

Package ‘BMTME’

October 18, 2019

Title Bayesian Multi-Trait Multi-Environment for Genomic Selection Analysis

Version 1.0.12

Date 2019-9-30

Language en-US

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Description Genomic selection and prediction models with the capacity to use multiple traits and environments, through ready-to-use Bayesian models. It consists a group of functions that help to create regression models for some genomic models proposed by Montesinos-López, et al. (2016) <doi:10.1534/g3.116.032359> also in Montesinos-López et al. (2018) <doi:10.1534/g3.118.200728> and Montesinos-López et al. (2018) <doi:10.2134/agronj2018.06.0362>.

Depends R (>= 3.5)

License LGPL-3

Encoding UTF-8

LazyData true

Type Package

RoxygenNote 6.1.1

URL <https://github.com/frahik/BMTME>

BugReports <https://github.com/frahik/BMTME/issues/new>

NeedsCompilation yes

Collate BME.R BMTME.R BMTME_Package.R BMORS.R BMORSEnv.R cholesky.R datasets.R detectCore.R RandomPartition.R RcppExports.R utils.R

Imports BGLR, doSNOW, dplyr, foreach, matrixcalc, mvtnorm, progress, snow, tidyr

LinkingTo Rcpp, RcppArmadillo

SystemRequirements C++11, GNU

Suggests covr, testthat,

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Repository CRAN

Date/Publication 2019-10-17 22:30:16 UTC

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barplot.BMORSENV *barplot BMORSENV graph*

Description

Creates a bar plot with vertical bars, showing the predictive capability of the model or the error rate.

Usage

```
## S3 method for class 'BMORSENV'
barplot(height, select = "Pearson", ...)
```

Arguments

- height an BMORSENV object for which the plot of model is meaningful.
- select character By default ('Pearson'), plot the Pearson Correlations of the BMORSENV Object, else ('MAAPE'), plot the MAAPE of the BMORSENV Object.
- ... Further arguments passed to or from other methods.

BME *Bayesian Multi-Environment Model (BME)*

Description

Bayesian Multi-Environment Model (BME)

Usage

```
BME(Y, Z1, nIter = 1000L, burnIn = 300L, thin = 2L,
     bs = ceiling(dim(Z1)[2]/6), parallelCores = 1, digits = 4,
     progressBar = TRUE, testingSet = NULL)
```

Arguments

Y	(matrix) Phenotypic response where each column is a different environment.
Z1	(matrix) Matrix design for the genetic effects.
nIter	(integer) Number of iterations to fit the model.
burnIn	(integer) Number of items to burn at the beginning of the model.
thin	(integer) Number of items to thin the model.
bs	(integer) Number of groups.
parallelCores	(integer) Number of cores to use.
digits	(integer) Number of digits of accuracy in the results.
progressBar	(Logical) Show the progress bar.
testingSet	(object or vector) Crossvalidation object or vector with the positions to use like testing in a cross-validation test.

Value

If the testingSet is NULL, the function returns the predictions.

Else, if the testingSet is not NULL, the function returns the correlation of the predictions of the cross-validation test.

References

Montesinos-Lopez, O.A., Montesinos-Lopez, A., Crossa, J., Toledo, F.H., Perez-Hernandez, O., Eskridge, K.M., ... Rutkoski, J. (2016). A Genomic Bayesian Multi-trait and Multi-environment Model. *G3: Genes|Genomes|Genetics*, 6(9), 2725–2744. <https://doi.org/10.1534/g3.116.032359>.

Examples

```
data("WheatMadaToy")
phenoMada <- (phenoMada[order(phenoMada$GID),])

#Matrix design
LG <- cholesky(genoMada)
ZG <- model.matrix(~0 + as.factor(phenoMada$GID))
Z.G <- ZG %*% LG

#Pheno data
Y <- as.matrix(phenoMada[, -c(1)])
# Check fitting
fm <- BME(Y = Y, Z1 = Z.G, nIter = 10000, burnIn = 5000, thin = 2, bs = 50)

# Check predictive capacities of the model with CrossValidation object
pheno <- data.frame(GID = phenoMada[, 1], Env = '', Response = phenoMada[, 3])
CrossV <- CV.RandomPart(pheno, NPartitions = 4, PTesting = 0.2, set_seed = 123)

pm <- BME(Y = Y, Z1 = Z.G, nIter = 10000, burnIn = 5000, thin = 2, bs = 50, testingSet = CrossV)
```

 BMORS

Bayesian Multi-Output Regression Stacking (BMORS)

Description

Bayesian Multi-Output Regression Stacking (BMORS)

