From event-labeled gene trees with horizontal gene transfer to species trees

Marc Hellmuth
University of Greifswald
Dpt. of Mathematics and Computer Science
Walther- Rathenau-Strasse 47, D-17487 Greifswald, Germany,
and
Saarland University, Center for Bioinformatics
Building E 2.1, P.O. Box 151150, D-66041 Saarbrücken, Germany
Email: mhellmuth@mailbox.org

Abstract

Evolutionary event relations such as orthology, paralogy and xenology provide important information on the evolutionary history of the investigated genes. It has recently been shown that there is an event-labeled gene tree that displays estimated event relations if and only if the (graph-representation of these) relations are so-called cographs, resp., uniformly non-prime 2-structures. In particular, the respective event-labeled gene trees can then be constructed in polynomial time by utilizing solely the information of these event relations.

In this contribution, we are concerned with the next conceptual step: the derivation of a species tree from an event-labeled gene tree \( T \) that contains horizontal gene transfer, speciation and duplication events. We show that there is a species tree \( S \) for \( T \) if and only if certain triples that are displayed in \( T \) are also displayed in \( S \). To this end, a reconciliation map from \( T \) to \( S \) is provided that is consistent with so-called DTL-scenarios. Moreover, we provide a polynomial-time algorithm to decide whether there is a species tree for a given gene tree, and in the positive case, to construct the species tree and the respective reconciliation map.

Keywords: DTL-scenario, Reconciliation, Horizontal gene transfer, Xenology, Gene tree, Species tree, Triples, Event-label

1 Introduction

The evolutionary history of genes is intimately linked with the history of the species in which they reside. Genes are passed from generation to generation to the offspring. Some of those genes are frequently duplicated, mutate, or get lost - a mechanism that also ensures that new species can evolve. In particular, genes that share a common origin (homologs) can be classified into the type of their “event relationship”, namely orthologs, paralogs and xenologs [16]. Two homologous genes are orthologous if at their most recent point of origin the ancestral gene is transmitted to two daughter lineages; a speciation event happened. They are paralogous if the ancestor gene at their most recent point of origin was duplicated within a single ancestral genome; a duplication event happened. Horizontal gene transfer (HGT) refers to the transfer of genes between organisms in a manner other than traditional reproduction and across different species and yield so-called xenologs.
The knowledge of evolutionary event relations such as orthology, paralogy or xenology is of fundamental importance in many fields of mathematical and computational biology, including the reconstruction of evolutionary relationships across species [10, 18, 20, 25, 24], as well as functional genomics and gene organization in species [17, 35, 36].

The type of event relationship is determined by the true history of the genes and species. However, the events of the past cannot be observed directly and hence, must be inferred from the genomic data available today. Tree-reconciliation methods [12, 13, 15, 18, 34, 37] provide one way to address this problem. Here a gene tree is mapped into a species tree such that certain optimization criteria are fulfilled. This mapping, eventually, identifies inner vertices of the gene tree as a duplication, speciation or HGT. These methods often require a gene and species tree as input. In most practical applications, however, neither the gene tree nor the species tree can be determined unambiguously. Intriguingly, there are methods to infer orthologs [2, 3, 4, 8, 27, 28, 29, 35, 38, 39] or to detect HGT [9, 11, 26, 30, 31] without the need to construct gene or species trees.

In [25, 19, 20, 24] we have therefore addressed the question: How much information about the gene tree, the species tree, and their reconciliation is already contained in such event relations between genes? One of the main results is the approach ParaPhylo [24] for the reconstruction of species trees and event-labeled gene trees. ParaPhylo is solely based on the knowledge of estimated orthology relations and it was shown that genome-wide data sets are sufficient to generate fully resolved species trees, see [22] for an overview. To establish ParaPhylo several of the following results were utilized: In [19] it was shown that (in the absence of HGT) a “valid” orthology, resp., paralogy relation (i.e., a set of pairs of estimated orthologs and paralogs that is not in conflict with some gene tree representing the history of the respective genes) is characterized in terms of so-called cographs. In [20] a characterization of “valid” sets of event relations that comprises orthologs, paralogs and xenologs by means of so-called uniformly non-prime (unp) 2-structures was given. Although cographs and unp 2-structures do not contain the full information on the event-labeled gene tree, they are equivalent to the gene tree’s homeomorphic image obtained by collapsing adjacent events of the same type. Thus, such event relations place strong and easily interpretable constraints on the gene tree. However, not all such computed gene trees provide biologically feasible trees in the sense that there is a species tree on which they can evolve. In [25], we characterized event-annotated trees (that do not contain HGT) for which there is a species tree by means of certain triples that are rooted at a speciation event.

In this contribution we generalize the results established in [25], that is, we are concerned with the derivation of a species tree from an event-labeled gene tree that contains speciation, duplication and HGT events. We want to understand in more detail when an event-annotated tree can be reconciled with a species tree and thus, when it can be considered as biological meaningful gene tree. We will approach this problem by reducing the reconciliation map from gene tree to species tree, also known as DTL-scenario [37, 5], to rooted triples of genes residing in three distinct species. Moreover, we provide a polynomial-time algorithm to decide whether there is a species tree for a given gene tree, and in the positive case, to construct the species tree and the respective reconciliation map.

2 Preliminaries

2.1 Phylogenetic Trees

A rooted tree $T = (V, E)$ (on $L$) is an acyclic connected simple graph with leaf set $L \subseteq V$, set of edges $E$, and set of interior vertices $V^0 = V \setminus L$ such that there is one distinguished vertex $r \in V$, called the root of $T$. In order to avoid uninteresting trivial cases, we always assume that $|L| \geq 3$.

The ancestor relation $\preceq_T$ on $V$ is the partial order defined, for all $x, y \in V$, by $x \preceq_T y$ whenever $y$ lies on the path from $x$ to the root and we call $x$ and $y$ comparable. If $x \preceq_T y$, then $x$ is called descendant of $y$ and $y$ ancestor of $x$. Furthermore, we write $x \prec_T y$ to mean $x \preceq_T y$ and $x \neq y$. Two
vertices \(x\) and \(y\) are incomparable iff \(x \not\leq_T y\) and \(y \not\leq_T x\). For \(x \in V\), we write \(L_T(x) := \{y \in L \mid y \leq x\}\) for the set of leaves in the subtree \(T(x)\) of \(T\) rooted in \(x\).

**Remark 1.** Although we do not consider rooted trees as directed graphs, it will be convenient to use a notation for edges \(e\) that implies which of the vertex in \(e\) is closer to the root. Therefore, the notation for edges \((u,v)\) of a tree is chosen such that \(u \succ_T v\).

For our discussion below we need to extend the ancestor relation \(\leq_T\) on \(V\) to the union of the edge and vertex sets of \(T\). More precisely, for the edge \(e = (u,v) \in E\) we put \(x \prec_T e\) if and only if \(x \leq_T v\) and \(e \prec_T x\) if and only if \(u \leq_T x\). For edges \(e = (u,v)\) and \(f = (a,b)\) in \(T\) we put \(e \preceq_T f\) if and only if \(v \preceq_T b\).

For a non-empty subset of leaves \(A \subseteq L\), we define \(lca_T(A)\), or the least common ancestor of \(A\), to be the unique \(\leq_T\)-minimal vertex of \(T\) that is an ancestor of every vertex in \(A\). In case \(A = \{x, y\}\), we put \(lca_T(x,y) := lca_T(\{x, y\})\) and if \(A = \{x, y, z\}\), we put \(lca_T(x,y,z) := lca_T(\{x, y, z\})\). For later reference, note that for all \(x \in V\) it hold that \(x = lca_T(L_T(x))\). For edges \(e = (u,v)\) and \(f = (u',v')\) in \(E\) we set \(lca_T(e,f) = lca_T(v,v')\).

A phylogenetic tree \(T\) (on \(L\)) is a rooted tree \(T = (V,E)\) (on \(L\)) such that no interior vertex in \(v \in V\) has in- and outdegree one and whose root \(\rho_T\) has in- and outdegree zero. If \(L\) corresponds to a set of genes \(G\) or species \(S\), we call a phylogenetic tree on a gene tree and species tree, respectively. The restriction \(T|_{L'}\) of a phylogenetic tree \(T\) to \(L' \subseteq L\) is the rooted tree with leaf set \(L'\) obtained from \(T\) by first forming the minimal spanning tree in \(T\) with leaf set \(L'\) and then by suppressing all vertices of degree two with the exception of \(\rho_T\) if \(\rho_T\) is a vertex of that tree.

### 2.2 Rooted Triples and Forests

Rooted triples are phylogenetic trees on three leaves with precisely two interior vertices. They constitute an important concept in the context of supertree reconstruction [32, 6, 14] and will also play a major role here. A rooted tree \(T\) on \(L\) displays a triple \((xy|z)\) if, \(x, y, z \in L\) and the path from \(x\) to \(y\) does not intersect the path from \(z\) to the root \(\rho_T\) and thus, having \(lca_T(x,y) \prec_T lca_T(x,y,z)\).

