Two metrics for general phylogenetic networks

Gabriel Cardona¹, Mercè Llabrés¹, Francesc Rosselló¹, and Gabriel Valiente²,³

¹ Department of Mathematics and Computer Science, University of the Balearic Islands, E-07122 Palma de Mallorca, {gabriel.cardona,merce.llabres,cesc.rossello}@uib.es
² Algorithms, Bioinformatics, Complexity and Formal Methods Research Group, Technical University of Catalonia, E-08034 Barcelona, valiente@lsi.upc.edu

Abstract. We prove that Nakhleh’s latest ‘metric’ for phylogenetic networks separates distinguishable phylogenetic networks, and that a slight modification of it provides a true distance on the class of all phylogenetic networks.

1 Introduction

L. Nakhleh has recently proposed a dissimilarity measure for the comparison of phylogenetic networks [4], but he has only proved that it satisfies the separation axiom for metrics (zero distance means isomorphism) on the class of all reduced phylogenetic networks in the sense of [3]. And, although we show that this measure separates phylogenetic networks more general than the reduced ones (for instance, the tree-child phylogenetic networks [1]), it does not satisfy the separation axiom on the whole class of all phylogenetic networks (see Remark 1 below).

In this note we complement Nakhleh’s work in two directions. On the one hand, we prove that, for this dissimilarity measure, zero distance implies indistinguishability up to reduction in the sense of [3], a goal that had already been pursued by Moret-Nakhleh-Warnow et al in loc. cit., failing in their attempt [2]. In this way, and to the best of our knowledge, Nakhleh’s dissimilarity measure turns out to be the first one that separates distinguishable networks. And, on the other hand, we show that a slight modification of Nakhleh’s definition does yield a true distance on the whole class of all phylogenetic networks. Again to the best of our knowledge, this is the first true metric defined on this class.

1.1 Notations

Let $N = (V, E)$ be a DAG (a finite directed acyclic graph). We say that a node $v \in V$ is a child of $u \in V$ if $(u, v) \in E$; we also say then that $u$ is a parent of $v$. We say that a node is a tree node when it has at most one parent, and that it is a hybrid node when it has more than one parent. A node that is not a leaf is called internal. A DAG is rooted when it has only one root: a node without parents.

A path in $N$ is a sequence of nodes $(v_0, v_1, \ldots, v_k)$ such that $(v_{i-1}, v_i) \in E$ for all $i = 1, \ldots, k$. We call $v_0$ the origin of the path, $v_1, \ldots, v_{k-1}$ its intermediate nodes, $v_k$ its end, and $k$ its length. We denote by $u \to v$ any path with origin $u$ and end $v$ and, whenever there exists a path $u \to v$, we say that $v$ is a descendant of $u$.

The height $h(v)$ of a node $v$ in a DAG $N$ is the largest length of a path from $v$ to a leaf. The absence of cycles implies that the nodes of a DAG can be stratified by means of their heights: the nodes of height 0 are the leaves, the nodes of height 1 are those nodes
all whose children are leaves, the nodes of height 2 are those nodes all whose children are leaves and nodes of height 1, and so on. If a node has height \( m \), then all its children have height smaller than \( m \), and at least one of them has height exactly \( m - 1 \).

Given a finite set \( S \), an \( S\text{-DAG} \) is a DAG whose leaves are bijectively labeled by elements of \( S \). We shall always identify, usually without any further notice, each leaf of an \( S\text{-DAG} \) with its label. Two \( S\text{-DAGs} \) \( N, N' \) are isomorphic, in symbols \( N \cong N' \), when they are isomorphic as directed graphs and the isomorphism preserves the leaves’ labels.

A phylogenetic network on a set \( S \) of taxa is a rooted \( S\text{-DAG} \).

