

by Tim James, 26 Oct 2023 15:03

Manuscript: <https://doi.org/10.1101/2023.04.14.536987> version 5

## Evaluation of your preprint

I want to thank the authors for carefully revising their paper and fully addressing most of the comments of the reviewers.

Before the final recommendation of the article I would like the authors to make the following changes.

1. Figure 4 is nicely improved. However, Reviewer 2 suggested that you convert this figure to a phylogram with branch lengths. The new figure legend says "the scale bar(e) represented the number of substitutions per site." However, this is clearly not the case as there are no meaningful branch lengths in the figure. This needs to either be corrected by using a phylogeny with branch lengths (highly recommended as this shows exactly how close the actual sequences are to each other in terms of nucleotide substitutions), or to delete that part of the legend and say that this is a cladogram and no branch lengths are shown. If you run PhyML on the data you should be able to get this phylogram with branch lengths, and then the bootstrap values are just mapped on top of that phylogram.

**Response:** Done

2. Since you will revise, please consider changing line 318 to "nucleotide" instead of "nucleotidic acid".

**Response:** Done

3. Also, lines 305-308 are basically two identical statements, so delete one.

**Response:** Done