Package: rptR (via r-universe)

November 20, 2026

Title Repeatability Estimation for Gaussian and Non-Gaussian Data

Version 0.9.24

Depends R (>= 3.2.1)

Date 2026-11-16

Description Estimating repeatability (intra-class correlation) from Gaussian, binary, proportion and Poisson data.

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Imports stats, lme4, parallel (>= 3.1.2), pbapply

Suggests testthat, knitr, rmarkdown, covr, tibble

RoxygenNote 7.3.2

VignetteBuilder knitr

URL https://github.com/mastoffel/rptR

BugReports https://github.com/mastoffel/rptR/issues

NeedsCompilation no

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Repository https://cran.r-universe.dev

Date/Publication 2026-11-20 07:30:02 UTC

RemoteUrl https://github.com/cran/rptR

RemoteRef HEAD

RemoteSha f8db055fbe2a8d23cab164dd5bd6afaa4e63bef3

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`BeetlesBody` *BeetlesBody dataset*

Description

BeetlesBody dataset

Details

This is an simulated dataset which was used as a toy example for a different purpose (Nakagawa & Schielzeth 2013). It offers a balanced dataset with rather simple structure, sizable effects and decent sample size, just right for demonstrating some features of `rptR`. Sufficient sample size is required in particular for the non-Gaussian traits, because those tend to be more computationally demanding and less rich in information per data point than simple Gaussian traits.

In brief the imaginary sampling design of the simulated dataset is as follows. Beetle larvae were sampled from 12 populations ('Population') with samples taken from two discrete microhabitats at each location ('Habitat'). Samples were split in equal proportion and raised in two dietary treatments ('Treatment'). Beetles were sexed at the pupal stage ('Sex') and pupae were kept in sex-homogeneous containers ('Container'). The phenotype in this dataset is body length ('BodyL').

References

Nakagawa, S. & Schielzeth, H. (2013) *A general and simple method for obtaining R2 from generalized linear mixed-effects models*. Methods in Ecology and Evolution 4: 133-142.

`BeetlesFemale` *BeetlesFemale dataset*

Description

BeetlesFemale dataset

Details

This is an simulated dataset which was used as a toy example for a different purpose (Nakagawa & Schielzeth 2013). It offers a balanced dataset with rather simple structure, sizable effects and decent sample size, just right for demonstrating some features of `rptR`. Sufficient sample size is required in particular for the non-Gaussian traits, because those tend to be more computationally demanding and less rich in information per data point than simple Gaussian traits.

In brief the imaginary sampling design of the simulated dataset is as follows. Beetle larvae were sampled from 12 populations ('Population') with samples taken from two discrete microhabitats at each location ('Habitat'). Samples were split in equal proportion and raised in two dietary treatments ('Treatment'). Beetles were sexed at the pupal stage ('Sex') and pupae were kept in sex-homogeneous containers ('Container'). The phenotype in this dataset is the number of eggs laid by female beetles ('Egg').

References

Nakagawa, S. & Schielzeth, H. (2013) *A general and simple method for obtaining R2 from generalized linear mixed-effects models*. Methods in Ecology and Evolution 4: 133-142.

`BeetlesMale` *BeetlesMale dataset*

Description

BeetlesMale dataset

Details

This is an simulated dataset which was used as a toy example for a different purpose (Nakagawa & Schielzeth 2013). It offers a balanced dataset with rather simple structure, sizable effects and decent sample size, just right for demonstrating some features of `rptR`. Sufficient sample size is required in particular for the non-Gaussian traits, because those tend to be more computationally demanding and less rich in information per data point than simple Gaussian traits.

In brief the imaginary sampling design of the simulated dataset is as follows. Beetle larvae were sampled from 12 populations ('Population') with samples taken from two discrete microhabitats at each location ('Habitat'). Samples were split in equal proportion and raised in two dietary treatments ('Treatment'). Beetles were sexed at the pupal stage ('Sex') and pupae were kept in sex-homogeneous containers ('Container'). The phenotype in this dataset is a binary variable containing the two distinct color morphs of males: dark and reddish-brown ('Colour').

References

Nakagawa, S. & Schielzeth, H. (2013) *A general and simple method for obtaining R2 from generalized linear mixed-effects models*. Methods in Ecology and Evolution 4: 133-142.

`plot.rpt` *Plot a rpt object*

Description

Plots the distribution of repeatability estimates from bootstrapping and permutation tests.

Usage

```
## S3 method for class 'rpt'
plot(
  x,
  grname = names(x$ngroups),
  scale = c("link", "original"),
  type = c("boot", "permut"),
  main = NULL,
  breaks = "FD",
  xlab = NULL,
  ...
)
```

Arguments

`x`	An rpt object returned from one of the rpt functions.
`grname`	The name of the grouping factor to plot.
`scale`	Either "link" or "original" scale results for results of non-Gaussian functions.
`type`	Either "boot" or "permut" for plotting the results of bootstraps or permutations.
`main`	Plot title
`breaks`	hist() argument
`xlab`	x-axis title
`...`	Additional arguments to the hist() function for customized plotting.

Value

A histogram of the distribution of bootstrapping or permutation test estimates of the repeatability including a confidence interval (CI).

Author(s)

Holger Schielzeth (holger.schielzeth@uni-jena.de), Shinichi Nakagawa (s.nakagawa@unsw.edu.au), Martin Stoffel (martin.adam.stoffel@gmail.com)

References

Nakagawa, S. & Schielzeth, H. (2010) *Repeatability for Gaussian and non-Gaussian data: a practical guide for biologists*. Biological Reviews 85: 935-956

print.rpt *Print a rpt object*

Description

Displays the results a rpt object (i.e. the result of a rpt function call) in a nice form.

Usage

```
## S3 method for class 'rpt'
print(x, ...)
```

Arguments

x	An rpt object returned from one of the rpt functions
...	Additional arguments; none are used in this method.

