Package 'minque'

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Type Package

Title Various Linear Mixed Model Analyses

Version 2.0.0

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Description This package offers three important components: (1) to construct a use-defined linear mixed model, (2) to employ one of linear mixed model approaches: minimum norm quadratic unbiased estimation (MINQUE) (Rao, 1971) for variance component estimation and random effect prediction; and (3) to employ a jackknife resampling technique to conduct various statistical tests. In addition, this package provides the function for model or data evaluations.This R package offers fast computations for large data sets analyses for various irregular data structures.

License GPL-3

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`minque-package` *Various Linear Mixed Model Analyses*

Description

This package offers three important components: (1) to construct a use-defined linear mixed model, (2) to employ one of linear mixed model approaches: minimum norm quadratic unbiased estimation (MINQUE) (Rao, 1971) for variance component estimation and random effect prediction;(3) to employ a jackknife resampling technique to conduct various statistical tests; and (4) to conduct various model evaluations. This R package offers fast computations for large data sets analyses for various irregular data structures.

Details

Package:	minque
Type:	Package
Version:	2.0
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License:	GPL-3

An overview of how to use the package, including the most important functions

Author(s)

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References

Miller, R. G. 1974. The jackknife - a review. Biometrika, 61:1- 15.

Patterson, H. D. and Thompson, R. 1971. Recovery of inter-block information when block sizes are unequal. Biometrika, 58: 545-554.

Rao, C.R. 1971. Estimation of variance and covariance components-MINQUE theory. J Multiva Ana 1:19

Rao, C. R. and Kleffe, J. 1980. Estimation of variance components. In Handbook of Statistics. Vol. l: 1-40. Krishnaiah, P. R. ed. New York. North-Holland.

Searle, S. R., Casella, G. and McCulloch, C. E. 1992. Variance Components. John Wiley & Sons, Inc. New York.

Wu J (2012) GenMod: An R package for various agricultural data analyses. ASA, CSSA, and SSSA 2012 International Annual Meetings, Cincinnati, OH, p 127

Wu J., Bondalapati K., Glover K., Berzonsky W., Jenkins J.N., McCarty J.C. 2013. Genetic analysis without replications: model evaluation and application in spring wheat. Euphytica. 190:447-458

Zhu J. 1989. Estimation of Genetic Variance Components in the General Mixed Model. Ph.D. Dissertation, NC State University, Raleigh, U.S.A

Zhu J. 1993. Methods of predicting genotype value and heterosis for offspring of hybrids. (Chinese). Journal of Biomathematics, 8(1): 32-44

`brate` *Cotton boll retention rate data*

Description

This data set contains boll retention of 10 cotton plants for 5 genotypes and 13 nodes. This data set can be analyzed in many ways: factorial factor design (genotype and position) or as split-plot design. For example, this data set can be analyzed by user-defined model as shown in the example.

Usage

```
data(brate)
```

Format

A data frame with 338 observations on the following 5 variables.

`Year` year of 2009

`Geno` genotypes from 1 to 5

`Pos` plant nodes from 5 to 17

`Rep` field blocks from 1 to 4

`Brate` mean boll retention for the first position over 10 plants

Details

No other details are needed

Source

No references or URLs available.

References

No reference available

Examples

```
library(minque)

data(brate)
head(brate)
brate$Geno=factor(brate$Geno)
brate$Pos=factor(brate$Pos)
brate$Rep=factor(brate$Rep)

res=lmm(Brate~1|Geno*Pos+Rep,data=brate)
res$Var
res$FixedEffect
res$RandomEffect

res=lmm.jack(Brate~1|Geno*Pos+Rep,data=brate,JacNum=10,JacRep=1,ALPHA=0.05)
res$Var
res$PVar
res$FixedEffect
res$RandomEffect
## end
```

---

cot *Twenty four cotton genotypes with four agronomic traits*

Description

Twentype four cotton genotypes were evaluated under two locations at the Mississippi State University Research Farm.

Usage

```
data(cot)
```

Format

A data frame with 288 observations on the following 7 variables.

