

Package ‘METAAB’

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Type Package

Title Multi Environment Trials Analysis using AMMI and BLUP

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Description This package compute has useful functions for computing stability analysis using AMMI and BLUP methods. Several procedures, including cross-validation, prediction, and stability parameters for AMMI and BLUP models are available. Tools for personalized graphics is also provided.

Depends R (>= 3.5.0)

License GPL-3

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gplots,
ggExtra,
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methods

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Suggests knitr,
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ReporteRs,
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kableExtra

URL <https://github.com/TiagoOlivoto/METAAB>

VignetteBuilder knitr

BugReports <https://github.com/TiagoOlivoto/METAAB/issues>

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AMMI_indexes

*AMMI-based indexes for stability and simultaneous selection***Description**

This function computes the following AMMI-based stability indexes: ASV, AMMI stability value (Purchase et al., 2000); SIPC, sums of the absolute value of the IPCA scores (Sneller et al. 1997); EV, averages of the squared eigenvector values (Sneller et al. 1997); and Za, absolute value of the relative contribution of IPCAs to the interaction (Zali et al. 2012).

Usage

```
AMMI_indexes(x, order.y = NULL)
```

Arguments

x An object of class WAAS.AMMI

order.y A vector of the same length of x used to order the response variable. Each element of the vector must be one of the "h" or "l". If "h" is used, the response variable will be ordered from maximum to minimum. If "l" is used then the response variable will be ordered from minimum to maximum.

Details

The ASV index is computed as follows:

$$ASV_i = \left[\left[\frac{r \lambda_1^2}{r \lambda_2^2} \times (\lambda_1^{0.5} a_{i1} t_{j1}) \right]^2 + (\lambda_2^{0.5} a_{i2} t_{j2})^2 \right]^{0.5}$$

where r is the number of replications included in the analysis,

The SIPC index is computed as follows:

$$SIPC_i = \sum_{k=1}^P |\lambda_k^{0.5} a_{ik}|$$

where P is the number of IPCA retained via F-tests.

The EV index is computed as follows:

$$EV_i = \sum_{k=1}^P a_{ik}^2 / P$$

The ZA index is computed as follows:

$$Za_i = \sum_{k=1}^P \theta_k a_{ik}$$

where θ_k is the percentage sum of squares explained by the k th IPCA.

Four simultaneous selection indexes (ssi) are also computed by summation of the ranks of the ASV, SIPC, EV and Za indexes and the ranks of the mean yields (Farshadfar, 2008), which results in ssiASV, ssiSIPC, ssiEV, and ssiZa, respectively.

Value

A dataframe containing the indexes

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

References

Purchase, J.L., H. Hatting, and C.S. van Deventer. 2000. Genotype vs environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. *South African J. Plant Soil* 17:101-107. doi:[10.1080/02571862.2000.10634878](https://doi.org/10.1080/02571862.2000.10634878)

Sneller, C.H., L. Kilgore-Norquest, and D. Dombek. 1997. Repeatability of Yield Stability Statistics in Soybean. *Crop Sci.* 37:383-390. doi:[10.2135/cropsci1997.0011183X003700020013x](https://doi.org/10.2135/cropsci1997.0011183X003700020013x)

Zali, H., E. Farshadfar, S.H. Sabaghpour, and R. Karimizadeh. 2012. Evaluation of genotype vs environment interaction in chickpea using measures of stability from AMMI model. *Ann. Biol. Res.* 3:3126-3136. <http://eprints.icrisat.ac.in/id/eprint/7173>

Examples

```
library(METAAB)
model = WAAS.AMMI(data_ge,
                  resp = c(GY, HM),
                  gen = GEN,
                  env = ENV,
                  rep = REP)
model_indexes = AMMI_indexes(model)
```

autoplot

Several types of residual plots

Description

Residual plots for a output model of class "WAAS.AMMI" and "WAASB". Six sets of plots are produced: (1) Residuals vs fitted, (2) normal Q-Q plot for the residuals, (3) scale-location plot (standardized residuals vs Fitted Values), (4) standardized residuals vs Factor-levels, (5) Histogram of raw residuals and (6) standardized residuals vs observation order. For a "WAASB" object, normal Q-Q plot for random effects may also be obtained declaring type = "re"

Usage

```
## S3 method for class 'WAAS.AMMI'
autoplot(x, conf = 0.95, labels = FALSE, theme = theme_waasb(),
         alpha = 0.2, fill.hist = "gray", col.hist = "black",
         col.point = "black", col.line = "red", col.lab.out = "red",
         size.lab.out = 2.5, size.tex.lab = 10, size.shape = 1.5,
         bins = 30, which = c(1:4), mfrow = c(2, 2), ...)
```

```
## S3 method for class 'WAASB'
```

```
autoplot(x, type = "res", conf = 0.95, out = "print",
         labels = FALSE, theme = theme_waasb(),
         alpha = 0.2, fill.hist = "gray", col.hist = "black",
         col.point = "black", col.line = "red", col.lab.out = "red",
         size.lab.out = 2.5, size.tex.lab = 10, size.shape = 1.5,
         bins = 30, which = c(1:4), mfrow = c(2, 2), ...)
```

Arguments

<code>x</code>	An object of class WAAS.AMMI or WAASB.
<code>type</code>	If <code>type = "re"</code> , normal Q-Q plots for the random effects are obtained.
<code>conf</code>	Level of confidence interval to use in the Q-Q plot (0.95 by default).
<code>out</code>	How the output is returned. Must be one of the "print" (default) or "return".
<code>labels</code>	Logical argument. If TRUE labels the points outside confidence interval limits.
<code>theme</code>	The theme to use in the graphics. Default is <code>theme = theme_waasb()</code> .
<code>alpha</code>	The transparency of confidence band in the Q-Q plot. Must be a number between 0 (opaque) and 1 (full transparency).
<code>fill.hist</code>	The color to fill the histogram. Default is "gray".
<code>col.hist</code>	The color of the border of the the histogram. Default is "black".
<code>col.point</code>	The color of the points in the graphic. Default is "black".
<code>col.line</code>	The color of the lines in the graphic. Default is "red".
<code>col.lab.out</code>	The color of the labels for the "outlying" points.
<code>size.lab.out</code>	The size of the labels for the "outlying" points.
<code>size.tex.lab</code>	The size of the text in axis text and labels.
<code>size.shape</code>	The size of the shape in the plots.
<code>bins</code>	The number of bins to use in the histogram. Default is 30.
<code>which</code>	Which graphics should be plotted. Default is <code>which = c(1:4)</code> that means that the first four graphics will be plotted.
<code>mfrow</code>	Allow creating a simple multi-paneled plot. Must be a vector of length 2. The first argument is the number of rows and the second the number of columns. Default is <code>mfrow = c(2, 2)</code> .
<code>...</code>	Additional parameter for the function

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(METAAB)
library(ggplot2)
model = WAAS.AMMI(data_ge,
                  resp = GY,
                  gen = GEN,
                  env = ENV,
                  rep = REP)
autoplot(model$GY)
```

```

model2 = WAASB(data_ge,
                resp = c(GY, HM),
                gen = GEN,
                env = ENV,
                rep = REP)
lapply(model2, function(x){
  autoplot.WAASB(x, which = 2, out = "return")
})

```

corr.ci	<i>Nonparametric confidence interval for Pearson's correlation coefficient</i>
---------	--

Description

Computes the half-width confidence interval for correlation coefficient based on the nonparametric method proposed by Olivoto et al. (2018).

Usage

```
corr.ci(data = NA, r = NULL, n = NULL)
```

Arguments

data	A dataset containing variables only or a symmetric correlation matrix.
r	If data is not available, provide the value for correlation coefficient.
n	The sample size if data is a correlation matrix or if r is informed.

Details

The half-width confidence interval is computed according to the following equation:

$$CI_w = 0.45304^r \times 2.25152 \times n^{-0.50089}$$

where n is the sample size and r is the correlation coefficient.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

References

Olivoto, T., A.D.C. Lucio, V.Q. Souza, M. Nardino, M.I. Diel, B.G. Sari, D.. K. Krysczun, D. Meira, and C. Meier. 2018. Confidence interval width for Pearson's correlation coefficient: a Gaussian-independent estimator based on sample size and strength of association. *Agron. J.* 110:1-8. doi:10.2134/agronj2017.09.0566.

Examples

