

# Package: gge (via r-universe)

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**Type** Package

**Title** Genotype Plus Genotype-by-Environment Biplots

**Version** 1.8

**Description** Create biplots for GGE (genotype plus genotype-by-environment) and GGB (genotype plus genotype-by-block-of-environments) models. See Laffont et al. (2013) <[doi:10.2135/cropsci2013.03.0178](https://doi.org/10.2135/cropsci2013.03.0178)>.

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**URL** <https://kwstat.github.io/gge/>, <http://kwstat.github.io/gge/>

**BugReports** <https://github.com/kwstat/gge/issues>

**Imports** nipals, reshape2

**Suggests** agridat, knitr, lattice, rgl, rmarkdown, testthat

**VignetteBuilder** knitr

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**Repository** <https://kwstat.r-universe.dev>

**RemoteUrl** <https://github.com/kwstat/gge>

**RemoteRef** HEAD

**RemoteSha** 0e9e6323f254b9e51c3f34b61b1a494442e63328

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`gge`*GGE and GGB biplots*

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**Description**

Fit a GGE (genotype + genotype \* environment) model and display the results.

**Usage**

```
gge(x, ...)  
  
## S3 method for class 'data.frame'  
gge(x, formula, gen.group = NULL, env.group = NULL, ggb = FALSE, ...)  
  
## S3 method for class 'formula'  
gge(formula, data, gen.group = NULL, env.group = NULL, ggb = FALSE, ...)  
  
## S3 method for class 'matrix'  
gge(  
  x,  
  center = TRUE,  
  scale = TRUE,  
  gen.group = NULL,  
  env.group = NULL,  
  ggb = FALSE,  
  comps = c(1, 2),  
  method = "svd",  
  ...  
)  
  
## S3 method for class 'gge'  
plot(x, main = substitute(x), ...)  
  
## S3 method for class 'gge'  
biplot(  
  x,  
  main = substitute(x),  
  subtitle = "",  
  xlab = "auto",  
  ylab = "auto",  
  cex.gen = 0.6,  
  cex.env = 0.5,  
  col.gen = "darkgreen",  
  col.env = "orange3",  
  pch.gen = 1,  
  lab.env = TRUE,  
  comps = 1:2,
```

```

    flip = "auto",
    origin = "auto",
    res.vec = TRUE,
    hull = FALSE,
    zoom.gen = 1,
    zoom.env = 1,
    ...
)

biplot3d(x, ...)

## S3 method for class 'gge'
biplot3d(
  x,
  cex.gen = 0.6,
  cex.env = 0.5,
  col.gen = "darkgreen",
  col.env = "orange3",
  comps = 1:3,
  lab.env = TRUE,
  res.vec = TRUE,
  zoom.gen = 1,
  ...
)

```

### Arguments

<code>x</code>	A matrix or data.frame.
<code>...</code>	Other arguments (e.g. <code>maxiter</code> , <code>gramschmidt</code> )
<code>formula</code>	A formula
<code>gen.group</code>	genotype group
<code>env.group</code>	env group
<code>ggb</code>	If TRUE, fit a GGB biplot model.
<code>data</code>	Data frame
<code>center</code>	If TRUE, center values for each environment
<code>scale</code>	If TRUE, scale values for each environment
<code>comps</code>	Principal components to use for the biplot. Default <code>c(1,2)</code> .
<code>method</code>	method used to find principal component directions. Either "svd" or "nipals".
<code>main</code>	Title, by default the name of the data. Use NULL to suppress the title.
<code>subtitle</code>	Subtitle to put in front of options. Use NULL to suppress the subtitle.
<code>xlab</code>	Label along axis. Default "auto" shows percent of variation explained. Use NULL to suppress.
<code>ylab</code>	Label along axis. Default "auto" shows percent of variation explained. Use NULL to suppress.

