

Package ‘METAAB’

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Type Package

Title Multi Environment Trials Analysis using AMMI and BLUP

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Author Tiago Olivoto

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Maintainer Tiago Olivoto <tiagoolivoto@gmail.com>

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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Imports dplyr, plyr, data.table, dendextend, heatmaply, gplots,
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AMMI_indexes	<i>AMMI-based indexes for stability and simultaneous selection</i>
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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)
```

Arguments

x An object of class WAAS.AMMI

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:

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

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
- 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
- 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(WAASBdata, GY, GEN, ENV, REP)
model_indexes = AMMI_indexes(model)
```

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, bins = 30, which = c(1:4),
         mfrow = c(2, 2), ...)

## S3 method for class 'WAASB'
autoplot(x, type = "res", 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, 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>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>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.

`mfrow` 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 `mfrow = c(2, 2)`.

`...` Additional parameter for the function

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(METAAB)
model = WAAS.AMMI(WAASBdata, GY, GEN, ENV, REP)
autoplot(model)

model2 = WAASB(WAASBdata, GY, GEN, ENV, REP)
autoplot(model2)
```

INT

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>

MEANS

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](#)

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

performs_ammi	<i>Performs Additive Main effects and Multiplicative Interaction</i>
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Description

Compute the Additive Main effects and Multiplicative interaction. This is a helper function for other procedures performed in the WAASB package.

Usage

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

Arguments

ENV	The name of the collum that contains the levels of the environments
GEN	The name of the collum that contains the levels of the genotypes
REP	The name of the collum 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

```
ammi_model = with(WAASBdata, performs_ammi(ENV, GEN, REP, GY))
```

plot.blup	<i>Plot the estimated BLUPs of genotypes</i>
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Description

Plot the predicted BLUP of the genotypes.

Usage

```
## S3 method for class 'blup'
plot(x, prob = 0.95, export = FALSE, file.type = "pdf",
      file.name = NULL, theme = theme_waasb(), width = 6, height = 6,
      size.err.bar = 0.5, size.shape = 3.5, 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

<code>x</code>	The WAASB object
<code>prob</code>	The probability to be considered in confidence interval prediction.
<code>export</code>	Export (or not) the plot. Default is TRUE.
<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>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>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.err.bar</code>	The size of the error bar for the plot. Default is 0.5.
<code>size.shape</code>	The size of the shape (both for genotypes and environments). Default is 3.5.
<code>height.err.bar</code>	The height for error bar. Default is 0.3.
<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>col.shape</code>	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> .
<code>x.lab</code>	The label of the x-axis in the plot. Default is "Predicted Grain Yield".
<code>y.lab</code>	The label of the y-axis in the plot. Default is "Genotypes".
<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)
model = WAASB(WAASBdata, resp = "GY", weight.response = 50, weight.WAAS = 50)
plot.blup(model)
```

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, y.lab = "Eigenvalue",
      y2.lab = "Accumulated variance", x.lab = "Number of multiplicative terms",
      resolution = 300, ...)
```

Arguments

x	The WAASB object
export	Export (or not) the plot. Default is TRUE.
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'
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 6.
height	The height "inch" of the plot. Default is 6.
size.shape	The size of the shape. Default is 3.5.
size.line	The size of the line. Default is 1.
y.lab	The label of the y-axis in the plot. Default is "Eigenvalue".
y2.lab	The label of the second y-axis in the plot. Default is "Accumulated variance".
x.lab	The label of the x-axis in the plot. Default is "Number of multiplicative terms".
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](#), [plot.WAASBY](#)

Examples

```
library(METAAB)
model = WAASB(WAASBdata, GY, GEN, ENV, REP)
plot.eigen(model)
```

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, 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 = 2.5, size.tex = 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

x	The object WAASB or WAAS.AMMI
type	Three types of graphics can be generated: 1 = PC1 x PC2, 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.
polygon	Logical argument. If TRUE, a polygon is drawn when type 1.
file.type	The type of file to be exported. Valid parameter if export = T TRUE. Default is "pdf". The graphic can also be exported in *.tiff format by declaring file.type = "tiff".
export	Export (or not) the plot. Default is FALSE.
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'

