

1 **partR2: Partitioning R^2 in generalized linear mixed models**

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29 **Abstract**

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

48 Introduction

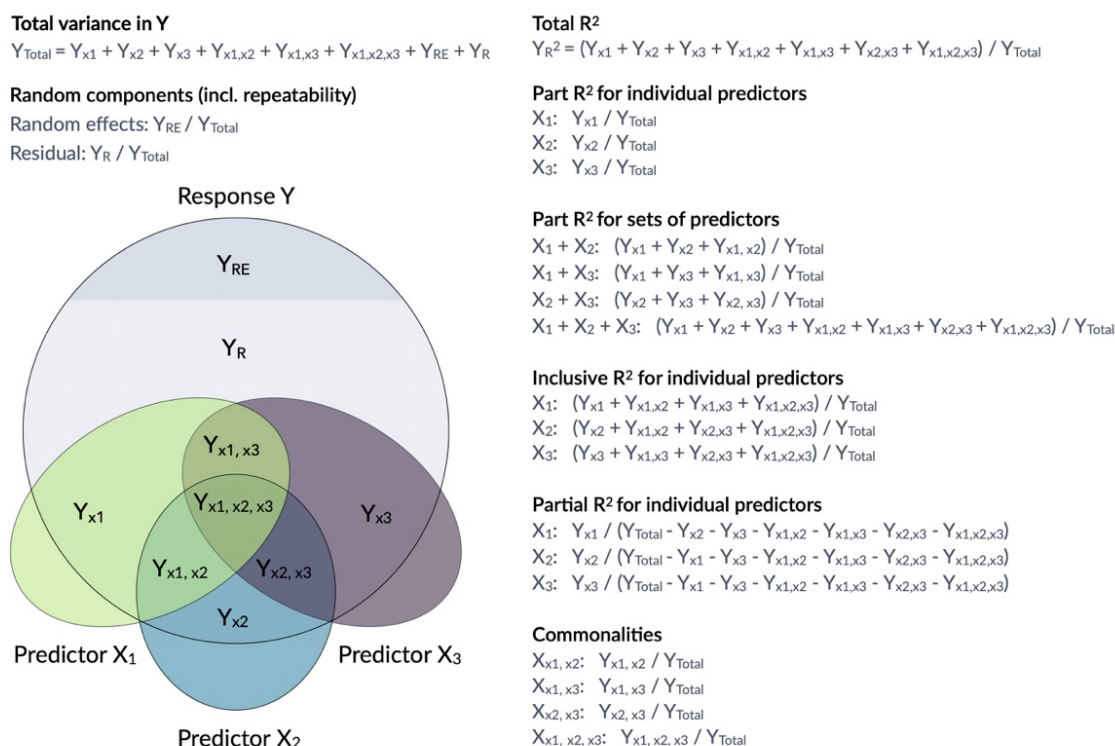
49 Coefficients of determination R^2 are of interest in the study of ecology and evolution, because they
50 quantify the amount of variation explained by a linear model (Edwards et al., 2008). By doing so, they
51 go beyond significance testing in putting effects in perspective of the phenotypic variance. R^2 is
52 expressed as a proportion of the total variance in the response, which represents a biologically
53 relevant quantity if the total variation is representative for the total population (de Villemereuil et al.,
54 2018). The total coefficient of determination quantifies the variance explained by all fixed effects
55 together (marginal R^2 *sensu* Nakagawa & Schielzeth (2013), also known as the total correlation
56 coefficient, Watanabe (1960)).

57
58 However, it is often of interest to attribute explained variation to individual predictors. Semi-partial
59 coefficients of determination, also known as part R^2 , decompose the variance of R^2 into components
60 uniquely explained by individual predictors (Jaeger et al., 2017) or sets of predictors (Figure 1). The
61 set of all predictors in the model yields the total proportion of variance explained by the fixed part
62 of the model (total R^2). With correlations among predictors, it often happens that predictors in
63 univariate regressions explain a large share of the variance, but do not show large part R^2 if other
64 correlated predictors are included in the model.