We denote by \(\mathcal{R}(T)\) the set of all triples that are displayed by the rooted tree \(T\).

A set \(R\) of triples is consistent if there is a rooted tree \(T\) on \(L_R = \cup_{r \in R} L_r(\rho_r)\) such that \(R \subseteq \mathcal{R}(T)\) and thus, \(T\) displays each triple in \(R\). Not all sets of triples are consistent of course. Nevertheless, given a triple set \(R\) there is a polynomial-time algorithm, referred to in [32, 33] as BUILD, that either constructs a phylogenetic tree \(T\) that displays \(R\) or that recognizes that \(R\) is not consistent [1].

Similar to the approaches in [37], we will consider phylogenetic trees \(T = (V,E)\) from which particular edges are removed. Let \(E' \subseteq E\) and consider the forest \(T_{E'} := (V,E \setminus E')\). We can preserve the order \(\leq_T\) for all vertices within one connected component of \(T_{E'}\) and define \(\leq_{T_{E'}}\) as follows: \(x \leq_{T_{E'}} y\) iff \(x \leq_T y\) and \(x, y\) are in same connected component of \(T_{E'}\). Since each connected component \(T'\) of \(T_{E'}\) is a tree, the ordering \(\leq_{T_{E'}}\) also implies a root \(\rho_{T_{E'}}\) for each \(T'\), that is, \(x \leq_{T_{E'}} \rho_{T_{E'}}\) for all \(x \in V(T')\). If \(L(T_{E'})\) is the leave set of \(T_{E'}\), we define \(L_{T_{E'}}(x) := \{y \in L(T_{E'}) \mid y \leq_{T_{E'}} x\}\) as the set of leaves in \(T_{E'}\) that are reachable from \(x\). Hence, all \(y \in L_{T_{E'}}(x)\) must be contained in the same connected component of \(T_{E'}\). We say that the forest \(T_{E'}\) displays a triple \(r\), if \(r\) is displayed by one of its connected components. Moreover, \(\mathcal{R}(T_{E'})\) denotes the set of all triples that are displayed by the forest \(T_{E'}\).

For later reference we give the following lemma:

**Lemma 2.1.** Two edges of the form \((u,x)\), \((u,y)\) that share a common vertex in a phylogenetic tree \(T\) on \(G\) are called siblings. Assume now that \(E\) does not contain siblings. Let \(T_1, \ldots, T_k\) be the connected components of \(T_{E'}\) with roots \(\rho_1, \ldots, \rho_k\), respectively. Then, \(\{L_{T_{E'}}(\rho_1), \ldots, L_{T_{E'}}(\rho_k)\}\) forms a partition of \(G\).
Proof. Since $L_{\mathcal{T}_T}(\rho_t) \subseteq V(T)$, it suffices to show that $L_{\mathcal{T}_T}(\rho_t)$ does not contain vertices of $V(T) \setminus G$. Note, $x \in L_{\mathcal{T}_T}(\rho_t)$ with $x \notin G$ is only possible if all edges $(x,y)$ are removed. Since $T$ is a phylogenetic tree, $x$ has at least two children. However, this amounts to removing siblings in $T$; a contradiction to the choice of $\mathcal{E}$.

\subsection{2.3 Event-Labeling, Reconciliation Map and DTL-scenario}

A gene tree $T$ arises through a series of events along a species tree $S$. Both, $T$ and $S$ are phylogenetic trees with leaf sets $G$ (the set of genes) and $S$ (the set of species), respectively. We consider gene duplications and horizontal gene transfer (HGT), which take place between speciation events, i.e., along the edges of $S$. Speciation events are modeled by transmitting the gene content of an ancestral lineage to each of its daughter lineages. HGT amounts to the transmission of genetic material across different species.

Arguing along the line in [25], we will restrict our attention to the observable part of the gene and species tree. Assume we know the true evolutionary history, that is, a true gene tree $\hat{T}$ that evolved along its corresponding true species tree $\hat{S}$. The true gene tree $\hat{T}$ represents all extant as well as all extinct genes, all duplication, all HGT, and all speciation events. Not all of these events are observable from extant genes data, however. In particular, extinct genes and events followed by a gene loss cannot be observed. The observable part $T = (V,E)$ of $\hat{T}$ is the restriction of $\hat{T}$ to the leaf set $G$ of extant genes, i.e., $T = \hat{T}|_G$. Furthermore, we can observe a map $\sigma : G \to S$ that assigns to each extant gene the species in which it resides. We set $\sigma(L) = \{ \sigma(x) \mid x \in L \}$ for any leaf set $L \subseteq G$. Here $S$ is the leaf set of the extant species tree, i.e., $S = \sigma(G)$. The observable part of the species tree $S = (W,F)$ is the restriction $\hat{S}|_S$ of $\hat{S}$ to $S$. In order to account for duplication events that occurred before the first speciation event, we need to add an extra vertex and an extra edge “above” the last common ancestor of all species: hence, we add an additional vertex to $W$ (that is known to be the new root $\rho_S$ of $S$) and the additional edge $(\rho_S, lca_S(S)) \in F$. Note that strictly speaking $S$ is not a phylogenetic tree anymore. In case there is no danger of confusion, we will from now on refer to a phylogenetic tree on $S$ with this extra edge and vertex added as a species tree on $S$.

The evolutionary scenario also implies an event-labeling map $t : V \cup E \to I \cup \{0,1\}$ with $I = \{\textbullet, \square, \Delta, \circ\}$ that assigns to each interior vertex $v$ of $T$ a value $t(v) \in I$ indicating whether $v$ is a speciation event (\textbullet), duplication event (\square) or HGT event (\Delta). It is convenient to use the special label $\circ$ for the leaves $x$ of $T$. Moreover, to each edge $e$ a value $t(e) \in \{0,1\}$ is added that indicates whether $e$ is a transfer edge (1) or not (0). Hence, $e = (x,y)$ and $t(e) = 1$ iff $t(x) = \Delta$ and the genetic material is transferred from the species containing $x$ to the species containing $y$. We remark that the restriction $t_W$ of $t$ to the vertex set $V$ was introduced as “symbolic dating map” in [7] and that there is a close relationship to so-called cographs [19, 21, 23].

Hereafter, we write $(T;t,\sigma)$ for the tree $T = (V,E)$ with event-labeling $t$ and corresponding map $\sigma$. Moreover, $\mathcal{E} = \{e \in E \mid t(e) = 1\}$ will always denote the set of transfer edges in $(T;t,\sigma)$.

Now, we follow an idea of Tofihg et al. [37] and consider gene trees $(T = (V,E);t,\sigma)$ from which the transfer edges have been removed, resulting in $T_{\mathcal{E}} = (V,E \setminus \mathcal{E})$ in which we preserve the event-labeling $t$, that is, we use the restriction $t_W$ on $T_{\mathcal{E}}$. Note, for each $x \in V$ with $t(x) = \Delta$ there is exactly one transfer edge $(x,y)$. Therefore, $\mathcal{E}$ does not contain sibling edges and Lemma 2.1 can be applied when appropriate. In particular, Lemma 2.1 implies that $\sigma(L_{\mathcal{T}_T}(x)) = \emptyset$ for all $x \in V(T)$. Clearly, the graph $T_{\mathcal{E}}$ is a forest and might contain interior vertices (distinct from the root) that have in- and outdegree one. Nevertheless, for each $x \preceq_{\mathcal{T}_T} y$ in $T_{\mathcal{E}}$ we have $x \preceq_T y$ in $T$. Hence, partial information (that in particular is “undisturbed” by transfer events) on the partial ordering of the vertices in $T$ can be inferred from $T_{\mathcal{E}}$.

Moreover, since $T_{\mathcal{E}}$ does not contain transfer edges, and hence, there is no genetic material transferred across different species within connected components of $T_{\mathcal{E}}$ we can make use of the following condition:

(C1) Let $x \in V$ be a speciation vertex, i.e., $t(x) = \bullet$, and let $T_{\mathcal{E}}(v)$ and $T_{\mathcal{E}}(w)$ be subtrees of $T_{\mathcal{E}}(x)$
rooted in two distinct children \(v, w\) of \(x\). Then,

\[ \sigma(L_{T_x}(v)) \cap \sigma(L_{T_x}(w)) = \emptyset. \]

Note that we do not require the converse, i.e., from the disjointedness of the species sets \(\sigma(L_{T_x}(y))\) and \(\sigma(L_{T_x}(y'))\) we do not conclude that their last common ancestor is a speciation vertex.

