Package ‘SciViews’

November 16, 2019

<table>
<thead>
<tr>
<th>Type</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>Version</td>
<td>0.9-13.1</td>
</tr>
<tr>
<td>Date</td>
<td>2018-01-05</td>
</tr>
<tr>
<td>Title</td>
<td>SciViews - Main package</td>
</tr>
<tr>
<td>Description</td>
<td>Functions to install SciViews additions to R, and more tools.</td>
</tr>
<tr>
<td>Maintainer</td>
<td>Philippe Grosjean <a href="mailto:phgrosjean@sciviews.org">phgrosjean@sciviews.org</a></td>
</tr>
<tr>
<td>Depends</td>
<td>R (&gt;= 2.6.0)</td>
</tr>
<tr>
<td>Imports</td>
<td>ellipse, grDevices, graphics, stats</td>
</tr>
<tr>
<td>Suggests</td>
<td>MASS, covr, knitr, testthat</td>
</tr>
<tr>
<td>Enhances</td>
<td>base</td>
</tr>
<tr>
<td>ByteCompile</td>
<td>yes</td>
</tr>
<tr>
<td>License</td>
<td>GPL-2</td>
</tr>
<tr>
<td>RoxygenNote</td>
<td>6.0.1</td>
</tr>
<tr>
<td>NeedsCompilation</td>
<td>no</td>
</tr>
<tr>
<td>Author</td>
<td>Philippe Grosjean [aut, cre]</td>
</tr>
<tr>
<td>Repository</td>
<td>CRAN</td>
</tr>
<tr>
<td>Date/Publication</td>
<td>2019-11-16 20:17:58 UTC</td>
</tr>
</tbody>
</table>

R topics documented:

<table>
<thead>
<tr>
<th>Topic</th>
<th>Pages</th>
</tr>
</thead>
<tbody>
<tr>
<td>SciViews-package</td>
<td>2</td>
</tr>
<tr>
<td>colors</td>
<td>2</td>
</tr>
<tr>
<td>correlation</td>
<td>3</td>
</tr>
<tr>
<td>enum</td>
<td>6</td>
</tr>
<tr>
<td>ln</td>
<td>7</td>
</tr>
</tbody>
</table>
Description

The SciViews package provides various functions to install the SciViews::R dialect. It also provides additional utilities besides base, recommended and tidyverse.

Important functions

TODO...

colors

Various color palettes.

Description

Create vectors of \( n \) contiguous colors.

Usage

\[
\begin{align*}
\text{rwb\_colors}(n, \alpha = 1, s = 0.9, v = 0.9) \\
\text{rwb\_colors}(n, \alpha = 1, s = 0.9, v = 0.9) \\
\text{rwg\_colors}(n, \alpha = 1, s = 0.9, v = 0.9) \\
\text{rwg\_colors}(n, \alpha = 1, s = 0.9, v = 0.9) \\
\text{ryg\_colors}(n, \alpha = 1, s = 0.9, v = 0.9) \\
\text{ryg\_colors}(n, \alpha = 1, s = 0.9, v = 0.9) \\
\text{cwm\_colors}(n, \alpha = 1, s = 0.9, v = 0.9) \\
\text{cwm\_colors}(n, \alpha = 1, s = 0.9, v = 0.9)
\end{align*}
\]
correlation

Arguments

- n: The number of colors (>= 1) to be in the palette.
- alpha: The alpha transparency, a number in [0, 1], see argument alpha = in [hsv()].
- s: The 'saturation' to be used to complete the HSV color descriptions.
- v: The 'value' to use for the HSV color descriptions.

Details

cwm_colors(s = 0.5, v = 1) gives very similar colors to cm.colors(). ryg_colors() is similar to rainbow(start = 0, end = 2/6). The xxx.colors() (tidyverse name-compatible) and 'xxx.colors" (grDevices name-compatible) functions are synonyms.

See Also

- cm.colors()
- colorRampPalette()

Examples

# Draw color wheels with various palettes
opar <- par(mfrow = c(2, 2))
pie(rep(1, 11), col = cwm.colors(11), main = "Cyan - white - magenta")
pie(rep(1, 11), col = rwb.colors(11), main = "Red - white - blue")
pie(rep(1, 11), col = rwg.colors(11), main = "Red - white - green")
pie(rep(1, 11), col = ryg.colors(11), main = "Red - yellow - green")
par(opar)

Description

Compute the correlation matrix between two variables, or more (between all columns of a matrix or data frame).

