

Package: gamlss.prepdata (via r-universe)

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Type Package

Title Preparing Data for Fitting a Generalized Additive Model for Location Scale and Shape

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Description Functions for preparing data to fit a Generalized Additive Models for Location Scale and Shape from the 'gamlss' or 'gamlss2' package, Stasinopoulos and Rigby (2007) <[doi:10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07)>, using for graphical methods 'ggplot2'.

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URL <https://www.gamlss.com/>

BugReports <https://github.com/gamlss-dev/gamlss.prepdata/issues>

Depends R (>= 3.5.0), gamlss.dist, gamlss (>= 4.3.3), gamlss.foreach

Imports methods, ggridges, ellipse, gamlss.inf, foreach, mgcv, ggplot2, yaImpute, gamlss.ggplots

Suggests glmnet, reshape2, igraph, networkD3, grid, gridExtra

LazyLoad yes

Repository <https://gamlss-dev.r-universe.dev>

RemoteUrl <https://github.com/gamlss-dev/gamlss.prepdata>

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Contents

gamlss.prepdata-package	2
data_cor	3
data_dim	6
data_inter	8
data_leverage	10

data_outliers	11
data_part	12
data_rm	15
data_scale	16
data_str	18
data_void	19
data_xyplot	22

Index	25
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gamlss.prepdata-package

*Prepering Data for Fitting a Generalized Additive Model for Location
Scale and Shape*

Description

Functions for prepering data to fit a Generalized Additive Models for Location Scale and Shape from the 'gamlss' or 'gamlss2' package, Stasinopoulos and Rigby (2007) <doi:10.18637/jss.v023.i07>, using for graphical methods 'ggplot2'.

Details

The DESCRIPTION file: This package was not yet installed at build time.

Index: This package was not yet installed at build time.

The following convention has been used to name the functions:

y_NAME: plots concerning fitted values from a single fitted model

data_NAME: plots concerning residuals from a single fitted model

where NAME refer to different characteristics.

Author(s)

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References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi:10.1201/9780429298547. An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M., Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi:10.18637/jss.v023.i07.

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi:10.1201/b21973

Stasinopoulos, M. D., Rigby, R. A., and De Bastiani F., (2018) GAMLSS: a distributional regression approach, *Statistical Modelling*, Vol. **18**, pp, 248-273, SAGE Publications Sage India: New Delhi, India.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[gamlss](#), [gamlss.family](#)

Examples

```
data(rent)
rent |> data_str()
```

data_cor

Plotting pairwise linear and partial correlations.

Description

The function `data_cor` takes a data frame and plots the pairwise Pearson's correlation coefficients of all continuous variables in the data.

The function `data_pcor` takes a data frame and plots the pairwise partial Pearson's correlation coefficients of all continuous variables in the data.

The function `data_association` takes a data frame and plots the pairwise association coefficients of all variables in the data. For continuous against continuous variables it shows the absolute value of the Pearson's correlation coefficient, for categorical against categorical it shows Cramer's ϕ , for continuous against categorical it fit an analysis of variance model and reports the square root of the R^2 .

The functions `high_val` and `low_val` take the square matrix generated by the above three functions and shows which pair-wise have a value larger or smaller respectively, than the value specified by the argument `val`.

Usage

```
data_cor(data, digits = 3, plot = TRUE, diag.off = TRUE,
         lower.tri.off = FALSE, method = c("square", "circle"),
         type = c("pearson", "kendall", "spearman"),
         outline.color = "gray", colors = c("blue", "white", "red"),
```

```

legend.title = "Corr", title, ggtheme = theme_minimal(),
tl.cex = 12, tl.col = "black", tl.srt = 45, lab = TRUE,
lab_col = "black", lab_size = 3, circle.size = 20, seed = 123,
percentage)

data_pcor(data, digits = 3, plot = TRUE, diag.off = TRUE,
lower.tri.off = FALSE, method = c("square", "circle"),
outline.color = "gray", colors = c("blue", "white", "red"),
legend.title = "Corr", title, ggtheme = theme_minimal(),
tl.cex = 12, tl.col = "black", tl.srt = 45, lab = TRUE,
lab_col = "black", lab_size = 3, circle.size = 20, seed = 123,
percentage)

data_association(data, digits = 3, plot = TRUE, diag.off = TRUE,
lower.tri.off = FALSE, method = c("square", "circle"),
outline.color = "gray", colors = c("blue", "white", "red"),
legend.title = "Assoc", title, ggtheme = ggplot2::theme_minimal(),
tl.cex = 12, tl.col = "black", tl.srt = 45, lab = TRUE,
lab_col = "black", lab_size = 3, circle.size = 20, seed = 123, percentage)

high_val(table, val = 0.90, digits = 3, plot = FALSE, igrph = TRUE)

low_val(table, val = 0.05, digits = 3, plot = FALSE, igrph = TRUE)