65
66 Structure coefficients provide a valuable addition to part R^2 in the decomposition of the phenotypic
67 variance (Nimon et al., 2008). Structure coefficients quantify the correlation between individual
68 predictors and the linear predictor ($\boldsymbol{\eta} = \mathbf{X}\boldsymbol{\beta}$, where \mathbf{X} is the design matrix for fixed effects and $\boldsymbol{\beta}$
69 is a vector of regression coefficients). Predictors that correlate well with a response, but are fitted
70 with collinear predictors may show large structure coefficients as they are correlated to the predicted
71 response, but low part R^2 as other predictors explain part of the same variance. Structure coefficients
72 range from -1 to 1 with their absolute value expressing the correlation relative to a perfect correlation
73 if a single predictor explains as much as the total fixed part of the model.

74
75 Structure coefficients are correlations and since the square of a correlation yields the variance
76 explained, we can use structure coefficients to estimate the total variance explained by a predictor
77 (Nimon et al., 2008). We call this the inclusive R^2 of a predictor and calculate it as the squared
78 structure coefficient, i.e. its contribution to the linear predictor independent of other predictors
79 (Nimon et al., 2008) times the proportion of variance explained by the linear predictor (which is the

80 'total' marginal R^2 of the model). As far as we are aware, inclusive R^2 has not been implemented
 81 before, but it provides valuable insights into the structure of the variance explained (Figure 1).
 82



83
 84 **Figure 1: Conceptual framework for the estimation of proportions of variance components in a mixed**
 85 **model.** The large grey circle symbolizes the variance in a response Y, the dark grey area on the top indicates
 86 the share explained by random effects and the coloured ellipses symbolize variance in covariates with
 87 intersections indicating jointly explained variances. `partR2` calculates total R^2 , part R^2 for individual predictors
 88 and sets of predictors as well as inclusive R^2 . The package does not report partial R^2 and commonalities,
 89 although they could be calculated from the `partR2` output.
 90

91 Here, we introduce `partR2`, a versatile package for estimating part R^2 , inclusive R^2 , structure
 92 coefficients and beta weights from mixed-effects models. The analysis is similar to, but not identical,
 93 to commonality analysis (Ray-Mukherjee et al., 2014; Seibold & McPhee, 1979; Zientek & Thompson,
 94 2006, Figure 1). We illustrate how to use `partR2` with real example datasets for Gaussian and
 95 binomial GLMMs, discuss how to estimate part R^2 in the presence of interactions and discuss some
 96 challenges and limitations.
 97

98 Other implementations in R packages

99 There are a few R packages that calculate part R^2 for linear models (`lm`), for example
 100 `rockchalk::getDeltaRsquare` (Johnson & Grothendieck, 2019). Other packages calculate

101 partial R^2 (not part R^2) such as `asbio::partial.R2` (Aho, 2020) and `rr2::R2` (Ives & Li, 2018) for
102 `lms` and `rsq::rsq.partial` (Zhang, 2020) for linear models and generalized linear models (glm).
103 Note that partial R^2 is different from part (semi-partial) R^2 (partial $R^2 >$ part R^2), since it represents the
104 unique variance explained by a particular predictor but after removing ('partialling out') the variance
105 explained by the other predictors (Yeatts et al., 2017, Figure 1). The package `yhat` features a suite
106 of functions for full communality analyses in glms (Nimon, Oswald & Roberts, 2020). None of these
107 packages estimates part R^2 for mixed-effects models that we focus on here.
108 Several packages estimate (marginal) R^2 as the variance explained by all fixed effects in linear mixed-
109 effects models. This includes `performance::r2_nakagawa` (Lüdtke et al., 2020),
110 `MuMIn::r.squaredGLMM` (Bartoń, 2019), and `rptR::rpt` (Stoffel, Nakagawa & Schielzeth, 2017).
111 These packages do not allow to estimate part R^2 . The only versatile package to estimate part R^2 from
112 linear mixed-models is `r2glmm` (Jaeger, 2017). The function `r2glmm::r2beta` computes part R^2
113 from `lmer`, `lme` and `glmmPQL` model fits (also for linear models `lm` and `glm`) based on Wald statistics.
114 However, it does neither support `lme4::glmer` for generalized linear model fits nor does it allow
115 to estimate R^2 for combinations of predictors. Furthermore, it does not estimate structure
116 coefficients, inclusive R^2 or part R^2 for multilevel factors as a unit.

