derived from *tree bisection and reconnection* (*TBR*) moves. (For a definition see, e.g., [9].) TBR moves generalize SPR moves and hence $d_{TBR}(\mathcal{T}_1, \mathcal{T}_2) \leq d_{SPR}(\mathcal{T}_1, \mathcal{T}_2)$ for all unrooted phylogenetic trees $\mathcal{T}_1, \mathcal{T}_2$ [9]. The fact that MP distance is a lower bound on d_{TBR} is a consequence of the fact that, as remarked at the end of [8, Theorem 1] — which is the main ingredient of our Theorem 3.8 — also holds for TBR distance. Alternatively, one can leverage [9, Lemma 5.1] to establish $d_{MP}(\mathcal{T}_1, \mathcal{T}_2) \leq d_{TBR}(\mathcal{T}_1, \mathcal{T}_2)$. We also have slightly larger examples (omitted) which show that MP distance is sometimes strictly lower than TBR distance. In any case, to better understand the attractiveness of MP distance as a lower bound for SPR (and TBR), it will be necessary to look more deeply into the mutual relationship between these three measures, building on the bounds given in [2] and subsequent articles.

To summarize: what exactly is the relationship between our new metric and SPR distance (and other phylogenetic measures)? And how far can the NP-hardness of our new metric be tamed in practice? In future research we will tackle these and other questions.

6. Appendix: Generalizing Lemma 4.5 to 3 states

Lemma 6.1. *Computing $d_{MP}^3(\mathcal{T}_1, \mathcal{T}_2)$ is NP-hard.*

Proof. We note that determining whether a 4-regular graph $G = (V, E)$ is 3-colorable, is NP-hard [14]. (The regularity restriction is not strictly essential but again makes the analysis cleaner). Let G be a 4-regular graph. Let $BICHROM(G)$ be the maximum number of bichromatic edges possible, ranging over all (proper or non-proper) colorings of V with at most 3 colors. Observe that G is 3-colorable if and only if $BICHROM(G) = |E|$. The following reduction shows that $BICHROM(G)$ can be computed using an oracle for $d_{MP}^3(\mathcal{T}_1, \mathcal{T}_2)$, from which hardness follows. The reduction differs only from that used in Lemma 4.5 in the choice of M and M^*.

Clearly, $|E| = 2|V|$. Let $\{0, 1, 2\}$ be the set of 3 character states. During this proof we will write "any character" as shorthand for "any character with at most 3 states".

The high-level idea is to construct two trees $\mathcal{T}_1$ and $\mathcal{T}_2$, henceforth referred to as $\mathcal{T}_V$ and $\mathcal{T}_E$, where $\mathcal{T}_V$ encodes the vertices and $\mathcal{T}_E$ the edges of G. In $\mathcal{T}_V$ the character states $\{0, 1, 2\}$ will be used to indicate the color assigned to each vertex. The mutations induced in $\mathcal{T}_E$ will be used to count the number of bichromatic edges induced by the coloring.

Let $V = \{v_1, \ldots, v_n\}$ and $E = \{e_1, \ldots, e_m\}$. Throughout the reduction we will utilize two large numbers, M and an even number M^*, such that $n << M << M^*$ but such that both are still at most $poly(n)$. In due course we will explain how these numbers are calculated. Both trees will have $4|V|M + M^*$ taxa.

To construct $\mathcal{T}_V$, we first introduce vertices $\rho^*, \rho, s, t, u,$ and $\{v_1, \ldots, v_n\}$. We add edges $\{\rho^*, \rho\}$, $\{\rho^*, u\}$, $\{u, s\}$, $\{u, t\}$, and $\{\rho, v_i\}$ for $1 \leq i \leq n$. We connect each v_i to $4M$ taxa. We connect s to $M^*/2$ taxa and t to $M^*/2$ taxa.

To construct $\mathcal{T}_E$ we introduce vertices $\rho^*, \rho, u,$ and $\{e_1, \ldots, e_m\}$. We add edges $\{\rho^*, \rho\}$, $\{\rho^*, u\}$, and $\{\rho, e_i\}$ for $1 \leq i \leq m$. To u we connect the M^* taxa that were connected to s and t in $\mathcal{T}_V$. Next we introduce mM vertices $e_{i,j}$ for $i \in \{1, \ldots, m\}$ and $j \in \{1, \ldots, M\}$. We connect each vertex e_i to all the $e_{i,j}$, for $j \in \{1, \ldots, M\}$. To each $e_{i,j}$ we connect two taxa, representing the endpoints (of the jth copy) of edge e_i. To determine which two taxa these are, suppose in G the edge e_i is connected to vertices v_a and v_b. Then one of the two taxa is taken from the clade of taxa we connected to v_a in $\mathcal{T}_V$, and the other from the clade of taxa beneath v_b in $\mathcal{T}_V$. The exact mapping chosen does not matter. This completes the construction.

