Package ‘qgtools’

October 13, 2022

Type Package
Title Generalized Quantitative Genetics Data Analyses
Version 2.0
Date 2019-12-17
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Description Two linear mixed model approaches: REML (restricted maximum likelihood) and MINQUE (minimum norm quadratic unbiased estimation) approaches and several resampling techniques are integrated for various quantitative genetics analyses. With these two types of approaches, various unbalanced data structures, missing data, and any irregular genetic mating designs can be analyzed and statistically tested. This package also offers fast computations for many large data sets.
License GPL-2
LazyLoad yes
Depends stats,utils
RoxygenNote 6.1.1
NeedsCompilation no
Repository CRAN
Date/Publication 2019-12-18 22:30:13 UTC

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Description

We integrated with two linear mixed model approaches (MIQUNE and REML) and several re-
sampling 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,
MIQUNE 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 tech-
nique is integrated for various statistical tests such as for variance components, fixed effects, and
random effects (Wu et al., 2012). Four commonly used genetic models: AD (additive-dominance),
ADC (AD model with cytoplasmic effects), ADM (AD model with maternal effects), and ADAA
(AD model with additive-by-additive interaction effects), are provided.

Author(s)

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Brookings, SD 57007
Maintainer: Jixiang Wu <jixiang.wu@sdstate.edu>

References

Australian Journal of Agricultural Research 14: 742-754.
Patterson, H. D. and Thompson, R. 1971. Recovery of inter-block information when block sizes are
unequal. Biometrika, 58: 545-554.

---

**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**

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

**Arguments**

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

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

Value

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

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


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.


Examples

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

Usage

ad.reml(Y, Ped)

Arguments

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

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

Value

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

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


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.


Examples

```r
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 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, proportional variance components, fixed effects, and random effects.

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


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.


Examples

```r
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**

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

**Arguments**

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

<table>
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<th>method</th>
<th>The default linear mixed model approach is MINQUE. Users can choose both or one of two linear mixed model approaches, REML and MINQUE.</th>
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</thead>
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<tr>
<td>ALPHA</td>
<td>A preset nominal probability level. The default is 0.05.</td>
</tr>
</tbody>
</table>

**Value**

Return list of simulated results for variance components.

**Author(s)**

Jixiang Wu <qgtools@gmail.com>

**References**


**Examples**

```r
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
```
An R function for AD model simulation

Description

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

Usage

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

Arguments

Y
A matrix of simulated data set

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

method
The default linear mixed model approach is MINQUE. Users can choose both or one of two linear mixed model approaches, REML and MINQUE.

JacNum
Number of jackknife groups. The default is 10.

JacRep
Repeating times for jackknife process. The default is 1.

ALPHA
A preset nominal probability level. The default is 0.05.

Value

Return list of simulated results for variance components.

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


Examples

```r
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
```

---

**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

```r
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**
  The number of simulations. The default number is 200.

### Details

The number of simulations. The default number is 200.

### Value

Return a simulated data set which is a matrix.

### Author(s)

Jixiang Wu <qgtools@gmail.com>
References


Examples

```r
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)
```
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


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.


Examples

```r
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
```
## 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

\[
\text{ad4.mq.jack}(Y, \text{Ped}, \text{JacNum} = \text{NULL}, \text{JacRep} = \text{NULL})
\]

## 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


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.


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
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


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.


Examples

```r
library(qgtools)
data(wheat)
n=nrow(wheat)
id=sample(n,200)
dat=wheat[id,]
Ped=dat[,c(1:6)]
Y=as.matrix(dat[,8])
colnames(Y)=colnames(dat)[8]
res=ad4.reml(Y,Ped)
res$Var
res$FixedEffect
res$RandomEffect
##End
```

---

**ad4.reml.jack**

*Additive-dominance (AD) model, multi-parent mating designs, REML, and jackknife*

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

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

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

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


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.


Examples

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

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

```r
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 columns. 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>

References


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.


ad4rc.mq.jack

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

Examples

```r
library(qgtools)
data(adrcdat)
str(adrcdat)
```

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

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

Arguments

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

References


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.


Examples

```r
library(qgtools)

data(wheat)
str(wheat)
```

---

ad4rc.reml

**AD model with row and column effects analyzed by REML approach**

Description

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

Usage

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

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

References

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.

Examples

library(qgtools)
data(adrcdat)
str(adrcdat)
AD model with row and column effects analyzed by MINQUE and jackknife

Description

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

Usage

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

Arguments

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


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.


Examples

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

colnames(Y)=colnames(dat)[8]
Row=dat$Row
Col=dat$Column

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

**ADAA model with MINQUE analysis**

Description

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

adaa.mq(Y, Ped)

Arguments

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

Details

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

Value

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

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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.
Examples

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

###Description

An additive-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

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

###Arguments

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

###Details

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

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

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


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.


Examples

```r
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
```
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
- 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.

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

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

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

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

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

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

Value

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

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


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.


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
An R function for AD model simulation.

Description

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

Usage

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

Arguments

Y A matrix of simulated data set
Ped A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
method The default linear mixed model approach is MINQUE. Users can choose both or one of two linear mixed model approaches, REML and MINQUE.
ALPHA A preset nominal probability level. The default is 0.05.

Value

Return list of simulated results for variance components.

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

Examples

```r
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
```
References


Examples

```r
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

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

Usage

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

Y    A matrix of trait with one or more than one trait.

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

v    A vector of preset variance components.

b    A vector of present fixed effects.

SimuNum  The number of simulations. The default number is 200.

Value

Return a simulated data set which is a matrix.

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


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
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

```r
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


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.mq.jack

An ADC model with MINQUE analyses and jackknife tests

Description

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

Usage

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

Arguments

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

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

Value

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

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


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.


