partR2: Partitioning R^2 in generalized linear mixed models

Martin A Stoffel [Corresp., 1, 2] , **Shinichi Nakagawa** [3] , **Holger Schielzeth** [Corresp. 1]

[1] Institute of Ecology and Evolution, Friedrich-Schiller Universität Jena, Jena, Germany

[2] Institute of Evolutionary Biology, University of Edinburgh, Edinburgh, United Kingdom

[3] Evolution & Ecology Research Centre and School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, Australia

Corresponding Authors: Martin A Stoffel, Holger Schielzeth
Email address: martin.stoffel@ed.ac.uk, holger.schielzeth@uni-jena.de

The coefficient of determination R^2 quantifies the amount of variance explained by regression coefficients in a linear model. It can be seen as the fixed-effects complement to the repeatability R (intra-class correlation) for the variance explained by random effects and thus as a tool for variance decomposition. The R^2 of a model can be further partitioned into the variance explained by a particular predictor or a combination of predictors using semi-partial (part) R^2 and structure coefficients, but this is rarely done due to a lack of software implementing these statistics. Here, we introduce partR2, an R package that quantifies part R^2 for fixed effect predictors based on (generalized) linear mixed-effect model fits. The package iteratively removes predictors of interest from the model and monitors the change in the variance of the linear predictor. The difference to the full model gives a measure of the amount of variance explained uniquely by a particular predictor or a set of predictors. partR2 also estimates structure coefficients as the correlation between a predictor and fitted values, which provide an estimate of the total contribution of a fixed effect to the overall prediction, independent of other predictors. Structure coefficients can be converted to the total variance explained by a predictor, here called 'inclusive' R^2, as the square of the structure coefficients times total R^2. Furthermore, the package reports beta weights (standardized regression coefficients). Finally, partR2 implements parametric bootstrapping to quantify confidence intervals for each estimate. We illustrate the use of partR2 with real example datasets for Gaussian and binomial GLMMs and discuss interactions, which pose a specific challenge for partitioning the explained variance among predictors.

1 **partR2: Partitioning R² in generalized linear mixed models**

3 Martin A. Stoffel[1,2], Shinichi Nakagawa[3], Holger Schielzeth[1]

4 [1] Institute of Ecology and Evolution, Friedrich Schiller University Jena, Germany

5 [2] Institute of Evolutionary Biology, University of Edinburgh, Edinburgh, UK

6 [3] Evolution & Ecology Research Centre and School of Biological, Earth and Environmental Sciences, University of

7 New South Wales, Sydney, Australia

8 ORCID: MAS 0000-0003-4030-3543, SN 0000-0002-7765-5182, HS 0000-0002-9124-2261

27 Corresponding authors

28 Martin A. Stoffel, martin.stoffel@ed.ac.uk

29 Holger Schielzeth, holger.schielzeth@uni-jena.de

30

31   **Abstract**

32   The coefficient of determination R^2 quantifies the amount of variance explained by regression coefficients in a linear

33   model. It can be seen as the fixed-effects complement to the repeatability R (intra-class correlation) for the variance

34   explained by random effects and thus as a tool for variance decomposition. The R^2 of a model can be further

35   partitioned into the variance explained by a particular predictor or a combination of predictors using semi-partial

36   (part) R^2 and structure coefficients, but this is rarely done due to a lack of software implementing these statistics.

37   Here, we introduce `partR2`, an R package that quantifies part R^2 for fixed effect predictors based on (generalized)

38   linear mixed-effect model fits. The package iteratively removes predictors of interest from the model and monitors

39   the change in the variance of the linear predictor. The difference to the full model gives a measure of the amount

40   of variance explained uniquely by a particular predictor or a set of predictors. `partR2` also estimates structure

41   coefficients as the correlation between a predictor and fitted values, which provide an estimate of the total

42   contribution of a fixed effect to the overall prediction, independent of other predictors. Structure coefficients can

43   be converted to the total variance explained by a predictor, here called 'inclusive' R^2, as the square of the structure

44   coefficients times total R^2. Furthermore, the package reports beta weights (standardized regression coefficients).

45   Finally, `partR2` implements parametric bootstrapping to quantify confidence intervals for each estimate. We

46   illustrate the use of `partR2` with real example datasets for Gaussian and binomial GLMMs and discuss interactions,

47   which pose a specific challenge for partitioning the explained variance among predictors.

Introduction

49 Coefficients of determination R^2 are of interest in the study of ecology and evolution, because they quantify the

50 amount of variation explained by a linear model (Edwards et al., 2008). By doing so, they go beyond significance

51 testing in putting effects in perspective of the phenotypic variance. R^2 is expressed as a proportion of the total

52 variance in the response, which represents a biologically relevant quantity if the total variation is representative for

53 the total population (de Villemereuil et al., 2018). The total coefficient of determination in a generalised linear

54 mixed model (GLMM) quantifies the variance explained by all fixed effects together (marginal R^2 *sensu* Nakagawa

55 & Schielzeth, 2013, also known as the total correlation coefficient, Watanabe (1960)).

56

57 However, it is often of interest to attribute explained variation to individual predictors. Semi-partial coefficients of

58 determination, also known as part R^2, decompose the variance of R^2 into components uniquely explained by

59 individual predictors (Jaeger et al., 2017; Jaeger, Edwards & Gurka, 2019) or sets of predictors (Figure 1). The set of

60 all predictors in the model yields the total proportion of variance explained by the fixed part of the model (total R^2).

61 With correlations among predictors, it often happens that predictors in univariate regressions explain a large share

62 of the variance, but do not show large part R^2 if other correlated predictors are included in the model. Note that

63 part R^2 estimates the proportion of the variance in the response explained by a predictor *while* accounting for

64 covariance between this predictor and the other predictors in the model, whereas the (arguably more familiar)

65 partial R^2 estimates the proportion of the variance that is explained by a predictor of interest *after* accounting for

66 the other predictors from the response as well as the predictor of interest. The difference is subtle, but important

67 (see more below). Therefore, part R^2 represents 'variance accounted for' in relation to the total variance, but partial

68 R^2 does not. Consequently, part R^2 will be conceptually easier to compare with (total) R^2.

69

70 Structure coefficients provide a valuable addition to part R^2 in the decomposition of the phenotypic variance

71 (Nimon et al., 2008; Yeatts et al., 2017). Structure coefficients quantify the correlation between individual

72 predictors and the linear predictor. Predictors that correlate well with a response, but are fitted with collinear

73 predictors may show large structure coefficients as they are correlated to the predicted response, but low part R^2

74 as other predictors explain part of the same variance. Structure coefficients range from -1 to 1 with their absolute

75 value expressing the correlation relative to a perfect correlation if a single predictor explains as much as the total

76 fixed part of the model.

