This paper deals with a quite important and interesting problem in phylogenetics, namely the construction of event-labeled gene trees and species networks to explain empirical estimates of orthology (genes that diverged after a speciation event (S)) or paralogy data (genes that diverged after a duplication event (D)). Such data is associated with a relation graph R whose vertex set is the set of considered genes and that contains an edge xy precisely if x and y are estimated orthologs (resp., paralogs). Relations graphs that can be "explained" by a gene tree having two labels S and D that can also be reconciled with a species tree have been characterized in the last years. Moreover, methods to correct such estimates to a closest relation graphs that can be explained in such a manner have been established.

In general, however, one may expect that errors in such relations graphs R may arise due to the existence of lateral gene transfer and the fact that the underlying species history is not tree-like. In this case, one may ask, whether there is a gene tree with an additional label "transfer" (T) that can be reconciled with a species network in a time-consistent manner. This question is addressed by the authors in the current paper.

It is shown that the problem of determining whether R is "N-consistent" is NP-hard. N-consistent means, for a given relation R and given network N, that there is a gene tree G together with reconciliation map α such that the type of events inferred by G, α and N determine the structure of R. The latter type of problem extends to allowing at most k-transfers, a problem that is shown to be W[1]-hard. Furthermore, a dynamic programming approach is provided to determine whether an event-labeled gene tree (G,ℓ) can be reconciled with a given network using a minimum number of transfer events. This algorithms runs in $O(f(k)p(|V(D)|,|V(N)|))$ time with f being a function on k (the maximum degree in the gene tree) and p a polynomial on the number of vertices in D and N and, thus, the problem is FPT. Finally, a characterization of relations graphs that are S-consistent is given and a polynomial time algorithm to decide if R is S-consistent is given for the case that S is a species tree. The latter problem becomes NP-hard, when only k transfers are allowed.

The results are very interesting and the paper is well-written. The proofs are correct as far as I checked. However, there are some issues (listed below) that should be addressed before publishing the paper.

Comments:

page 2, line 19 "using sequence similarity [29,7,among others]" seems a bit sloppy - maybe provide further references or a survey here.

page 2, line 2-4: [line 2] remove "reconciled" from "given a reconciled gene tree"
[line 3] add "set" to "displays a given [set] of relations"
[line 4] add "can" to "that [can] be reconciled"

page 4 [line 2] what does "LGT" abbreviate?
[line 8] What does it mean that a vertex is "contracted", do you mean "suppress"?
[line 5-10] Is it possible that one arc incident to the root of N is contained in $E_S$? In this case, the root of N' has only one outgoing arc since N is binary. However, to obtain $T_0(N)$ only vertices with in- and out-degree 1 are "contracted", which means that $T_0(N)$ may have a root with a single arc. Is this intended and possible, or does this yield problems in upcoming proofs?
[def "time-consistent"]. It took me some time to understand, when a DAG is not time-consistent. Maybe provide a small example for this case (e.g. 3-vertex DAG with arcs (a,b), (b,c), (a,c)). Maybe out of scope, but is there a neat characterization of time-consistent DAGs?

In addition, I cannot see in the proofs that this time-map for N is ever used except for Lemma 8. In Lemma 8, you write "add secondary arcs to S in a time-consistent manner". It seems, that you show - by using the time-map as a vehicle - that you create a DAG. So is time-consistency needed here at all?
[line -4] Def of gene tree: can you specify, what you mean with "tree"? must it be binary, phylogenetic, rooted?
Def 1 seems to be different from the definition in [31] where switched-on/off edges are used - clarify.

The constraint (b.7) seems to be redundant, since then (b.5) is already satisfied - clarify.

The definition of $\alpha$ allows to map leaves of the gene tree to paths in the network, as also used in your example and then they get label $\mathbb{S}L$ or $\mathbb{T}L$. Why not mapping every leaf directly to the species in which it resides and thus, forbid to map gene-leaves to paths in $N$?

Moreover, a reconciliation map between gene tree and species network should be time-consistent to ensure that genes do not travel through time when mapped onto the species network. I guess that the map $\alpha$ is always time-consistent, but this needs some verification.