Furthermore, assume that \(t(x) = \triangle\) and \((x, y) \in E\) is a transfer edge. Therefore, \(T_x(x)\) and \(T_x(y)\) are subtrees of distinct connected components of \(T_x\). Since HGT amounts to the transfer of genetic material across distinct species, the genes \(x\) and \(y\) must be from distinct species. Since \(T_x\) does not contain transfer edges and thus, there is no genetic material transferred across distinct species between distinct connected components in \(T_x\), we can lay down the next condition:

(C2) Let \((x, y) \in E\). Then,

\[ \sigma(L_{T_x}(x)) \cap \sigma(L_{T_x}(y)) = \emptyset. \]

We are now in the position to define a reconciliation map that “embeds” a given gene tree into a given species tree.

**Definition 1.** Suppose that \(\mathbb{S}\) is a set of species, \(S = (W, F)\) is a phylogenetic tree on \(\mathbb{S}\), \(T = (V, E)\) is a gene tree with leaf set \(\mathbb{G}\) and that \(\sigma : \mathbb{G} \to \mathbb{S}\) and \(t : V \to \{\bullet, \square, \triangle, \triangledown\} \cup \{0, 1\}\) are the maps described above. Then we say that \(S\) is a species tree for \((T; t, \sigma)\) if there is a map \(\mu : V \to W \cup F\) such that, for all \(x \in V\):

(M1) Leaf Constraint. If \(t(x) = \circ\) then \(\mu(x) = \sigma(x)\).

(M2) Event Constraint.

(i) If \(t(x) = \bullet\), then \(\mu(x) \in W^0 = W \setminus \mathbb{S}\) and \(\mu(x) = \text{lca}_S(\sigma(L_{T_x}(x)))\).

(ii) If \(t(x) \in \{\square, \triangle\}\), then \(\mu(x) \in F\).

(iii) If \(t(x) = \triangle\) and \((x, y) \in E\), then \(\mu(x)\) and \(\mu(y)\) are incomparable in \(S\).

(M3) Ancestor Constraint.

Let \(x, y \in V\) with \(x \prec_{T_x} y\). Note, the latter implies that the path connecting \(x\) and \(y\) in \(T\) does not contain transfer edges. We distinguish two cases:

(i) If \(t(x), t(y) \in \{\square, \triangle\}\), then \(\mu(x) \preceq_S \mu(y)\).

(ii) otherwise, i.e., at least one of \(t(x)\) and \(t(y)\) is a speciation \(\bullet\), \(\mu(x) \prec_S \mu(y)\).

We call \(\mu\) the reconciliation map from \((T; t, \sigma)\) to \(S\).

Condition (M1) ensures that each leaf of \(T\), i.e., an extant gene in \(\mathbb{G}\), is mapped to the species in which it resides. Condition (M2i) and (M2ii) ensure that each vertex of \(T\) is either mapped to a vertex or an edge in \(S\) such that a vertex of \(T\) is mapped to an interior vertex of \(S\) if and only if it is a speciation vertex. Additionally, (M2i) implies that a speciation vertex is mapped to the least common ancestor of the species where the genes in \(L_{T_x}(x)\) reside. Condition (M2iii) maps the vertices of a transfer edge in a way that they are incomparable in the species tree, since a HGT occurs between distinct (co-existing) species. Finally, (M3) implies that each vertex of \(T\) is mapped to \(S\) in such a way that the ancestor order \(\preceq_T\) of \(T\) along the paths that do not contain transfer edges is preserved.

Definition 1 is a natural generalization of the map defined in [25], that is, in the absence of horizontal gene transfer, Condition (M2iii) vanishes and thus, the proposed reconciliation map precisely coincides with the one given in [25].

In case that the event-labeling of \(T\) is unknown, but a species tree \(S\) is given, the authors in [37] gave an axiom set, called DTL-scenario, to reconcile \(T\) with \(S\). This reconciliation is then used to infer the event-labeling of \(T\). Instead of defining a DTL-scenario as octuple [37], we use the notation established above:
Definition 2 (DTL-scenario). For a given gene tree \( (T,t, \sigma) \) on \( \mathbb{G} \) and a species tree \( S \) on \( \mathbb{S} \) the map \( \gamma : V(T) \to V(S) \) maps the gene tree into the species tree such that

1. For each leaf \( x \in \mathbb{G} \), \( \gamma (u) = \sigma (u) \).
2. If \( u \in V(S) \setminus S \) with children \( v,w \), then
   - (a) \( \gamma (u) \) is not a proper descendant of \( \gamma (v) \) or \( \gamma (w) \), and
   - (b) at least one of \( \gamma (v) \) or \( \gamma (w) \) is a descendant of \( \gamma (u) \).
3. \((u,v)\) is a transfer edge if and only if \( \gamma (u) \) and \( \gamma (v) \) are incomparable.
4. If \( u \in V(S) \setminus S \) with children \( v,w \), then
   - (a) \( t(u) = \triangle \) if and only if either \((u,v)\) or \((u,w)\) is a transfer-edge,
   - (b) If \( t(u) = \bullet \), then \( \gamma (u) = \text{lca}_S(\gamma (v), \gamma (w)) \) and \( \gamma (v), \gamma (w) \) are incomparable,
   - (c) If \( t(u) = \square \), then \( \gamma (u) \supseteq \text{lca}_S(\gamma (v), \gamma (w)) \).

As we shall see later, our notion of reconciliation map - which is more convenient to establish the results - is consistent with the definition of a DTL-scenario [37, 5].

3 Main Results

3.1 Properties of the Reconciliation Map \( \mu \)

For later reference we provide a couple of useful properties of reconciliation maps.

Lemma 3.1. Let \( \mu \) be a reconciliation map from \( (T,t, \sigma) \) to \( S \). Then the following conditions are satisfied:

1. \( \mu (u) \succeq_S \text{lca}_S(\sigma (L_{T_S}(u))) \) for any \( u \in V(T) \).
2. If \( v,w \in V(T) \) are in the same connected component of \( T_S \), then \( \mu (\text{lca}_{T_S}(v,w)) \succeq_S \text{lca}_S(\mu (v), \mu (w)) \).

Let \( u \) be an arbitrary interior vertex of \( T \) with children \( v,w \), then:

3. \( \mu (u) \) and \( \mu (v) \) are incomparable in \( S \) if and only if \( (u,v) \in E \).
4. If \( t(u) = \bullet \), then \( \mu (v) \) and \( \mu (w) \) are incomparable in \( S \).
5. If \( \mu (v), \mu (w) \) are comparable or \( \mu (u) \succeq_S \text{lca}_S(\mu (v), \mu (w)) \), then \( t(u) = \square \).

Proof. We prove the Items 1 - 5 separately. Recall, Lemma 2.1 implies that \( \sigma (L_{T_S}(x)) \neq \emptyset \) for all \( x \in V(T) \).

Proof of Item 1: If \( u \) is a leaf, then by Condition (M1) \( \mu (u) = \sigma (u) \) and we are done. Thus, let \( u \) be an interior vertex. By Condition (M3), \( z \preceq_S \mu (u) \) for all \( z \in \sigma (L_{T_S}(u)) \). Hence, if \( \mu (u) \sim_S \text{lca}_S(\sigma (L_{T_S}(u))) \) or if \( \mu (u) \) and \( \text{lca}_S(\sigma (L_{T_S}(u))) \) are incomparable in \( S \), then there is a \( z \in \sigma (L_{T_S}(u)) \) such that \( z \) and \( \mu (u) \) are not comparable; a contradiction.

Proof of Item 2: Let \( v \) and \( w \) be distinct vertices of \( T \) that are in the same connected component of \( T_S \). Consider the unique path \( P \) connecting \( w \) with \( v \) in \( T_S \). This path \( P \) is uniquely subdivided into a path \( P' \) and a path \( P'' \) from \( \text{lca}_{T_S}(v,w) \) to \( v \) and \( w \), respectively. Condition (M3) implies that the images of the vertices of \( P' \) and \( P'' \) under \( \mu \), resp., are ordered in \( S \) with regards to \( \preceq_S \) and hence, are contained in the intervals \( Q' \) and \( Q'' \) that connect \( \mu (\text{lca}_{T_S}(v,w)) \) with \( \mu (v) \) and \( \mu (w) \), respectively. In particular, \( \mu (\text{lca}_{T_S}(v,w)) \) is the largest element (w.r.t. \( \preceq_S \)) in the union of \( Q \cup Q'' \) which contains the unique path from \( \mu (v) \) to \( \mu (w) \) and hence also \( \text{lca}_S(\mu (v), \mu (w)) \).

Proof of Item 3: The if-part is equivalent to Condition (M2ii). Let \( \mu (u) \) and \( \mu (v) \) be incomparable in \( S \). Item (M3) implies that for any edge \( (x,y) \in E(T_S) \) we have \( \mu (y) \preceq_S \mu (x) \). However, since \( \mu (u) \) and \( \mu (v) \) are incomparable it must hold that \( (u,v) \notin E(T_S) \). Since \( (u,v) \) is an edge in the gene tree \( T \), \( (u,v) \in E \) is a transfer edge.
Hence, moreover, labeled with one event, we have \( \mu \).

