Package 'qgtools'

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Type Package

Title Generalized Quantitative Genetics Data Analyses

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Description

Two linear mixed model approaches: REML(restricted maximum likelihood) and MINQUE (minimum norm quadratic unbiased estimation) approaches and several resampling techniques are integrated for various quantitative genetics analyses. With these two types of approaches, various unbalanced data structures, missing data, and any irregular genetic mating designs can be analyzed and statistically tested. This package also offers fast computations for many large data sets.

License GPL-2

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`qgtools-package` *A Tool Set for Quantitative Genetics Analyses*

Description

We integrated with two linear mixed model approaches (MIQNUE and REML) and several resampling techniques for various genetics models. With these two types of approaches, various unbalanced data structures, missing data, and any irregular genetic mating designs can be analyzed and statistically tested. This package also offers fast computations for many large data sets.

Details

Package:	qgtools
Type:	Package
Version:	2.0
Date:	2019-12-17
License:	GPL -2

The current version includes two major components: (1) genetic model analyses for various genetic mating genetic and breeding data and (2) yield stability. Both components have been integrated with resampling approaches. Regarding the first component, two linear mixed model approaches, MINQUE and REML are employed to analyze various genetic mating designs and data structures. The adjusted unbiased prediction (AUP) method is employed to predict random effects (Zhu, 1993). Functions for model/data evaluations are provided too. Randomized group-based jackknife technique is integrated for various statistical tests such as for variance components, fixed effects, and random effects (Wu et al., 2012). Four commonly used genetic models: AD (additive-dominance), ADC (AD model with cytoplasmic effects), ADM (AD model with maternal effects), and ADAA (AD model with additive-by-additive interaction effects), are provided.

Author(s)

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References

Crossa J., Gauch H.G. and Zobel R.W. (1990) Additive main effect and multiplicative interaction analysis of two international maize cultivar trials. Crop Sci 30:493-500.

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Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

Wu, J., K. Glover, W. Berzonsky, 2012. Statistical tests for stability analysis with resampling techniques. 25th Conference of Applied Statistics in Agriculture. p88-108. April 29-May 01, 2012. Manhattan, KS

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Unbalanced Genetic Data Analysis: model evaluation and application. 2010 ASA, CSSA, & SSSA International Annual Meetings, Long Beach, CA.

Wu, J., J. N. Jenkins, and J.C., McCarty. 2011. A generalized approach and computer tool for quantitative genetics study. Proceedings Applied Statistics in Agriculture, April 25-27, 2010, Manhattan, KS. p.85-106.

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.

`ad.mq` *Additive-dominance (AD) model with MINQUE analysis*

Description

An AD model can be analyzed by MINQUE approach, requiring no specific genetic mating designs or balance data. For reliable results, parents and F1s, parents and F2s, are preferred.

Usage

```
ad.mq(Y, Ped)
```

Arguments

`Y`	A trait matrix including one or more than one traits.
`Ped`	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects.

Author(s)

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References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

Wu, J., J. N. Jenkins, and J.C., McCarty. 2011. A generalized approach and computer tool for quantitative genetics study. Proceedings Applied Statistics in Agriculture, April 25-27, 2010, Manhattan, KS. p.85-106.

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(qgtools)
data(cotf2)
Ped=cotf2[,c(1:5)]
Y=cotf2[,-c(1:5)]
## star
# res=ad.mq(Y,Ped)
# res$Var
# res$FixedEffect
# res$RandomEffect

##End
```

ad.mq.jack *Additive-dominance (AD) model with MINQUE analysis and jackknife*

Description

An AD model can be analyzed by MINQUE approach, requiring no specific genetic mating design or balance data. For reliable results, parents and F1s, parents and F2s, are preferred.

Usage

```
ad.mq.jack(Y, Ped, JacNum = NULL, JacRep = NULL)
```

Arguments

`Y`	A trait matrix including one or more traits.
`Ped`	A pedigree matrix including Env, Female, Male, Generation, with or without block is required. The matrix should include either 4 or 5 columns.
`JacNum`	Number of jackknife groups. The default is 10.
`JacRep`	Repeating times for jackknife process. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated Variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects, and their statistical tests

Author(s)

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References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

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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

```
data(cotf12)
#names(cotf12)
dat=cotf12[which(cotf12$Year==1),]
Ped=dat[,c(1,3:6)]
Y=dat[,-c(1:6)]
res=ad.mq.jack(Y,Ped)
res$Var
res$PVar
res$FixedEffect
res$RandomEffect

##End
```

---

ad.reml *Additive-dominance (AD) model with REML analysis*

Description

An AD model can be analyzed by REML approach, requiring no specific genetic mating designs or balance data. For reliable results, parents and F1s, parents and F2s, are preferred.

Usage

```
ad.reml(Y, Ped)
```

Arguments

`Y`	A trait matrix including one or more than one traits.
`Ped`	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

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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(qgtools)
data(cotf2)
dat=cotf2[which(cotf2$Env==1),]
Ped=dat[,c(1:5)]
Y=dat[,-c(1:5)]

res=ad.reml(Y,Ped)
res$Var
res$FixedEffect
res$RandomEffect
```

```
##End
```

`ad.reml.jack` *AD model with REML analysis and jackknife resampling test*

Description

AD model can be analyzed by REML approach for variance components, fixed effects, random effects and tested by a jackknife approach

Usage

```
ad.reml.jack(Y, Ped, JacNum = NULL, JacRep = NULL)
```

Arguments

`Y`	A trait matrix including one or more than one traits.
`Ped`	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
`JacNum`	Number of groups to be jackknifed. The default is 10.
`JacRep`	Number of jackknife process to be repeated. The default is 1

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: variance components, propotional variance components, fixed effects, and random effects.

Author(s)

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References

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

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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(qgtools)
data(cotf2)
dat=cotf2[which(cotf2$Env==1),]
Ped=dat[,c(1:5)]
Y=dat[,-c(1:5)]

res=ad.reml.jack(Y,Ped)
res$Var
res$FixedEffect
res$RandomEffect

##End
```

`ad.simu` *An R function for AD model simulation.*

Description

An R function for AD model simulation with generated data set.

Usage

```
ad.simu(Y, Ped, method = NULL, ALPHA = NULL)
```

Arguments

Y	A matrix of simulated data set
Ped	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.

`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.The default is 0.05.

Value

Return list of simulated results for variance components.

Author(s)

Jixiang Wu <qgtools@gmail.com>

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.

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(qgtools)
data(cotf2)
Ped=cotf2[,c(1:5)]
Y=cotf2[,-c(1:5)]
Y=data.frame(Y)
YS=ad.simudata(Y,Ped,v=rep(20,7),b=c(100),SimuNum=10)
res=ad.simu(YS,Ped,method="minque",ALPHA=0.05)
res
##End
```

`ad.simu.jack` *An R function for AD model simulation*

Description

An R function for AD model simulation with generated data set.