Usage

```
BMORS(Y = NULL, ETA = NULL, covModel = "BRR",
      predictor_Sec_complete = FALSE, nIter = 2500, burnIn = 500,
      thin = 5, progressBar = TRUE, testingSet = NULL,
      parallelCores = 1, digits = 4)
```

Arguments

Y	(matrix) Phenotypic response where each column is a different trait
ETA	(matrix) This is a two-level list used to specify the regression function (or linear predictor).
covModel	(string) Name of the covariates model to implement (BRR, BayesA, BayesB, BayesC).
predictor_Sec_complete	FALSE by default
nIter	(integer) Number of iterations to fit the model.
burnIn	(integer) Number of items to burn at the beginning of the model.
thin	(integer) Number of items to thin the model.
progressBar	(Logical) Show the progress bar.
testingSet	(object or vector) Crossvalidation object or vector with the positions to use like testing in a cross-validation test.
parallelCores	(integer) Number of cores to use.
digits	(integer) Number of digits of accuracy in the results.

Examples

```
data("WheatToy")
phenoWheatToy <- phenoWheatToy[order(phenoWheatToy$Env, phenoWheatToy$Gid),]

#Matrix Design
LG <- cholesky(genoWheatToy)
ZG <- model.matrix(~0 + as.factor(phenoWheatToy$Gid))
Z.G <- ZG %*% LG
```

```

#Linear Predictor
ETA <- list(Gen = list(X = Z.G, model = 'BRR'))

pheno <- phenoWheatToy[, c(1:3)] #Use only the first trait to do a cv
colnames(pheno) <- c('Line', 'Env', 'Response')
CrossValidation <- CV.RandomPart(pheno, NPartitions = 10, PTesting = 0.2, set_seed = 123)

#Pheno
Y <- as.matrix(phenoWheatToy[, c(3,4)])
#Check predictive capacities of the model
pm <- BMORS(Y, ETA = ETA, nIter = 10000, burnIn = 5000, thin = 2,
            testingSet = CrossValidation, digits = 4)

```

 BMORS_Env

Bayesian Multi-Output regression stacking for specific environment estimations

Description

Bayesian Multi-Output regression stacking for specific environment estimations

Usage

```

BMORS_Env(data = NULL, testingEnv = "", ETA = NULL,
          covModel = "BRR", predictor_Sec_complete = FALSE, nIter = 2500,
          burnIn = 500, thin = 5, progressBar = TRUE, digits = 4)

```

Arguments

data	(data.frame) Phenotypic response where each column is a different trait and the first column are the name of the environment where it was evaluated.
testingEnv	(string) Name of the Environment to test.
ETA	(matrix) This is a two-level list used to specify the regression function (or linear predictor).
covModel	(string) Name of the covariates model to implement (BRR, BayesA, BayesB, BayesC).
predictor_Sec_complete	(Logical) FALSE by default.
nIter	(integer) Number of iterations to fit the model.
burnIn	(integer) Number of items to burn at the beginning of the model.
thin	(integer) Number of items to thin the model.
progressBar	(Logical) Show the progress bar.
digits	(integer) Number of digits of accuracy in the results.

Examples

```

data('MaizeToy')
phenoMaizeToy <- phenoMaizeToy[order(phenoMaizeToy$Env, phenoMaizeToy$Line),]

#Matrix design
LG <- cholesky(genoMaizeToy)
ZG <- model.matrix(~0 + as.factor(phenoMaizeToy$Line))
Z.G <- ZG %**% LG
#Linear Predictor
ETA <- list(Gen = list(X = Z.G, model = 'BRR'))

dataset <- phenoMaizeToy[, 2:5] #Must Include in the first column the environments
#Check predictive capacities of the model
pm <- BMORS_Env(dataset, testingEnv = 'EBU', ETA = ETA, covModel = 'BRR', nIter = 10000,
                burnIn = 5000, thin = 2, progressBar = FALSE, digits = 3)

```

BMTME

Bayes Multi-Trait Multi-Environment Model (BMTME)

Description

The Bayesian Multi-Trait Multi-Environment models (BMTME) package was developed to implement...

Usage

```

BMTME(Y, X, Z1, Z2, nIter = 1000L, burnIn = 300L, thin = 2L,
      bs = ceiling(dim(Z1)[2]/6), parallelCores = 1, digits = 4,
      progressBar = TRUE, testingSet = NULL)

```

Arguments

Y	(matrix) Phenotypic response where each column is a different trait.
X	(matrix) Matrix design for the environment effects.
Z1	(matrix) Matrix design for the genetic effects.
Z2	(matrix) Matrix design for the genetic effects interaction with the environment effects.
nIter	(integer) Number of iterations to fit the model.
burnIn	(integer) Number of items to burn at the beginning of the model.
thin	(integer) Number of items to thin the model.
bs	(integer) Number of groups.
parallelCores	(integer) Number of cores to use.

digits (integer) Number of digits of accuracy in the results.

progressBar (Logical) Show the progress bar.

testingSet (object or vector) Crossvalidation object or vector with the positions to use like testing in a cross-validation test.