```

Arguments

data	a data frame
table	a correlation table obtained by <code>data_cor(,plot=FALSE)</code> or <code>data_pcor(,plot=FALSE)</code>
digits	the digits for printing the correlation coefficients
plot	whether to plot or not
diag.off	whether to show the diagonal elements
lower.tri.off	whether to show the lower part of the matrix
method	plotting in "square" or "circle"
type	type of correlation <code>c("pearson", "kendall", "spearman")</code>
outline.color	the outline colour
colors	the range of colours
legend.title	title for the legend
title	the main title
ggtheme	the theme for the plot, see package ggthemes for more themes
tl.cex	the text size for the marginal labels
tl.col	the colour of the marginal labels
tl.srt	the angle of the text in the bottom labels of the table
lab	whether to show the correlation coefficients in the table
lab_col	the colour of the lettering of the correlation coefficients

lab_size	the size of the lettering of the correlation coefficients, increase (or decrease) if the default 3 is not appropriate
circle.size	the size of the circles, increase (or decrease) if the default 20 is not appropriate
percentage	this is for big data sets. if more than a million only 10% is plotted, if from 100.00 to a million, 20%, if 50.000 to 100.000, 50% otherwise 100% of the data.
seed	Setting a seed value for selection of the percentage of data (for big data sets)
val	the threshold value so if the actual value is greater than val it will be reported in high_val()
igraph	if in high_val(), the option plot=TRUE is set, then there are two options for plotting; i) igraph::graph_from_data_frame() with igraph=TRUE or ii) networkD3::simpleNetwork with igraph=FALSE

Value

creates a correlation matrix plot.

Author(s)

Mikis Stasinopoulos

References

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. doi:10.1201/9780429298547.

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi:10.1201/b21973

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. 56). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

mcor

Examples

```
data_cor(rent99)
Pearson.cor <- data_cor(rent99, plot=FALSE)
```

```
data_pcor(rent99)
partial.cor <- data_cor(rent99, plot=FALSE)
```

```
high_val(partial.cor, val=0.5)
high_val(Pearson.cor, val=0.5)
```

`data_dim`*Function to get information from data.*

Description

This is a set of function are designed to help the user to deal with new data sets.

`data_dim()`: the class, the dimension and the % NA's in the data

`data_which_na()`: which variables have NA's and how many

`data_omit()`: omit the NA's from the data.

`data_names()`: The names of the variables in the data.

`data_shorter_names()`: abbreviate the names up to specified digits.

`data_rename()` renames some of of the variables.

Usage

```
data_dim(data)
```

```
data_which_na(data)
```

```
data_omit(data)
```

```
data_names(data)
```

```
data_shorter_names(data, max = 5, newnames)
```

```
data_rename(data, oldnames, newnames)
```

Arguments

<code>data</code>	a data frame
<code>max</code>	the maximum number of characters allowed, with default 5. Make sure that you are using enough characters otherwise you could end up with variables with the same name
<code>newnames</code>	New names if not abbreviation is required, as characters
<code>oldnames</code>	the old names as characters

Details

The function `data_dim()` gives the the class, the dimension and the % NA's in the data.

The function `data_which_na()` gives the number of missing observation for each variable in the data.

The function `data_omit()`: omits the NA's from the data.

The function `data_names()` gives the names of the variables.

The function `data_shorter_names()` takes the current names and abbreviates to max characters.

