Package ‘qgtools’

February 20, 2015

Type Package
Title Tools for Quantitative Genetics Data Analyses
Version 1.0
Date 2014-09-05
Author Jixiang Wu (South Dakota State University), Johnie N. Jenkins and Jack C. McCarty (USDA-ARS)
Maintainer Jixiang Wu <qgtools@gmail.com>
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. Other functions will be added to this R tool in the future.
License GPL-2
LazyLoad yes
Depends stats,utils,Matrix, MASS
NeedsCompilation no
Repository CRAN
Date/Publication 2014-09-17 18:12:26

R topics documented:

qgtools-package .................................................. 3
ad.mq .................................................................. 4
ad.mq.jack .......................................................... 6
ad.reml .............................................................. 7
ad.reml.jack ......................................................... 9
ad.simu .............................................................. 10
ad.simu.jack ......................................................... 12
ad.simudata ......................................................... 13
ad4.mq ............................................................... 14
R topics documented:

<table>
<thead>
<tr>
<th>Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>ad4.mq.jack</td>
<td>16</td>
</tr>
<tr>
<td>ad4.reml</td>
<td>17</td>
</tr>
<tr>
<td>ad4.reml.jack</td>
<td>19</td>
</tr>
<tr>
<td>adaa.mq</td>
<td>21</td>
</tr>
<tr>
<td>adaa.mq.jack</td>
<td>22</td>
</tr>
<tr>
<td>adaa.reml</td>
<td>24</td>
</tr>
<tr>
<td>adaa.reml.jack</td>
<td>25</td>
</tr>
<tr>
<td>adaa.simu</td>
<td>27</td>
</tr>
<tr>
<td>adaa.simu.jack</td>
<td>28</td>
</tr>
<tr>
<td>adaa.simudata</td>
<td>30</td>
</tr>
<tr>
<td>adc.mq</td>
<td>31</td>
</tr>
<tr>
<td>adc.mq.jack</td>
<td>32</td>
</tr>
<tr>
<td>adc.reml</td>
<td>34</td>
</tr>
<tr>
<td>adc.reml.jack</td>
<td>35</td>
</tr>
<tr>
<td>adc.simu</td>
<td>37</td>
</tr>
<tr>
<td>adc.simu.jack</td>
<td>38</td>
</tr>
<tr>
<td>adc.simudata</td>
<td>40</td>
</tr>
<tr>
<td>adc4.mq</td>
<td>41</td>
</tr>
<tr>
<td>adc4.mq.jack</td>
<td>42</td>
</tr>
<tr>
<td>adc4.reml</td>
<td>44</td>
</tr>
<tr>
<td>adc4.reml.jack</td>
<td>46</td>
</tr>
<tr>
<td>adm.mq</td>
<td>47</td>
</tr>
<tr>
<td>adm.mq.jack</td>
<td>49</td>
</tr>
<tr>
<td>adm.reml</td>
<td>50</td>
</tr>
<tr>
<td>adm.reml.jack</td>
<td>52</td>
</tr>
<tr>
<td>adm.simu</td>
<td>53</td>
</tr>
<tr>
<td>adm.simu.jack</td>
<td>54</td>
</tr>
<tr>
<td>adm.simudata</td>
<td>56</td>
</tr>
<tr>
<td>adrc.mq</td>
<td>57</td>
</tr>
<tr>
<td>adrc.mq.jack</td>
<td>58</td>
</tr>
<tr>
<td>adrc.reml</td>
<td>60</td>
</tr>
<tr>
<td>adrc.reml.jack</td>
<td>62</td>
</tr>
<tr>
<td>adrcdat</td>
<td>63</td>
</tr>
<tr>
<td>cotf12</td>
<td>65</td>
</tr>
<tr>
<td>cotf2</td>
<td>66</td>
</tr>
<tr>
<td>maize</td>
<td>67</td>
</tr>
<tr>
<td>stab.fw</td>
<td>68</td>
</tr>
<tr>
<td>stab.mean</td>
<td>69</td>
</tr>
<tr>
<td>stab.var</td>
<td>70</td>
</tr>
<tr>
<td>wheat</td>
<td>72</td>
</tr>
</tbody>
</table>