Usage

```
ad.simu.jack(Y, Ped, method = NULL, JacNum = NULL, JacRep = NULL, ALPHA = NULL)
```

Arguments

`Y`	A matrix of simulated data set
`Ped`	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
`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`	Number of jackknife groups. The default is 10.
`JacRep`	Repeating times for jackknife process. The default is 1.
`ALPHA`	A preset nominal probability level.The default is 0.05.

Value

Return list of simulated results for variance components.

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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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(qgtools)
data(cotf2)
Ped=cotf2[,c(1:5)]
Y=cotf2[,6]
Y=data.frame(Y)
YS=ad.simudata(Y,Ped,v=rep(20,7),b=c(100),SimuNum=10)
res=ad.simu.jack(YS,Ped,JacNum=5)
res
##End
```

---

ad.simudata — *An R function to generate an AD model simulated data set*

Description

An R function to generate an AD model simulated data set with given parameters and data structure.

Usage

```
ad.simudata(Y, Ped, v, b, SimuNum = NULL)
```

Arguments

Y	A matrix of trait with one or more than one trait.
Ped	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
v	A vector of preset variance components.
b	A vector of present fixed effects.
SimuNum	

Details

The number of simulations. The default number is 200.

Value

Return a simulated data set which is a matrix.

Author(s)

Jixiang Wu <qgtools@gmail.com>

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.

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(qgtools)
data(cotf2)
Ped=cotf2[,c(1:5)]
Y=cotf2[,-c(1:5)]
Y=data.frame(Y)

YS=ad.simudata(Y,Ped,v=rep(20,7),b=c(100),SimuNum=10)

##End
```

---

ad4.mq — *Additive-dominance (AD) model with MINQUE analysis for multi-parent mating designs*

Description

An AD model from multi-parent mating designs can be analyzed by MINQUE approach, requiring no specific genetic mating designs or balance data. For reliable results, parents and F1s, parents and F2s, are preferred.

Usage

```
ad4.mq(Y,Ped)
```

Arguments

Y	A trait matrix including one or more than one traits.
Ped	A pedigree matrix including Environment, Female1, Male1, Female2, Male2, Generation, with or without block is required. So the matrix should include either 6 columns or 7 columns.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female1(column 2), Male1(column 3), Female2(column 4), Male2(column 5),Generation (column 6). Column 7 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

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References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

Wu, J., J. N. Jenkins, and J.C., McCarty. 2011. A generalized approach and computer tool for quantitative genetics study. Proceedings Applied Statistics in Agriculture, April 25-27, 2010, Manhattan, KS. p.85-106.

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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(qgtools)
data(wheat)
n=nrow(wheat)
id=sample(n,200)
dat=wheat[id,]
Ped=dat[,c(1:6)]
Y=as.matrix(dat[,8])
colnames(Y)=colnames(dat)[8]

res=ad4.mq(Y,Ped)
res$Var
```

```
res$FixedEffect
res$RandomEffect

##End
```

---

ad4.mq.jack *Additive-dominance (AD) model, multi-parent mating designs, MINQUE, and jackknife*

Description

An AD model from multi-parent mating designs can be analyzed by MINQUE and jackknife methods, requiring no specific genetic mating designs or balance data.

Usage

```
ad4.mq.jack(Y, Ped, JacNum = NULL, JacRep = NULL)
```

Arguments

`Y`	A trait matrix including one or more than one traits.
`Ped`	A pedigree matrix including Environment, Female1, Male1, Female2, Male2, Generation, with or without block is required. So the matrix should include either 6 columns or 7 columns.
`JacNum`	Number of groups to be jackknifed. The default is 10
`JacRep`	Number of jackknife process to be repeated. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female1(column 2), Male1(column 3), Female2(column 4), Male2(column 5),Generation (column 6). Column 7 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects

Author(s)

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References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

Wu, J., J. N. Jenkins, and J.C., McCarty. 2011. A generalized approach and computer tool for quantitative genetics study. Proceedings Applied Statistics in Agriculture, April 25-27, 2010, Manhattan, KS. p.85-106.

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Examples

```
library(qgtools)
data(wheat)
n=nrow(wheat)
id=sample(n,200)
dat=wheat[id,]
Ped=dat[,c(1:6)]
Y=as.matrix(dat[,8])
colnames(Y)=colnames(dat)[8]

res=ad4.mq.jack(Y,Ped,JacNum=5)
res$Var
res$PVar
res$FixedEffect
res$RandomEffect

##End
```

---

ad4.reml *Additive-dominance (AD) model with REML analysis for multi-parent mating designs*

Description

An AD model from multi-parent mating designs can be analyzed by REML approach, requiring no specific genetic mating designs or balance data. For reliable results, parents and F1s, parents and F2s, are preferred.

Usage

```
ad4.reml(Y, Ped)
```

Arguments

`Y`	A trait matrix including one or more than one traits.
`Ped`	A pedigree matrix including Environment, Female1, Male1, Female2, Male2, Generation, with or without block is required. So the matrix should include either 6 columns or 7 columns.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female1(column 2), Male1(column 3), Female2(column 4), Male2(column 5),Generation (column 6). Column 7 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

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References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

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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(qgtools)
data(wheat)
n=nrow(wheat)
id=sample(n,200)
dat=wheat[id,]
Ped=dat[,c(1:6)]
Y=as.matrix(dat[,8])
colnames(Y)=colnames(dat)[8]

res=ad4.reml(Y,Ped)
res$Var
res$FixedEffect
res$RandomEffect

##End
```

---

ad4.reml.jack — *Additive-dominance (AD) model, multi-parent mating designs, REML, and jackknife*

Description

An AD model from multi-parent mating designs can be analyzed by REML and jackknife methods, requiring no specific genetic mating designs or balance data.