References

Montesinos-Lopez, O.A., Montesinos-Lopez, A., Crossa, J., Toledo, F.H., Perez-Hernandez, O., Eskridge, K.M., ... Rutkoski, J. (2016). A Genomic Bayesian Multi-trait and Multi-environment Model. *G3: Genes|Genomes|Genetics*, 6(9), 2725–2744. <https://doi.org/10.1534/g3.116.032359>.

Examples

```
data("WheatIranianToy")

# Matrix Design
LG <- cholesky(genoIranianToy)
ZG <- model.matrix(~0 + as.factor(phenoIranianToy$GID))
Z.G <- ZG %%% LG
Z.E <- model.matrix(~0 + as.factor(phenoIranianToy$Env))
ZEG <- model.matrix(~0 + as.factor(phenoIranianToy$GID):as.factor(phenoIranianToy$Env))
G2 <- kronecker(diag(length(unique(phenoIranianToy$Env))), data.matrix(genoIranianToy))
LG2 <- cholesky(G2)
Z.EG <- ZEG %%% LG2

#Pheno
Y <- as.matrix(phenoIranianToy[, -c(1, 2)])

#Check fitting
fm <- BMTME(Y = Y, X = Z.E, Z1 = Z.G, Z2 = Z.EG,
           nIter = 10000, burnIn = 5000, thin = 2, bs = 50)
fm

# Check predictive capacities of the model
pheno <- data.frame(GID = phenoIranianToy[, 1],
                  Env = phenoIranianToy[, 2],
                  Response = phenoIranianToy[, 3])
CrossV <- CV.RandomPart(pheno, NPartitions = 4, PTesting = 0.2, set_seed = 123)

pm <- BMTME(Y = Y, X = Z.E, Z1 = Z.G, Z2 = Z.EG,
           nIter = 10000, burnIn = 5000, thin = 2,
           bs = 50, testingSet = CrossV)
pm
```

boxplot.BMECV	<i>boxplot.BMECV</i>
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Description

Produce box-and-whisker plot(s) of the given BMECV object.

Usage

```
## S3 method for class 'BMECV'
boxplot(x, select = "Pearson", ordered = TRUE, ...)
```

Arguments

x	an BMECV object for which the plot of model is meaningful.
select	character By default ('Pearson'), plot the Pearson Correlations of the BMECV Object, else ('MAAPE'), plot the MAAPE of the BMECV Object.
ordered	logic The graph should be sorted by the median? by default is TRUE.
...	Further arguments passed to or from other methods.

boxplot.BMORSCV	<i>boxplot.BMORSCV</i>
-----------------	------------------------

Description

Produce box-and-whisker plot(s) of the given BMORSCV object.

Usage

```
## S3 method for class 'BMORSCV'
boxplot(x, select = "Pearson", ordered = TRUE, ...)
```

Arguments

x	an BMORSCV object for which the plot of model is meaningful.
select	character By default ('Pearson'), plot the Pearson Correlations of the BMORSCV Object, else ('MAAPE'), plot the MAAPE of the BMORSCV Object.
ordered	logic The graph should be sorted by the median? by default is TRUE.
...	Further arguments passed to or from other methods.

<code>boxplot.BMTMECV</code>	<i>boxplot.BMTMECV</i>
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Description

Produce box-and-whisker plot(s) of the given BMTMECV object.

Usage

```
## S3 method for class 'BMTMECV'
boxplot(x, select = "Pearson", ordered = TRUE, ...)
```

Arguments

<code>x</code>	an BMTMECV object for which the plot of model is meaningful.
<code>select</code>	character By default ('Pearson'), plot the Pearson Correlations of the BMTMECV Object, else ('MAAPE'), plot the MAAPE of the BMTMECV Object.
<code>ordered</code>	logic The graph should be sorted by the median? by default is TRUE.
<code>...</code>	Further arguments passed to or from other methods.

<code>cholesky</code>	<i>Cholesky</i>
-----------------------	-----------------

Description

Compute the Cholesky factorization of a non-real symmetric positive-definite square matrix.

Usage

```
cholesky(G, tolerance = 1e-10)
```

Arguments

<code>G</code>	(numeric - matrix) an object to apply this method, it could be non positive-definite matrices.
<code>tolerance</code>	(double) Tolerance level, by default is 1e-10.

