

Line 353: isn't " $D_{i,j}$ " also squared? The function used in `ulam()` was "`cov_GPL2`" and not "`cov_GPL1`".

Evaluation round #2

DOI or URL of the preprint: <https://ecoevorxiv.org/rc8na/>

Version of the preprint: 4

Author's Reply, None

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Decision by [Matthieu Paquet](#), 07 Jun 2022

Dear Authors,

Your manuscript has been reviewed by one of the previous referees and based on their reviews and my reading, I am inviting you to revise it slightly according to their comments and suggestions.

You will find their reviews below. In addition, I also have some comments:

Line 41 "mediate". Although I appreciate that it is indeed a statistical "mediator", perhaps using a less causal terminology would be less ambiguous e.g. relationship between rank and reproductive success were conditional on life history?

Lines 46-49: I would suggest avoiding the use of the term "complex" here as it can be rather subjective and such complexity levels are not referred to nor defined in the main text.

Line 93: it sounds like all social mammals were included. Perhaps delete "all".

Line 292-299 Apologies for not suggesting it earlier on but could it be possible to provide the resulting consensus phylogenetic tree used in the study as a Figure, possibly with illustrations (animal characteristic shapes) for different taxa? It would provide the reader with a fast and intuitive assessment of the phylogenetic diversity and representativity of the dataset.

Line 306: not sure "estimated all models" is the best wording (they are rather built and fitted to the data, then parameters are estimated). I'd suggest merging with the following sentence e.g.: We fit meta-analytic multilevel mixed-effects models with moderators via linear models (function "`rma.mv`" in the package `metafor`; Viechtbauer 2010)...

Line 312: this sounds like the sampling variance was ignored when using the `metafor` package. Is that the case? It is also unclear in the text whether there is a difference in the way phylogeny was accounted for with the two approaches. See my main comment below based on previous reviews: a mathematical notation of the models (equations) would really help understanding what statistical models were built and whether they differ between the two approaches (beyond the existence of priors for the Bayesian approach). See e.g. Edwards & Auger-Méthé 2018 for guidance (<https://doi.org/10.1111/2041-210X.13105>).