77

78 Structure coefficients are correlations and since the square of a correlation yields the variance explained, we can

79 use structure coefficients to estimate the total variance explained by a predictor (Nimon et al., 2008). We call this

80 the inclusive R^2 of a predictor and calculate it as the squared structure coefficient, i.e. its contribution to the linear

81 predictor independent of other predictors (Nimon et al., 2008) times the proportion of variance explained by the

82 linear predictor (which is the 'total' marginal R^2 of the model) (see also Nathans, Oswald & Nimon, 2012). As far as
83 we are aware, inclusive R^2 has not been implemented before, but it provides valuable insights into the structure of
84 the variance explained (Figure 1).

86 Here, we introduce `partR2`, a versatile package for estimating part R^2, inclusive R^2, structure coefficients and beta
87 weights from mixed-effects models. Figure 1 gives an overview of how variances are calculated and how they relate
88 to partial R^2 and to commonality analysis (Ray-Mukherjee et al., 2014; Seibold & McPhee, 1979; Zientek &
89 Thompson, 2006). We illustrate how to use `partR2` with real example datasets for Gaussian and binomial GLMMs,
90 discuss how to estimate part R^2 in the presence of interactions and discuss some challenges and limitations.

92 **Figure 1:** Conceptual framework for the estimation of proportions of variance components in a mixed model.
93

94 **Mathematical representation**

95 **Part R^2**

97 A Gaussian mixed-effects model can be written as:

98 $$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \sum \boldsymbol{\alpha}_k + \boldsymbol{\varepsilon} \qquad \text{(Eq. 1)}$$

99 $$\alpha_k \sim N(0, \sigma^2_{\alpha_k})$$

100 $$\varepsilon \sim N(0, \sigma^2_\varepsilon)$$

101 Where $\mathbf{y}$ is a vector of response values (outcomes), $\mathbf{X}$ is the design matrix of fixed effects, $\boldsymbol{\beta}$ is a vector of
102 regression coefficients, $\sum \boldsymbol{\alpha}_k$ is the random part of the model that might contain multiple random effects and $\boldsymbol{\varepsilon}$
103 is a vector of residual deviations. The linear predictor $\boldsymbol{\eta}$ represents the vector of predicted values from the fixed
104 part of the model as $\boldsymbol{\eta} = \mathbf{X}\boldsymbol{\beta}$. Note that we dealing with estimates of regression coefficients and variance
105 components throughout (hence all $\boldsymbol{\beta}$ should be read as $\hat{\boldsymbol{\beta}}$).

107 Since we are interested in the proportion of the phenotypic variance explained, we symbolize variance components
108 by upper case Y and index by the source of variance (als in Figure 1). While variances are frequently represented as
109 V with the source of variance as an index, this leads to ambiguity for V_X which might represent variance in y
110 explained by x or variance in x itself, which is why we use this alternative notation. The total variance in the response
111 is $Y_{Total} = \text{var}(y)$ and is estimated from the raw data or from the model (see below). The variance of the residuals
112 is estimated by the model as $Y_R = \text{var}(\varepsilon)$. The variance of the (sum of) random effects is estimated by the model

113   as $Y_{RE} = \mathrm{var}(\sum \alpha_k)$ and the variance explained by fixed effects can be estimated as the variance in the linear

114   predictor $Y_X = \mathrm{var}(\mathbf{X\beta})$.

115

116   The coefficient of determination R^2 estimates the proportion of variance in the response that is explained by fixed

117   effects. The coefficient of determination R^2 for the total fixed part of the model is thus:

118     $$R_x^2 = \frac{Y_X}{Y_X + Y_{RE} + Y_R} = \frac{Y_X}{Y_{Total}} \qquad \text{(Eq. 2)}$$

119   Note that the sum of the components in the denominator might deviate numerically from the total outcome

120   variance in the raw data. However, conceptually they are the same in that they represent the population-level

121   outcome variance. The variance in the outcome is an estimate from the specific sample, while the sum of

122   components of the mixed model represents a population-level estimate given the data and the model.

123

124   A reduced model with a (set of) fixed effect predictors X^* removed but the same random effect structure can be

125   fitted as (now using the tilde to highlight the differences from Eq. 1):

126     $$\mathbf{y} = \widetilde{\mathbf{X}}\widetilde{\boldsymbol{\beta}} + \sum \widetilde{\alpha}_k + \widetilde{\boldsymbol{\varepsilon}} \qquad \text{(Eq. 3)}$$

127     $$\widetilde{\alpha}_k \sim N(0, \sigma_{\widetilde{\alpha}_k}^2)$$

128     $$\widetilde{\varepsilon} \sim N(0, \sigma_{\widetilde{\varepsilon}}^2)$$

129   with the variance in the linear predictor of the reduced model being $Y_{\widetilde{X}} = \mathrm{var}(\widetilde{\mathbf{X}}\widetilde{\boldsymbol{\beta}})$.

130

131   The variance uniquely explained by X^* is then the difference between the variance explained by fixed effects in

132   the full and the reduced model $Y_{X^*} = Y_X - Y_{\widetilde{X}}$. Part R^2 sets this variance in proportion to the total outcome

133   variance:

134     $$R_{X^*}^2 = \frac{Y_X - Y_{\widetilde{X}}}{Y_X + Y_{RE} + Y_R} = \frac{Y_X - Y_{\widetilde{X}}}{Y_{Total}} \qquad \text{(Eq. 4)}$$

135   The process of fitting a reduced model, estimation of Y_{X^*} and estimation of $R_{X^*}^2$ can be repeated for all

136   predictors and combinations of predictors. At the limit for a model with all fixed effects removed, $R_{x^*}^2 = R_X^2$.

137

138   **Side-note on partial R^2**

139

140   For completeness we note that the partial R^2 could be calculated as:

141     $$R_{X^*}^2 = \frac{Y_X - Y_{\widetilde{X}}}{Y_{Total} - Y_{\widetilde{X}}} \qquad \text{(Eq. 5)}$$

142   However, this estimate does not put the explained variance in perspective of the total variance in the response. It

143   has the major disadvantage that the denominator depends on $Y_{\tilde{X}}$. The same effect in terms of Y_{X^*} thus appears

144   larger if the reduced model explains more variance (larger $Y_{\tilde{X}}$). Even in the case of independent additive predictors,

145   the contributions of the different fixed effects do not sum up to R^2_X, because of the change in the denominator

146   that different Y_{X^*} are compared to. Finally, since we are interested in explaining phenotypic variation in some

147   biological response (the phenomenon to be explained), we think that part R^2 is the more relevant quantity, as it

148   represents the proportion of variance in the response uniquely explained by X^*.