CV.KFold	<i>Cross-Validation with K Folds</i>
----------	--------------------------------------

Description

This method consists of randomly dividing the training data set and the test data set.

Usage

```
CV.KFold(DataSet, DataSetID = "Line", K = 5, set_seed = NULL)
```

Arguments

DataSet	(data.frame) The object need contain three columns in the Tidy data format: \$Line is the Line or genotype identifier, and the name of this column could change. \$Env is the name of the evaluated environment (s). \$Response Variable response obtained for the row corresponding to line and environment.
DataSetID	(string) The ID of the lines.
K	(integer) Number of groups to the cross-validation.
set_seed	(integer) Seed number for reproducible research. Is NULL by default

Value

Returns a nested list, with a positions to use as testing.

Examples

```
data("WheatMadaToy")
phenoMada <- (phenoMada[order(phenoMada$GID),])
pheno <- data.frame(GID = phenoMada[, 1], Response = phenoMada[, 3])

CV.KFold(pheno)
CV.KFold(pheno, set_seed = 123)
CV.KFold(pheno, DataSetID = 'GID', set_seed = 123)
CV.KFold(pheno, DataSetID = 'GID', K = 10, set_seed = 123)
```

Description

This method consists of randomly dividing the training data set and the test data set. For each division, the approximation function is adjusted from the training data and calculates the output values for the test data set. The result corresponds to the arithmetic mean of the values obtained for the different divisions.

Usage

```
CV.RandomPart(DataSet, NPartitions = 10, PTesting = 0.35,
  Traits.testing = NULL, set_seed = NULL)
```

Arguments

DataSet	data.frame	The data set object is a data.frame object that contains 4 columns in the Tidy data format: \$Line is the Line or genotype identifier, and the name of this column could change. \$Env is the name of the evaluated environment (s). \$Trait is the name of the evaluated trait (s). \$Response Variable response obtained for the row corresponding to line, trait and environment.
NPartitions	integer	Number of Partitions for the Cross-Validation. Is 10 by default.
PTesting	Double	Percentage of Testing for the Cross-Validation. Is 0.35 by default.
Traits.testing	character	By default is null and use all the traits to fit the model, else only part of the traits specified be used to fit the model.
set_seed	integer	Seed number for reproducible research. Is NULL by default.

Value

List A list object with length of NPartitions, every index has a the positions to use like testing.

Examples

```
library(BMTME)
data("WheatIranianToy")
phenoIranianToy <- phenoIranianToy[order(phenoIranianToy$Env, phenoIranianToy$GID), ]
pheno <- data.frame(GID = phenoIranianToy[, 1], Env = phenoIranianToy$Env,
  Trait = rep(colnames(phenoIranianToy)[3:4], each = dim(phenoIranianToy)[1]),
  Response = c(phenoIranianToy[, 3], phenoIranianToy[, 4]))

CV.RandomPart(pheno)
CV.RandomPart(pheno, NPartitions = 10)
CV.RandomPart(pheno, Traits.testing = 'DTM')
CV.RandomPart(pheno, NPartitions = 10, PTesting = .35)
CV.RandomPart(pheno, NPartitions = 10, Traits.testing = 'DTH')
```

```
CV.RandomPart(pheno, NPartitions = 10, PTesting = .35, set_seed = 5)
CV.RandomPart(pheno, NPartitions = 10, PTesting = .35, Traits.testing = 'DTH')
CV.RandomPart(pheno, NPartitions = 10, PTesting = .35, Traits.testing = 'DTM', set_seed = 5)
```

genoIranianToy

Genomic values of Iranian toy dataset.

Description

A data set based on a portion of the data used in the study of (Crossa et al., 2016).

Usage

genoIranianToy

Format

30 x 30 matrix

Source

International Maize and Wheat Improvement Center (CIMMYT), Mexico.

References

Crossa, J., Jarquín, D., Franco, J., Pérez-Rodríguez, P., Burgueño, J., Saint-Pierre, C., Singh, S. (2016). Genomic Prediction of Gene Bank Wheat Landraces. *G3: Genes|Genomes|Genetics*, 6(7), 1819–1834. <https://doi.org/10.1534/g3.116.029637>

genoJapa30

Genomic values of Japa dataset.

Description

A data set based on a portion of the data used in the study of (Ben Hassen et al., 2018).

Usage

genoJapa30

Format

30 x 30 matrix

References

Ben Hassen, M., Bartholomé, J., Valè, G., Cao, T.-V., & Ahmadi, N. (2018). Genomic Prediction Accounting for Genotype by Environment Interaction Offers an Effective Framework for Breeding Simultaneously for Adaptation to an Abiotic Stress and Performance Under Normal Cropping Conditions in Rice. *G3: Genes|Genomes|Genetics*, 8(July), 2319–2332. <https://doi.org/10.1534/g3.118.200098>

genoJapa50

Genomic values of Japa dataset.