<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 2.5.
<code>size.tex</code>	The size of the text in the background of the plot. Default is 3.5.
<code>size.line</code>	The size of the line that indicate the means in the biplot. Default is 0.5.
<code>size.segm.line</code>	The size of the segment that start in the origin of the biplot and end in the scores values. Default is 0.5.
<code>leg.lab</code>	The labs of legend. Default is Gen and Env.
<code>line.type</code>	The type of the line that indicate the means in the biplot. Default is "solid". Other values that can be attributed are: "blank", no lines in the biplot, "dashed", "dotted", "dotdash".
<code>line.alpha</code>	The alpha value that combine the line with the background to create the appearance of partial or full transparency. Default is 0.4. Values must be between "0" (full transparency) to "1" (full color).
<code>col.line</code>	The color of the line that indicate the means in the biplot. Default is "gray"
<code>col.gen</code>	The shape color for genotypes. Default is "blue". Other values can be attributed. For example, "transparent", will make a plot with only an outline around the shape area.
<code>col.env</code>	The shape color for environments. Default is "red". The same usability than "col.gen".
<code>col.alpha</code>	The alpha value for the color. Default is 0.9. Values must be between 0 (full transparency) to 1 (full color).
<code>col.segm.gen</code>	The color of segment for genotypes. Default is "transparent". Parameter valid for <code>type = 1</code> and <code>type = 2</code> graphics. This segment start in the origin of the biplot and end in the scores values.
<code>col.segm.env</code>	The color of segment for environments. Default is "gray50". The same usability than "col.segm.gen"
<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

Details

The plots type 1 and 2 have the same interpretation than those used in traditional-usage AMMI analysis (well know as AMMI2 and AMMI1, respectively). In the plot type 3, the scores of both genotypes and environments are plotted considering the response variable and the WAASB (stability index that considers all significant principal component axis of traditional AMMI models or all principal component axis estimated with BLUP-interaction effects. Plot type 4 may be used to better understand the well known "which-won-where" pattern, facilitating the recommendation of appropriate genotypes targeted for specific environments, thus allowing the exploitation of narrow adaptations.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

See Also

[plot.WAASBY](#)

Examples

```
library(METAAB)
model = WAASB(WAASBdata, resp = "GY", weight.response = 50, weight.WAAS = 50)
plot.scores(model, 1, file.type = "tiff", width = 8, height = 7, col.gen = "green")
# PC1 x PC2.tiff

plot.scores(model, 2, width = 8, height = 7, col.gen = "green", shape.gen = 23)
# GY x PC1.pdf

plot.scores(model, 3, col.gen = "blue", col.env = "red",
  theme = theme_waasb() + theme(axis.title = element_text(size = 14)))
# GY x WAAS.pdf

plot.scores(model, 4)
# no file exported
```

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, 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

<code>x</code>	An object of class <code>validation.AMMIF</code> .
<code>violin</code>	Define if a violine plot is used with boxplot. Default is "TRUE"
<code>export</code>	Export (or not) the plot. Default is T.
<code>x.lab</code>	The label of x-axis. New arguments can be inserted as <code>x.lab = "my x label"</code> .
<code>y.lab</code>	The label of y-axis. New arguments can be inserted as <code>y.lab = "my y label"</code> .
<code>file.type</code>	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>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>width</code>	The width "inch" of the plot. Default is 6.
<code>height</code>	The height "inch" of the plot. Default is 6.
<code>resolution</code>	The resolution of the plot. Parameter valid if <code>file.type = "tiff"</code> is used. Default is 300 (300 dpi)
<code>col.violin</code>	Parameter valid if <code>violin = T</code> . Define the color of the violin plot. Default is "gray90.
<code>col.boxplot</code>	Define the color for boxplot. Default is "gray70".
<code>width.boxplot</code>	The width of boxplots. Default is 0.2.
<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>...</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

```
library(METAAB)
validation = validation.AMMIF(WAASBdata, GY, GEN, ENV, REP,
                              nboot = 100, nrepval = 2)

#A plot without a violin plot exported to a *.pdf file
plot(validation, violin = F, export = T)
```

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,
     col.shape = c("blue", "red"), 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.
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").
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)
# plotting the WAASBY values based on blup procedure
#model = WAASBYratio(WAASBdata, resp = "GY", increment = 5, saveWAASY = 60)
#plot.WAASBY(model)

# plotting the WAASY value based on traditional AMMI model
#model2 = WAASratio.AMMI(WAASBdata, resp = "GY", increment = 5, saveWAASY = 60)
#plot.WAASBY(model2)
```

plot.WAASBYratio	<i>Plot heat maps with genotype ranking</i>
------------------	---

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, ...)
```

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>

See Also

[plot.scores](#)

