

Dear Editor,

Please consider our manuscript “babette: BEAUti 2, BEAST2 and Tracer for R” for publication in *Methods in Ecology & Evolution*.

Many of us use BEAST2, as it is one of the most widely used phylogenetic software tool. One of the likely causes for its success is that it is accompanied by programs that have a user-friendly graphical user interface. However, when doing an intensive theoretical exploration, with thousands of DNA alignments and/or model settings, a workflow of graphical user interfaces would be repetitive, plain dumb or impossible.

This manuscript describes ***babette***, an R package that solves this problem. There have been many partial solutions to work with BEAST2 from R. Next to the partial solutions cited in this manuscript, there are many more uncitable code snippets that automate part of the BEAST2 workflow. ***babette*** unifies this scattered landscape of partial BEAST2 solutions, as it is the first R package that offers a complete begin-to-end workflow to work with BEAST2 from R. This manuscript gives the reader an idea of the scope and ease of use of ***babette***, thanks to the examples supplied.

We believe that our manuscript helps increase the joy and thoroughness of future studies within phylogenetics and should therefore appeal to a wide audience. Hence, we feel that *Methods in Ecology & Evolution* is the ideal platform for our manuscript.

Kind regards,

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