Package ‘gge’

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Title  Genotype Plus Genotype-by-Environment Biplots
Version  1.4
Date  2018-05-12
Description  Create biplots for GGE (genotype plus genotype-by-environment) and GGB (genotype plus genotype-by-block-of-environments) models.
Type  Package
Imports nipals, rgl, reshape2
Suggests agridat, knitr, lattice, testthat
License  GPL-3
LazyData  yes
URL  https://github.com/kwstat/gge
BugReports  https://github.com/kwstat/gge/issues
VignetteBuilder  knitr
RoxygenNote  6.0.1
NeedsCompilation  no
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**GGE and GGB biplots**

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

### Usage

```r
gge(x, ...)  
```

**Description**

GGE and GGB biplots

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

### Arguments

- `x`: A matrix or data.frame.
- `...`: Other arguments (e.g. `maxiter`, `gramschmidt`)
- `formula`: A formula
- `data`: Data frame
- `gen.group`: genotype group
- `env.group`: env group
center
If TRUE, center values for each environment
scale
If TRUE, scale values for each environment
comps
Principal components to use for the biplot. Default c(1,2).
method
method used to find principal component directions
main
Title, by default the name of the data. Use NULL to suppress the title.
subtitle
Subtitle to put in front of options. Use NULL to suppress the subtitle.
xlab
Label along axis. Default "auto" shows percent of variation explained. Use NULL to suppress.
ylab
Label along axis. Default "auto" shows percent of variation explained. Use NULL to suppress.
cex.gen
Character expansion for genotypes, default 0.6. Use 0 to omit genotypes.
cex.env
Character expansion for environments
col.gen
Color for genotypes
col.env
Color for environments
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:

x The filled-in data
x.orig The original data
genCoord genotype coordinates
locCoord loc coordinates
blockCoord block coordinates
gen.group If not NULL, this specifies a classification of genotypes into groups.
env.group If not NULL, this specifies a classification of environments into groups.
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


Examples

# Example 1. Data is a data.frame in 'matrix' format
B <- matrix(c(50, 67, 90, 98, 128,
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)
RedGrayBlue

Function to create a Red-Gray-Blue palette

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

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