

# Package: smvgraph (via r-universe)

November 4, 2024

**Type** Package

**Title** Visualization and Clustering of Data in a Shiny App

**Version** 0.2.0

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**Description** Various visualisations of univariate and multivariate graphs (e.g. mosaic diagram, scatterplot matrix, Andrews curves, parallel coordinate diagram, radar diagram and Chernoff plots) as well as clustering methods (e.g. k-means, agglomerative, EM clustering and DBSCAN) are implemented as a Shiny app. The app allows interactive changes, e.g. of the order of variables. It is intended for use in teaching.

**License** GPL-3

**URL** <https://github.com/sigbertklinke/smvgraph> (development version)

**Encoding** UTF-8

**Imports** tools, devtools, formatR, highlight, shiny, DT, base64enc, shinyWidgets, shinydashboardPlus, sortable, mrfDepth

**RoxygenNote** 7.2.2

**Roxygen** list(markdown = TRUE)

**Suggests** MASS, knitr, rmarkdown

**Depends** R (>= 2.10)

**LazyData** true

**VignetteBuilder** knitr

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

**RemoteUrl** <https://github.com/sigbertklinke/smvgraph>

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---

andrews	<i>andrews</i>
---------	----------------

---

## Description

Andrews curves for visualization of multidimensional data. `step` determines the number of line segments for each curve. If `ymax==NA` then the maximum y coordinate will be determined from the curves. Note that for `type==3` the x range is  $[0, 4 * \pi]$  otherwise  $[-\pi, \pi]$ . Observations containing NA, Nan, -Inf, or +Inf will be deleted before plotting

## Usage

```
andrews(x, type = 1, step = 100, ..., normalize = 1, ymax = NA)
```

## Arguments

<code>x</code>	data frame or matrix
<code>type</code>	type of curve (default: 1) <ul style="list-style-type: none"> <li>1: <math>f(t) = x1/(2^{0.5}) + x2 * \sin(t) + x3 * \cos(t) + x4 * \sin(2 * t) + x5 * \cos(2 * t) + \dots</math></li> <li>2: <math>f(t) = x1 * \sin(t) + x2 * \cos(t) + x3 * \sin(2 * t) + x4 * \cos(2 * t) + \dots</math></li> <li>3: <math>f(t) = x1 * \cos(t) + x2 * \cos((2 * t)^{0.5}) + x3 * \cos((3 * t)^{0.5}) + \dots</math></li> <li>4: <math>f(t) = 1/(2^{0.5}) * (x1 + x2 * (\sin(t) + \cos(t)) + x3 * (\sin(t) - \cos(t)) + x4 * (\sin(2 * t) + \cos(2 * t)) + x5 * (\sin(2 * t) - \cos(2 * t)) + \dots)</math></li> </ul>
<code>step</code>	smoothness of curves
<code>...</code>	further parameters given to <a href="#">graphics::plot</a> and <a href="#">graphics::lines</a>
<code>normalize</code>	integer: normalization method (default: 1) <ul style="list-style-type: none"> <li>0: no rescaling</li> <li>1: <math>(x - \min(x)) / (\max(x) - \min(x))</math></li> <li>2: <math>(x - \text{mean}(x)) / \text{sd}(x)</math></li> </ul>
<code>ymax</code>	numeric: maximum of y coordinate (default: NA)

## Value

nothing

**References**

- Andrews, D. F. (1972) Plots of High-Dimensional Data. *Biometrics*, vol. 28, no. 1, pp. 125-136.
- Khatree, R., Naik, D. N. (2002) Andrews Plots for Multivariate Data: Some New Suggestions and Applications. *Journal of Statistical Planning and Inference*, vol. 100, no. 2, pp. 411-425.

**See Also**

In package [andrews](#) or at [CRAN](#)

**Examples**

```
andrews(iris[,-5], col=as.factor(iris[,5]))
andrews(iris[,-5], type=4, col=as.factor(iris[,5]), ymax=2)
```

---

as\_param

*as\_param*

---

**Description**

Create a parameter list or a function call. For a function call fun must be explicitly given.

**Usage**

```
as_param(..., fun = NULL)

txt(x)
```

**Arguments**

...	list of named and unnamed parameters
fun	character:
x	character: replaces "x" by "'x'"

**Value**

a character as parameter list of function call

**Examples**

```
as_param(letters[1:5])
as_param(txt(letters[1:5]))
as_param(a=txt("a"))
as_param(txt(letters[1:5]), fun="c")
```

availablePlots

*availablePlots*

## Description

Returns a data frame with columns about the available plots in smvgraph:

- `module`: the internal name used. If you want to call the Shiny app then you might need this.
- `label`: the label used in the Shiny app
- `help`: the R help topic for the plot
- `packages`: packages which are required to make the plot
- `code`: if code block exists, should always be TRUE
- `ui`: if plot specific interactive UI elements exists
- `condition`: the condition when a plot is offered in the Shiny app to the user

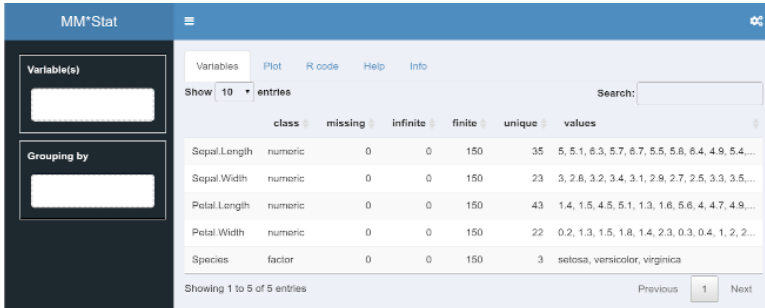
## Usage

```
availablePlots()
```

## Details

To understand `condition`:

- `nrow(analysis)`: the number of variables in "Analysis" field
- `nrow(group)`: the number of variables in "Grouping by" field
- `xxx$unique`: the number of unique values in a variable, for other elements then unique see the "Variable" panel of the Shiny app



The screenshot shows the MM\*Stat Shiny app interface. On the left, there are two input fields: "Variable(s)" and "Grouping by". The main area displays a table with the following columns: class, missing, infinite, finite, unique, and values. The table contains data for five variables: Sepal.Length, Sepal.Width, Petal.Length, Petal.Width, and Species. The 'unique' column shows the number of unique values for each variable: 35 for Sepal.Length, 23 for Sepal.Width, 43 for Petal.Length, 22 for Petal.Width, and 3 for Species. The 'values' column shows the unique values for each variable.

