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Dear Editor-in-Chief Shawn Narum,

I hope you will consider our manuscript entitled: **"slimr: An R package for integrating data and tailor-made population genomic simulations over space and time"** for publication in Molecular Ecology Resources.

The manuscript describes a new R package designed to integrate the popular and powerful population genetic simulation software SLiM with the data analysis, visualisation, and manipulation features of R. We think it will be of interest to readers of Molecular Ecology Resources as it makes complex simulation of population genetics accessible for inclusion in standard molecular biological workflows mediated by the R language.

slimr is much more than just a wrapper around SLiM, it creates a hybrid domain specific language that enhances the already powerful SLiM, acting as a workflow manager and providing metaprogramming tools to generate thousands of parameterised simulations easily. It also offers a simple approach to capture the output from simulations for downstream analysis using R's extensive suite of data tools. Importantly for the readers of Molecular Ecology Resources, slimr allows the passing of genomic, genetic, and other types of data easily between R and SLiM, both into and out of simulations. In doing this, we provide a tool for user's who wish to estimate simulation parameters through fitting to empirical data obtained from Approximate Bayesian Computation or other advanced likelihood-free methods available in R.

We have incorporated a detailed application of the package as supplementary material and links to many more examples through the website (https://rdinnager.github.io/slimr/) and including a 1-day workshop, developed and run by the authors, on how to use the package.

This manuscript has previously been posted as a preprint here:
https://www.biorxiv.org/content/10.1101/2021.08.05.455258v2

Thank you for your consideration of this manuscript. On behalf of all coauthors,

Sincerely,

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