

# Package: minque (via r-universe)

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**Type** Package

**Title** Various Linear Mixed Model Analyses

**Version** 2.0.0

**Author** Jixiang Wu

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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

**Encoding** UTF-8

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**RoxygenNote** 7.0.2

**NeedsCompilation** no

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minque-package	<i>Various Linear Mixed Model Analyses</i>
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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;(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  
 Date: 2019-12-18  
 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. 1: 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

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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

Twenty 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
```

---

Imm

*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)**

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. 1: 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

**Examples**

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

---

`Imm.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**

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

**Arguments**

<code>formula</code>	A linear mixed model formula
<code>data</code>	A data frame used for modelling. It can be default

**Value**

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

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

**Author(s)**

Jixiang Wu <jixiang.wu@sdstate.edu>

**Examples**

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

#End
```

Imm.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**

```
Imm.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. 1: 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

### 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
```

---

Imm.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)

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. 1: 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

## Examples

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

---

Imm.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

```
Imm.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. 1: 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

**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
- Rao, C. R. and Kleffe, J. 1980. Estimation of variance components. In *Handbook of Statistics*. Vol. 1: 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

**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)**

Jixiang Wu <jixiang.wu@sdstate.edu>

## 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. 1: 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

## 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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