	class	missing	infinite	finite	unique	values
Sepal.Length	numeric	0	0	150	35	5, 5.1, 6.3, 5.7, 6.7, 5.5, 5.6, 6.4, 4.9, 5.4,...
Sepal.Width	numeric	0	0	150	23	3, 2.6, 3.2, 3.4, 3.1, 2.9, 2.7, 2.5, 3.3, 3.5,...
Petal.Length	numeric	0	0	150	43	1.4, 1.5, 4.5, 5.1, 1.3, 1.6, 5.6, 4, 4.7, 4.9,...
Petal.Width	numeric	0	0	150	22	0.2, 1.3, 1.5, 1.6, 1.4, 2.3, 0.3, 0.4, 1, 2, 2,...
Species	factor	0	0	150	3	setosa, versicolor, virginica

13 was chosen because twelve has the largest number of divisors below 20 and 43 was chosen because forty-two is the answer of the **ultimate question** ;)

## Value

a data frame with information about all available plots

## Examples

```
availablePlots()
```

---

 bagplot2

*bagplot*


---

## Description

A non-ggplot2 bagplot based on [mrfDepth::bagplot](#).

## Usage

```
bagplot2(
  x,
  y = NULL,
  colorbag = NULL,
  colorloop = NULL,
  colorchull = NULL,
  databag = TRUE,
  dataloop = TRUE,
  plot.fence = FALSE,
  type = "hdepth",
  sizesubset = 500,
  extra.directions = FALSE,
  options = NULL,
  ...
)
```

## Arguments

<code>x, y</code>	the <code>x</code> and <code>y</code> arguments provide the <code>x</code> and <code>y</code> coordinates for the bagplot. Any reasonable way of defining the coordinates is acceptable. See the function <code>xy.coords</code> for details. If supplied separately, they must be of the same length.
<code>colorbag</code>	The color of the bag (which contains the 50% observations with largest depth).
<code>colorloop</code>	The color of the loop (which contains the regular observations).
<code>colorchull</code>	When the bagplot is based on halfspace depth, the depth region with maximal depth is plotted. This argument controls its color.
<code>databag</code>	Logical indicating whether data points inside the bag need to be plotted. Defaults to TRUE.
<code>dataloop</code>	Logical indicating whether data points inside the fence need to be plotted. Defaults to TRUE.
<code>plot.fence</code>	Logical indicating whether the fence should be plotted. Defaults to FALSE.
<code>type</code>	Determines the depth function used to construct the bagplot: "hdepth" for halfspace depth, "projdepth" for projection depth and "sprojdepth" for skewness-adjusted projection depth. Defaults to "hdepth".

sizesubset	When computing the bagplot based on halfspace depth, the size of the subset used to perform the main computations. See Details for more information. Defaults to 500.
extra.directions	Logical indicating whether additional directions should be considered in the computation of the fence for the bagplot based on projection depth or skewness-adjusted projection depth. If set to TRUE an additional 250 equispaced directions are added to the directions defined by the points in <code>x</code> themselves and the center. If FALSE only directions determined by the points in <code>x</code> are considered. Defaults to FALSE.
options	A list of options to pass to the <code>projdepth</code> or <code>sprojdepth</code> function. In addition the following option may be specified: <ul style="list-style-type: none"> <li><code>max.iter</code> The maximum number of iterations in the bisection algorithm used to compute the depth contour corresponding to the cutoff. See <code>depthContour</code> for more information. Defaults to 100.</li> </ul>
...	further parameters given to <code>plot</code>

### Details

The bagplot has been proposed by Rousseeuw et al. (1999) as a generalisation of the boxplot to bivariate data. It is constructed based on halfspace depth and as such is invariant under affine transformations. Similar graphical representations can be obtained by means of other depth functions, as illustrated in Hubert and Van der Veeken (2008) and in Hubert et al. (2015). See [mrfDepth::compBagplot](#) for more details.

The deepest point is indicated with a "\*" sign, the outlying observations with red points.

### Value

Invisibly the result of the call to [mrfDepth::compBagplot](#)

### References

- Rousseeuw P.J., Ruts I., Tukey, J.W. (1999). The bagplot: a bivariate boxplot. *The American Statistician*, 53, 382–387.
- Hubert M., Van der Veeken S. (2008). Outlier detection for skewed data. *Journal of Chemometrics*, 22, 235–246.
- Hubert M., Rousseeuw P.J., Segaert, P. (2015). Rejoinder to 'Multivariate functional outlier detection'. *Statistical Methods & Applications*, 24, 269–277.

### See Also

[mrfDepth::compBagplot](#) and [mrfDepth::bagplot](#)

**Examples**

```

bagplot2(iris$Sepal.Length, iris$Sepal.Width)
bagplot2(iris[,1:2])
bagplot2(iris[,3:4], title="Bagplot with Tukey depth", xlab="Petal.Length", ylab="Petal.Width")
#
library("mrfDepth")
data("bloodfat")
result <- compBagplot(bloodfat)
bagplot(result, colorbag = rgb(0.2,0.2,0.2), colorloop = "green")

```

binData

*binData***Description**

Bins each variable in data in bins Bins. It can return a data frame (out="data.frame"), a table with the counts (out="table"), or a table converted to a data frame with an additional variable Freq. The values can be either the bin mids (val="mids") or the bin numbers (val="interval"). If possible all variables contain an attribute breaks with breaks used.

**Usage**

```

binData(
  data,
  bins,
  out = c("data.frame", "table", "binned"),
  val = c("mid", "interval"),
  pretty = TRUE,
  numeric = TRUE
)

```

**Arguments**

data	object: a data.frame or object that can be converted to a data frame with variables to bin
bins	integer: number of bins, will be recycled if necessary
out	character: output type, either "data.frame", "table", or "binned"
val	character: values for outer, either "mids" (interval centers), or "interval" (interval number)
pretty	logical: should be <code>base::pretty</code> used or minimum and maximum (default: TRUE)
numeric	logical: return output a factor or as numeric (default: TRUE)

**Value**

a data frame or table with the results



**Examples**

```
df <- data.frame(x=runif(25), y=runif(25))
binData(df, 5, 'data.frame')
binData(df, 5, 'table')
binData(df, 5, 'binned')
```

---

character_data	<i>character_data</i>
----------------	-----------------------

---

**Description**

Converts a matrix or data frame into a character vector, matrix or data frame. If `na.action` is a character then all NAs are replaced by `na.action` (default: `na.action="NA"`). If `na.action` is a function then the function will be applied to the result.