```
corr.ci(iris[,1:3])
```

corr.ss	<i>Sample size planning for a desired Pearson's correlation confidence interval.</i>
---------	--

Description

Find the required (sufficient) sample size for computing a Pearson correlation coefficient with a desired confidence interval (Olivoto et al., 2018).

Usage

```
corr.ss(r, CI)
```

Arguments

r	The magnitude of the correlation coefficient.
CI	The half-width for confidence interval at $p < 0.05$.

Details

The required (sufficient) sample size is computed as follows:

$$n = [CI_w / 0.45304^r \times 2.25152]^{-0.50089}$$

where CI_w is desired confidence interval and r is the correlation coefficient.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

References

Olivoto, T., A.D.C. Lucio, V.Q. Souza, M. Nardino, M.I. Diel, B.G. Sari, D.. K. Kryszun, D. Meira, and C. Meier. 2018. Confidence interval width for Pearson's correlation coefficient: a Gaussian-independent estimator based on sample size and strength of association. Agron. J. 110:1-8. doi:10.2134/agronj2017.09.0566.

Examples

```
corr.ss(r = 0.60, CI = 0.1)
```

data_ge	<i>A replicate-based data of 10 genotypes cultivated in 14 environments</i>
---------	---

Description

This dataset contain data on two variables assessed in 10 genotypes growing in 11 environments. The experimental design was a RCBD with 3 replicates(blocks). This data provide examples for several functions of **METAAB** package.

Arguments

The following columns in data_ge are:

ENV	A factor with 14 levels; each level represents one cultivation environment.
GEN	A factor with 10 levels; each level represents one genotype.
REP	A factor with 3 levels; each level represents one replication/block.
GY	A continuous variable (grain yield) observed in each plot.
HM	A continuous variable (hectoliter mass) observed in each plot.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

FAI.BLUP	<i>Multitrait index based on factor analysis and ideotype-design</i>
----------	--

Description

Multitrait index based on factor analysis and ideotype-design proposed by Rocha et al. (2018).

Usage

```
FAI.BLUP(x, DI, UI, show = TRUE, SI = NULL, mineval = 1)
```

Arguments

x	An object of class WAASB
DI, UI	A vector of the same length of x to construct the desirable/undesirable ideotype. For each element of the vector, allowed values are "max", "min", "mean", or a numeric value.
show	Logical value. If TRUE the results are shown in console.
SI	An integer [0-100]. The selection intensity in percentage of the total number of genotypes.
mineval	The minimum value so that an eigenvector is retained in the factor analysis.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

References

Rocha, J.R.A.S.C.R, J.C. Machado, and P.C.S. Carneiro. 2018. Multitrait index based on factor analysis and ideotype-design: proposal and application on elephant grass breeding for bioenergy. GCB Bioenergy 10:52-60. doi: [doi:10.1111/gcbb.12443](https://doi.org/10.1111/gcbb.12443).

Examples

```
multivariate = WAASB(data_ge,
                      resp = c(GY, HM),
                      gen = GEN,
                      env = ENV,
                      rep = REP)

FAI = FAI.BLUP(multivariate,
               SI = 15,
               DI = c("max", "max"),
               UI = c("min", "min"))

plot(FAI)
```

int.effects

Dataset with genotype-by-environment interaction effects

Description

This dataset contains a matrix with interaction effects of 10 genotypes cultivated in 5 environments.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

See Also

[meansGxE](#)

meansGxE

A dataset with means of 10 genotypes cultivated in 5 environments

Description

This dataset contains the means for grain yield of 10 genotypes cultivated in 5 environments. The interaction effects for this data is found in [int.effects](#)

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

mmat

Make a two-way table based on categorical and numerical arguments

Description

This function help users to easly make a two-way table from a "long format" data.

Usage

```
mmat(data, row, col, value)
```

Arguments

data	The dataset. Must contains at least two categorical columns.
row	The column of data in which the mean of each level will correspond to one line in the output.
col	The column of data in which the mean of each level will correspond to one column in the output.
value	The column of data that contains the values to fill the two-way table.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
datage = expand.grid(ENV = paste("E", 1:8, sep = ""),
                    GEN = paste("G", 1:20, sep = ""),
                    REP = paste(c("I", "II", "III")))
datage$Y = rnorm(480, 50, 20)
matrix = mmat(datage, row = GEN, col = ENV, val = Y)
matrix
```

MTSI

Multitrait stability index

Description

Multitrait stability index in analysis of multi-environment trials using AMMI or BLUP methods.

Usage

```
MTSI(x, index = "WAASB", show = TRUE, SI = 15, mineval = 1)
```

Arguments

x	An object of class WAASB or WAAS.AMMI.
index	If index = "WAASB" (Default) the multitrait index will be computed considering the stability of genotypes only. If index = "WAASBY" both stability and mean performance are considered. More details can be seen in WAASB and WAAS.AMMI functions.
show	If show = TRUE (Default) some results are shown in the console.
SI	An integer [0-100]. The selection intensity in percentage of the total number of genotypes.
mineval	The minimum value so that an eigenvector is retained in the factor analysis.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(METAAB)
# Based on stability only
MTSI_MODEL = WAASB(data_ge,
                    resp = c(GY, HM),
                    gen = GEN,
                    env = ENV,
                    rep = REP)

MTSI_index = MTSI(MTSI_MODEL)

# Based on mean performance and stability
MTSI_MODEL2 = WAASB(data_ge,
                    resp = c(GY, HM),
                    gen = GEN,
                    env = ENV,
                    rep = REP,
                    mresp = c(100, 100), #Default
                    wresp = c(65, 65))
MTSI_index2 = MTSI(MTSI_MODEL2,
                  index = "WAASBY")
plot(MTSI_index2)
```

partial.corr

Partial correlation coefficient

Description

Estimates of partial correlation coefficient based on data raw or correlation matrices.

Usage

```
partial.corr(data, n = NULL, method = "pearson")
```

Arguments

data	The data, must be a dataframe or a symmetric correlation matrix.
n	The number of subjects used if data is a correlation matrix.
method	If data is a correlation matrix, then codemethod is the method for computing the correlation; one of the "pearson" (default), "kendall", or "spearman"

Value

linear.mat	The matrix of linear correlation.
partial.mat	The matrix of partial correlations.
results	Hypothesis testing for each pairwise comparison
call	The function call

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
partial.corr(iris[,1:4])
```

performs_amm

Performs Additive Main effects and Multiplicative Interaction

Description

Compute the Additive Main effects and Multiplicative interaction. This is a helper function for other procedures performed in the WAASB package such as [WAAS.AMMI](#), [validation.AMMI](#), [validation.AMMIF](#), and [predict.WAAS.AMMI](#).