Usage

```
ad4.reml.jack(Y, Ped, JacNum = NULL, JacRep = NULL)
```

Arguments

Y	A trait matrix including one or more than one traits.
Ped	A pedigree matrix including Environment, Female1, Male1, Female2, Male2, Generation, with or without block is required. So the matrix should include either 6 columns or 7 columns.
JacNum	Number of groups to be jackknifed. The default is 10
JacRep	Number of jackknife process to be repeated. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female1(column 2), Male1(column 3), Female2(column 4), Male2(column 5),Generation (column 6). Column 7 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

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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(qgtools)
data(wheat)
summary(wheat)
 ##End
```

---

ad4rc.mq — *AD model with row and column effects*

Description

An AD model with row and column effects included is used for controlling field variation. The data set can be irregular or missing but the field layout should be rectangular. It can analyze any genetic mating designs and data including F1, F2, or F3 with parents..

Usage

```
ad4rc.mq(Y, Ped, Row = NULL, Col = NULL)
```

Arguments

`Y`	A data matrix for one or more traits
`Ped`	A pedigree matrix including Environment, Female1, Male1, Female2, Male2, Generation is required.
`Row`	A vector for field rows. It can be default.
`Col`	A vector for field colums.It can be default.

Details

If only row or column vector is included, this is equivallent to an AD model with block effects.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

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Wu, J., J. N. Jenkins, and J.C., McCarty. 2011. A generalized approach and computer tool for quantitative genetics study. Proceedings Applied Statistics in Agriculture, April 25-27, 2010, Manhattan, KS. p.85-106.

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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(qgtools)
data(adrcdat)
str(adrcdat)
```

`ad4rc.mq.jack` *AD model with row and column effects analyzed by MINQUE and jackknife*

Description

An AD model with row and column effects included is used for controlling field variation. This model will be analyzed by MINQUE approach and tested by jackknife technique. The data set can be irregular or missing but the field layout should be rectangular. It can analyze any genetic mating designs and data including F1, F2, or F3 with parents..

Usage

```
ad4rc.mq.jack(Y, Ped, Row = NULL, Col = NULL, JacNum = NULL, JacRep = NULL)
```

Arguments

`Y`	A data matrix for one or more traits
`Ped`	A pedigree matrix including Environment, Female1, Male1, Female2, Male2,Generation is required.
`Row`	A vector for field rows. It can be default.
`Col`	A vector for field colums.It can be default.
`JacNum`	Number of jackknife groups to be used. The default is 10.
`JacRep`	Repeating times for jackknife process. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female1(column 2), Male1(column 3), Female2(column 4), Male2(column 5),Generation (column 6). Even though there is only one environment, this first column is needed.If only row or column vector is included, this is equivallent to an AD model with block effects.

Value

Return a list of results: estimated Variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects, and their statistical tests

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

Wu, J., J. N. Jenkins, and J.C., McCarty. 2011. A generalized approach and computer tool for quantitative genetics study. Proceedings Applied Statistics in Agriculture, April 25-27, 2010, Manhattan, KS. p.85-106.

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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(qgtools)

data(wheat)
str(wheat)
```

---

ad4rc.reml — *AD model with row and column effects analyzed by REML approach*

Description

An AD model with row and column effects included is used for controlling field variation. This model is analyzed by the REML approach. The data set can be irregular or missing but the field layout should be rectangular. It can analyze any genetic mating designs and data including F1, F2, or F3 with parents..

Usage

```
ad4rc.reml(Y, Ped, Row = NULL, Col = NULL)
```

Arguments

`Y`	A data matrix for one or more traits
`Ped`	A pedigree matrix including Environment, Female1, Male1, Female2, Male2, Generation is required.
`Row`	A vector for field rows. It can be default.
`Col`	A vector for field colums.It can be default.

Details

If only row or column vector is included, this is equivallent to an AD model with block effects.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

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Wu, J., J. N. Jenkins, and J.C., McCarty. 2011. A generalized approach and computer tool for quantitative genetics study. Proceedings Applied Statistics in Agriculture, April 25-27, 2010, Manhattan, KS. p.85-106.

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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(qgtools)
data(adrcdat)
str(adrcdat)
```

`ad4rc.reml.jack` *AD model with row and column effects analyzed by MINQUE and jackknife*

Description

An AD model with row and column effects included is used for controlling field variation. This model will be analyzed by MINQUE approach and tested by jackknife technique. The data set can be irregular or missing but the field layout should be rectangular. It can analyze any genetic mating designs and data including F1, F2, or F3 with parents..

Usage

```
ad4rc.reml.jack(Y, Ped, Row = NULL, Col = NULL, JacNum = NULL, JacRep = NULL)
```

Arguments

`Y`	A data matrix for one or more traits
`Ped`	A pedigree matrix including Environment, Female1, Male1, Female2, Male2, Generation is required.
`Row`	A vector for field rows. It can be default.
`Col`	A vector for field colums.It can be default.
`JacNum`	Number of jackknife groups to be used. The default is 10.
`JacRep`	Repeating times for jackknife process. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Even though there is only one environment, this first column is needed.If only row or column vector is included, this is equivallent to an AD model with block effects.

Value

Return a list of results: estimated Variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects, and their statistical tests

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

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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(qgtools)
data(adrcdat)
dat=adrcdat[which(adrcdat$Env==1&adrcdat$Row<=3),]
Ped=dat[,c(1,4,5,6)]
Y=as.matrix(dat[,8])

colnames(Y)=colnames(dat)[8]

Row=dat$Row
Col=dat$Column


##run AD model with field row and column effects
res=adrc.reml.jack(Y,Ped,Row=Row,JacNum=5)
res$Var
res$PVar
res$FixedEffect
res$RandomEffect
```

---

adaa.mq *ADAA model with MINQUE analysis*

Description

An ADAA model can be analyzed by MINQUE approach, requiring no specific genetic mating design or balance data. For reliable results, three generations such as (parents,F1s,F2s) or (parents, F2s,F3s) are preferred.

Usage

```
adaa.mq(Y, Ped)
```

Arguments

Y	A trait matrix including one or more traits.
Ped	pedigree matrix including Env, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., J. N. Jenkins, Jack C. McCarty, and D. Wu. 2006b Variance component estimation using the ADAA model when genotypes vary across environments. Crop Science 46: 174-179.

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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(qgtools)
data(cotf12)
names(cotf12)
dat=cotf12[which(cotf12$Year==1),]
Ped=dat[,c(1,3:6)]
Y=dat[,-c(1:6)]
#Ped=cotf12[,c(1,3:6)]
#Y=cotf12[,-c(1:6)]
res=adaa.mq(Y,Ped)
res$Var
res$FixedEffect
res$RandomEffect

##End
```

---

adaa.mq.jack — *ADAA model with MINQUE and jacknife analyses*

Description

An dditive-dominance (AD) model and additive-by-additive interaction effects (ADAA model) can be analyzed by MINQUE approach, requiring no specific genetic mating design or balance data. For reliable results, three generations such as (parents,F1s,F2s) or (parents, F2s,F3s) are preferred. The jackknife method will conduct all statistical tests.