What is the difference / similarities between the map $\mu$ as e.g. used in Ref [26,30] and your map $\alpha$ when $N$ is restricted to be a tree?

This example does not help without a figure, that is, an explicit drawing of the gene tree embedded into the network (the reader must do this either way to understand your example). Please, provide such a drawing.

Typo: $e(\alpha_1(b_1)) = e(\alpha_1(b_1)) = \emptyset$.

Typo: $e(\alpha(c_1))$ should be $e(\alpha_1(c_1))$.

"xenologs could be "interpreted" as either orthologs [] or paralogs."

This sentence is confusing, since you wrote before Sec 2.2 that it is defined based on the labeling of the lca - in which case there is no room for interpretation.

Do you mean, when inferred from sequence data? Why could orthologs or paralogs not be interpreted as transfers?

The definition of $e^*(u,i)$ seems only be used in the proof of Lemma 2 as a vehicle and there it is defined a 2nd time. Is there a way to streamline Def 2 by just using $e(u,i)$ instead?

Moreover, it is not obvious that Def 2 covers all cases, or to be more precise: what happens if e.g. $e^*(\text{LCA}_G(x,y),\text{LAST}) = \mathbb{S}L$ ? is this forbidden by definition?

[Text below Def 2] .. and that can be reconciled with $N$" replace by ".. and that can be reconciled with a given network $N$".

Why does the statement hold: "Note that, if $(G,\alpha)$ and $R$ are known, there is only one relabeling $e^*$ that ensures that $(G,\alpha)$ displays $R$"? Please, give a reference or verify.

[line -1] missing reference "??"

All the theory in Sec 2.3 goes back to the seminal paper


and should be cited here. Maybe a few words to the structural properties (e.g. cograph) would be good to have for the reader.

Are there examples of non-cographs $R$ that are $N$-consistent? If so, can you provide one?

"we show that given a set of relations $R$" - I think $R$ is a relation but not a set of relations.

In Ref [17] it was shown that a DS-tree can always be reconciled with some network (Thm 6) and it is characterized when a DS-tree can be reconciled with a given network $N$ (Thm 7) – at least in terms of the reconciliation map used in [17] – again how does your $\alpha$ differs from the map $\mu$ used there and how do these result fit into your results?

In this context it might also be worth to say that, given an event-labeled gene tree $(G,\ell)$ where also transfer edges in $G$ have been specified, it is possible to determine in polynomial time if $(D,\ell)$ is $S$-reconcilable with some species tree $S$ (even if $S$ is not known a priory), see the work of Hellmuth M. Biologically feasible gene trees, reconciliation maps and informative triples. Algorithms Mol
In other words, the problem of finding a species tree $S$ and a time-consistent reconciliation map between a given gene tree $(G, \ell)$ gets easy, if $G$ and its event-labels incl. transfer edges are known. In this case, a time-consistent network can readily be found just by adding arcs in $S$ on which a transfer happens (=two comparable genes in $G$ for which their images are mapped in an incomparable way in $S$).

To this end, however, it would be nice to see the differences / similarities between the map $\mu$ as e.g. used in Ref [17,26,30] and your map $\alpha$ when $N$ is restricted to be a tree.

Can you provide an example of an event-labeled gene tree $(D, \ell)$ that is not $S$-reconcilable with any species tree $S$ (where $S$-reconcilable is in terms of the map defined in [26,30]) but $N$-reconcilable with some species network (latter reconcilable w.r.t. $\alpha$)?

**page 16, Def 5** is the species network considered in this definition still an LGT-network? please clarify.

**page 16** [1st paragraph below Def 5.] Can you give an example-figure for such a ”peculiar case”?

[1st paragraph below Lemma 6.] ”We make every internal node of $D$ a transfer node.” This sentence is misleading, since $(D, \ell)$ and thus the labeling $\ell$ is already given. It seems however, that you change $\ell$ such that all internal nodes $u$ satisfy $\ell(u) = \top$. please clarify.

**page 18** ”We invite the interested reader to consult the Appendix for the details.”

Can you explain where the details can be found in the appendix?