**Definition 1.** Let \( \sigma \) be a reconciliation map for the gene tree \( T \) and the species tree \( S \) as in Definition 1. Set for all \( u \in V(T) \):

\[
\mu(u) = \text{lca}_S(\sigma(L_{T_u}(v))) = \text{lca}_S(\sigma(L_{T_u}(v)) \cup \sigma(L_{T_{\gamma(u)}}(v)))
\]

Thus, \( \mu(u) \) is comparable to both \( \mu(v) \) and \( \mu(w) \) and thus, (M2ii) implies that \( t(u) \neq \emptyset \). Item 4 implies that \( \mu(v) \) and \( \mu(w) \) are comparable in \( S \). Assume for contradiction that \( \mu(v) \) and \( \mu(w) \) are comparable, say, \( \mu(w) \geq_S \mu(v) \).

**Proof of Item 4:** Let \( \mu(u), \mu(v) \) be comparable in \( S \). Item 4 implies that \( t(u) \neq \emptyset \). Assume for contradiction that \( t(u) = \emptyset \). Since only one of the edges \((u,v)\) or \((u,w)\) is a transfer edge, we have either \((u,v) \in E \) or \((u,w) \in E \). W.l.o.g. let \((u,v) \in E \) and \((u,w) \in E \). By Condition (M3), \( \mu(u) \geq_S \mu(w) \). However, since \( \mu(v) \) and \( \mu(w) \) are comparable in \( S \), also \( \mu(u) \) and \( \mu(v) \) are comparable in \( S \); a contradiction to Item 3. Thus, \( t(u) \neq \emptyset \). Since each interior vertex is labeled with one event, we have \( t(u) = \emptyset \).

Assume now that \( \mu(u) >_S \text{lca}_S(\mu(v), \mu(w)) \). Hence, \( \mu(u) \) is comparable to both \( \mu(v) \) and \( \mu(w) \) and thus, (M2ii) implies that \( t(u) \neq \emptyset \). Item 4 implies that \( \mu(v) \geq_S \text{lca}_S(\sigma(L_{T_u}(v))) \) and \( \mu(w) \geq_S \text{lca}_S(\sigma(L_{T_{\gamma(u)}}(v))) \). Thus,

\[
\text{lca}_S(\mu(v), \mu(w)) \geq_S \text{lca}_S(\sigma(L_{T_u}(v))) \cup \sigma(L_{T_{\gamma(u)}}(v))) = \text{lca}_S(\sigma(L_{T_{\gamma(u)}}(v)))) = \text{lca}_S(\sigma(L_{T_{\gamma(u)}}(v))))
\]

Hence, \( \mu(u) \square_S \text{lca}_S(\sigma(L_{T_u}))) \). Now, (M2ii) applies \( t(u) = \emptyset \). Since each interior vertex is labeled with one event, we have \( t(u) = \emptyset \).

The choice of our notion of reconciliation in Definition 1 is a natural generalization of the map given in [26] and more convenient to establish our results. Nevertheless, we show in the following lemma that it is consistent with the definition of a DTL-scenario [37, 5].

**Lemma 3.2.** Let \( \mu \) be a reconciliation map for the gene tree \( T; t, \sigma \) and the species tree \( S \) as in Definition 1. Set for all \( u \in V(T) \):

\[
\gamma(u) = \begin{cases} 
\mu(u), & \text{if } \mu(u) \in V(S) \\
\gamma(v), & \text{if } \mu(u) = (x,y) \in E(S)
\end{cases}
\]

Then \( \gamma : V(T) \to V(S) \) is a map according to the DTL-scenario.

**Proof.** We first emphasize that, by construction, \( \mu(u) \geq_S \gamma(u) \) for all \( u \in V(T) \). Moreover, \( \mu(u) = \mu(v) \) implies that \( \gamma(u) = \gamma(v) \) and \( \gamma(u) = \gamma(v) \) implies that \( \mu(u) \) and \( \mu(v) \) are comparable.

Furthermore, \( \mu(u) \leq_S \mu(v) \) implies \( \gamma(u) \leq_S \gamma(v) \), while \( \gamma(u) \leq_S \gamma(v) \) implies that \( \mu(u) \leq_S \mu(v) \).

Item (I) and (M1) are equivalent.

For Item (II) let \( u \in V(S) \backslash S \) be an interior vertex with children \( v, w \). If \((u,w) \notin E \), then \( w \leq_{\gamma(u)} u \). Applying Condition (M3) yields \( \mu(w) \leq_S \mu(u) \) and thus, by construction, \( \gamma(w) \leq_S \gamma(u) \). Therefore, \( \gamma(u) \) is not a proper descendant of \( \gamma(w) \) and \( \gamma(w) \) is a descendant of \( \gamma(u) \). If one of the edges, say \((u,v)\), is a transfer edge, then \( t(u) = \emptyset \) and by Condition (M2ii) \( \mu(u) \) and \( \mu(v) \) are incomparable. Hence, \( \gamma(u) \) and \( \gamma(v) \) are incomparable. Therefore, \( \gamma(u) \) is a proper descendant of \( \gamma(v) \). Note, for each vertex \( u \in V(S) \backslash S \) at least one of its outgoing edges must be a non-transfer edge, which implies that \( \gamma(w) \leq_S \gamma(u) \) or \( \gamma(v) \leq_S \gamma(u) \) as shown before. Hence, Item (IIa) and (IIb) are satisfied.

For Item (III) observe that (M2ii) implies that \( \gamma(u) \) and \( \gamma(v) \) are incomparable. Now assume that \((u,v)\) is an edge in the gene tree \( T \) and \( \gamma(u) \) and \( \gamma(v) \) are incomparable. Therefore, \( \mu(u) \) and \( \mu(v) \) are incomparable. Now, apply Lemma 3.1(3).
Hence, as the subset of all triples displayed in $T$ implies that $\gamma(v)$ and $\gamma(w)$ be the set of triples in $T$. If $\gamma(v)$ is mapped on the edge $(x,y)$ in $T$, then $\gamma(v) = y$. By definition of lca for edges, $\text{lca}_S(\mu(v),\mu(w)) = \text{lca}_S(\gamma(v),\gamma(w))$. The same argument applies if $\mu(w)$ is mapped on an edge. Since for all $z \in V(T)$ either $\mu(z) >_S \gamma(z)$ (if $\mu(z)$ is mapped on an edge) or $\mu(z) = \gamma(z)$, we always have

$$\text{lca}_S(\gamma(v),\gamma(w)) = \text{lca}_S(\mu(v),\mu(w)) = \mu(u).$$

Since $\mu(u) >_S \mu(v), \mu(w)$, it holds that $\gamma(u) >_S \gamma(v), \gamma(w)$. Moreover, since $\gamma(v)$ and $\gamma(w)$ are incomparable, we obtain $\gamma(u) >_S \text{lca}_S(\gamma(v),\gamma(w))$. The latter together with $\mu(u) >_S \gamma(v), \gamma(w)$. If $\gamma(v)$ and $\gamma(w)$ are comparable, then $\gamma(u) >_S \gamma(v), \gamma(w)$ implies that $\gamma(u) >_S \text{lca}_S(\gamma(v),\gamma(w))$. If $\gamma(v)$ and $\gamma(w)$ are comparable, say $\gamma(v) >_S \gamma(w)$, then $\gamma(u) >_S \gamma(v) = \text{lca}_S(\gamma(v),\gamma(w))$. Hence, Statement (IVc) is satisfied.

### 3.2 From Gene Trees to Species Trees

Since a gene tree $T$ is uniquely determined by its induced triple set $\mathcal{R}(T)$, it is reasonable to expect that a lot of information on the species tree(s) for $(T,t,\sigma)$ is contained in the images of the triples in $\mathcal{R}(T)$, (or more precisely their leaves) under $\sigma$. However, not all triples in $\mathcal{R}(T)$ are informative, see Figure 1 for an illustrative example. In the absence of HGT, it has already been shown by Hernandez-Rosales et al. [25] that the informative triples $r \in \mathcal{R}(T)$ are precisely those that are rooted at a speciation event and where the genes in $r$ reside in three distinct species. However, in the presence of HGT we need to further subdivide the informative triples as follows.

**Definition 3.** Let $(T;t,\sigma)$ be a given event-labeled gene tree with respective set of transfer-edges $\mathcal{E} = \{e_1, \ldots, e_h\}$ and $T_\mathcal{E}$ as defined above. We define

$$\mathcal{R}_\sigma(T_\mathcal{E}) = \{(ab|c) \in \mathcal{R}(T_\mathcal{E}) : \sigma(a), \sigma(b), \sigma(c) \text{ are pairwise distinct}\}$$

as the subset of all triples displayed in $T_\mathcal{E}$ such that the leaves are from pairwise distinct species. Let

$$\mathcal{R}_0(T_\mathcal{E}) := \{(ab|c) \in \mathcal{R}_\sigma(T_\mathcal{E}) : t(\text{lca}_{T_\mathcal{E}}(a,b,c)) = \bullet\}$$

be the set of triples in $\mathcal{R}_\sigma(T_\mathcal{E})$ that are rooted at a speciation event.