149

150   **Inclusive R^2**

151

152   Structure coefficients are the Pearson correlations between a particular predictor of interest x^* and the linear

153   predictor η. Note that we now use a lower case x^* to indicate that we are dealing with a single predictor. Structure

154   coefficients are quantified from the full model as:

155   $$SC_{x^*} = \mathrm{cor}(\eta, x^*) \qquad\qquad\qquad (Eq.\ 6)$$

156

157   The squared correlation between two variables a and b gives the variance explained for these variables

158   $\mathrm{cor}(a,b)^2 = R^2_a$. The squared structure correlations thus quantify the proportion of variance in the linear

159   predictor Y_X that is explained by a the predictor of interest x^*. Since the proportion of outcome variance

160   explained by the linear predictor in the full model is R^2_x, the inclusive variance explained by predictor x^* is:

161   $$IR^2_{x^*} = SC^2 \cdot R^2_X \qquad\qquad\qquad (Eq.\ 7)$$

162

163   Inclusive R^2 as we define it here, complements part R^2 by giving additional insights. While part R^2 quantifies the

164   variance uniquely explained by a predictor (or set of predictors), inclusive R^2 quantifies the total proportion of

165   variance explained in the model, both uniquely and jointly with other predictors. In the special case of a single

166   predictor in a model $SC_{x^*} = \mathrm{cor}(\eta, x^*) = 1$, such that $IR^2_{x^*} = R^2_x$.

167

168   **Part R^2 in non-Gaussian models**

169

170   For Gaussian models there is a single residual error term ε with variance $Y_R = \mathrm{var}(\varepsilon)$. For non-Gaussian models,

171   however, there is additional error that arises from the link function that translates latent-level predictions to

172   observed outcomes. This variance can be approximated for a variety of link functions and error distributions

173   (Nakagawa & Schielzeth, 2010; Nakagawa, Johnson & Schielzeth, 2017). Our R package currently implements

174 distribution-specific variances for Poisson models with log and square root link functions and binomial models with

175 logit and probit link functions. For Poisson models and non-binary binomial models (proportion models), `partR2`

176 also fits an observational level random effect (if none is fitted already) to estimate variance due to overdispersion

177 (Harrison, 2014). Both the overdispersion variance, now denoted Y_R and the distribution-specific variance Y_D are

178 included in the denominator of the part R2 calculation:

179

180 $$R^2_{X*} = \frac{Y_X - Y_{\tilde{X}}}{Y_X + Y_{RE} + Y_D + Y_R}$$ (Eq. 8).

181

182
183 Notably, there are other estimation methods for R^2 for non-Gaussian models or GLMM (Jaeger et al., 2017; Piepho,

2019). Currently, `partR2` only implements the method based on Nakagawa & Schielzeth (2013) and Nakagawa,

184 Johnson & Schielzeth (2017).

185 **Other implementations in R packages**

186 There are a few R packages that calculate part R^2 for linear models (lm), for example

187 `rockchalk::getDeltaRsquare` (Johnson & Grothendieck, 2019). Other packages calculate partial R^2 (not

188 part R^2) such as `asbio::partial.R2` (Aho, 2020) and `rr2::R2` (Ives & Li, 2018) for lms and

189 `rsq::rsq.partial` (Zhang, 2020) for linear models and generalized linear models (glm). Note that partial R^2 is

190 different from part (semi-partial) R^2 (partial R^2 > part R^2), since it represents the unique variance explained by a

191 particular predictor but after removing ('partialling out') the variance explained by the other predictors (Yeatts et

192 al., 2017, Figure 1). The ppcor package calculates semi-partial and partial correlations, but does not work on fitted

193 GLM or GLMM models (Kim, 2015). The package `yhat` features functions for commonality analyses in glms

194 (Nimon, Oswald & Roberts, 2020). None of these packages estimates part R^2 for mixed-effects models that we

195 focus on here.

196 Several packages estimate (marginal) R^2 as the variance explained by all fixed effects in linear mixed-effects models.

197 This includes `performance::r2_nakagawa` (Lüdecke et al., 2020), `MuMIn::r.squaredGLMM` (Bartoń,

198 2019), and `rptR::rpt` (Stoffel, Nakagawa & Schielzeth, 2017). These packages do not allow to estimate part R^2.

199 The only versatile package to estimate part R^2 from linear mixed-models is `r2glmm` (Jaeger, 2017). The function

200 `r2glmm::r2beta` computes part R^2 from lmer, lme and glmmPQL model fits (also for linear models lm and glm)

201 based on Wald statistics. However, it does neither support `lme4::glmer` for generalized linear model fits nor

202 does it allow to estimate R^2 for combinations of predictors. Furthermore, it does not estimate structure coefficients,

203 inclusive R^2 or part R^2 for multilevel factors as a unit.

204

205 **Features of `partR2`**

206 `partR2` takes a fitted (generalized) linear mixed-model (GLMM), from the popular mixed model package `lme4`

207 (Bates et al., 2015) and estimates part R^2 by iteratively removing fixed effects (Nimon et al., 2008). The specific fixed

208 effects of interest are specified by the `partvars` and/or by the `partbatch` argument. The package estimates

209 part R^2 for all predictors specified in `partvars` individually and in all possible combinations (the maximum level

210 of combinations can be set by the `max_level` argument). A custom specification of fixed effects of interest saves

211 computation time as compared to an all-subset specification and is therefore required in `partR2`.

212 The central function `partR2` will work for Gaussian, Poisson and binomial GLMMs. Since the model fit is done

213 externally, there is no need to supply a family argument. For non-Gaussian GLMMs, the package estimates link-

214 scale R^2 *(sensu* Nakagawa & Schielzeth, 2013*)*. We implement parametric bootstrapping to quantify sampling

215 variance and thus uncertainty in the estimates. Parametric bootstrapping works through repeated model fitting on

216 simulated data based on fitted values (Faraway, 2015). The number of bootstrap iterations is controlled by the

217 `nboot` argument. We recommend a low number of `nboot` for testing purposes and a large number (e.g. `nboot`

218 `= 1000`) for the final analysis.

219 The package returns an object of class `partR2` that contains elements for part R^2, inclusive R^2, structure

220 coefficients, beta weights (standardized regression slopes), bootstrapping iterations and some other information.