Usage

correlation(x, ...)

Correlation(x, ...)

## S3 method for class 'formula'
correlation(formula, data = NULL, subset, na.action, ...)

## Default S3 method:
correlation(x, y = NULL, use = "everything",
method = c("pearson", "kendall", "spearman"), ...)
correlation

is.Correlation(x)

is.correlation(x)

as.Correlation(x)

as.correlation(x)

## S3 method for class 'Correlation'
print(x, digits = 3, cutoff = 0, ...)

## S3 method for class 'Correlation'
summary(object, cutpoints = c(0.3, 0.6, 0.8, 0.9, 0.95),
    symbols = c(" ", ".", ",", "+", 
    ",", "B"), ...)

## S3 method for class 'summary.Correlation'
print(x, ...)

## S3 method for class 'Correlation'
plot(x, y = NULL, outline = TRUE, cutpoints = c(0.3,
    0.6, 0.8, 0.9, 0.95), palette = rwb.colors, col = NULL, numbers = TRUE,
    digits = 2, type = c("full", "lower", "upper"), diag = (type == "full"),
    cex.lab = par("cex.lab"), cex = 0.75 * par("cex"), ...)

## S3 method for class 'Correlation'
lines(x, choices = 1L:2L, col = par("col"), lty = 2,
    ar.length = 0.1, pos = NULL, cex = par("cex"), labels = rownames(x),
    ...)

Arguments

x A numeric vector, matrix or data frame (or any object for is.Correlation(),
as.Correlation()).

... Further arguments passed to functions.

formula A formula with no response variable, referring only to numeric variables.

data An optional data frame (or similar: see model.frame()) containing the vari-
    ables in the formula formula. By default the variables are taken from environment(formula).

subset An optional vector used to select rows (observations) of the data matrix x.

na.action A function which indicates what should happen when the data contain NAs. The
default is set by the na.action = setting of options() and na.fail() is used if that is not set. The 'factory-fresh' default is na.omit().

y NULL (default), or a vector, matrix or data frame with compatible dimensions to
    x for Correlation(). The default is equivalent to x = y, but more efficient.

use An optional character string giving a method for computing correlations in the
    presence of missing values. This must be (an abbreviation of) one of the strings
    "everything","all.obs","complete.obs","na.or.complete",or "pairwise.complete.obs".
### Method
A character string indicating which correlation coefficient is to be computed. One of "pearson" (default), "kendall", or "spearman", can be abbreviated.

### Digits
Digits to print after the decimal separator.

### Cutoff
Correlation coefficients lower than this (in absolute value) are suppressed.

### Object
A 'Correlation' object.

### Cutpoints
The cut points to use for categories. Specify only positive values (absolute value of correlation coefficients are summarized, or negative equivalents are automatically computed for the graph. Do not include 0 or 1 in the cutpoints).

### Symbols
The symbols to use to summarize the correlation matrix.

### Outline
Do we draw the outline of the ellipse?

### Palette
A function that can produce a palette of colors.

### Col
Color of the ellipse. If NULL (default), the colors will be computed using cutpoints = and palette =.

### Numbers
Do we print correlation values in the center of the ellipses?

### Type
Do we plot a complete matrix, or only lower or upper triangle?

### Diag
Do we plot items on the diagonal? They have always a correlation of one.

### Cex.lab
The expansion factor for labels.

### Cex
The expansion factor for text.

### Choices
The items to select

### Lty
The line type to draw.

### Ar.length
The length of the arrow head.

### Pos
The position relative to arrows.

### Labels
The label to draw near arrows.

### Value
Correlation() and as.Correlation() create a 'Correlation' object, while is.Correlation() tests for it.

There are print() and summary() methods for the 'Correlation' object that differ in the symbolic encoding of the correlations in summary(), using symnum(), which makes large correlation matrices more readable.

The method plot() returns nothing, but it draws ellipses on a graph that represent the correlation matrix visually. This is essentially the plotcorr() function from package ellipse, with slightly different default arguments and with default cutpoints equivalent to those used in the summary() method.

### Author(s)
Philippe Grosjean phgrosjean@sciviews.org, wrapping code in package ellipse, function plotcorr() for the plot.Correlation() method.