Index

73
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

<table>
<thead>
<tr>
<th>Package</th>
<th>qgtools</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>Package</td>
</tr>
<tr>
<td>Version</td>
<td>1.0</td>
</tr>
<tr>
<td>Date</td>
<td>2014-09-05</td>
</tr>
<tr>
<td>License</td>
<td>GPL -2</td>
</tr>
</tbody>
</table>

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. For the second component, we add regression based yield stability with integration of bootstrapping and permutation tests included. Genotypic means, ranks, and variations across test environments can be calculated with resampling techniques integrated. Please refer to each function and its example R codes and data sets for detailed information and better understanding. More functions for genetic data analyses will be provided in the future.

Author(s)

Jixiang Wu: Plant Science Department, South Dakota State University, Brookings, SD 57007
Maintainer: Jixiang Wu <qgtools@gmails.com>

References


---

**Additive-dominance (AD) model with MINQUE analysis**

**Description**

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

**Usage**

`ad.mq(Y, Ped)`
Arguments

\( Y \)  
A trait matrix including one or more than one traits.

\( \text{Ped} \)  
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)]
```
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


Examples

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

---

ad.reml

**Additive-dominance (AD) model with REML analysis**

---

Description

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

Usage

```r
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

library(qgtools)
data(cotf2)
dat=cotf2[which(cotf2$Env==1),]
ad.reml.jack

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

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

##End

---

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

### Description

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

### Usage

```r
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.
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

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

An R function for AD model simulation

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

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Y</td>
<td>A matrix of simulated data set</td>
</tr>
<tr>
<td>Ped</td>
<td>A pedigree matrix including Environment, Female, Male, Generation, with or</td>
</tr>
<tr>
<td></td>
<td>without block is required. So the matrix should include either 4 columns or</td>
</tr>
<tr>
<td></td>
<td>5 columns.</td>
</tr>
<tr>
<td>method</td>
<td>The default linear mixed model approach is MINQUE. Users can choose both</td>
</tr>
<tr>
<td></td>
<td>or one of two linear mixed model approaches, REML and MINQUE.</td>
</tr>
<tr>
<td>JacNum</td>
<td>Number of jackknife groups. The default is 10.</td>
</tr>
<tr>
<td>JacRep</td>
<td>Repeating times for jackknife process. The default is 1.</td>
</tr>
<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
Ana 1:19
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
**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 = rep(20, 7), b = c(100), SimuNum = 10)
```

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 preset 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)]

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

## End

### ad4.mq

Additive-dominance (AD) model with MINQUE analysis for multi-parent mating designs

Description

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

Usage

`ad4.mq(Y, Ped)`

Arguments

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

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

Value

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

Author(s)

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

---

**ad4.reml**

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

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

Usage

ad4.reml(Y, Ped)

Arguments

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

Details

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

Value

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

Author(s)

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
```

---

**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

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

```r
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

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 model with MINQUE and jacknife analyses

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

Arguments

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

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

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

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

References
   Ana 1:19
   Wu, J., J. N. Jenkins, Jack C. McCarty, and D. Wu. 2006b Variance component estimation using
   "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 quan-
titative 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
   Dissertation, NC State University, Raleigh, U.S.A
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
```

### adaarem1

*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

`adaarem1(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(cotf12)
#names(cotf12)
dat=icotf12[which(cotf12$Year==1),]
Ped=dat[,c(1,3:6)]
Y=dat[,c(1:6)]
#Ped=icotf12[,c(1,3:6)]
#Y=icotf12[,c(1:6)]
res=adaa.reml(Y,Ped)
res$Var
res$FixedEffect
res$RandomEffect
```

---

**Examples**

```r
library(qgtools)
data(cotf12)
#names(cotf12)
dat=icotf12[which(cotf12$Year==1),]
Ped=dat[,c(1,3:6)]
Y=dat[,c(1:6)]
#Ped=icotf12[,c(1,3:6)]
#Y=icotf12[,c(1:6)]
res=adaa.reml(Y,Ped)
res$Var
res$FixedEffect
res$RandomEffect
```

---

**ADA 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

```r
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
```

###Description

An R function for AD model simulation.