221 An extended summary, that includes inclusive R^2, structure coefficients and beta weights can be viewed using the

222 `summary` function. The `forestplot` function shows a graphical representation of the variance explained by

223 individual predictors and sets of predictors along with their bootstrapping uncertainties. All computations can be

224 parallelized across many cores based on the `future` and `furrr` packages (Vaughan & Dancho, 2018; Bengtsson,

225 2020). An extended vignette with details on the complete functionality accompanies the package.

226

227 **Example with Gaussian data**

228 We use an example dataset with hormone data collected from a population of captive guinea pigs to illustrate the

229 features of `partR2`. The dataset contains testosterone measurements of 31 male guinea pigs, each measured at 5

230 time points (age between 120 and 240 days at 30-day intervals). We analyze log-transformed testosterone titers

231 and fit male identity as a random effect. As covariates the dataset contains the time point of measurement and a

232 rank index derived from behavioral observations around the time of measurement (Mutwill et al., in prep.).

233 *Rank* and *Time* are correlated in the dataset ($r = 0.40$), since young individuals are typically low rank, while older

234 individuals tend to hold a high rank. *Time* might be fitted as a continuous predictor or as a factor with five levels.

235 Here we present the version of a factorial predictor to illustrate the estimation of part R^2 for interactions terms.

236 Hence, an interaction between time and rank will also be fitted.

237 First, the package needs to be loaded (after successful installation) in an R session (R Core Team, 2019). The package
238 comes with the guinea pig dataset that also needs to be loaded using the data function.
239
240 `library(partR2)`

241 `data(GuineaPigs)`

242

243 A single record contains missing values for testosterone measurements. Missing records can be problematic to
244 handle in `partR2` and are better removed prior to the analysis. We also log-transform the response and convert
245 *Time* to a factor and filter for the first three time points to simplify the output.

246
247 `GuineaPigs <- subset(GuineaPigs,`

248 `        !is.na(Testo) & !is.na(Rank) & (Time %in% c(1,3,5)))`

249 `GuineaPigs$TestoTrans <- log(GuineaPigs$Testo)`

250 `GuineaPigs$Time <- factor(GuineaPigs$Time)`

251

252 We then fit a linear mixed effects model using `lmer` from the `lme4` package (Bates et al., 2015). Further exploration
253 of the data and model checks are omitted here for simplicity, but are advisable in real data analysis.
254
255 `library(lme4)`

256 `mod <- lmer(TestoTrans ~ Rank * Time + (1|MaleID), data=GuineaPigs)`

257

258 The `partR2` analysis takes the `lmer` model fit (an `merMod` object) and a character vector `partvars` indicating
259 the fixed effects to be evaluated. Interactions are specified with the colon syntax (see the package's vignette for
260 further details).

261

262 `res <- partR2(mod, partvars = c("Rank", "Time", "Rank:Time"),`

263 `        nboot=100)`

264

265   The function returns a `partR2` object. The `print` function reports the part coefficients of determination and a

266   more extensive summary can be viewed with the `summary` function which also shows inclusive R^2, structure

267   coefficients and beta weights (standardized slopes) (Figure 2).

268
269   `print(res)`

270   `summary(res, round_to = 2)`

271

272

273   **Figure 2:** Summary output for example data analysis with Gaussian data (guinea pig analysis).
274

275

276   The variances appear largely additive, since combinations of predictors explain about the sum of the variance

277   explained by individual predictors. The main components of the `partR2` object can be accessed for further

278   processing as `res$R2` for part R^2 (with point estimates and confidence intervals), `res$SC` for structure

279   coefficients, `res$IR2` for inclusive R^2 and `res$BW` for beta weights.

280

281   **Dealing with interactions**

282   Models with interactions are problematic, because the variance explained by a main factor can be estimated in

283   multiple ways (Figure 3) and because of the internal parametrization of the model matrix.

284

285

286   **Figure 3:** Conceptual framework for dealing with interactions.
287
288
289

290   The model output above shows the number of parameters fitted in each model (Figure 2, each row in the R2 part

291   refers to a reduced model). In the `print` and `summary` output this is visible as a column labelled 'ndf'. A close

292   inspection shows that the removal of rank did not change the number of parameters (6 for the full model, 6 for the

293   model excluding rank). This is because the model matrix is reparametrized in the reduced model and `lmer` will fit

294   three terms for the interaction (here `Time1:Rank`, `Time3:Rank`, `Time5:Rank`) rather than just two for the

295   interaction in the full model. Dummy coding of the factor can be usefully combined with centering of dummy coded

296   variables (Schielzeth, 2010) and gives more control over this re-parametrisation. It allows for example to estimate

297 the part R^2 for the average effect of *Rank* by constraining the average *Rank* effect to zero, so that only the two

298 contrasts are fitted (here `Time3:Rank`, `Time5:Rank`):

299
300
```
GuineaPigs <- cbind(GuineaPigs, model.matrix(~ 0 + Time,
```
301
```
    data=GuineaPigs))
```
302
```
GuineaPigs$Time3 <- GuineaPigs$Time3 - mean(GuineaPigs$Time3)
```
303
```
GuineaPigs$Time5 <- GuineaPigs$Time5 - mean(GuineaPigs$Time5)
```
304

305 The model can then be fitted with dummy predictors. Since the usual specification in `partR2` via `partvars` would

306 fit all possible combinations, including combinations of the different *Time* terms, such a run can take a long time.

307 However we are mostly interested in fitting and removing all dummy predictors at a time. The package therefore

308 features an additional argument `partbatch` to specify a list of character vectors containing the sets of predictors

309 that should always be kept together. In the example, the list has two elements, a character vector for the dummy-

310 coded main effects and a character vector for the interaction terms. The analysis yields part R^2 for two batches of

311 predictors as well as *Rank* and their combinations.

312
313
```
mod <- lmer(TestoTrans ~ (Time3 + Time5) * Rank + (1|MaleID),
```
314
```
    data=GuineaPigs)
```
315
```
batch <- c("Time3", "Time5")
```
316
```
partR2(mod, partvars=c("Rank"), partbatch=list(Time=batch,
```
317
```
    `Time:Rank`= paste0(batch, ":Rank")), nboot=100)
```
318

319 This, however, is only one way of dealing with interactions (Option A in Figure 3). It represents the variance uniquely

320 explained by main effects even in the presence of an interaction. Since interactions are the products of main effects,

321 interaction terms are typically correlated with main effects and the part R^2 calculated above might not represent a

322 biologically relevant quantity. There are two alternative ways of how to deal with interactions. Both are possible in

323 `partR2`, but since requirements differ between applications, we do not implement one with priority.