Usage

```
adaa.mq.jack(Y, Ped, JacNum = NULL, JacRep = NULL)
```

Arguments

`Y`	A trait matrix including one or more traits.
`Ped`	A pedigree matrix including Env, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
`JacNum`	Number of jackknife groups. The default is 10.
`JacRep`	Repeating times for jackknife process. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated Variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects, and their statistical tests

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., J. N. Jenkins, Jack C. McCarty, and D. Wu. 2006b Variance component estimation using the ADAA model when genotypes vary across environments. Crop Science 46: 174-179.

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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(qgtools)

data(cotf12)
names(cotf12)
dat=cotf12[which(cotf12$Year==1),]
Ped=dat[,c(1,3:6)]
Y=dat[,-c(1:6)]
#Ped=cotf12[,c(1,3:6)]
#Y=cotf12[,-c(1:6)]

res=adaa.mq.jack(Y,Ped,JacNum=5)
res$Var
res$FixedEffect
res$RandomEffect

##End
```

adaa.reml *Additive-dominance (AD) with additive-additive interaction model with REML analysis*

Description

An ADAA model can be analyzed by REML approach, requiring no specific genetic mating designs or balance data. For reliable results, parents and F1s, parents and F2s, are preferred.

Usage

```
adaa.reml(Y, Ped)
```

Arguments

Y	A trait matrix including one or more than one traits.
Ped	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

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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(qgtools)
data(cotf12)
#names(cotf12)
dat=cotf12[which(cotf12$Year==1),]
Ped=dat[,c(1,3:6)]
Y=dat[,-c(1:6)]
#Ped=cotf12[,c(1,3:6)]
#Y=cotf12[,-c(1:6)]
res=adaa.reml(Y,Ped)
res$Var
res$FixedEffect
res$RandomEffect

##End
```

---

adaa.reml.jack   *ADAA model with REML and jacknife analyses*

Description

An dditive-dominance (AD) model and additive-by-additive interaction effects (ADAA model) can be analyzed by REML approach, requiring no specific genetic mating design or balance data. For reliable results, three generations such as (parents,F1s,F2s) or (parents, F2s,F3s) are preferred. The jackknife method will conduct all statistical tests.

Usage

```
adaa.reml.jack(Y, Ped, JacNum = NULL, JacRep = NULL)
```

Arguments

`Y`	A trait matrix including one or more traits.
`Ped`	A pedigree matrix including Env, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
`JacNum`	Number of jackknife groups. The default is 10.
`JacRep`	Repeating times for jackknife process. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated Variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects, and their statistical tests

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

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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(qgtools)

data(cotf2)
dat=cotf2[which(cotf2$Env==1),]
Ped=dat[,c(1:5)]
Y=dat[,-c(1:5)][,1:2]
res=adaa.reml.jack(Y,Ped,JacNum=5)
res$Var
res$FixedEffect
res$RandomEffect

##End
```

`adaa.simu` *An R function for AD model simulation.*

Description

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

Usage

```
adaa.simu(Y, Ped, method = NULL, ALPHA = NULL)
```

Arguments

`Y`	A matrix of simulated data set
`Ped`	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
`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.The default is 0.05.

Value

Return list of simulated results for variance components.

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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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(qgtools)
data(cotf2)
dat=cotf2[which(cotf2$Env==1),]
Ped=dat[,c(1:5)]
Y=dat[,-c(1:5)]
Y=data.frame(Y)
#Ped=cotf2[,c(1:5)]
#Y=cotf2[,-c(1:5)]
YS=adaa.simudata(Y,Ped,v=rep(20,5),b=c(100),SimuNum=10)
res=adaa.simu(YS,Ped,ALPHA=0.05)
res
##End
```

---

adaa.simu.jack *An R function for AD model simulation*

Description

An R function for AD model simulation with generated data set.

Usage

```
adaa.simu.jack(Y, Ped, method = NULL, JacNum = NULL, JacRep = NULL, ALPHA = NULL)
```

Arguments

Y	A matrix of simulated data set
Ped	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
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	Number of jackknife groups. The default is 10.
JacRep	Repeating times for jackknife process. The default is 1.
ALPHA	A preset nominal probability level.The default is 0.05.

Value

Return list of simulated results for variance components.

Author(s)

Jixiang Wu <qgtools@gmail.com>

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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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(qgtools)
data(cotf2)
dat=cotf2[which(cotf2$Env==1),]
Ped=dat[,c(1:5)]
Y=dat[,-c(1:5)]
Y=data.frame(Y)
#Ped=cotf2[,c(1:5)]
#Y=cotf2[,-c(1:5)]
YS=adaa.simudata(Y,Ped,v=rep(20,5),b=c(100),SimuNum=10)
res=adaa.simu.jack(YS,Ped,JacNum=5)
res
##End
```

---

adaa.simudata *An R function to generate an ADAA model simulated data set*

Description

An R function to generate an ADAA model simulated data set with given parameters and data structure.

Usage

```
adaa.simudata(Y, Ped, v, b, SimuNum = NULL)
```

Arguments

`Y`	A matrix of trait with one or more than one trait.
`Ped`	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
`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 <qgtools@gmail.com>

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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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(qgtools)
data(cotf2)
Ped=cotf2[,c(1:5)]
Y=cotf2[,-c(1:5)]
Y=data.frame(Y)

YS=adaa.simudata(Y,Ped,v=rep(20,9),b=c(100),SimuNum=10)

##End
```

adc.mq *An ADC with MINQUE analysis*

Description

An ADC model can be analyzed by MINQUE approach, requiring no specific genetic mating design or balance data. For reliable results, parents and F1s, parents and F2s, are preferred.

Usage

```
adc.mq(Y, Ped)
```

Arguments

`Y` A trait matrix including one or more traits.

