Package ‘pbkrtest’

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Title Parametric Bootstrap, Kenward-Roger and Satterthwaite Based Methods for Test in Mixed Models

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Description Test in mixed effects models. Attention is on mixed effects models as implemented in the 'lme4' package. For linear mixed models, this package implements (1) a parametric bootstrap test, (2) a Kenward-Roger-typ modification of F-tests for linear mixed effects models and (3) a Satterthwaite-type modification of F-tests for linear mixed effects models. The package also implements a parametric bootstrap test for generalized linear mixed models. The facilities of the package are documented in the paper by Halehoh and Højsgaard, (2012, <doi:10.18637/jss.v059.i09>). Please see 'citation(``pbkrtest'')' for citation details.

URL https://people.math.aau.dk/~sorenh/software/pbkrtest/

Depends R (>= 3.5.0), lme4 (>= 1.1.10)

Imports broom, dplyr, magrittr, MASS, Matrix (>= 1.2.3), methods, numDeriv, parallel, knitr

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ZipData no

License GPL (>= 2)

ByteCompile Yes

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VignetteBuilder knitr

NeedsCompilation no

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`data-beets` *Sugar beets data*

Description

Yield and sugar percentage in sugar beets from a split plot experiment. Data is obtained from a split plot experiment. There are 3 blocks and in each of these the harvest time defines the "whole plot" and the sowing time defines the "split plot". Each plot was $25m^2$ and the yield is recorded in kg. See 'details' for the experimental layout.

Usage

```
beets
```

Format

A dataframe with 5 columns and 30 rows.

Details

```
Experimental plan
Sowing times            1        4. april
                        2       12. april
                        3       21. april
                        4       29. april
                        5       18. may
Harvest times           1        2. october
                        2       21. october
Plot allocation:
               Block 1     Block 2     Block 3
            +-----------|-----------|-----------+
```

```
Plot  | 1 1 1 1 1 | 2 2 2 2 2 | 1 1 1 1 1 | Harvest time
 1-15 | 3 4 5 2 1 | 3 2 4 5 1 | 5 2 3 4 1 | Sowing time
      |-----------|-----------|-----------|
Plot  | 2 2 2 2 2 | 1 1 1 1 1 | 2 2 2 2 2 | Harvest time
16-30 | 2 1 5 4 3 | 4 1 3 2 5 | 1 4 3 2 5 | Sowing time
      +-----------|-----------|-----------+
```

References

Ulrich Halekoh, Søren Højsgaard (2014)., A Kenward-Roger Approximation and Parametric Bootstrap Methods for Tests in Linear Mixed Models - The R Package pbkrtest., Journal of Statistical Software, 58(10), 1-30., https://www.jstatsoft.org/v59/i09/

Examples

```
data(beets)

beets$bh <- with(beets, interaction(block, harvest))
summary(aov(yield ~ block + sow + harvest + Error(bh), beets))
summary(aov(sugpct ~ block + sow + harvest + Error(bh), beets))
```

`data-budworm` *budworm data*

Description

Effect of Insecticide on survivial of tobacco budworms number of killed budworms exposed to an insecticidepp mortality of the moth tobacco budworm 'Heliothis virescens' for 6 doses of the pyrethroid trans-cypermethrin differentiated with respect to sex

Usage

```
budworm
```

Format

This data frame contains 12 rows and 4 columns:

sex: sex of the budworm

dose: dose of the insecticide trans-cypermethrin in [μg]

ndead: budworms killed in a trial

ntotal: total number of budworms exposed per trial

Source

Collet, D. (1991) Modelling Binary Data, Chapman & Hall, London, Example 3.7

References

Venables, W.N; Ripley, B.D.(1999) Modern Applied Statistics with S-Plus, Heidelberg, Springer, 3rd edition, chapter 7.2