### See Also
cov(), cov2cor(), cov.wt(), symnum(), plotcorr() and look at panel_cor()
Examples

# This is a simple correlation coefficient
cor(rnorm(10), runif(10))
Correlation(rnorm(10), runif(10))

# 'Correlation' objects allow better inspection of the correlation matrices
# than the output of default R cor() function
(longley.cor <- Correlation(longley))
summary(longley.cor) # Synthetic view of the correlation matrix
plot(longley.cor) # Graphical representation

# Use of the formula interface
(mtcars.cor <- Correlation(~ mpg + cyl + disp + hp, data = mtcars,  
method = "spearman", na.action = "na.omit"))

mtcars.cor2 <- Correlation(mtcars, method = "spearman")
print(mtcars.cor2, cutoff = 0.6)
summary(mtcars.cor2)
plot(mtcars.cor2, type = "lower")

mtcars.cor2["mpg", "cyl"] # Extract a correlation from the correlation matrix

---

enum

Enumerate items in an object.

Description

enum() is creating a vector of integers to enumerate items in an object. It is particularly useful in
the for(i in enum(object)) construct.

Usage

enum(x)

Arguments

x Any object.

Note

The pattern for(i in 1:length(object)) is often found, but it fails in case length(object) ==
0! enum() is indeed a synonym of seq_along(), but the later one is less expressive in the context.

See Also

seq_along()
Examples

```r
enum(letters)
enum(numeric(0))
# Compare with:
1:length(numeric(0))
enum(NULL)
letters5 <- letters[1:5]
for (i in enum(letters5)) cat("letter", i, ", ", letters5[i], "\n")
```

Description

To avoid confusion using the default `log()` function, which is natural logarithm, but spells out like base 10 logarithm in the mind of some beginners, we define `ln()` and `ln1p()` as wrappers for `log()` with default base = `exp(1)` argument and for `log1p()`, respectively. For similar reasons, `lg()` is a wrapper of `log10()` (there is no possible confusion here, but 'lg' is another common notation for base 10 logarithm). `lg1p()` is a convenient way to use the optimized code to calculate the logarithm of `x + 1`, but returning the result in base 10 logarithm. `E` is the Euler constant and is provided for convenience as `exp(1)`. Finally `lb()` is a synonym of `log2()`.

Usage

```r
ln(x)
ln1p()
lg()
lg1p(x)
E
lb()
```

Arguments

| x | A numeric or complex vector. |

Format

An object of class numeric of length 1.

See Also

`log()`
Examples

\[ \ln(\exp(3)) \] # Same as log(exp(3))
\[ \ln1p(c(0, 1, 10, 100)) \] # Wrapper for log1p()
\[ \lg(10^3) \] # Same as log10(10^3)
\[ \lg1p(c(0, 1, 10, 100)) \] # log10(x + 1), but optimized for x << 1
\[ E^4 \] # Similar to exp(4), but different calculation!
\[ lb(1:3) \] # Wrapper for log2()

nr

Convenience functions for rows or columns manipulations.

Description

nr() and nc() are synonyms of the ugly NROW() or NCOL() that still provide a result, even if dim attribute of the object is not set, on the contrary to nrow() or ncol(). ROWS and COLS are constants that makes call to apply() more expressive.

Usage

nr(x)
nc(x)
ROWS
COLS

Arguments

x Any object.

Format

An object of class numeric of length 1.

See Also

NROW()

Examples

mm <- matrix(1:6, nrow = 3)
nr(mm)
nc(mm)
vv <- 1:6
nr(vv)
nc(vv)
# ROWS and COLS constants used with apply()
apply(mm, ROWS, mean) # Idem apply(mm, 1, mean)
apply(mm, COLS, mean) # Idem apply(mm, 2, mean)
Description

Several panel plots that can be used with functions like `coplot()` and `pairs()`:

[pairs]): R:pairs()

Usage

panel.reg(x, y, col = par("col"), bg = par("bg"), pch = par("pch"),
         cex = par("cex"), lwd = par("lwd"), line.reg = lm, line.col = "red",
         line.lwd = lwd, untf = TRUE, ...)

panel_reg(x, y, col = par("col"), bg = par("bg"), pch = par("pch"),
         cex = par("cex"), lwd = par("lwd"), line.reg = lm, line.col = "red",
         line.lwd = lwd, untf = TRUE, ...)

panel_ellipse(x, y, col = par("col"), bg = par("bg"), pch = par("pch"),
              cex = par("cex"), el.level = 0.7, el.col = "cornsilk",
              el.border = "red", major = TRUE, ...)

panel.ellipse(x, y, col = par("col"), bg = par("bg"), pch = par("pch"),
              cex = par("cex"), el.level = 0.7, el.col = "cornsilk",
              el.border = "red", major = TRUE, ...)