Usage

```
performs_amm(ENV, GEN, REP, Y)
```

Arguments

ENV	The name of the column that contains the levels of the environments
GEN	The name of the column that contains the levels of the genotypes
REP	The name of the column that contains the levels of the replications/blocks
Y	The response variable

Value

ANOVA	The analysis of variance for the AMMI model.
analysis	The principal component analysis
means	means of genotype vs environment
biplot	scores for genotypes and environments in all the possible axes.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(METAAB)
ammi_model = with(data_ge, performs_ammi(ENV, GEN, REP, GY))
```

plot.blup

Plot the BLUPs for genotypes

Description

Plot the predicted BLUP of the genotypes.

Usage

```
## S3 method for class 'blup'
plot(x, prob = 0.05, export = FALSE, file.type = "pdf",
      file.name = NULL, theme = theme_waasb(), width = 6,
      height = 6, size.err.bar = 0.5, size.shape = 3.5,
      size.tex.lab = 12, height.err.bar = 0.3, x.lim = NULL,
      x.breaks = waiver(), col.shape = c("blue", "red"),
      y.lab = "Genotypes", x.lab = "Predicted Grain Yield",
      resolution = 300, ...)
```

Arguments

x	The WAASB object
prob	The probability error for constructing confidence interval.
export	Export (or not) the plot. Default is TRUE.
file.type	If export = TRUE, define the type of file to be exported. Default is pdf, Graphic can also be exported in *.tiff format by declaring file.type = "tiff".
file.name	The name of the file for exportation, default is NULL, i.e. the files are automatically named.
theme	The graphical theme of the plot. Default is 'theme = theme_waasb()'. Please, see '?WAASB::theme_waasb'. An own theme can be applied using the arguments: 'theme = theme_waasb() + theme(some stuff here)'. For more details, please, see '?ggplot2::theme'
width	The width "inch" of the plot. Default is 6.
height	The height "inch" of the plot. Default is 6.
size.err.bar	The size of the error bar for the plot. Default is 0.5.
size.shape	The size of the shape (both for genotypes and environments). Default is 3.5.
size.tex.lab	The size of the text in axis text and labels.
height.err.bar	The height for error bar. Default is 0.3.
x.lim	The range of x-axis. Default is NULL (maximum and minimum values of the data set). New arguments can be inserted as x.lim = c(x.min, x.max).

x.breaks	The breaks to be plotted in the x-axis. Default is automatic breaks. New arguments can be inserted as <code>x.breaks = c(breaks)</code>
col.shape	A vector of length 2 that contains the color of shapes for genotypes above and below of the mean, respectively. Default is <code>c("blue", "red")</code> .
x.lab	The label of the x-axis in the plot. Default is "Predicted Grain Yield".
y.lab	The label of the y-axis in the plot. Default is "Genotypes".
resolution	The resolution of the plot. Parameter valid if <code>file.type = "tiff"</code> is used. Default is 300 (300 dpi)
...	Other arguments of the function

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

See Also

[plot.scores](#), [plot.WAASBY](#)

Examples

```
library(METAAB)
BLUP = WAASB(data_ge,
              resp = c(GY, HM),
              gen = GEN,
              env = ENV,
              rep = REP)
plot.blup(BLUP$GY)
```

plot.eigen

Plot the eigenvalues

Description

Plot the eigenvalues for from singular value decomposition of BLUP interaction effects matrix.

Usage

```
## S3 method for class 'eigen'
plot(x, export = FALSE, theme = theme_waasb(),
     file.type = "pdf", file.name = NULL, width = 6, height = 6,
     size.shape = 3.5, size.line = 1, size.tex.lab = 12,
     y.lab = "Eigenvalue", y2.lab = "Accumulated variance",
     x.lab = "Number of multiplicative terms", resolution = 300, ...)
```

Arguments

<code>x</code>	The WAASB object
<code>export</code>	Export (or not) the plot. Default is TRUE.
<code>theme</code>	The graphical theme of the plot. Default is <code>'theme = theme_waasb()'</code> . Please, see <code>'?WAASB::theme_waasb'</code> . An own theme can be applied using the arguments: <code>'theme = theme_waasb() + theme(some stuff here)'</code> . For more details, please, see <code>'?ggplot2::theme'</code>
<code>file.type</code>	If <code>export = TRUE</code> , define the type of file to be exported. Default is pdf, Graphic can also be exported in *.tiff format by declaring <code>file.type = "tiff"</code> .
<code>file.name</code>	The name of the file for exportation, default is NULL, i.e. the files are automatically named.
<code>width</code>	The width "inch" of the plot. Default is 6.
<code>height</code>	The height "inch" of the plot. Default is 6.
<code>size.shape</code>	The size of the shape. Default is 3.5.
<code>size.line</code>	The size of the line. Default is 1.
<code>size.tex.lab</code>	The size of the text in axis text and labels.
<code>y.lab</code>	The label of the y-axis in the plot. Default is "Eigenvalue".
<code>y2.lab</code>	The label of the second y-axis in the plot. Default is "Accumulated variance".
<code>x.lab</code>	The label of the x-axis in the plot. Default is "Number of multiplicative terms".
<code>resolution</code>	The resolution of the plot. Parameter valid if <code>file.type = "tiff"</code> is used. Default is 300 (300 dpi)
<code>...</code>	Other arguments of the function

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

See Also

[plot.scores](#), [plot.WAASBY](#)

Examples

```
library(METAAB)
BLUP = WAASB(data_ge,
              resp = c(GY, HM),
              gen = GEN,
              env = ENV,
              rep = REP)
plot.eigen(BLUP$GY)
```

plot.FAI.BLUP

Multitrait index based on factor analysis and ideotype-design

Description

Plot the multitrait index based on factor analysis and ideotype-design proposed by Rocha et al. (2018).

Usage

```
## S3 method for class 'FAI.BLUP'
plot(x, ideotype = 1, SI = 15, radar = TRUE,
     size.point = 2, col.sel = "red",
     col.nonsel = "black", ...)
```

Arguments

x	An object of class WAASB
ideotype	The ideotype to be plotted. Default is 1.
SI	An integer [0-100]. The selection intensity in percentage of the total number of genotypes.
radar	Logical argument. If true (default) a radar plot is generated after using coord_polar().
size.point	The size of the point in graphic.
col.sel	The colour for selected genotypes.
col.nonsel	The colour for nonselected genotypes.
...	Other arguments of the function.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

References

Rocha, J.R.A.S.C.R, J.C. Machado, and P.C.S. Carneiro. 2018. Multitrait index based on factor analysis and ideotype-design: proposal and application on elephant grass breeding for bioenergy. GCB Bioenergy 10:52-60. doi: [doi:10.1111/gcbb.12443](https://doi.org/10.1111/gcbb.12443).

Examples

```
multivariate = WAASB(data_ge,
                     resp = c(GY, HM),
                     gen = GEN,
                     env = ENV,
                     rep = REP)

FAI = FAI.BLUP(multivariate,
               SI = 15,
               DI = c("max", "max"),
               UI = c("min", "min"))

plot(FAI)
```

plot.MTSI	<i>Plot the multitrait stability index</i>
-----------	--

Description

Plot the multitrait stability index using ggplot-generated graphics. .

Usage

```
## S3 method for class 'MTSI'
plot(x, SI = 15, radar = TRUE, size.point = 2,
      col.sel = "red", col.nonsel = "black", ...)
```

Arguments

x	An object of class MTSI
SI	An integer [0-100]. The selection intensity in percentage of the total number of genotypes.
radar	Logical argument. If true (default) a radar plot is generated after using coord_polar().
size.point	The size of the point in graphic.
col.sel	The colour for selected genotypes.
col.nonsel	The colour for nonselected genotypes.
...	Other arguments of the function.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(METAAB)
MTSI_MODEL = WAASB(data_ge,
                    resp = c(GY, HM),
                    gen = GEN,
                    env = ENV,
                    rep = REP)

MTSI_index = MTSI(MTSI_MODEL)
plot(MTSI_index)
```

plot.ratios

*Plot heat maps with genotype ranking***Description**

Plot heat maps with genotype ranking in two ways.