Examples

```
data(budworm)

## function to caclulate the empirical logits
empirical.logit<- function(nevent,ntotal) {
   y <- log((nevent + 0.5) / (ntotal - nevent + 0.5))
   y
}


# plot the empirical logits against log-dose

log.dose <- log(budworm$dose)
emp.logit <- empirical.logit(budworm$ndead, budworm$ntotal)
plot(log.dose, emp.logit, type='n', xlab='log-dose',ylab='emprirical logit')
title('budworm: emprirical logits of probability to die ')
male <- budworm$sex=='male'
female <- budworm$sex=='female'
lines(log.dose[male], emp.logit[male], type='b', lty=1, col=1)
lines(log.dose[female], emp.logit[female], type='b', lty=2, col=2)
legend(0.5, 2, legend=c('male', 'female'), lty=c(1,2), col=c(1,2))

## Not run:
* SAS example;
data budworm;
infile 'budworm.txt' firstobs=2;
input sex dose ndead ntotal;
run;

## End(Not run)
```

---

getkr *Extract (or "get") components from a* `KRmodcomp` *object.*

Description

Extract (or "get") components from a `KRmodcomp` object, which is the result of the `KRmodcomp` function.

Usage

```
getKR(
  object,
 name = c("ndf", "ddf", "Fstat", "p.value", "F.scaling", "FstatU", "p.valueU", "aux")
)
```

Arguments

object	A KRmodcomp object, which is the result of the KRmodcomp function
name	The available slots. If name is missing or NULL then everything is returned.

Author(s)

Søren Højsgaard <sorenh@math.aau.dk>

References

Ulrich Halekoh, Søren Højsgaard (2014)., A Kenward-Roger Approximation and Parametric Bootstrap Methods for Tests in Linear Mixed Models - The R Package pbkrtest., Journal of Statistical Software, 58(10), 1-30., https://www.jstatsoft.org/v59/i09/

See Also

KRmodcomp, PBmodcomp, vcovAdj

Examples

```
data(beets, package='pbkrtest')
lg <- lmer(sugpct ~ block + sow + harvest + (1|block:harvest),
              data=beets, REML=FALSE)
sm <- update(lg, .~. - harvest)
modcomp <- KRmodcomp(lg, sm)
getKR(modcomp, "ddf") # get denominator degrees of freedom.
```

---

get_ddf_Lb *Adjusted denomintor degress freedom for linear estimate for linear mixed model.*

Description

Get adjusted denomintor degress freedom for testing Lb=0 in a linear mixed model where L is a restriction matrix.

Usage

```
get_Lb_ddf(object, L)

## S3 method for class 'lmerMod'
get_Lb_ddf(object, L)

get_ddf_Lb(object, Lcoef)

## S3 method for class 'lmerMod'
get_ddf_Lb(object, Lcoef)

Lb_ddf(L, V0, Vadj)

ddf_Lb(VVa, Lcoef, VV0 = VVa)
```

Arguments

`object`	A linear mixed model object.
`L`	A vector with the same length as `fixef(object)` or a matrix with the same number of columns as the length of `fixef(object)`
`Lcoef`	Linear contrast matrix
`V0, Vadj`	Unadjusted and adjusted covariance matrix for the fixed effects parameters. Undjusted covariance matrix is obtained with `vcov()` and adjusted with `vcovAdj()`.
`VVa`	Adjusted covariance matrix
`VV0`	Unadjusted covariance matrix

Value

Adjusted degrees of freedom (adjusment made by a Kenward-Roger approximation).

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

References

Ulrich Halekoh, Søren Højsgaard (2014)., A Kenward-Roger Approximation and Parametric Bootstrap Methods for Tests in Linear Mixed Models - The R Package pbkrtest., Journal of Statistical Software, 58(10), 1-30., https://www.jstatsoft.org/v59/i09/

See Also

KRmodcomp, vcovAdj, model2remat, remat2model

Examples

```
(fmLarge <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy))
## removing Days
(fmSmall <- lmer(Reaction ~ 1 + (Days|Subject), sleepstudy))
anova(fmLarge,fmSmall)

KRmodcomp(fmLarge, fmSmall)  ## 17 denominator df's
get_Lb_ddf(fmLarge, c(0,1))  ## 17 denominator df's

# Notice: The restriction matrix L corresponding to the test above
# can be found with
L <- model2remat(fmLarge, fmSmall)
L
```

`internal` *Internal functions for the pbkrtest package*

Description

These functions are not intended to be called directly.