###Usage

```r
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

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

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

Description

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

Usage

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

**Y**
A matrix of simulated data set

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

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

**JacNum**
Number of jackknife groups. The default is 10.

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

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

Value

Return list of simulated results for variance components.

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


Examples

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

```r
adaaNsimudata(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

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

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

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


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=adc.mq(y, Ped)

res$Var
res$FixedEffect
res$RandomEffect

##End
```

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

dc.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.
**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


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
```
Description

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

Usage

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

Arguments

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

Details

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

Value

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

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


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

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

##End
```

---

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

**Description**

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

**Usage**

```r
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

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

Ped=dat[,c(1:5)]
Y=dat[,c(6,7)]
#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
```r
adc.simu.jack(Y, Ped, method = NULL, JacNum = NULL, JacRep = NULL, ALPHA = NULL)
```

Arguments

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

Value

Return list of simulated results for variance components.

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


Examples

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

An R function to generate an ADC model simulated data set

Description

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

Usage

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

Arguments

Y  A matrix of trait with one or more than one trait.
Ped A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
v  A vector of preset variance components.
b  A vector of present fixed effects.
SimuNum The number of simulations. The default number is 200.

Value

Return a simulated data set which is a matrix.

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

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


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(adc4.mq.jack)
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
```

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.


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

Examples
library(qgtools)
data(wheat)
n=nrow(wheat)
id=sample(n,200)
dat=wheat[id,]
Ped=dat[,c(1:6)]
Y=as.matrix(dat[,8])
colnames(Y)=colnames(dat)[8]
res=adc4.mq.jack(Y,Ped,JacNum=5)
res$Var
res$PVar
res$FixedEffect
res$RandomEffect

### End
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
**Description**

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

**Usage**

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

**Arguments**

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

**Details**

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

**Value**

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

**Author(s)**

Jixiang Wu <qgtools@gmail.com>

**References**


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

###End

An ADM model with MINQUE analysis

Description

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

Usage

adm.mq(Y, Ped)

Arguments

Y A trait matrix including one or more traits.

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

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

Value

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

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


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 with MINQUE analysis and jackknife test

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

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

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

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

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

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

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

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

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)]

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

###End
```
ADM model 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

```r
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


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$Env==1),]
Ped=dat[,c(1:5)]
Y=dat[,,-c(1:5)]
res=adm.mq.jack(Y,Ped,JacNum=5)
res$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**

```r
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

```
library(qgtools)
data(cotf2)

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

adm.simu.jack

An R function for ADM model simulation

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

Usage

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

y
A matrix of simulated data set

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

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

JacNum
Number of jackknife groups. The default is 10.

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

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

Value
Return list of simulated results for variance components.

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

References

Examples

library(qgtools)
data(cotf2)

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

An R function to generate an ADM model simulated data set

Description

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

Usage

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

Arguments

- **Y**: A matrix of trait with one or more than one trait.
- **Ped**: A pedigree matrix including Environment, Female, Male, Generation, with or without block is required. So the matrix should include either 4 columns or 5 columns.
- **v**: A vector of preset variance components.
- **b**: A vector of present fixed effects.
- **SimuNum**: The number of simulations. The default number is 200.

Value

Return a simulated data set which is a matrix.

Author(s)

Jixiang Wu <qgtools@gmail.com>

References

Examples

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

YS=adm.simudata(Y, Ped, v=rep(20,11), b=c(100))

##End

adrc.mq

AD model with row and column effects

Description

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

Usage

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

Arguments

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


Examples

```
library(ggtools)
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
```

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.
adrc.mq.jack

Usage
adrc.mq.jack(Y, Ped, Row = NULL, Co1 = 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.
Co1  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**

```r
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
```
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


Examples

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

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

adrcdat  
F2 spring wheat data with row and column

Description

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

data(adrcdat)

Format

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

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

Details

No other details

Source


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)
```

---

**Description**

A cotton data set 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**

```r
data(cotf12)
```

