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Dear Professor Hurley,

We thank you, the associate editor, and the reviewers for another helpful round of helpful comments on our paper “Bootstrapping Clustered Data in R using `lmeresampler`” (2021-94). We have made the recommended revisions to the manuscript and are resubmitting the manuscript for your consideration. Our responses to the reviewers can be found in the file `reviewer_response.pdf`.

Our paper provides an overview of the add-on package **`lmeresampler`**, which implements five bootstrap procedures for linear mixed-effects (LME) models fit to nested data fit using `nlme::lme()` or `lme4::lmer()`. **`lmeresampler`** expands the bootstrap procedures available to R users, saving them from manually coding procedures for each analysis, so we believe it will be of substantial interest to the readership. We provide a unified `bootstrap()` command that can be used to implement the parametric, residual, cases (i.e., nonparametric), random effects block, and wild bootstraps for LME models. Further, the parametric, residual, and cases procedures work with generalized linear mixed-effects models fit via `lme4::glmer()`.

In addition to discussing new contributions of the package, we discuss points that are not specific to the package:

- We illustrate how the lineup protocol can be used to conduct residual analysis for LME models. While **`lmeresampler`** makes this implementation quite easy (with the help of **`nullabor`**), the discussion helps readers discover this tool for model diagnostics.
- We illustrate that bootstrap procedures make it easy to construct interval estimates of complex functions of model parameters. The example we include shows an easy way to build a confidence interval for the intraclass correlation, which is also called repeatability in the biological literature. While this may seem like an obvious application, we believe it will appeal to a broader set of readers than formally trained statisticians.
- We include a brief overview of parallel computing in R and illustrate how the user can take advantage of the embarrassingly parallel nature of bootstrap procedures.

We have no conflicts of interest to disclose. Please address all correspondence concerning this manuscript to me at aloy@carleton.edu. Thank you for your consideration of this manuscript.

Sincerely,

Adam Loy
with Jenna Korobova