117

118 **Features of `partR2`**

119 `partR2` takes a fitted (generalized) linear mixed-model (GLMM), from the popular mixed model
120 package `lme4` (Bates et al., 2015) and estimates part R^2 by iterative removal of fixed effects (Nimon
121 et al., 2008). The specific fixed effects of interest are specified by the `partvars` and/or by the
122 `partbatch` argument. The package estimates part R^2 for all predictors specified in `partvars`
123 individually and in all possible combinations (the maximum level of combinations can be set by the
124 `max_level` argument). A custom specification of fixed effects of interest saves computation time as
125 compared to an all-subset specification and is therefore required in `partR2`.

126 The central function `partR2` will work for Gaussian, Poisson and binomial GLMMs. Since the model
127 fit is done externally, there is no need to supply a family argument. For non-Gaussian GLMMs, the
128 package estimates link-scale R^2 (*sensu* Nakagawa & Schielzeth, 2013). We implement parametric
129 bootstrapping to quantify sampling variance and thus uncertainty in the estimates. Parametric
130 bootstrapping works through repeated model fitting on simulated data based on fitted values
131 (Faraway, 2015). The number of bootstrap iterations is controlled by the `nboot` argument. We
132 recommend a low number of `nboot` for testing purposes and a large number (e.g. `nboot = 1000`)
133 for the final analysis.

134 The package returns an object of class `partR2` that contains elements for part R^2 , inclusive R^2 ,
135 structure coefficients, beta weights (standardized regression slopes), bootstrapping iterations and
136 some other information. An extended summary, that includes inclusive R^2 , structure coefficients and
137 beta weights can be viewed using the `summary` function. The `forestplot` function shows a
138 graphical representation of the variance explained by individual predictors and sets of predictors
139 along with their bootstrapping uncertainties. All computations can be parallelized across many cores
140 based on the `future` and `furrr` packages (Vaughan & Dancho, 2018; Bengtsson, 2020). An
141 extended vignette with details on the complete functionality accompanies the package.

142

143 **Example with Gaussian data**

144 We use an example dataset with hormone data collected from a population of captive guinea pigs
145 to illustrate the features of `partR2`. The dataset contains testosterone measurements of 31 male
146 guinea pigs, each measured at 5 time points (age between 120 and 240 days at 30-day intervals).
147 We analyze log-transformed testosterone titers and fit male identity as a random effect. As covariates
148 the dataset contains the time point of measurement and a rank index derived from behavioral
149 observations around the time of measurement (Mutwill et al., in prep.).

150 *Rank* and *Time* are correlated in the dataset ($r = 0.40$), since young individuals are typically low rank,
151 while older individuals tend to hold a high rank. *Time* might be fitted as a continuous predictor or as
152 a factor with five levels. Here we present the version of a factorial predictor to illustrate the estimation
153 of part R^2 for interactions terms. Hence, an interaction between time and rank will also be fitted.

154 First, the package needs to be loaded (after successful installation) in an R session (R Core Team,
155 2019). The package comes with the guinea pig dataset that also needs to be loaded using the `data`
156 function.

157

```
158 library(partR2)
```

```
159 data(GuineaPigs)
```

160

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

165

```
166 GuineaPigs <- subset(GuineaPigs,
```

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

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

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

```
170
```

171 We then fit a linear mixed effects model using `lmer` from the `lme4` package (Bates et al., 2015).

172 Further exploration of the data and model checks are omitted here for simplicity, but are advisable
173 in real data analysis.

```
174
```

```
175 library(lme4)
```

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

```
177
```

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

```
181
```

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

```
183         data=GuineaPigs, nboot=100)
```

```
184
```