**Format**

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

- **Year**  Codes for years
- **Entry**  Codes for 50 entries
- **Female**  Codes for female parents
- **Male**  Codes for male parents
- **Gen**  Codes for generations: 0=parent, 1=F1, and 2=F2
- **Blk**  Code for field blocks
- **CtYld**  Cotton seed yield
- **TlnY**  Total lint yield
- **LintY**  Lint yield
- **Bolls**  Boll numeric per plant
- **Bsize**  Boll size

**Details**

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

**Source**

Not available

**References**

To be added
Examples

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

#End

cotf2

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

Description

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

Usage

data(cotf2)

Format

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

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

Details

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

Source

Not available

References

No reference available.
Examples

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

#End
```

---

### Maize variety trial

**Description**

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

**Usage**

```r
data(maize)
```

**Format**

A data frame with 260 observations on the following 4 variables.

- **Cultivar**: test cultivar
- **Year**: test years
- **Location**: test locations
- **Yld**: maize yield

**Details**

No other details available

**Source**


**References**


**Examples**

```r
library(qgtools)
data(maize)
names(maize)
```

## stab.fw

**Regression based stability analysis**

**Description**

A simple and multiple linear regression based method for stability analysis

**Usage**

```r
stab.fw(y, Gen, Env, times, Rep, X = NULL, alpha = NULL, ...)
```

**Arguments**

- `y`: A response variable vector used for stability analysis
- `Gen`: A vector of genotypes
- `Env`: A vector of environments
- `times`: Times of resampling used for stability analysis.
- `Rep`: An argument with replication: Rep=TRUE or with replication: Rep=FALSE
- `X`: A vector or matrix of other predictable variables. Default is NULL.
- `alpha`: A nominal probability values used for statistical tests
- `...`: 

**Value**

Return the stability parameter estimates and their confidence interval of (1-alpha) for each genotype

**Author(s)**

Jixiang Wu <qgtools@gmail.com>

**References**


stab.mean

See Also

stab.mean
stab.var
stab.ammi

Examples

library(qgtools)
data(maize)
#names(maize)

Geno=as.vector(maize$Cultivar)
Env=paste(maize$Location,maize$Year,sep=":")
y=maize$Yld

res=stab.fw(y,Geno=Geno,Env=Env,times=10,Rep=TRUE)
res

##end

stab.mean  Group mean and rank calculator

Description

A function to calculate group means and ranks with two resampling techniques

Usage

stab.mean(Y, class, cls2 = NULL, resample, times = NULL, alpha = NULL, ...)

Arguments

Y        A matrix including One or more traits
class    A vector of the first factor for calculating variance. For example, a vector of genotypes.
cls2     A vector of the second factor used within-group bootstraping for variance. It can be default
resample Resampling technique option. resample="Boot" is for bootstrapping. resample="Perm" is for permutation.
times    Number of resampling used. The default is 1000.
alpha    A nominal probability used for statistical test. The default value is 0.05.
Value

Return ranks and means and their (1-alpha) confidence intervals

Author(s)

Jixiang Wu <qgtools@gmail.com>

References


Examples

```r
# Sample R codes for the function genmod.rank
library(qgtools)
data(maize)
#names(maize)

Geno=as.vector(maize$Cultivar)
Env=paste(maize$Location,maize$Year,sep=" ")
y=maize$Yld

res=stab.mean(y,class=Geno,cls2=Env,resample="Boot",times=10)
res

res=stab.mean(y,class=Geno,resample="Perm",times=10)
res

## end
```

---

**stab.var**

*Within-group variance calculation with resampling techniques*

Description

Within-group variance calculation with resampling techniques: permutation and bootstrapping

Usage

```r
stab.var(Y, class, cls2 = NULL, resample, times = NULL, alpha = NULL, ...)
```
**Arguments**

- `y`: A matrix including one or more traits
- `class`: A vector of the first factor for calculating variance. For example, a vector of genotypes.
- `cls2`: A vector of the second factor used within-group bootstrapping for variance. It can be default.
- `resample`: Resampling technique option. `resample="Boot"` is for bootstrapping. `resample="Perm"` is for permutation.
- `times`: Number of resampling used. The default number is 1000.
- `alpha`: A nominal probability used for statistical test. The default value is 0.05.

**Value**

Return a list of variance and (1-alpha) confidence interval for each level in the class.

**Author(s)**

Jixiang Wu <qgtools@gmail.com>

**References**


**Examples**

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

Geno=as.vector(maize$Cultivar)
Env=paste(maize$Location,maize$Year,sep=":")
y=maize$Yld

res=stab.var(y,class=Geno,cls2=Env,resample="Boot",times=10)
res

res=stab.var(y,class=Geno,resample="Perm",times=10)
res
```

##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.

