Package 'qgtools'

October 13, 2022

Type Package

Title Generalized Quantitative Genetics Data Analyses

Version 2.0
Date 2019-12-17
Author Jixiang Wu (South Dakota State University), Johnie N. Jenkins and Jack C. McCarty (USDA-ARS)
Maintainer Jixiang Wu <jixiang.wu@sdstate.edu></jixiang.wu@sdstate.edu>
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
LazyLoad yes
Depends stats,utils
RoxygenNote 6.1.1
NeedsCompilation no
Repository CRAN
Date/Publication 2019-12-18 22:30:13 UTC
R topics documented:
qgtools-package
ad.mq
ad.mq.jack
ad.reml
ad.reml.jack
ad.simu
ad.simu.jack
ad.simudata

74

Index

d4.mq	14
d4.mq.jack	16
d4.reml	17
d4.reml.jack	19
d4rc.mq	20
d4rc.mq.jack	22
d4rc.reml	23
d4rc.reml.jack	25
daa.mq	26
daa.mq.jack	28
daa.reml	30
daa.reml.jack	31
daa.simu	33
daa.simu.jack	34
daa.simudata	35
dc.mq	37
dc.mq.jack	38
dc.reml	40
dc.reml.jack	41
dc.simu	43
dc.simu.jack	44
dc.simudata	45
dc4.mq	47
dc4.mq.jack	48
dc4.reml	50
dc4.reml.jack	51
dm.mq	53
13	54
	56
3	57
	59
3	6 0
dm.simudata	61
drc.mq	63
drc.mq.jack	64
drc.reml	66
drc.reml.jack	67
	69
	71
otf2	72
vheat	73

qgtools-package 3

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)

Jixiang Wu: Agronomy, Horticulture & Plant Science Department, South Dakota State University, Brookings, SD 57007

Maintainer: Jixiang Wu <jixiang.wu@sdstate.edu>

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.

Finlay, K.W., G.N. Wilkinson 1963. The analysis of adaptation in a plant breeding programme. Australian Journal of Agricultural Research 14: 742-754.

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.

4 ad.mq

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., 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

Υ

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.

ad.mq 5

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.

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

6 ad.mq.jack

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)

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.

ad.reml 7

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

```
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
```

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

Υ

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.

8 ad.reml

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.

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)
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
```

ad.reml.jack 9

##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)

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.

10 ad.simu

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)
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

Ped

Y A matrix of simulated data set

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.

ad.simu 11

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.

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)]
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
```

12 ad.simu.jack

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

Υ	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. 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

ad.simudata 13

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>

14 ad4.mq

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

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)]
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 multiparent 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

Υ

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.

ad4.mq 15

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.

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(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
```

16 ad4.mq.jack

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)

Jixiang Wu <qgtools@gmail.com>

ad4.reml

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(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

18 ad4.reml

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)

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.

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

ad4.reml.jack

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
```

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.

20 ad4rc.mq

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.

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(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..

ad4rc.mq 21

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.

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

22 ad4rc.mq.jack

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

Υ	A data	matrix	for	one	or	more	traits

Ped A pedigree matrix including Environment, Female 1, Male 1, Female 2, Male 2, 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 equivalent 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>

ad4rc.reml 23

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(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)
```

24 ad4rc.reml

Arguments

Υ	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.

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(adrcdat)
str(adrcdat)

ad4rc.reml.jack 25

jackknife	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

Υ	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 equivalent 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>

26 adaa.mq

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(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</pre>
```

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.

adaa.mq 27

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.

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

28 adaa.mq.jack

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.

adaa.mq.jack 29

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.

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(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
```

30 adaa.reml

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.

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.

adaa.reml.jack 31

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(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

Υ	A	trait ma	trix inc	luding	one or	more trai	ts.
---	---	----------	----------	--------	--------	-----------	-----

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.

32 adaa.reml.jack

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.

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)
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 33

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

Υ	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. 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

34 adaa.simu.jack

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

Υ	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>

adaa.simudata 35

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(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)
```

36 adaa.simudata

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. 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(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 37

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.

38 adc.mq.jack

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)
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.

adc.mq.jack 39

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.

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(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
```

40 adc.reml

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.

adc.reml.jack 41

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)
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

Υ	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.
TacNum	Number of groups to be jackknifed. The default is 10

JacNum Number of groups to be jackknifed. The default is 10.

JacRep Number of jackknife process to be repeated. The default is 1

42 adc.reml.jack

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.

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)
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
```

adc.simu 43

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.

