Package ‘prettyGraphs’

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Author Derek Beaton
Maintainer Derek Beaton <exposition.software@gmail.com>
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contributionBars

Description

Produces bar charts for multivariate analyses. Plots the contribution to the variance from each data point for upwards of two axes (components).

Usage

contributionBars(factor_scores, contributions, x_axis = 1, y_axis = 2, col = NULL, main = NULL, upper = 'steelblue4', lower = 'firebrick2', threshold = NULL, sortcontributions = TRUE, pretty = FALSE, show.bg.bars = FALSE)

Arguments

factor_scores  The factor scores, or x- and y-axis points of a data set.
contributions  The amount of contribution to the variance (between 0-1) by each data point.
x_axis  Which axis is the x-axis? Default is 1.
y_axis  Which axis is the y-axis? Default is 2.
col  A single-column matrix of colors for each data point.
main  A title to be placed at the top of the graph.
upper  The color used to identify the upper bound items that contribute above average variance.
lower  The color used to identify the lower bound items that contribute above average variance.
threshold  A threshold (between 0-1) to draw upper and lower bounds for important items. Default is 1/number of items.
sortcontributions  boolean, if TRUE, items will be sorted by contribution. if FALSE, items will appear in their row order.
pretty  a boolean. If FALSE, use the current version. If TRUE, make the bars with prettyBars.
show.bg.bars  a boolean. Only used if pretty is TRUE. If TRUE, background bars are plotted for a fill effect.

Author(s)

Derek Beaton
correlationPlotter

correlationPlotter correlationPlotter

Description

Computes and plots a correlation circle (used in multivariate analyses). Correlation is computed between measured items and components (factors, dimensions, principal axes, etc...).

Usage

correlationPlotter(data_matrix, factor_scores, x_axis = 1, y_axis = 2, col = NULL, pch = NULL, xlab = NULL, ylab = NULL, main = "", asp = 1, dev.new = TRUE)

Arguments

data_matrix A set of data (i.e., original measures and observations)
factor_scores One set of factor scores that were computed from the original data matrix.
x_axis Which axis is the x-axis? Default is 1.
y_axis Which axis is the y-axis? Default is 2.
col A single-column matrix of colors for each data point.
pch A single-column matrix of pch for each data point. Indicates which point style to use for each item. See par.
xlab A label to be placed along the x-axis.
ylab A label to be placed along the y-axis.
main A title to be placed at the top of the graph.
asp numeric. Aspect ratio (see asp in par).
dev.new boolean. If TRUE, dev.new is called internally to create new device. If FALSE, a device must already be open.

Author(s)

Derek Beaton

colorCreate

colorCreate
colorCreate

colorCreate

colorCreate

Description

Produces a color vector for items by using a design matrix.
Usage

createColorVectorsByDesign(design_matrix, hsv = TRUE, offset = NULL)

Arguments

design_matrix  A dummy coded design matrix.
hsv            a boolean. If TRUE, use prettyGraphsHSVColorSelection. If FALSE, use prettyGraphsColorSelection.
offset         numeric. An offset value to be passed to prettyGraphsHSVColorSelection or prettyGraphsColorSelection.

Value

Produces a list with the following items

oc             The colors of the observations (based on group)
 gc            The colors of the groups

Author(s)

Derek Beaton

---

Description

Computes the x- and y- axis constraints for all prettyGraphs functions.

Usage

minmaxHelper(mat1, mat2 = NULL, axis1 = 1, axis2 = 2, findBounds = TRUE)

Arguments

mat1           Matrix that will be plotted. Must be at least 2 rows by 2 columns.
mat2           if NULL, mat2=mat2. Second matrix that will be plotted (if a biplot). Must be at least 2 rows by 2 columns.
axis1          Which column of the matrix will be the x-axis? Default = 1.
axis2          Which column of the matrix will be the y-axis? Default = 2.
findBounds     a boolean. If TRUE, min and max values are found for positive and negative on axis1 and axis2. If FALSE, one value is used for all constraints.
**Value**

```
minMaxList  # A list with the following values: minx, miny, maxx, maxy
```

**Author(s)**

Derek Beaton

**Examples**

```r
data(beavers)
minMaxList <- minmaxHelper(as.matrix(beaver1),as.matrix(beaver1),1,2)
```

---

**Description**

Computes and plots a peeled hull around a set of points onto a current graphics device.