For every node \( u \) of a phylogenetic network \( N = (V, E) \), let \( C(u) \) be the set of all its descendants in \( N \) and \( N(u) \) the subgraph of \( N \) supported on \( C(u) \); it is still a phylogenetic network, with root \( u \) and leaves labeled in the subset \( C_L(u) \subseteq S \) of labels of the leaves that are descendants of \( u \). We shall call \( N(u) \) the rooted subnetwork of \( N \) generated by \( u \), and the set of leaves \( C_L(u) \) the cluster of \( u \).

A clade of a phylogenetic network \( N \) is a rooted subnetwork of \( N \) all whose nodes are tree nodes in \( N \) (and, in particular, it is a rooted tree).

### 1.2 Moret-Nakhleh-Warnow-et al’s reduction process

Let \( N = (V, E) \) be a phylogenetic network on a set \( S \) of taxa. A subset \( U \) of internal nodes of \( V \) is said to be convergent when it has more than one element, and all nodes in it have exactly the same cluster.

The removal of convergent sets is the basis of the reduction procedure introduced in [3]:

1. Replace every clade by a new ‘symbolic leaf’ labeled with the names of all leaves in it.
2. For every maximal convergent set \( U \), remove all internal descendants of its nodes (including the nodes of \( U \)).
3. Append to every symbolic leaf representing a clade the corresponding clade, with an arc from the symbolic leaf to the root of the clade, and remove the label of the symbolic leaf.
4. Replace every node with only one parent and one child by an arc from its parent to its only child.

(These are the only nodes that have to be removed in this step.)

The output of this procedure applied to a phylogenetic network \( N \) on \( S \) is a (non-necessarily rooted) \( S\text{-DAG} \), called the reduced version of \( N \) and denoted by \( R(N) \). A network \( N \) is reduced when \( R(N) = N \). It should be noticed that the only possible convergent sets in \( R(N) \) consist of a hybrid node and its only child (more specifically, the hybrid node corresponding to a symbolic leaf with more than one parent, and the root of the corresponding clade) [2].

Two networks \( N_1 \) and \( N_2 \) are said to be indistinguishable when they have isomorphic reduced versions, that is, when \( R(N_1) \cong R(N_2) \). Moret, Nakhleh, Warnow, et al argue in [3, p. 19] that for reconstructible phylogenetic networks this notion of indistinguishability (isomorphism after simplification) is more suitable than the existence of an isomorphism between the original networks.
2 Nakhleh’s ‘metric’

Nakhleh defines in [4] an equivalence on the set of nodes of a pair of S-DAGs inductively as follows.

Definition 1. Let \( N_1 = (V_1, E_1) \) and \( N_2 = (V_2, E_2) \) be S-DAGs (not necessarily different). Two nodes \( u \in V_1 \) and \( v \in V_2 \) are equivalent, in symbols \( u \equiv v \), when:

- \( u \) and \( v \) are both leaves labeled with the same taxon, or
- for some \( k \geq 1 \), node \( u \) has exactly \( k \) children \( u_1, \ldots, u_k \), node \( v \) has exactly \( k \) children \( v_1, \ldots, v_k \), and \( u_i \equiv v_i \) for every \( i = 1, \ldots, k \).

Thus, in this case, \( u \equiv v \).

The following characterization of node equivalence will be useful.

Definition 2. Let \( N = (V, E) \) be a DAG. The nested labeling \( \ell(v) \) of the nodes \( v \) of \( N \) is defined by induction on \( h(v) \) as follows:

- If \( h(v) = 0 \), that is, if \( v \) is a leaf, then \( \ell(v) = \{v\} \), the one-element set consisting of its label.
- If \( h(v) = m > 0 \), then all its children \( v_1, \ldots, v_k \) have height smaller then \( m \), and hence they have been already labeled: then, \( \ell(v) \) is the multiset of their nested labels,

\[
\ell(v) = \{\ell(v_1), \ldots, \ell(v_k)\}.
\]

Notice that the nested label of a node is, in general, a nested multiset (a multiset of multisets of multisets of...), hence its name. Moreover, the height of a node \( u \) is the highest level of nesting of a leaf in \( \ell(u) \) minus 1.