`LOC` location

`Geno` genotypes

`REP` field blocks

`BN` Boll number

`BS` Boll size

`LP` Lint percentage

`LY` Lint yield

Details

No other details are needed

Source

Not available

References

To be added

Examples

```
##Sample R codes used to analyze the data set: cot
 library(minque)
 data(cot)
 names(cot)
 cot$Geno=factor(cot$Geno)
 cot$Loc=factor(cot$LOC)
 cot$Rep=factor(cot$REP)

 res=lmm(LY~1|Geno*Loc+Loc:Rep,data=cot)
 res$Var
 res$FixedEffect
 res$RandomEffect

 res=lmm.jack(LY~1|Geno*Loc+Loc:Rep,data=cot,JacNum=10,JacRep=1,ALPHA=0.05)
 res$Var
 res$PVar
 res$FixedEffect
 res$RandomEffect



 ##End
```

`lmm` *An R function for linear mixed model analysis.*

Description

An R function for linear mixed model analysis with REML and/or MINQUE approaches

Usage

```
lmm(formula,data = list(), method = NULL, ALPHA = NULL)
```

Arguments

formula	A linear mixed model formula.
data	Data frame. It can be default.
method	The default linear mixed model approach is MINQUE. Users can choose both or one of two linear mixed model approaches, REML and MINQUE.
ALPHA	A preset nominal probability level.

Details

No data frame is needed when more than one response variables are analyzed

Value

Return list of simulated results for variance components

Author(s)

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References

Miller, R. G. 1974. The jackknife - a review. Biometrika, 61:1- 15.

Rao, C.R. 1971. Estimation of variance and covariance components-MINQUE theory. J Multiva Ana 1:19

Rao, C. R. and Kleffe, J. 1980. Estimation of variance components. In Handbook of Statistics. Vol. l: 1-40. Krishnaiah, P. R. ed. New York. North-Holland.

Searle, S. R., Casella, G. and McCulloch, C. E. 1992. Variance Components. John Wiley & Sons, Inc. New York.

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Wu J., Bondalapati K., Glover K., Berzonsky W., Jenkins J.N., McCarty J.C. 2013. Genetic analysis without replications: model evaluation and application in spring wheat. Euphytica. 190:447-458

Zhu J. 1989. Estimation of Genetic Variance Components in the General Mixed Model. Ph.D. Dissertation, NC State University, Raleigh, U.S.A

Examples

```
library(minque)
data(ncii)
res=lmm(Yld~1|Female*Male+Rep,data=ncii)
res$Var
res$FixedEffect
res$RandomEffect
#End
```

`lmm.check` *An R function to obtain information from a linear mixed model*

Description

Sometimes users may need run some simulations for a given data structure and/or a model. This function will give users the information used for simulation.

Usage

```
lmm.check(formula, data = list())
```

Arguments

`formula`	A linear mixed model formula
`data`	A data frame used for modelling. It can be default

Value

Return the information that will be used to preset values for simulation

`comp1`	Number of variance components including one for random error
`comp2`	Names for all variance components not including the one for random error
`comp3`	Levels of effects for each fixed effect component
`comp4`	Names of all fixed effects

Author(s)

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Examples

```
library(minque)
data(ncii)
ncii$Female=factor(ncii$Female)
lmm.inf=lmm.check(Yld~Female|Female*Male+Rep,data=ncii)
lmm.inf

#End
```

lmm.jack *An R function for linear mixed model analysis*

Description

An R function for linear mixed model analysis with integration two linear mixed model approaches (REML and MINQUE) and a jackknife technique.

Usage

```
lmm.jack(formula, data=list(),method = NULL, JacNum = NULL,
 JacRep = NULL, ALPHA = NULL)
```

Arguments

formula	A linear mixed model formula.
data	A data frame used for analysis,it can be default.
method	The default linear mixed model approach is MINQUE. Users can choose both or one of two linear mixed model approaches, REML and MINQUE.
JacNum	The groups of jackknife to be used. The default number is 10.
JacRep	The times of jackknife process being repeated. The default is 1
ALPHA	The nomial alpha value being used for statistical tests. The default value is 0.05

Value

Return a list of matrices each including mean estimated variance components, standard error, and power

Author(s)

Jixiang Wu <jixiang.wu@sdstate.edu>

References

Miller, R. G. 1974. The jackknife - a review. Biometrika, 61:1- 15.

Rao, C.R. 1971. Estimation of variance and covariance components-MINQUE theory. J Multiva Ana 1:19

Rao, C. R. and Kleffe, J. 1980. Estimation of variance components. In Handbook of Statistics. Vol. l: 1-40. Krishnaiah, P. R. ed. New York. North-Holland.