Value

Abbreviations in the print.rpt output:

R	Repeatability.
SE	Standard error of R.
CI	Confidence interval of R derived from parametric bootstrapping.
P	P-value
LRT	Likelihood-ratio test
Permutation	Permutation of residuals

Author(s)

Holger Schielzeth (holger.schielzeth@uni-jena.de), Shinichi Nakagawa (s.nakagawa@unsw.edu.au), Martin Stoffel (martin.adam.stoffel@gmail.com)

References

Nakagawa, S. & Schielzeth, H. (2010) *Repeatability for Gaussian and non-Gaussian data: a practical guide for biologists*. Biological Reviews 85: 935-956

print.summary.rpt *Prints the summary of a rpt object*

Description

Displays the summary of an rpt object (i.e. the result of a rpt function call) in an extended form.

Usage

```
## S3 method for class 'summary.rpt'
print(x, ...)
```

Arguments

x	An rpt object returned from one of the rpt functions
...	Additional arguments; none are used in this method.

Author(s)

Holger Schielzeth (holger.schielzeth@uni-jena.de), Shinichi Nakagawa (s.nakagawa@unsw.edu.au), Martin Stoffel (martin.adam.stoffel@gmail.com)

References

Nakagawa, S. and Schielzeth, H. (2010) *Repeatability for Gaussian and non-Gaussian data: a practical guide for biologists*. Biological Reviews 85: 935-956

rpt *Repeatability Estimation for Gaussian and Non-Gaussian Data*

Description

A wrapper function for (adjusted) repeatability estimation from generalized linear mixed-effects models fitted by restricted maximum likelihood (REML). Calls specialised functions depending of the choice of datatype and method.

Usage

```
rpt(
  formula,
  grname,
  data,
  datatype = c("Gaussian", "Binary", "Proportion", "Poisson"),
  link = c("logit", "probit", "log", "sqrt"),
  CI = 0.95,
```

```
  nboot = 1000,
  npermut = 0,
  parallel = FALSE,
  ncores = NULL,
  ratio = TRUE,
  adjusted = TRUE,
  expect = "meanobs",
  rptObj = NULL,
  update = FALSE,
  ...
)
```

Arguments

formula	Formula as used e.g. by lmer. The grouping factor(s) of interest needs to be included as a random effect, e.g. '(1|groups)'. Covariates and additional random effects can be included to estimate adjusted repeatabilities.
grname	A character string or vector of character strings giving the name(s) of the grouping factor(s), for which the repeatability should be estimated. Spelling needs to match the random effect names as given in `formula` and terms have to be set in quotation marks. The reseved terms "Residual", "Overdispersion" and "Fixed" allow the estimation of overdispersion variance, residual variance and variance explained by fixed effects, respectively.
data	A dataframe that contains the variables included in the `formula` and `grname` arguments.
datatype	Character string specifying the data type ('Gaussian', 'Binary', 'Proportion', 'Poisson').
link	Character string specifying the link function. Ignored for 'Gaussian' datatype.
CI	Width of the required confidence interval between 0 and 1 (defaults to 0.95).
nboot	Number of parametric bootstraps for interval estimation (defaults to 1000). Larger numbers of bootstraps give a better asymtotic CI, but may be time-consuming. Bootstrapping can be switch off by setting `nboot = 0`. See also **Details** below.
npermut	Number of permutations used when calculating asymptotic p-values (defaults to 0). Larger numbers of permutations give a better asymtotic p-values, but may be time-consuming (in particular when multiple grouping factors are specified). Permutaton tests can be switch off by setting `npermut = 0`. See also **Details** below.
parallel	Boolean to express if parallel computing should be applied (defaults to FALSE). If TRUE, bootstraps and permutations will be distributed across multiple cores.
ncores	Specifying the number of cores to use for parallelization. On default, all but one of the available cores are used.
ratio	Boolean to express if variances or ratios of variance should be estimated. If FALSE, the variance(s) are returned without forming ratios. If TRUE (the default) ratios of variances (i.e. repeatabilities) are estimated.

adjusted	Boolean to express if adjusted or unadjusted repeatabilities should be estimated. If TRUE (the default), the variances explained by fixed effects (if any) will not be part of the denominator, i.e. repeatabilities are calculated after controlling for variation due to covariates. If FALSE, the varianced explained by fixed effects (if any) will be added to the denominator.
expect	A character string specifying the method for estimating the expectation in Poisson models with log link and in Binomial models with logit link (in all other cases the agrument is ignored). The only valid terms are 'meanobs' and 'latent' (and 'liability for binary and proportion data). With the default 'meanobs', the expectation is estimated as the mean of the observations in the sample. With 'latent', the expectation is estimated from estiamtes of the intercept and variances on the link scale. While this is a preferred solution, it is susceptible to the distribution of fixed effect covariates and gives appropriate results typically only when all covariances are centered to zero. With 'liability' estimates follow formulae as presented in Nakagawa & Schielzeth (2010). Liability estimates tend to be slightly higher.
rptObj	The output of a rptR function. Can be specified in combination with update = TRUE to update bootstraps and permutations
update	If TRUE, the rpt object to be updated has to be inputted with the rptObj argument. The function just updates the permutations and bootstraps, so make sure to specify all other arguments excactly like for the rpt object specified in rptObj.
...	Other parameters for the lmer or glmer call, such as optimizers.

Details

For `datatype='Gaussian'` calls function rptGaussian, for `datatype='Poisson'` calls function rptPoisson, for `datatype='Binary'` calls function rptBinary, for `datatype='Proportion'` calls function rptProportion.