Proposition 1. Let \( N_1 = (V_1, E_1) \) and \( N_2 = (V_2, E_2) \) be DAGs (not necessarily different) labeled in a set \( S \). For every \( u \in V_1 \) and \( v \in V_2 \), \( u \equiv v \) if, and only if, \( \ell(u) = \ell(v) \).

Proof. We prove the equivalence by induction on the height of one of the nodes, say \( u \).

If \( h(u) = 0 \), then it is a leaf, and \( \ell(u) \) is the one-element set consisting of its label. Thus, in this case, \( u \equiv v \) if, and only if, \( v \) is the leaf of \( N_2 \) with the same label as \( u \), and \( \ell(u) = \ell(v) \) if, and only if, \( v \) is the leaf of \( N_2 \) with the same label as \( u \), too.

Consider now the case when \( h(u) = m > 0 \) and assume that the thesis holds for all nodes \( u' \in V_1 \) of height smaller than \( m \). Let \( u_1, \ldots, u_k \) be the children of \( u \). Then:

- \( u \equiv v \) if and only if \( v \) has exactly \( k \) children and they can be ordered \( v_1, \ldots, v_k \) in such a way that \( u_i \equiv v_i \) for every \( i = 1, \ldots, k \).
- \( \ell(u) = \ell(v) \) if and only if \( v \) has exactly \( k \) children and the multiset of their nested labels is equal to the multiset of nested labels of \( u_1, \ldots, u_k \), which means that \( v \)’s children can be ordered \( v_1, \ldots, v_k \) in such a way that \( \ell(u_i) = \ell(v_i) \) for every \( i = 1, \ldots, k \).

Since, by induction, the children of \( u \) satisfy the thesis, it is clear that \( u \equiv v \) is equivalent to \( \ell(u) = \ell(v) \).

We shall say that a nested label \( \ell(v) \) is contained in a nested label \( \ell(u) \), in symbols \( \ell(v) \preceq \ell(u) \), when \( \ell(v) \) is the nested label of a descendant of \( u \). Notice that if \( \ell(v) \) is contained in \( \ell(u) \), then \( v \) is equivalent to some descendant of \( u \), but \( v \) itself need not be a descendant of \( u \): several instances of this fact can be detected in the networks depicted in Fig. 1. Notice moreover that \( \ell(u) \in \ell(u) \) if, and only if, \( \ell(v) \) is the nested label of a child of \( u \).

Nakhleh defines in [4] the following dissimilarity measure.
Definition 3. For every S-DAG $N$, let $\mathcal{Y}(N)$ be the multiset of equivalence classes of its nodes (where each equivalence class appears with multiplicity the number of nodes in it).

Definition 4. For every pair of phylogenetic networks $N_1$ and $N_2$ on the same set $S$ of taxa, let

$$m(N_1, N_2) = \frac{1}{2}|\mathcal{Y}(N_1) \triangle \mathcal{Y}(N_2)|,$$

where $\triangle$ denotes the symmetric difference of multisets: if a class belongs to $\mathcal{Y}(N_1)$ with multiplicity $a$ and to $\mathcal{Y}(N_2)$ with multiplicity $b$, then it contributes $|a-b|$ to $|\mathcal{Y}(N_1) \triangle \mathcal{Y}(N_2)|$.

Notice that $\mathcal{Y}(N)$ can be also understood as the multiset of nested labels of the nodes of $N$, each nested label appearing with multiplicity the number of nodes labeled with it.

Lemma 1. Let $N_1$ and $N_2$ be two S-DAGs such that no one of them contains any pair of equivalent nodes. Then, $m(N_1, N_2) = 0$ if, and only if, $N_1 \cong N_2$.