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

*Topic AD model
  ad.mq, 4
  ad.mq.jack, 6
  ad.reml, 7
  ad.reml.jack, 9
  ad.simu.jack, 12
  ad.simudata, 13
  adc.mq, 31
  adc.mq.jack, 38
  adrc.dat, 63
  cotf12, 65
  cotf2, 66

*Topic ADAA model
  ada.mq, 21
  ada.mq.jack, 22
  adaa.reml, 25
  adaa.simu, 27
  adaa.simudata, 30
  cotf12, 65

*Topic ADC model
  ad.simu, 10
  adc.mq, 31
  adc.mq.jack, 32
  adrc.mq, 57
  adrc.mq.jack, 58
  adrc.dat, 63
  cotf12, 65
  cotf2, 66

*Topic ADM model
  adm.mq, 47
  adm.mq.jack, 49
  adm.reml, 50
  adm.reml.jack, 52
  adm.simu, 53
  adm.simudata, 56
  cotf12, 65
  cotf2, 66

*Topic F1
  cotf12, 65

*Topic F2
  cotf12, 65

*Topic MINQUE
  ad.mq, 4
  ad.mq.jack, 6
  ad.simu, 10
  ad.simu.jack, 12
  ad4.mq, 14
  ad4.mq.jack, 16
  adaa.mq, 21
  adaa.simu, 27
  adaa.simu.jack, 28
  adc.mq, 31
  adc.simu, 37
  adc.simu.jack, 38
  adc4.mq, 41
  adc4.mq.jack, 42
  ad.mq, 47
  ad.simu, 53
  ad.simu.jack, 54
  adrc.mq, 57
  adrc.mq.jack, 58
  cotf12, 65
  cotf2, 66