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

44 adc.simu.jack

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

Υ	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>

adc.simudata 45

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(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)
```

46 adc.simudata

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. 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(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 47

adc4.mg

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.

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.

48 adc4.mq.jack

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(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
```

 $\mathsf{adc4}.\mathsf{mq.jack}$

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

Υ	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.

adc4.mq.jack 49

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.

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(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
```

50 adc4.reml

```
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.

adc4.reml.jack 51

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(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)
```

52 adc4.reml.jack

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.

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

adm.mq 53

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

54 adm.mq.jack

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.

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)

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.

adm.mq.jack 55

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.

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

56 adm.reml

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>

adm.reml.jack 57

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)
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)
```

58 adm.reml.jack

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.

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)

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

adm.simu 59

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

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. 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.

60 adm.simu.jack

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)

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

Υ	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.

adm.simudata 61

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. 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(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.

62 adm.simudata

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.

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(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 63

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

Υ	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.

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.

64 adrc.mq.jack

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(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 re-

quired.

adrc.mq.jack 65

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 equivalent 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.

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

66 adrc.reml

```
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 re-

quired.

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 equivalent 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>

adrc.reml.jack 67

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(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
```

AD model with row and column effects analyzed by MINQUE and jackknife

68 adrc.reml.jack

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

Υ	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 equivalent 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.

adrcdat 69

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(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</pre>
```

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

70 adredat

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.

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(adrcdat)
names(adrcdat)

cotf12 71

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

72 cotf2

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

#End

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

wheat 73

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)
```

Index

* AD model	adm.mq, 53
ad.mq,4	adm.mq.jack,54
ad.mq.jack, 6	adm.reml, <u>56</u>
ad.reml,7	adm.reml.jack,57
ad.reml.jack,9	adm.simu,59
ad.simu.jack, 12	adm.simudata,61
ad.simudata, 13	cotf12, 7 1
ad4.mq, 14	cotf2, 72
ad4.mq.jack, 16	* F1
ad4.reml, 17	cotf12, 7 1
ad4.reml.jack, 19	* F2
adaa.simu.jack,34	cotf12, 7 1
adc4.reml, 50	* MINQUE
adm.simu.jack,60	ad.mq,4
cotf12, 71	ad.mq.jack,6
cotf2, <mark>72</mark>	ad.simu, 10
* ADAA model	ad.simu.jack, 12
adaa.mq, 26	ad4.mq, 14
adaa.mq.jack,28	ad4.mq.jack, 16
adaa.reml, 30	ad4rc.mq, 20
adaa.reml.jack,31	ad4rc.mq.jack,22
adaa.simu,33	adaa.mq, 26
adaa.simudata,35	adaa.simu,33
cotf12, 7 1	adaa.simu.jack,34
* ADC model	adc.mq, 37
ad.simu, 10	adc.simu,43
adc.mq, 37	adc.simu.jack,44
adc.mq.jack,38	adc4.mq, 47
adc.reml,40	adc4.mq.jack,48
adc.reml.jack,41	adm.mq, 53
adc.simu,43	adm.simu,59
adc.simu.jack,44	adm.simu.jack,60
adc.simudata,45	adrc.mq,63
adc4.mq,47	adrc.mq.jack,64
adc4.mq.jack,48	adrcdat, 69
adc4.reml.jack,51	cotf12, 7 1
cotf12, 71	cotf2, 72
cotf2, 72	* REML
* ADM model	ad.reml,7

INDEX 75

ad.reml.jack,9	adaa.mq.jack,28
ad.simu, 10	adaa.reml.jack,31
ad.simu.jack, 12	adc.mq.jack,38
ad4.reml, 17	adm.mq.jack,54
ad4.reml.jack,19	adm.reml.jack,57
ad4rc.rem1,23	* cotf2
ad4rc.reml.jack,25	ad.mq,4
adaa.reml,30	ad.reml,7
adaa.reml.jack,31	ad.reml.jack, 9
adaa.simu,33	ad.simudata,13
adaa.simu.jack,34	adaa.reml, 30
adc.reml,40	adaa.simudata,35
adc.reml.jack,41	adc.mq, 37
adc.simu,43	adc.reml, 40
adc.simu.jack,44	adc.reml.jack,41
adc4.reml, 50	adc.simudata,45
adc4.reml.jack, 51	adm.mq, 53
adm.reml,56	adm.reml,56
adm.reml.jack,57	adm.simudata,61
adm.simu,59	* cotton
adm.simu.jack,60	ad.mq,4
adrc.reml, 66	ad.reml, 7
adrc.reml.jack,67	ad.reml.jack, 9
ad model	ad.simu, 10
ad4rc.mq, 20	ad.simu.jack, 12
ad4rc.mq.jack,22	ad.simudata, 13
ad4rc.rem1,23	adaa.mq, 26
ad4rc.reml.jack,25	adaa.reml, 30
adrc.mq, 63	adaa.simu,33
adrc.mq.jack,64	adaa.simu.jack,34
adrc.reml, 66	adaa.simudata,35
adrc.reml.jack,67	adc.mq, 37
adrcdat, 69	adc.reml, 40
boll number	adc.reml.jack,41
cotf2, 72	adc.simu,43
column effect	adc.simu.jack,44
ad4rc.mq, 20	adc.simudata,45
ad4rc.mq.jack,22	adm.mq, 53
ad4rc.reml, 23	adm.reml,56
ad4rc.reml.jack,25	adm.simu,59
adrc.mq,63	adm.simu.jack,60
adrc.mq.jack,64	adm.simudata,61
adrc.reml, 66	cotf12, 71
adrc.reml.jack,67	* datasets
adrcdat, 69	adrcdat, 69
cotf12	cotf12, 7 1
ad.mq.jack, 6	cotf2, 72
adaa.mq, 26	wheat, 73