panel.cor(x, y, use = "everything", method = c("pearson", "kendall",
      "spearman"), alternative = c("two.sided", "less", "greater"), digits = 2,
      prefix = "", cex = par("cex"), cor.cex = cex, stars.col = "red", ...)

panel.cor(x, y, use = "everything", method = c("pearson", "kendall",
      "spearman"), alternative = c("two.sided", "less", "greater"), digits = 2,
      prefix = "", cex = par("cex"), cor.cex = cex, stars.col = "red", ...)

panel_smooth(x, y, col = par("col"), bg = NA, pch = par("pch"), cex = 1,
             col.smooth = "red", span = 2/3, iter = 3, ...)

Arguments

x
A numeric vector.

y
A numeric vector of same length as x.

col
The color of the points.

bg
The background color for symbol used for the points.

pch
The symbol used for the points.

cex
The expansion factor used for the points.
lwd  The line width.
line.reg A function that calculates coefficients of a straight line, for instance, `lm()`, or `rlm()` for robust linear regression.
line.col The color of the line.
line.lwd The width of the line.
untf Logical asking whether to untransform the straight line in case one or both axis are in log scale.
...
Further arguments to plot functions.
el.level The confidence level for the bivariate normal ellipse around data; the default value of 0.7 draws an ellipse of roughly +/-1 sd.
el.col The color used to fill the ellipse.
el.border The color used to draw the border of the ellipse and the standardized major axis.
major If TRUE, the standardized major axis is also drawn.
use One of "everything", "all.obs", "complete.obs", "na.or.complete", or "pairwise.complete.obs" (can be abbreviated). Defines how the cor() function behaves with missing observations.
method One of the three correlation coefficients "pearson" (default), "kendall", or "spearman". Can be abbreviated.
alternative The alternative hypothesis in correlation test, see cor.test().
digits The number of decimal digits to print when the correlation coefficient is printed in the graph.
prefix A prefix (character string) to use before the correlation coefficient printed in the graph.
cor.cex Expansion coefficient for text in printing correlation coefficients.
stars.col The color used for significance stars (with: *** p < 0.001, ** p < 0.1, * p < 0.05, . p < 0.1.
col.smooth Color to be used by lines for drawing the smooths.
span Smoothing parameter f for lowess(), see there.
iter Number of robustness iterations for lowess().

Details
Theses functions should be used outside of the diagonal in pairs(), or with coplot(), as they are bivariate plots.

Value
These functions return nothing and are used for their side effect of plotting in panels of composite plots.

Author(s)
Philippe Grosjean phgrosjean@sciviews.org, but code inspired from panel.smooth() in graphics and panel.car() in package car.
See Also

coplot(), pairs(), panel.smooth(), lm(), ellipse(), cor() and cor.test()

Examples

# Smooth lines in lower graphs and straight lines in upper graphs
pairs(trees, lower.panel = panel_smooth, upper.panel = panel_reg)
# Robust regression lines
library(MASS) # For rlm()
pairs(trees, panel = panel_reg, diag.panel = panel_boxplot,
    reg.line = rlm, line.col = "blue", line.lwd = 2)
# A Double log graph
pairs(trees, lower.panel = panel_smooth, upper.panel = panel_reg, log = "xy")

# Graph suitable to explore correlations (take care there are potentially
# many simultaneous tests done here... So, you loose much power in the whole
# analysis... use it just as an indication!)
# Pearson's r
pairs(trees, lower.panel = panel_ellipse, upper.panel = panel_cor)
# Spearman's rho (ellipse and straight lines not suitable here!)
pairs(trees, lower.panel = panel_smooth, upper.panel = panel_cor,
    method = "spearman", span = 1)
# Several groups (visualize how bad it is to consider the whole set at once!)
pairs(iris[, -5], lower.panel = panel_smooth, upper.panel = panel_cor,
    method = "kendall", span = 1,
    col = c("red3", "blue3", "green3")[iris$Species])
# Now analyze correlation for one species only
pairs(iris[iris$Species == "virginica", -5], lower.panel = panel_ellipse,
    upper.panel = panel_cor)

# A coplot with custom panes
coplot(Petal.Length ~ Sepal.Length | Species, data = iris,
    panel = panel_ellipse)

panels.diag

More univariate panel plots.

Description

Several panel plots that can be used with pairs().