For each $e_i = (x,y) \in \mathcal{E}$ define

$$\mathcal{R}_i(T_\mathcal{E}) := \{(ab|c) : \sigma(a), \sigma(b), \sigma(c) \text{ are pairwise distinct and either } a,b \in L_{T_\mathcal{E}}(x), c \in L_{T_\mathcal{E}}(y) \text{ or } c \in L_{T_\mathcal{E}}(x), a,b \in L_{T_\mathcal{E}}(y)\}.$$

Hence, $\mathcal{R}_i(T_\mathcal{E})$ contains for any $a,b \in L_{T_\mathcal{E}}(x),c \in L_{T_\mathcal{E}}(y)$ that reside in pairwise distinct species a triple $(ab|c)$. Analogously, for any $a,b \in L_{T_\mathcal{E}}(y),c \in L_{T_\mathcal{E}}(x)$ there is a triple $(ab|c) \in \mathcal{R}_i(T_\mathcal{E})$, if $\sigma(a), \sigma(b), \sigma(c)$ are pairwise distinct.

The informative triples of $T$ are comprised in the set

$$\mathcal{R}(T;t,\sigma) = \bigcup_{i=0}^h \mathcal{R}_i.$$
Finally, we define the species triple set

\[ S(T; t, \sigma) := \{(\sigma(a)\sigma(b)|\sigma(c)) : (ab|c) \in \mathcal{R}(T; t, \sigma)\} \]

that can be inferred from the informative triples of \((T; t, \sigma)\).

In [25] the following characterization was established.

**Theorem 3.1.** For a given gene tree \((T; t, \sigma)\) on \(\mathbb{G}\) that does not contain HGT and \(\mathcal{G} := \{(\sigma(a)\sigma(b)|\sigma(c)) : (ab|c) \in \mathcal{R}_0(T)\}\), the following statement is satisfied:

There is a species tree on \(\hat{S} = \sigma(\mathcal{G})\) for \((T; t, \sigma)\) if and only if the triple set \(\mathcal{G}\) is consistent.

In what follows, we generalize the latter result and show that consistency of \(S(T; t, \sigma)\) characterizes whether there is a species tree \(S\) for \((T; t, \sigma)\).

**Lemma 3.3.** If \(\mu\) is a reconciliation map from \((T; t, \sigma)\) to \(S\) and \((ab|c) \in \mathcal{R}(T; t, \sigma)\), then \((\sigma(a)\sigma(b)|\sigma(c))\) is displayed in \(S\).

**Proof.** Recall that \(\mathcal{G}\) is the leaf set of \(T = (V, E)\) and, by Lemma 2.1, of \(T_{\mathcal{G}}\). In what follows, we write \(\mathcal{L}(u)\) instead of the more complicated writing \(L_{T_{\mathcal{G}}}(u)\). Let \((a, b, c) \in \mathcal{G}\) and assume w.l.o.g. \((ab|c) \in \mathcal{R}(T; t, \sigma)\).

First assume that \((ab|c) \in \mathcal{R}_0\), that is \((ab|c)\) is displayed in \(T_{\mathcal{G}}\) and \(\mu = \mu_{(ab|c)}\). For simplicity set \(u = \text{lca}_{T_{\mathcal{G}}}(a, b, c)\) and let \(v, w\) be its children in \(T_{\mathcal{G}}\). Condition (M2) implies that

\[ \mu(v) = \text{lca}_{\hat{S}}(\sigma(\mathcal{L}(v))) = \text{lca}_{\hat{S}}(\sigma(\mathcal{L}(w))) = \mu(w). \]

By Lemma 3.1(1), \(\mu(v) \succeq_{\hat{S}} \text{lca}_{\hat{S}}(\sigma(\mathcal{L}(v)))\) and \(\mu(w) \succeq_{\hat{S}} \text{lca}_{\hat{S}}(\sigma(\mathcal{L}(w)))\). Moreover, Lemma 3.1(4) implies that \(\mu(v)\) and \(\mu(w)\) are incomparable. The latter two arguments imply that

\[ \text{lca}_{\hat{S}}(\mu(v), \mu(w)) = \text{lca}_{\hat{S}}(\text{lca}_{\hat{S}}(\sigma(\mathcal{L}(v))), \text{lca}_{\hat{S}}(\sigma(\mathcal{L}(w)))) = \mu(u). \]

Since \((ab|c) \in \mathcal{R}_0\) we can assume w.l.o.g. that \(v \succeq_{T_{\mathcal{G}}} \text{lca}_{T_{\mathcal{G}}}(a, b) \succ_{T_{\mathcal{G}}} a, b\) and \(w \succeq_{T_{\mathcal{G}}} c\). Hence, \(\sigma(a), \sigma(b) \in \sigma(\mathcal{L}(v))\) and \(\sigma(c) \in \sigma(\mathcal{L}(w))\). Moreover, Condition (M1) and (M3) imply that \(\mu(u) \succeq_{\hat{S}} \mu(v) \succeq_{\hat{S}} \sigma(a), \sigma(b)\) and \(\mu(u) \succeq_{\hat{S}} \mu(w) \succeq_{\hat{S}} \sigma(c)\). Since \(\mu(v)\) and \(\mu(w)\) are incomparable and \(\mu(u) = \text{lca}_{\hat{S}}(\mu(v), \mu(w))\) we can conclude that \(\mu(u) = \text{lca}_{\hat{S}}(\sigma(a), \sigma(b), \sigma(c))\).

Hence \(S\) must display the triple \((\sigma(a)\sigma(b)|\sigma(c))\), since \(\sigma(a), \sigma(b), \sigma(c)\) are pairwise distinct leaves of \(S\).

Now assume that \((ab|c) \in \mathcal{R}_t\) for some transfer edge \(e_i = (x, y) \in \mathcal{E}\). For \(e_i = (x, y)\) we either have \(a, b \in \mathcal{L}(x)\) and \(c \in \mathcal{L}(y)\) or \(c \in \mathcal{L}(x)\) and \(a, b \in \mathcal{L}(y)\). If \(a, b \in \mathcal{L}(x)\), then \(x \succeq_{T_{\mathcal{G}}} \text{lca}_{T_{\mathcal{G}}}(a, b)\), and \(y \succeq_{T_{\mathcal{G}}} c\). Condition (M3) implies that \(\mu(y) \succeq_{\hat{S}} \mu(c) = \sigma(c)\). Moreover, Condition (M3) and Lemma 3.1(2) imply that \(\mu(x) \succeq_{\hat{S}} \mu(\text{lca}_{T_{\mathcal{G}}}(a, b)) \succeq_{\hat{S}} \text{lca}_{\hat{S}}(\mu(a), \mu(b)) = \text{lca}_{\hat{S}}(\sigma(a), \sigma(b))\). Since \(t(x) = \Delta\), we can apply (M2ii) and conclude that \(\mu(x)\) and \(\mu(y)\) are incomparable in \(S\). Hence, \(\sigma(c)\) and \(\text{lca}_{\hat{S}}(\sigma(a), \sigma(b))\) are incomparable. Thus, the triple \((\sigma(a)\sigma(b)|\sigma(c))\) must be displayed in \(S\). Analogously, \((\sigma(a)\sigma(b)|\sigma(c))\) must be displayed in \(S\) if \(c \in \mathcal{L}(x)\) and \(a, b \in \mathcal{L}(y)\). \qed

**Lemma 3.4.** Let \(S\) be species tree on \(\mathbb{S}\). Then there is reconciliation map \(\mu\) from \((T; t, \sigma)\) to \(S\) whenever \(S\) displays all triples in \(S(T; t, \sigma)\).
Proof. Recall that $G$ is the leaf set of $T = (V, E)$ and, by Lemma 2.1, of $T_G$. In what follows, we write $L(u)$ instead of the more complicated writing $L_T(u)$. Put $S = (W, F)$ and $S = S(T, t, \sigma)$. We first consider the subset $U = \{x \in V \mid t(x) \in \{\emptyset, \bullet\}\}$ of $V$ comprising the leaves and speciation vertices of $T$.

In what follows we will explicitly construct $\mu : V \to W \cup F$ and verify that $\mu$ satisfies Conditions (M1), (M2) and (M3). To this end, we first set for all $x \in V$:

(S1) $\mu(x) = \sigma(x)$, if $t(x) = \emptyset$,

(S2) $\mu(x) = \text{lca}_S(\sigma(L(x)))$, if $t(x) = \bullet$.

Conditions (S1) and (M1) are equivalent.