Examples

```r
library(qgtools)
data(cotf12)
names(cotf12)
dat=cotf12[which(cotf12$Year==1),]
Ped=dat[,c(1,3:6)]
Y=dat[,-c(1:6)]
#Ped=cotf12[,c(1,3:6)]
#Y=cotf12L,-c(1:6)]
res=adc.mq.jack(Y,Ped,JacNum=5)
res$Var
res$FixedEffect
```
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

```r
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


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.


Examples

```r
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**

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

**Arguments**

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Y</td>
<td>A trait matrix including one or more than one traits.</td>
</tr>
<tr>
<td>Ped</td>
<td>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.</td>
</tr>
<tr>
<td>JacNum</td>
<td>Number of groups to be jackknifed. The default is 10.</td>
</tr>
<tr>
<td>JacRep</td>
<td>Number of jackknife process to be repeated. The default is 1</td>
</tr>
</tbody>
</table>
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, proportional variance components, fixed effects, and random effects.

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


Wu, 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.


Examples

```r
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
```
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


adc.simu.jack

An R function for ADC model simulation

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

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

Arguments

Y
A matrix of simulated data set

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

method
The default linear mixed model approach is MINQUE. Users can choose both or one of two linear mixed model approaches, REML and MINQUE.

JacNum
Number of jackknife groups. The default is 10.

JacRep
Repeating times for jackknife process. The default is 1.

ALPHA
A preset nominal probability level. The default is 0.05.

Value
Return list of simulated results for variance components.

Author(s)
Jixiang Wu <qgtools@gmail.com>
adc.simudata

An R function to generate an ADC model simulated data set

Description

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

Usage

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

Y  A matrix of trait with one or more than one trait.

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

v A vector of preset variance components.

b A vector of present fixed effects.

SimuNum The number of simulations. The default number is 200.

Value

Return a simulated data set which is a matrix.

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


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
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


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.

adc4.mq.jack

ADC model, multi-parent mating designs, MINQUE, and jackknife

Description

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

Usage

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

Arguments

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

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

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

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

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

Value

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

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


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.


Examples

```r
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
```
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


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.


Examples

```r
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**

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

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

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

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

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

Details

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

Value

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

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


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.


Examples

```r
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

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

Arguments

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

Details

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

Value

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

Jixiang Wu <qgtools@gmail.com>

References


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.


Examples

```r
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 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

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


"Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.


Examples

```r
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**

```r
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

ADM model analysis with REML analysis and jackknife test

Description

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

Usage

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

Y  A trait matrix including one or more traits.

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

JacNum  Number of jackknife groups. The default is 10.

JacRep  Repeating times for jackknife process. The default is 1.

Details

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

Value

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

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


"Unbalanced Genetic Data Analysis: model evaluation and application" was offered at ASA, CSSA, & SSSA 2010 International Annual Meetings, Long Beach, CA.

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

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

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


Examples

```r
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
```

adm.simu.jack

An R function for ADM model simulation

Description

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

Usage

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

Arguments

- `Y` A matrix of simulated data set
- `Ped` A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
- `method` The default linear mixed model approach is MINQUE. Users can choose both or one of two linear mixed model approaches, REML and MINQUE.
- `JacNum` Number of jackknife groups. The default is 10.
- `JacRep` Repeating times for jackknife process. The default is 1.
- `ALPHA` A preset nominal probability level. The default is 0.05.
adm.simudata

Value

Return list of simulated results for variance components.

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


Examples

```r
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
```

Description

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

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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
Dissertation, NC State University, Raleigh, U.S.A

Examples

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

## End
**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**

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

**Arguments**

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

**References**


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.
adrc.mq.jack


Examples

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

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

---

adrc.mq.jack

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

Description

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

Usage

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

Arguments

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

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

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

---

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

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

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

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


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.


Examples

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

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

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

adrc.reml.jack

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

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

Usage

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

Arguments

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


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.
Examples

```r
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])

rownames(Y)=rownames(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
```

Description

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

Usage

data(adrcdat)

Format

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

Env  Location code
**Row**  Field row code  
**Column**  Field column  
**Female**  Female parent  
**Male**  Male parent  
**Gen**  Generation. 0=parent and 2=F2  
**Rep**  Field replication  
**YIELD**  Grain yield  
**HEIGHT**  Plant height  
**HEADING**  Heading date  

**Details**

No other details  

**Source**


**References**

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.  

**Examples**

```r
library(qgtools)
data(adrcdat)
names(adrcdat)
```
Cotton F1 and F2 data

Description
A cotton data dataset contains 10 parents, 20 F1 hybrids, and 20 F2 hybrids, which were evaluated at one research at Zhejiang Agricultural University 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
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 available

References

No reference available.

Examples

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

#End
Description

A F2 wheat 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.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Env</td>
<td>Code for year</td>
</tr>
<tr>
<td>P1</td>
<td>Codes for female 1</td>
</tr>
<tr>
<td>P2</td>
<td>Codes for male 1</td>
</tr>
<tr>
<td>P3</td>
<td>Codes for female 2</td>
</tr>
<tr>
<td>P4</td>
<td>Code for male 2</td>
</tr>
<tr>
<td>Gen</td>
<td>Codes for generation: 0=parent and 2=F2</td>
</tr>
<tr>
<td>REP</td>
<td>Codes for replication</td>
</tr>
<tr>
<td>Average</td>
<td>Pre-harvest sprout index</td>
</tr>
</tbody>
</table>

Details

No other details available

Source

Not available

References

To be added

Examples

library(qgtools)
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