Usage

```
## S3 method for class 'WAASBYratio'
plot(x, type, export = FALSE, file.type = "pdf",
      file.name = NULL, width = 6, height = 5, size.lab = 1,
      margins = c(5, 4), y.lab = NULL, x.lab = NULL,
      key.lab = "Genotype ranking", resolution = 300, ...)

## S3 method for class 'WAASratio.AMMI'
plot(x, type, export = FALSE, file.type = "pdf",
      file.name = NULL, width = 6, height = 5, size.lab = 1,
      margins = c(5, 4), y.lab = NULL, x.lab = NULL,
      key.lab = "Genotype ranking", resolution = 300, ...)
```

Arguments

x	The WAASYratio object
type	1 = Heat map Ranks: this graphic shows the genotype ranking considering the WAAS estimated with different numbers of Principal Components; 2 = Heat map WAASY-GY ratio: this graphic shows the genotype ranking considering the different combinations in the WAAS/GY ratio.
export	Export (or not) the plot. Default is TRUE.
file.type	If export = TRUE define the type of file to be exported. Default is pdf, Graphic can also be exported in *.tiff format by declaring file.type = "tiff".
file.name	The name of the file for exportation, default is NULL, i.e. the files are automatically named.
width	The width "inch" of the plot. Default is 8.
height	The height "inch" of the plot. Default is 7.
size.lab	The label size of the plot. It is suggested attribute 1
margins	Numeric vector of length 2 containing the margins for column and row names, respectively. Default is c(5, 4).
y.lab	The label of y axis. Default is "Genotypes".
x.lab	The label of x axis. Default is "Number of axes".
key.lab	The label of color key. Default is "Genotype ranking".
resolution	Valid parameter if file.type = "tiff". Define the resolution of the plot. Default is "300".
...	Other arguments of the function

Details

The first type of heatmap shows the genotype ranking depending on the number of principal component axis used for estimating the WAASB index. An euclidian distance-based dendrogram is used for grouping the genotype ranking for both genotypes and principal component axis. The second type of heatmap shows the genotype ranking depending on the WAASB/GY ratio. The ranks obtained with a ratio of 100/0 considers exclusively the stability for the genotype ranking. On the other hand, a ratio of 0/100 considers exclusively the productivity for the genotype ranking. Four clusters are estimated (1) unproductive and unstable genotypes; (2) productive, but unstable genotypes; (3) stable, but unproductive genotypes; and (4), productive and stable genotypes.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(METAAB)
#wratio = WAASBYratio(data_ge,
#                      resp = GY,
#                      gen = GEN,
#                      env = ENV,
#                      rep = REP,
#                      increment = 10)
#plot(wratio, type = 1)

#wratio2 = WAASRatio.AMMI(data_ge,
#                          resp = GY,
#                          gen = GEN,
#                          env = ENV,
#                          rep = REP,
#                          increment = 5)
#plot(wratio2, type = 2)
```

plot.scores

Plot scores in different graphical interpretations

Description

Plot scores of genotypes and environments in different graphics. 1 = PC1 x PC2, 2 = GY x PC1, 3 = GY x WAASB, and 4 = Nominal yield x EPCA1.

Usage

```
## S3 method for class 'scores'
plot(x, type = 1, polygon = FALSE, file.type = "pdf",
     export = FALSE, file.name = NULL, theme = theme_waasb(),
     axis.expand = 1.1, width = 8, height = 7, x.lim = NULL,
     x.breaks = waiver(), x.lab = NULL, y.lab = NULL, y.lim = NULL,
     y.breaks = waiver(), shape.gen = 21, shape.env = 23,
     size.shape = 2.2, size.bor.tick = 0.3, size.tex.lab = 12,
     size.tex.pa = 3.5, size.line = 0.5, size.segm.line = 0.5,
     leg.lab = c("Gen", "Env"), line.type = "solid", line.alpha = 0.9,
```

```
col.line = "gray", col.gen = "blue", col.env = "darkgreen",
col.alpha = 0.9, col.segm.gen = "transparent",
col.segm.env = "darkgreen", resolution = 300, ...)
```

Arguments

<code>x</code>	The object WAASB or WAAS.AMMI
<code>type</code>	Three types of graphics can be generated: 1 = PC1 x PC2, default, to make inferences related to the interaction effects; 2 = GY x PC1 to make inferences related to stability and productivity; 3 = GY x WAASB, and 4 = Nominal yield x Environment PC1.
<code>polygon</code>	Logical argument. If TRUE, a polygon is drawn when type 1.
<code>file.type</code>	The type of file to be exported. Valid parameter if <code>export = T TRUE</code> . Default is "pdf". The graphic can also be exported in *.tiff format by declaring <code>file.type = "tiff"</code> .
<code>export</code>	Export (or not) the plot. Default is FALSE.
<code>file.name</code>	The name of the file for exportation, default is NULL, i.e. the files are automatically named.
<code>theme</code>	The graphical theme of the plot. Default is 'theme = theme_waasb()'. Please, see '?WAASB::theme_waasb'. An own theme can be applied using the arguments: 'theme = theme_waasb() + theme(some stuff here)'. For more details, please, see '?ggplot2::theme'
<code>axis.expand</code>	Multiplication factor to expand the axis limits by to enable fitting of labels. Default is 1.1.
<code>width</code>	The width "inch" of the plot. Default is 8.
<code>height</code>	The height "inch" of the plot. Default is 7.
<code>x.lim</code>	The range of x-axis. Default is NULL (maximum and minimum values of the data set). New arguments can be inserted as <code>x.lim = c(x.min, x.max)</code> .
<code>x.breaks</code>	The breaks to be plotted in the x-axis. Default is automatic breaks. New arguments can be inserted as <code>x.breaks = c(breaks)</code>
<code>x.lab</code>	The label of x-axis. Each plot has a default value. New arguments can be inserted as <code>x.lab = "my label"</code> .
<code>y.lab</code>	The label of y-axis. Each plot has a default value. New arguments can be inserted as <code>y.lab = "my label"</code> .
<code>y.lim</code>	The range of x-axis. Default is NULL. The same arguments than <code>x.lim</code> can be used.
<code>y.breaks</code>	The breaks to be plotted in the x-axis. Default is automatic breaks. The same arguments than <code>x.breaks</code> can be used.
<code>shape.gen</code>	The shape for genotype indication in the biplot. Default is 21 (circle). Values must be between 21-25: 21 (circle), 22 (square), 23 (diamond), 24 (up triangle), and 25 (low triangle).
<code>shape.env</code>	The shape for environment indication in the biplot. Default is 23 (diamond). The same arguments than "shape.gen".
<code>size.shape</code>	The size of the shape (both for genotypes and environments). Default is 2.2.
<code>size.bor.tick</code>	The size of tick of shape. Default is 0.3. The size of the shape will be <code>size.shape + size.bor.tick</code>
<code>size.tex.lab</code>	The size of the text in the axes text and labels. Default is 12.

Examples

```
library(METAAB)
library(ggplot2)
scores = WAASB(data_ge,
                resp = GY,
                gen = GEN,
                env = ENV,
                rep = REP)

# PC1 x PC2
plot.scores(scores$GY,
            type = 1,
            polygon = TRUE)

# GY x PC1
plot.scores(scores$GY,
            type = 2,
            col.env = "olivedrab",
            col.gen = "orange2",
            x.lab = "My own x label")

# GY x WAASB
plot.scores(scores$GY,
            type = 3,
            size.tex.pa = 2,
            size.tex.lab = 16)
```

plot.validation.AMMIF *Plot the RMSPD of all AMMI-family tested models*

Description

Boxplot showing the Root Means Square Prediction Difference of all AMMI family models obtained in a cross-validation procedure.

Usage

```
## S3 method for class 'validation.AMMIF'
plot(x, violin = FALSE, export = FALSE, x.lab = NULL,
     y.lab = NULL, size.tex.lab = 12, file.type = "pdf",
     file.name = NULL, theme = theme_waasb(), width = 6,
     height = 6, resolution = 300, col.violin = "gray90",
     col.boxplot = "gray70", width.boxplot = 0.2,
     x.lim = NULL, x.breaks = waiver(), ...)
```

Arguments

x	An object of class validation.AMMIF.
violin	Define if a violine plot is used with boxplot. Default is "TRUE"
export	Export (or not) the plot. Default is T.
x.lab	The label of x-axis. New arguments can be inserted as x.lab = "my x label".

y.lab	The label of y-axis. New arguments can be inserted as <code>y.lab = "my y label"</code> .
size.tex.lab	The size of the text in axis text and labels.
file.type	The type of file to be exported. Default is pdf, Graphic can also be exported in *.tiff format by declaring <code>file.type = "tiff"</code> .
file.name	The name of the file for exportation, default is NULL, i.e. the files are automatically named.
theme	The graphical theme of the plot. Default is <code>'theme = theme_waasb()'</code> . Please, see <code>'?WAASB::theme_waasb'</code> . An own theme can be applied using the arguments: <code>'theme = theme_waasb() + theme(some stuff here)'</code> . For more details, please, see <code>'?ggplot2::theme'</code>
width	The width "inch" of the plot. Default is 6.
height	The height "inch" of the plot. Default is 6.
resolution	The resolution of the plot. Parameter valid if <code>file.type = "tiff"</code> is used. Default is 300 (300 dpi)
col.violin	Parameter valid if <code>violin = T</code> . Define the color of the violin plot. Default is "gray90.
col.boxplot	Define the color for boxplot. Default is "gray70".
width.boxplot	The width of boxplots. Default is 0.2.
x.lim	The range of x-axis. Default is NULL (maximum and minimum values of the dataset). New arguments can be inserted as <code>x.lim = c(x.min, x.max)</code> .
x.breaks	The breaks to be plotted in the x-axis. Default is automatic breaks. New arguments can be inserted as <code>x.breaks = c(breaks)</code>
...	Other arguments of the function

Details

Five statistics are shown in this type of plot. The lower and upper hinges correspond to the first and third quartiles (the 25th and 75th percentiles). The upper whisker extends from the hinge to the largest value no further than $1.5 * \text{IQR}$ from the hinge (where IQR is the inter-quartile range). The lower whisker extends from the hinge to the smallest value at most $1.5 * \text{IQR}$ of the hinge. Data beyond the end of the whiskers are considered outlying points.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

See Also

plot.scores, plot.WAASBY

Examples