Proof. Let $R(N_1) = (V_1, E_1)$ and $R(N_2) = (V_2, E_2)$. If neither $N_1$ nor $N_2$ contain any pair of equivalent nodes, then $\mathcal{Y}(N_1)$ and $\mathcal{Y}(N_2)$ are sets, and the quotient mappings $V_i \rightarrow \mathcal{Y}(N_i)$ are bijections, for $i = 1, 2$.

Now, assume that $|\mathcal{Y}(N_1) \triangle \mathcal{Y}(N_2)| = 0$. Then $\mathcal{Y}(N_1) = \mathcal{Y}(N_2)$ and hence there exists a well-defined bijection $\alpha : V_1 \rightarrow V_2$ that sends each node in $N_1$ to the only node in $N_2$ equivalent to it. In particular it sends each leaf of $N_1$ to the leaf of $N_2$ with the same label. To see that $\alpha$ is an isomorphism of graphs, let $(u, v) \in E_1$ be any arc in $N_1$. Since $u \equiv \alpha(u)$, the node $\alpha(u)$ must have a child equivalent to $v$, and since $N_2$ does not contain any pair of equivalent nodes, this child is $\alpha(v)$, which implies that $(\alpha(u), \alpha(v)) \in E_2$. This shows that $\alpha$ preserves arcs, and a similar argument applied to $\alpha^{-1} : V_2 \rightarrow V_1$ shows that it also reflects them. This proves that $\alpha : N_1 \rightarrow N_2$ is an isomorphism of S-DAGs.

The converse implication is obvious.

A first consequence of this lemma is the following result, which is essentially Theorem 2 in Nakhleh’s paper [4].

Proposition 2. Let $R(N_1)$ and $R(N_2)$ be the reduced versions of two phylogenetic networks on the same set $S$ of taxa. Then, $m(R(N_1), R(N_2)) = 0$ if, and only if, $R(N_1) \cong R(N_2)$.

Proof. The reduced version of a phylogenetic network does not contain any pair of equivalent nodes [4, Obs. 2].

Corollary 1. Let $N_1$ and $N_2$ be two reduced phylogenetic networks on the same set $S$ of taxa. Then, $m(N_1, N_2) = 0$ if, and only if, $N_1 \cong N_2$.

Another type of phylogenetic networks not containing any pair of equivalent nodes are the tree-child phylogenetic networks: phylogenetic networks where every internal node has a child that is a tree node. Tree-child phylogenetic networks were introduced in [1], and a metric and an alignment method for them was proposed, and they have been recently proposed by S. J. Willson as the class where meaningful phylogenetic networks should be searched [7].

Proposition 3. A tree-child phylogenetic network does not contain any pair of equivalent nodes.
Proof. Let \( u \) and \( v \) be two nodes of a tree-child phylogenetic network \( N \). If \( u \equiv v \), then \( C_L(u) = C_L(v) \) and \( h(u) = h(v) \). Let now \( s \) be a leaf for which there exists a path \( u \leadsto s \) with all intermediate nodes and \( s \) itself tree nodes (which exists by [2, Lem. 2]). Then \( s \in C_L(u) = C_L(v) \), which implies that there is also a path \( v \leadsto s \). By [2, Lem. 1], this implies that \( u \) and \( v \) are connected by a path. If they have moreover the same height, they must be the same node.

Corollary 2. Let \( N_1 \) and \( N_2 \) be two tree-child phylogenetic networks on the same set \( S \) of taxa. Then, \( m(N_1, N_2) = 0 \) if, and only if, \( N_1 \cong N_2 \).

Remark 1. It is false in general that if two arbitrary phylogenetic networks \( N_1 \) and \( N_2 \) on the same set \( S \) of taxa are such that \( m(N_1, N_2) = 0 \), then \( N_1 \cong N_2 \). For instance, it is easy to check that the networks depicted in Fig. 1 have the same multisets \( \Upsilon \), but they are not isomorphic.

