Package ‘GGEBiplots’

February 9, 2022

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), grDevices (>= 3.3.1), stats (>= 3.3.1), grid (>= 3.3.1)

RoxygenNote 7.1.2

NeedsCompilation no

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Repository CRAN

Date/Publication 2022-02-09 16:20:02 UTC

R topics documented:

<table>
<thead>
<tr>
<th>Topic</th>
<th>Pages</th>
</tr>
</thead>
<tbody>
<tr>
<td>CompareGens</td>
<td>2</td>
</tr>
<tr>
<td>DiscRep</td>
<td>2</td>
</tr>
<tr>
<td>EnvRelationship</td>
<td>3</td>
</tr>
<tr>
<td>ExamineEnv</td>
<td>3</td>
</tr>
<tr>
<td>ExamineGen</td>
<td>4</td>
</tr>
<tr>
<td>GGEModel</td>
<td>4</td>
</tr>
<tr>
<td>GGEPlot</td>
<td>6</td>
</tr>
<tr>
<td>MeanStability</td>
<td>8</td>
</tr>
<tr>
<td>Ontario</td>
<td>8</td>
</tr>
</tbody>
</table>
CompareGens

**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**

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

DiscRep

**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`
**EnvRelationship**

**Examples**

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

---

**EnvRelationship**  
*Relationship between environments*

**Description**

Relationship between environments

**Usage**

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

**Arguments**

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

---

**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
data(Ontario)
GGE1 <- GGEModel(Ontario)
ExamineEnv(GGE1)
```
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**


**Examples**

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

GGE bipo[ets 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 genotypes 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 and not equal to selectedG1

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

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

Examples
data(Ontario)
RankEnv

Description
Ranking environments with respect to the ideal environment

Usage
RankEnv(GGEModel, ...)

Arguments
GGEModel  An object of class GGEModel or gge
...

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

RankGen

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.
...

Examples
data(Ontario)
GGE1<-GGEModel(Ontario)
RankGen(GGE1)
sttable  

Produce a two-way summary table of results

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

Usage
\begin{verbatim}
sttable(rowfactor, columnfactor, outcome, FUN = mean, ...)
\end{verbatim}

Arguments
- \texttt{rowfactor} variable to be included in the rows
- \texttt{columnfactor} variable to be included in the columns
- \texttt{outcome} vector containing outcome values
- \texttt{FUN} name of summary function to use
- \texttt{...} other arguments for \texttt{FUN}

Examples
\begin{verbatim}
simdata<-data.frame(expand.grid(Genotype=1:10,Environment=1:10,Rep=1:3),Outcome=rnorm(300))
meantab<-sttable(simdata$Genotype,simdata$Environment,simdata$Outcome,FUN=mean,na.rm=TRUE)
GGEPlot(GGEModel(meantab))
\end{verbatim}

WhichWon  

Which Won Where/What Biplot

Description
Identifying the 'best' cultivar in each environment

Usage
\begin{verbatim}
WhichWon(GGEModel, ...)
\end{verbatim}

Arguments
- \texttt{GGEModel} An object of class \texttt{GGEModel} or \texttt{gge}
- \texttt{...} Other arguments sent to \texttt{GGEPlot}

Examples
\begin{verbatim}
data(Ontario)
GGE1<-GGEModel(Ontario)
WhichWon(GGE1)
\end{verbatim}
Index

* 2way  sttable, 10
* Biplot  GGEPlot, 6
* GGEBiplotGUI  sttable, 10
* GGE  
  CompareGens, 2
  DiscRep, 2
  EnvRelationship, 3
  ExamineEnv, 3
  ExamineGen, 4
  GGEModel, 4
  GGEPlot, 6
  MeanStability, 8
  RankEnv, 9
  RankGen, 9
  WhichWon, 10
* biplot  GGEModel, 4
* datasets  Ontario, 8
* ggplot2  GGEModel, 4
* means  sttable, 10
* statistics  sttable, 10
* summary  sttable, 10
* table  sttable, 10

  CompareGens, 2, 6
  DiscRep, 2, 7
  EnvRelationship, 3, 6
  ExamineEnv, 3, 6
  ExamineGen, 4, 6

ga, 4, 6
GGEModel, 4, 6, 10
GGEPlot, 2–5, 6, 8–10
MeanStability, 7, 8
Ontario, 8
RankEnv, 7, 9
RankGen, 7, 9
sttable, 10
WhichWon, 6, 10

stattable, 10

stattable, 10