```
validation <- validation.AMMIF(data_ge,  
                               resp = GY,  
                               gen = GEN,  
                               env = ENV,  
                               rep = REP,  
                               nboot = 5,  
                               nrepval = 2)  
  
plot(validation)
```

plot.WAASBY

*Plot WAASBY values for genotype ranking***Description**

Plot heat maps with genotype ranking in two ways.

Usage

```
## S3 method for class 'WAASBY'
plot(x, export = F , file.type = "pdf", file.name = NULL,
     theme = theme_waasb(), width = 6, height = 6, size.shape = 3.5,
     size.tex.lab = 12, col.shape = c("blue", "red"), x.lab = "WAASBY",
     y.lab = "Genotypes", x.breaks = waiver(), resolution = 300, ...)
```

Arguments

x	The WAASBY object
export	Export (or not) the plot. Default is T.
file.type	The type of file to be exported. Default is pdf, Graphic can also be exported in *.tiff format by declaring file.type = "tiff".
file.name	The name of the file for exportation, default is NULL, i.e. the files are automatically named.
theme	The graphical theme of the plot. Default is 'theme = theme_waasb()'. Please, see '?WAASB::theme_waasb'. An own theme can be applied using the arguments: 'theme = theme_waasb() + theme(some stuff here)'. For more details, please, see '?ggplot2::theme'
width	The width "inch" of the plot. Default is 8.
height	The height "inch" of the plot. Default is 7.
size.shape	The size of the shape in the plot. Default is 3.5.
size.tex.lab	The size of the text in axis text and labels.
col.shape	A vector of length 2 that contains the color of shapes for genotypes above and below of the mean, respectively. Default is c("blue", "red").
x.lab	The label of the x axis in the plot. Default is "WAASBY".
y.lab	The label of the y axis in the plot. Default is "Genotypes".
x.breaks	The breaks to be plotted in the x-axis. Default is automatic breaks. New arguments can be inserted as x.breaks = c(breaks)
resolution	The resolution of the plot. Parameter valid if file.type = "tiff" is used. Default is 300 (300 dpi)
...	Other arguments of the function

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

See Also

[plot.scores](#)

Examples

```
library(METAAB)
library(ggplot2)
waasby = WAASB(data_ge,
               resp = GY,
               gen = GEN,
               env = ENV,
               rep = REP)
waasby2 = WAAS.AMMI(data_ge,
                   resp = GY,
                   gen = GEN,
                   env = ENV,
                   rep = REP)
plot.WAASBY(waasby$GY)
plot.WAASBY(waasby2$GY) +
  theme_gray() +
  theme(legend.position = "bottom",
        legend.background = element_blank(),
        legend.title = element_blank(),
        legend.direction = "horizontal")
```

predict.WAAS.AMMI

Predict the means of a WAAS.AMMI object

Description

Predict the means of a WAAS.AMMI object considering a specific number of axis.

Usage

```
## S3 method for class 'WAAS.AMMI'
predict(object, naxis, ...)
```

Arguments

object	An object of class WAAS.AMMI
naxis	The the number of axis to be use in the prediction. If object has more than one variable, then naxis must be a vector.
...	Additional parameter for the function

Details

This function is used to predict the response variable of a two-way table (for examples the yielding of the i -th genotype in the j -th environment) based on AMMI model. This prediction is based on the number of multiplicative terms used. If $naxis = 0$, only the main effects (AMMI0) are used. In this case, the predicted mean will be the predicted value from OLS estimation. If $naxis = 1$ the AMMI1 (with one multiplicative term) is used for predicting the response variable. If $naxis = \min(\text{gen}-1; \text{env}-1)$, the AMMIF is fitted and the predicted value will be the cell mean, i.e. the mean of R-replicates of the i -th genotype in the j -th environment. The number of axis to be used must be carrefully chosen. Precures based on Postdictive sucess (such as Gollob's d.f.) or Predictive sucess (such as cross-validation) should be used to do this. This package provide both.

`WAAS.AMMI` function compute traditional AMMI analysis showing the number of significant axis. On the other hand, `validation.AMMIF` function provide a cross-validation, estimating the RMSE of all AMMI-family models, based on resampling procedure.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(METAAB)
model = WAAS.AMMI(data_ge,
                  resp = c(GY, HM),
                  gen = GEN,
                  env = ENV,
                  rep = REP)
# Predict GY with 3 IPCA and HM with 1 IPCA
predict = predict.WAAS.AMMI(model, naxis = c(3, 1))
```

rbind_fill

Helper function for combining data.frames by row, filling missing values.

Description

Helper function similar to `plyr::rbind.fill` that combines data.frames by row and fills with . missing values

Usage

```
rbind_fill(...)
```

Arguments

... Input dataframes.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
df1 = data.frame(v1 = c(1, 2), v2 = c(2, 3))
df2 = data.frame(v3 = c(4, 5))
rbind_fill(df1, df2)
```

resca	<i>Rescale a continuous vector to have specified minimum and maximum values</i>
-------	---

Description

Helper function used in the WAASB package. It rescales a continuous vector to have specified minimum and maximum values. Missing values are not allowed.

Usage

```
resca(values, new_min = 0, new_max = 100)
```

Arguments

values	continuous vector of values to manipulate.
new_min	The minimum value of the new scale. Default is 0.
new_max	The maximum value of the new scale. Default is 100

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
resca(1:10)
resca(c(20, 30, 40), new_min = 5, new_max = 10)
```

Resende_indexes	<i>Stability indexes proposed by Resende based on a mixed-effect model.</i>
-----------------	---

Description

This function computes the following indexes proposed by Resende (2007): the harmonic mean of genotypic values (HMGV), the relative performance of the genotypic values (RPGV) and the harmonic mean of the relative performance of genotypic values (HMRPGV).

Usage

```
Resende_indexes(x)
```

Arguments

x	An object of class WAASB
---	--------------------------

Details

The indexes computed with this function have been used to select genotypes with stability performance in a mixed-effect model framework. Some examples are in Alves et al (2018), Azevedo Peixoto et al. (2018), Dias et al. (2018) and Colombari Filho et al. (2013).

The HMGV index is computed as

$$HMGV_i = \frac{1}{E} \sum_{j=1}^E \frac{1}{Gv_{ij}}$$

where E is the number of environments included in the analysis, Gv_{ij} is the genotypic value (BLUP) for the i th genotype in the j th environment.

The RPGV index is computed as

$$RPGV_i = \frac{1}{e} \sum_{j=1}^e BLUP_{ij} / \mu_j$$

The HMRPGV index is computed as

$$HMRPGV_i = \frac{1}{E} \sum_{j=1}^E \frac{1}{Gv_{ij} / \mu_j}$$

Value

A dataframe containing the indexes

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

References

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- Resende MDV (2007) *Matemática e estatística na análise de experimentos e no melhoramento genético*. Embrapa Florestas, Colombo

Examples

```
library(METAAB)
res_ind = WAASB(data_ge,
                 resp = c(GY, HM),
                 gen = GEN,
                 env = ENV,
                 rep = REP)
model_indexes = Resende_indexes(res_ind)
```

summary.MTSI

*Summary a MTSI object***Description**

Summary a MTSI object in two ways. By default, the results are shown in the R console. The results can also be exported to the directory.