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Zhu J. 1989. Estimation of Genetic Variance Components in the General Mixed Model. Ph.D. Dissertation, NC State University, Raleigh, U.S.A

Examples

```
library(minque)
data(ncii)
res=lmm.jack(Yld~1|Female*Male+Rep,data=ncii,
   JacNum=10,JacRep=1,ALPHA=0.05)
res$Var
res$PVar
res$FixedEffect
res$RandomEffect
#End
```

`lmm.perm` *An R function for linear mixed model analysis and permutation test*

Description

An R function for linear mixed model analysis with integration two linear mixed model approaches (REML and MINQUE) and a permutation test.

Usage

```
lmm.perm(formula, data = list(), method = NULL, PermNum = NULL)
```

Arguments

`formula`	A linear mixed model formula.
`data`	Data frame. It can be default.
`method`	The default linear mixed model approach is MINQUE. Users can choose both or one of two linear mixed model approaches, REML and MINQUE.
`PermNum`	Permutation number. The default number is 100

Value

Return a list of matrices each including mean estimated variance components, standard error, and power

Author(s)

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References

Miller, R. G. 1974. The jackknife - a review. Biometrika, 61:1- 15.

Rao, C.R. 1971. Estimation of variance and covariance components-MINQUE theory. J Multiva Ana 1:19

Rao, C. R. and Kleffe, J. 1980. Estimation of variance components. In Handbook of Statistics. Vol. l: 1-40. Krishnaiah, P. R. ed. New York. North-Holland.

Searle, S. R., Casella, G. and McCulloch, C. E. 1992. Variance Components. John Wiley & Sons, Inc. New York.

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Zhu J. 1989. Estimation of Genetic Variance Components in the General Mixed Model. Ph.D. Dissertation, NC State University, Raleigh, U.S.A

Examples

```
library(minque)
data(ncii)
res=lmm.perm(Yld~1|Female*Male+Rep,data=ncii)
res
#End
```

`lmm.simu` *An R function for linear mixed model simulation.*

Description

An R function for linear mixed model simulation with generated data set and a given model.

Usage

```
lmm.simu(formula, method = NULL, ALPHA = NULL)
```

Arguments

`formula`	A linear mixed model formula.
`method`	The default linear mixed model approach is MINQUE. Users can choose both or one of two linear mixed model approaches, REML and MINQUE.
`ALPHA`	A preset nominal probability level.

Details

No data frame is needed when more than one response variables are analyzed

Value

Return list of simulated results for variance components

Author(s)

Jixiang Wu <jixiang.wu@sdstate.edu>

References

Miller, R. G. 1974. The jackknife - a review. Biometrika, 61:1- 15.

Rao, C.R. 1971. Estimation of variance and covariance components-MINQUE theory. J Multiva Ana 1:19

Rao, C. R. and Kleffe, J. 1980. Estimation of variance components. In Handbook of Statistics. Vol. l: 1-40. Krishnaiah, P. R. ed. New York. North-Holland.

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Zhu J. 1989. Estimation of Genetic Variance Components in the General Mixed Model. Ph.D. Dissertation, NC State University, Raleigh, U.S.A

Examples

```
library(minque)
data(ncii)

lmm.inf=lmm.check(Yld~1|Female*Male+Rep,data=ncii)

lmm.inf  ##there are five variance components
v=c(20,20,20,20,20) ##there are five variance components
b=as.vector(100)    ##there is only population mean as fixed effect
Y=lmm.simudata(Yld~1|Female*Male+Rep,data=ncii,v=v,b=b,SimuNum=50)
Female=factor(ncii$Female)
Male=factor(ncii$Male)
Rep=factor(ncii$Rep)
res=lmm.simu(Y~1|Female*Male+Rep)
res
#End
```

`lmm.simu.jack` *An R function for linear mixed model simulation.*

Description

An R function for linear mixed model simulation with integration two linear mixed model approaches (REML and MINQUE) and a jackknife technique.

Usage

```
lmm.simu.jack(formula, method = NULL, JacNum = NULL, JacRep = NULL, ALPHA = NULL)
```

Arguments

`formula`	A linear mixed model formula.
`method`	The default linear mixed model approach is MINQUE. Users can choose both or one of two linear mixed model approaches, REML and MINQUE.
`JacNum`	The groups of jackknife to be used. The default number is 10.
`JacRep`	The times of jackknife process being repeated. The default is 1
`ALPHA`	The nomial alpha value being used for statistical tests. The default value is 0.05

Value

Return a list of matrices each including mean estimated variance components, standard error, and power

Author(s)

Jixiang Wu <jixiang.wu@sdstate.edu>

References

Miller, R. G. 1974. The jackknife - a review. Biometrika, 61:1- 15.