`Ped` A pedigree matrix including Env, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

Wu, J., J. N. Jenkins, and J.C., McCarty. 2011. A generalized approach and computer tool for quantitative genetics study. Proceedings Applied Statistics in Agriculture, April 25-27, 2010, Manhattan, KS. p.85-106.

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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(qgtools)

data(cotf2)
dat=cotf2[which(cotf2$Env==1),]

Ped=dat[,c(1:5)]
Y=dat[,-c(1:5)]

res=adc.mq(Y,Ped)

res$Var
res$FixedEffect
res$RandomEffect

##End
```

`adc.mq.jack` *An ADC model with MINQUE analyses and jackknife tests*

Description

An AD model can be analyzed by MINQUE approach, requiring no specific genetic mating design or balance data. For reliable results, parents and F1s, parents and F2s, are preferred.

Usage

```
adc.mq.jack(Y, Ped, JacNum = NULL, JacRep = NULL)
```

Arguments

`Y`	A trait matrix including one or more traits.
`Ped`	A pedigree matrix including Env, Female, Male, Generation, with or without block is required. The matrix should include either 4 or 5 columns.
`JacNum`	Number of groups to be jackknifed. The default is 10.
`JacRep`	Repeating times for jackknife process. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed. Please refer to the example.

Value

Return a list of results: estimated Variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects, and their statistical tests

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

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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(qgtools)
data(cotf12)
names(cotf12)
dat=cotf12[which(cotf12$Year==1),]
Ped=dat[,c(1,3:6)]
Y=dat[,-c(1:6)]
#Ped=cotf12[,c(1,3:6)]
#Y=cotf12[,-c(1:6)]
res=adc.mq.jack(Y,Ped,JacNum=5)
res$Var
res$FixedEffect
```

```
res$RandomEffect

##End
```

---

adc.reml *ADC model with REML analysis*

Description

ADC model can be analyzed by REML approach, requiring no specific genetic mating designs or balance data. For reliable results, parents and F1s, parents and F2s, are preferred.

Usage

```
adc.reml(Y, Ped)
```

Arguments

Y	A trait matrix including one or more than one traits.
Ped	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

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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(qgtools)
data(cotf2)
dat=cotf2[which(cotf2$Env==1),]

Ped=dat[,c(1:5)]
Y=dat[,c(6,7)]

res=adc.reml(Y,Ped)
res$Var
res$FixedEffect
res$RandomEffect

##End
```

`adc.reml.jack` *ADC model with REML analysis and jackknife resampling test*

Description

ADC model can be analyzed by REML approach for variance components, fixed effects, random effects and tested by a jackknife approach

Usage

```
adc.reml.jack(Y, Ped, JacNum = NULL, JacRep = NULL)
```

Arguments

`Y`	A trait matrix including one or more than one traits.
`Ped`	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
`JacNum`	Number of groups to be jackknifed. The default is 10.
`JacRep`	Number of jackknife process to be repeated. The default is 1

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: variance components, propotional variance components, fixed effects, and random effects.

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

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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(qgtools)
data(cotf2)
dat=cotf2[which(cotf2$Env==1),]
#Ped=dat[,c(1,3:6)]
#Y=dat[,-c(1:6)]
Ped=dat[,c(1:5)]
Y=dat[,c(6,7)]

res=adc.reml.jack(Y,Ped,JacNum=5)
res$Var
res$PVar
res$FixedEffect
```

```
res$RandomEffect

##End
```

---

adc.simu *An R function for ADC model simulation.*

Description

An R function for ADC model simulation with generated data set.

Usage

```
adc.simu(Y, Ped, method = NULL, ALPHA = NULL)
```

Arguments

Y	A matrix of simulated data set
Ped	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
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.The default is 0.05.

Value

Return list of simulated results for variance components.

Author(s)

Jixiang Wu <qgtools@gmail.com>

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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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(qgtools)
data(cotf2)
dat=cotf2[which(cotf2$Env==1),]

Ped=dat[,c(1:5)]
Y=dat[,6]
Y=data.frame(Y)
#Ped=cotf2[,c(1:5)]
#Y=cotf2[,-c(1:5)]
YS=adc.simudata(Y,Ped,v=rep(20,5),b=c(100),SimuNum=10)
res=adc.simu(YS,Ped)
res
##End
```

---

adc.simu.jack *An R function for ADC model simulation*

Description

An R function for ADC model simulation with generated data set.

Usage

```
adc.simu.jack(Y, Ped, method = NULL, JacNum = NULL, JacRep = NULL, ALPHA = NULL)
```

Arguments

Y	A matrix of simulated data set
Ped	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
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	Number of jackknife groups. The default is 10.
JacRep	Repeating times for jackknife process. The default is 1.
ALPHA	A preset nominal probability level.The default is 0.05.

Value

Return list of simulated results for variance components.

Author(s)

Jixiang Wu <qgtools@gmail.com>

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.

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

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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(qgtools)
data(cotf2)
dat=cotf2[which(cotf2$Env==1),]
Ped=dat[,c(1:5)]
Y=dat[,c(6,7)]
Y=data.frame(Y)
#Ped=cotf2[,c(1:5)]
#Y=cotf2[,-c(1:5)]
YS=adc.simudata(Y,Ped,v=rep(20,5),b=c(100),SimuNum=5)
res=adc.simu.jack(YS,Ped,JacNum=5)
res
##End
```

`adc.simudata` *An R function to generate an ADC model simulated data set*

Description

An R function to generate an ADC model simulated data set with given parameters and data structure.

Usage

```
adc.simudata(Y, Ped, v, b, SimuNum = NULL)
```

Arguments

`Y`	A matrix of trait with one or more than one trait.
`Ped`	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
`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 <qgtools@gmail.com>

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.