`internal-pbkrtest` *pbkrtest internal*

Description

pbkrtest internal

`kr-modcomp` *F-test and degrees of freedom based on Kenward-Roger approximation*

Description

An approximate F-test based on the Kenward-Roger approach.

Usage

```
KRmodcomp(largeModel, smallModel, betaH = 0, details = 0)

## S3 method for class 'lmerMod'
KRmodcomp(largeModel, smallModel, betaH = 0, details = 0)
```

Arguments

largeModel	An lmer model
smallModel	An lmer model or a restriction matrix
betaH	A number or a vector of the beta of the hypothesis, e.g. L beta=L betaH. betaH=0 if modelSmall is a model not a restriction matrix.
details	If larger than 0 some timing details are printed.

Details

The model object must be fitted with restricted maximum likelihood (i.e. with REML=TRUE). If the object is fitted with maximum likelihood (i.e. with REML=FALSE) then the model is refitted with REML=TRUE before the p-values are calculated. Put differently, the user needs not worry about this issue.

An F test is calculated according to the approach of Kenward and Roger (1997). The function works for linear mixed models fitted with the lmer function of the **lme4** package. Only models where the covariance structure is a sum of known matrices can be compared.

The largeModel may be a model fitted with lmer either using REML=TRUE or REML=FALSE. The smallModel can be a model fitted with lmer. It must have the same covariance structure as largeModel. Furthermore, its linear space of expectation must be a subspace of the space for largeModel. The model smallModel can also be a restriction matrix L specifying the hypothesis $L\beta = L\beta_H$, where L is a $k \times p$ matrix and β is a p column vector the same length as fixef(largeModel).

The β_H is a p column vector.

Notice: if you want to test a hypothesis $L\beta = c$ with a k vector c, a suitable β_H is obtained via $\beta_H = Lc$ where L_n is a g-inverse of L.

Notice: It cannot be guaranteed that the results agree with other implementations of the Kenward-Roger approach!

Note

This functionality is not thoroughly tested and should be used with care. Please do report bugs etc.

Author(s)

Ulrich Halekoh <uhalekoh@health.sdu.dk>, Søren Højsgaard <sorenh@math.aau.dk>

References

Ulrich Halekoh, Søren Højsgaard (2014)., A Kenward-Roger Approximation and Parametric Bootstrap Methods for Tests in Linear Mixed Models - The R Package pbkrtest., Journal of Statistical Software, 58(10), 1-30., https://www.jstatsoft.org/v59/i09/

Kenward, M. G. and Roger, J. H. (1997), *Small Sample Inference for Fixed Effects from Restricted Maximum Likelihood*, Biometrics 53: 983-997.

See Also

getKR, lmer, vcovAdj, PBmodcomp

Examples

```
(fmLarge <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy))
## removing Days
(fmSmall <- lmer(Reaction ~ 1 + (Days|Subject), sleepstudy))
anova(fmLarge,fmSmall)
KRmodcomp(fmLarge,fmSmall)

## The same test using a restriction matrix
L <- cbind(0,1)
KRmodcomp(fmLarge, L)

## Same example, but with independent intercept and slope effects:
m.large  <- lmer(Reaction ~ Days + (1|Subject) + (0+Days|Subject), data = sleepstudy)
m.small  <- lmer(Reaction ~ 1 + (1|Subject) + (0+Days|Subject), data = sleepstudy)
anova(m.large, m.small)
KRmodcomp(m.large, m.small)
```

---

kr-vcov *Ajusted covariance matrix for linear mixed models according to Kenward and Roger*

Description

Kenward and Roger (1997) describbe an improved small sample approximation to the covariance matrix estimate of the fixed parameters in a linear mixed model.

