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rr2: An R package to calculate R^2s for regression models

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Software

- Review
- Repository
- Archive

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Summary

Reporting the variance explained by a model (an R^2) is common for many simple statistical tests. However, conceptual challenges exist in defining R^2 for models that include correlated data. Ives (2018) proposed three R^2s (R^2_{lik}, R^2_{resid}, and R^2_{pred}) for a variety of regression models that include correlation among data such as linear mixed models (LMMs), generalized linear mixed models (GLMMs), and phylogenetic regressions (Ives & Garland, 2014; PGLMMs, Ives & Helmus, 2011). These three R^2s can also be used as partial R^2s to compare the contributions of predictor variables (fixed effects) and/or correlation structures (random effects) to the fit of the models.

The `rr2` package provides R functions to implement the R^2s proposed by Ives (2018). The main function, `R2()`, calculates all three R^2s by default, with arguments available to select which R^2(s) to calculate by users. Alternatively, individual R^2s can be calculated with corresponding functions (`R2_lik()`, `R2_resid()`, and `R2_pred()`). Supported models include linear models (`lm`), generalized linear models (`glm`), linear mixed models (`lmerMod`), generalized linear mixed models (`glmerMod`), phylogenetic generalized least squares models (`phylolm`), phylogenetic logistic regression (`phyloglm`), and phylogenetic generalized linear mixed models (`binaryPGLMM` and `communityPGLMM`).

The R package `rr2` is available on Github, where issues can be opened.

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