185 The function returns a `partR2` object. The `print` function reports the part coefficients of
186 determination and a more extensive summary can be viewed with the `summary` function which also
187 shows inclusive R^2 , structure coefficients and beta weights (standardized slopes) (Figure 2).

```
188
```

```
189 print(res)
```

```
190 summary(res, round_to = 2)
```

```
R2 (marginal) and 95% CI for the full model:
R2   CI_lower CI_upper nboot ndf
0.17 0.1      0.31    100  6

-----

Part (semi-partial) R2:
Predictor(s)      R2   CI_lower CI_upper nboot ndf
Model             0.17 0.10    0.31    100  6
Rank              0.00 0.00    0.14    100  6
Time              0.02 0.00    0.16    100  4
Rank:Time         0.03 0.00    0.17    100  4
Rank+Time         0.02 0.00    0.16    100  4
Rank+Rank:Time    0.15 0.08    0.29    100  3
Time+Rank:Time    0.04 0.00    0.17    100  2
Rank+Time+Rank:Time 0.17 0.10    0.31    100  1

-----

Inclusive R2 (SC^2 * R2):
Predictor IR2   CI_lower CI_upper
Rank      0.13 0.06    0.22
Time3     0.00 0.00    0.04
Time5     0.00 0.00    0.05
Rank:Time3 0.05 0.01    0.14
Rank:Time5 0.01 0.00    0.07

-----

Structure coefficients r(Yhat,x):
Predictor SC   CI_lower CI_upper
Rank      0.87 0.61    0.97
Time3     0.14 -0.20   0.46
Time5     0.16 -0.13   0.55
Rank:Time3 0.56 0.21    0.78
Rank:Time5 0.28 -0.03   0.64

-----

Beta weights (standardised estimates)
Predictor BW   CI_lower CI_upper
Rank      0.50 0.08    0.98
Time3     -0.19 -0.55   0.17
Time5     0.17 -0.14   0.55
Rank:Time3 0.17 -0.48   0.75
Rank:Time5 -0.36 -1.00   0.24

-----
```

```
Parametric bootstrapping resulted in warnings or messages:
Check r2obj$boot_warnings and r2obj$boot_messages.
```

191

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

193

194 The variances appear largely additive, since combinations of predictors explain about the sum of the
195 variance explained by individual predictors. The main components of the `partR2` object can be
196 accessed for further processing as `res$R2` for part R^2 (with point estimates and confidence intervals),
197 `res$SC` for structure coefficients, `res$IR2` for inclusive R^2 and `res$BW` for beta weights.

198

199 Dealing with interactions

200 Models with interaction are problematic, because the variance explained by a main factor can be
201 estimated in multiple ways (Figure 3) and because of internal parametrization of the model matrix.




202

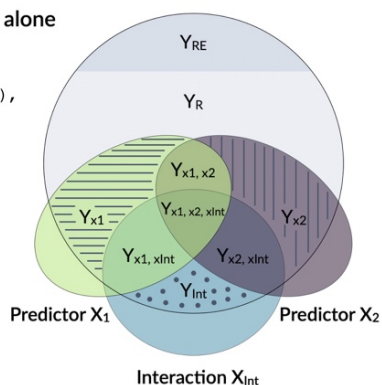
(A) Main effect and interaction alone

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



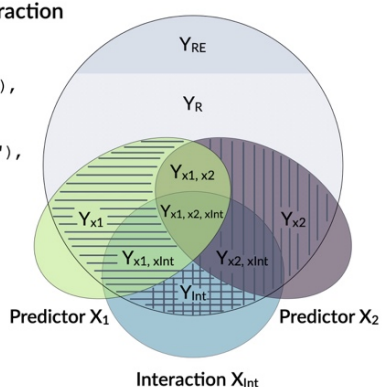
(B) Main effects with their interaction

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






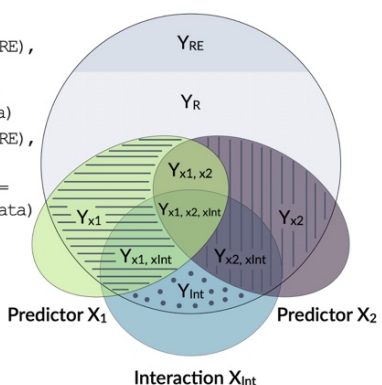
(C) Main effect priority

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



203

204 **Figure 3:** Conceptual framework for dealing with interactions. An interaction is the product of two main
 205 effects and thus often correlated with each of the main effects. The figure shows three options for estimating
 206 the part R^2 for main effects that are involved in an interaction.