Usage

```
## S3 method for class 'MTSI'
summary(object, export = FALSE, file.name = NULL, digits = 4, ...)
```

Arguments

object	The MTSI object
export	A logical argument. If TRUE T, a *.txt file is exported to the working directory
file.name	The name of the file if export = TRUE
digits	The significant digits to be shown.
...	Other arguments of the function

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(METAAB)
# Based on stability only
MTSI_MODEL = WAASB(data_ge,
                   resp = c(GY, HM),
                   gen = GEN,
                   env = ENV,
                   rep = REP)

MTSI_index = MTSI(MTSI_MODEL)
summary(MTSI_index)
summary(MTSI_index,
        export = TRUE,
        file.name = "my results")
```

summary.WAAS.AMMI	<i>Summary a WAAS.AMMI object</i>
-------------------	-----------------------------------

Description

Summary the WAAS.AMMI object in two ways. By default, the results are shown in the R console. The results can also be exported to the directory.

Usage

```
## S3 method for class 'WAAS.AMMI'
summary(object, export = FALSE, file.name = NULL, digits = 4, ...)
```

Arguments

object	The WAAS.AMMI object
export	A logical argument. If TRUE T, a *.txt file is exported to the working directory
file.name	The name of the file if export = TRUE
digits	The significant digits to be shown.
...	Other arguments of the function

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(METAAB)
model = WAAS.AMMI(data_ge,
                   resp = c(GY, HM),
                   gen = GEN,
                   env = ENV,
                   rep = REP)

summary(model)
```

summary.WAASB	<i>Summary a WAASB object</i>
---------------	-------------------------------

Description

Summary the WAASB object in two ways. By default, the results are shown in the R console. The results can also be exported to the directory.

Usage

```
## S3 method for class 'WAASB'
summary(object, export = FALSE, blup = FALSE,
        file.name = NULL, digits = 4, ...)
```

Arguments

object	The WAASB object
export	A logical argument. If TRUE T, a *.txt file is exported to the working directory
blup	A logical argument. If TRUE T, the blups are shown.
file.name	The name of the file if export = TRUE
digits	The significant digits to be shown.
...	Other arguments of the function

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(METAAB)
model = WAASB(data_ge,
               resp = c(GY, HM),
               gen = GEN,
               env = ENV,
               rep = REP)
summary(model)
```

 theme_waasb

A personalized theme for the WAASB ggplot2-based graphics

Description

The function theme_waasb() is a personalized theme for the WAASB ggplot2-based graphics. An own theme can be applied in all graphics by using the following arguments in the plot. functions of the package: theme = theme_waasb() + theme(some stuff here...). See ?ggplot2::theme for more details.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

 validation.AMMI

Cross-validation for estimation of AMMI model

Description

Cross-validation for estimation of AMMI models

Usage

```
validation.AMMI(data, resp, gen, env, rep, design = "RCBD",
                nboot, nrepval, naxis, progbar = TRUE)
```

Arguments

data	The dataset containing the columns related to Environments, Genotypes, replication/block and response variable(s).
resp	The response variable, for example <code>resp = "RG"</code> .
gen	The name of the column that contains the levels of the genotypes.
env	The name of the column that contains the levels of the environments.
rep	The name of the column that contains the levels of the replications/blocks.
design	The experimental design to be considered. Default is RCBD (Randomized complete Block Design). For Completely Randomized Designs inform <code>design = "CRD"</code> .
nboot	The number of resamples to be used in the cross-validation
nrepval	The number of replicates (r) from total number of replicates (R) to be used in the modeling dataset. Only one replicate is used as validating data each step, so, <code>Nrepval</code> must be equal $R-1$
naxis	The number of axis to be considered for estimation of GE effects.
progbar	A logical argument to define if a progress bar is shown. Default is TRUE.

Details

For each iteration, the original dataset is split into two datasets: modeling and validating data. The dataset "modeling" has all combinations (genotype x environment) with the number of replications informed in `nrepval`. The dataset "validating" has one replication. The splitting of the dataset into modeling and validating data depends on the design informed. For Completely Randomized Block Design (default), completely blocks are selected within environments. The remained block serves validation data. If `design = "RCD"` is informed, completely randomly samples are made for each genotype-by-environment combination. The estimated values (depending on NAXIS informed) are compared with the "validating" data. the Root Means Square error is computed. At the end of boots, a list is returned with the following values.

Value

RMSE	A vector with <code>Nboot</code> -estimates of the root mean squared error estimated with the difference between predicted and validating data.
RSMEmean	The mean of RMSE estimates.
Estimated	A data frame that contain the values (predicted, observed, validation) of the last loop.
Modeling	The dataset used as modeling data in the last loop.
Testing	The dataset used as testing data in the last loop.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

See Also

[validation.AMMIF](#)

Examples

```
library(METAAB)
model = validation.AMMI(data_ge,
                        resp = GY,
                        gen = GEN,
                        env = ENV,
                        rep = REP,
                        nboot = 5,
                        nrepval = 2,
                        naxis = 2)
```

validation.AMMIF	<i>Cross-validation for estimation of all AMMI-family models</i>
------------------	--

Description

Cross-validation for estimation of all AMMI-family models

Usage

```
validation.AMMIF(data, resp, gen, env, rep, design = "RCBD",
                 nboot, nrepval, progbars = TRUE)
```

Arguments

data	The dataset containing the columns related to Environments, Genotypes, replication/block and response variable(s).
resp	The response variable, for example resp = GY.
gen	The name of the column that contains the levels of the genotypes.
env	The name of the column that contains the levels of the environments.
rep	The name of the column that contains the levels of the replications/blocks.
design	The experimental design to be considered. Default is RCBD (Randomized complete Block Design). For Completely Randomized Designs inform design = "CRD".
nboot	The number of resamples to be used in the cross-validation
nrepval	The number of replicates (r) from total number of replicates (R) to be used in the modeling dataset. Only one replicate is used as validating data each step, so, Nrepval must be equal R-1
progbars	A logical argument to define if a progress bar is shown. Default is TRUE.

Details

This function provides a complete cross-validation of replicate-based data using AMMI-family models. By default, the first validation is carried out considering the AMMIF (all possible axis used). Considering this model, the original dataset is split up into two datasets: training set and validation set. The "training" set has all combinations (genotype x environment) with the number of replications informed in nrepval. The dataset "validation" set has the remaining replication. The splitting of the dataset into modeling and validating data depends on the design informed. For

Completely Randomized Block Design (default), completely blocks are selected within environments. The remained block serves validation data. If `design = "RCD"` is informed, completely randomly samples are made for each genotype-by-environment combination. The estimated values (depending on the naxis informed) are compared with the "validation" data. the Root Mean Square Prediction Difference (RMSPD) is computed. At the end of boots, a list is returned.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

See Also

[validation.AMMI](#)

Examples

```
library(METAAB)
model = validation.AMMIF(data_ge,
  resp = GY,
  gen = GEN,
  env = ENV,
  rep = REP,
  nboot = 2,
  nrepval = 2)
```

validation.blup

Cross-validation for blup prediction

Description

Cross-validation for blup prediction.

Usage