Usage

```
vcovAdj(object, details = 0)

## S3 method for class 'lmerMod'
vcovAdj(object, details = 0)
```

Arguments

object	An `lmer` model
details	If larger than 0 some timing details are printed.

Value

phiA	the estimated covariance matrix, this has attributed P, a list of matrices used in `KR_adjust` and the estimated matrix W of the variances of the covariance parameters of the random effetcs
SigmaG	list: Sigma: the covariance matrix of Y; G: the G matrices that sum up to Sigma; n.ggamma: the number (called M in the article) of G matrices)

Note

If N is the number of observations, then the `vcovAdj()` function involves inversion of an $N x N$ matrix, so the computations can be relatively slow.

Author(s)

Ulrich Halekoh <uhalekoh@health.sdu.dk>, Søren Højsgaard <sorenh@math.aau.dk>

References

Ulrich Halekoh, Søren Højsgaard (2014)., A Kenward-Roger Approximation and Parametric Bootstrap Methods for Tests in Linear Mixed Models - The R Package pbkrtest., Journal of Statistical Software, 58(10), 1-30., https://www.jstatsoft.org/v59/i09/

Kenward, M. G. and Roger, J. H. (1997), *Small Sample Inference for Fixed Effects from Restricted Maximum Likelihood*, Biometrics 53: 983-997.

See Also

getKR, KRmodcomp, lmer, PBmodcomp, vcovAdj

Examples

```
fm1 <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy)
class(fm1)

## Here the adjusted and unadjusted covariance matrices are identical,
## but that is not generally the case:

v1 <- vcov(fm1)
v2 <- vcovAdj(fm1, details=0)
v2 / v1

## For comparison, an alternative estimate of the variance-covariance
## matrix is based on parametric bootstrap (and this is easily
## parallelized):

## Not run:
nsim <- 100
sim <- simulate(fm.ml, nsim)
B <- lapply(sim, function(newy) try(fixef(refit(fm.ml, newresp=newy))))
B <- do.call(rbind, B)
v3 <- cov.wt(B)$cov
v2/v1
v3/v1

## End(Not run)
```

model-coerce — *Conversion between a model object and a restriction matrix*

Description

Testing a small model under a large model corresponds imposing restrictions on the model matrix of the larger model and these restrictions come in the form of a restriction matrix. These functions converts a model to a restriction matrix and vice versa.

Usage

```
model2remat(largeModel, smallModel, sparse = FALSE)

remat2model(largeModel, L, REML = TRUE, ...)

make_modelmat(X, L)

make_remat(X, X2)
```

Arguments

`largeModel, smallModel`	Model objects of the same "type". Possible types are linear mixed effects models and linear models (including generalized linear models)
`sparse`	Should the restriction matrix be sparse or dense?
`L`	A restriction matrix; a full rank matrix with as many columns as ‘X‘ has.
`REML`	Controls if new model object should be fitted with REML or ML.
`...`	Additional arguments; not used.
`X, X2`	Model matrices. Must have same numer of rows.

Details

‘make_remat‘ Make a restriction matrix. If span(X2) is in span(X) then the corresponding restriction matrix ‘L‘ is returned.

Value

`model2remat`: A restriction matrix. `remat2model`: A model object.

Note

That these functions are visible is a recent addition; minor changes may occur.