**Usage**

```r
peeledHull(data_matrix, x_axis = 1, y_axis = 2, percentage = 1, col = "black", lwd = 3, lty = 1)
```

**Arguments**

- `data_matrix` A set of data you would like to plot on 2 dimensions (e.g., a scatter plot). Can be original data or factor scores or anything with at least 2 columns.
- `x_axis` Which axis is the x-axis? Default is 1.
- `y_axis` Which axis is the y-axis? Default is 2.
- `percentage` The percentage of points that should be enveloped by the hull.
- `col` The color of the hull (see `col` in `plot()`).
- `lwd` The thickness of the hull line (see `lwd` in `plot()`).
- `lty` The line type (see `lty` in `plot()`).

**Note**

The code for this function was (barely) adapted from Michael Greenacre’s book on correspondence analysis. All credit for this code should go to Michael Greenacre; I only turned it into a function. The original code can be found at [http://carme-n.org/?sec=code2](http://carme-n.org/?sec=code2)

**Author(s)**

Derek Beaton turned Michael Greenacre’s code into a function.

**References**

prettyBars creates simple, crisp, publication-style quality bar graphs.

Usage

prettyBars(data, axis = 1, cex.names = 0.5, fg.col = NULL, axis.lims = NULL,
show.bg.bars = FALSE, threshold.line = FALSE, main = "", bg.border = "white",
bg.col = NULL, bg.lims = NULL, sort.data = TRUE, horiz = TRUE, dev.new = TRUE)

Arguments

data A set of data you would like to plot with bars for 1 dimension. Can be original
data or factor scores or anything with at least 1 column.
axis which axis (column of data) should be plotted?
cex.names size of the text
fg.col a matrix (single column) of colors for bars corresponding to rows of data.
axis.lims two values in the form of c(min, max) for plot limits. If NULL, the min and
max are computed.
show.bg.bars a set of bars to be plotted under the bars in data. Used for a fill effect.
threshold.line boolean. If TRUE, a line perpendicular to the bars is plotted. The lines appear
at bg.lims.
main A title to be placed at the top of the graph.
bg.border color for show.bg.bars borders (see border in barplot)
bg.col a matrix (single column) of colors for background bars to be plotted under
fg.col.
bg.lims two values in the form of c(min, max) for where to plot background bars or
threshold line.
sort.data a boolean. Will sort the bars by descending values.
horiz see horiz in barplot.
dev.new boolean. If TRUE, dev.new is called internally to create new device. If FALSE, a
device must already be open.

Value

bp.cols locations of bars (as would be returned by barplot).

Author(s)

Derek Beaton
**prettyGraphs**

**See Also**

`barplot`, `prettyPlot`

**Examples**

```r
# stolen from ?barplot
# tN <- table(Ni <- stats::rpois(100, lambda = 5))
# the.colors <- rainbow(length(tN))
# dev.new()
# r <- barplot(tN, col = the.colors)
# prettyBars(as.matrix(tN), axis=1, fg.col=as.matrix(the.colors), horiz=FALSE, dev.new=TRUE)
```

---

**prettyGraphs**

`prettyGraphs`: for publication-quality graphics.

**Description**

`prettyGraphs` is a package that produces simple, crisp, publication-quality graphics for multivariate analyses.

**Details**

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**Author(s)**

Derek Beaton <exposition.software@gmail.com>

**References**

Two functions were copied/derived for use in `prettyGraphs`: `peeledHull` and `repmat`.

For `peeledHull` see:

http://carme-n.org/?sec=code2

For `repmat` see:
http://cran.r-project.org/doc/contrib/R-and-octave.txt

See Also

`prettyPlot contributionBars correlationPlotter peeledHull minmaxHelper repmat`

---

### prettyGraphsColors

**Description**

A function to return only a subset of R colors used by the prettyGraphs package.