*Topic REML
  ad.reml, 7
  ad.reml.jack, 9
  ad.simu, 10
ad.simu.jack, 12
ad4.reml, 17
ad4.reml.jack, 19
adaa.reml, 24
adaa.reml.jack, 25
adaa.simu, 27
adaa.simu.jack, 28
adc.reml, 34
adc.reml.jack, 35
adc.simu, 37
adc.simu.jack, 38
adc4.reml, 44
adc4.reml.jack, 46
adm.reml, 50
adm.reml.jack, 52
adm.simu, 53
adm.simu.jack, 54
adrc.reml, 60
adrc.reml.jack, 62
adrcdat, 63
*Topic \textbf{ad model}
adrc.mq, 57
adrc.mq.jack, 58
adrc.reml, 60
adrc.reml.jack, 62
adrcdat, 63
*Topic \textbf{boll number}
cotf2, 66
*Topic \textbf{bootstrapping}
stab.mean, 69
*Topic \textbf{column effect}
adrc.mq, 57
adrc.mq.jack, 58
adrc.reml, 60
adrc.reml.jack, 62
adrcdat, 63
*Topic \textbf{cotf12}
ad.mq.jack, 6
adaa.mq, 21
adaa.mq.jack, 22
adaa.reml.jack, 25
adc.mq.jack, 32
adm.mq.jack, 49
adm.reml.jack, 52
*Topic \textbf{cotf2}
ad.mq, 4
ad.reml, 7
ad.reml.jack, 9
ad.simudata, 13
adaa.reml, 24
adaa.simudata, 30
adc.mq, 31
adc.reml, 34
adc.reml.jack, 35
adc.simudata, 40
adm.mq, 47
adm.reml, 50
adm.simudata, 56
*Topic \textbf{cotton}
ad.mq, 4
ad.reml, 7
ad.reml.jack, 9
ad.simu, 10
ad.simu.jack, 12
ad.simudata, 13
adaa.mq, 21
adaa.reml, 24
adaa.simu, 27
adaa.simu.jack, 28
adaa.simudata, 30
adc.mq, 31
adc.reml, 34
adc.reml.jack, 35
adc.simu, 37
adc.simu.jack, 38
adc.simudata, 40
adm.mq, 47
adm.reml, 50
adm.simu, 53
adm.simu.jack, 54
adm.simudata, 56
cotf12, 65
*Topic \textbf{datasets}
adrcdat, 63
cotf12, 65
cotf2, 66
maize, 67
wheat, 72
*Topic \textbf{fw stability analysis}
stab.fw, 68
*Topic \textbf{genetic models}
cotf2, 66
*Topic \textbf{jackknife}
ad.mq.jack, 6
adaa.mq.jack, 22
adaa.reml.jack, 25
adc.mq.jack, 32
adm.mq.jack, 49
adm.reml.jack, 52
*Topic jackknife
ad.reml.jack, 9
ad.simu.jack, 12
ad4.mq.jack, 16
ad4.reml.jack, 19
adaa.simu.jack, 28
adc.reml.jack, 35
adc.simu.jack, 38
adc4.mq.jack, 42
adc4.reml.jack, 46
ad.reml.jack, 52
adm.reml.jack, 52
*Topic regression
stab.fw, 68
*Topic resampling
stab.fw, 68
stab.mean, 69
*Topic row effect
adrc.mq, 57
adrc.mq.jack, 58
adrc.reml, 60
adrc.reml.jack, 62
adrc.dat, 63
*Topic simulated data
ad.simudata, 13
adaa.simudata, 30
adc.simudata, 40
adm.simudata, 56
*Topic stab.fw
maize, 67
*Topic stab.mean
maize, 67
stab.mean, 69
*Topic stab.var
maize, 67
stab.var, 70
*Topic stability analysis
maize, 67
stab.var, 70
*Topic stability
stab.fw, 68
stab.mean, 69
*Topic variation
stab.var, 70
*Topic wheat
ad4.mq, 14
ad4.mq.jack, 16
ad4.reml, 17
ad4.reml.jack, 19
adc4.mq, 41
adc4.mq.jack, 42
adc4.reml, 44
adc4.reml.jack, 46
adm.mq, 4
ad.mq.jack, 6
ad.reml, 7
ad.reml.jack, 9
ad.simu, 10
ad.simu.jack, 12
ad.simudata, 13
*Topic lint percentage
cotf2, 66
*Topic lint size
cotf2, 66
*Topic lint yield
cotf2, 66
*Topic maize
maize, 67
stab.fw, 68
stab.mean, 69
stab.var, 70
*Topic mean
stab.mean, 69
*Topic minque
adaa.mq.jack, 22
adc.mq.jack, 32
adm.mq.jack, 49
*Topic multi-parent mating design
ad4.mq, 14
ad4.mq.jack, 16
ad4.reml, 17
ad4.reml.jack, 19
adc4.mq, 41
adc4.mq.jack, 42
adc4.reml, 44
adc4.reml.jack, 46
*Topic permutation
stab.mean, 69
*Topic rank
stab.mean, 69
ad4.mq, 14
ad4.mq.jack, 16
ad4.reml, 17
ad4.reml.jack, 19
adaa.mq, 21
adaa.mq.jack, 22
adaa.reml, 24
adaa.reml.jack, 25
adaa.simu, 27
adaa.simu.jack, 28
adaa.simudata, 30
adc.mq, 31
adc.mq.jack, 32
adc.reml, 34
adc.reml.jack, 35
adc.simu, 37
adc.simu.jack, 38
adc.simudata, 40
adc4.mq, 41
adc4.mq.jack, 42
adc4.reml, 44
adc4.reml.jack, 46
adm.mq, 47
adm.mq.jack, 49
adm.reml, 50
adm.reml.jack, 52
adm.simu, 53
adm.simu.jack, 54
adm.simudata, 56
adrcc.mq, 57
adrcc.mq.jack, 58
adrcc.reml, 60
adrcc.reml.jack, 62
adrcc.dat, 63
cotf12, 65
cotf2, 66

maize, 67

qgtools (qgtools-package), 3
qgtools-package, 3

stab.fw, 68
stab.mean, 69
stab.var, 70

wheat, 72