Rao, C.R. 1971. Estimation of variance and covariance components-MINQUE theory. J Multiva Ana 1:19

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Searle, S. R., Casella, G. and McCulloch, C. E. 1992. Variance Components. John Wiley & Sons, Inc. New York.

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Examples

```
library(minque)
data(ncii)

lmm.inf=lmm.check(Yld~1|Female*Male+Rep,data=ncii)

lmm.inf  ##there are five variance components
v=c(20,20,20,20,20) ##there are five variance components
b=as.vector(100)    ##there is only population mean as fixed effect
Y=lmm.simudata(Yld~1|Female*Male+Rep,data=ncii,v=v,b=b,SimuNum=50)
Female=factor(ncii$Female)
Male=factor(ncii$Male)
Rep=factor(ncii$Rep)
res=lmm.simu.jack(Y~1|Female*Male+Rep)
res

#End
```

`lmm.simudata` *An R function to generate a simulated data set*

Description

An R function to generate a simulated data set with given parameters, model, and data structure.

Usage

```
lmm.simudata(formula, data = list(), v, b, SimuNum = NULL)
```

Arguments

`formula`	A linear mixed model formula
`data`	A data frame. It can be default.
`v`	A vector of preset variance components
`b`	A vector of present fixed effects.
`SimuNum`	The number of simulations. The default number is 200.

Value

Return a simulated data set which is a matrix.

Author(s)

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References

Rao, C.R. 1971. Estimation of variance and covariance components-MINQUE theory. J Multiva Ana 1:19

Rao, C. R. and Kleffe, J. 1980. Estimation of variance components. In Handbook of Statistics. Vol. l: 1-40. Krishnaiah, P. R. ed. New York. North-Holland.

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Examples

```
library(minque)
data(ncii)

lmm.inf=lmm.check(Yld~1|Female*Male+Rep,data=ncii)

lmm.inf  ##there are five variance components
v=c(20,20,20,20,20) ##there are five variance components
b=as.vector(100)    ##there is only population mean as fixed effect
Y=lmm.simudata(Yld~1|Female*Male+Rep,data=ncii,v=v,b=b,SimuNum=50)



#End
```

`maize` *Maize variety trial*

Description

Maize variety trial with two years and multi-locations in China.

Usage

```
data(maize)
```

Format

A data frame with 260 observations (rows) on the following 4 variables (columns).

`Cultivar` cultivar names

`Year` testing year

`Location` testing locations

`Yld` maize yield

Details

No other details available

Source

Fan X.M., Kang M.S., Chen H.M., Zhang Y.D., Tan J., Xu C.X. (2007) Yield stability of maize hybrids evaluated in multi-environment trials in Yunnan, China. Agronomy Journal.99:220-228

References

Fan X.M., Kang M.S., Chen H.M., Zhang Y.D., Tan J., Xu C.X. (2007) Yield stability of maize hybrids evaluated in multi-environment trials in Yunnan, China. Agronomy Journal.99:220-228

Examples

```
library(minque)
data(maize)
#names(maize)

res=lmm(Yld~1|Cultivar*Year+Cultivar*Location+Year*Location,data=maize)
res$Var
res$FixedEffect
res$RandomEffect

res=lmm.jack(Yld~1|Cultivar*Year+Cultivar*Location+Year*Location,
   data=maize,JacNum=10,JacRep=1,ALPHA=0.05)
res$Var
res$PVar
res$FixedEffect
res$RandomEffect

##End
```

ncii *NC design II F1 data*

Description

A genetic data set can be analyzed by ANOVA or MIQNUE approaches.

Usage

```
data(ncii)
```

Format

A data frame with 60 observations on the following 4 variables.

`Female` female parents

`Male` male parents

`Rep` replications

`Yld` yield

Details

No other details available

Source

Not available

References

To be added

Examples

```
library(minque)
data(ncii)

res=lmm(Yld~1|Female*Male+Rep,data=ncii)
res$Var
res$FixedEffect
res$RandomEffect

res=lmm.jack(Yld~1|Female*Male+Rep,data=ncii,
   JacNum=10,JacRep=1,ALPHA=0.05)
res$Var
res$PVar

res$FixedEffect
res$RandomEffect
```

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