

Package ‘pbkrtest’

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Title Parametric bootstrap and Kenward Roger based methods for mixed model comparison

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Description Test in linear mixed effects models.

Attention is on linear mixed effects models as implemented in the lme4 package.

The package implements a parametric bootstrap test

The package implements a Kenward-Roger modification of F-tests

URL <http://people.math.aau.dk/~sorenh/software/pbkrtest/>

Depends MASS,lme4,parallel

Imports Matrix

Suggests gplots

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beets	<i>Yield and sugar percentage in sugar beets from a split plot experiment.</i>
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Description

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

```
data(beets)
```

Format

The format is: chr "beets"

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
	+++++	+++++	+++++	

Examples

```
data(beets)
## maybe str(beets) ; plot(beets) ...

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

budworm

Effect of Insecticide on survival of tobacco budworms

Description

number of killed budworms exposed to an insecticide

Usage

```
data(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

Details

mortality of the moth tobacco budworm 'Heliothis virescens' for 6 doses of the pyrethroid trans-cypermethrin differentiated with respect to sex

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)

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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)
xx<-KRmodcomp(lg, sm)
getKR(xx, "ddf") # get denominator degrees of freedom.
```

 KenwardRoger

Ftest 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 'mer'
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.
 ... Additional arguments to print function

Details

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)

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References

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)
```

```
KRmodcomp_init      Model input check
```

Description

Utility functions check the models for KRmodcomp.lmer function. Not to be used directly by the user

Usage

```
KRmodcomp_init(m1, m2, matrixOK=FALSE)
## S3 method for class 'mer'
KRmodcomp_init(m1, m2, matrixOK=FALSE)
## S3 method for class 'lmerMod'
KRmodcomp_init(m1, m2, matrixOK=FALSE)
```

Arguments

m1	lmer model
m2	lmer model or restriction matrix
matrixOK	if FALSE then m2 must not be a restriction matrix but a lmer model, if TRUE m2 may also be a restriction matrix

Details

The function checks whether m1 is an lmer model and m2 either an lmer model or a restriction matrix. Furthermore, it is checked whether the fixed effects space of m2 is a subspace of m1. In the following $\langle m1 \rangle$ is the fixed effects space of model m1.

Value

code -1: $\langle m1 \rangle = \langle m2 \rangle$, 0: $\langle m1 \rangle < \langle m2 \rangle$, 1: $\langle m1 \rangle > \langle m2 \rangle$

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See Also

[lmer.](#)

PBmodcomp	<i>Model comparison of mixed models using parametric bootstrap methods.</i>
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Description

Model comparison of mixed models using parametric bootstrap methods.

Usage

```
PBmodcomp(largeModel, smallModel, nsim = 1000, ref = NULL, cl = NULL, details = 0)
```

Arguments

largeModel	A linear mixed effects model as fitted with the <code>lmer()</code> function in the lme4 package. This model must be larger than <code>smallModel</code> (see below).
smallModel	A linear mixed effects model as fitted with the <code>lmer()</code> function in the lme4 package. This model must be smaller than <code>largeModel</code> (see above).
nsim	The number of simulations to form the reference distribution.
ref	Vector containing samples from the reference distribution. If <code>NULL</code> , this vector will be generated using <code>PBrefdist()</code> .
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.

Details

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

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 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.

Note

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

Author(s)

Søren Højsgaard <sorenh@math.aau.dk>

See Also

[KRmodcomp](#) [PBrefdist](#)

Examples

```
data(beets)
head(beets)
beet0<-lmer(supct~block+sow+harvest+(1|block:harvest), data=beets, REML=FALSE)
beet_no.harv <- update(beet0, .~-harvest)
PBmodcomp(beet0, beet_no.harv, nsim=20)

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

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

## Vanilla
PBmodcomp(beet0, beet_no.harv, nsim=1000)

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

## 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=1000, cl=cl)
PBmodcomp(beet0, beet_no.harv, ref=refdist)

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

## End(Not run)
```

PBrefdist

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)
```

Arguments

largeModel	A linear mixed effects model as fitted with the <code>lmer()</code> function in the lme4 package. This model must be larger than <code>smallModel</code> (see below).
smallModel	A linear mixed effects model as fitted with the <code>lmer()</code> function in the lme4 package. This model must be smaller than <code>largeModel</code> (see above).
nsim	The number of simulations to form the reference distribution.
seed	Seed for the random number generation.
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.

Value

A numeric vector

Author(s)

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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)
rr <- PBrefdist(beet0, beet_no.harv, nsim=20)
rr

## Note clearly many more than 10 simulations must be made in practice.

## Computations can be made in parallel using several processors:
## Not run:
cl <- makeSOCKcluster(rep("localhost", 4))
clusterEvalQ(cl, library(lme4))
clusterSetupSPRNG(cl)
rr <- PBrefdist(beet0, beet_no.harv, nsim=20)
stopCluster(cl)

## End(Not run)
## Above, 4 cpu's are used and 5 simulations are made on each cpu.

```

vcovAdj

Adjusted covariance matrix for linear mixed models according to Kenward and Roger

Description

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

Usage

```

vcovAdj(object, details=0)
LMM_Sigma_G(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 effects
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

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

Author(s)

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References

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

```
(fmLarge <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy))  
## removing Day  
(vcovAdj(fmLarge,detail=0))
```

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