**Usage**

```
character_data(
  x,
  select = NULL,
  out = c("data.frame", "matrix", "vector"),
  na.action = "NA",
  ...,
  title = NULL
)
```

**Arguments**

<code>x</code>	vector, matrix or data frame
<code>select</code>	vector: indicating columns to select (default: NULL)
<code>out</code>	output as <code>data.frame</code> (default), <code>matrix</code> , or <code>vector</code>
<code>na.action</code>	function or character: indicates what should happen when the data contain NAs
<code>...</code>	unused
<code>title</code>	character: title attribute (default NULL)

**Value**

the desired R object

**Examples**

```
character_data(iris)
character_data(iris, out="matrix")
character_data(iris, out="vector")
```

---

checkPackages	<i>checkPackages, installPackages</i>
---------------	---------------------------------------

---

## Description

Checks if a package is installed without loading it. Returns a logical vector with TRUE or FALSE for each package checked.

## Usage

```
checkPackages(
  ...,
  plotmodule = NULL,
  add = c("tools", "devtools", "formatR", "highlight", "shiny", "shinydashboard",
    "shinydashboardPlus", "shinyWidgets", "DT", "sortable", "base64enc"),
  error = FALSE
)

installPackages(
  plotmodule = NULL,
  add = c("tools", "devtools", "formatR", "highlight", "shiny", "shinydashboard",
    "shinydashboardPlus", "shinyWidgets", "DT", "sortable", "base64enc")
)
```

## Arguments

...	character: name(s) of package
plotmodule	character: name(s) of plot modules to check for packages
add	character: names of default packages to check (default: c("highlight", "formatR", "shiny", "shinydashboard", "shinydashboardPlus", "DT"))
error	logical: should a error thrown if one or more package are missing? (default: FALSE)

## Value

TRUE if successful otherwise an error will be thrown

## Examples

```
checkPackages("graphics", add=NULL)           # checks if 'graphics' is installed
if (interactive()) checkPackages("graphics") # checks if 'graphics', 'shiny', ... are installed
if (interactive()) installPackages()          # installs all packages to show ALL plots
```

---

color_data	<i>color_data</i>
------------	-------------------

---

**Description**

Assigns a color to the data `x` based on the color palette `colpal`.

**Usage**

```
color_data(x, colpal = grDevices::hcl.colors, select = NULL, ..., title = NULL)
```

**Arguments**

<code>x</code>	vector, matrix, or data frame
<code>colpal</code>	color palette (default: <a href="#">grDevices::hcl.colors</a> )
<code>select</code>	vector: indicating columns to select (default: 1)
<code>...</code>	further parameters to <a href="#">factor_data</a>
<code>title</code>	character: title attribute (default NULL)

**Value**

a color vector

**Examples**

```
color_data(iris)
color_data(iris$Species)
```

---

color_hclust	<i>color_hclust</i>
--------------	---------------------

---

**Description**

Determines colors for `x` based on [stats::hclust](#). `x` is normalized according [normalize](#).

**Usage**

```
color_hclust(
  x,
  normalize = 1,
  ncol = 2,
  colpal = grDevices::hcl.colors,
  dist = "euclidean",
  na.action = stats::na.pass,
  ...
)
```

**Arguments**

x	a numeric matrix, data frame or "dist" object.
normalize	integer: normalization method (default: 1) <ul style="list-style-type: none"> <li>• 0: no rescaling</li> <li>• 1: <math>(x - \min(x)) / (\max(x) - \min(x))</math></li> <li>• 2: <math>(x - \text{mean}(x)) / \text{sd}(x)</math></li> </ul>
ncol	integer: maximal number colors
colpal	color palette: a function which generates "ncol" colors with "colpal(ncol)" (default: <a href="#">grDevices::hcl.colors</a> )
dist	the distance measure to be used. This must be one of "euclidean", "maximum", "manhattan", "canberra" or "binary"(default: euclidean)
na.action	a function which indicates what should happen when the data contain NAs (default: na.pass)
...	further parameters given to <a href="#">stats::hclust</a>

**Value**

a color vector

**Examples**

```
color_hclust(iris[,-5], ncol=6)
```

---

convertTo

*convertTo*

---

**Description**

Converts an input object (vector, matrix or data frame) to an output according to the format in out. Variable, Row and column names are set, if possible as well as a attribute title.

**Usage**

```
convertTo(x, coln, rown, title, out = c("data.frame", "matrix", "vector"))
```

**Arguments**

x	vector, matrix, or data frame: input
coln	character: column names if possible
rown	character: row names if possible
title	character: for title attribute
out	character: either

**Value**

the desired output object

**Examples**

```
str(convertTo(pi, "Col1", "Row1", "Title", out='data.frame'))
str(convertTo(pi, "Col1", "Row1", "Title", out='matrix'))
str(convertTo(pi, "Col1", "Row1", "Title", out='vector'))
```

---

factor\_data

*factor\_data*

---

**Description**

Creates a single group variable from the data x.

**Usage**

```
factor_data(
  x,
  select = NULL,
  out = c("data.frame", "matrix", "vector"),
  exclude = NULL,
  na.action = stats::na.pass,
  ...,
  title = NULL
)
```

**Arguments**

x	vector, matrix, or data frame
select	vector: indicating columns to select (default: NULL)
out	output as data.frame (default), matrix, or vector
exclude	vector: values to be excluded when forming the set of levels (default: NULL)
na.action	a function which indicates what should happen when the data contain NAs (default: <a href="#">stats::na.pass</a> )
...	further parameters to <a href="#">character_data</a>
title	character: title attribute (default NULL)

**Value**

a one-column matrix with the merged groups

**Examples**

```
factor_data(iris$Species, out="vector")
factor_data(iris)
```

---

formatCommands	<i>formatCommands</i>
----------------	-----------------------

---

**Description**

formatCommands

**Usage**

```
formatCommands(cmds)
```

**Arguments**

cmds                    character: R code

**Value**

HTML code for the splot app

**Examples**

```
formatCommands('print("Hello World!")')
```

---

getModules	<i>getModules</i>
------------	-------------------

---

**Description**

Returns a list of available module as a list.