Note, for $x$ in $T$ with $t(x) = \emptyset$, there are two children in $v$ and $w$ in $T_G$. By Lemma 2.1, both $L(v)$ and $L(w)$ are non-empty subsets of $G$. Condition (C1) claims that $\sigma(L(v)) \cap \sigma(L(w)) = \emptyset$. Thus, there are two leaves $a, b \in L(x)$ such that $\sigma(a) \neq \sigma(b)$. Hence, \text{lca}_S(\sigma(L(x))) \in W^0 = W \setminus S$. The latter together with (S2) implies that (M2i) is satisfied.

Claim 1: For all $x, y \in U$ with $x \prec_{T_G} y$ we have $\mu(x) \preceq_S \mu(y)$.

Note, $y$ must be an interior vertex, since $x \prec_{T_G} y$. Hence $t(y) = \bullet$. If $x$ is a leaf, then $\mu(x) = \sigma(x) \in S$. As argued above, $\mu(y) \in W \setminus S$. Since $x \in L(y)$ and $\sigma(L(y)) \neq \emptyset$ (cf. Lemma 2.1), we have $\sigma(x) \in \sigma(L(y)) \subseteq S$ and thus, $\mu(x) \preceq_S \mu(y)$.

Now assume that $x$ is an interior vertex and hence, $t(x) = \bullet$. Again, there are leaves $a, b \in L(x)$ with $A = \sigma(a)$ and $B = \sigma(b)$ with $A \neq B$. Since $x \prec_{T_G} y$ and $t(y) = \bullet$, we can apply Condition (C1) and conclude that for all vertices $c \in L(y) \setminus L(x)$ it holds that $\sigma(c) = C \neq A, B$. In particular, $(a,b,c) \in R_0$ and therefore, $(AB,C) \in S$. Hence, $\text{lca}_S(\sigma(L(x))) \subseteq \text{lca}_S(\sigma(L(y)))$. Such an edge exists for $v = \text{lca}_S(\sigma(L(x)))$ in $S$ by construction. Every speciation vertex $y$ with $x \prec_{T_G} x$ therefore necessarily maps on the vertex $u$ or above, i.e., $\mu(y) \preceq_S u$ must hold. Thus, we set:

(S3) $\mu(x) = (u, \text{lca}_S(\sigma(L(x))))$, if $t(x) \in \{\triangle, \square\}$,

which now makes $\mu$ a map from $V$ to $W \cup F$.

By construction of $\mu$, Conditions (M1), (M2i), (M2ii) are satisfied by $\mu$.

We proceed with showing (M3).

Claim 2: For all $x, y \in V(T)$ with $x \prec_{T_G} y$, Condition (M3) is satisfied.

If both $x$ and $y$ are speciation vertices, then we can apply the Claim 1 to conclude that $\mu(x) \preceq_S \mu(y)$. If $x$ is a leaf, then we argue similarly as in the proof of Claim 1 to conclude that $\mu(x) \preceq_S \mu(y)$.

Now assume that both $x$ and $y$ are interior vertices of $T$ and at least one vertex of $x, y$ is not a speciation vertex. Since, $L(x) \subseteq L(y)$ we also have $\sigma(L(x)) \subseteq \sigma(L(y))$.

We start with the case $t(y) = \emptyset$ and $t(x) \in \{\square, \triangle\}$. Since $t(y) = \emptyset$, vertex $y$ has two children $y', y''$ in $T_G$ such that $x \preceq_{T_G} y'$. Since $L(x) \subseteq L(y') \subseteq L(y)$, we have $L(y) \setminus L(x) \neq \emptyset$. If $\sigma(L(x))$ contains only one species $A$, then $\mu(x) = (u, A) \preceq_S u \preceq_S \text{lca}_S(\sigma(L(y)))) = \mu(y)$. If $\sigma(L(x))$ contains at least two species, then there are $a, b \in L(x)$ with $\sigma(a) = A \neq \sigma(b) = B$ and $c \in L(y) \setminus L(x)$ with $\sigma(c) = C \neq A, B$. By construction, $\sigma(c) \in R_0$ and hence $(AB,C) \in S$. Now we can argue similar as in the proof of the Claim 1, to see that

$$\mu(x) = (u, \text{lca}_S(\sigma(L(x)))) \preceq_S u \preceq_S \text{lca}_S(\sigma(L(y))) = \mu(y).$$

If $t(x) = \bullet$ and $t(y) \in \{\square, \triangle\}$, then $\sigma(L(x)) \subseteq \sigma(L(y))$ implies that

$$\mu(x) = \text{lca}_S(\sigma(L(x))) \preceq_S \text{lca}_S(\sigma(L(y))) \preceq_S (u, \text{lca}_S(\sigma(L(y)))) = \mu(y).$$
Finally assume that \( t(x), t(y) \in \{\square, \triangle\} \). If \( \sigma(\mathcal{L}(x)) = \sigma(\mathcal{L}(y)) \), then \( \mu(x) = \mu(y) \). Now let \( \sigma(\mathcal{L}(x)) \subsetneq \sigma(\mathcal{L}(y)) \) which implies that \( \text{lca}_S(\sigma(\mathcal{L}(x))) \preceq_S \text{lca}_S(\sigma(\mathcal{L}(y))) \). If \( \text{lca}_S(\sigma(\mathcal{L}(x))) = \text{lca}_S(\sigma(\mathcal{L}(y))) \), then \( \mu(x) = \mu(y) \). If \( \text{lca}_S(\sigma(\mathcal{L}(x))) \prec_S \text{lca}_S(\sigma(\mathcal{L}(y))) \), then

\[
\mu(x) = (u, \text{lca}_S(\sigma(\mathcal{L}(x)))) \prec_S u \preceq_S \text{lca}_S(\sigma(\mathcal{L}(y))) \prec (u', \text{lca}_S(\sigma(\mathcal{L}(y)))) = \mu(y).
\]

It remains to show (M2iii), that is, if \( e_i = (x, y) \) is a transfer-edge, then \( \mu(x) \) and \( \mu(y) \) are incomparable in \( S \). Since \((x, y)\) is a transfer edge and by Condition (C2), \( \sigma(\mathcal{L}(x)) \cap \sigma(\mathcal{L}(y)) = \emptyset \).

If \( \sigma(\mathcal{L}(x)) = \{A\} \) and \( \sigma(\mathcal{L}(y)) = \{C\} \), then \( \mu(x) = (u, A) \) and \( \mu(y) = (u', C) \). Since \( A \) and \( C \) are distinct leaves in \( S \), \( \mu(x) \) and \( \mu(y) \) are incomparable. Assume that \( |\sigma(\mathcal{L}(x))| > 1 \). Hence, there are leaves \( a, b \in \mathcal{L}(x) \) with \( A = \sigma(a) \neq \sigma(b) = B \) and \( c \in \mathcal{L}(y) \) with \( \sigma(c) = C \neq A, B \). By construction, \( (ab|c) \in \mathcal{R}_i \) and hence, \( (AB|C) \in S \). The latter is fulfilled for all triples \((x''|c) \in \mathcal{R}_i \) with \( x', x'' \in \mathcal{L}(x) \), and, therefore, \( \text{lca}_S(\sigma(\mathcal{L}(x))) \cup \{C\} \Rightarrow_S \text{lca}_S(\sigma(\mathcal{L}(x))) \). Set \( v = \text{lca}_S(\sigma(\mathcal{L}(x))) \cup \{C\} \).

Thus, there is an edge \((v, v') \in S \) with \( v' \geq_S \text{lca}_S(\sigma(\mathcal{L}(x))) \) and an edge \((v, v'') \) such that \( v'' \geq_S C \). Hence, either \( \mu(x) = (v, v') \) or \( \mu(x) = (u, \text{lca}_S(\sigma(\mathcal{L}(x)))) \) and \( v' \geq_S u \). Assume that \( \sigma(\mathcal{L}(y)) \) contains only the species \( C \) and thus, \( \mu(y) = (u', C) \). Since \( v'' \geq_S C \), we have either \( v'' = C \) which implies that \( \mu(y) = (v, v'') \) or \( v'' \geq_S C \) which implies that \( \mu(y) = (u', C) \) and \( v'' \geq_S u' \).

Since both vertices \( v' \) and \( v'' \) are incomparable in \( S \) and \( \mu(x) \) and \( \mu(y) \) are.

If \( |\sigma(\mathcal{L}(y))| > 1 \), then we set \( v = \text{lca}_S(\sigma(\mathcal{L}(x))) \cup \{C\} \) and we can argue analogously as above and conclude that there are edges \((v, v') \) and \((v, v'') \) in \( S \) such that \( v' \geq_S \text{lca}_S(\sigma(\mathcal{L}(x))) \) and \( v'' \geq_S \text{lca}_S(\sigma(\mathcal{L}(y))) \). Again, since \( v' \) and \( v'' \) are incomparable in \( S \) and by construction of \( \mu \), \( \mu(x) \) and \( \mu(y) \) are incomparable.