Usage

panel_boxplot(x, col = par("col"), box.col = "cornsilk", ...)

panel.boxplot(x, col = par("col"), box.col = "cornsilk", ...)

panel_density(x, adjust = 1, rug = TRUE, col = par("col"),
    lwd = par("lwd"), line.col = col, line.lwd = lwd, ...)
panel.density(x, adjust = 1, rug = TRUE, col = par("col"),
   lwd = par("lwd"), line.col = col, line.lwd = lwd, ...)

panel.hist(x, breaks = "Sturges", hist.col = "cornsilk",
   hist.border = NULL, hist.density = NULL, hist.angle = 45, ...)

panel.hist(x, breaks = "Sturges", hist.col = "cornsilk",
   hist.border = NULL, hist.density = NULL, hist.angle = 45, ...)

panel.qqnorm(x, pch = par("pch"), col = par("col"), bg = par("bg"),
   cex = par("cex"), lwd = par("lwd"), qq.pch = pch, qq.col = col,
   qq.bg = bg, qq.cex = cex, qqline.col = qq.col, qqline.lwd = lwd, ...)

panel.qqnorm(x, pch = par("pch"), col = par("col"), bg = par("bg"),
   cex = par("cex"), lwd = par("lwd"), qq.pch = pch, qq.col = col,
   qq.bg = bg, qq.cex = cex, qqline.col = qq.col, qqline.lwd = lwd, ...)

Arguments

x       A numeric vector.
col     The color of the points.
box.col The filling color of the boxplots.
...     Further arguments to plot functions, or functions that construct items, like density(),
         depending on the context.
adjust  The bandwidth adjustment factor, see density().
rug     Do we add a rug representation (1-d plot) of the points too?
lwd     The line width.
line.col The color of the line.
line.lwd The width of the line.
brakes   The number of breaks, the name of a break algorithm, a vector of breakpoints,
         or any other acceptable value for breaks = argument of hist().
hist.col The filling color for the histograms.
hist.border The border color for the histograms.
hist.density The density for filling lines in the histograms.
hist.angle The angle for filling lines in the histograms.
pch     The symbol used for the points.
bg      The background color for symbol used for the points.
cex     The expansion factor used for the points.
qq.pch  The symbol used to plot points in the QQ-plots.
qq.col  The color of the symbol used to plot points in the QQ-plots.
qq.bg   The background color of the symbol used to plot points in the QQ-plots.
qq.cex  The expansion factor for points in the QQ-plots.
qqline.col The color for the QQ-plot lines.
qqline.lwd The width for the QQ-plot lines.
Details

Panel functions `panel_boxplot()`, `panel_density()`, `panel_hist()` and `panel_qqnorm()` should be used only to plot univariate data on the diagonals of pair plots (or scatterplot matrix).

Value

These functions return nothing and are used for their side effect of plotting in panels of composite plots.

Author(s)

Philippe Grosjean phgrosjean@sciviews.org, but code inspired from `spm()` in package `car`.

See Also

`pairs()`, `boxplot()`, `hist()`, `density()`, `qqnorm()`

Examples

```r
# Example of scatterplot matrices with custom plots on the diagonal
# Boxplots
pairs(trees, panel = panel_smooth, diag.panel = panel_boxplot)
pairs(trees, diag.panel = panel_boxplot, box.col = "gray")
# Densities
pairs(trees, panel = panel_smooth, diag.panel = panel_density)
pairs(trees, diag.panel = panel_density, line.col = "red", adjust = 0.5)
# Histograms
pairs(trees, panel = panel_smooth, diag.panel = panel_hist)
pairs(trees, diag.panel = panel_hist, hist.col = "gray", breaks = "Scott")
# QQ-plots against Normal theoretical distribution
pairs(trees, panel = panel_smooth, diag.panel = panel_qqnorm)
pairs(trees, diag.panel = panel_qqnorm, qqline.col = 2, qq.cex = .5, qq.pch = 3)
```

---

**pcomp**

Principal Components Analysis.

Description

Perform a principal components analysis on a matrix or data frame and return a pcomp object.

Usage

```r
pcomp(x, ...)
```

## S3 method for class 'formula'
```r
pcomp(formula, data = NULL, subset, na.action,
       method = c("svd", "eigen"), ...)
```
## Default S3 method:
pcomp(x, method = c("svd", "eigen"), scores = TRUE,
    center = TRUE, scale = TRUE, tol = NULL, covmat = NULL,
    subset = rep(TRUE, nrow(as.matrix(x))), ...)  