Examples

```
library(METAAB)
model = WAASBYratio(WAASBdata, resp = "GY")

# plot the heatmap considering the ranks in different number of PC axis.
plot.WAASBYratio(model, type = 1)

# plot the heatmap considering the ranks in WAASY/GY ratio and export to a *.tiff file
plot.WAASBYratio(model, type = 2, export = TRUE, file.type = "tiff")
```

predict.WAAS.AMMI	<i>Predict the means of a WAAS.AMMI object</i>
-------------------	--

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, digits = 4, ...)
```

Arguments

<code>object</code>	An object of class <code>WAAS.AMMI</code>
<code>naxis</code>	The the number of axis to be use in the prediction.
<code>digits</code>	The significant digits to be shown.
<code>...</code>	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(gen-1; 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 carefully 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(WAASBdata, GY, GEN, ENV, REP)
predict = predict.AMMI(model, naxis = 3)
```

<code>resca</code>	<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

<code>values</code>	continuous vector of values to manipulate.
<code>new_min</code>	The minimum value of the new scale. Default is 0.
<code>new_max</code>	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

Stability indexes proposed by Resende based on a mixed-effect model.

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 for to select genotypes with stability performance in a mixed-effect model framewor. 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

$$RPGV_i = \frac{1}{E} \left(\sum_{j=1}^E Gv_{ij} / \mu_j \right)$$

The HMRPGV index is computed as

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

Value

A dataframe contaning the indexes

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

References

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- Azevedo Peixoto, L. de, P.E. Teodoro, L.A. Silva, E.V. Rodrigues, B.G. Laviola, and L.L. Bhering. 2018. *Jatropha* half-sib family selection with high adaptability and genotypic stability. *PLoS One* 13:e0199880. doi:10.1371/journal.pone.0199880.
- Resende MDV (2007) *Matematica e estatistica na analise de experimentos e no melhoramento genetico*. Embrapa Florestas, Colombo

Examples

```
library(METAAB)
model = WAASB(WAASBdata, GY, GEN, ENV, REP)
model_indexes = Resende_indexes(model)
```

summary.WAAS.AMMI

Summary a WAAS.AMMI object

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(WAASBdata, GY, GEN, ENV, REP)
summary(model, digits = 2)
summary(model, export = T, file.name = "my results")
```

summary.WAASB

Summary a WAASB object

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, 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
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(WAASBdata, GY, GEN, ENV, REP)
summary(model, digits = 2)
summary(model, export = T, file.name = "my results")
```

theme_waasb	<i>A personalized theme for the WAASB ggplot2-based graphics</i>
-------------	--

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	<i>Cross-validation for estimation of AMMI model</i>
-----------------	--

Description

Cross-validation for estimation of AMMI models

Usage

```
validation.AMMI(data, resp, gen, env, rep, design = "RCBD",
  nboot, nrepval, naxis, 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 = "RG"</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>design</code>	The experimental design to be considered. Default is RCBD (Randomized complete Block Design). For Completely Randomized Designs inform <code>design = "CRD"</code> .
<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>naxis</code>	The number of axis to be considered for estimation of GE effects.
<code>progbar</code>	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 random 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)
validation = validation.AMMI(WAASBdata, GY, GEN, ENV, REP,
                             nboot = 100, nrepval = 2, naxis = 4)
```

validation.AMMIF

Cross-validation for estimation of all AMMI-family models

Description

Cross-validation for estimation of all AMMI-family models

Usage

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

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

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.
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
progbar	A logical argument to define if a progress bar is shown. Default is TRUE.

Details

This function provides a cross-validation of replicate-based data using mixed models. By default, complete blocks are randomly selecte each environment. In 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 estimated values are compared with the "validating" data. the Root Means Square error is computed. At the end of boots, a list is returned.

Value

RMSE	The root mean squared error estimated with the difference between predicted and validating data.
------	--

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

See Also

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

Examples

```
library(METAAB)
validation = validation.blup(WAASBdata, GY, GEN, ENV, REP,
                             nboot = 100, nrepval = 2)
```

WAAS.AMMI	<i>Weighted Average of Absolute Scores for AMMI analysis</i>
-----------	--

Description

Compute the Weighted Average of Absolute Scores for AMMI analysis.

Usage

```
WAAS.AMMI(data, resp, gen, env, rep, p.valuePC = 0.05,
           naxis = NULL, weight.response = 50, weight.WAAS = 50)
```

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.
p.valuePC	The p-value for considering the PC significant. The number of significant Principal Components to be used for calculating the WAAS will be chosen based on this probability.
naxis	The number of axis to be used for computing the WAAS value. Default it NULL. If informed some values, the number of axis informed is used for computing the WAAS.
weight.response	The weight for the response variable.
weight.WAAS	The weight for the WAAS (stability).