```
validation.blup(data, resp, gen, env, rep,
  nboot, nrepval, progbar = TRUE)
```

Arguments

<code>data</code>	The dataset containing the columns related to Environments, Genotypes, replication/block and response variable(s).
<code>resp</code>	The response variable, for example <code>resp = GY</code> .
<code>gen</code>	The name of the column that contains the levels of the genotypes.
<code>env</code>	The name of the column that contains the levels of the environments.
<code>rep</code>	The name of the column that contains the levels of the replications/blocks.
<code>nboot</code>	The number of resamples to be used in the cross-validation
<code>nrepval</code>	The number of replicates (r) from total number of replicates (R) to be used in the modeling dataset. Only one replicate is used as validating data each step, so, <code>Nrepval</code> must be equal $R-1$
<code>progbar</code>	A logical argument to define if a progress bar is shown. Default is TRUE.

Details

This function provides a cross-validation procedure for mixed models using replicate-based data. By default, complete blocks are randomly selected within each environment. In each iteration, the original dataset is split up into two datasets: training and validation data. The "training" set has all combinations (genotype x environment) with the number of replications informed in `nrepval`. The "validation" set has the remaining replication. The estimated values are compared with the "validation" data and the Root Means Square Prediction Difference is computed. At the end of boots, a list is returned.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

See Also

[plot.scores](#), [plot.WAASBY](#)

Examples

```
library(METAAB)
model = validation.blup(data_ge,
                        resp = GY,
                        gen = GEN,
                        env = ENV,
                        rep = REP,
                        nboot = 5,
                        nrepval = 2)
```

WAAS.AMMI

Weighted Average of Absolute Scores for AMMI analysis

Description

Compute the Weighted Average of Absolute Scores for AMMI analysis.

Usage

```
WAAS.AMMI(data, resp, gen, env, rep, mresp = NULL,
           wresp = NULL, prob = 0.05, naxis = NULL,
           verbose = TRUE)
```

Arguments

<code>data</code>	The dataset containing the columns related to Environments, Genotypes, replication/block and response variable(s).
<code>resp</code>	The response variable(s). To analyze multiple variables in a single procedure a vector of variables may be used. For example <code>resp = c(var1, var2, var3)</code> .
<code>gen</code>	The name of the column that contains the levels of the genotypes.
<code>env</code>	The name of the column that contains the levels of the environments.
<code>rep</code>	The name of the column that contains the levels of the replications/blocks.

mresp	A numeric vector of the same length of resp. The mresp will be the new maximum value after rescaling. By default, all variables in resp are rescaled so that the maximum value is 100 and the minimum value is 0.
wresp	The weight for the response variable(s) for computing the WAASBY index. Must be a numeric vector of the same length of resp. Default is 50, i.e., equal weights for stability and mean performance.
prob	The p-value for considering a IPCA significant.
naxis	The number of IPCAs to be used for computing the WAAS index. Default is NULL (Significant IPCAs are used). If values are informed, the number of IPCAs will be used independently on its significance. Note that if two or more variables are included in resp, then naxis must be a vector.
verbose	Logical argument. If verbose = FALSE the code is run silently.

Details

This function compute the weighted average of absolute scores, estimated as follows:

$$WAAS_i = \sum_{k=1}^p |IPCA_{ik} \times EP_k| / \sum_{k=1}^p EP_k$$

where $WAAS_i$ is the weighted average of absolute scores of the i th genotype; $IPCA_{ik}$ is the score of the i th genotype in the k th IPCA; and EP_k is the explained variance of the k th IPCA for $k = 1, 2, \dots, p$, considering p the number of significant PCAs, or a declared number of PCAs. For example if $prob = 0.05$, all axis that are significant considering this probability level are used. The number of axis can be also informed by declaring $naxis = x$. This comand ignores the `p.valuePC` comand.

Value

individual	A within-environments ANOVA considering a fixed-effect model.
model	A data frame with the response variable, the scores of all Principal Components, the estimates of Weighted Average of Absolute Scores, and WAASY (the index that consider the weights for stability and productivity in the genotype ranking).
MeansGxE	The means of genotypes in the environments, with observed, predicted and residual values.
PCA	Principal Component Analysis.
anova	Joint analysis of variance for the main effects and Principal Component analysis of the interaction effect.
Details	A list summarizing the results. The following information are showed. WgtResponse, the weight for the response variable in estimating WAASB, WgtWAAS the weight for stability, Ngen the number of genotypes, Nenv the number of environments, OVmean the overall mean, Min the minimum observed (returning the genotype and environment), Max the maximum observed, Max the maximum observed, MinENV the environment with the lower mean, MaxENV the environment with the larger mean observed, MinGEN the genotype with the lower mean, MaxGEN the genotype with the larger.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

See Also[WAAS.AMMI](#)**Examples**

```
library(METAAB)

# Considering p-value <= 0.05 to compute the WAAS

model <- WAAS.AMMI(data_ge,
  resp = GY,
  gen = GEN,
  env = ENV,
  rep = REP)

# Declaring the number of axis to be used for computing WAAS
# and assigning a larger weight for the response variable when
# computing the WAASBY index.

model2 <- WAAS.AMMI(data_ge,
  resp = GY,
  gen = GEN,
  env = ENV,
  rep = REP,
  naxis = 3,
  wresp = 60)

# Analyzing multiple variables (GY and HM) at the same time
# considering that smaller values of HM are better and higher
# values of GY are better, assigning a larger weight for the GY
# and a smaller weight for HM when computing WAASBY index.

model3 <- WAAS.AMMI(data_ge,
  resp = c(GY, HM),
  gen = GEN,
  env = ENV,
  rep = REP,
  mresp = c(100, 0),
  wresp = c(60, 40))
```

WAASB

Weighted Average of Absolute Scores for the BLUP'S GxE effects matrix generated by a mixed-effect model

Description

Compute the Weighted Average of Absolute Scores for quantifying the stability in multienvironment trials using mixed-effect models.

Usage

```
WAASB(data, resp, gen, env, rep, mresp = NULL, wresp = NULL,
  random = "gen", prob = 0.05, verbose = TRUE)
```

Arguments

<code>data</code>	The dataset containing the columns related to Environments, Genotypes, replication/block and response variable(s).
<code>resp</code>	The response variable(s). To analyze multiple variables in a single procedure a vector of variables may be used. For example <code>resp = c(var1, var2, var3)</code> .
<code>gen</code>	The name of the column that contains the levels of the genotypes.
<code>env</code>	The name of the column that contains the levels of the environments.
<code>rep</code>	The name of the column that contains the levels of the replications/blocks.
<code>mresp</code>	A numeric vector of the same length of <code>resp</code> . The <code>mresp</code> will be the new maximum value after reescalating. By default, all variables in <code>resp</code> are rescaled so that the maximum value is 100 and the minimum value is 0.
<code>wresp</code>	The weight for the response variable(s) for computing the WAASBY index. Must be a numeric vector of the same length of <code>resp</code> . Default is 50, i.e., equal weights for stability and mean performance.
<code>random</code>	The effects of the model assumed to be random. Default is <code>random = "gen"</code> (genotype and genotype-vs-environment as random effects. Other values allowed are <code>random = "env"</code> (environment, genotype-vs-environment and block-within-environment random effects) or <code>random = "all"</code> all effects except the intercept are assumed to be random effects.
<code>prob</code>	The probability for estimating confidence interval for BLUP's prediction.
<code>verbose</code>	Logical argument. If <code>verbose = FALSE</code> the code are run silently.

Details

This function compute the weighted average of absolute scores considering all principal component axis from the Singular Value Decomposition (SVD) of the BLUP'S GxE effects matrix generated by a linear mixed-effect model. The main advantage of this procedure in relation to the WAAS.AMMI function is that random effects can be included in the model. In addition, unbalanced datasets can also be modeled.

Value

The function returns the results in a list for each analyzed variable. For each variable, the following objects are returned.

<code>individual</code>	A within-environments ANOVA considering a fixed-effect model.
<code>fixed</code>	Test for fixed effects.
<code>random</code>	Variance components for random effects.
<code>LRT</code>	The Likelihood Ratio Test for the random effects.
<code>model</code>	A data frame with the response variable, the scores of all Principal Components, the estimates of Weighted Average of Absolute Scores, and WAASY (the index that consider the weights for stability and productivity in the genotype ranking).
<code>blupGEN</code>	The estimated BLUPS for genotypes (If <code>random = "gen"</code> or <code>random = "all"</code>)
<code>BLUPenv</code>	The estimated BLUPS for environments, (If <code>random = "env"</code> or <code>random = "all"</code>).
<code>BLUPge</code>	The estimated BLUPS of all genotypes in all environments "BLUPij".
<code>PCA</code>	The results of Principal Component Analysis with eigenvalues and explained variance of BLUP-interaction matrix.

MeansGxE	The phenotypic means of genotypes in the environments, with observed, predicted and OLS residual prediction.
Details	A list summarizing the results. The following information are showed. WgtResponse, the weight for the response variable in estimating WAASB, WgtWAAS the weight for stability, Ngen the number of genotypes, Nenv the number of environments, OVmean the overall mean, Min the minimum observed (returning the genotype and environment), Max the maximum observed, Max the maximum observed, MinENV the environment with the lower mean, MaxENV the environment with the larger mean observed, MinGEN the genotype with the lower mean, MaxGEN the genotype with the larger.
ESTIMATES	A list with the following values: GEV the genotype-by-environment variance (and percentage of phenotypic variance); GV the genotypic variance (and percentage of phenotypic variance); EV the environmental variance; RV the residual variance (and percentage of phenotypic variance); FV the phenotypic variance; h2g the heritability of the trait; GER2 the coefficient of determination of the interaction effects; h2mg the heritability of the mean; AccuGen the selective accuracy; rge the genotype-environment correlation; CVg the genotypic coefficient of variation; CVr the residual coefficient of variation; CVratio the ratio between genotypic and residual coefficient of variation.
residuals	The residuals of the model.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

See Also

[WAAS.AMMI](#)

Examples

