

# Package ‘GGEbiplots’

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**Title** GGE Biplots with 'ggplot2'

**Version** 0.1.1

**Description** Genotype plus genotype-by-environment (GGE) biplots rendered using 'ggplot2'. Provides a command line interface to all of the functionality contained within '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), GGEbiplotGUI (>=  
1.0-9), grid (>= 3.3.1), utils (>= 3.3.1), gge (>= 1.2)

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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 <a href="#">GGEPlot</a>

### Examples

```
library(GGEBiplotGUI)
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 <a href="#">GGEPlot</a>

**Examples**

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

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EnvRelationship	<i>Relationship between environments</i>
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**Description**

Relationship between environments

**Usage**

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

**Arguments**

GGEModel	An object of class GGEModel or gge
...	Other arguments sent to <a href="#">GGEPlot</a>

**Examples**

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

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ExamineEnv	<i>Examine an environment</i>
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**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 <a href="#">GGEPlot</a>

**Examples**

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

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ExamineGen	<i>Examine a genotype biplot</i>
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**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 <a href="#">GGEPlot</a>

**Examples**

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

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GGEModel	<i>Produces genotype plus genotype-by-environment model from a 2-way table of means</i>
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**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**

```
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 <code>GGEP1ot</code> 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. <http://dx.doi.org/10.2134/agronj2002.0990>

**Examples**

```
library(GGEBiplotGUI)
data(Ontario)
GGE1<-GGEModel(Ontario)
GGEP1ot(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

```
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

<code>GGEModel</code>	An object of class <code>GGEModel</code> or <code>gge</code>
<code>type</code>	type of biplot to produce. <ol style="list-style-type: none"> <li>1. Basic biplot.</li> <li>2. Examine environment. See <a href="#">ExamineEnv</a></li> <li>3. Examine genotype. See <a href="#">ExamineGen</a></li> <li>4. Relationship among environments. See <a href="#">EnvRelationship</a></li> <li>5. Compare two genotypes. See <a href="#">CompareGens</a></li> <li>6. Which won where/what. See <a href="#">WhichWon</a></li> <li>7. Discrimination vs. representativeness. See <a href="#">DiscRep</a></li> <li>8. Ranking environments. See <a href="#">RankEnv</a></li> <li>9. Mean vs. stability. See <a href="#">MeanStability</a></li> <li>10. Ranking genotypes See <a href="#">RankGen</a></li> </ol>
<code>d1</code>	PCA component to plot on x axis. Defaults to 1
<code>d2</code>	PCA component to plot on y axis. Defaults to 2
<code>selectedE</code>	name of the environment to examine when <code>type=2</code> . Must be a string which matches an environment label
<code>selectedG</code>	name of the genotype to examine when <code>type=3</code> . Must be a string which matches a genotype label
<code>selectedG1</code>	name of a genotype to compare when <code>type=5</code> . Must be a string which matches a genotype label
<code>selectedG2</code>	name of a genotype to compare when <code>type=5</code> . Must be a string which matches a genotype label and not equal to <code>selectedG1</code>
<code>colGen</code>	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 footbote

### 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

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

#using 'gge' instead

library(gge)
GGE2<-gge(as.matrix(Ontario))
GGEPlot(GGE2)
```

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MeanStability	<i>Mean vs. Stability Biplot</i>
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**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 <a href="#">GGEPlot</a>

**Examples**

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

---

RankEnv	<i>Ranking Environments Biplot</i>
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**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 <a href="#">GGEPlot</a>

**Examples**

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



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RankGen	<i>Ranking genotypes with respect to the ideal genotype</i>
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**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 <a href="#">GGEPlot</a>

**Examples**

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

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stattable	<i>Produce a two-way summary table of results</i>
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**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))
```

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WhichWon

*Which Won Where/What Biplot*

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**Description**

Identifying the 'best' cultivar in each environment

**Usage**

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

**Arguments**

GGEModel	An object of class GGEModel or gge
...	Other arguments sent to <a href="#">GGEPlot</a>

**Examples**

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

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