324 One way to think about variance explained by main effects and their interactions is to pool the variance explained

325 by a main effect with the variance explained by interactions that the term is involved in (Option B in Figure 3). In the

326 guinea pig example, for instance, *Rank* might be considered important either as a main effect or in interaction with

327 time and we might want to estimate the total effect of rank. This can be done for the guinea pig dataset by using

328 `partbatch`:

329

```
330   mod <- lmer(Testo ~ Time * Rank + (1|MaleID), data=GuineaPigs)

331   partR2(mod, partbatch = list(Time=c("Time", "Time:Rank"),

332       Rank=c("Rank", "Time:Rank")), nboot=100)
```

333

334   A third, which we think usually preferable option is to prioritize main effects by assigning the proportion of variance
335   that is explained by a main effect together with the variance jointly explained with its interaction to the main effect
336   (Option C in Figure 3). This implies that part R^2 for a main effect is estimated when its own interaction is excluded
337   from the model (`mod1` and `part1` below). The variance explained by the interaction is then estimated in a
338   separate model (`mod2` and `part2` below). We have implemented a helper function `mergeR2` that allows to merge
339   two `partR2` runs.

340
```
341   mod1 <- lmer(Testo ~ Time * Rank + (1|MaleID), data=GuineaPigs)

342   part1 <- partR2(mod1, partvars = c("Time:Rank"), nboot=100)

343   mod2 <- lmer(Testo ~ Time + Rank + (1|MaleID), data=GuineaPigs)

344   part2 <- partR2(mod2, partvars = c("Time", "Rank"), nboot=100)

345   mergeR2(part1, part2)
```

346

347   All these results can be viewed by `print`, `summary` and plotted by `forestplot`. It is important to bear in mind
348   the differences in the interpretation as illustrated in Figure 3.
349

350   **An example with proportion data**

351   As an example for proportion data, we analyze a dataset on spatial variation in color morph ratios in a color-
352   polymorphic species of grasshopper. Individuals of this species occur either in a green or a brown color variant and
353   the dataset contains counts of brown and green individuals (separated for females and males) from 42 sites sampled
354   in the field (Dieker et al., 2018). Site identity will be fitted as a random effect. As covariates the dataset contains a
355   range of Bioclim variable that describe various aspects of ecologically relevant climatic conditions (Karger et al.,
356   2017). The aim is to identify the climatic conditions that favour one or the other colour variant.

357 We first load the grasshopper dataset. We standardise all Bioclim variables using the `scale` function and add an
358 observation-level counter that will be used as an observation-level random effect (OLRE) to account for
359 overdispersion (Harrison, 2014).
360
361 ```
data(Grasshoppers)
```
362  ```
for (i in which(substr(colnames(Grasshoppers),1,3)=="Bio")){
```
363 ```
    Grasshoppers[,i] <- scale(Grasshoppers[,i])
```
364  ```
}
```
365 ```
Grasshoppers$OLRE <- 1:nrow(Grasshoppers)
```
366
367  We first fit a GLMM with binomial error structure and logit link using the `glmer` function from the `lme4` package
368  (Bates et al., 2015). A previous analysis has shown that the first principle component of the Bioclim data explains a
369  small, but significant part of variation in morph ratios (Dieker et al., 2018). For illustration, we use the four Bioclim
370  variables that show a loading of more than 0.30 on the first principle component.
371
372  ```
mod <- glmer(cbind(nGreen, nBrown) ~ Bio7 + Bio14 + Bio17 + Bio19 +
```
373 ```
    (1|SiteID) + (1|OLRE), data=Grasshoppers, family="binomial")
```
374  ```
res <- partR2(mod, partvars=c("Bio7", "Bio14", "Bio17", "Bio19"),
```
375 ```
    max_level = 1, nboot=100)
```
376
377  The `summary` output informs us (at the bottom) that there have been warnings in the bootstrapping processes.
378  This is not unusual since bootstrapping frequently generates data, for which one of the parameters is estimated at
379  the boundary (in particular if one of the variance components is very small). The results can be visualised using the
380  `forestplot` function (Figure 4). Plotting is based on `ggplot2` (Wickham, 2016), and multiple forest plots can
381  easily be assembled using the `patchwork` package (Pedersen, 2020). Forest plots show the effect sizes
382  graphically and can be set to either show part $R^2$ when `type = "R2"` (the default), inclusive $R^2$ when `type =`
383  `"IR2"`, structure coefficients when `type = "SC"`, and beta weights (standardized model estimates) with `type`
384  `= "BW"`.
385
386  ```
p1 <- forestplot(res, type = "R2")
```
387 ```
p2 <- forestplot(res, type = "IR2")
```

```
388   p3 <- forestplot(res, type = "SC")

389   p4 <- forestplot(res, type = "BW")

390

391   library(patchwork)

392   (p1 + p2) / (p3 + p4) + plot_annotation(tag_levels = "A",   tag_prefix

393   = "(", tag_suffix = ")")

