# Package ‘BMTME’

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

**Version** 1.0.19

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**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** 7.1.1

**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, Rcpp

**LinkingTo** Rcpp, RcppArmadillo

**SystemRequirements** C++11, GNU

**Suggests** covr, testthat

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**Repository** CRAN

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# R topics documented:

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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 Milti-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` *boxplot.BMECV*

---

## 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 *boxplot.BMORSCV*

---

## 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. |

---

boxplot.BMTMECV *boxplot.BMTMECV*

---

## 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

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

---

## `cholesky` *Cholesky*

---

### Description

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

### Usage

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

### Arguments

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

---

## `CV.KFold` *Cross-Validation with K Folds*

---

### 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)
```

---

## CV.RandomPart *Cross-Validation with Random Partitions*

---

### 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 × 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` *Phenotypic 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

```
phenoWheatToy
```

## Format

data.frame, 90 row per 4 columns.

## Source

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

## plot.BME *plot.BME*

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

### 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` *plot.BMTME Simple scatter plot comparing the observed values against the predicted values.*

## 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` *Print BME information object*

## 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 *Print BMECV information object*

## 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 *Print BMORS information object*

## 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 — *Print BMORSCV information object*

### 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 *Print BMTMECV information object*

### 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 *residuals.BME*

### 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 *residuals.BMTME*

### 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 *summary.BMECV*

### 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 *summary.BMORSCV*

### 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 *summary.BMORSENV*

### 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 *summary.BMTMECV*

### 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` *Wheat Iranian Toy Data*

## 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

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`WheatJapa50` *Wheat Japa 50 Data*

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## 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

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`WheatMadaToy` *Wheat Mada Data*

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## 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

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`WheatToy` *Phenotypic values and Genetic values of Wheat toy dataset.*

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## 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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