207

208 The model output above shows the number of parameters fitted in each model (Figure 2, each row
 209 in the R^2 part refers to a reduced model). In the `print` and `summary` output this is visible as a column

210 labelled 'ndf'. A close inspection shows that the removal of rank did not change the number of
 211 parameters (6 for the full model, 6 for the model excluding rank). This is because the model matrix

212 is reparametrized in the reduced model and `lmer` will fit three terms for the interaction (here
 213 `Time1:Rank`, `Time3:Rank`, `Time5:Rank`) rather than just two for the interaction in the full model.

214 Dummy coding of the factor can be usefully combined with centering of dummy coded variables

215 (Schielzeth, 2010) and gives more control over this re-parametrisation. It allows for example to
216 estimate the part R^2 for the average effect of *Rank* by constraining the average *Rank* effect to zero,
217 so that only the two contrasts are fitted (here `Time3:Rank`, `Time5:Rank`):

```
218  
219 GuineaPigs <- cbind(GuineaPigs, model.matrix(~ 0 + Time,  
220           data=GuineaPigs))  
221 GuineaPigs$Time3 <- GuineaPigs$Time3 - mean(GuineaPigs$Time3)  
222 GuineaPigs$Time5 <- GuineaPigs$Time5 - mean(GuineaPigs$Time5)
```

223
224 The model can then be fitted with dummy predictors. Since the usual specification in `partR2` via
225 `partvars` would fit all possible combinations, including combinations of the different *Time* terms,
226 such a run can take a long time, while we are mostly interested in fitting and removing all dummy
227 predictors at a time. The package therefore features an additional argument `partbatch` to specify
228 a list of character vectors containing the sets of predictors that should always be kept together. In
229 the example, the list has two elements, a character vector for the dummy-coded main effects and a
230 character vector for the interaction terms. The analysis yields part R^2 for two batches of predictors as
231 well as *Rank* and their combinations.

```
232  
233 mod <- lmer(TestoTrans ~ (Time3 + Time5) * Rank + (1|MaleID),  
234           data=GuineaPigs)  
235 batch <- c("Time3", "Time5")  
236 partR2(mod, partvars=c("Rank"), partbatch=list(Time=batch,  
237           `Time:Rank`= paste0(batch, ":Rank")), data=GuineaPigs,  
238           nboot=100)
```

239
240 This, however, is only one way of dealing with interactions (Option A in Figure 3). It represents the
241 variance explained uniquely by main effects even in the presence of an interaction. Since interactions
242 are the products of main effects, interaction terms are typically correlated with main effects and the
243 part R^2 calculated above might not represent a biologically relevant quantity. There are two
244 alternative ways of how to deal with interactions. Both are possible in `partR2`, but since
245 requirements differ between applications, we do not implement one with priority.

246 One way to think about variance explained by main effects and their interactions is to pool the
247 variance explained by a main effect with the variance explained by interactions that the term is

248 involved in (Option B in Figure 3). In the guinea pig example, for instance, *Rank* might be considered
249 important either as a main effect or in interaction with time and we might want to estimate the total
250 effect of rank. This can be done for the guinea pig dataset by using `partbatch`:

```
251  
252 mod <- lmer(Testo ~ Time * Rank + (1|MaleID), data=GuineaPigs)  
253     partR2(mod, partbatch = list(Time=c("Time", "Time:Rank"),  
254     Rank=c("Rank", "Time:Rank")), data=GuineaPigs, nboot=100)
```

255

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

```
262  
263 mod1 <- lmer(Testo ~ Time * Rank + (1|MaleID), data=GuineaPigs)  
264 part1 <- partR2(mod1, partvars = c("Time:Rank"), data=GuineaPigs,  
265     nboot=100)  
266 mod2 <- lmer(Testo ~ Time + Rank + (1|MaleID), data=GuineaPigs)  
267 part2 <- partR2(mod2, partvars = c("Time", "Rank"), data=GuineaPigs,  
268     nboot=100)  
269 mergeR2(part1, part2)
```

270

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

273

274 **An example with proportion data**

275 As an example for proportion data, we analyze a dataset on spatial variation in color morph ratios in
276 a color-polymorphic species of grasshopper. Individuals of this species occur either in a green or a
277 brown color variant and the dataset contains counts of brown and green individuals (separated for
278 females and males) from 42 sites sampled in the field (Dieker et al., 2018). Site identity will be fitted
279 as a random effect. As covariates the dataset contains a range of Bioclim variable that describe

280 various aspects of ecologically relevant climatic conditions (see Karger *et al.* 2017). The aim is to
281 identify the climatic conditions that favour one or the other colour variant.