## S3 method for class 'pcomp'
print(x, ...)  

## S3 method for class 'pcomp'
summary(object, loadings = TRUE, cutoff = 0.1, ...)  

## S3 method for class 'summary.pcomp'
print(x, digits = 3, loadings = x$print.loadings,
    cutoff = x$cutoff, ...)  

## S3 method for class 'pcomp'
plot(x, which = c("screeplot", "loadings", "correlations",
    "scores"), choices = 1L:2L, col = par("col"), bar.col = "gray",
    circle.col = "gray", ar.length = 0.1, pos = NULL, labels = NULL,
    cex = par("cex"), main = paste(deparse(substitute(x)), which, sep = "+"),
    xlab, ylab, ...)  

## S3 method for class 'pcomp'
screepplot(x, npcs = min(10, length(x$sdev)),
    type = c("barplot", "lines"), col = "cornsilk",
    main = deparse(substitute(x)), ...)  

## S3 method for class 'pcomp'
points(x, choices = 1L:2L, type = "p", pch = par("pch"),
    col = par("col"), bg = par("bg"), cex = par("cex"), ...)  

## S3 method for class 'pcomp'
lines(x, choices = 1L:2L, groups, type = c("p", "e"),
    col = par("col"), border = par("fg"), level = 0.9, ...)  

## S3 method for class 'pcomp'
text(x, choices = 1L:2L, labels = NULL, col = par("col"),
    cex = par("cex"), pos = NULL, ...)  

## S3 method for class 'pcomp'
biplot(x, choices = 1L:2L, scale = 1, pc.biplot = FALSE,
    ...)  

## S3 method for class 'pcomp'
pairs(x, choices = 1L:3L, type = c("loadings", "correlations"),
    col = par("col"), circle.col = "gray",
    ar.col = par("col"), ar.length = 0.05, pos = NULL,
    ar.cex = par("cex"), cex = par("cex"), ...)
## S3 method for class 'pcomp'
predict(object, newdata, dim = length(object$sdev), ...)

## S3 method for class 'pcomp'
correlation(x, newvars, dim = length(x$sdev), ...)

scores(x, ...)

## S3 method for class 'pcomp'
scores(x, labels = NULL, dim = length(x$sdev), ...)

### Arguments

- **x**: A matrix or data frame with numeric data.
- **...**: Arguments passed to or from other methods. If 'x' is a formula one might specify `scale = TRUE`, `tol = 0`, or `covmat =`. 
- **formula**: A formula with no response variable, referring only to numeric variables.
- **data**: An optional data frame (or similar: see `model.frame()`) containing the variables in the formula `formula =`. By default the variables are taken from `environment(formula)`. 
- **subset**: An optional vector used to select rows (observations) of the data matrix `x`.
- **na.action**: A function which indicates what should happen when the data contain NAs. The default is set by the `na.action` setting of `options()`, and is `na.fail()` if that is not set. The 'factory-fresh' default is `na.omit()`. 
- **method**: Either "svd" (using `prcomp()`), "eigen" (using `princomp()`), or an abbreviation. 
- **scores**: A logical value indicating whether the score on each principal component should be calculated. 
- **center**: A logical value indicating whether the variables should be shifted to be zero centered. Alternately, a vector of length equal the number of columns of `x` can be supplied. The value is passed to `scale =`. Note that this argument is ignored for `method = "eigen"` and the dataset is always centered in this case. 
- **scale**: A logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is `TRUE`, which in general, is advisable. Alternatively, a vector of length equal the number of columns of `x` can be supplied. The value is passed to `scale()`. 
- **tol**: Only when `method = "svd"`. A value indicating the magnitude below which components should be omitted. (Components are omitted if their standard deviations are less than or equal to `tol` times the standard deviation of the first component.) With the default null setting, no components are omitted. Other settings for `tol` could be `tol = 0` or `tol = sqrt(.Machine$double.eps)`, which would omit essentially constant components. 
- **covmat**: A covariance matrix, or a covariance list as returned by `cov.wt()` (and `cov.mve()` or `cov.mcd()` from package `MASS`). If supplied, this is used rather than the covariance matrix of `x`. 
object  A 'pcomp' object.
loadings Do we also summarize the loadings?
cutoff  The cutoff value below which loadings are replaced by white spaces in the table. That way, larger values are easier to spot and to read in large tables.
digits  The number of digits to print.
which The graph to plot.
choices Which principal axes to plot. For 2D graphs, specify two integers.
col The color to use in graphs.
bar.col The color of bars in the screeplot.
circle.col The color for the circle in the loadings or correlations plots.
ar.length The length of the arrows in the loadings and correlations plots.
pos The position of text relative to arrows in loadings and correlation plots.
lables The labels to write. If NULL default values are computed.
cex The factor of expansion for text (labels) in the graphs.
main The title of the graph.
xlab The label of the x-axis.
ylab The label of the y-axis.
npcs The number of principal components to represent in the screeplot.
type The type of screeplot ("barplot" or "lines") or pairs plot ("loadings" or "correlations").
pch The type of symbol to use.
bg The background color for symbols.
groups A grouping factor.
border The color of the border.
level The probability level to use to draw the ellipse.
pc.biplot Do we create a Gabriel’s biplot (see biplot())?
ar.col Color of arrows.
ar.cex Expansion factor for text on arrows.
newdata New individuals with observations for the same variables as those used for calculating the PCA. You can then plot these additional individuals in the scores plot.
dim The number of principal components to keep.
newvars New variables with observations for same individuals as those used for mcalculating the PCA. Correlation with PCs is calculated. You can then plot these additional variables in the correlation plot.
Details

