Decision 2

This is an excellent paper, and the revision is much improved. The author provided substantive responses to all comments in the previous reviews. I think some of this is important enough to include in the text of the article rather than being relegated to the author's response. For this reason, I'm going to ask for a third draft. Details follow.

100: The text here fails to mention that $t_1 + 2N_e$ is not really the expected coalescence time for the $A|B$ split. I pointed this out in my previous review, and the author acknowledged it in his response. The text should make clear that the present formulation is an approximation that should work well when $t_2 - t_1 \gg 2N_e$ but may introduce bias otherwise.

193: Section 2.6 should mention the point, raised by reviewer 2, that a genomic segment long enough to include mutations will probably also include recombinations. This issue is addressed at length later, but I would anticipate it briefly here.

210–211: It's worth mentioning that Aphid performs well in these simulations even though the parameters chosen make Aphid's approximation (see comment above on line 100) rather poor. For these parameter values, the expected coalescence time for the $A|B$ split is $t_1 + 0.69 \times 2N_e$, which is substantially smaller than the value $(t_1 + 2N_e)$ assumed by Aphid. I would have expected this to generate substantial bias. Yet Aphid does a good job of recovering the simulation parameters. This should be advertized a bit.

264–267: The difficulty in anotating ILS trees might arise from the problem discussed in my comment on line 100. If so, these problems should be greatest when $z = 2(\tau_2 - \tau_1)/\theta$ is small. (For details, see my comment on lines 97–99 in the previous review.)

374–375: I've never seen scientific notation written this way. I would write 1.15×10^{-2} rather than $1.15 \ 10^{-2}$. While I'm on typography, in this paper dashes look like "-" rather than like "—". The latter is conventional. To get longer dashes in LaTeX, use "---". These are just suggestions.

459–460: Legofit has also been used to study chimpanzees [1].

References

[1] Colin M. Brand et al. "Estimating bonobo (*Pan paniscus*) and chimpanzee (*Pan troglodytes*) evolutionary history from nucleotide site patterns". *Proceedings of the National Academy of Sciences, USA* 119.17 (2022), e2200858119. DOI: 10.1073/pnas.2200858119.