Confidence intervals and standard errors are estimated by **parametric bootstrapping**. Under the assumption that the model is specified correctly, the fitted model can be used to generate response values that could potentially be obversed. Differences between the original data and the simulated response from the fitted model arise from sampling variation. The full model is then fitted to each simuated response vector. The distribution of estimates across all `nboot` replicates represents the design- and model-specific sampling variance and hence uncertainty of the estimates.

In addition to the likelihood-ratio test, the package uses **permutation tests** for null hypothesis testing. The general idea is to randomize data under the null hypothesis of no effect and then test in how many cases the estimates from the model reach or exceed those in the observed data. In the simplest case, a permutation test randomizes the vector of group identities against the response vector many times, followed by refitting the model and recalculating the repeatabilities. This provides a null distribution for the case that group identities are unrelated to the response. However, in more complex models involving multiple random effects and/or fixed effects, such a procedure will also break the data structure between the grouping factor of interest and other aspects of the experimental design. Therefore `rptR` implements a more robust alternative which works by fitting a model withouth the grouping factor of interest. It then adds the randomized residuals to the fitted values of this model, followed by recalculating the repeatability from the full model. This procedure maintains the general data structure and any effects other than the grouping effect of interest. The number of permutations can be adjusted with the `nperm` argument. By the logic of a null hypothsis testing, the

observed data is one possible (albeit maybe unlikely) outcome under the null hypothesis. So the observed data is always included as one 'randomization' and the P value can thus never be lower than `1/nperm`, because at least one randomization is as exteme as the observed data.

Note also that the **likelihood-ratio test**, since testing variances at the boundary of the possible parameter range (i.e. against zero), uses a mixture distribution of Chi-square distrbutions with zero and one degree of freedom as a reference. This ist equivalent to deviding the P value derived from a Chi-square distribution with one degree of freedom by two.

Value

Returns an object of class `rpt`. See specific functions for details.

Author(s)

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References

Nakagawa, S. & Schielzeth, H. (2010) *Repeatability for Gaussian and non-Gaussian data: a practical guide for biologists*. Biological Reviews 85: 935-956.

See Also

rptR

Examples

```
# load data
data(BeetlesBody)
data(BeetlesMale)
data(BeetlesFemale)

#  prepare proportion data
BeetlesMale$Dark <- BeetlesMale$Colour
BeetlesMale$Reddish <- (BeetlesMale$Colour-1)*-1
BeetlesColour <- aggregate(cbind(Dark, Reddish) ~ Treatment + Population + Container,
     data=BeetlesMale, FUN=sum)

# Note: nboot and npermut are set to 0 for speed reasons. Use larger numbers
# for the real analysis.

# gaussian data (example with a single random effect)
rpt(BodyL ~ (1|Population), grname="Population", data=BeetlesBody,
     nboot=0, npermut=0, datatype = "Gaussian")

# poisson data (example with two grouping levels and adjusted for fixed effect)
rpt(Egg ~ Treatment + (1|Container) + (1|Population), grname=c("Population"),
     data = BeetlesFemale, nboot=0, npermut=0, datatype = "Poisson")

## Not run:
```

```
# binary data (example with estimation of the fixed effect variance)
rpt(Colour ~ Treatment + (1|Container) + (1|Population),
     grname=c("Population", "Container", "Fixed"),
     data=BeetlesMale, nboot=0, npermut=0, datatype = "Binary", adjusted = FALSE)

# proportion data (example for the estimation of raw variances,
# including residual and fixed-effect variance)
rpt(cbind(Dark, Reddish) ~ Treatment + (1|Population),
     grname=c("Population", "Residual", "Fixed"), data=BeetlesColour,
     nboot=0, npermut=0, datatype = "Proportion", ratio=FALSE)


## End(Not run)
```

`rptBinary` *GLMM-based Repeatability Estimation for Binary Data*

Description

Estimates repeatability from a generalized linear mixed-effects models fitted by restricted maximum likelihood (REML).

Usage

```
rptBinary(
  formula,
  grname,
  data,
  link = c("logit", "probit"),
  CI = 0.95,
  nboot = 1000,
  npermut = 0,
  parallel = FALSE,
  ncores = NULL,
  ratio = TRUE,
  adjusted = TRUE,
  expect = "meanobs",
  rptObj = NULL,
  update = FALSE,
  ...
)
```

Arguments

`formula`	Formula as used e.g. by lmer. The grouping factor(s) of interest needs to be included as a random effect, e.g. '(1|groups)'. Covariates and additional random effects can be included to estimate adjusted repeatabilities.

grname	A character string or vector of character strings giving the name(s) of the grouping factor(s), for which the repeatability should be estimated. Spelling needs to match the random effect names as given in formula and terms have to be set in quotation marks. The reseved terms "Residual", "Fixed" allow the estimation of residual variance and variance explained by fixed effects, respectively. "Overdispersion" is not available for rptBinary.
data	A dataframe that contains the variables included in the formula and grname arguments.
link	Link function. logit and probit are allowed, defaults to logit.
CI	Width of the required confidence interval between 0 and 1 (defaults to 0.95).
nboot	Number of parametric bootstraps for interval estimation (defaults to 1000). Larger numbers of bootstraps give a better asymtotic CI, but may be time-consuming. Bootstrapping can be switch off by setting nboot = 0. See also **Details** below.
npermut	Number of permutations used when calculating asymptotic p-values (defaults to 0). Larger numbers of permutations give a better asymtotic p-values, but may be time-consuming (in particular when multiple grouping factors are specified). Permutaton tests can be switch off by setting npermut = 0. See also **Details** below.
parallel	Boolean to express if parallel computing should be applied (defaults to FALSE). If TRUE, bootstraps and permutations will be distributed across multiple cores.
ncores	Specifying the number of cores to use for parallelization. On default, all but one of the available cores are used.
ratio	Boolean to express if variances or ratios of variance should be estimated. If FALSE, the variance(s) are returned without forming ratios. If TRUE (the default) ratios of variances (i.e. repeatabilities) are estimated.
adjusted	Boolean to express if adjusted or unadjusted repeatabilities should be estimated. If TRUE (the default), the variances explained by fixed effects (if any) will not be part of the denominator, i.e. repeatabilities are calculated after controlling for variation due to covariates. If FALSE, the varianced explained by fixed effects (if any) will be added to the denominator.
expect	A character string specifying the method for estimating the expectation in Poisson models with log link and in Binomial models with logit link (in all other cases the agrument is ignored). The only valid terms are 'meanobs' and 'latent' (and 'liability for binary and proportion data). With the default 'meanobs', the expectation is estimated as the mean of the observations in the sample. With 'latent', the expectation is estimated from estiamtes of the intercept and variances on the link scale. While this is a preferred solution, it is susceptible to the distribution of fixed effect covariates and gives appropriate results typically only when all covariances are centered to zero. With 'liability' estimates follow formulae as presented in Nakagawa & Schielzeth (2010). Liability estimates tend to be slightly higher.
rptObj	The output of a rptR function. Can be specified in combination with update = TRUE to update bootstraps and permutations
update	If TRUE, the rpt object to be updated has to be inputted with the rptObj argument. The function just updates the permutations and bootstraps, so make sure to specify all other arguments excactly like for the rpt object specified in rptObj.

