Dear Editor,

Please consider our manuscript "babette: BEAUti 2, BEAST2 and Tracer for R" for publication as an Application in Methods in Ecology & Evolution.

BEAST2 is one of the most widely used phylogenetic software tools. A probable cause for its success is that it is accompanied by programs that have a user-friendly graphical user interface. However, when doing an intensive exploration, with thousands of DNA alignments and/or model settings, a workflow of graphical user interfaces is repetitive and inefficient. Furthermore, a large part of the scientific community in ecology and evolution uses R and many phylogenetic tools are available for R, except the actual tree construction.

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` stands out in 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`, by providing various examples.

We believe that our manuscript substantially facilitates phylogenetic studies 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,

Richèl J.C. Bilderbeek and Rampal S. Etienne