Details

This function compute the weighted average of absolute scores considering the significant principal component axis. The number of axis to be used depends on the probability level informed in p.valuePC. For example if p.valuePC = 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>

Examples

```
# Considering p-value <= 0.05 to compute the WAAS
library(METAAB)
model = WAAS.AMMI(WAASBdata, GY, GEN, ENV, REP,
                  weight.response = 40, weight.WAAS = 60)

# Declaring the number of axis to be used for computing WAAS

model = WAAS.AMMI(WAASBdata, resp = GY, gen = GEN, env = ENV, rep = REP,
                  naxis = 3, weight.response = 40, weight.WAAS = 60)
```

WAASB

Weighted Average of Absolute Scores for BLUP-based PCA analysis

Description

Compute the Weighted Average of Absolute Scores for PCA analysis based on the GE-interaction matrix.

Usage

```
WAASB(data, resp, gen, env, rep, random = "gen",
      prob = 0.95, weight.response = 50, weight.WAAS = 50)
```

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 = RG</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>random</code>	The effect to be considered as random. Default is genotype "gen". A random effects model can be fitted using <code>random = "all"</code> .
<code>prob</code>	The probability for estimating confidence interval for BLUP's prediction.
<code>weight.response</code>	The weight for the response variable. Default is 50.
<code>weight.WAAS</code>	The weight for the WAAS (stability). Default is 50.

Details

This function compute the weighted average of absolute scores considering all principal component axis from Singular Value Decomposition of BLUP-interaction effects matrix. As the matrix of genotypic effects (free from error and interaction effects) is used, all multiplicative terms can be used without a noise-adding effect. The main advantage of this procedure in relation to the `WAAS.AMMI` function is that, by using mixed model-based analysis, random effects can be included in the model. In addition, unbalanced datasets can also be modeled.

Value

<code>individual</code>	A within-environments ANOVA considering a fixed-effect model.
<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.
<code>BLUPenv</code>	The estimated BLUPS for environments, if <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.
<code>MeansGxE</code>	The phenotypic means of genotypes in the environments, with observed, predicted and OLS residual prediction.
<code>Details</code>	A list summarizing the results. The following information are showed. <code>WgtResponse</code> , the weight for the response variable in estimating WAASB, <code>WgtWAAS</code> the weight for stability, <code>Ngen</code> the number of genotypes, <code>Nenv</code> the number of environments, <code>OVmean</code> the overall mean, <code>Min</code> the minimum observed (returning the genotype and environment), <code>Max</code> the maximum observed, <code>MinENV</code> the environment with the lower mean, <code>MaxENV</code> the environment with the larger mean observed, <code>MinGEN</code> the genotype with the lower mean, <code>MaxGEN</code> the genotype with the larger.
<code>REML</code>	A list with the following data frames: <code>fixed</code> , that contains the ANOVA table with F-tests and p-values for fixed effects (If <code>random = "gen"</code>); and <code>random</code> that contains the estimated variance components of the random effects.

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.
LRT	The Likelihood Ratio Test for the random effects of the model.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
# Ggenotypes as random effects and equal weights for both response variable and stability

library(METAAB)
model = WAASB(WAASBdata, GY, GEN, ENV, REP)

# Higher weight for stability
model2 = WAASB(WAASBdata, rep = REP, env = ENV, resp = GY, gen = GEN,
               weight.response = 70, weight.WAAS = 30)

# A random-effect model
model3 = WAASB(WAASBdata, GY, GEN, ENV, REP, random = "all")
```

WAASBdata

A replicate-based data of 10 genotypes cultivated in 11 environments

Description

This dataset contain the observed grain yield of 10 genotypes cultivated in 11 environments. The experimental design was a RCBD with 3 replicates(blocks). This data provide examples for several functions of WAAS package.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

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, 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 <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.
progbars	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 provides the option of attributing weights for stability and productivity 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 with 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 default, 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 weight 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
library(METAAB)
model = WAASBYratio(WAASBdata, GY, GEN, ENV, REP)

# Incrementing 2-by-2 and saving the WAASY values when weight is 70

model2 = WAASBYratio(WAASBdata, GY, GEN, ENV, REP,
                      increment = 2, saveWAASY = 70)
```

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.
progbars	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
library(METAAB)
model= WAASratio.AMMI(WAASBdata, GY, GEN, ENV, REP)

# Incrementing 2-by-2 and saving the WAASY values when weight is 70

model2 = WAASratio.AMMI(WAASBdata, GY, GEN, ENV, REP,
                        increment = 2, saveWAASY = 70)
```

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