Lemma 3.3 implies that consistency of the triple set \( S(T; t, \sigma) \) is necessary for the existence of a reconciliation map from \((T; t, \sigma)\) to a species tree on \( S \). Lemma 3.4, on the other hand, establishes that this is also sufficient. Thus, we have

**Theorem 3.2.** There is a species tree on \( S = \sigma(\mathcal{G}) \) for a gene tree \((T; t, \sigma)\) on \( \mathcal{G} \) if and only if the triple set \( S(T; t, \sigma) \) is consistent.

The proof of Lemma 3.4 is constructive and we summarize the latter findings in Algorithm 1, see Figure 1 for an illustrative example.

**Lemma 3.5.** Algorithm 1 returns a species tree \( S \) for \((T; t, \sigma)\) and a reconciliation map \( \mu \) in polynomial time, if one exits and otherwise, recognizes \((T; t, \sigma)\) as “biologically infeasible”.

**Proof.** Theorem 3.2 and the construction of \( \mu \) in the proof of Lemma 3.4 implies the correctness of the algorithms.

For the runtime observe that all tasks, computing \( S(T; t, \sigma) \), using the BUILD algorithm \([1, 32]\) and the construction of the map \( \mu \) \([25, \text{Cor}7]\) can be done in polynomial time.

In our examples, the species trees that display \( S(T; t, \sigma) \) is computed using the \( O(|L_R||R|) \) time algorithm BUILD, that either constructs a tree \( S \) that displays all triples in a given triple set \( R \) or recognizes that \( R \) is not consistent. However, any other supertree method might be conceivable, see \([6]\) for an overview. The tree \( T \) returned by BUILD is least resolved, i.e., if \( T' \) is obtained from \( T \) by contracting an edge, then \( T' \) does not display \( R \) anymore. However, the trees generated by BUILD do not necessarily have the minimum number of internal vertices, i.e., the trees may resolve multifurcations in an arbitrary way that is not implied by any of the triples in \( R \). Thus, depending on \( R \), not all trees consistent with \( R \) can be obtained from BUILD. Nevertheless, in \([24, \text{Prop. 2(SI)}]\) the following result was established.

**Lemma 3.6.** Let \( R \) be a consistent triple set. If the tree \( T \) obtained with BUILD applied on \( R \) is binary, then \( T \) is a unique tree on \( L_R \) that displays \( R \), i.e., for any tree \( T' \) on \( L_R \) that displays \( R \), we have \( T' \simeq T \).
Figure 1: Left: An example of a “true” history of a gene tree that evolves along the (tube-like) species tree (taken from [24]). The set of extant genes $G$ comprises $a, b, c_1, c_2$ and $d$ and $\sigma$ maps each gene in $G$ to the species (capitals below the genes) $A, B, C, D \in S$. Upper Right: Shown is the observable gene tree $(T; t, \sigma)$ that can be constructed from (estimated) orthology or xenology relations, cf. [19, 20, 24]. Note, if we would consider $R_0(T)$ we obtain the triples $(ac_1|d)$ and $(c_2|d|a)$ which leads to the two contradicting species triples $(AC|D)$ and $(CD|A)$. Thus, we restrict $R_0$ to $T_E$ and obtain $R_0(T_E) = \{(ac_1|d)\}$. However, this triple alone would not provide enough information to obtain a species tree such that a valid reconciliation map $\mu$ can be constructed. Hence, we take $R_1(T_E) = \{(bc_2|d)\}$ into account and obtain $\overline{S}(T; t, \sigma) = \{(AC|D), (BC|D)\}$. Lower Right: A least resolved species tree $S$ (obtained with BUILD) that displays all triples in $\overline{S}(T; t, \sigma)$ together with the reconciled gene tree $(T; t, \sigma)$ is shown. Although $S$ does not display the triple $(AB|C)$ as in the true history, this tree $S$ does not pretend a higher resolution than actually supported by $(T; t, \sigma)$. Clearly, as more gene trees (gene families) are available as more information about the resolution of the species tree can be provided.

Algorithm 1 ReconcT

Input: $(T; t, \sigma)$ on $G$

Output: Species tree $S$ for $T$ and a reconciliation map $\mu$, if one exists

1: Compute $\overline{S}(T; t, \sigma)$;
2: if BUILD recognizes $\overline{S}(T; t, \sigma)$ as not consistent then
3: write “There is no species tree for $(T; t, \sigma)$” and stop;
4: else
5: for all $x \in V(T)$ do
6: if $t(x) = \odot$ then set $\mu(x) = \sigma(x)$;
7: else if $t(x) = \bullet$ then set $\mu(x) = \text{lca}_S(\sigma(L_{TE}(x))) \in W^0$;
8: else set $\mu(x) = (u, \text{lca}_S(\sigma(L_{TE}(x)))) \in F$;
9: return $S$ and $\mu$;
4 Open Problems and Outlook

Event-labeled gene trees can be obtained by combining the reconstruction of gene phylogenies with methods for orthology and HGT detection. We showed that event-labeled gene trees \((T; t, \sigma)\) for which a species tree exists – in terms of the reconciliation map \(\mu\) and thus, of a DTL-scenario – can be characterized by a set of species triples \(S(T; t, \sigma)\) that is easily constructed from a subset of triples of \(T\).

From a biological point of view, however, it is necessary to reconcile a gene tree with a species tree such that genes do not “travel through time”, an issue that we have not considered so-far. Although, we do not assume to have dated trees with “time stamp” \([13]\) we can make the following observation: If we have two transfer edges \(\{u, v\}\) and \(\{u', v'\}\) (ignoring the directions for the moment) and a map \(\mu\) from \(T\) to \(S\) with \(\mu(v) \succ_S \mu(v')\), then we should ensure that never \(\mu(u) \prec_S \mu(u')\). If the latter is satisfied for all transfer-edges and the reconciliation map \(\mu\), then we call \(\mu\) acyclic.

![Diagram](image)

Figure 2: Example adapted from [37]. Given the gene tree \((T; t, \sigma)\), we obtain \(S(T; t, \sigma) = \{(AB|E), (AC|E), (BC|A), (BC|D), (BC|E), (DE|C)\}\). A (tube-like) species tree (obtained with BUILD) that displays all triples in \(S(T; t, \sigma)\) is shown. The reconciliation map \(\mu\) for \(T\) and \(S\) is given implicitly by drawing the gene tree within the species tree. However, although \(\mu\) satisfies the conditions of Def. 1, it is cyclic since \(\mu(v) \succ_S \mu(v')\) and \(\mu(u) \prec_S \mu(u')\). As argued in the text, there is no species tree for \(T\) such that there is an acyclic reconciliation map.

Clearly, consistency of \(S(T; t, \sigma)\) is still necessary for the existence of acyclic reconciliation maps, however not sufficient. To see this, consider the example in Figure 2 that shows a cyclic scenario. Applying the BUILD algorithm on \(S(T; t, \sigma)\) yields the species tree \(S\) as shown in Figure 2. The map \(\mu\) is constructed as in Algorithm 1 and is implicitly shown by drawing \(T\) within \(S\). It is easy to see that there is no degree of freedom to shift \(\mu(x)\) to some other vertex or edge in \(S\) for any \(x \in V(T)\). Hence, \(\mu\) is the only reconciliation map from \(T\) to \(S\). Lemma 3.6 implies that \(S\) is the unique tree that displays \(S(T; t, \sigma)\). Lemma 3.3 implies that any species tree for \(T\) must display \(S(T; t, \sigma)\). Since \(S\) is unique for \(S(T; t, \sigma)\) and there is only one (but cyclic) reconciliation map \(\mu\) from \(T\) to \(S\), we can conclude that there is no acyclic reconciliation map from \(T\) to any species tree. We summarize the latter observation in the following

**Lemma 4.1.** If there is an acyclic reconciliation map from \(T\) to \(S\), then \(S(T; t, \sigma)\) is consistent. The converse is in general not true.
In the latter example the tree $S$ that displays all triples in $S(T; t, \sigma)$ is unique. However, in general there might be different species trees for $T$ that display $S(T; t, \sigma)$ for which some of them may have an acyclic reconciliation map with $T$ and some might have not. Therefore, additional constraints for the characterization of acyclic reconciliation maps are needed, an issue that will be part of future work.

References

[1] A. V. Aho, Y. Sagiv, T. G. Szymanski, and J. D. Ullman. Inferring a tree from lowest common ancestors with an application to the optimization of relational expressions. SIAM J. Comput., 10:405–421, 1981.

[2] A M Altenhoff and C. Dessimoz. Phylogenetic and functional assessment of orthologs inference projects and methods. PLoS Comput Biol., 5:e1000262, 2009.

[3] A M Altenhoff, M Gil, G H Gonnet, and C Dessimoz. Inferring hierarchical orthologous groups from orthologous gene pairs. PLoS ONE, 8(1):e53786, 2013.