Author(s)

Ulrich Halekoh <uhalekoh@health.sdu.dk>, Søren Højsgaard <sorenh@math.aau.dk>

References

Ulrich Halekoh, Søren Højsgaard (2014)., A Kenward-Roger Approximation and Parametric Bootstrap Methods for Tests in Linear Mixed Models - The R Package pbkrtest., Journal of Statistical Software, 58(10), 1-30., https://www.jstatsoft.org/v59/i09/

See Also

PBmodcomp, PBrefdist, KRmodcomp

Examples

```
library(pbkrtest)
data("beets", package = "pbkrtest")
sug <- lm(sugpct ~ block + sow + harvest, data=beets)
sug.h <- update(sug, .~. - harvest)
sug.s <- update(sug, .~. - sow)

## Construct restriction matrices from models
L.h <- model2remat(sug, sug.h); L.h
L.s <- model2remat(sug, sug.s); L.s

## Construct submodels from restriction matrices
mod.h <- remat2model(sug, L.h); mod.h
mod.s <- remat2model(sug, L.s); mod.s

## Sanity check: The models have the same fitted values and log likelihood
plot(fitted(mod.h), fitted(sug.h))
plot(fitted(mod.s), fitted(sug.s))
logLik(mod.h)
logLik(sug.h)
logLik(mod.s)
logLik(sug.s)
```

---

pb-modcomp *Model comparison using parametric bootstrap methods.*

Description

Model comparison of nested models using parametric bootstrap methods. Implemented for some commonly applied model types.

Usage

```
PBmodcomp(
  largeModel,
  smallModel,
  nsim = 1000,
  ref = NULL,
  seed = NULL,
```

```
  cl = NULL,
  details = 0
)

## S3 method for class 'merMod'
PBmodcomp(
  largeModel,
  smallModel,
  nsim = 1000,
  ref = NULL,
  seed = NULL,
  cl = NULL,
  details = 0
)

## S3 method for class 'lm'
PBmodcomp(
  largeModel,
  smallModel,
  nsim = 1000,
  ref = NULL,
  seed = NULL,
  cl = NULL,
  details = 0
)

seqPBmodcomp(largeModel, smallModel, h = 20, nsim = 1000, cl = 1)
```

Arguments

`largeModel`	A model object. Can be a linear mixed effects model or generalized linear mixed effects model (as fitted with `lmer()` and `glmer()` function in the **lme4** package) or a linear normal model or a generalized linear model. The `largeModel` must be larger than `smallModel` (see below).
`smallModel`	A model of the same type as `largeModel` or a restriction matrix.
`nsim`	The number of simulations to form the reference distribution.
`ref`	Vector containing samples from the reference distribution. If NULL, this vector will be generated using PBrefdist().
`seed`	A seed that will be passed to the simulation of new datasets.
`cl`	A vector identifying a cluster; used for calculating the reference distribution using several cores. See examples below.
`details`	The amount of output produced. Mainly relevant for debugging purposes.
`h`	For sequential computing for bootstrap p-values: The number of extreme cases needed to generate before the sampling proces stops.

Details

The model `object` must be fitted with maximum likelihood (i.e. with `REML=FALSE`). If the object is fitted with restricted maximum likelihood (i.e. with `REML=TRUE`) then the model is refitted with `REML=FALSE` before the p-values are calculated. Put differently, the user needs not worry about this issue.

Under the fitted hypothesis (i.e. under the fitted small model) `nsim` samples of the likelihood ratio test statistic (LRT) are generetated.

Then p-values are calculated as follows:

LRT: Assuming that LRT has a chi-square distribution.

PBtest: The fraction of simulated LRT-values that are larger or equal to the observed LRT value.

Bartlett: A Bartlett correction is of LRT is calculated from the mean of the simulated LRT-values

Gamma: The reference distribution of LRT is assumed to be a gamma distribution with mean and variance determined as the sample mean and sample variance of the simulated LRT-values.

F: The LRT divided by the number of degrees of freedom is assumed to be F-distributed, where the denominator degrees of freedom are determined by matching the first moment of the reference distribution.

Note

It can happen that some values of the LRT statistic in the reference distribution are negative. When this happens one will see that the number of used samples (those where the LRT is positive) are reported (this number is smaller than the requested number of samples).