Fig. 1. These phylogenetic networks have the same multisets of equivalence classes of nodes, but they are not isomorphic.

Now, it turns out that this metric \( m \) separates networks that are distinguishable up to reduction. We would like to recall here that this was the (unaccomplished [2]) goal of the error metric defined in [3].

Theorem 1. Let \( N_1 \) and \( N_2 \) be two phylogenetic networks on the set \( S \) of taxa. If \( m(N_1, N_2) = 0 \), then \( N_1 \) and \( N_2 \) are indistinguishable.

Proof. In this proof, we shall take \( \Upsilon(N) \) as the multiset of nested labels of a network \( N \). Let \( N_1 = (V_1, E_1) \) and \( N_2 = (V_2, E_2) \) be two phylogenetic networks such that \( \Upsilon(N_1) = \Upsilon(N_2) \). We shall prove that the reduction process of both networks modifies exactly in the same way their multisets of nested labels, and thus the reduced versions \( R(N_1) \) and \( R(N_2) \) also have the same multisets of nested labels. Then, by Proposition 2, the latter are isomorphic.
To begin with, notice that two nodes are convergent when the set of $S$-labels appearing in their nested labels are the same (without taking into account nesting levels or multiplicities). In particular, $N_1$ and $N_2$ have the same sets of nested labels of convergent nodes.

Step (0) in the reduction process consists of replacing every clade by a symbolic leaf. This corresponds to remove the nested labels of the nodes belonging to clades (except their roots) and to replace, in all remaining nested labels, each nested label of a root of a clade by the label of the corresponding symbolic leaf. We must prove now that we can decide from the multisets of nested labels alone which are the nested labels of nodes of clades and of roots of clades.

Since the clades of a phylogenetic network are subtrees, a node belonging to a clade is only equivalent to itself (if $v$ is a node of a clade and $v \equiv u$, then $C_L(u) = C_L(v)$, but in this case, since $v$ is the least common ancestor of $C_L(v)$ in the clade it belongs, $v$ must be a descendant of $u$, and since $u$ and $v$ have the same height —because they are equivalent—they must be the same node). In particular, a node of a clade does not share its nested label with any other node.

Then, the nested labels of nodes $v \in V_i$ belonging to some clade of $N_i$ ($i = 1, 2$) are characterized by the following two properties: $\ell(v)$ and each one of the nested labels contained in it appear with multiplicity 1 in $\Upsilon(N_i) = \Upsilon(N_2)$ (and in particular $v$ and its descendants are characterized by their nested labels); and $\ell(v)$ and each one of the nested labels contained in it belong at most to one nested label (this means that $v$ and its descendants are tree nodes, and in particular that the rooted subnetwork generated by $v$ is a tree consisting only of tree nodes from $N_i$). And therefore the roots of clades of $N_i$ are the nodes $v$ with nested label $\ell(v)$ maximal with these properties, and the nodes of the clade rooted at $v$ are those nodes with nested labels contained in $\ell(v)$. This shows that the nested labels of roots of clades and the nested labels of nodes belonging to clades in $N_1$ are the same as in $N_2$.

So, we remove the same nested labels in $N_1$ and $N_2$ and we replace the same nested labels by symbolic leaves. As a consequence, the networks resulting after this step have the same nested labels.

In step (1), all nodes that are convergent with some other node are removed, and all nodes other than symbolic leaves that are descendant of some removed node are also removed. So, in this step we remove the nested labels of convergent nodes, and the nested labels other than singletons that are contained in some nested label of convergent node (notice that if $\ell(v)$ is not a singleton and it is contained in $\ell(u)$ and $u$ is convergent, then either $v$ is a descendant of $u$, and then it has to be removed, or it is equivalent to a descendant of $u$, and then it forms a convergent set with this descendant and it has to be removed, too). This shows that the nested labels of the nodes removed in both networks are the same, and hence that the nested labels of the nodes that remain in both networks are also the same.