[4] A M Altenhoff et al. The OMA orthology database in 2015: function predictions, better plant support, synteny view and other improvements. Nucleic Acids Res, 43(D1):D240–D249, 2015.

[5] Mukul S. Bansal, Eric J. Alm, and Manolis Kellis. Efficient algorithms for the reconciliation problem with gene duplication, horizontal transfer and loss. Bioinformatics, 28(12):i283–i291, 2012.

[6] O.R.P Bininda-Emonds. Phylogenetic Supertrees. Kluwer Academic Press, Dordrecht, NL, 2004.

[7] Sebastian Böcker and Andreas W. M. Dress. Recovering symbolically dated, rooted trees from symbolic ultrametrics. Adv. Math., 138:105–125, 1998.

[8] F Chen, A J Mackey, C J Stoeckert, and D S Roos. OrthoMCL-db: querying a comprehensive multi-species collection of ortholog groups. Nucleic Acids Res, 34(S1):D363–D368, 2006.

[9] G. D. Paul Clarke, Robert G. Beiko, Mark A. Ragan, and Robert L. Charlebois. Inferring genome trees by using a filter to eliminate phylogenetically discordant sequences and a distance matrix based on mean normalized BLASTP scores. Journal of Bacteriology, 184(8):2072–2080, 2002.

[10] Frédéric Delsuc, Henner Brinkmann, and Hervé Philippe. Phylogenomics and the reconstruction of the tree of life. Nature Reviews Genetics, 6(5):361–375, 2005.

[11] C Dessimoz, D Margadant, and G H Gonnet. DLIGHT – lateral gene transfer detection using pairwise evolutionary distances in a statistical framework. In Proceedings RECOMB 2008, pages 315–330, Berlin, Heidelberg, 2008. Springer.

[12] Jean-Philippe Doyon, Vincent Ranwez, Vincent Daubin, and Vincent Berry. Models, algorithms and programs for phylogeny reconciliation. Briefings in bioinformatics, 12(5):392–400, 2011.

[13] Jean-Philippe Doyon, Celine Scornavacca, K. Yu. Gorbunov, Gergely J. Szöllősi, Vincent Ranwez, and Vincent Berry. An Efficient Algorithm for Gene/Species Trees Parsimonious Reconciliation with Losses, Duplications and Transfers, pages 93–108. Springer Berlin Heidelberg, Berlin, Heidelberg, 2010.

[14] Andreas W. M. Dress, Katharina T. Huber, Jacobus Koolen, Vincent Moulton, and Andreas Spillner. Basic Phylogenetic Combinatorics. Cambridge University Press, Cambridge, 2011.

[15] Oliver Eulenstein, Snehalata Huzurbazar, and David A Liberles. Reconciling phylogenetic trees. Evolution after gene duplication, pages 185–206, 2010.
[16] Walter M. Fitch. Homology: a personal view on some of the problems. *Trends Genet.*, 16:227–231, 2000.

[17] T. Gabaldón and EV. Koonin. Functional and evolutionary implications of gene orthology. *Nat. Rev. Genet.*, 14(5):360–366, 2013.

[18] Morris Goodman, John Czelusniak, G. William Moore, A. E. Romero-Herrera, and Genji Matsuda. Fitting the gene lineage into its species lineage, a parsimony strategy illustrated by cladograms constructed from globin sequences. *Systematic Biology*, 28(2):132–163, 1979.

[19] M. Hellmuth, M. Hernandez-Rosales, K. T. Huber, V. Moulton, P. F. Stadler, and N. Wieseke. Orthology relations, symbolic ultrametrics, and cographs. *J. Math. Biology*, 66(1-2):399–420, 2013.

[20] M. Hellmuth, P F Stadler, and N Wieseke. The mathematics of xenology: Di-cographs, symbolic ultrametrics, 2-structures and tree- representable systems of binary relations. *Journal of Mathematical Biology*, 2016. DOI: 10.1007/s00285-016-1084-3.

[21] M. Hellmuth and N. Wieseke. On symbolic ultrametrics, cotree representations, and cograph edge decompositions and partitions. In Dachuan Xu, Donglei Du, and Dingshu Du, editors, *Computing and Combinatorics: 21st International Conference, COCOON 2015, Beijing, China, August 4-6, 2015, Proceedings*, pages 609–623, Cham, 2015. Springer International Publishing.

[22] M. Hellmuth and N. Wieseke. *From Sequence Data Including Orthologs, Paralogs, and Xenologs to Gene and Species Trees*, pages 373–392. Springer, Cham, 2016.

[23] M. Hellmuth and N. Wieseke. On tree representations of relations and graphs: Symbolic ultrametrics and cograph edge decompositions. *J. Comb. Opt.*, 2017. (in press) DOI 10.1007/s10878-017-0111-7.

[24] Marc Hellmuth, Nicolas Wieseke, Marcus Lechner, Hans-Peter Lenhof, Martin Middendorf, and Peter F. Stadler. Phylogenomics with paralogs. *Proceedings of the National Academy of Sciences*, 112(7):2058–2063, 2015. DOI: 10.1073/pnas.1412770112.

[25] M. Hernandez-Rosales, M. Hellmuth, N. Wieseke, K. T. Huber, and P. F. Moulton, V. and Stadler. From event-labeled gene trees to species trees. *BMC Bioinformatics*, 13(Suppl 19):S6, 2012.

[26] J G Lawrence and D L Hartl. Inference of horizontal genetic transfer from molecular data: an approach using the bootstrap. *Genetics*, 131(3):753–760, 1992.

[27] Marcus Lechner, Sven Findeiß, Lydia Steiner, Manja Marz, Peter F. Stadler, and Sonja J. Prohaska. Proteinorthoh: detection of (co-)orthologs in large-scale analysis. *BMC Bioinformatics*, 12:124, 2011.

[28] Marcus Lechner, Maribel Hernandez-Rosales, D. Doerr, N. Wiesecke, A. Thevenin, J. Stoye, Roland K. Hartmann, Sonja J. Prohaska, and Peter F. Stadler. Orthology detection combining clustering and synteny for very large datasets. *PLoS ONE*, 9(8):e105015, 08 2014.

[29] Gabriel Ostlund, Thomas Schmitt, Kristoffer Forslund, Tina Köstler, David N Messina, Sanjit Roopra, Oliver Frings, and Erik LL Sonnhammer. InParanoid 7: new algorithms and tools for eukaryotic orthology analysis. *Nucleic acids research*, 38(suppl 1):D196–D203, 2010.

[30] Matteo Pellegrini, Edward M. Marcotte, Michael J. Thompson, David Eisenberg, and Todd O. Yeates. Assigning protein functions by comparative genome analysis: Protein phylogenetic profiles. *Proc. Natl. Acad. Sci. U.S.A.*, 96(8):4285–4288, 1999.

[31] Matt Ravenhall, Nives Škunca, Florent Lassalle, and Christophe Dessimoz. Inferring horizontal gene transfer. *PLoS Comput Biol*, 11(5):e1004095, 2015.

[32] Charles Semple and Mike Steel. *Phylogenetics*, volume 24 of *Oxford Lecture Series in Mathematics and its Applications*. Oxford University Press, Oxford, UK, 2003.
[33] Mike Steel. *Phylogeny: Discrete and Random Processes in Evolution*, CBMS-NSF Regional conference series in Applied Mathematics. SIAM, Philadelphia, USA, 2016.

[34] Gergely J Szöllősi, Eric Tannier, Vincent Daubin, and Bastien Boussau. The inference of gene trees with species trees. *Systematic biology*, page syu048, 2014.

[35] R L Tatusov, M Y Galperin, D A Natale, and E V Koonin. The COG database: a tool for genome-scale analysis of protein functions and evolution. *Nucleic Acids Research*, 28(1):33–36, 2000.

[36] Roman L Tatusov, Eugene V Koonin, and David J Lipman. A genomic perspective on protein families. *Science*, 278(5338):631–637, 1997.

[37] A. Tofigh, M. Hallett, and J. Lagergren. Simultaneous identification of duplications and lateral gene transfers. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(2):517–535, 2011.

[38] K Trachana, T A Larsson, S Powell, W-H Chen, T Doerks, J Muller, and P Bork. Orthology prediction methods: A quality assessment using curated protein families. *BioEssays*, 33(10):769–780, 2011.

[39] D L Wheeler, T Barrett, D A Benson, S H Bryant, K Canese, V Chetverinin, D M Church, M DiCuccio, R Edgar, S Federhen, M Feolo, L Y Geer, W Helmberg, Y Kapustin, O Khojoyko, D Landsman, D J Lipman, T L Madden, D R Maglott, V Miller, J Ostell, K D Pruitt, G D Schuler, M Shumway, E Sequeira, S T Sherry, K Sirotkin, A Souvorov, G Starchenko, R L Tatusov, T A Tatusova, L Wagner, and E Yaschenko. Database resources of the national center for biotechnology information. *Nucleic Acids Res.*, 36:D13–D21, 2008.