**Usage**

```
getModules(pattern, path = getShinyOption("smvgraph.path"))
```

**Arguments**

pattern                character: character string containing a regular expression, currently are used plot\_\*.R and color\_\*.R

path                    character: containing the path where to search the modules

**Value**

a list with the modules

**Examples**

```
library("shiny")
getModules('plot_*.R') # get plots
getModules('color_*.R') # get colors
```

---

getval                      *getval*

---

**Description**

Returns val if `length(val)>1`. Otherwise it runs through `args=list(...)` until it finds an element with `length(args[[i]])>0` and returns it. If everything fails NULL will be returned.

**Usage**

```
getval(val, ...)
```

**Arguments**

val	current value
...	sequence of alternative values

**Value**

a value

**Examples**

```
getval(NULL, 0)
getval(1, 0)
```

---

getVariableInfo            *getVariableInfo*

---

**Description**

Returns a data frame with one row for each variable in data:

**Usage**

```
getVariableInfo(data, n = 47)
```

**Arguments**

data	data frame: input data set
n	integer: character length for values (default: 47)

**Details**

- class the [base::class](#) of the variable
- missing the number of missing values
- infinite the number of infinite values
- unique the number of unique values
- valid the number of unique valid values (see [valid](#))
- values the values with the decreasing frequency

**Value**

a data frame with information about the variables of the input data set

**Examples**

```
getVariableInfo(iris)
```

---

<code>getVariableNames</code>	<i>getVariableNames</i>
-------------------------------	-------------------------

---

**Description**

Extracts variable names from a data frame or matrix (column names).

**Usage**

```
getVariableNames(x, xvar = NULL, num = TRUE)
```

**Arguments**

<code>x</code>	data frame/matrix: data set to analyse
<code>xvar</code>	character: variable names to analyse (default: <code>character(0)</code> = all variables)
<code>num</code>	logical: should numerical or non-numerical variable use (default: TRUE)

**Value**

character vector with variable names

**Examples**

```
getVariableNames(iris)
getVariableNames(iris, num=FALSE)
getVariableNames(normalize(iris, 0))
getVariableNames(normalize(iris, 0), num=FALSE)
```



---

jitter_min	<i>jitter_min</i>
------------	-------------------

---

**Description**

Add a small amount of noise to a numeric vector. The result is  $x + \text{runif}(n, -a, a)$  where  $n \leftarrow \text{length}(x)$  and  $a \leftarrow \text{abs}(\text{factor} * \text{amount})$  argument. If  $\text{amount} == 0$  then amount is set to  $1e-6$  times the smallest non-zero distance between adjacent unique  $x$  values. In case of no non-zero distances amount is set to  $1e-6 * (1 + \min(\text{abs}(x)))$ . Note that `jitter_min` delivers different results than [base::jitter](#).

**Usage**

```
jitter_min(x, factor = 1, amount = 0)
```

**Arguments**

<code>x</code>	numeric: vector to which jitter should be added
<code>factor</code>	numeric: multiplier for amount (default: 1)
<code>amount</code>	numeric: amount for jittering (default: 0)

**Value**

jittered data

**Examples**

```
jitter_min(runif(6))
jitter_min(rep(0, 7))
jitter_min(rep(10000, 5))
```

---

loggit	<i>loggit</i>
--------	---------------

---

**Description**

Stores in a temporary file the log messages including messages, warnings and errors.

**Usage**

```
loggit(log_lvl, log_msg)

read_logs()

set_logfile()
```

**Arguments**

`log_lvl` character: Level of log output. In actual practice, one of "DEBUG", "INFO", "WARN", and "ERROR" are common, but any string may be supplied

`log_msg` character: Main log message

**Value**

Nothing.

**Examples**

```
if (interactive()) {
  set_logfile() # create a temporary file for logging
  loggit("DEBUG", "Hello world")
  read_logs() # get a data frame with the current messages.
}
```

---

normalize *normalize*

---

**Description**

Extracts the numeric vectors from a data frame and normalizes each vector. Note: In case that a variable is constant for `method==1` (minmax) the entries will be replaced by 0.5 and for `method==2` (standardization) the entries will be replaced by 0.

**Usage**

```
normalize(x, method = 1)
```

**Arguments**

`x` data.frame or matrix

`method` integer: normalization method (default: 1)

- 0: no rescaling
- 1:  $(x - \min(x)) / (\max(x) - \min(x))$
- 2:  $(x - \text{mean}(x)) / \text{sd}(x)$

**Value**

numeric matrix

**See Also**

In package [normalize](#) or at [CRAN](#)

**Examples**

```
normalize(iris, 2)
```

---

numeric_data	<i>numeric_data</i>
--------------	---------------------

---

## Description

Converts a vector, matrix or data frame into a numeric vector, matrix or data frame.

## Usage

```
numeric_data(  
  x,  
  select = NULL,  
  out = c("data.frame", "matrix", "vector"),  
  na.action = stats::na.pass,  
  ...,  
  title = NULL  
)
```

## Arguments

x	vector, matrix or data frame
select	vector: indicating columns to select (default: NULL)
out	output as data.frame (default), matrix, or vector
na.action	a function which indicates what should happen when the data contain NAs (default: <a href="#">stats::na.pass</a> )
...	unused
title	character: title attribute (default NULL)

## Value

the desired R object

## Examples

```
numeric_data(iris)  
numeric_data(iris, out="matrix")  
numeric_data(iris, out="vector")
```

---

order_andrews	<i>order_andrews</i>
---------------	----------------------

---

**Description**

Returns a reordering of the columns of  $x$  to visualize outliers or clusters better. If no column names are given then  $V1, V2, \dots$  will be used.

**Usage**

```
order_andrews(x, method = 1)
```

**Arguments**

$x$	data matrix
method	numeric: order method (default: 1) <ul style="list-style-type: none"> <li>• 1: interquartile range</li> <li>• 2: <math>\max(x - \text{median}(x))/IQR(x)</math> (outlier)</li> <li>• 3: fit to a Ward cluster solution with euclidean distance</li> </ul>

**Value**

order of column vectors

**Examples**

```
order_andrews(iris)
```

---

order_parcoord	<i>order_parcoord</i>
----------------	-----------------------

---

**Description**

Returns a reordering of the columns of  $x$  to visualize highly correlated variable pairs based on a cluster analysis of the correlation matrix. If no column names are given then  $V1, V2, \dots$  will be used.