282 We first load the grasshopper dataset. We standardise all Bioclim variables using the `scale` function
283 and add an observation-level counter that will be used as an observation-level random effect (OLRE)
284 to account for overdispersion (Harrison, 2014).

```
285  
286 data(Grasshoppers)  
287 for (i in which(substr(colnames(Grasshoppers),1,3)=="Bio")) {  
288     Grasshoppers[,i] <- scale(Grasshoppers[,i])  
289 }  
290 Grasshoppers$OLRE <- 1:nrow(Grasshoppers)
```

291
292 We first fit a GLMM with binomial error structure and logit link using the `glmer` function from the
293 `lme4` package (Bates *et al.*, 2015). A previous analysis has shown that the first principle component
294 of the Bioclim data explains a small, but significant part of variation in morph ratios (Dieker *et al.*,
295 2018). For illustration, we use the four Bioclim variables that show a loading of more than 0.30 on
296 the first principle component.

```
297  
298 mod <- glmer(cbind(nGreen, nBrown) ~ Bio7 + Bio14 + Bio17 + Bio19 +  
299     (1|SiteID) + (1|OLRE), data=Grasshoppers, family="binomial")  
300 res <- partR2(mod, partvars=c("Bio7", "Bio14", "Bio17", "Bio19"),  
301     data=Grasshoppers, max_level = 1, nboot=100)
```

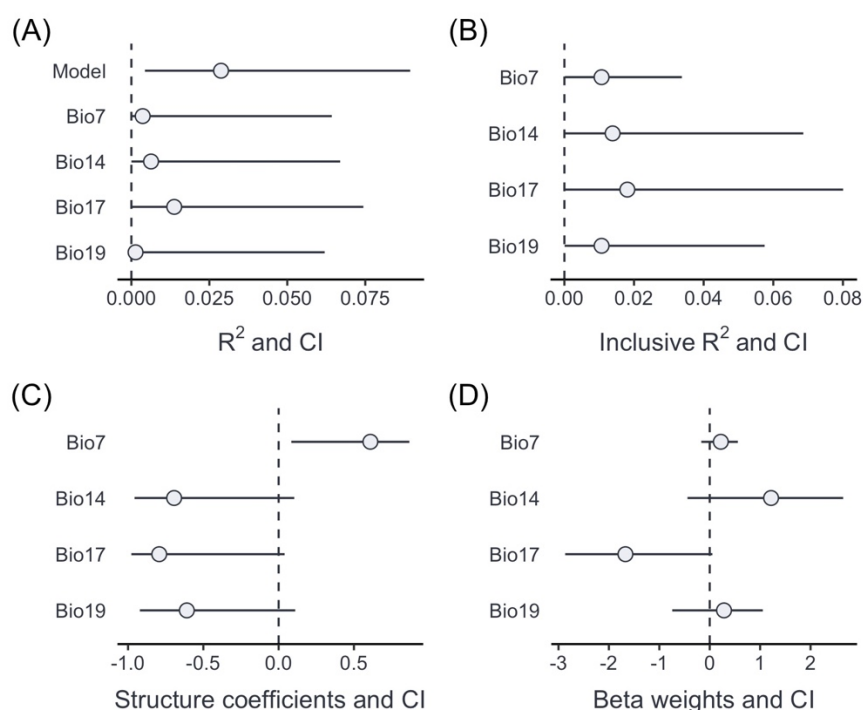
302
303 The summary output informs us (at the bottom) that there have been warnings in the bootstrapping
304 processes. This is not unusual since bootstrapping frequently generates data, for which one of the
305 parameters is estimated at the boundary (in particular if one of the variance components is very
306 small). The results can be visualised using the `forestplot` function (Figure 4). Plotting is based on
307 `ggplot2` (Wickham, 2016), and multiple forest plots can easily be assembled using the `patchwork`
308 package (Pedersen, 2020). Forest plots show the effect sizes graphically and can be set to either
309 show part R^2 when `type = "R2"` (the default), inclusive R^2 when `type = "IR2"`, structure
310 coefficients when `type = "SC"`, and beta weights (standardized model estimates) with `type =`
311 `"BW"`.