...	Other parameters for the lmer or glmer call, such as optimizers.

Details

see details section of `rpt` for details on parametric bootstrapping, permutation and likelihood-ratio tests.

Value

Returns an object of class `rpt` that is a a list with the following elements:

`call`	Function call.
`datatype`	Response distribution (here: 'Binary').
`CI`	Coverage of the confidence interval as specified by the `CI` argument.
`R`	`data.frame` with point estimates for repeatabilities. Columns represent grouping factors of interest. Rows show original and link scale repeatabilites (in this order).
`se`	`data.frame` with approximate standard errors (*se*) for repeatabilities. Columns are groups of interest. Rows are original and link scale (in this order). Note that the distribution might not be symmetrical, in which case the *se* is less informative.
`CI_emp`	`list` of two elements containing the confidence intervals for repeatabilities on the link and original scale, respectively. Within each list element, lower and upper CI are columns and each row for each grouping factor of interest.
`P`	`data.frame` with p-values from a significance test based on likelihood-ratios in the first column and significance test based on permutation of residuals for both the original and link scale in the second and third column. Each row represents a grouping factor of interest.
`R_boot_link`	Parametric bootstrap samples for *R* on the link scale. Each `list` element is a grouping factor.
`R_boot_org`	Parametric bootstrap samples for *R* on the original scale. Each `list` element is a grouping factor.
`R_permut_link`	Permutation samples for *R* on the link scale. Each `list` element is a grouping factor.
`R_permut_org`	Permutation samples for *R* on the original scale. Each `list` element is a grouping factor.
`LRT`	List of two elements. *LRT_mod* is the likelihood for the full model and (2) *LRT_table* is a data.frame for the reduced model(s) including columns for the likelihood *logl_red*, the likelihood ratio(s) *LR_D*, p-value(s)*LR_P* and degrees of freedom for the likelihood-ratio test(s) *LR_df*.
`ngroups`	Number of groups for each grouping level.
`nobs`	Number of observations.
`mod`	Fitted model.
`ratio`	Boolean. TRUE, if ratios have been estimated, FALSE, if variances have been estimated

adjusted	Boolean. TRUE, if estimates are adjusted
all_warnings	list with two elements. 'warnings_boot' and 'warnings_permut' contain warnings from the lme4 model fitting of bootstrap and permutation samples, respectively.

Author(s)

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References

Carrasco, J. L. & Jover, L. (2003) *Estimating the generalized concordance correlation coefficient through variance components*. Biometrics 59: 849-858.

Faraway, J. J. (2006) *Extending the linear model with R*. Boca Raton, FL, Chapman & Hall/CRC.

Nakagawa, S. & Schielzeth, H. (2010) *Repeatability for Gaussian and non-Gaussian data: a practical guide for biologists*. Biological Reviews 85: 935-956

See Also

rpt

Examples

```
data(BeetlesMale)

# Note: nboot and npermut are set to 0 for speed reasons.

# repeatability with one grouping level
rptBinary(Colour ~ (1|Population), grname=c("Population"),
data=BeetlesMale, nboot=0, npermut=0)

# unadjusted repeatabilities with  fixed effects and
# estimation of the fixed effect variance
rptBinary(Colour ~ Treatment + (1|Container) + (1|Population),
                  grname=c("Container", "Population", "Fixed"),
                  data=BeetlesMale, nboot=0, npermut=0, adjusted=FALSE)


## Not run:
# variance estimation of random effects and residual
R_est <- rptBinary(Colour ~ Treatment + (1|Container) + (1|Population),
                  grname=c("Container","Population","Residual"),
                  data = BeetlesMale, nboot=0, npermut=0, ratio = FALSE)

## End(Not run)
```

rptGaussian *LMM-based Repeatability Estimation for Gaussian Data*

Description

Estimates the repeatability from a general linear mixed-effects models fitted by restricted maximum likelihood (REML).