**Usage**

```
order_parcoord(x, method = "spearman", ...)
```

**Arguments**

$x$	data matrix
method	numeric: order method (default: "spearman")
$\dots$	further parameters given to <a href="#">stats::cor</a>

**Value**

order of column vectors

**Examples**

```
order_parcoord(iris)
```

---

pyramid

*pyramid*

---

**Description**

pyramid

**Usage**

```
pyramid(
  tab,
  gap = 0,
  left = list(col = "red"),
  right = list(col = "blue"),
  ...
)
```

**Arguments**

tab	table: a table with two columns
gap	numeric(2): relative size of gap in y- and x-direction (default: c(0,0))
left	list: parameters for the left polygons (default: list(col="red"))
right	list: parameters for the right polygons (default: list(col="blue"))
...	further parameters to use in <a href="#">graphics::plot.default</a>

**Value**

a pyramid plot

**Examples**

```
data("Boston", package="MASS")
tab <- table(data.frame(Boston$rad, Boston$chas))
pyramid(tab, main="Absolute frequencies")
pyramid(tab, gap=c(0.2, 0.2))
rtab <- tab/sum(tab)
pyramid(rtab, gap=c(0.2, 0.2), main="Relative frequencies")
ctab <- proportions(tab, 2)
pyramid(ctab, gap=c(0.2, 0.2), main="Conditional frequencies on columns")
rtab <- proportions(tab, 1)
```

```

pyramid(rtab, gap=c(0.2, 0.2), main="Conditional frequencies on rows")
# zebraing
pyramid(tab, gap=c(0.2, 0.2),
        left=list(list(col="black"), list(col="white")),
        right=list(list(col="blue"), list(col="green")))

```

---

resetpar	<i>resetpar</i>
----------	-----------------

---

### Description

Resets the par if necessary.

### Usage

```
resetpar(oldpar)
```

### Arguments

oldpar            graphical parameters

### Value

nothing

### Examples

```
# no examples
```

---

sandrews	<i>sandrews</i>
----------	-----------------

---

### Description

Shiny app for creating an Andrews curve diagram with interactive variable selection.

### Usage

```
sandrews(data, xvar = character(0), ...)
```

### Arguments

data            matrix or data frame  
xvar            character: names of selected variables for the plot  
...            unused

**Value**

nothing

**Examples**

```
if (interactive()) sandrews(iris)
```

---

schernoff

*schernoff*

---

**Description**

Shiny app for creating a Chernoff faces plot with interactive variable selection.

**Usage**

```
schernoff(data, xvar = character(0), ...)
```

**Arguments**

data	matrix or data.frame
xvar	character: names of selected variables for the plot
...	further parameters given to <a href="#">DescTools::PlotFaces</a>

**Value**

nothing

**Examples**

```
if (interactive()) schernoff(normalize(iris))
```

---

sdbscan

*sdbscan*

---

**Description**

Shiny app which allows to run a cluster analysis with DBSCAN with interactive choice of variables, core distance, and minimal neighbours.

**Usage**

```
sdbscan(data, xvar = character(0), ...)
```

**Arguments**

data	matrix or data.frame
xvar	character: names of selected variables for the clustering
...	unused

**Value**

nothing

**Examples**

```
if (interactive()) sdbscan(iris)
```

---

sdistance	<i>sdistance</i>
-----------	------------------

---

**Description**

Shiny app which shows the contribution of each variable to the distance between two observations with interactive variable selection. If  $d_{ijk}$  is the distance between observations  $i$  and  $j$  in variable  $k$  then the contribution is computed:

**Usage**

```
sdistance(data, xvar = character(0), ...)
```

**Arguments**

data	matrix or data.frame
xvar	character: names of selected variables for the plot
...	unused

**Details**

- Total variance:  $var_k/sum(var_k)$  with  $var_k$  the variance of the  $k$ th variable
- Minimum:  $d_{ijk} == \min_k(d_{ijk})$
- Manhattan:  $d_{ijk}/sum(d_{ijk})$
- Gower:  $d_{ijk}$  is rescaled to  $[0, 1]$  in each variable and then  $d_{ijk}/sum(d_{ijk})$
- Euclidean:  $d_{ijk}^2/sum(d_{ijk}^2)$
- Manhattan:  $d_{ijk}/sum(d_{ijk})$
- Maximum:  $d_{ijk} == \max_k(d_{ijk})$

**Value**

nothing



**Examples**

```
if (interactive()) sdistance(iris)
```

---

sfactor	<i>sfactor</i>
---------	----------------

---

**Description**

Shiny app for doing a factor analysis with interactive variable selection.

**Usage**

```
sfactor(data, xvar = character(0), ...)
```

**Arguments**

data	matrix or data frame
xvar	character: names of selected variables for the plot
...	unused

**Value**

nothing

**Examples**

```
if (interactive()) sfactor(iris)
```

---

shclust	<i>shclust</i>
---------	----------------

---

**Description**

Shiny app which allows to run a hierarchical cluster analysis with interactive choice of variables, distance, and agglomeration method.

**Usage**

```
shclust(data, xvar = character(0), ...)
```

**Arguments**

data	matrix or data.frame
xvar	character: names of selected variables for the clustering
...	unused

**Value**

nothing

**Examples**

```
if (interactive()) shclust(iris)
```

---

skmeans

*skmeans*

---

**Description**

Shiny app which allows to run a k-means cluster analysis with interactive choice of variables.

**Usage**

```
skmeans(data, xvar = character(0), ...)
```

**Arguments**

data	matrix or data.frame
xvar	character: names of selected variables for the clustering
...	unused

**Value**

nothing

**Examples**

```
if (interactive()) skmeans(iris)
```

---

smclust

*smclust*

---

**Description**

Shiny app which allows to run a EM clustering with interactive choice of variables.

**Usage**

```
smclust(data, xvar = character(0), ...)
```

**Arguments**

data	matrix or data.frame
xvar	character: names of selected variables for the clustering
...	unused

**Value**

nothing

**Examples**

```
if (interactive()) smclust(iris)
```

---

smosaic	<i>smosaic</i>
---------	----------------

---

**Description**

Shiny app for creating a Mosaic plot with interactive variable selection.