dcomp() is a generic function with "formula" and "default" methods. It is essentially a wrapper around 
prcomp() and princomp() to provide a coherent interface and object for both methods.

A 'pcomp' object is created. It inherits from 'pca' (as in labdsv package, but not compatible with
the 'pca' object of package ade4) and of 'princomp'.

For more information on calculation done, refer to prcomp() for method = "svd" or princomp() 
for method = "eigen".

Value

A c("pcomp","pca","princomp") object.

Note

The signs of the columns of the loadings and scores are arbitrary, and so may differ between func-
tions for PCA, and even between different builds of R.

Author(s)

Philippe Grosjean phgrosjean@sciviews.org, but the core code is indeed in package stats.

See Also

vectorplot(), prcomp(), princomp(), loadings(), Correlation()

Examples

# We will analyze mtcars without the Mercedes data (rows 8:14)
data(mtcars)
cars.pca <- pcomp(~ mpg + cyl + disp + hp + drat + wt + qsec, data = mtcars, 
subset = -(8:14))
cars.pca
summary(cars.pca)
screepplot(cars.pca)

# Loadings are extracted and plotted like this
(cars.ldg <- loadings(cars.pca))
plot(cars.pca, which = "loadings") # Equivalent to vectorplot(cars.ldg)

# Similarly, correlations of variables with PCs are extracted and plotted
(cars.cor <- Correlation(cars.pca))
plot(cars.pca, which = "correlations") # Equivalent to vectorplot(cars.cor)
# One can add supplementary variables on this graph
lines(Correlation(cars.pca,
newvars = mtcars[-(8:14), c("vs", "am", "gear", "carb")])

# Plot the scores
plot(cars.pca, which = "scores", cex = 0.8) # Similar to plot(scores(x)[, 1:2])
# Add supplementary individuals to this plot (labels), also points() or lines()
text(predict(cars.pca, newdata = mtcars[8:14, ]), col = "gray", cex = 0.8)
# Pairs plot for 3 PCs
iris.pca <- pcomp(iris[, -5])
pairs(iris.pca, col = (2:4)[iris$Species])

## timing

**Timing of R expressions.**

### Description

Similar to `system.time()` but returns a more convenient `difftime` object.

### Usage

```r
timing(expr, gc.first = TRUE)
```

### Arguments

- **expr**: Valid R expression to be timed. If missing, `proc.time()` is used instead.
- **gc.first**: Logical - should a garbage collection be performed immediately before the timing? Default is `TRUE`.

### See Also

`system.time()`

### Examples

```r
test <- timing(Sys.sleep(0.5))
test	none
attr(test, "details")
```

## vectorplot

**Plot vectors inside a unit circle (PCA loadings or correlations plots).**

### Description

Plots vectors with $0 < \text{norms} < 1$ inside a circle. These plots are mainly designed to represent variables in principal components space for PCAs.
vectorplot

Usage

vectorplot(x, ...)

### Default S3 method:
vectorplot(x, y, col = par("col"), circle.col = "gray",
ar.length = 0.1, pos = NULL, cex = par("cex"), labels = NULL, ...)

### S3 method for class 'loadings'
vectorplot(x, choices = 1L:2L, col = par("col"),
circle.col = "gray", ar.length = 0.1, pos = NULL, cex = par("cex"),
labels = rownames(x), main = deparse(substitute(x)), ...)