Description

A data set based on a portion of the data used in the study of (Ben Hassen et al., 2018).

Usage

genoJapa50

Format

50 x 50 matrix

References

Ben Hassen, M., Bartholomé, J., Valè, G., Cao, T.-V., & Ahmadi, N. (2018). Genomic Prediction Accounting for Genotype by Environment Interaction Offers an Effective Framework for Breeding Simultaneously for Adaptation to an Abiotic Stress and Performance Under Normal Cropping Conditions in Rice. *G3: Genes|Genomes|Genetics*, 8(July), 2319–2332. <https://doi.org/10.1534/g3.118.200098>

genoMada

Genomic values of Mada dataset.

Description

A data set based on a portion of the data used in the study of (Ben Hassen et al., 2018).

Usage

genoMada

Format

50 x 50 matrix

References

Ben Hassen, M., Bartholomé, J., Valè, G., Cao, T.-V., & Ahmadi, N. (2018). Genomic Prediction Accounting for Genotype by Environment Interaction Offers an Effective Framework for Breeding Simultaneously for Adaptation to an Abiotic Stress and Performance Under Normal Cropping Conditions in Rice. *G3: Genes|Genomes|Genetics*, 8(July), 2319–2332. <https://doi.org/10.1534/g3.118.200098>

genoMaizeToy *Genomic values of Maize dataset.*

Description

A data set based on a portion of the data used in the study of (Montesinos-López et al., 2017).

Usage

genoMaizeToy

Format

30 x 30 matrix

References

Montesinos-López, O. A., Montesinos-López, A., Crossa, J., Montesinos-López, J. C., Luna-Vázquez, F. J., Salinas, J., ... Buenrostro-Mariscal, R. (2017). A Variational Bayes Genomic-Enabled Prediction Model with Genotype × Environment Interaction. *G3: Genes|Genomes|Genetics*, 7(8), g3.117.041202. <https://doi.org/10.1534/g3.117.041202>

genoWheatToy *Genomic values of Wheat toy dataset.*

Description

A data set based on a portion of the data used in the study from a collection of 599 historical CIMMYT wheat lines. The wheat data set is from CIMMYT's Global Wheat Program.

Usage

genoWheatToy

Format

30 x 30 data.frame

Source

International Maize and Wheat Improvement Center (CIMMYT), Mexico.

MaizeToy

Maize Data

Description

This data set is based on the data set used in the study of (Montesinos-López et al., 2017). The original dataset is composed of a sample of 309 maize lines evaluated for three traits: anthesis-silking interval (ASI), plant height (PH), grain yield (GY), each of them was evaluated in three optimal environments (Env1, Env2 and Env3). The total numbers of GBS data were 681,257 SNPs, and, after filtering for missing values and minor allele frequency, were used 158,281 SNPs for the analyses. To load this dataset in the package we only use 30 lines, and we have identified this data set as MaizeToy. For more details, see the study of (Montesinos-López et al., 2017).

Usage

```
data(MaizeToy)
```

Format

2 objects are loaded (phenoMaizeToy and genoMaizeToy)

References

Montesinos-López, O. A., Montesinos-López, A., Crossa, J., Montesinos-López, J. C., Luna-Vázquez, F. J., Salinas, J., ... Buenrostro-Mariscal, R. (2017). A Variational Bayes Genomic-Enabled Prediction Model with Genotype \times Environment Interaction. *G3: Genes|Genomes|Genetics*, 7(8), g3.117.041202. <https://doi.org/10.1534/g3.117.041202>

phenoIranianToy*Phenotypic values of Iranian toy dataset.*

Description

A data set based on a portion of the data used in the study of (Crossa et al., 2016).

Usage

```
phenoIranianToy
```

Format

data.frame, 60 row per 4 columns.

Source

International Maize and Wheat Improvement Center (CIMMYT), Mexico.

References

Crossa, J., Jarquín, D., Franco, J., Pérez-Rodríguez, P., Burgueño, J., Saint-Pierre, C., Singh, S. (2016). Genomic Prediction of Gene Bank Wheat Landraces. *G3: Genes|Genomes|Genetics*, 6(7), 1819–1834. <https://doi.org/10.1534/g3.116.029637>

phenoJapa30 *Phenotypic values of Japa dataset.*

Description

A data set based on a portion of the data used in the study of (Ben Hassen et al., 2018).

Usage

phenoJapa30

Format

data.frame, 30 row per 7 columns.