In theory one can not have a negative value of the LRT statistic but in practice on can: We speculate that the reason is as follows: We simulate data under the small model and fit both the small and the large model to the simulated data. Therefore the large model represents - by definition - an overfit; the model has superfluous parameters in it. Therefore the fit of the two models will for some simulated datasets be very similar resulting in similar values of the log-likelihood. There is no guarantee that the the log-likelihood for the large model in practice always will be larger than for the small (convergence problems and other numerical issues can play a role here).

To look further into the problem, one can use the `PBrefdist()` function for simulating the reference distribution (this reference distribution can be provided as input to `PBmodcomp()`). Inspection sometimes reveals that while many values are negative, they are numerically very small. In this case one may try to replace the negative values by a small positive value and then invoke `PBmodcomp()` to get some idea about how strong influence there is on the resulting p-values. (The p-values get smaller this way compared to the case when only the originally positive values are used).

Author(s)

Søren Højsgaard <sorenh@math.aau.dk>

References

Ulrich Halekoh, Søren Højsgaard (2014)., A Kenward-Roger Approximation and Parametric Bootstrap Methods for Tests in Linear Mixed Models - The R Package pbkrtest., Journal of Statistical Software, 58(10), 1-30., https://www.jstatsoft.org/v59/i09/

See Also

KRmodcomp, PBrefdist

Examples

```
data(beets, package="pbkrtest")
head(beets)

NSIM <- 50 ## Simulations in parametric bootstrap

## Linear mixed effects model:
sug   <- lmer(sugpct ~ block + sow + harvest + (1|block:harvest),
              data=beets, REML=FALSE)
sug.h <- update(sug, .~. -harvest)
sug.s <- update(sug, .~. -sow)

anova(sug, sug.h)
PBmodcomp(sug, sug.h, nsim=NSIM, cl=1)
anova(sug, sug.h)
PBmodcomp(sug, sug.s, nsim=NSIM, cl=1)

## Linear normal model:
sug <- lm(sugpct ~ block + sow + harvest, data=beets)
sug.h <- update(sug, .~. -harvest)
sug.s <- update(sug, .~. -sow)

anova(sug, sug.h)
PBmodcomp(sug, sug.h, nsim=NSIM, cl=1)
anova(sug, sug.s)
PBmodcomp(sug, sug.s, nsim=NSIM, cl=1)

## Generalized linear model
counts    <- c(18, 17, 15, 20, 10, 20, 25, 13, 12)
outcome   <- gl(3, 1, 9)
treatment <- gl(3, 3)
d.AD      <- data.frame(treatment, outcome, counts)
head(d.AD)
glm.D93   <- glm(counts ~ outcome + treatment, family = poisson())
glm.D93.o <- update(glm.D93, .~. -outcome)
glm.D93.t <- update(glm.D93, .~. -treatment)

anova(glm.D93, glm.D93.o, test="Chisq")
PBmodcomp(glm.D93, glm.D93.o, nsim=NSIM, cl=1)
anova(glm.D93, glm.D93.t, test="Chisq")
PBmodcomp(glm.D93, glm.D93.t, nsim=NSIM, cl=1)

## Generalized linear mixed model (it takes a while to fit these)
## Not run:
(gm1 <- glmer(cbind(incidence, size - incidence) ~ period + (1 | herd),
              data = cbpp, family = binomial))
(gm2 <- update(gm1, .~.-period))
```

```
anova(gm1, gm2)
PBmodcomp(gm1, gm2, cl=2)

## End(Not run)


## Not run:
(fmLarge <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy))
## removing Days
(fmSmall <- lmer(Reaction ~ 1 + (Days|Subject), sleepstudy))
anova(fmLarge, fmSmall)
PBmodcomp(fmLarge, fmSmall, cl=1)

## The same test using a restriction matrix
L <- cbind(0,1)
PBmodcomp(fmLarge, L, cl=1)

## Vanilla
PBmodcomp(beet0, beet_no.harv, nsim=NSIM, cl=1)

## Simulate reference distribution separately:
refdist <- PBrefdist(beet0, beet_no.harv, nsim=1000)
PBmodcomp(beet0, beet_no.harv, ref=refdist, cl=1)

## Do computations with multiple processors:
## Number of cores:
(nc <- detectCores())
## Create clusters
cl <- makeCluster(rep("localhost", nc))

## Then do:
PBmodcomp(beet0, beet_no.harv, cl=cl)

## Or in two steps:
refdist <- PBrefdist(beet0, beet_no.harv, nsim=NSIM, cl=cl)
PBmodcomp(beet0, beet_no.harv, ref=refdist)

## It is recommended to stop the clusters before quitting R:
stopCluster(cl)

## End(Not run)

## Linear and generalized linear models:

m11 <- lm(dist ~ speed + I(speed^2), data=cars)
m10 <- update(m11, ~.-I(speed^2))
anova(m11, m10)

PBmodcomp(m11, m10, cl=1, nsim=NSIM)
PBmodcomp(m11, ~.-I(speed^2), cl=1, nsim=NSIM)
PBmodcomp(m11, c(0, 0, 1), cl=1, nsim=NSIM)

m21 <- glm(dist ~ speed + I(speed^2), family=Gamma("identity"), data=cars)
```

```
m20 <- update(m21, ~.-I(speed^2))
anova(m21, m20, test="Chisq")

PBmodcomp(m21, m20, cl=1, nsim=NSIM)
PBmodcomp(m21, ~.-I(speed^2), cl=1, nsim=NSIM)
PBmodcomp(m21, c(0, 0, 1), cl=1, nsim=NSIM)
```