**Usage**

```
smosaic(data, xvar = character(0), yvar = character(0), ...)
```

**Arguments**

data	table or data.frame
xvar	character: names of selected variables for x-axis
yvar	character: names of selected variables for y-axis
...	further parameters given to <a href="#">graphics::mosaicplot</a>

**Value**

nothing

**Examples**

```
if (interactive()) smosaic(Titanic)
dfTitanic <- toDataframe(Titanic)
if (interactive()) smosaic(dfTitanic)
```

---

sortbin	<i>sortbin</i>
---------	----------------

---

### Description

Sorts and bins the rows of the data frame `x` according the sorting columns in `sortCol`. `decreasing` and `na.last` are recycled is necessary. If `equibin` is `TRUE` and `nBins==NA` then `nBins` is set to 100. If `equibin` is `FALSE` and `nBins==NA` then the bins are returned as they come from sorting; only identical values are in one bin. If `nBins` is positive then the bins are merged until `nBins` reached. Note that the numbers of observations per bin may vary.

### Usage

```
sortbin(
  x,
  sortCol = 1,
  decreasing = FALSE,
  na.last = TRUE,
  nBins = NA,
  equibin = TRUE
)
```

### Arguments

<code>x</code>	data frame
<code>sortCol</code>	numeric/character: names or indices of variable used for sorting (default: 1)
<code>decreasing</code>	logical: should the sort order be increasing or decreasing (default: FALSE)
<code>na.last</code>	logical: for controlling the treatment of NAs (default: TRUE)
<code>nBins</code>	integer: maximal number of bins (default: NA).
<code>equibin</code>	logical: should the number of observations equal per bin (default: TRUE)

### Value

(non-sequential) bin numbers as integer

### Examples

```
data("Boston", package="MASS")
tableplot(Boston, bin=sortbin(Boston))
```

---

spairs	<i>spairs</i>
--------	---------------

---

**Description**

Shiny app for creating a scatterplot matrix with interactive variable selection.

**Usage**

```
spairs(data, xvar = character(0), ...)
```

**Arguments**

data	matrix or data.frame
xvar	character: names of selected variables for the plot
...	further parameters given to <a href="#">graphics::pairs</a>

**Value**

nothing

**Examples**

```
if (interactive()) spairs(iris)
```

---

sparcoord	<i>sandrews</i>
-----------	-----------------

---

**Description**

Shiny app for creating a Parallel Coordinate plot with interactive variable selection.

**Usage**

```
sparcoord(data, xvar = character(0), ...)
```

**Arguments**

data	matrix or data.frame
xvar	character: names of selected variables for the plot
...	further parameters given to <a href="#">MASS::parcoord</a>

**Value**

nothing

**Examples**

```
if (interactive()) sparcoord(iris)
```

---

splot

*splot*

---

**Description**

Shiny app for choosing a specific plot.

**Usage**

```
splot(data, xvar = character(0), path = NULL)
```

**Arguments**

data	data.frame: input data
xvar	character: selected variables (default: character(0))
path	character: path where to read the plot modules (default: NULL)

**Value**

nothing

**Examples**

```
if (interactive()) splot(iris)
```

---

sradar

*sradar*

---

**Description**

Shiny app for creating radar charts with interactive variable selection.

**Usage**

```
sradar(data, xvar = character(0), ...)
```

**Arguments**

data	matrix or data.frame
xvar	character: names of selected variables for the plot
...	unused

**Value**

nothing

**Examples**

```
if (interactive()) sradar(iris)
```

---



*tableplot*


---

**Description**

A tableplot is a visualisation of multivariate data sets. Each column represents a variable and each row bin is an aggregate of a certain number of records. For numeric variables, a value box is plotted with minimum, mean (black line) and maximum value. If any missing values in a bin of a numeric variable appear the box left from the value box is plotted in gray. For categorical variables, a stacked bar chart is depicted of the proportions of categories. Missing values are taken into account.

**Usage**

```
tableplot(
  x,
  select = NULL,
  subset = NULL,
  bin = NULL,
  yj = NA,
  IQR_bias = 5,
  colpal = grDevices::rainbow,
  color.NA_num = "gray75",
  color.NA = "grey75",
  color.num = "lightblue",
  color.box = "deepskyblue",
  color.line = "black",
  box.lower = NULL,
  box.upper = NULL,
  box.line = NULL,
  cex.main = 1,
  cex.legend = 1,
  width = 1,
  height = 0.15
)
```

**Arguments**

x	data frame
select	numeric/character: variable to show in the plot (default: NULL)

subset	numeric: index of observations to show
bin	integer: bin numbers to which a observations belongs (default: NULL = all)
yj	numeric: Yeo Johnson coefficient (default: NA). If NA then it will be set to 0 (=log) or 1 (=identity)
IQR_bias	numeric: parameter that determines when a logarithmic scale is used when yj is set to NA. The argument IQR_bias is multiplied by the interquartile range as a test.
colpal	color palette to draw (default: rainbow)
color.NA_num	color for missing of infinity values for numeric variables (default: gray75)
color.NA	color for missing values for categorical variables (default: grey75)
color.num	color for lower box for numeric variables (default: lightblue)
color.box	color for upper box for numeric variables (default: deepskyblue)
color.line	color for line in upper box for numeric variables (default: black)
box.lower	function: determine lower border in upper box for numeric variables (default: NULL). If NULL then <code>min(., na.rm=TRUE)</code> is used.
box.upper	function: determine upper border in upper box for numeric variables (default: NULL). If NULL then <code>max(., na.rm=TRUE)</code> is used.
box.line	function: determine line position in upper box for numeric variables (default: NULL). If NULL then <code>mean(., na.rm=TRUE)</code> is used.
cex.main	number: magnification to be used for the titles (default: 1)
cex.legend	number: magnification to be used for the legends (default: 1)
width	number: width of percentage axis (default: 1). If 1 then the width is as wide as a plot.
height	number: percentage of the height of the legends (default: 0.15)

### Details

The idea and some code of the tableplot is taken from [tableplot package](#) by Martijn Tennekes and Edwin de Jonge. It differs from their package by

- multicolumn sorting is possible, and
- no support for 'ff' (out of memory vectors).