In step (2), the paths from the remaining nodes to the labels are restored. It means to replace in each remaining nested label $\ell(x)$, each maximal nested label $\ell(x) \preceq \ell(v)$ of a removed node $v$ by the singletons $\{s_1\}, \{s_2\}, \ldots, \{s_p\}$ of the symbolic leaves appearing in $\ell(v)$. Again, this operation only depends on the nested labels, and therefore after this step the resulting DAGs have the same multisets of nested labels.

In step (3), clades are restored. This is simply done by replacing in the nested labels each symbolic leaf $s$ by the nested label of the root of the clade it replaced, between brackets (because we append it to the node corresponding to the symbolic leaf). Since the
same clades were removed in both networks and replaced by the same symbolic leaves, after this step the resulting DAGs still have the same multisets of nested labels.

Finally, in step (4), the nodes with only one parent and only one child are removed. This corresponds to remove nested labels of the form \{\ldots\} that are children of only one parent (that is, that belong to only one nested label), and hence the same nested labels are removed in both DAGs.

So, at the end of this procedure, the resulting DAGs \(R(N_1)\) and \(R(N_2)\) have the same multisets of nested labels. By Proposition 2, this implies that \(R(N_1)\) and \(R(N_2)\) are isomorphic.

The converse implication is, of course false: since the reduction process may remove parts with different topologies that yield differences in the multisets of equivalence classes, two phylogenetic networks with isomorphic reduced versions may have different multisets of equivalence classes.

The value \(m(N_1, N_2)\) can be computed in time polynomial in the sizes of the networks \(N_1, N_2\) by performing a simultaneous bottom-up traversal of the two networks [5, 6].

### 3 A metric for arbitrary phylogenetic networks

If instead of the equivalence classes of the nodes (or, equivalently, their nested labels) we consider the whole rooted subnetworks generated by the nodes, we can define a true distance on the whole class of all phylogenetic networks.

**Remark 2.** It is clear that if \(u\) and \(v\) are two nodes of two phylogenetic networks \(N_1\) and \(N_2\), respectively (it can happen that \(N_1 = N_2\)), such that the rooted subnetworks \(N_1(u)\) and \(N_2(v)\) generated by them are isomorphic, then \(u \equiv v\) (because the equivalence can be computed within these rooted subnetworks). But the converse implication is false: node equivalence in phylogenetic networks does not imply isomorphism of the rooted subnetworks. Consider for instance the non-isomorphic phylogenetic networks depicted in Fig. 1: it is easy to check that their roots are equivalent.

**Definition 5.** For every \(S\)-DAG \(N\), let \(\Sigma(N)\) be the multiset of isomorphism classes of the rooted subnetworks generated by its nodes.

**Definition 6.** For every pair of phylogenetic networks \(N_1\) and \(N_2\) on the same set \(S\) of taxa, let

\[
\sigma(N_1, N_2) = \frac{1}{2} | \Sigma(N_1) \triangle \Sigma(N_2) |
\]

where \(\triangle\) denotes the symmetric difference of multisets.

**Theorem 2.** Let \(N_1\) and \(N_2\) be two phylogenetic networks on the same set \(S\) of taxa. Then, \(\sigma(N_1, N_2) = 0\) if, and only if, \(N_1 \cong N_2\).

**Proof.** Assume that \(\sigma(N_1, N_2) = 0\), that is, \(\Sigma(N_1) = \Sigma(N_2)\). Since each \(N_i\) is its rooted subnetwork generated by its root, we conclude that \(N_1\) contains a rooted subnetwork isomorphic to \(N_2\) and \(N_2\) contains a rooted subnetwork isomorphic to \(N_1\). The only possibility is then that \(N_1\) and \(N_2\) are isomorphic (otherwise, \(N_1\) would contain a rooted subnetwork isomorphic to it and strictly contained in it, something that in finite graphs is impossible).