394

395
```

396 **Figure 4:** Comparison of part R^2 for individual predictors (A), inclusive R^2 (B), structure coefficients (C) and beta
397 weights (D) for an example dataset with proportion data from grasshoppers.
398

399

400
401 A comparison of part R^2, inclusive R^2, structure coefficients beta weights shows the different insights that can be

402 gained from these different summaries of the model fit (Figure 3). In this case, three of the Bioclim variables (*Bio14*,

403 *Bio17*, *Bio19*) are highly positively correlated ($r \geq 0.93$), while a fourth one (*Bio7*) is moderately negatively correlated

404 to all three of them ($r \leq -0.63$). Part R^2 are thus low, because none of the parameters uniquely explains a large share

405 of the variance. *Bio17* seems to be the best predictor of morph ratios, with the largest (negative) beta weight, largest

406 part R^2, largest structure coefficients and largest inclusive R^2. Beta weights for the two positively correlated (but

407 slightly weaker) predictors, *Bio14* and *Bio19*, switch sign as is not unusual for collinear predictors. This means that

408 after accounting for the effect of *Bio17*, they contribute positively to prediction. However, structure coefficients

409 show that both variables load negatively on the linear predictor, as does *Bio17*.

410

411 **Challenges**

412 Using transformation or functions in the formula argument can lead to issues with matching the terms of the model

413 with the `partvars` argument of `partR2`. It is therefore important that the names in `partvars` match exactly

414 the terms in the `merMod` object. However, any complications are easily circumvented by implementing the

415 transformations before fitting the model and storing them in the data frame used in the analysis. It is also worth to

416 be aware that unusual names may cause complications and renaming can offer an easy solution.

417 We have repeatedly seen model outputs where the point estimate does not fall within the confidence interval. This

418 might seem like in the bug in the package, but in our experience usually indicates issues with the data and/or the

419   model. In fact, parametric bootstrapping can be seen as a limited form of posterior predictive model checks

420   (Gelman & Hill, 2006). If generating new data from the fitted model (as done with parametric bootstrapping) results

421   in data that are dissimilar to the original data, then the model is probably not a good fit to the data.

422   Bootstrap iterations can sometimes yield slightly negative estimates of part R^2, in particular if the variance

423   explained by a predictor is low. These negative estimates happen in mixed-effects models, because estimates of

424   random-effect variance might change when a predictor is removed and this can lead to a slight decrease in the

425   residual variance, and hence a proportional increase in R^2 (see also Rights & Sterba, 2019). By default, partR2 sets

426   negative R^2 values to 0, but this can be changed by setting `allow_neg_r2` to `TRUE`. It also happens that inclusive

427   R^2 is estimated slightly lower than part R^2 when the contribution of a particular predictor is very large. We consider

428   both cases as sampling error that should serve as a reminder that variance components are estimated with relatively

429   large uncertainly and minor differences should not be over-interpreted.

430   A warning needs to be added for the estimation of R^2 (and, in fact, also repeatability R) from small datasets. In

431   particular if the number of levels of random effect is low, variance components might be slightly overestimated (Xu,

432   2003). This issue applies similarly to the variance explained by fixed effects, in particular if the number of predictors

433   is large relative to the number of data points.

434

435   **Code and data availability**

436   The current stable version of `partR2` can be downloaded from CRAN ([https://cran.r-](https://cran.r-project.org/web/packages/partR2/index.html)

437   [project.org/web/packages/partR2/index.html](https://cran.r-project.org/web/packages/partR2/index.html)) and the development version can be obtained from GitHub

438   (https://github.com/mastoffel/partR2). The data used in the examples is part of the package.

439

440

441   **Acknowledgements**

442   We thank Alexandra Mutwill for providing the guinea pig data.

443

444   **References**

445   Aho K. 2020.asbio: A Collection of Statistical Tools for Biologists. *Available at https://CRAN.R-*

446   *project.org/package=asbio* (accessed July 25, 2020).

447   Bartoń K. 2019.MuMIn: Multi-Model Inference. *Available at https://CRAN.R-project.org/package=MuMIn* (accessed

448   July 25, 2020).

449   Bates D, Mächler M, Bolker B, Walker S. 2015. Fitting linear mixed-effects models using lme4. *Journal of Statistical*

450   *Software* 67. DOI: 10.18637/jss.v067.i01.

451   Bengtsson H. 2020.future: Unified Parallel and Distributed Processing in R for Everyone. *Available at*

452   *https://CRAN.R-project.org/package=future* (accessed July 25, 2020).

453   Dieker P, Beckmann L, Teckentrup J, Schielzeth H. 2018. Spatial analyses of two colour polymorphisms in an

454   alpine grasshopper reveal a role of small-scale heterogeneity. *Ecology and Evolution* 8:7273–7284. DOI:

455   10.1002/ece3.4156.

456   Edwards LJ, Muller KE, Wolfinger RD, Qaqish BF, Schabenberger O. 2008. An R2 statistic for fixed effects in the

457   linear mixed model. *Statistics in Medicine* 27:6137–6157. DOI: 10.1002/Sim.3429.

458   Faraway JJ. 2015. *Linear models with R*. Boca Raton: CRC Press, Taylor & Francis Group.

459   Gelman A, Hill J. 2006. *Data analysis using regression and multilevel/hierarchical models*. Cambridge university

460   press.

461   Harrison XA. 2014. Using observation-level random effects to model overdispersion in count data in ecology and

462   evolution. *PeerJ* 2:e616. DOI: 10.7717/peerj.616.

463   Ives A, Li D. 2018. rr2: An R package to calculate R2s for regression models. *Journal of Open Source Software*

464   3:1028.

465   Jaeger B. 2017.r2glmm: Computes R Squared for Mixed (Multilevel) Models. *Available at https://CRAN.R-*

466   *project.org/package=r2glmm* (accessed July 25, 2020).

467   Jaeger BC, Edwards LJ, Das K, Sen PK. 2017. An R2 statistic for fixed effects in the generalized linear mixed model.

468   *Journal of Applied Statistics* 44:1086–1105. DOI: 10.1080/02664763.2016.1193725.

469   Jaeger BC, Edwards LJ, Gurka MJ. 2019. An R 2 statistic for covariance model selection in the linear mixed model.

470   *Journal of Applied Statistics* 46:164–184.

471   Johnson PE, Grothendieck G. 2019.rockchalk: Regression Estimation and Presentation. *Available at*

472   *https://CRAN.R-project.org/package=rockchalk* (accessed July 25, 2020).

473   Karger DN, Conrad O, Böhner J, Kawohl T, Kreft H, Soria-Auza RW, Zimmermann NE, Linder HP, Kessler M. 2017.