---

pb-refdist *Calculate reference distribution using parametric bootstrap*

Description

Calculate reference distribution of likelihood ratio statistic in mixed effects models using parametric bootstrap

Usage

```
PBrefdist(
  largeModel,
  smallModel,
  nsim = 1000,
  seed = NULL,
  cl = NULL,
  details = 0
)

## S3 method for class 'lm'
PBrefdist(
  largeModel,
  smallModel,
  nsim = 1000,
  seed = NULL,
  cl = NULL,
  details = 0
)

## S3 method for class 'merMod'
PBrefdist(
  largeModel,
  smallModel,
  nsim = 1000,
  seed = NULL,
  cl = NULL,
  details = 0
)
```

Arguments

- `largeModel` — A linear mixed effects model as fitted with the `lmer()` function in the **lme4** package. This model muse be larger than `smallModel` (see below).
- `smallModel` — A linear mixed effects model as fitted with the `lmer()` function in the **lme4** package. This model muse be smaller than `largeModel` (see above).
- `nsim` — The number of simulations to form the reference distribution.
- `seed` — Seed for the random number generation.
- `cl` — Used for controlling parallel computations. See sections 'details' and 'examples' below.
- `details` — The amount of output produced. Mainly relevant for debugging purposes.

Details

The model `object` must be fitted with maximum likelihood (i.e. with `REML=FALSE`). If the object is fitted with restricted maximum likelihood (i.e. with `REML=TRUE`) then the model is refitted with `REML=FALSE` before the p-values are calculated. Put differently, the user needs not worry about this issue.

The argument 'cl' (originally short for 'cluster') is used for controlling parallel computations. 'cl' can be NULL (default), positive integer or a list of clusters.

Special care must be taken on Windows platforms (described below) but the general picture is this:

The recommended way of controlling cl is to specify the component `pbcl` in options() with e.g. `options("pbcl"=4)`.

