Package ‘GGEBiplots’

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**CompareGenets**

*Compare two genotypes biplot*

**Description**

Compare the performance of two genotypes across all environments

**Usage**

```r
CompareGenets(GGEMo델, G1, G2, ...)
```

**Arguments**

- `GGEMo델`: An object of class `GGEMo델` 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**

```r
library(GGEBiplotGUI)
data(Ontario)
GGEmodel <- GGEMoдель(Ontario)
CompareGenets(GGEmodel,"cas","luc")
```

---

**DiscRep**

*Discrimination vs. representativeness biplot*

**Description**

Evaluating the environments based on both discriminating ability and representativeness

**Usage**

```r
DiscRep(GGEMo델, ...)
```

**Arguments**

- `GGEMoдель`: An object of class `GGEMoдель` or `gge`.
- `...`: Other arguments sent to `GGEPlot`.

**Examples**

```r
```
EnvRelationship

**Examples**

```r
library(GGEBiplotGUI)
data(Ontario)
GGE1<-GGEModel(Ontario)
DiscRep(GGE1)
```

**Description**

Relationship between environments

**Usage**

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

**Arguments**

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

**Examples**

```r
library(GGEBiplotGUI)
data(Ontario)
GGE1<-GGEModel(Ontario)
EnvRelationship(GGE1)
```

---

ExamineEnv

**Examine an environment**

**Description**

Ranking the cultivars based on their performance in any given environment

**Usage**

```r
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

```r
library(GGEBiplotGUI)
data(Ontario)
GGEl<-GGEModel(Ontario)
ExamineEnv(GGE1,"WP93")
```

ExamineGen

*Examine a genotype biplot*

Description

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

Usage

```r
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 GGEPPlot

Examples

```r
library(GGEBiplotGUI)
data(Ontario)
GGEl<-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 GGEBiplot. For dealing with missing data then a better implementation is available through gge.

Usage

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

**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 `GGModel` 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**


**Examples**

```r
library(GGEBiplotGUI)
data(Ontario)
GGEl<-GGModel(Ontario)
GGEPlot(GGE1)
```
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

```r
GGEPlot(GGEModel, type = 1, d1 = 1, d2 = 2, selectedE = NA,
        selectedG = NA, selectedG1 = NA, selectedG2 = NA,
        colGen = "forestgreen", colEnv = "blue", colSegment = "red",
        colHull = "black", sizeGen = 4, sizeEnv = 4, largeSize = 4.5,
        axis_expand = 1.2, axislabels = TRUE, axes = TRUE, limits = TRUE,
        titles = TRUE, footnote = TRUE)
```

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`
- `colGen`: colour for genotype attributes on biplot. Defaults to "forestgreen"
colEnv  colour for environment attributes on biplot. Defaults to "blue"
colSegment  colour for segment or circle lines. Defaults to "red"
colHull  colour for hull when type=6. Defaults to "black"
sizeGen  text size for genotype labels. Defaults to 4
sizeEnv  text size for environment labels. Defaults to 4
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

Value

A biplot of class ggplot

References


Examples

library(GGEBiplotGUI)
data(Ontario)
GGE1<-GGEModel(Ontario)
GGEPlot(GGE1)

#using 'gge' instead

library(gge)
GGE2<-gge(as.matrix(Ontario))
GGEPlot(GGE2)
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**
```r
library(GGEBiplotGUI)
data(Ontario)
GGE1 <- GGEModel(Ontario)
MeanStability(GGE1)
```

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**
```r
library(GGEBiplotGUI)
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_expanded = 1.4, ...)
```

**Arguments**

- **GGEModel**: An object of class GGEModel or gge
- **axis_expanded**: 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**

```
library(GGEBiplotGUI)
data(Ontario)
GGEl <- 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))

<table>
<thead>
<tr>
<th>WhichWon</th>
<th>Which Won Where/What Biplot</th>
</tr>
</thead>
</table>

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

library(GGEBiplotGUI)
data(Ontario)
GGE1<-GGEModel(Ontario)
WhichWon(GGE1)
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