cex.gen	Character expansion for genotype labels, default 0.6. Use 0 to omit genotype labels.
cex.env	Character expansion for environment labels/symbols. Use lab.env=FALSE to omit labels.
col.gen	Color for genotype labels. May be a single color for all genotypes, or a vector of colors for each genotype.
col.env	Color for environments. May be a single color for all environments, or a vector of colors for each environment.
pch.gen	Plot character for genotypes
lab.env	Label environments if TRUE.
flip	If "auto" then each axis is flipped so that the genotype ordinate is positively correlated with genotype means. Can also be a vector like c(TRUE,FALSE) for manual control.
origin	If "auto", the plotting window is centered on genotypes, otherwise the origin is at the middle of the window.
res.vec	If TRUE, for each group, draw residual vectors from the mean of the locs to the individual locs.
hull	If TRUE, show a which-won-where polygon.
zoom.gen	Zoom factor for manual control of genotype xlim,ylim The default is 1. Values less than 1 may be useful if genotype names are long.
zoom.env	Zoom factor for manual control of environment xlim,ylim. The default is 1. Values less than 1 may be useful if environment names are long. Not used for 3D biplots.

### Details

If there is replication in G\*E, then the replications are averaged together before constructing the biplot.

The singular value decomposition of  $x$  is used to calculate the principal components for the biplot. Missing values are NOT allowed.

The argument `method` can be either 'svd' for complete-data or 'nipals' for missing-data.

### Value

A list of class `gge` containing:

<code>x</code>	The filled-in data
<code>x.orig</code>	The original data
<code>genCoord</code>	genotype coordinates
<code>locCoord</code>	loc coordinates
<code>blockCoord</code>	block coordinates
<code>gen.group</code>	If not NULL, use this to specify a column of the data.frame to classify genotypes into groups.

env.group	If not NULL, use this to specify a column of the data.frame to classify environments into groups.
ggb	If TRUE, create a GGB biplot
genMeans	genotype means
mosdat	mosaic plot data
R2	variation explained by each PC
center	Data centered?
scale	Data scaled?
method	Method used to calculate principal components.
pctMiss	Percent of x that is missing values
maxPCs	Maximum number of PCs

### Author(s)

Kevin Wright, Jean-Louis Laffont  
Jean-Louis Laffont, Kevin Wright

### References

Jean-Louis Laffont, Kevin Wright and Mohamed Hanafi (2013). Genotype + Genotype x Block of Environments (GGB) Biplots. *Crop Science*, 53, 2332-2341. doi:10.2135/cropsci2013.03.0178.

Kroonenberg, Pieter M. (1997). *Introduction to Biplots for GxE Tables*, Research Report 51, Centre for Statistics, The University of Queensland, Brisbane, Australia. <https://three-mode.leidenuniv.nl/document/biplot.pdf>

Yan, W. and Kang, M.S. (2003). *GGE Biplot Analysis*. CRC Press.

### Examples

```
# Example 1. Data is a data.frame in 'matrix' format
B <- matrix(c(50, 67, 90, 98, 120,
             55, 71, 93, 102, 129,
             65, 76, 95, 105, 134,
             50, 80, 102, 130, 138,
             60, 82, 97, 135, 151,
             65, 89, 106, 137, 153,
             75, 95, 117, 133, 155), ncol=5, byrow=TRUE)
rownames(B) <- c("G1", "G2", "G3", "G4", "G5", "G6", "G7")
colnames(B) <- c("E1", "E2", "E3", "E4", "E5")

library(gge)
m1 = gge(B)
plot(m1)
biplot(m1, main="Example biplot")
# biplot3d(m1)

if(require(agridat)){
  # crossa.wheat biplot
```

```
# Specify env.group as column in data frame
data(crossa.wheat)
dat2 <- crossa.wheat
m2 <- gge(dat2, yield~gen*loc, env.group=locgroup, scale=FALSE)
plot(m2)
biplot(m2, lab.env=TRUE, main="crossa.wheat")
# biplot3d(m2)
}
```

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RedGrayBlue

*Function to create a Red-Gray-Blue palette*

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### **Description**

A function to create a Red-Gray-Blue palette.

### **Usage**

```
RedGrayBlue(n)
```

### **Arguments**

n                      Number of colors to create

### **Details**

Using gray instead of white allows missing values to appear as white (actually, transparent).

### **Value**

A vector of n colors.

### **Author(s)**

Kevin Wright

### **Examples**

```
pie(rep(1,11), col=RedGrayBlue(11))
title("RedGrayBlue(11)")
```

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