# Package 'biplotbootGUI'

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**Encoding** latin1

**Type** Package

**Title** Bootstrap on Classical Biplots and Clustering Disjoint Biplot

**Version** 1.1

**Date** 2015-06-20

**Author** Ana Belen Nieto Librero<ananieto@usal.es>, Purificacion Galindo Villardon<pgalindo@usal.es>

**Maintainer** Ana Belen Nieto Librero <ananieto@usal.es>

**Description** A GUI with which the user can construct and interact with Bootstrap methods on Classical Biplots and with Clustering and/or Disjoint Biplot.

**License** GPL (>= 2)

**Depends** R (>= 3.1.1)

**Imports** rgl, tkrplot, tcltk, tcltk2, shapes, cluster, dendroextras, MASS

**SystemRequirements** Tcl/Tk package BWidget.

**Repository** CRAN

**NeedsCompilation** no

**Date/Publication** 2015-06-22 01:46:27

## R topics documented:

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| biplotbootGUI-package | *biplotbootGUI: Bootstrap on Classical Biplots and Clustering Disjoint Biplot* |

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**Description**

The biplotbootGUI package is a graphical user interface to construct and interact with Classical Biplots and, combined with Bootstrap methods, provides confidence intervals based on percentiles, t-bootstrap and BCa to measure the accuracy of the estimators of the parameters given by them.

**Details**

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|---|---|
| Package: | biplotbootGUI |
| Type: | Package |
| Version: | 1.1 |
| Date: | 2015-06-20 |
| License: | GPL>=2 |

**Author(s)**

Ana Belen Nieto Librero <ananieto@usal.es>, Purificacion Galindo Villardon <pgalindo@usal.es>

Maintainer: Ana Belen Nieto Librero <ananieto@usal.es>

**References**

- Gabriel, K. R. (1971). The Biplot graphic display of matrices with applications to principal components analysis. Biometrika, 58(3), 453-467.
- Galindo, M. P. (1986). Una alternativa de representacion simultanea: HJ-Biplot. Questiio, 10(1), 13-23.
- Efron, B. (1979). Bootstrap methods: Another look at the jackknife. Annals of Statistics, 7, 1-26.
- Efron, B. (1987). Better bootstrap confidence intervals. Journal of the American Statistical Association, 82, 171-185.
- Efron, B., & Tibshirani, R. J. (1993). An introduction into the bootstrap. New York: Chapman and Hall.
- Nieto, A. B., & Galindo, M. P., & Leiva, V., & Vicente-Galindo, P. (2014). A methodology for biplots based on bootstrapping with R. Revista Colombiana de Estadistica, 37(2), 367-397.

**Examples**

```
data(iris)
biplotboot(iris[,-5])
```

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| biplotboot | *biplotbootGUI: Bootstrap on Classical Biplots and Clustering Disjoint Biplot* |
|---|---|

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## Description

The biplotboot function is a graphical user interface to construct and interact with Classical Biplots and, combined with Bootstrap methods, provides confidence intervals based on percentiles and t-bootstrap to measure the accuracy of the estimators of the parameters given by them.

## Usage

```
biplotboot(x)
```

## Arguments

x                    A data frame with the information to be analyzed

## Details

When the function is launched, firstly, it is necessary to select the number of resamples to be extracted, the conficende level to calculate the intervals presented in the results and the parameters whose inferential form want to be calculated. Then, an option window is displayed where you can change the color, the size, the label and/or the symbol of an element or of a set of elements; to select the kind of Biplot factorization to be applied, to select the transformation data, to change the window size containing the graphs and to tick the checkbox to show the axes in the graph. Press the Graph button and then choose the number of axes to be retained. When the graph will be shown, the function will allow you to change characteristics of the points with the mouse. Press the right mouse button and a window will be displayed to change the color, the size, the label and/or the symbol of the nearest point of position clicked. Press the left mouse button and a window will be displayed to select one option: Change the position label, Remove label or Do nothing. It is also possible to select the dimensions shown in the graph and to change the limits of the axes. In the window there are five menus with their corresponding submenus:

- File
    - Copy image
    - Save image
        * PDF file
        * Eps file
        * Png file
        * Jpg/Jpeg file
    - Exit
- 3D
    - 3D
- Projections

        – Variables
        – Back to original data
- Options
        – Change title
        – Show/Hide axes
- Cluster
        – Hierarchical cluster with biplot coordinates
        – K-means with biplot coordinates
        – K-medoids with biplot coordinates
        – Back to original graph

The File menu provides different options to save the graph and permits to exit the program. The second menu shows the graph in 3 dimensions. The third menu allows the user to project the individuals onto the direction representing one variable selected from a listbox. This menu permits to go back to original graph. The following menu permits to change the title and to show/hide the axes in the graph. The fifth menu allows the user to analyze the biplot coordinates with clustering techniques. The results in an inferential form have saved in a file and together with it graphs with histograms and QQ-plots generated with the bootstrap replications are saved.

### Value

A graph showing the data representation, an output file containing the contributions, qualities of representation, goodness of fit, coordinates and eigen values and another output file containing these results in an inferential form.

### Author(s)

Ana Belen Nieto Librero <ananieto@usal.es>, Purificacion Galindo Villardon <pgalindo@usal.es>

### References

- Gabriel, K. R. (1971). The Biplot graphic display of matrices with applications to principal components analysis. Biometrika, 58(3), 453-467.
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### Examples

```
data(iris)
biplotboot(iris[,-5])
```

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CDBiplot                    *Clustering and/or Disjoint Biplot*

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## Description

The CDBiplot function is a graphical user interface to construct and interact with Clustering and/or Disjoint Biplot.

## Usage

```
CDBiplot(data, clase)
```

## Arguments

data            A data frame with the information to be analyzed

clase           A vector containing the real classification of the objects in the data

## Details

When the function is launched, firstly, it is necessary to select the kind of analysis to be used on the data. Then, a window to select the number of clusters, components, the tolerance, the number of iterations and the repetitions of the algorithm. Press the OK button and the graph will be shown. Press the left mouse button and a window will be displayed to select one option: Change the position label, Remove label or Do nothing. It is also possible to select the dimensions shown in the graph and to change the limits of the axes. In the window there are four menus:

- File
    - Copy image
    - Save image
        * PDF file
        * Eps file
        * Png file
        * Jpg/Jpeg file
    - Exit
- 3D
    - 3D
- Options
    - Change title
    - Show/Hide axes
    - Show/Hide variables
    - Show/Hide row labels
- Cluster
    - Convex-hull

The File menu provides different options to save the graph and permits to exit the program. The second menu shows the graph in 3 dimensions. The third menu allows the user to change the title and to show/hide the axes, the variables and the row labels in the graph. The last menu permits the user to draw (filled or empty) convex-hull on each cluster. The program saves a file containing the main results of the analysis.

**Value**

A graph showing the data representation and an output file containing the information about the results.

**Author(s)**

Ana Belen Nieto Librero `<ananieto@usal.es>`, Purificacion Vicente Galindo `<purivg@usal.es>`, Purificacion Galindo Villardon `<pgalindo@usal.es>`

**References**

- Gabriel, K. R. (1971). The Biplot graphic display of matrices with applications to principal components analysis. Biometrika, 58(3), 453-467.

- Galindo, M. P. (1986). Una alternativa de representacion simultanea: HJ-Biplot. Questiio, 10(1), 13-23.

- Vichi, M and Saporta, G. (2009). Clustering and disjoint principal component analysis. *Computational Statistics and Data Analysis*, 53, 3194-3208.

- Macedo, E. and Freitas, A. (2015). The alternating least-squares algorithm for CDPCA. *Communications in Computer and Information Science (CCIS), Springer Verlag (to appear)*.

**Examples**

```
data(iris)
CDBiplot(iris[,-5], iris[,5])
```

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