**Usage**

```r
prettyGraphsColors()
```

**Value**

`possibleColors`  A list of colors used by prettyGraphs

**Author(s)**

Derek Beaton

---

### prettyGraphsColorSelection

**Description**

*Algorithmically select colors from prettyGraphs*

**Usage**

```r
prettyGraphsColorSelection(n.colors = 1, offset = NULL, starting.color = 163)
```

**Arguments**

- `n.colors`  number of colors needed
- `offset`  numeric. Should be a prime number, if it is not, the closest prime is selected. This number decides the distance between indices for color selection.
- `starting.color`  numeric. This is the starting location (e.g., color) in a matrix of `prettyGraphsColors`. 
prettyGraphsHSVColorSelection

Value

a matrix a matrix of colors are returned.

Author(s)

Derek Beaton

prime number selection from here:
http://stackoverflow.com/questions/3789968/generate-a-list-of-primes-in-r-up-to-a-certain-number

See Also

prettyGraphsColors, prettyGraphsHSVColorSelection

prettyGraphsHSVColorSelection

Algorithmically select HSV colors.

Description

This function uses an HSV color selection algorithm to create HSV color palletes.

Usage

prettyGraphsHSVColorSelection(n.colors = 1, offset = NULL, h = 13, s = 0.75, v = 0.75)

Arguments

n.colors number of colors needed
offset numeric (decimal/percentage). This number decides the distance between indices for color selection. If NULL, the golden ratio is selected.
h numeric. The initial hue (see hsv).
s numeric. The initial saturation (see hsv).
v numeric. The initial value (see hsv).

Value

a matrix a matrix of colors are returned.

Author(s)

Derek Beaton

HSV selection from here:
prettyPlot

See Also

prettyGraphsColors, prettyGraphsColorSelection

Description

prettyPlot creates simple, crisp, publication-style quality graphics for multivariate analyses.

Usage

prettyPlot(data_matrix, x_axis=1, y_axis=2, col=NULL, pch=NULL, cex=NULL, text.cex=NULL, pos=3, xlab="", ylab="", main="", display_names=TRUE, display_points=TRUE, constraints=NULL, contributionCircles=false, contributions=NULL, axes=TRUE, fg.line.width=3, fg.type="l", fg.col="black", bg.line.width=1.5, bg.lty=3, bg.col="black", flip=FALSE, asp=1, findBounds=TRUE, dev.new=TRUE, new.plot=TRUE)

Arguments

data_matrix A set of data you would like to plot on 2 dimensions (e.g., a scatter plot). Can be original data or factor scores or anything with at least 2 columns.
x_axis Which axis is the x-axis? Default is 1.
y_axis Which axis is the y-axis? Default is 2.
col any acceptable color format. A single-column matrix of colors for each data point. A single value can be used.
pch A single-column matrix of pch for each data point. A single value can be used. Indicates which point style to use for each item. See \texttt{par}.
cex a single column of continuous values. A single value can be used. Indicates the size of the points. See \texttt{par}. Used multiplicatively for points with contributions.
text.cex A replacement for the cex parameter in text() (to avoid collisions with cex). Used additively for points with contributions. See \texttt{par} and \texttt{text}.
pos integer between 1-4. Determines position of text for points. See \texttt{par}.
xlab A label to be placed along the x-axis.
ylab A label to be placed along the y-axis.
main A title to be placed at the top of the graph.
display_names boolean. If TRUE, the names of the points will be displayed on the plot.
display_points boolean. If TRUE, the points will be displayed on the plot.
constraints A list that contains the plot constraints. Default is NULL (constraints are computed each time).
contributionCircles
boolean. If TRUE, items plotted will vary in size, dependent on amount of contribution to the variance.

ccontributions
A matrix of contribution values for data_matrix (should also be the same size & dimensionality as data_matrix)

axes
boolean. If TRUE, a new set of axes are plotted.

fg.line.width
integer. Determines thickness of foreground (default: solid) axis lines, see points and lwd under par.

fg.type
character or string Determines type of points for foreground (default: solid) axis lines, see points and type under par.

fg.col
any acceptable color format. Determines color for foreground (default: solid) axis lines, see points and col under par.