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(qgtools)
 data(cotf2)
 Ped=cotf2[,c(1:5)]
 Y=cotf2[,-c(1:5)]

 YS=adc.simudata(Y,Ped,v=rep(20,9),b=c(100))

 ##End
```

`adc4.mq` *ADC model with MINQUE analysis for multi-parent mating designs*

Description

An ADC model from multi-parent mating designs can be analyzed by MINQUE approach, requiring no specific genetic mating designs or balance data.

Usage

```
adc4.mq(Y, Ped)
```

Arguments

`Y`	A trait matrix including one or more than one traits.
`Ped`	A pedigree matrix including Environment, Female1, Male1, Female2, Male2, Generation, with or without block is required. So the matrix should include either 6 columns or 7 columns.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female1(column 2), Male1(column 3), Female2(column 4), Male2(column 5),Generation (column 6). Column 7 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

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Wu, J., J. N. Jenkins, and J.C., McCarty. 2011. A generalized approach and computer tool for quantitative genetics study. Proceedings Applied Statistics in Agriculture, April 25-27, 2010, Manhattan, KS. p.85-106.

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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(qgtools)
data(wheat)
n=nrow(wheat)
id=sample(n,200)
dat=wheat[id,]
Ped=dat[,c(1:6)]
Y=as.matrix(dat[,8])
colnames(Y)=colnames(dat)[8]

res=adc4.mq(Y,Ped)
res$Var
res$FixedEffect
res$RandomEffect

##End
```

---

adc4.mq.jack *ADC model, multi-parent mating designs, MINQUE, and jackknife*

Description

An ADC model from multi-parent mating designs can be analyzed by MINQUE and jackknife methods, requiring no specific genetic mating designs or balance data.

Usage

```
adc4.mq.jack(Y, Ped, JacNum = NULL, JacRep = NULL)
```

Arguments

`Y`	A trait matrix including one or more than one traits.
`Ped`	A pedigree matrix including Environment, Female1, Male1, Female2, Male2, Generation, with or without block is required. So the matrix should include either 6 columns or 7 columns.
`JacNum`	Number of groups to be jackknifed. The default is 10
`JacRep`	Number of jackknife process to be repeated. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female1(column 2), Male1(column 3), Female2(column 4), Male2(column 5),Generation (column 6). Column 7 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

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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(qgtools)
data(wheat)
n=nrow(wheat)
id=sample(n,200)
dat=wheat[id,]
Ped=dat[,c(1:6)]
Y=as.matrix(dat[,8])
colnames(Y)=colnames(dat)[8]

res=adc4.mq.jack(Y,Ped,JacNum=5)
res$Var
```

```
res$PVar
res$FixedEffect
res$RandomEffect

##End
```

`adc4.reml` *ADC model with REML analysis for multi-parent mating designs*

Description

An ADC model from multi-parent mating designs can be analyzed by REML approach, requiring no specific genetic mating designs or balance data.

Usage

```
adc4.reml(Y, Ped)
```

Arguments

`Y`	A trait matrix including one or more than one traits.
`Ped`	A pedigree matrix including Environment, Female1, Male1, Female2, Male2, Generation, with or without block is required. So the matrix should include either 6 columns or 7 columns.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female1(column 2), Male1(column 3), Female2(column 4), Male2(column 5),Generation (column 6). Column 7 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

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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(qgtools)
data(wheat)
n=nrow(wheat)
id=sample(n,200)
dat=wheat[id,]
Ped=dat[,c(1:6)]
Y=as.matrix(dat[,8])
colnames(Y)=colnames(dat)[8]

res=adc4.reml(Y,Ped)
res$Var
res$FixedEffect
res$RandomEffect

##End
```

---

adc4.reml.jack *ADC model, multi-parent mating designs, REML, and jackknife*

Description

An ADC model from multi-parent mating designs can be analyzed by REML and jackknife methods, requiring no specific genetic mating designs or balance data.

Usage

```
adc4.reml.jack(Y, Ped, JacNum = NULL, JacRep = NULL)
```

Arguments

Y	A trait matrix including one or more than one traits.
Ped	A pedigree matrix including Environment, Female1, Male1, Female2, Male2, Generation, with or without block is required. So the matrix should include either 6 columns or 7 columns.
JacNum	Number of groups to be jackknifed. The default is 10
JacRep	Number of jackknife process to be repeated. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female1(column 2), Male1(column 3), Female2(column 4), Male2(column 5),Generation (column 6). Column 7 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

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Wu, J., J. N. Jenkins, and J.C., McCarty. 2011. A generalized approach and computer tool for quantitative genetics study. Proceedings Applied Statistics in Agriculture, April 25-27, 2010, Manhattan, KS. p.85-106.

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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(qgtools)
data(wheat)
n=nrow(wheat)
id=sample(n,200)
dat=wheat[id,]
Ped=dat[,c(1:6)]
Y=as.matrix(dat[,8])
colnames(Y)=colnames(dat)[8]

res=adc4.reml.jack(Y,Ped,JacNum=5)
res$Var
res$PVar
res$FixedEffect
res$RandomEffect

##End
```

---

adm.mq *An ADM model with MINQUE analysis*

Description

An ADM model can be analyzed by MINQUE approach, requiring no specific genetic mating design or balance data. For reliable results, parents and F1s, parents and F2s, are preferred.

Usage

```
adm.mq(Y, Ped)
```

Arguments

`Y`	A trait matrix including one or more traits.
`Ped`	A pedigree matrix including Env, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

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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(qgtools)
data(cotf2)

dat=cotf2[which(cotf2$Env==1),]
Ped=dat[,c(1:5)]
Y=dat[,-c(1:5)]

res=adm.mq(Y,Ped)
res$Var
res$FixedEffect
res$RandomEffect
##End
```

---

adm.mq.jack *ADM model awith MINQUE analysis and jackknife test*

Description

An ADM model can be analyzed by MINQUE approach, requiring no specific genetic mating design or balance data. For reliable results, parents and F1s, parents and F2s, are preferred.

Usage

```
adm.mq.jack(Y, Ped, JacNum = NULL, JacRep = NULL)
```

Arguments

`Y`	A trait matrix including one or more traits.
`Ped`	A pedigree matrix including Env, Female, Male, Generation, with or without block is required. The matrix should include either 4 or 5 columns.
`JacNum`	Number of jackknife groups. The default is 10.
`JacRep`	Repeating times for jackknife process. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated Variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects, and their statistical tests

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

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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(qgtools)
data(cotf2)

dat=cotf2[which(cotf2$Env==1),]
Ped=dat[,c(1:5)]
Y=dat[,-c(1:5)]
res=adm.mq.jack(Y,Ped,JacNum=5)
res$Var
res$PVar
res$FixedEffect
res$RandomEffect

##End
```

---

adm.reml *ADM model with REML analysis*

Description

ADM model can be analyzed by REML approach, requiring no specific genetic mating designs or balance data. For reliable results, parents and F1s, parents and F2s, are preferred.

Usage

```
adm.reml(Y, Ped)
```

Arguments

Y	A trait matrix including one or more than one traits.
Ped	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

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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(qgtools)
data(cotf2)
 dat=cotf2[which(cotf2$Env==1),]
Ped=dat[,c(1:5)]
Y=dat[,-c(1:5)]

res=adm.reml(Y,Ped)
res$Var
res$FixedEffect
res$RandomEffect

##End
```

`adm.reml.jack` *ADM model awith REML analysis and jackknife test*

Description

An ADM model can be analyzed by REML approach, requiring no specific genetic mating design or balance data. For reliable results, parents and F1s, parents and F2s, are preferred.