The converse implication is obvious.
Corollary 3. The mapping $\sigma$ is a metric on the class of all phylogenetic networks on the set $S$ of taxa, that is, it satisfies the following properties: for every phylogenetic networks $N_1, N_2, N_3$ on the set $S$,

(a) Non-negativity: $\sigma(N_1, N_2) \geq 0$
(b) Separation: $\sigma(N_1, N_2) = 0$ if and only if $N_1 \cong N'_2$
(c) Symmetry: $\sigma(N_1, N_2) = \sigma(N_2, N_1)$
(d) Triangle inequality: $\sigma(N_1, N_3) \leq \sigma(N_1, N_2) + \sigma(N_2, N_3)$

Proof. Properties (a) and (d) are straightforward, property (b) is a consequence of the last theorem, and property (d) is a consequence of the triangle inequality of the symmetric difference of multisets.

The computation of $\sigma$ has at least the same complexity as the $S$-DAG isomorphism problem (because the latter can be decided using $\sigma$), and isomorphism of general DAGs can be reduced to $S$-DAG isomorphism. Therefore, the problem of deciding whether $\sigma$ can be computed in polynomial time for arbitrary phylogenetic networks remains open. But if we bound the in and out-degree of the nodes, the $S$-DAG isomorphism problem is in P, and therefore $\sigma$ can be computed in polynomial time by performing a simultaneous bottom-up traversal of the two networks.

4 Conclusion

In this paper we have complemented Luay Nakhleh’s latest proposal of a metric $m$ for phylogenetic networks by (a) showing that $m$ separates distinguishable networks, and (b) proposing a modification of its definition that provides a true metric $\sigma$ on the class of all phylogenetic networks. When both distances $m$ and $\sigma$ are applied to phylogenetic trees, they both yield half the symmetric differences of the sets of (isomorphism classes of) subtrees.

The measure $m$ can be computed in time polynomial in the size of the networks, but since $\sigma$ can be used to decide the isomorphism problem for $S$-DAGs, we are lead to conjecture that it cannot be computed in polynomial time (as any other dissimilarity measure for phylogenetic networks satisfying the separation property). Any way, $\sigma$ can also computed in polynomial time on subspaces of phylogenetic trees with bounded in and out-degree.

Given a set $S$ of $n \geq 2$ labels, there exists no upper bound for the values of $\sigma(N_1, N_2)$ and $m(N_1, N_2)$, as there exist arbitrarily large phylogenetic networks with $n$ leaves and no internal node of any one of them equivalent to an internal node of the other one.

References

1. G. Cardona, F. Rosselló, and G. Valiente, “Comparison of tree-child phylogenetic networks,” IEEE T. Comput. Biol., 2007, in press.
2. ——, “Tripartitions do not always discriminate phylogenetic networks,” Math. Biosci., 2007, in press.
3. B. M. E. Moret, L. Nakhleh, T. Warnow, C. R. Linder, A. Tholse, A. Padolina, J. Sun, and R. Timme, “Phylogenetic networks: Modeling, reconstructibility, and accuracy,” IEEE T. Comput. Biol., vol. 1, no. 1, pp. 13–23, 2004.
4. L. Nakhleh, “A metric for comparing phylogenetic network topologies,” 2007, submitted.
5. G. Valiente, *Algorithms on Trees and Graphs*. Springer, 2002.
6. ——, “Efficient algorithms on trees and graphs with unique node labels,” in *Applied Graph Theory in Computer Vision and Pattern Recognition*, ser. Studies in Computational Intelligence, A. Kandel, H. Bunke, and M. Last, Eds. Springer, 2007, vol. 52, pp. 137–149.
7. S. J. Wilson, “Restrictions on meaningful phylogenetic networks,” 2007, accepted contributed talk at the Workshop *Current Challenges and Problems in Phylogenetics* (Isaac Newton Institute, Cambridge, UK, September 2007).