312

```

313 p1 <- forestplot(res, type = "R2")
314 p2 <- forestplot(res, type = "IR2")
315 p3 <- forestplot(res, type = "SC")
316 p4 <- forestplot(res, type = "BW")
317
318 library(patchwork)
319 (p1 + p2) / (p3 + p4) + plot_annotation(tag_levels = "A", tag_prefix =
320 "(", tag_suffix = ")")
321

```



322

323 **Figure 4:** Comparison of part R^2 for individual predictors (A), inclusive R^2 (B), structure coefficients
324 (C) and beta weights (D) for an example dataset with proportion data from grasshoppers.
325
326 A comparison of part R^2 , inclusive R^2 , structure coefficients beta weights shows the different insights
327 that can be gained from these different summaries of the model fit (Figure 3). In this case, three of
328 the Bioclim variables (*Bio14*, *Bio17*, *Bio19*) are highly positively correlated ($r \geq 0.93$), while a fourth
329 one (*Bio7*) is moderately negatively correlated to all three of them ($r \leq -0.63$). Part R^2 are thus low,
330 because none of the parameters uniquely explains a large share of the variance. *Bio17* seems to be
331 the best predictor of morph ratios, with the largest (negative) beta weight, largest part R^2 , largest
332 structure coefficients and largest inclusive R^2 . Beta weights for the two positively correlated (but
333 slightly weaker) predictors, *Bio14* and *Bio19*, switch sign as is not unusual for collinear predictors.

334 This means that after accounting for the effect of *Bio17*, they contribute positively to prediction.
335 However, structure coefficients show that both variables load negatively on the linear predictor, as
336 does *Bio17*.

337

338 **Challenges**

339 Using transformation or functions in the formula argument can lead to issues with matching the terms
340 of the model with the `partvars` argument of `partR2`. It is therefore important that the names in
341 `partvars` match exactly the terms in the `merMod` object. However, any complications are easily
342 circumvented by implementing the transformations before fitting the model and storing them in the
343 data frame used in the analysis. It is also worth to be aware that unusual names may cause
344 complications and renaming can offer an easy solution.

345 We have repeatedly seen model outputs where the point estimate does not fall within the confidence
346 interval. This might seem like a bug in the package, but in our experience usually indicates issues
347 with the data and/or the model. In fact, parametric bootstrapping can be seen as a limited form of
348 posterior predictive model checks (Gelman & Hill, 2007). If generating new data from the fitted
349 model (as done with parametric bootstrapping) results in data that are dissimilar to the original data,
350 then the model is probably not a good fit to the data.

351 Bootstrap iterations can sometimes yield slightly negative estimates of R^2 , in particular if the
352 variance explained by a predictor is low. These negative estimates happen in mixed-effects models,
353 because estimates of random-effect variance might change when a predictor is removed and this
354 can lead to a slight decrease in the residual variance, and hence a proportional increase in R^2 (see
355 also Rights & Sterba, 2019). By default, `partR2` sets negative R^2 values to 0, but this can be changed
356 by setting `allow_neg_r2` to `TRUE`. It also happens that inclusive R^2 is estimated slightly lower than
357 R^2 when the contribution of a particular predictor is very large. We consider both cases as
358 sampling error that should serve as a reminder that variance components are estimated with
359 relatively large uncertainty and minor differences should not be over-interpreted.

360 A warning needs to be added for the estimation of R^2 (and, in fact, also repeatability R) from small
361 datasets. In particular if the number of levels of random effect is low, variance components might be
362 slightly overestimated (Xu, 2003). This issue applies similarly to the variance explained by fixed
363 effects, in particular if the number of predictors is large relative to the number of data points.

364

365 **Code and data availability**

366 The development version of `partR2` can be obtained from GitHub
367 (<https://github.com/mastoffel/partR2>) and includes the data used in the examples. The package will
368 be uploaded to CRAN after peer-review.

369

370 **Author contributions**

371 SN and HS conceived the idea. HS and MAS wrote the manuscript with contributions from SN. MAS
372 wrote the package and the vignette, supervised by HS. All authors contributed critically to the
373 manuscript, package and vignette and gave final approval for publication.

374

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