Usage

```
rptGaussian(
  formula,
  grname,
  data,
  CI = 0.95,
  nboot = 1000,
  npermut = 0,
  parallel = FALSE,
  ncores = NULL,
  ratio = TRUE,
  adjusted = TRUE,
  rptObj = NULL,
  update = FALSE,
  ...
)
```

Arguments

formula	Formula as used e.g. by lmer. The grouping factor(s) of interest needs to be included as a random effect, e.g. '(1|groups)'. Covariates and additional random effects can be included to estimate adjusted repeatabilities.
grname	A character string or vector of character strings giving the name(s) of the grouping factor(s), for which the repeatability should be estimated. Spelling needs to match the random effect names as given in formula and terms have to be set in quotation marks. The reseved terms "Residual", "Overdispersion" and "Fixed" allow the estimation of overdispersion variance, residual variance and variance explained by fixed effects, respectively.
data	A dataframe that contains the variables included in the formula and grname arguments.
CI	Width of the required confidence interval between 0 and 1 (defaults to 0.95).
nboot	Number of parametric bootstraps for interval estimation (defaults to 1000). Larger numbers of bootstraps give a better asymtotic CI, but may be time-consuming. Bootstrapping can be switch off by setting nboot = 0. See also **Details** below.
npermut	Number of permutations used when calculating asymptotic p-values (defaults to 0). Larger numbers of permutations give a better asymtotic p-values, but may

	be time-consuming (in particular when multiple grouping factors are specified). Permutaton tests can be switch off by setting `npermut = 0`. See also **Details** below.
`parallel`	Boolean to express if parallel computing should be applied (defaults to FALSE). If TRUE, bootstraps and permutations will be distributed across multiple cores.
`ncores`	Specifying the number of cores to use for parallelization. On default, all but one of the available cores are used.
`ratio`	Boolean to express if variances or ratios of variance should be estimated. If FALSE, the variance(s) are returned without forming ratios. If TRUE (the default) ratios of variances (i.e. repeatabilities) are estimated.
`adjusted`	Boolean to express if adjusted or unadjusted repeatabilities should be estimated. If TRUE (the default), the variances explained by fixed effects (if any) will not be part of the denominator, i.e. repeatabilities are calculated after controlling for variation due to covariates. If FALSE, the varianced explained by fixed effects (if any) will be added to the denominator.
`rptObj`	The output of a rptR function. Can be specified in combination with update = TRUE to update bootstraps and permutations
`update`	If TRUE, the rpt object to be updated has to be inputted with the rptObj argument. The function just updates the permutations and bootstraps, so make sure to specify all other arguments excactly like for the rpt object specified in rptObj.
`...`	Other parameters for the lmer or glmer call, such as optimizers.

Details

see details section of `rpt` for details on parametric bootstrapping, permutation and likelihood-ratio tests.

Value

Returns an object of class `rpt` that is a a list with the following elements:

`call`	Function call.
`datatype`	Response distribution (here: 'Gaussian').
`CI`	Coverage of the confidence interval as specified by the `CI` argument.
`R`	`data.frame` with point estimates for repeatabilities for each grouping factor of interest.
`se`	`data.frame` with approximate standard errors (*se*) for repeatabilities. Rows repsresent grouping factors of interest. Note that the distribution might not be symmetrical, in which case the *se* is less informative.
`CI_emp`	`data.frame` containing the (empirical) confidence intervals for the repeatabilities estiamted based parametric bootstrapping. Each row represents a grouping factor of interest.
`P`	`data.frame` with p-values based on likelihood-ratio tests (first column) and permutation tests (second column). Each row represents a grouping factor of interest.

R_boot	Vector(s) of parametric bootstrap samples for *R*. Each list element respesents a grouping factor.
R_permut	Vector(s) of permutation samples for *R*. Each list element represents a grouping factor.
LRT	list with two elements. (1) The likelihood for the full model and a data.frame called LRT_table for the reduced model(s), which includes columns for the respective grouping factor(s), the likelihood(s) *logL_red*, likelihood ratio(s) *LR_D*, p-value(s) *LRT_P* and degrees of freedom *LRT_df*
ngroups	Number of groups for each grouping level.
nobs	Number of observations.
mod	Fitted model.
ratio	Boolean. TRUE, if ratios have been estimated, FALSE, if variances have been estimated
adjusted	Boolean. TRUE, if estimates are adjusted
all_warnings	list with two elements. 'warnings_boot' and 'warnings_permut' contain warnings from the lme4 model fitting of bootstrap and permutation samples, respectively.

Author(s)

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References

Carrasco, J. L. & Jover, L. (2003) *Estimating the generalized concordance correlation coefficient through variance components*. Biometrics 59: 849-858.

Nakagawa, S. & Schielzeth, H. (2010) *Repeatability for Gaussian and non-Gaussian data: a practical guide for biologists*. Biological Reviews 85: 935-956

See Also

rpt

Examples

```
data(BeetlesBody)

# Note: nboot and npermut are set to 3 for speed reasons. Use larger numbers
# for the real analysis.

# one random effect
rpt_est <- rptGaussian(BodyL ~ (1|Population), grname="Population",
                  data=BeetlesBody, nboot=3, npermut=3, ratio = FALSE)

# two random effects
rptGaussian(BodyL ~ (1|Container) + (1|Population), grname=c("Container", "Population"),
```

```
                    data=BeetlesBody, nboot=3, npermut=3)

# unadjusted repeatabilities with fixed effects and
# estimation of the fixed effect variance
rptGaussian(BodyL ~ Sex + Treatment + Habitat + (1|Container) + (1|Population),
                  grname=c("Container", "Population", "Fixed"),
                  data=BeetlesBody, nboot=3, npermut=3, adjusted=FALSE)


# two random effects, estimation of variance (instead repeatability)
R_est <- rptGaussian(formula = BodyL ~ (1|Population) + (1|Container),
            grname= c("Population", "Container", "Residual"),
            data=BeetlesBody, nboot=3, npermut=3, ratio = FALSE)
```

`rptPoisson` *GLMM-based Repeatability Estimation for Poisson-distributed Data*

Description

Estimates repeatability from a generalized linear mixed-effects models fitted by restricted maximum likelihood (REML).