References

Ben Hassen, M., Bartholomé, J., Valè, G., Cao, T.-V., & Ahmadi, N. (2018). Genomic Prediction Accounting for Genotype by Environment Interaction Offers an Effective Framework for Breeding Simultaneously for Adaptation to an Abiotic Stress and Performance Under Normal Cropping Conditions in Rice. *G3: Genes|Genomes|Genetics*, 8(July), 2319–2332. <https://doi.org/10.1534/g3.118.200098>

phenoJapa50 *Phenotypic values of Japa dataset.*

Description

A data set based on a portion of the data used in the study of (Ben Hassen et al., 2018).

Usage

phenoJapa50

Format

data.frame, 50 row per 4 columns.

References

Ben Hassen, M., Bartholomé, J., Valè, G., Cao, T.-V., & Ahmadi, N. (2018). Genomic Prediction Accounting for Genotype by Environment Interaction Offers an Effective Framework for Breeding Simultaneously for Adaptation to an Abiotic Stress and Performance Under Normal Cropping Conditions in Rice. *G3: Genes|Genomes|Genetics*, 8(July), 2319–2332. <https://doi.org/10.1534/g3.118.200098>

phenoMada

Phenotypic values of Mada dataset.

Description

A data set based on a portion of the data used in the study of (Ben Hassen et al., 2018).

Usage

phenoMada

Format

data.frame, 50 row per 7 columns.

References

Ben Hassen, M., Bartholomé, J., Valè, G., Cao, T.-V., & Ahmadi, N. (2018). Genomic Prediction Accounting for Genotype by Environment Interaction Offers an Effective Framework for Breeding Simultaneously for Adaptation to an Abiotic Stress and Performance Under Normal Cropping Conditions in Rice. *G3: Genes|Genomes|Genetics*, 8(July), 2319–2332. <https://doi.org/10.1534/g3.118.200098>

phenoMaizeToy

Phenotypic values of Maize dataset.

Description

A data set based on a portion of the data used in the study of (Montesinos-López et al., 2017).

Usage

phenoMaizeToy

Format

data.frame, 90 row per 5 columns.

References

Montesinos-López, O. A., Montesinos-López, A., Crossa, J., Montesinos-López, J. C., Luna-Vázquez, F. J., Salinas, J., . . . Buenrostro-Mariscal, R. (2017). A Variational Bayes Genomic-Enabled Prediction Model with Genotype × Environment Interaction. *G3: Genes|Genomes|Genetics*, 7(8), g3.117.041202. <https://doi.org/10.1534/g3.117.041202>

phenoWheatToy	<i>Phenotypic values of Wheat toy dataset.</i>
---------------	--

Description

A data set based on a portion of the data used in the study from a collection of 599 historical CIMMYT wheat lines. The wheat data set is from CIMMYT's Global Wheat Program.

Usage

```
phenoWheatToy
```

Format

data.frame, 90 row per 4 columns.

Source

International Maize and Wheat Improvement Center (CIMMYT), Mexico.

plot.BME	<i>plot.BME</i>
----------	-----------------

Description

Simple scatter plot comparing the observed values against the predicted values.

Usage

```
## S3 method for class 'BME'
plot(x, trait = "", ...)
```

Arguments

x	an BME object for which the plot of model is meaningful.
trait	string Name of the trait to plot.
...	Further arguments passed to or from other methods.

plot.BMORSCV	<i>Plot BMORSCV Simple scatter plot comparing the observed values against the predicted values.</i>
--------------	---

Description

Plot BMORSCV Simple scatter plot comparing the observed values against the predicted values.

Usage

```
## S3 method for class 'BMORSCV'
plot(x, select = "Pearson", ...)
```

Arguments

x	an BMORS object for which the plot of model is meaningful.
select	character By default ('Pearson'), plot the Pearson Correlations of the BMORSCV Object, else ('MAAPE'), plot the MAAPE of the BMORSCV Object.
...	Further arguments passed to or from other methods.

plot.BMTME	<i>plot.BMTME Simple scatter plot comparing the observed values against the predicted values.</i>
------------	---

Description

plot.BMTME
Simple scatter plot comparing the observed values against the predicted values.