For $x \in \mathbb{R}$, let $round(x)$ be x rounded to the nearest integer. (By construction we will actually only use values of x that are at most $1/3$ above or below the nearest integer; this will become clearer later.) We shall prove the following:

$$BICHROM(G) = round\left(\frac{d_{MP}^3(\mathcal{T}_V, \mathcal{T}_E) - M^*/2}{M}\right). \tag{6.1}$$

Moreover, we will show how any optimal character f can be transformed in polynomial-time into a coloring that has $BICHROM(G)$ edges.

Note that in $\mathcal{T}_V$ the subtree rooted at u is a refinement of the subtree rooted at u in $\mathcal{T}_E$. This means that, for any character f, a (crude) upper bound on $l_f(\mathcal{T}_V) - l_f(\mathcal{T}_E)$ is $4|V|M$. To see this, observe that for any character the number of mutations incurred in $\mathcal{T}_V$ in the subtree rooted at u, is less than or equal to the number of mutations incurred in the corresponding subtree of $\mathcal{T}_E$. Therefore, mutations in this subtree can never contribute to an increase in $l_f(\mathcal{T}_V) - l_f(\mathcal{T}_E)$. Hence, an upper bound on $l_f(\mathcal{T}_V) - l_f(\mathcal{T}_E)$ can be achieved by maximizing the number of mutations that occur in $\mathcal{T}_V$ on edges that are not in this subtree, and minimizing the number of mutations that occur in $\mathcal{T}_E$ on edges that are not in this subtree. A (trivial) lower bound on the latter is 0, while a (trivial) upper bound on the former is $4|V|M$ (e.g., by assigning the same state to all internal nodes of $\mathcal{T}_V$).

On the other hand, consider a character f such that the $M^*/2$ taxa underneath s in $\mathcal{T}_V$ are allocated, without loss of generality, state 0, and all other taxa are allocated, without loss of generatlity, state 1. Then $l_f(\mathcal{T}_V) = 1$ and $l_f(\mathcal{T}_E) \geq M^*/2$. For this

reason we choose M^* such that

$$M^*/2 - 1 > 4|V|M.$$

After choosing M^* this way we know that $d_{MP}^3(\mathcal{T}_V, \mathcal{T}_E) \geq (M^*/2) - 1$ and, more importantly, that for every optimal character f, $l_f(\mathcal{T}_V) < l_f(\mathcal{T}_E)$.

From Observation 4.4 we can therefore assume that, for each vertex of $\mathcal{T}_V$ in the set $\{s, t, v_1, \ldots, v_n\}$, all the taxa beneath the vertex are allocated the same state by f. (The same observation tells us that it is safe to assume that all the taxa in the s clade have the same state, and all the taxa in the t clade have the same state, and that these two states are distinct.)

Such a character naturally induces a coloring of the vertices. The core observation is that if an edge e_i is bichromatic (i.e., the colors at its endpoints are different) then f will induce at least M mutations in the subtree of $\mathcal{T}_E$ rooted at e_i. On the other hand, if an edge e_i is monochromatic this will induce 0 mutations in the subtree rooted at e_i.

More formally, suppose f induces k bichromatic edges. The parameter k does not, in itself, give us enough information to *exactly* determine $l_f(\mathcal{T}_V)$ and $l_f(\mathcal{T}_E)$, but we can get close enough. Counting crudely,

$$0 \leq l_f(\mathcal{T}_V) \leq |V|,$$

where the upper bound of $|V|$ can be obtained by applying Fitch (and observing that, by the earlier assumption, the taxa in the s clade have a different state to the taxa in the t clade). Also,

$$M \cdot k + M^*/2 \leq l_f(\mathcal{T}_E) \leq M \cdot k + |E| + 2 + M^*/2.$$

(The $|E| + 2$ on the right-hand side of the above expression is an upper bound on the number of mutations incurred on the $|E|$ edges leaving ρ and the 2 edges leaving ρ^*.) From this, it follows that

$$M \cdot k + M^*/2 - |V| \leq l_f(\mathcal{T}_E) - l_f(\mathcal{T}_V) \leq M \cdot k + |E| + 2 + M^*/2.$$

Assuming M has been chosen such that $M > |V| + |E| + 2$, we observe that $l_f(\mathcal{T}_E) - l_f(\mathcal{T}_V)$ — and thus also $d_{MP}^3(\mathcal{T}_V, \mathcal{T}_E)$ — will be maximized by selecting k as large as possible, i.e., by making as many edges as possible bichromatic. So,

$$BICHROM(G) - \frac{|V|}{M} \leq \frac{d_{MP}^3(\mathcal{T}_V, \mathcal{T}_E) - M^*/2}{M} \leq BICHROM(G) + \frac{|E| + 2}{M}$$

Taking $M > 3(|V| + |E| + 2)$ is therefore sufficient. This completes the reduction. ∎

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