### Value

nothing

### References

Tennekes, M., Jonge, E. de, Daas, P.J.H. (2013), Visualizing and Inspecting Large Datasets with Tableplots, *Journal of Data Science* 11 (1), 43-58.

### Examples

```
data("Boston", package="MASS")
tableplot(Boston, bin=sortbin(Boston))
```



---

template	<i>template</i>
----------	-----------------

---

**Description**

Each line of a code template consists of condition based on the unnamed parameters and R code in which replacements with named parameters done.

**Usage**

```
template(text, ...)
```

**Arguments**

text	a code template
...	further parameters

**Value**

a character vector

**Examples**

```
template("
1: 'Hello {{letter}}'
!1: 'Good-bye {{letter}}'
",
  letter=sample(LETTERS, 1),
  runif(1)<0.5 #1 = first unnamed parameter
)
```

---

testdata	<i>Test data</i>
----------	------------------

---

**Description**

A data frame containing various variable types and special values.

**Usage**

```
testdata
```

**Format**

A data frame with n=25 rows and 8 variables:

```

xu  runif(n) with a NA, NaN, Inf, -Inf
xn  rnorm(n, 0, 2) with a NA, NaN
x0  rep(0, n)
xi  as.integer(rnorm(n, 0, 2) with a NA, NaN
x2  sample(c(0,1), size=n, replace=TRUE)
gf  factor(as.integer(rnorm(n, 0, 2)) with a NA
go  ordered(as.integer(rnorm(n, 0, 2)) with a new level 10
gn  ordered(as.integer(rnorm(n, 0, 2)) with a NA
gc  as.character(as.integer(rnorm(n, 0, 2)) with a NA and ""
gl  sample(c(T,F), size=n, replace=TRUE) with a NA
g0  rep("constant, n)
g2  sample(c(T,F), size=n, replace=TRUE)

```

---

toChoice

*toChoice*


---

**Description**

The elements in ... will coerced into one text vector. The entries will either the text (method==NA) or integer number starting at method. The first letter of the list element names will be capitalized.

**Usage**

```
toChoice(method = NA, ...)
```

**Arguments**

```

method      integer: which method is used for creating the list elements
...         character: choice values

```

**Value**

a list

**Examples**

```

txt <- c("the", "quick", "brown", "fox", "jumps", "over", "the", "lazy", "dog")
toChoice(NA, txt)
toChoice(0, txt) # integer sequence starts at zero

```

---

toDataframe	<i>toDataframe</i>
-------------	--------------------

---

**Description**

Converts a table to a full data frame.

**Usage**

```
toDataframe(obj, name = NULL, ...)
```

**Arguments**

obj	R object (table or ts) to convert to a data frame
name	character: vector of variable name(s), only use for a ts object
...	further parameters given to <a href="#">base::as.data.frame.table</a>

**Value**

a data frame

**Examples**

```
toDataframe(Titanic)
toDataframe(austres)
```

---

toLayout	<i>toLayout</i>
----------	-----------------

---

**Description**

Given a (minimal) length len and the number unused entries a layout is generated. If sel<0 then less rows and more columns are used and if sel>0 then more rows and less columns are used.

**Usage**

```
toLayout(len, sel = 0, unused = 0)
```

**Arguments**

len	integer: minimal size of layout
sel	integer: select less or more rows (default: 0)
unused	integer: number of unused entries (default: 0)

**Value**

a matrix

**Examples**

```
toLayout(13)
```

---

toRDS

*toRDS*

---

**Description**

Saves one or more data sets in RDS format to a temporary directory (`tmpdir()`). Data sets must have the class `ts` or something that can be converted to a data frame, e.g. `matrix`, `table`, etc.

**Usage**

```
toRDS(...)
```

**Arguments**

... data sets to save

**Value**

returns the name of the created files

**Examples**

```
toRDS(Titanic) # saves to tmpdir/Titanic.rds
```

---

trend\_season

*Trend and aeasonality estimation of a univariate time series*

---

**Description**

Estimate a trend and seasonality for a time series. Available functions:

- `trend_season` to generate an estimate
- `print` to print the estimate
- `summary` to summarize the estimate result
- `plot` to plot the time series, its estimation and the residuals
- `coef` to extract the coefficients if a seasonality estimation was done
- `residuals` to extract the residuals of the model
- `fitted` to the fitted values

**Usage**

```

trend_season(t, ...)

## Default S3 method:
trend_season(
  t,
  trend = c("constant", "linear", "exponential"),
  season = c("none", "additive", "multiplicative"),
  ...
)

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

## S3 method for class 'trend_season'
summary(object, ...)

## S3 method for class 'trend_season'
plot(x, y, which = 1, ...)

```

**Arguments**

t	ts: time series object
...	unused
trend	character: trend method, either none (default), linear or exponential
season	character: seasonality method, either none (default), additive or multiplicative
x, object	trend_season: estimated time series
y	unused
which	integer: what to plot, 1 time series and estimation (default) or 2 residuals

**Value**

trend\_season returns a trend\_season object with

- call the function call
- ts the input time series
- trend the trend estimation (ts object)
- trend.residuals the residuals of the trend estimation (ts object)
- season the trend and season estimation (ts object)
- season.residuals the residuals of the trend and season estimation (ts object)
- coefficients the coefficients used in the seasonality estimation
- residuals the residuals of the model
- fitted.values the fitted values of the model

**Examples**

```
tts <- trend_season(austres, "linear")
print(tts)
summary(tts)
plot(tts)
plot(tts, which=2)
residuals(tts)
fitted(tts)
coef(tts) # if NULL then no seasonality was estimated
```

---

UIdatanormalization    *General UI elements*

---

**Description**

Some general UI elements for common use where last selected value is stored for reuse:

- UIplotype plot type, defines smvgraph\_type
- UIpointsymbol plot symbol for point, defines smvgraph\_pch
- UIpointsize point size, defines smvgraph\_cex
- UIlinetype line type, defines smvgraph\_lty
- UIlinewidth line width, defines smvgraph\_lwd
- UItextsize text size, defines smvgraph\_tex
- UIlegend legend position, defines smvgraph\_legend
- UIlegendsize legend size, defines smvgraph\_lex
- UIdatanormalization should data be rescaled, defines smvgraph\_normalize (no, minMax, mstandardization)
- UIdistance distance to use, defines smvgraph\_distance
- UIobservations range of observations, defines smvgraph\_obs
- UImergegroups should a set of grouping variables merged into one group variable, defines smvgraph\_single

From the top menu are the following input elements are defined

- input\$smvgraph\_pch point symbol,
- input\$smvgraph\_cex point size,
- input\$smvgraph\_lty line type,
- input\$smvgraph\_lwd line width,
- input\$smvgraph\_tex text size, and
- input\$smvgraph\_legend legend position.