474   Climatologies at high resolution for the earth's land surface areas. *Scientific data* 4:170122.

475   Kim S. 2015. ppcor: an R package for a fast calculation to semi-partial correlation coefficients. *Communications for*

476   *statistical applications and methods* 22:665.

477   Lüdecke D, Makowski D, Waggoner P, Patil I. 2020.performance: Assessment of Regression Models Performance.

478   *Available at https://CRAN.R-project.org/package=performance* (accessed July 25, 2020).

479   Mutwill AM, Schielzeth H, Zimmermann TD, Richter H, Kaiser S, Sachser N. in prep. Endocrine mechanisms

480   underlying dominance rank acquisition in males: individuality meets plasticity in a complex social

481   environment.

482   Nakagawa S, Johnson PCD, Schielzeth H. 2017. The coefficient of determination R^2 and intra-class correlation

483   coefficient from generalized linear mixed-effects models revised and expanded. *Journal of the Royal*

484   *Society Interface* 14:20170213. DOI: 10.1098/rsif.2017.0213.

485   Nakagawa S, Schielzeth H. 2010. Repeatability for Gaussian and non-Gaussian data: a practical guide for

486   biologists. *Biological Reviews* 85:935–956.

487   Nakagawa S, Schielzeth H. 2013. A general and simple method for obtaining R^2 from generalized linear mixed-

488   effects models. *Methods in Ecology and Evolution* 4:133–142.

489   Nathans LL, Oswald FL, Nimon K. 2012. Interpreting multiple linear regression: A guidebook of variable

490   importance. *Practical Assessment, Research, and Evaluation* 17:9.

491   Nimon K, Lewis M, Kane R, Haynes RM. 2008. An R package to compute commonality coefficients in the multiple

492   regression case: an introduction to the package and a practical example. *Behavior Research Methods*

493   40:457–66. DOI: 10.3758/brm.40.2.457.

494   Nimon K, Oswald F, Roberts JK. 2020.yhat: Interpreting Regression Effects. *Available at https://CRAN.R-*

495   *project.org/package=yhat* (accessed July 25, 2020).

496   Pedersen TL. 2020.patchwork: The Composer of Plots. *Available at https://CRAN.R-*

497   *project.org/package=patchwork* (accessed July 25, 2020).

498   Piepho H-P. 2019. A coefficient of determination (R^2) for generalized linear mixed models. *Biometrical Journal*

499   61:860–872.

500   R Core Team. 2019. *R: A language and environment for statistical computing. R Foundation for Statistical*

501   *Computing*. Vienna, Austria.

502 Ray Mukherjee J, Nimon K, Mukherjee S, Morris DW, Slotow R, Hamer M. 2014. Using commonality analysis in

503   multiple regressions: a tool to decompose regression effects in the face of multicollinearity. *Methods in*

504   *Ecology and Evolution* 5:320–328. DOI: 10.1111/2041-210X.12166.

505 Rights JD, Sterba SK. 2019. New recommendations on the Use of R-squared differences in multilevel model

506   comparisons. *Multivariate Behavioral Research*:1–32. DOI: 10.1080/00273171.2019.1660605.

507 Schielzeth H. 2010. Simple means to improve the interpretability of regression coefficients. *Methods in Ecology*

508   *and Evolution*.

509 Seibold DR, McPhee RD. 1979. Commonality analysis: a method for decomposing explained variance in multiple

510   regression analyses. *Human Communication Research* 5:355–365.

511 Stoffel MA, Nakagawa S, Schielzeth H. 2017. rptR: repeatability estimation and variance decomposition by

512   generalized linear mixed-effects models. *Methods in Ecology and Evolution* 8:1639–1644. DOI:

513   10.1111/2041-210X.12797.

514 Vaughan D, Dancho M. 2018.furrr: Apply Mapping Functions in Parallel using Futures. *Available at https://CRAN.R-*

515   *project.org/package=furrr* (accessed July 25, 2020).

516 de Villemereuil P, Morrissey M, Nakagawa S, Schielzeth H. 2018. Fixed effect variance and the estimation of

517   repeatabilities and heritabilities: Issues and solutions. *Journal of Evolutionary Biology* 31:621–632. DOI:

518   10.1111/jeb.13232.

519 Watanabe S. 1960. Information theoretical analysis of multivariate correlation. *IBM Journal of Research and*

520   *Development* 4:66–82. DOI: DOI 10.1147/rd.41.0066.

521 Xu RH. 2003. Measuring explained variation in linear mixed effects models. *Statistics in Medicine* 22:3527–3541.

522   DOI: Doi 10.1002/Sim.1572.

523 Yeatts PE, Barton M, Henson RK, Martin SB. 2017. The use of structure coefficients to address multicollinearity in

524   sport and exercise science. *Measurement in Physical Education and Exercise Science* 21:83–91.

525 Zhang D. 2020.rsq: R-Squared and Related Measures. *Available at https://CRAN.R-project.org/package=rsq*

526   (accessed July 25, 2020).

527 Zientek LR, Thompson B. 2006. Commonality analysis: Partitioning variance to facilitate better understanding of

528   data. *Journal of Early Intervention* 28:299–307.

529

Figure 1

Conceptual framework for the estimation of proportions of variance components in a mixed model.

The large grey circle symbolizes the variance in a response Y, the dark grey area on the top indicates the share explained by random effects and the coloured ellipses symbolize variance in covariates with intersections indicating jointly explained variances. partR2 calculates total R^2, part R^2 for individual predictors and sets of predictors as well as inclusive R^2. The package does not report partial R^2 and commonalities, although they could be calculated from the partR2 output.

Total variance in Y
$Y_{Total} = Y_{x1} + Y_{x2} + Y_{x3} + Y_{x1,x2} + Y_{x1,x3} + Y_{x1,x2,x3} + Y_{RE} + Y_R$

Random components (incl. repeatability)
Random effects: Y_{RE} / Y_{Total}
Residual: Y_R / Y_{Total}

Total R²
$Y_{R}^2 = (Y_{x1} + Y_{x2} + Y_{x3} + Y_{x1,x2} + Y_{x1,x3} + Y_{x2,x3} + Y_{x1,x2,x3}) / Y_{Total}$

Part R² for individual predictors
X_1: Y_{x1} / Y_{Total}
X_2: Y_{x2} / Y_{Total}
X_3: Y_{x3} / Y_{Total}

Part R² for sets of predictors
$X_1 + X_2$: $(Y_{x1} + Y_{x2} + Y_{x1, x2}) / Y_{Total}$
$X_1 + X_3$: $(Y_{x1} + Y_{x3} + Y_{x1, x3}) / Y_{Total}$
$X_2 + X_3$: $(Y_{x2} + Y_{x3} + Y_{x2, x3}) / Y_{Total}$
$X_1 + X_2 + X_3$: $(Y_{x1} + Y_{x2} + Y_{x3} + Y_{x1,x2} + Y_{x1,x3} + Y_{x2,x3} + Y_{x1,x2,x3}) / Y_{Total}$

Inclusive R² for individual predictors
X_1: $(Y_{x1} + Y_{x1,x2} + Y_{x1,x3} + Y_{x1,x2,x3}) / Y_{Total}$
X_2: $(Y_{x2} + Y_{x1,x2} + Y_{x2,x3} + Y_{x1,x2,x3}) / Y_{Total}$
X_3: $(Y_{x3} + Y_{x1,x3} + Y_{x2,x3} + Y_{x1,x2,x3}) / Y_{Total}$

Partial R² for individual predictors
X_1: $Y_{x1} / (Y_{Total} - Y_{x2} - Y_{x3} - Y_{x1,x2} - Y_{x1,x3} - Y_{x2,x3} - Y_{x1,x2,x3})$
X_2: $Y_{x2} / (Y_{Total} - Y_{x1} - Y_{x3} - Y_{x1,x2} - Y_{x1,x3} - Y_{x2,x3} - Y_{x1,x2,x3})$
X_3: $Y_{x3} / (Y_{Total} - Y_{x1} - Y_{x3} - Y_{x1,x2} - Y_{x1,x3} - Y_{x2,x3} - Y_{x1,x2,x3})$

Commonalities
$X_{x1, x2}$: $Y_{x1, x2} / Y_{Total}$
$X_{x1, x3}$: $Y_{x1, x3} / Y_{Total}$
$X_{x2, x3}$: $Y_{x2, x3} / Y_{Total}$
$X_{x1, x2, x3}$: $Y_{x1, x2, x3} / Y_{Total}$

Figure 2

Summary output for example data analysis with Gaussian data (guinea pig analysis).