76 INDEX

* genetic models	ad4rc.mq.jack,22
cotf2, 72	ad4rc.reml, 23
* jaccknife	ad4rc.reml.jack,25
ad.mq.jack,6	adrc.mq, 63
adaa.mq.jack, 28	adrc.mq.jack,64
adaa.reml.jack,31	adrc.reml, 66
adc.mq.jack,38	adrc.reml.jack,67
adm.mq.jack, 54	adrcdat, 69
adm.reml.jack,57	* simuated data
* jackknife	ad.simudata,13
ad.reml.jack,9	adaa.simudata,35
ad.simu.jack, 12	adc.simudata,45
ad4.mq.jack, 16	adm.simudata,61
ad4.reml.jack,19	* wheat
ad4rc.mq.jack,22	ad4.mq, 14
ad4rc.reml.jack,25	ad4.mq.jack, 16
adaa.simu.jack,34	ad4.reml, 17
adc.reml.jack,41	ad4.reml.jack,19
adc.simu.jack,44	adc4.mq, 47
adc4.mq.jack,48	adc4.mq.jack, 48
adc4.reml.jack,51	adc4.reml, 50
adm.simu.jack,60	adc4.reml.jack, 51
adrc.mq.jack,64	- d 4
adrc.reml.jack,67	ad.mq, 4
adrcdat, 69	ad.mq.jack, 6
cotf12, 71	ad.reml, 7
cotf2, <mark>72</mark>	ad.reml.jack, 9
* lint percentage	ad.simu, 10
cotf2, 72	ad.simu.jack, 12
* lint size	ad.simudata,13
cotf2, <mark>72</mark>	ad4.mq, 14
* lint yield	ad4.mq.jack,16 ad4.reml,17
cotf2, 72	ad4.reml.jack, 19
* minque	ad4.remi1.jack, 19 ad4rc.mq, 20
adaa.mq.jack, 28	ad4rc.mq.jack,22
adc.mq.jack,38	ad4rc.rem1, 23
adm.mq.jack, 54	ad4rc.reml.jack, 25
* multi-parent mating design	adaa.mq, 26
ad4.mq, 14	adaa.mq.jack, 28
ad4.mq.jack, 16	adaa.reml, 30
ad4.reml, 17	adaa.reml.jack,31
ad4.reml.jack,19	adaa.simu, 33
adc4.mq, 47	adaa.simu.jack,34
adc4.mq.jack,48	adaa.simudata,35
adc4.reml, 50	ada.simdata, 33
adc4.reml.jack,51	adc.mq.jack, 38
* row effect	adc.reml, 40
ad4rc.mg. 20	adc.reml.jack.41

INDEX 77

```
adc.simu, 43
adc.simu.jack,44
adc.simudata, 45
adc4.mq, 47
adc4.mq.jack, 48
adc4.reml, 50
adc4.reml.jack, 51
adm.mq, 53
adm.mq.jack, 54
adm.reml, 56
adm.reml.jack, 57
adm.simu,59
adm.simu.jack, 60
adm.simudata, 61
adrc.mq, 63
{\tt adrc.mq.jack,}\, {\tt 64}
\mathsf{adrc.reml}, \textcolor{red}{\mathbf{66}}
adrc.reml.jack, 67
adrcdat, 69
cotf12, 71
cotf2, 72
qgtools (qgtools-package), 3
qgtools-package, 3
wheat, 73
```