### S3 method for class 'Correlation'
vectorplot(x, choices = 1L:2L, col = par("col"),
circle.col = "gray", ar.length = 0.1, pos = NULL, cex = par("cex"),
labels = rownames(x), main = deparse(substitute(x)), ...)

Arguments

x An object that has a vectorplot() method, like 'loadings' or 'correlation', or a numeric vector with 0 < values < 1.
...
Further arguments passed to plot functions.
y A numeric vector with 0 < values < 1 of same length as 'x.'
col Color of the arrows and labels.
circle.col The color for the circle around the vector plot.
ar.length The length of the arrows.
pos The position of text relative to arrows. If NULL, a suitable position is calculated according to the direction where the arrows are pointing.
cex The factor of expansion for labels in the graph.
labels The labels to draw near the arrows.
choices A vector of two integers indicating the axes to plot.
main The title of the plot.

Value

The object 'x' is returned invisibly. These functions are called for their side-effect of drawing a vector plot.

See Also

pcomp(), loadings(), Correlation()
Examples

# Create a PCA and plot loadings and correlations
iris.pca <- pcomp(iris[, -5])
vectorplot(loadings(iris.pca))
vectorplot(Correlation(iris.pca))
# Note: on screen devices, change aspect ratio of the graph by resizing
# the window to reveal cropped labels...
Index

*Topic aplot
  panels, 9
  panels.diag, 11
  vectorplot, 18
*Topic color
  colors, 2
*Topic datasets
  ln, 7
  nr, 8
*Topic distribution
  correlation, 3
*Topic math
  ln, 7
*Topic models
  pcomp, 13

as.Correlation (correlation), 3
as.correlation (correlation), 3

biplot(), 16
biplot.pcomp (pcomp), 13
boxplot(), 13

cm.colors(), 3
colorRampPalette(), 3
colors, 2
COLS (nr), 8
coplot(), 9–11
cor(), 10, 11
cor.test(), 10, 11
Correlation (correlation), 3
correlation, 3
Correlation(), 17, 19
correlation.pcomp (pcomp), 13
cov(), 5
cov.mcd(), 15
cov.mve(), 15
cov.wt(), 5, 15
cov2cor(), 5
cwm.colors (colors), 2
cwm.colors (colors), 2
density(), 12, 13
E (ln), 7
ellipse(), 11
enum, 6

hist(), 12, 13
is.Correlation (correlation), 3
is.correlation (correlation), 3

lb (ln), 7
lg (ln), 7
lg1p (ln), 7
lines.Correlation (correlation), 3
lines.pcomp (pcomp), 13
lm(), 10, 11
ln, 7
ln1p (ln), 7
loadings(), 17, 19
log(), 7
lowess(), 10

model.frame(), 4, 15

na.fail(), 15
na.omit(), 15
nc (nr), 8
nr, 8
NROW(), 8

options(), 15

pairs(), 10, 11, 13
pairs.pcomp (pcomp), 13
panel.boxplot (panels.diag), 11
panel.cor (panels), 9
panel.density (panels.diag), 11
panel.ellipse (panels), 9
INDEX

panel.hist (panels.diag), 11
panel.qqnorm (panels.diag), 11
panel.reg (panels), 9
panel.smooth (), 10, 11
panel_boxplot (panels.diag), 11
panel_boxplot (), 13
panel_cor (panels), 9
panel_cor (), 5
panel_density (panels.diag), 11
panel_density (), 13
panel_ellipse (panels), 9
panel_hist (panels.diag), 11
panel_hist (), 13
panel_qqnorm (panels.diag), 11
panel_qqnorm (), 13
panel_reg (panels), 9
panel_smooth (panels), 9
panels, 9
panels.diag, 11
pcomp, 13
pcomp (), 19
plot.Correlation (correlation), 3
plot.pcomp (pcomp), 13
plotcorr (), 5
points.pcomp (pcomp), 13
prcomp (), 15, 17
predict.pcomp (pcomp), 13
princomp (), 15, 17
print.Correlation (correlation), 3
print.pcomp (pcomp), 13
print.summary.Correlation (correlation), 3
print.summary.pcomp (pcomp), 13
proc.time (), 18

qqnorm (), 13

rlm (), 10
ROWS (nr), 8
rwb.colors (colors), 2
rwb_colors (colors), 2
rwg.colors (colors), 2
rwg_colors (colors), 2
ryg.colors (colors), 2
ryg_colors (colors), 2

scale (), 15
SciViews-package, 2
scores (pcomp), 13

timings, 18

vectorplot, 18
vectorplot (), 17, 19