**Usage**

```

UIdataNormalization(
  sel = getShinyOption("smvgraph.current")$smvgraph_normalize
)

UIdistance(sel = getShinyOption("smvgraph.current")$smvgraph_distance)

UIobservations(n, sel = getShinyOption("smvgraph.current")$smvgraph_obs)

UImergegroups(n, sel = getShinyOption("smvgraph.current")$smvgraph_single)

UIpointsize(n, sel = getShinyOption("smvgraph.current")$smvgraph_cex)

UIpointsymbol(n, sel = getShinyOption("smvgraph.current")$smvgraph_pch)

UIlinewidth(n, sel = getShinyOption("smvgraph.current")$smvgraph_lwd)

UIlinetype(n, sel = getShinyOption("smvgraph.current")$smvgraph_lty)

UITextsize(n, sel = getShinyOption("smvgraph.current")$smvgraph_tex)

UIlegend(n, sel = getShinyOption("smvgraph.current")$smvgraph_legend)

UIlegendsize(n, sel = getShinyOption("smvgraph.current")$smvgraph_lex)

UIplottype(n, sel = getShinyOption("smvgraph.current")$smvgraph_type)

```

**Arguments**

sel	selected element
n	integer: number of observations

**Value**

an UI element for shiny

**Examples**

```
# none
```

---

 valid

*valid, invalid*


---

**Description**

Computes the number a logical matrix or vector if all values are valid in x or each column or row of x. Valid values for numeric variables are `is.finite(v)` and for other types `!is.na`

Computes the number a logical matrix or vector if any values are valid in x or each column or row of x.

**Usage**

```
valid(x, margin = 1:2, n = FALSE)
```

```
invalid(x, margin = 1:2, n = FALSE)
```

**Arguments**

x	object: anything taht can be coerced to a data frame checked for valid/invalid values
margin	integer: a vector giving the subscripts for which valid/invalid values looked for, e.g. <code>margin==1</code> indicates rows, <code>margin==2</code> indicates columns, otherwise indicates rows and columns.
n	logical: should just the number of valid/invalid values returned or a logical matrix/vector

**Value**

a logical data frame, a logical vector or an integer

**Examples**

```
data("testdata")
valid(testdata)           # matrix with logical entries if x has valid entry
valid(testdata, n=TRUE)  # number of valid entries in x
valid(testdata, 1)       # vector with logical entries if each row if x has valid entries
valid(testdata, 1, n=TRUE) # number of rows with valid entries in x
valid(testdata$xu)
```

---

with\_progress

*Progress*

---

**Description**

Reports progress to the user during long-running operations.

**Usage**

```
with_progress(...)
```

```
set_progress(...)
```

```
inc_progress(...)
```



**Arguments**

... see [\[shiny::withProgress\]](#)

**Value**

see [\[shiny::withProgress\]](#)

**Examples**

```
## Only run examples in interactive R sessions
if (interactive()) {
  options(device.ask.default = FALSE)
  ui <- fluidPage(plotOutput("plot"))
  #
  server <- function(input, output) {
    output$plot <- renderPlot({
      with_progress(message = 'Calculation in progress',
                    detail = 'This may take a while...', value = 0, {
        for (i in 1:15) {
          inc_progress(1/15)
          Sys.sleep(0.25)
        }
      })
    plot(cars)
  })
}
#
shinyApp(ui, server)
}
```

---

yeo.johnson

*yeo.johnson*

---

**Description**

Computes the Yeo-Johnson transformation, which is a normalizing transformation. The code and documentation is taken from the **VGAM** package (see function `yeo.johnson`) with some slight modifications, e.g. NA's are kept and do not produce an error.

**Usage**

```
yeo.johnson(
  y,
  lambda,
  derivative = 0,
  epsilon = sqrt(.Machine$double.eps),
  inverse = FALSE
)
```

**Arguments**

<code>y</code>	numeric: a vector or matrix.
<code>lambda</code>	numeric: It is recycled to the same length as <code>y</code> if necessary.
<code>derivative</code>	non-negative integer: the default is the ordinary function evaluation, otherwise the derivative with respect to <code>lambda</code> (default: 0)
<code>epsilon</code>	numeric and positive value: the tolerance given to values of <code>lambda</code> when comparing it to 0 or 2.
<code>inverse</code>	logical: return the inverse transformation? (default: FALSE)

**Details**

The Yeo-Johnson transformation can be thought of as an extension of the Box-Cox transformation. It handles both positive and negative values, whereas the Box-Cox transformation only handles positive values. Both can be used to transform the data so as to improve normality.

**Value**

The Yeo-Johnson transformation or its inverse, or its derivatives with respect to `lambda`, of `y`.

**Note**

If `inverse = TRUE` then the argument `derivative = 0` is required.

**References**

Yeo, I.-K. and Johnson, R. A. (2000). A new family of power transformations to improve normality or symmetry. *Biometrika*, **87**, 954–959.

**See Also**

VGAM: `yeo.johnson`, [boxcox](#).

**Examples**

```

y <- seq(-4, 4, len = (nn <- 200))
ltry <- c(0, 0.5, 1, 1.5, 2) # Try these values of lambda
lltry <- length(ltry)
psi <- matrix(as.numeric(NA), nn, lltry)
for (ii in 1:lltry)
  psi[, ii] <- yeo.johnson(y, lambda = ltry[ii])
matplot(y, psi, type = "l", ylim = c(-4, 4), lwd = 2, lty = 1:lltry,
        ylab = "Yeo-Johnson transformation", col = 1:lltry, las = 1,
        main = "Yeo-Johnson transformation with some values of lambda")
abline(v = 0, h = 0)
legend(x = 1, y = -0.5, lty = 1:lltry, legend = as.character(ltry),
      lwd = 2, col = 1:lltry)

```

---

zzz

zzz

---

**Description**

Runs all s . . . functions for test purposes if interactively called.

**Usage**

zzz()

**Value**

nothing

**Examples**

zzz()

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