Usage

```
## S3 method for class 'BMTME'
plot(x, trait = "", ...)
```

Arguments

x	an BMTME object for which the plot of model is meaningful.
trait	string Name of the trait to plot.
...	Further arguments passed to or from other methods.

print.BME	<i>Print BME information object</i>
-----------	-------------------------------------

Description

Print BME information object

Usage

```
## S3 method for class 'BME'  
print(x, ...)
```

Arguments

x	an BME object used to print.
...	Further arguments passed to or from other methods.

print.BMECV	<i>Print BMECV information object</i>
-------------	---------------------------------------

Description

Print BMECV information object

Usage

```
## S3 method for class 'BMECV'  
print(x, ...)
```

Arguments

x	an BMECV object used to print.
...	Further arguments passed to or from other methods.

print.BMORS	<i>Print BMORS information object</i>
-------------	---------------------------------------

Description

Print BMORS information object

Usage

```
## S3 method for class 'BMORS'  
print(x, ...)
```

Arguments

x	an BMORS object used to print.
...	Further arguments passed to or from other methods.

print.BMORSCV	<i>Print BMORSCV information object</i>
---------------	---

Description

Print BMORSCV information object

Usage

```
## S3 method for class 'BMORSCV'  
print(x, ...)
```

Arguments

x	an BMORSCV object used to print.
...	Further arguments passed to or from other methods.

print.BMORSENV *Print BMORSENV information object*

Description

Print BMORSENV information object

Usage

```
## S3 method for class 'BMORSENV'  
print(x, ...)
```

Arguments

x an BMORSENV object used to print.
... Further arguments passed to or from other methods.

Value

test

print.BMTME *Print BMTME information object*

Description

Print BMTME information object

Usage

```
## S3 method for class 'BMTME'  
print(x, ...)
```

Arguments

x an BMTME object used to print.
... Further arguments passed to or from other methods.

print.BMTMECV	<i>Print BMTMECV information object</i>
---------------	---

Description

Print BMTMECV information object

Usage

```
## S3 method for class 'BMTMECV'
print(x, ...)
```

Arguments

x	an BMTMECV object used to print.
...	Further arguments passed to or from other methods.

residuals.BME	<i>residuals.BME</i>
---------------	----------------------

Description

extracts model residuals from BME objects returned by modeling function BME.

Usage

```
## S3 method for class 'BME'
residuals(object, digits = 4, ...)
```

Arguments

object	an BME object for which the extraction of model residuals is meaningful.
digits	number of digits.
...	Further arguments passed to or from other methods.

residuals.BMTME	<i>residuals.BMTME</i>
-----------------	------------------------

Description

extracts model residuals from BMTME objects returned by modeling function BMTME.

Usage

```
## S3 method for class 'BMTME'
residuals(object, digits = 4, ...)
```

Arguments

object	an BMTME object for which the extraction of model residuals is meaningful.
digits	number of digits.
...	Further arguments passed to or from other methods.

summary.BMECV	<i>summary.BMECV</i>
---------------	----------------------

Description

Produces a summary of the results of the fitted model adding the predictive capabilities of the model, as well as the MAAPE error rate and the respective standard errors.

Usage

```
## S3 method for class 'BMECV'
summary(object, information = "compact", digits = 4,
...)
```

Arguments

object	BMECV object an BMECV object for which a summary is desired.
information	The type of summary to obtain from the model (compact, extended, complete), by default is compact.
digits	number of digits.
...	Further arguments passed to or from other methods.

summary.BMORSCV	<i>summary.BMORSCV</i>
-----------------	------------------------

Description

Produces a summary of the results of the fitted model adding the predictive capabilities of the model, as well as the MAAPE error rate and the respective standard errors.

Usage

```
## S3 method for class 'BMORSCV'
summary(object, information = "compact", digits = 4,
        ...)
```

Arguments

object	BMORSCV object an BMORSCV object for which a summary is desired.
information	The type of summary to obtain from the model (compact, extended, complete), by default is compact.
digits	number of digits.
...	Further arguments passed to or from other methods.

summary.BMORSENV	<i>summary.BMORSENV</i>
------------------	-------------------------

Description

Produces a summary of the results of the fitted model adding the predictive capabilities of the model, as well as the MAAPE error rate and the respective standard errors.

Usage

```
## S3 method for class 'BMORSENV'
summary(object, digits = 4, ...)
```

Arguments

object	BMORSENV object an BMORSENV object for which a summary is desired.
digits	number of digits.
...	Further arguments passed to or from other methods.

summary.BMTMECV	<i>summary.BMTMECV</i>
-----------------	------------------------

Description

Produces a summary of the results of the fitted model adding the predictive capabilities of the model, as well as the MAAPE error rate and the respective standard errors.

Usage

```
## S3 method for class 'BMTMECV'
summary(object, information = "compact", digits = 4,
        ...)
```

Arguments

object	BMTMECV object an BMTMECV object for which a summary is desired.
information	The type of summary to obtain from the model (compact, extended, complete), by default is compact.
digits	number of digits.
...	Further arguments passed to or from other methods.