Usage

```
rptPoisson(
  formula,
  grname,
  data,
  link = c("log", "sqrt"),
  CI = 0.95,
  nboot = 1000,
  npermut = 0,
  parallel = FALSE,
  ncores = NULL,
  ratio = TRUE,
  adjusted = TRUE,
  expect = "meanobs",
  rptObj = NULL,
  update = FALSE,
  ...
)
```

Arguments

`formula`	Formula as used e.g. by lmer. The grouping factor(s) of interest needs to be included as a random effect, e.g. '(1|groups)'. Covariates and additional random effects can be included to estimate adjusted repeatabilities.

grname	A character string or vector of character strings giving the name(s) of the grouping factor(s), for which the repeatability should be estimated. Spelling needs to match the random effect names as given in formula and terms have to be set in quotation marks. The reseved terms "Residual", "Overdispersion" and "Fixed" allow the estimation of overdispersion variance, residual variance and variance explained by fixed effects, respectively.
data	A dataframe that contains the variables included in the formula and grname arguments.
link	Link function. logit and probit are allowed, defaults to logit.
CI	Width of the required confidence interval between 0 and 1 (defaults to 0.95).
nboot	Number of parametric bootstraps for interval estimation (defaults to 1000). Larger numbers of bootstraps give a better asymtotic CI, but may be time-consuming. Bootstrapping can be switch off by setting nboot = 0. See also **Details** below.
npermut	Number of permutations used when calculating asymptotic p-values (defaults to 0). Larger numbers of permutations give a better asymtotic p-values, but may be time-consuming (in particular when multiple grouping factors are specified). Permutaton tests can be switch off by setting npermut = 0. See also **Details** below.
parallel	Boolean to express if parallel computing should be applied (defaults to FALSE). If TRUE, bootstraps and permutations will be distributed across multiple cores.
ncores	Specifying the number of cores to use for parallelization. On default, all but one of the available cores are used.
ratio	Boolean to express if variances or ratios of variance should be estimated. If FALSE, the variance(s) are returned without forming ratios. If TRUE (the default) ratios of variances (i.e. repeatabilities) are estimated.
adjusted	Boolean to express if adjusted or unadjusted repeatabilities should be estimated. If TRUE (the default), the variances explained by fixed effects (if any) will not be part of the denominator, i.e. repeatabilities are calculated after controlling for variation due to covariates. If FALSE, the varianced explained by fixed effects (if any) will be added to the denominator.
expect	A character string specifying the method for estimating the expectation in Poisson models with log link and in Binomial models with logit link (in all other cases the agrument is ignored). The only valid terms are 'meanobs' and 'latent' (and 'liability for binary and proportion data). With the default 'meanobs', the expectation is estimated as the mean of the observations in the sample. With 'latent', the expectation is estimated from estiamtes of the intercept and variances on the link scale. While this is a preferred solution, it is susceptible to the distribution of fixed effect covariates and gives appropriate results typically only when all covariances are centered to zero. With 'liability' estimates follow formulae as presented in Nakagawa & Schielzeth (2010). Liability estimates tend to be slightly higher.
rptObj	The output of a rptR function. Can be specified in combination with update = TRUE to update bootstraps and permutations
update	If TRUE, the rpt object to be updated has to be inputted with the rptObj argument. The function just updates the permutations and bootstraps, so make sure to specify all other arguments excactly like for the rpt object specified in rptObj.

...	Other parameters for the lmer or glmer call, such as optimizers.

Details

see details section of `rpt` for details on parametric bootstrapping, permutation and likelihood-ratio tests.

Value

Returns an object of class `rpt` that is a a list with the following elements:

`call`	Function call
`datatype`	Response distribution (here: 'Poisson').
`CI`	Coverage of the confidence interval as specified by the `CI` argument.
`R`	`data.frame` with point estimates for repeatabilities. Columns represent grouping factors of interest. Rows show original and link scale repeatabilites (in this order).
`se`	`data.frame` with approximate standard errors (*se*) for repeatabilities. Columns are groups of interest. Rows are original and link scale (in this order). Note that the distribution might not be symmetrical, in which case the *se* is less informative.
`CI_emp`	`list` of two elements containing the confidence intervals for repeatabilities on the link and original scale, respectively. Within each list element, lower and upper CI are columns and each row for each grouping factor of interest.
`P`	`data.frame` with p-values from a significance test based on likelihood-ratios in the first column and significance test based on permutation of residuals for both the original and link scale in the second and third column. Each row represents a grouping factor of interest.
`R_boot_link`	Parametric bootstrap samples for *R* on the link scale. Each `list` element is a grouping factor.
`R_boot_org`	Parametric bootstrap samples for *R* on the original scale. Each `list` element is a grouping factor.
`R_permut_link`	Permutation samples for *R* on the link scale. Each `list` element is a grouping factor.
`R_permut_org`	Permutation samples for *R* on the original scale. Each `list` element is a grouping factor.
`LRT`	List of two elements. *LRT_mod* is the likelihood for the full model and (2) *LRT_table* is a data.frame for the reduced model(s) including columns for the likelihood *logl_red*, the likelihood ratio(s) *LR_D*, p-value(s)*LR_P* and degrees of freedom for the likelihood-ratio test(s) *LR_df*.
`ngroups`	Number of groups for each grouping level.
`nobs`	Number of observations.
`mod`	Fitted model.
`ratio`	Boolean. TRUE, if ratios have been estimated, FALSE, if variances have been estimated

adjusted	Boolean. TRUE, if estimates are adjusted
all_warnings	list with two elements. 'warnings_boot' and 'warnings_permut' contain warnings from the lme4 model fitting of bootstrap and permutation samples, respectively.

Author(s)

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References

Carrasco, J. L. & Jover, L. (2003) *Estimating the generalized concordance correlation coefficient through variance components*. Biometrics 59: 849-858.

Faraway, J. J. (2006) *Extending the linear model with R*. Boca Raton, FL, Chapman & Hall/CRC.