Usage

```
adm.reml.jack(Y, Ped, JacNum = NULL, JacRep = NULL)
```

Arguments

Y	A trait matrix including one or more traits.
Ped	A pedigree matrix including Env, Female, Male, Generation, with or without block is required. The matrix should include either 4 or 5 columns.
JacNum	Number of jackknife groups. The default is 10.
JacRep	Repeating times for jackknife process. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Column 5 for block can be default. Even though there is only one environment, this column is needed.

Value

Return a list of results: estimated Variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects, and their statistical tests

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., J. N. Jenkins, J. C. McCarty, K. Glover, and W. Berzonsky. 2010. Presentation titled by "Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

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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(qgtools)
data(cotf2)

dat=cotf2[which(cotf2$Env==1),]
Ped=dat[,c(1:5)]
```

```
Y=dat[,-c(1:5)]
res=adm.mq.jack(Y,Ped,JacNum=5)
res$Var
res$PVar
res$FixedEffect
res$RandomEffect

##End
```

---

adm.simu *An R function for ADM model simulation.*

Description

An R function for ADM model simulation with generated data set.

Usage

```
adm.simu(Y, Ped, method = NULL, ALPHA = NULL)
```

Arguments

Y	A matrix of simulated data set
Ped	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
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.The default is 0.05.

Value

Return list of simulated results for variance components.

Author(s)

Jixiang Wu <qgtools@gmail.com>

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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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(qgtools)
data(cotf2)

dat=cotf2[which(cotf2$Env==1),]
Ped=dat[,c(1:5)]
Y=dat[,6]
Y=data.frame(Y)
YS=adm.simudata(Y,Ped,v=rep(20,6),b=c(100),SimuNum=10)
res=adm.simu(YS,Ped)
res
##End
```

`adm.simu.jack` *An R function for ADM model simulation*

Description

An R function for ADM model simulation with generated data set.

Usage

```
adm.simu.jack(Y, Ped, method = NULL, JacNum = NULL, JacRep = NULL, ALPHA = NULL)
```

Arguments

`Y`	A matrix of simulated data set
`Ped`	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
`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`	Number of jackknife groups. The default is 10.
`JacRep`	Repeating times for jackknife process. The default is 1.
`ALPHA`	A preset nominal probability level.The default is 0.05.

Value

Return list of simulated results for variance components.

Author(s)

Jixiang Wu <qgtools@gmail.com>

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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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(qgtools)
data(cotf2)

dat=cotf2[which(cotf2$Env==1),]
Ped=dat[,c(1:5)]
Y=dat[,6]
Y=data.frame(Y)
YS=adm.simudata(Y,Ped,v=rep(20,6),b=c(100),SimuNum=10)
res=adm.simu.jack(YS,Ped,JacNum=5)
res
##End
```

---

adm.simudata *An R function to generate an ADM model simulated data set*

Description

An R function to generate an ADM model simulated data set with given parameters and data structure.

Usage

```
adm.simudata(Y, Ped, v, b, SimuNum = NULL)
```

Arguments

Y	A matrix of trait with one or more than one trait.
Ped	A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
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 <qgtools@gmail.com>

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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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(qgtools)
 data(cotf2)
 Ped=cotf2[,c(1:5)]
 #Y=cotf2[,-c(1:5)]
 Y=cotf2[,6]
 Y=data.frame(Y)
 YS=adm.simudata(Y,Ped,v=rep(20,11),b=c(100))

 ##End
```

adrc.mq *AD model with row and column effects*

Description

An AD model with row and column effects included is used for controlling field variation. The data set can be irregular or missing but the field layout should be rectangular. It can analyze any genetic mating designs and data including F1, F2, or F3 with parents..

Usage

```
adrc.mq(Y, Ped, Row = NULL, Col = NULL)
```

Arguments

`Y`	A data matrix for one or more traits
`Ped`	A pedigree matrix including Environment, Female, Male, Generation is required.
`Row`	A vector for field rows. It can be default.
`Col`	A vector for field colums.It can be default.

Details

If only row or column vector is included, this is equivallent to an AD model with block effects.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

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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(qgtools)
data(adrcdat)
dat=adrcdat[which(adrcdat$Env==1),]
Ped=dat[,c(1,4,5,6)]
Y=dat[,c(8:10)]
Row=dat$Row
Col=dat$Column

res=adrc.mq(Y,Ped,Row=Row,Col=Col) ##run AD model without jackknifing under row and column effects
res$Var
res$FixedEffect
res$RandomEffect
```

`adrc.mq.jack` *AD model with row and column effects analyzed by MINQUE and jackknife*

Description

An AD model with row and column effects included is used for controlling field variation. This model will be analyzed by MINQUE approach and tested by jackknife technique. The data set can be irregular or missing but the field layout should be rectangular. It can analyze any genetic mating designs and data including F1, F2, or F3 with parents..

Usage

```
adrc.mq.jack(Y, Ped, Row = NULL, Col = NULL, JacNum = NULL, JacRep = NULL)
```

Arguments

`Y`	A data matrix for one or more traits
`Ped`	A pedigree matrix including Environment, Female, Male, Generation is required.

`Row`	A vector for field rows. It can be default.
`Col`	A vector for field colums.It can be default.
`JacNum`	Number of jackknife groups to be used. The default is 10.
`JacRep`	Repeating times for jackknife process. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Even though there is only one environment, this first column is needed.If only row or column vector is included, this is equivallent to an AD model with block effects.

Value

Return a list of results: estimated Variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects, and their statistical tests

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

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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(qgtools)
data(adrcdat)
dat=adrcdat[which(adrcdat$Env==1),]
Ped=dat[,c(1,4,5,6)]
```

```
Y=dat[,c(8:10)]
Row=dat$Row
Col=dat$Column

##run AD model with field row and column effects
res=adrc.mq.jack(Y,Ped,Row=Row,Col=Col,JacNum=5)
res$Var
res$PVar
res$FixedEffect
res$RandomEffect
```

`adrc.reml` *AD model with row and column effects analyzed by REML approach*

Description

An AD model with row and column effects included is used for controlling field variation. This model is analyzed by the REML approach. The data set can be irregular or missing but the field layout should be rectangular. It can analyze any genetic mating designs and data including F1, F2, or F3 with parents..

