Package ‘GGEBiplots’

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Title GGE Biplots with 'ggplot2'

Version 0.1.3

Description Genotype plus genotype-by-environment (GGE) biplots rendered using 'ggplot2'. Provides a command line interface to all of the functionality contained within the archived package 'GGEBiplotGUI'.

Depends R (>= 3.3.1)

License GPL-3

Encoding UTF-8

LazyData true

Imports ggplot2 (>= 2.2.0), ggforce (>= 0.1.1), scales (>= 0.4.1),
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R topics documented:

`CompareGens` *Compare two genotypes biplot*

Description

Compare the performance of two genotypes across all environments

Usage

```
CompareGens(GGEModel, G1, G2, ...)
```

Arguments

`GGEModel`	An object of class `GGEModel` or gge
`G1`	genotype to compare. Must be a string which matches a genotype label
`G2`	genotype to compare. Must be a string which matches a genotype label and not equal to G1
`...`	Other arguments sent to `GGEPlot`

Examples

```
data(Ontario)
GGE1<-GGEModel(Ontario)
CompareGens(GGE1,"cas","luc")
```

`DiscRep` *Discrimination vs. representativeness biplot*

Description

Evaluating the environments based on both discriminating ability and representativeness

Usage

```
DiscRep(GGEModel, ...)
```

Arguments

`GGEModel`	An object of class `GGEModel` or gge
`...`	Other arguments sent to `GGEPlot`

Examples

```
data(Ontario)
GGE1<-GGEModel(Ontario)
DiscRep(GGE1)
```

`EnvRelationship` *Relationship between environments*

Description

Relationship between environments

Usage

```
EnvRelationship(GGEModel, ...)
```

Arguments

`GGEModel`	An object of class `GGEModel` or gge
`...`	Other arguments sent to `GGEPlot`

Examples

```
data(Ontario)
GGE1<-GGEModel(Ontario)
EnvRelationship(GGE1)
```

`ExamineEnv` *Examine an environment*

Description

Ranking the cultivars based on their performance in any given environment

Usage

```
ExamineEnv(GGEModel, Env, ...)
```

Arguments

`GGEModel`	An object of class `GGEModel` or gge
`Env`	environment to examine. Must be a string which matches an environment label
`...`	Other arguments sent to `GGEPlot`

Examples

```
data(Ontario)
GGE1<-GGEModel(Ontario)
ExamineEnv(GGE1,"WP93")
```

`ExamineGen` *Examine a genotype biplot*

Description

Ranking the environments based on the relative performance of any given cultivar

Usage

```
ExamineGen(GGEModel, Gen, ...)
```

Arguments

`GGEModel`	An object of class `GGEModel` or gge
`Gen`	genotype to examine. Must be a string which perfectly matches an genotype label
`...`	Other arguments sent to `GGEPlot`

Examples

```
data(Ontario)
GGE1<-GGEModel(Ontario)
ExamineGen(GGE1,"cas")
```

`GGEModel` *Produces genotype plus genotype-by-environment model from a 2-way table of means*

Description

Calculates the GGE model where presented with a two way table of means with genotypes in rows, where genotype names are set as row names, and environments in columns, where environment names are set as column names. This function serves as a command line interface to the internal code contained within the archived package 'GGEBiplotGUI'. For dealing with missing data then a better implementation is available through `gge`.

Usage

```
GGEModel(Data, centering = "tester", scaling = "none", SVP = "column")
```

Arguments

`Data`	a data frame or matrix containing genotype by environment means with the genotypes in rows and the environments in columns. row names and column names should be set to indicate the genotype names and environment names.
`centering`	centering method. Either "tester" for tester centered (G+GE), "global" for global centered (E+G+GE), "double" for double centred (GE) or "none" for no centering. Models produced without centering cannot be used in the `GGEPlot` function.
`scaling`	scaling method. Either "sd" for standard deviation or "none" for no scaling.
`SVP`	method for singular value partitioning. Either "row","column","dual" or "symmetrical".

Value

A list of class `GGEModel` containing:

`coordgenotype`	plotting coordinates for genotypes from all components
`coordenviroment`	plotting coordinates for environments from all components
`eigenvalues`	vector of eigenvalues from each component
`vartotal`	overall variance
`varexpl`	percentage of variance explained by each component
`labelgen`	genotype names
`labelenv`	environment names
`axes`	axis labels
`Data`	scaled and centered input data
`centering`	name of centering method
`scaling`	name of scaling method
`SVP`	name of SVP method

References

Yan W, Kang M (2003). *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists*. CRC Press.

Yan W, Kang M (2002). *Singular-Value Partitioning in Biplot Analysis of Multienvironment Trial Data*. Agronomy Journal, 94, 990-996. doi: 10.2134/agronj2002.0990

Examples

```
data(Ontario)
GGE1<-GGEModel(Ontario)
GGEPlot(GGE1)
```

`GGEPlot` *GGE biplots with* **ggplot2**

Description

Produces the GGE biplot as an object of class 'ggplot' from a model produced by a call to either `GGEModel` or `gge`. Nearly all stylistic attributes of output can either be customised within the function or disabled so that the user can customise output to their own liking.

Usage

```
GGEPlot(
  GGEModel,
  type = 1,
  d1 = 1,
  d2 = 2,
  selectedE = NA,
  selectedG = NA,
  selectedG1 = NA,
  selectedG2 = NA,
  colSegment = "red",
  colHull = "black",
  largeSize = 4.5,
  axis_expand = 1.2,
  axislabels = TRUE,
  axes = TRUE,
  limits = TRUE,
  titles = TRUE,
  footnote = TRUE,
 textGen = element_text(family = "", face = 1, color = "forestgreen", size = 4, hjust
    = 0, vjust = 0, angle = 0),
 textEnv = element_text(family = "", face = 1, color = "blue", size = 4, hjust = 0,
    vjust = 0, angle = 0)
)
```

Arguments

`GGEModel` An object of class `GGEModel` or `gge`

`type` type of biplot to produce.