Nakagawa, S. & Schielzeth, H. (2010) *Repeatability for Gaussian and non-Gaussian data: a practical guide for biologists*. Biological Reviews 85: 935-956

See Also

rpt

Examples

```
# load data
data(BeetlesFemale)

# Note: nboot and npermut are set to 0 for speed reasons.

# estimating adjusted repeatabilities for two random effects
rptPoisson(Egg ~ Treatment + (1|Container) + (1|Population),
                  grname=c("Container", "Population"),
                  data = BeetlesFemale, nboot=0, npermut=0)

# unadjusted repeatabilities with  fixed effects and
# estimation of the fixed effect variance
rptPoisson(Egg ~ Treatment + (1|Container) + (1|Population),
                  grname=c("Container", "Population", "Fixed"),
                  data=BeetlesFemale, nboot=0, npermut=0, adjusted=FALSE)


# variance estimation of random effects, residual and overdispersion
rptPoisson(formula = Egg ~ Treatment + (1|Container) + (1|Population) ,
                  grname=c("Container","Population","Residual", "Overdispersion"),
                  data = BeetlesFemale, nboot=0, npermut=0, ratio = FALSE)
```

`rptProportion` *GLMM-based Repeatability Estimation for Proportion Data*

Description

Estimates repeatability from a generalized linear mixed-effects models fitted by restricted maximum likelihood (REML).

Usage

```
rptProportion(
  formula,
  grname,
  data,
  link = c("logit", "probit"),
  CI = 0.95,
  nboot = 1000,
  npermut = 0,
  parallel = FALSE,
  ncores = NULL,
  ratio = TRUE,
  adjusted = TRUE,
  expect = "meanobs",
  rptObj = NULL,
  update = FALSE,
  ...
)
```

Arguments

`formula`	Formula as used e.g. by lmer. The grouping factor(s) of interest needs to be included as a random effect, e.g. '(1|groups)'. Covariates and additional random effects can be included to estimate adjusted repeatabilities.
`grname`	A character string or vector of character strings giving the name(s) of the grouping factor(s), for which the repeatability should be estimated. Spelling needs to match the random effect names as given in `formula` and terms have to be set in quotation marks. The reseved terms "Residual", "Overdispersion" and "Fixed" allow the estimation of overdispersion variance, residual variance and variance explained by fixed effects, respectively.
`data`	A dataframe that contains the variables included in the `formula` and `grname` arguments.
`link`	Link function. `logit` and `probit` are allowed, defaults to `logit`.
`CI`	Width of the required confidence interval between 0 and 1 (defaults to 0.95).
`nboot`	Number of parametric bootstraps for interval estimation (defaults to 1000). Larger numbers of bootstraps give a better asymtotic CI, but may be time-consuming. Bootstrapping can be switch off by setting `nboot = 0`. See also **Details** below.

npermut	Number of permutations used when calculating asymptotic p-values (defaults to 0). Larger numbers of permutations give a better asymtotic p-values, but may be time-consuming (in particular when multiple grouping factors are specified). Permutaton tests can be switch off by setting `npermut = 0`. See also **Details** below.
parallel	Boolean to express if parallel computing should be applied (defaults to FALSE). If TRUE, bootstraps and permutations will be distributed across multiple cores.
ncores	Specifying the number of cores to use for parallelization. On default, all but one of the available cores are used.
ratio	Boolean to express if variances or ratios of variance should be estimated. If FALSE, the variance(s) are returned without forming ratios. If TRUE (the default) ratios of variances (i.e. repeatabilities) are estimated.
adjusted	Boolean to express if adjusted or unadjusted repeatabilities should be estimated. If TRUE (the default), the variances explained by fixed effects (if any) will not be part of the denominator, i.e. repeatabilities are calculated after controlling for variation due to covariates. If FALSE, the varianced explained by fixed effects (if any) will be added to the denominator.
expect	A character string specifying the method for estimating the expectation in Poisson models with log link and in Binomial models with logit link (in all other cases the agrument is ignored). The only valid terms are 'meanobs' and 'latent' (and 'liability for binary and proportion data). With the default 'meanobs', the expectation is estimated as the mean of the observations in the sample. With 'latent', the expectation is estimated from estiamtes of the intercept and variances on the link scale. While this is a preferred solution, it is susceptible to the distribution of fixed effect covariates and gives appropriate results typically only when all covariances are centered to zero. With 'liability' estimates follow formulae as presented in Nakagawa & Schielzeth (2010). Liability estimates tend to be slightly higher.
rptObj	The output of a rptR function. Can be specified in combination with update = TRUE to update bootstraps and permutations
update	If TRUE, the rpt object to be updated has to be inputted with the rptObj argument. The function just updates the permutations and bootstraps, so make sure to specify all other arguments excactly like for the rpt object specified in rptObj.
...	Other parameters for the lmer or glmer call, such as optimizers.

Details

see details section of `rpt` for details on parametric bootstrapping, permutation and likelihood-ratio tests.

Value

Returns an object of class `rpt` that is a a list with the following elements:

call	Function call
datatype	Response distribution (here: 'Proportion').