Usage

```
adrc.reml(Y, Ped, Row = NULL, Col = NULL)
```

Arguments

`Y`	A data matrix for one or more traits
`Ped`	A pedigree matrix including Environment, Female, Male, Generation is required.
`Row`	A vector for field rows. It can be default.
`Col`	A vector for field colums.It can be default.

Details

If only row or column vector is included, this is equivallent to an AD model with block effects.

Value

Return a list of results: estimated variance components, estimated fixed effects, and predicted random effects

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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

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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(qgtools)
data(adrcdat)
dat=adrcdat[which(adrcdat$Env==1),]
Ped=dat[,c(1,4,5,6)]
Y=dat[,c(8:10)]
Row=dat$Row
Col=dat$Column

##run AD model without jackknifing under row and column effects

res=adrc.reml(Y,Ped,Row=Row,Col=Col)
res$Var
res$FixedEffect
res$RandomEffect
```

---

adrc.reml.jack *AD model with row and column effects analyzed by MINQUE and jackknife*

Description

An AD model with row and column effects included is used for controlling field variation. This model will be analyzed by MINQUE approach and tested by jackknife technique. The data set can be irregular or missing but the field layout should be rectangular. It can analyze any genetic mating designs and data including F1, F2, or F3 with parents..

Usage

```
adrc.reml.jack(Y, Ped, Row = NULL, Col = NULL, JacNum = NULL, JacRep = NULL)
```

Arguments

`Y`	A data matrix for one or more traits
`Ped`	A pedigree matrix including Environment, Female, Male,Generation is required.
`Row`	A vector for field rows. It can be default.
`Col`	A vector for field colums.It can be default.
`JacNum`	Number of jackknife groups to be used. The default is 10.
`JacRep`	Repeating times for jackknife process. The default is 1.

Details

A pedigree matrix used for analysis is required in the order of Environment (column 1), Female(column 2), Male(column 3), Generation (column 4). Even though there is only one environment, this first column is needed.If only row or column vector is included, this is equivallent to an AD model with block effects.

Value

Return a list of results: estimated Variance components, estimated proportional variance components, estimated fixed effects, and predicted random effects, and their statistical tests

Author(s)

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References

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

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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(qgtools)
data(adrcdat)
dat=adrcdat[which(adrcdat$Env==1&adrcdat$Row<=3),]
Ped=dat[,c(1,4,5,6)]
Y=as.matrix(dat[,8])

colnames(Y)=colnames(dat)[8]

Row=dat$Row
Col=dat$Column


##run AD model with field row and column effects
res=adrc.reml.jack(Y,Ped,Row=Row,JacNum=5)
res$Var
res$PVar
res$FixedEffect
res$RandomEffect
```

---

adrcdat *F2 spring wheat data with row and column*

Description

F2 spring wheat data with row and column can be used to separate field variation. It can be integrated with a AD model using the functions:adrc.mq or adrc.mq.jack.

Usage

```
data(adrcdat)
```

Format

A data frame with 358 observations on the following 10 variables.

`Env` Location code

`Row` Field row code

`Column` Field column

`Female` Female parent

`Male` Male parent

`Gen` Generation. 0=parent and 2=F2

`Rep` Field replication

`YIELD` Grain yield

`HEIGHT` Plant height

`HEADING` Heading date

Details

No other details

Source

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

References

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

Wu, J., McCarty Jr., J.C., Jenkins, J.N. 2010. Cotton chromosome substitution lines crossed with cultivars: Genetic model evaluation and seed trait analyses. Theoretical and Applied Genetics 120:1473-1483.

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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(qgtools)
data(adrcdat)
names(adrcdat)
```

`cotf12` *Cotton F1 and F2 data*

Description

A cotton data dat set contains 10 parents, 20 F1 hybrids, and 20 F2 hybrids, which were evaluated at one research at Zhejiang Agricultural Univsersity in 1992 and 1993.

Usage

```
data(cotf12)
```

Format

A data frame with 300 observations on the following 11 variables.

`Year` Codes for years

`Entry` Codes for 50 entries

`Female` Codes for female parents

`Male` Codes for male parents

`Gen` Codes for generations: 0=parent, 1=F1, and 2=F2

`Blk` Code for field blocks

`CtYld` Cotton seed yield

`TlnY` Total lint yield

`LintY` Lint yield

`Bolls` Boll numeric per plant

`Bsize` Boll size

Details

This data set can be analyzed by different genetic models: AD, ADC, ADM, and ADAA models as showed in the examples.

Source

Not available

References

To be added

Examples

```
library(qgtools)
data(cotf12)
names(cotf12)

#End
```

cotf2 *A cotton F2 data set from a 2*6 factorial genetic mating design.*

Description

Twelve F2 hybrids and their 8 parents were evaluated under two years each an randomized complete block design.

Usage

```
data(cotf2)
```

Format

A data frame with 240 observations on the following 9 variables.

- `Env` Codes for years
- `Female` Codes for female parents
- `Male` Codes for male parents
- `Gen` Codes for generations: 0=parent, 2=F2
- `rep` Codes for field block within each year
- `BN` Boll number
- `BS` Boll size
- `LP` Lint percentage
- `LY` Lint yield

Details

Please refer to the example R codes for more information. This data set can be analyzed by different models.

Source

Not availble

References

No reference available.

Examples

```
library(qgtools)
data(cotf2)
names(cotf2)

#End
```

wheat — *Multi-parental mating design data*

Description

A F2 what data set includes parents, two-way, three-way, and four-way crosses.

Usage

```
data(wheat)
```

Format

A data frame with 802 observations on the following 8 variables.

`Env` Code for year

`P1` Codes for female 1

`P2` Codes for male 1

`P3` Codes for female 2

`P4` Code for male 2

`Gen` Codes for generation: 0=parent and 2=F2

`REP` Codes for replication

`Average` Pre-harvest sprout index

Details

No other details available

Source

Not available

References

To be added

Examples

```
library(qgtools)
data(wheat)
summary(wheat)
```

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