1. Basic biplot.
2. Examine environment. See `ExamineEnv`
3. Examine genotype. See `ExamineGen`
4. Relationship among environments. See `EnvRelationship`
5. Compare two genotypes. See `CompareGens`
6. Which won where/what. See `WhichWon`

7. Discrimination vs. representativeness. See DiscRep
8. Ranking environments. See RankEnv
9. Mean vs. stability. See MeanStability
10. Ranking gentoypes See RankGen

`d1`	PCA component to plot on x axis. Defaults to 1
`d2`	PCA component to plot on y axis. Defaults to 2
`selectedE`	name of the environment to examine when type=2. Must be a string which matches an environment label
`selectedG`	name of the genotype to examine when type=3. Must be a string which matches a genotype label
`selectedG1`	name of a genotype to compare when type=5. Must be a string which matches a genotype label
`selectedG2`	name of a genotype to compare when type=5. Must be a string which matches a genotype label and not equal to selectedG1
`colSegment`	colour for segment or circle lines. Defaults to "red"
`colHull`	colour for hull when type=6. Defaults to "black"
`largeSize`	text size to use for larger labels where type=5, used for the two selected genotypes, and where type=6, used for the outermost genotypes. Defaults to 4.5
`axis_expand`	multiplication factor to expand the axis limits by to enable fitting of labels. Defaults to 1.2
`axislabels`	logical. If TRUE then include automatically generated labels for axes
`axes`	logical. If TRUE then include x and y axes going through the origin
`limits`	logical. If TRUE then automatically rescale axes
`titles`	logical. If TRUE then include automatically generated titles
`footnote`	logical. If TRUE then include automatically generated footnote
`textGen`	element_text for genotype labels
`textEnv`	element_text for environment labels

Value

A biplot of class `ggplot`

References

Yan W, Kang M (2003). *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists*. CRC Press.

Examples

```
data(Ontario)
GGE1<-GGEModel(Ontario)
GGEPlot(GGE1)
```

`MeanStability` *Mean vs. Stability Biplot*

Description

Evaluating cultivars based on both average yield and stability

Usage

```
MeanStability(GGEModel, ...)
```

Arguments

`GGEModel`	An object of class `GGEModel` or `gge`
`...`	Other arguments sent to `GGEPlot`

Examples

```
data(Ontario)
GGE1<-GGEModel(Ontario)
MeanStability(GGE1)
```

`Ontario` *Ontario winter wheat (1993)*

Description

The sample data are yields from the 1993 Ontario winter wheat (Triticum aestivum L.) performance trials, in which 18 cultivars were tested at nine locations (Yan and Kang 2003). Duplicated from the archived package 'GGEBiplotGUI'.

Usage

```
data(Ontario)
```

Format

A data frame with 18 observations on the following 10 variables.

Source

Yan W, Kang MS (2003). "GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists." *CRC Press, Boca Raton, FL, USA*.

Examples

```
data(Ontario)
```

`RankEnv` *Ranking Environments Biplot*

Description

Ranking environments with respect to the ideal environment

Usage

```
RankEnv(GGEModel, ...)
```

Arguments

`GGEModel`	An object of class `GGEModel` or `gge`
`...`	Other arguments sent to `GGEPlot`

Examples

```
data(Ontario)
GGE1<-GGEModel(Ontario)
RankEnv(GGE1)
```

`RankGen` *Ranking genotypes with respect to the ideal genotype*

Description

Ranking genotypes with respect to the ideal genotype

Usage

```
RankGen(GGEModel, axis_expand = 1.4, ...)
```

Arguments

`GGEModel`	An object of class `GGEModel` or `gge`
`axis_expand`	multiplication factor to expand the axis limits by to enable fitting of labels. Defaults to 1.4 for genotype ranking plot as the circles usually extend beyond limits of the other biplot types.
`...`	Other arguments sent to `GGEPlot`

Examples

```
data(Ontario)
GGE1<-GGEModel(Ontario)
RankGen(GGE1)
```

`stattable` *Produce a two-way summary table of results*

Description

Transforms raw data into a simple two-way table for use in `GGEModel` with row names and column names. By design rather than just a side-effect of combining `list` with `tapply`

Usage

```
stattable(rowfactor, columnfactor, outcome, FUN = mean, ...)
```

Arguments

`rowfactor`	variable to be included in the rows
`columnfactor`	variable to be included in the columns
`outcome`	vector containing outcome values
`FUN`	name of summary function to use
`...`	other arguments for `FUN`

Examples

```
simdata<-data.frame(expand.grid(Genotype=1:10,Environment=1:10,Rep=1:3),Outcome=rnorm(300))
meantab<-stattable(simdata$Genotype,simdata$Environment,simdata$Outcome,FUN=mean,na.rm=TRUE)
GGEPlot(GGEModel(meantab))
```

`WhichWon` *Which Won Where/What Biplot*

Description

Identifying the 'best' cultivar in each environment

Usage

```
WhichWon(GGEModel, ...)
```

Arguments

`GGEModel`	An object of class `GGEModel` or `gge`
`...`	Other arguments sent to `GGEPlot`

Examples

```
data(Ontario)
GGE1<-GGEModel(Ontario)
WhichWon(GGE1)
```

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