

Dear PCI Evolutionary Biology editor,

We have uploaded a revision of our manuscript *MaxTiC: Fast ranking of a phylogenetic tree by Maximum Time Consistency with lateral gene transfers*.

In this version we take into consideration the remarks from the second round of peer-review. They are mainly minor suggestions of style, an additional citation and some grammar check.

We provide a detailed point by point answer to the reviews.

For the authors,
Eric Tannier.

Reviewed by Mukul Bansal, 2017-10-18 03:44

The authors have addressed my major concerns and the updated manuscript is a clear improvement over the initial submission. The manuscript now provides an improved description of the heuristic algorithm and of the experimental analysis. The work is definitely interesting, and the proposed method has the potential to be quite useful for species tree dating in prokaryotes. I only have a single minor comment, which the authors can address as they see fit: The new text added to the manuscript has more grammatical errors than the original text from the initial submission. Carefully proofreading the newly added text would help.

Reply: we made several proofreads in this revision, correcting many formulations and improving the readability of the text, in particular the added parts.

Reviewed by anonymous reviewer, 2017-10-07 02:12

This paper seems now in mostly good shape, following the previous reviews and the revisions the authors have made in response to those earlier comments (I was not one of the previous reviewers). The idea of developing algorithms to rank nodes in trees using transfer events is a timely one, and the two algorithms described for minimizing conflicts (one heuristic and one exact) appear to be both new and sound. Accordingly I am happy to recommend publication, however, I have a few suggestions that will be easy for the authors to address.

1. The authors should cite and briefly discuss this paper A Method for Investigating Relative Timing Information on Phylogenetic Trees Daniel Ford, Frederick A. Matsen and Tanja Stadler Systematic biology, 58 (2): 167-183, 2009. While it doesn't directly deal with transfers, nevertheless the ideas in it are very relevant to this paper.

Reply: We have added this paper as a reference and briefly discuss its relevance in the context of this submission in our introduction. Precisely we added in the text the sentence:

Ranked trees provide a relative timing of diversification. They can be used for example to detect events of diversification burst and to relate them with known events in the history of life (Ford et al, 2009).

2. [optional] In the proof of Theorem 1, the authors could point out that the choice of a comb tree (line 3) is entirely arbitrary. Also, with slightly more work (and more "dummy" leaves o_i) one could also even ensure that each node is associated with just one arrow (unlike fig 3(b) where some nodes are associated with 2 and 3 arrows).

Reply: We have added the remark that the comb is arbitrary. Indeed, there are ways to improve this proof. We did not fully understand the reviewer's suggestion to associate only one arrow to each node, neither in its rationale nor in its technical details. We are nonetheless happy that this part of the paper can generate new ideas.

3. page 11 "Figure 6" - in my version I see the caption but no figure (>?!)

Reply: This is our mistake in the version we uploaded, apologies. It has been corrected.

4. Proof of Theorem 2. I'd suggest starting it with $\{\em Proof\}$

Reply: Done.

5. Maybe also flag at the start that the algorithm is based on dynamic programming techniques. Then replace "Indeed, call, ..., the sequence" -> "Let... denote the sequence" line 4 of proof: "note C_N the set" -> "let C_N denote the set" Figure 4 - make the arrows on the end of the transfer arrows bigger next para: "Note $N_{ij} = \dots$ Let then" -> "Let $N_{ij} = \dots$, and let" page 9 - may put the usual square box for \end{proof} just before the para "Applying the mixing..."

Reply: All these corrections have been done.