bg.line.width
integer. Determines thickness of background (default: dashed) axis lines, see abline and lwd under par.

bg.lty
integer. Determines type of background (default: dashed) axis lines, see abline and lty under par.

bg.col
any acceptable color format. Determines color of background (default: dashed) axis lines, see abline and col under par.

flip
boolean. If TRUE, exchanges bg and col for all applicable pch values.

asp
numeric. Aspect ratio, see par.

findBounds
boolean. If TRUE, finds the min and max of each plotted axes. If FALSE, the largest value is used for all constraints.

dev.new
boolean. If TRUE, dev.new is called internally to create new device. If FALSE, a device must already be open.

new.plot
boolean. If TRUE, plot is called for a new plot on the current device. If FALSE, items will be overlayed much like points.

Details
All items after contributions (i.e., axes onward) are parameters for very fine-grained detail. They are quite powerful but in most cases not required.

Value
Returns a three item list:

col
A matrix of colors where each element is the color for each item plotted.

pch
A matrix of pch values where each element is the pch number for each item plotted.

constraints
A list (from minmaxHelper) of the plot constraints (i.e., min and max for axes)

Author(s)
Derek Beaton
prettyScree

Description

prettyScree creates simple, crisp, publication-style scree plots and “tests” for SVD-based analyses.

Usage

prettyScree(eigs, retain.col = "mediumorchid4", dismiss.col = "gray", perc.exp = 1, n.comps = NULL, broken.stick = TRUE, kaiser = TRUE, main = "")

Arguments

eigs a vector of positive eigenvalues.
retain.col a color for components that are kept.
dismiss.col a color for components that are dismissed.
perc.exp a value between 0 and 1. Used to retain components that explain perc.comp * 100 variance. Note: perc.exp retains cumsum(explained variance) < (perc.exp * 100) + 1 component.
n.comps a value between 1 and length(eigs). Used to retain n.comps number of components.
broken.stick a boolean. If TRUE (default), the broken-stick test is performed (see details).
kaiser a boolean. If TRUE (default), all components with eigenvalues greater than the mean(eigs) are retained.
main A title to be placed at the top of the graph.

Details

prettyScree visualizes the distribution of eigenvalues/explained variance from SVD-based analyses. Further, prettyScree performs several rudimentary “tests”. Two rudimentary criteria are implemented: 1) user selected explained variance, and 2) user selected number of components. Additionally, two rudimentary “tests” are implemented: 1) the “broken-stick” distribution of variance model, and 2) the “Kaiser criterion” where all components that explain more variance than the mean are kept.

prettyScree colors components that “pass” all selected tests with retain.col. Any components that do not pass tests are colored by a more transparent version of retain.col. Components that do not meet any criteria for retention are colored by dismiss.col.

prettyScree should be considered “under development” as of 12.09.2013. The function works, but we will be adding more features in the near future.
Value

comps.tests  a matrix with boolean values. Rows indicate which criteria are used, and columns correspond to components. If TRUE, a component is considered “retained” by that test/criteria. If FALSE, the component is “dismissed” according to that test/criteria.

Note

A private function (add.alpha) was copied from http://lamages.blogspot.com/2013/04/how-to-change-alpha-value-of-colours-in.html

Author(s)

Derek Beaton

References


See Also

Also see (some of) the other packages that perform a wide array of SVD-based analyses: ExPosition, FactoMineR, ca, ade4

Examples

```r
prcomp.res <- prcomp(USArests, scale = TRUE)
prettyScree(prcomp.res$sdev^2)
# or
princomp.res <- princomp(USArests, cor = TRUE)
prettyScree(princomp.res$sdev^2)
```

Description

A function to match repmat in Matlab (Mathworks, Natick, MA)

Usage

```r
repmat(a, n, m)
```
Arguments

- **a**: Matrix or vector to repeat.
- **n**: Number of row repetitions.
- **m**: Number of column repetitions.

Note

This code was created by Robin Hankin. Derek Beaton included the code in prettyGraphs because it is a versatile function and used in prettyGraphs.

Author(s)

Robin Hankin.

References

For `repmat` see:
http://cran.r-project.org/doc/contrib/R-and-octave.txt
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