If cl is NULL, the function will look at if the pbcl has been set in the options list with `getOption("pbcl")`

If cl=N then N cores will be used in the computations. If cl is NULL then the function will look for

Value

A numeric vector

Author(s)

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References

Ulrich Halekoh, Søren Højsgaard (2014)., A Kenward-Roger Approximation and Parametric Bootstrap Methods for Tests in Linear Mixed Models - The R Package pbkrtest., Journal of Statistical Software, 58(10), 1-30., https://www.jstatsoft.org/v59/i09/

See Also

PBmodcomp, KRmodcomp

Examples

```
data(beets)
head(beets)
beet0 <- lmer(sugpct ~ block + sow + harvest + (1|block:harvest), data=beets, REML=FALSE)
beet_no.harv <- update(beet0, . ~ . -harvest)
rd <- PBrefdist(beet0, beet_no.harv, nsim=20, cl=1)
rd
## Not run:
## Note: Many more simulations must be made in practice.

# Computations can be made in parallel using several processors:

# 1: On OSs that fork processes (that is, not on windows):
# --------------------------------------------------------

if (Sys.info()["sysname"] != "Windows"){
  N <- 2 ## Or N <- parallel::detectCores()

# N cores used in all calls to function in a session
  options("mc.cores"=N)
  rd <- PBrefdist(beet0, beet_no.harv, nsim=20)

# N cores used just in one specific call (when cl is set,
# options("mc.cores") is ignored):
  rd <- PBrefdist(beet0, beet_no.harv, nsim=20, cl=N)
}

# In fact, on Windows, the approach above also work but only when setting the
# number of cores to 1 (so there is to parallel computing)

# In all calls:
# options("mc.cores"=1)
# rd <- PBrefdist(beet0, beet_no.harv, nsim=20)
# Just once
# rd <- PBrefdist(beet0, beet_no.harv, nsim=20, cl=1)

# 2. On all platforms (also on Windows) one can do
# ------------------------------------------------
library(parallel)
N <- 2 ## Or N  <- detectCores()
clus <- makeCluster(rep("localhost", N))

# In all calls in a session
options("pb.cl"=clus)
rd <- PBrefdist(beet0, beet_no.harv, nsim=20)

# Just once:
rd <- PBrefdist(beet0, beet_no.harv, nsim=20, cl=clus)
stopCluster(clus)

## End(Not run)
```

sat-modcomp — *F-test and degrees of freedom based on Satterthwaite approximation*

Description

An approximate F-test based on the Satterthwaite approach.

Usage

```
SATmodcomp(
  largeModel,
  smallModel,
  details = 0,
  eps = sqrt(.Machine$double.eps)
)

## S3 method for class 'lmerMod'
SATmodcomp(
  largeModel,
  smallModel,
  details = 0,
  eps = sqrt(.Machine$double.eps)
)
```

Arguments

`largeModel`	An `lmerMod` model.
`smallModel`	An `lmerMod` model, a restriction matrix or a model formula. See example section.
`details`	If larger than 0 some timing details are printed.
`eps`	A small number.

Details

Notice: It cannot be guaranteed that the results agree with other implementations of the Satterthwaite approach!

Note

This code is greatly inspired by code in the lmerTest package. This is a recent addition to the pbkrtest package; please report unexpected behaviour.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

References

Ulrich Halekoh, Søren Højsgaard (2014)., A Kenward-Roger Approximation and Parametric Bootstrap Methods for Tests in Linear Mixed Models - The R Package pbkrtest., Journal of Statistical Software, 58(10), 1-30., https://www.jstatsoft.org/v59/i09/

See Also

getKR, lmer, vcovAdj, PBmodcomp

Examples

```
(fm1 <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy))
L1 <- cbind(0,1)
SATmodcomp(fm1, L1)

(fm2 <- lmer(Reaction ~ Days + I(Days^2) + (Days|Subject), sleepstudy))

## Test for no effect of Days. There are three ways of using the function:

## 1) Define 2-df contrast - since L has 2 (linearly independent) rows
## the F-test is on 2 (numerator) df:
L2 <- rbind(c(0, 1, 0), c(0, 0, 1))
SATmodcomp(fm2, L2)

## 2) Use two model objects
fm3 <- update(fm2, ~. - Days - I(Days^2))
SATmodcomp(fm2, fm3)

## 3) Specify restriction as formula
SATmodcomp(fm2, ~. - Days - I(Days^2))
```

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