CI	Width of the confidence interval.
R	data.frame with point estimates for repeatabilities. Columns represent grouping factors of interest. Rows show original and link scale repeatabilites (in this order).
se	data.frame with approximate standard errors (*se*) for repeatabilities. Columns are groups of interest. Rows are original and link scale (in this order). Note that the distribution might not be symmetrical, in which case the *se* is less informative.
CI_emp	list of two elements containing the confidence intervals for repeatabilities on the link and original scale, respectively. Within each list element, lower and upper CI are columns and each row for each grouping factor of interest.
P	data.frame with p-values from a significance test based on likelihood-ratios in the first column and significance test based on permutation of residuals for both the original and link scale in the second and third column. Each row represents a grouping factor of interest.
R_boot_link	Parametric bootstrap samples for *R* on the link scale. Each list element is a grouping factor.
R_boot_org	Parametric bootstrap samples for *R* on the original scale. Each list element is a grouping factor.
R_permut_link	Permutation samples for *R* on the link scale. Each list element is a grouping factor.
R_permut_org	Permutation samples for *R* on the original scale. Each list element is a grouping factor.
LRT	List of two elements. *LRT_mod* is the likelihood for the full model and (2) *LRT_table* is a data.frame for the reduced model(s) including columns for the likelihood *logl_red*, the likelihood ratio(s) *LR_D*, p-value(s)*LR_P* and degrees of freedom for the likelihood-ratio test(s) *LR_df*.
ngroups	Number of groups for each grouping level.
nobs	Number of observations.
overdisp	Overdispersion parameter. Equals the variance in the observational factor random effect
mod	Fitted model.
ratio	Boolean. TRUE, if ratios have been estimated, FALSE, if variances have been estimated
adjusted	Boolean. TRUE, if estimates are adjusted
all_warnings	list with two elements. 'warnings_boot' and 'warnings_permut' contain warnings from the lme4 model fitting of bootstrap and permutation samples, respectively.

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References

Carrasco, J. L. & Jover, L. (2003) *Estimating the generalized concordance correlation coefficient through variance components*. Biometrics 59: 849-858.

Faraway, J. J. (2006) *Extending the linear model with R*. Boca Raton, FL, Chapman & Hall/CRC.

Nakagawa, S. & Schielzeth, H. (2010) *Repeatability for Gaussian and non-Gaussian data: a practical guide for biologists*. Biological Reviews 85: 935-956

See Also

rpt

Examples

```
data(BeetlesMale)

# prepare proportion data
BeetlesMale$Dark <- BeetlesMale$Colour
BeetlesMale$Reddish <- (BeetlesMale$Colour-1)*-1
BeetlesColour <- aggregate(cbind(Dark, Reddish) ~ Treatment + Population + Container,
     data=BeetlesMale, FUN=sum)

# Note: nboot and npermut are set to 0 for speed reasons.

# repeatability with one grouping level
rptProportion(cbind(Dark, Reddish) ~ (1|Population),
     grname=c("Population"), data=BeetlesColour, nboot=3, npermut=3)

# unadjusted repeatabilities with  fixed effects and
# estimation of the fixed effect variance
rptProportion(cbind(Dark, Reddish) ~ Treatment + (1|Container) + (1|Population),
     grname=c("Population", "Fixed"),
     data=BeetlesColour, nboot=0, npermut=0, adjusted=FALSE)

# variance estimation of random effects, residual and overdispersion
rptProportion(cbind(Dark, Reddish) ~ Treatment + (1|Container) + (1|Population),
     grname=c("Container","Population","Residual", "Overdispersion"),
     data = BeetlesColour, nboot=0, npermut=0, ratio = FALSE)
```

---

rptR *rptR: Repeatability Estimation for Gaussian and Non-Gaussian data*

Description

A collection of functions for calculating point estimates, interval estimates and significance tests of the repeatability (intra-class correlation coefficient) as well as variance components in mixed effects models. The function rpt is a wrapper function that calls more specialised functions as required. Specialised functions can also be called directly (see rpt for details). All functions return lists of

values in the form of an S3 object `rpt`. The function summary.rpt produces summaries in a detailed format and plot.rpt plots bootstraps or permutation results.

Note

Currently there four different functions depending on the distribution and type of response: (1) rptGaussian for a Gaussian response distributions, (2) rptPoisson for Poisson-distributed data, (3) rptBinary for binary response following binomial distributions and (4) rptProportion for response matrices with a column for successes and a column for failures that are analysed as proportions following binomial distributions. All function use a mixed model framework in `lme4`, and the non-Gaussian functions use an observational level random effect to account for overdispersion.

All functions use the argument `formula`, which is the same formula interface as in the `lme4` package (indeed models are fitted by `lmer` or `glmer`). Repeatabilites are calculated for the response variable, while one or more grouping factors of interest can be assigned as random effects in the form (1|group) and have to be specified with the `grname` argument. This allows to estimate adjusted repeatabilities (controlling for fixed effects) and the estimation of multiple variance components simultaneously (multiple random effects). All variables have to be columns in a `data.frame` given in the `data` argument. The `link` argument specifies the link function for a given non-Gaussian distribtion.

The argument `ratio` allows switching to raw variances rather than ratios of variances to be estimated and The argument `adjusted` allows switching to an estimation where the variance explained by fixed effects is included in the denominator of the repeatability calculation. The reserved `grname` terms "Residual", "Overdispersion" and "Fixed" allow the estimation of oversipersion variance, residual variance and variance explained by fixed effects, respectively. All computation can be parallelized with the `parallel` argument, which enhances computation speed for larger computations.

When using `rptR` please cite:

Stoffel, M., Nakagawa, S. & Schielzeth, H. (2017) *rptR: Repeatability estimation and variance decomposition by generalized linear mixed-effects models.*. Methods Ecol Evol. Accepted Author Manuscript. doi:10.1111/2041-210X.12797

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References

Nakagawa, S. & Schielzeth, H. (2010) *Repeatability for Gaussian and non-Gaussian data: a practical guide for biologists*. Biological Reviews 85: 935-956

See Also

Useful links:

- https://github.com/mastoffel/rptR
- Report bugs at https://github.com/mastoffel/rptR/issues

summary.rpt *Summary of a rpt object*

Description

Summary of a rpt object

Usage

```
## S3 method for class 'rpt'
summary(object, ...)
```

Arguments

object	An rpt object returned from one of the rpt functions
...	Additional arguments; none are used in this method.

Author(s)

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References

Nakagawa, S. and Schielzeth, H. (2010) *Repeatability for Gaussian and non-Gaussian data: a practical guide for biologists*. Biological Reviews 85: 935-956

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