WheatIranianToy	<i>Wheat Iranian Toy Data</i>
-----------------	-------------------------------

Description

This data set is based on the data set used in the study of (Crossa et al., 2016). The original dataset was composed of 2374 wheat lines that were evaluated in field (D) and heat (H) drought experiments at the CIMMYT experimental station near Obregón City, Sonora, Mexico (27°20' N, 109°54' W, 38 meters above sea level), during the Obregón 2010-2011 cycle. Two traits were evaluated (DTM days at maturity and DTH days to heading). From a total of 40,000 markers, after quality control 39,758 markers were used. To load this dataset in the package we only use 30 lines, and we have identified this data set as WheatIranianToy. For more details, see the study of (Crossa et al., 2016).

Usage

```
data(WheatIranianToy)
```

Format

2 objects are loaded (phenoIranianToy and genoIranianToy)

References

Crossa, J., Jarquín, D., Franco, J., Pérez-Rodríguez, P., Burgueño, J., Saint-Pierre, C., Singh, S. (2016). Genomic Prediction of Gene Bank Wheat Landraces. *G3: Genes|Genomes|Genetics*, 6(7), 1819–1834. <https://doi.org/10.1534/g3.116.029637>

WheatJapa30

Wheat Japa 30 Data

Description

This data set is also based on the data used in the study of (Ben Hassen et al., 2018). The original dataset was composed of a sample of 167 lines evaluated for six traits each of them was evaluated in one environment. The total numbers of genome by sequencing (GBS) data were 32,066 SNPs and they were obtained with a heterozygosity rate <5

Usage

```
data(WheatJapa30)
```

Format

2 objects are loaded (phenoJapa30 and genoJapa30)

References

Ben Hassen, M., Bartholomé, J., Valè, G., Cao, T.-V., & Ahmadi, N. (2018). Genomic Prediction Accounting for Genotype by Environment Interaction Offers an Effective Framework for Breeding Simultaneously for Adaptation to an Abiotic Stress and Performance Under Normal Cropping Conditions in Rice. *G3: Genes|Genomes|Genetics*, 8(July), 2319–2332. <https://doi.org/10.1534/g3.118.200098>

WheatJapa50

Wheat Japa 50 Data

Description

This data set is also based on the data used in the study of (Ben Hassen et al., 2018). The original dataset was composed of a sample of 230 lines evaluated for three traits. Each of them was evaluated in one environment. The total numbers GBS data were 32,066 SNPs was obtained with a heterozygosity rate <5

Usage

```
data(WheatJapa50)
```

Format

2 objects are loaded (phenoJapa50 and genoJapa50)

References

Ben Hassen, M., Bartholomé, J., Valè, G., Cao, T.-V., & Ahmadi, N. (2018). Genomic Prediction Accounting for Genotype by Environment Interaction Offers an Effective Framework for Breeding Simultaneously for Adaptation to an Abiotic Stress and Performance Under Normal Cropping Conditions in Rice. *G3: Genes|Genomes|Genetics*, 8(July), 2319–2332. <https://doi.org/10.1534/g3.118.200098>

WheatMadaToy

Wheat Mada Data

Description

This data set is based on the data used in the study of (Ben Hassen, Bartholomé, Valè, Cao, & Ahmadi, 2018). The original dataset was composed of a sample of 188 wheat lines evaluated for six traits. Each of them was evaluated in one environment. The total numbers of genome by sequencing (GBS) data were 32,066 single nucleotide polymorphisms (SNPs) that was obtained with a heterozygosity rate < 5

Usage

`data(WheatMadaToy)`

Format

2 objects are loaded (phenoMada and genoMada)

References

Ben Hassen, M., Bartholomé, J., Valè, G., Cao, T.-V., & Ahmadi, N. (2018). Genomic Prediction Accounting for Genotype by Environment Interaction Offers an Effective Framework for Breeding Simultaneously for Adaptation to an Abiotic Stress and Performance Under Normal Cropping Conditions in Rice. *G3: Genes|Genomes|Genetics*, 8(July), 2319–2332. <https://doi.org/10.1534/g3.118.200098>

WheatToy

Phenotypic values and Genetic values of Wheat toy dataset.

Description

A data set based on a portion of the data used in the study from a collection of 599 historical CIMMYT wheat lines. The wheat data set is from CIMMYT's Global Wheat Program.

The variables that import the dataset are as follows:

* 'phenoWheatToy': Phenotypic values. * 'genoWheatToy': Genomic values.

Usage

```
data(WheatToy)
```

Format

2 objects are loaded (phenoWheatToy and genoWheatToy)

Source

International Maize and Wheat Improvement Center (CIMMYT), Mexico.

References

McLaren, C. G., R. Bruskiewich, A.M. Portugal, and A.B. Cosico. 2005. The International Rice Information System. A platform for meta-analysis of rice crop data. *Plant Physiology* **139**: 637-642.

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