```
R2 (marginal) and 95% CI for the full model:
 R2   CI_lower CI_upper ndf
 0.17 0.09     0.36      6

__________

Part (semi-partial) R2:
 Predictor(s)         R2    CI_lower CI_upper ndf
 Model                0.17 0.09      0.36      6
 Rank                 0.00 0.00      0.18      6
 Time                 0.02 0.00      0.20      4
 Rank:Time            0.04 0.00      0.21      4
 Rank+Time            0.02 0.00      0.20      4
 Rank+Rank:Time       0.16 0.08      0.34      3
 Time+Rank:Time       0.04 0.00      0.22      2
 Rank+Time+Rank:Time  0.17 0.09      0.36      1

__________

Inclusive R2 (SC^2 * R2):
 Predictor  IR2  CI_lower CI_upper
 Rank       0.13 0.03     0.26
 Time3      0.00 0.00     0.04
 Time5      0.00 0.00     0.04
 Rank:Time3 0.05 0.01     0.13
 Rank:Time5 0.01 0.00     0.07

__________

Structure coefficients r(Yhat,x):
 Predictor  SC    CI_lower CI_upper
 Rank       0.87  0.56     0.94
 Time3      0.14 -0.18     0.43
 Time5      0.16 -0.26     0.48
 Rank:Time3 0.56  0.22     0.75
 Rank:Time5 0.28 -0.14     0.57

__________

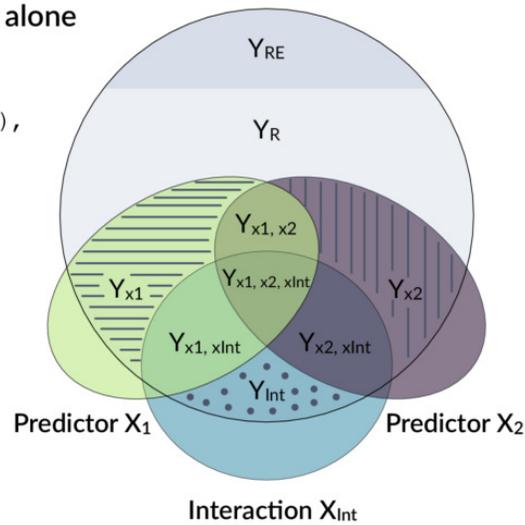
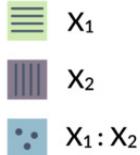
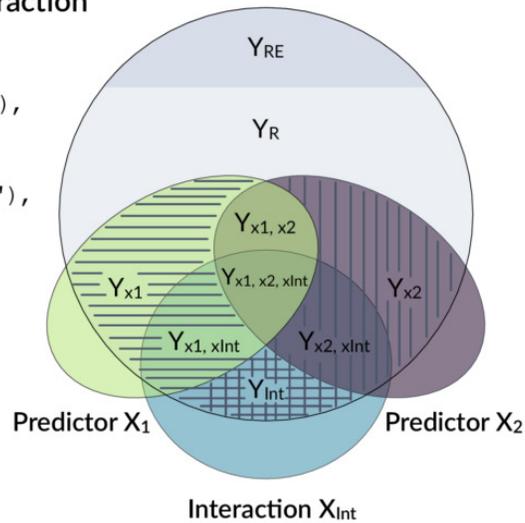
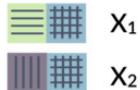
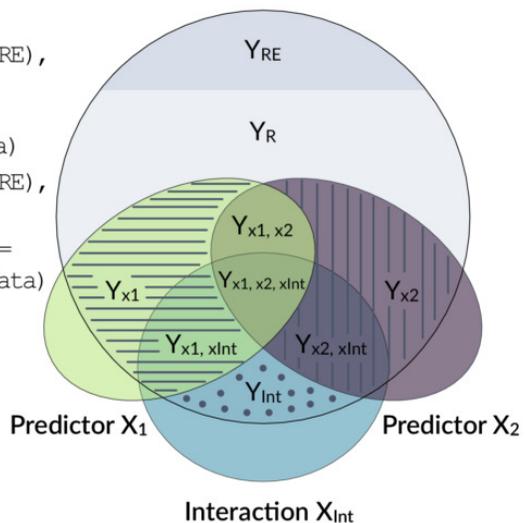
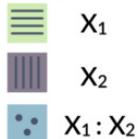
Beta weights (standardised estimates)
 Predictor  BW    CI_lower CI_upper
 Rank        0.50 -0.08    0.94
 Time3      -0.19 -0.53    0.14
 Time5       0.17 -0.20    0.55
 Rank:Time3  0.17 -0.36    0.83
 Rank:Time5 -0.36 -0.95    0.38

__________
```

Figure 3

Conceptual framework for dealing with interactions.

An interaction is the product of two main effects and thus often correlated with each of the

main effects. The figure shows three options for estimating the part R^2 for main effects that

are involved in an interaction.

(A) Main effect and interaction alone

Generic syntax

```
mod <- lmer(Y ~ X1 * X2 + (1|RE),
       data)
partR2(mod, partvars = c('X1',
     'X2', 'X1:X2'), data)
```

Components estimated

X₁

X₂

X₁ : X₂

(B) Main effects with their interaction

Generic syntax

```
mod <- lmer(Y ~ X1 * X2 + (1|RE),
       data)
partR2(mod, partbatch =
     list(X1 = c('X1', 'X1:X2'),
     X2 = c('X2', 'X1:X2')),
     data)
```

Components estimated

X₁

X₂

(C) Main effect priority

Generic syntax

```
mod1  <- lmer(Y ~ X1 * X2 + (1|RE),
         data)
part1 <- partR2(mod, partvars =
           c('X1:X2'), data)
mod2  <- lmer(Y ~ X1 + X2 + (1|RE),
         data)
part2 <- partR2(mod2, partvars =
           c('X1','X2'), data)
mergeR2(part1, part2)
```

Components estimated

X₁

X₂

X₁ : X₂

Figure 4

Comparison of part R^2 for individual predictors (A), inclusive R^2 (B), structure coefficients (C) and beta weights (D) for an example dataset with proportion data from grasshoppers.