January 31st, 2023

Dear Dr. Sanmartín:

We are excited to submit our paper entitled, *Potential survival of some, but not all, diversification methods* for consideration as a Point of View in *Systematic Biology.*

Molecular phylogenies are powerful sources of data for understanding diversification dynamics of a set of organisms and have become crucial in multiple areas of ecology and evolution. In theory, if birth and death rates are constant across a phylogeny, estimating them separately is possible because each has distinguishable effects on the tree shape and branch length distributions. The assumption of constant rates is, of course, rarely, if ever, true, which has led to extensions that infer lines showing speciation and extinction rates scrolling into the past, like the pen of a seismometer tracking vibrations through time. However, it was recently pointed out by Louca and Pennell (2020) that for this particular class of models any given phylogeny is described by an infinite array of *congruent models*, each having unique functions of speciation and/or extinction rates smoothly varying through time. That is, they have identical likelihood and so are indistinguishable from each other despite telling very different stories about the diversification history.

These findings have led many empiricists and theoreticians to assume that any attempt to learn anything about diversification rates from molecular phylogenies is a completely futile enterprise. The issues raised by Louca and Pennell (and Kubo and Iwasa 25 years earlier in 1995) do represent substantial methodological problems for comparative biology. However, in our view, this does not signal the complete demise of studying diversification rates on molecular phylogenies, as some have claimed – these problems do not extend to *all* models of diversification. Here, we provide a brief review of the key findings of Louca and Pennell (2020) and put them in the context of other fields. For instance, model congruence readily occurs in areas as different as coin flipping and Brownian motion and this it does not mean these models must be given up, only that certain questions are infeasible. We also demonstrate how other classes of models, such as the popular state-speciation and extinction (SSE) methods use information beyond that in a lineage through time curve and their utility remains intact in the face of Louca and Pennell (2020). Finally, we emphasize examining uncertainty in parameter estimates. Pulled speciation rates (Louca and Pennell 2020) may be identifiable, but they fail to incorporate the substantial uncertainty in rate reconstructions as one approaches the root.

We believe this manuscript is broadly appealing to comparative biologists, who after three years remain confused as to the status of diversification rate analyses. We should also point that this this work was submitted as a preprint on EcoRxiv in 2022 (https://ecoevorxiv.org/repository/view/3912/) and it has already garnered 11 citations, which we feel speaks to the potential impact of our message.

Thank you very much for your consideration, and we look forward to hearing from you.

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