```
library(METAAB)

# Genotypes as random effects and equal weights for both

# response variable and stability

model <- WAASB(data_ge,
               resp = GY,
               gen = GEN,
               env = ENV,
               rep = REP,
               wresp = 70)

# Higher weight for response variable

model2 <- WAASB(data_ge,
               resp = GY,
               gen = GEN,
               env = ENV,
               rep = REP,
               wresp = 65)

# Environment as random effects analyzing more than one variables
```

```
# considering that smaller values of HM are better and higher
# values of GY are better, assigning a larger weight for the GY
# and a smaller weight for HM when computing WAASBY index.
```

```
model3 <- WAASB(data_ge,
  random = "env",
  resp = c(GY, HM),
  gen = GEN,
  env = ENV,
  rep = REP,
  mresp = c(100, 0),
  wresp = c(60, 40))
```

WAASBYratio	<i>Weighted Average of Absolute Scores from SVD of BLUP-interaction effects matrix in different scenarios of WAASB/GY ratio</i>
-------------	---

Description

Compute the Weighted Average of Absolute Scores for AMMI analysis in different combinations of weights for stability and productivity.

Usage

```
WAASBYratio(data, resp, gen, env, rep, increment = 5,
  saveWAASY = 50, progbar = TRUE)
```

Arguments

data	The dataset containing the columns related to Environments, Genotypes, replication/block and response variable(s).
resp	The response variable, for example <code>resp = RG</code> .
gen	The name of the column that contains the levels of the genotypes.
env	The name of the column that contains the levels of the environments.
rep	The name of the column that contains the levels of the replications/blocks.
increment	The range of the increment for WAASB/GY ratio. Default is 5. The function compute the WAASBY values starting with a weight of 100 for stability and 0 for response variable. With the default, the first scenario will be a WAASB/GY ratio = 100/0. In the next scenario, the WAASBY values are computed based on a WAASB/GY ratio = 95/5.
saveWAASY	Automatically save the WAASY values when the weight for WAAS (stability) in the WAAS/GY ratio is "saveWAASY". Default is 100. The value of "saveWAASY" must be multiple of "Increment". If this assumption is not valid, an error will occur.
progbar	A logical argument to define if a progress bar is shown. Default is TRUE.

Details

This function considers both stability (weighted average of absolute scores based on SVD of BLUP-interaction effects matrix) and productivity for genotype ranking. This function provide the option of attributing weights for stability and productive in genotype ranking. This is important depending on the goal of a selection strategy. For example, if a goal of a breeding program is to select a genotype whith high yielding (independently on the stability performance), that genotype with the first rank in an $WAASB/GY = 0/100$ ratio should be selected. The reciprocal is true. Aiming at selecting a high-stable genotype (independently on the productivity), that genotype with the first rank in an $WAASB/GY = 100/0$ ratio should be selected. By defalut, the increment on the $WAASB/GY$ ratio is equal to 5. In other words, twenty one different combinations are computed. Each combination, the genotypes are ranked regarding the WAASY value.

Value

anova	Joint analysis of variance for the main effects and Principal Component analysis of the interaction effect.
PC	Principal Component Analysis.
MeansGxE	The means of genotypes in the environments, with observed, predicted and residual values.
WAAS	A data frame with the response variable, the scores of all Principal Components, the estimates of Weighted Average of Absolute Scores, and WAASY (the index that consider the weights for stability and productivity in the genotype ranking.
WAASY	The values of the WAASY estimated when the wheight for the stability in the loop match with argument "saveWAASY".
WAASY.values	All the values of WAASY estimated in the different scenarios of WAAS/GY weighting ratio.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(METAAB)

# Default, with increment of 5 and saving the WAASY values when weight is 50
# wratio = WAASBYratio(data_ge,
#                       resp = GY,
#                       gen = GEN,
#                       env = ENV,
#                       rep = REP)

# Incrementing 2-by-2
wratio2 = WAASBYratio(data_ge,
                      resp = GY,
                      gen = GEN,
                      env = ENV,
                      rep = REP,
                      increment = 50)
```

WAASratio.AMMI	<i>Weighted Average of Absolute Scores for AMMI analysis in different scenarios of WAAS/GY ratio</i>
----------------	--

Description

Compute the Weighted Average of Absolute Scores for AMMI analysis in different combinations of weights for stability and productivity.

Usage

```
WAASratio.AMMI(data, resp, gen, env, rep, p.valuePC = 0.05,
               increment = 5, saveWAASY = 50, progbar = TRUE)
```

Arguments

data	The dataset containing the columns related to Environments, Genotypes, replication/block and response variable(s).
resp	The response variable, for example resp = RG.
gen	The name of the column that contains the levels of the genotypes.
env	The name of the column that contains the levels of the environments.
rep	The name of the column that contains the levels of the replications/blocks.
p.valuePC	The p-value for considering the PC significant. Default is 0.05. The number of significant Principal Components to be used for calculating the WAASB will be chosen based on this probability.
increment	The range of the increment for WAAS/GY ratio. Default is 5. The function compute the WAASY values starting with a weight o 100 for stability and 0 for response variable. With the default, the first scenario will be a WAAS/GY ratio = 100/0. In the next scenario, the WAASY values are computed based on a WAAS/GY ratio = 95/5.
saveWAASY	Automatically save the WAASY values when the wheight for WAAS (stability) in the WAAS/GY ratio is "saveWAASY". Default is 100. The value of "save-WAASY" must be multiple of "Increment". If this assumption is not valid, an error will be occur.
progbar	A logical argument to define if a progress bar is shown. Default is TRUE.

Details

This function is very similar to the WAASBYratio. The main difference is that here, the WAASBY values are computed considering a traditional AMMI model.

Value

anova	Joint analysis of variance for the main effects and Principal Component analysis of the interaction effect.
PC	Principal Component Analysis.
MeansGxE	The means of genotypes in the environments, with observed, predicted and residual values.

WAAS	A data frame with the response variable, the scores of all Principal Components, the estimates of Weighted Average of Absolute Scores, and WAASY (the index that consider the weights for stability and productivity in the genotype ranking.
WAASY	The values of the WAASY estimated when the wheight for the stability in the loop match with argument "saveWAASY".
WAASY.values	All the values of WAASY estimated in the different scenarios of WAAS/GY weighting ratio.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
# Default, with increment of 5 and saving the WAASY values when weight is 50
#wratio = WAASratio.AMMI(data_ge,
#                          resp = GY,
#                          gen = GEN,
#                          env = ENV,
#                          rep = REP)

# Incrementing 2-by-2
wratio2 = WAASratio.AMMI(data_ge,
                          resp = GY,
                          gen = GEN,
                          env = ENV,
                          rep = REP,
                          increment = 50)
```

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