Dear Editor,

Here we present our manuscript "Quantifying the importance of an inference model in Bayesian phylogenetics". We hope you will consider it for publication as an Application in Methods in Ecology & Evolution.

Current computational techniques allow phylogenetic reconstruction from sequence alignments of extant organisms. BEAST2 is one of the most popular tools to perform such task: it operates in a Bayesian framework and, therefore, requires an underlying tree prior model to yield a posterior distribution of phylogenies. Tree priors contain the rules according to which diversification should occur. They can be developed and implemented by third-party users to be integrated in BEAST2. However, it is not possible, at the current state, to assess whether the implementation of a novel tree prior is actually needed or if current BEAST2 options could already perform the task to a satisfactory extent.

With this manuscript we introduce pirouette, an R package that allows to quantitatively assess the goodness of the inference on novel diversification processes, adopting standard BEAST2 priors. The package is completely black-boxed and documented, allowing for an easy use by third-party users that desire to test their own diversification models. The package features also a model selection across several available priors and a parallel pipeline to evaluate the baseline error. The manuscript describes through working examples the functionalities of pirouette and guides the reader in the usage.

As we deem pirouette to be a potential useful tool for theoretical evolutionary biologists, we think that Methods in Ecology & Evolution will be a suitable journal to host our work.

All authors have agreed to this submission and we declare no conflict of interests.

Kind regards,

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