The function `data_rename()` renames variable from the data.

Value

The function `data_dim()` after printing gives the original data set.

The function `data_which_na()` prints the number of missing observations for each variable in the data and passes the original data set.

The function `data_omit()`: omits the NA's from the data and passes the new data set.

The function `data_names()` prints the names of the variables in the data and passes the original data.

The function `data_shorter_names()` takes the current names and abbreviates to max characters and returns the data with shorter names.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <https://www.jstatsoft.org/v23/i07/>.

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[data_cor](#)

Examples

```
data_dim(rent)
data_which_na(rent)
data_omit(rent)
data_names(rent)
data_shorter_names(rent)
pp=data_rename(rent, c("R", "F1"), c("rent", "floor"))
data_names(pp)
```

data_inter *Identifying Pair-Wise Interactions in the Data Frames*

Description

The function `data_inter()` is trying to identify pair-wise interactions given the response variable using linear regression methodology. At the moment it works only with continuous response variables.

Usage

```
data_inter(data, response, weights, digits = 3, plot = TRUE,
           lower.tri.off = TRUE,
           method = c("circle", "square"), fit.method = c("linear", "nonlinear"),
           outline.color = "gray", colors = c("blue", "white", "red"),
           legend.title = "Inter", title, ggtheme = theme_minimal(),
           tl.cex = 12, tl.col = "black", tl.srt = 45, lab = TRUE,
           lab_col = "black", lab_size = 3, circle.size = 20, seed = 123,
           percentage)
```

Arguments

<code>data</code>	a data frame
<code>response</code>	the response variable
<code>weights</code>	prior weights
<code>digits</code>	the number of digits in the plot
<code>plot</code>	whether to plot the results
<code>lower.tri.off</code>	whether to show the lower part of the matrix
<code>method</code>	plotting in "square" or "circle"
<code>fit.method</code>	whether in "linear" or "nonlinear"
<code>outline.color</code>	the outline colour
<code>colors</code>	the range of colours
<code>legend.title</code>	title for the legend
<code>title</code>	the main title
<code>ggtheme</code>	the theme for the plot, see package ggthemes for more themes
<code>tl.cex</code>	the text size for the marginal labels
<code>tl.col</code>	the colour of the marginal labels
<code>tl.srt</code>	the angle of the text in the bottom labels of the table
<code>lab</code>	whether to show the correlation coefficients in the table
<code>lab_col</code>	the colour of the lettering of the correlation coefficients
<code>lab_size</code>	the size of the lettering of the correlation coefficients, increase (or decrease) if the default 3 is not appropriate

circle.size	the size of the circles, increase (or decrease) if the default 20 is not appropriate
percentage	the percentage of data to show if the observation number is too big
seed	Setting a seed value for selection of the percentage of data (for big data sets)

Details

The function `data_inter()` uses the function `z_scores()` to standardized the continuous response variable and then uses linear model fits to establish whether the first order interactions between the the x 's are significant or not. It reports the significant level based on Chi-square tests. Note that for large data sets it uses the function `data_cut()` to cut randomly the size of the data in order to use `ggplo2` graphs to plot it.

Typically for linear model first order interaction it fits the models $y \sim x_1 + x_2$ and $y \sim x_1 * x_2$, respectively, and calculated significant level based on the difference in deviances. Under the H_0 hypothesis the difference in deviances follow be a Chi-square distribution with degrees of freedom based on the difference of the degrees of freedom of the two fitted models.

Value

It produce a plot `plot=TRUE` or a square upper triangular table.

Note

The function `data_inter()` works only for continuous responses.

Author(s)

Mikis Stasinopoulos

References

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. doi:10.1201/9780429298547.

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi:10.1201/b21973

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. 56). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[data_cor](#)

Examples

```
data_inter(rent[, -4,5], response=R)
```

data_leverage *Finding high leverage points*

Description

The function `data_leverage()` uses linear model methodology to identify unusual observations in the explanatory variables.

Usage

```
data_leverage(data, response, weights, quan.val = 0.99, annotate = TRUE,
               line.col = "steelblue4", point.col = "steelblue4", annot.col = "darkred",
               plot = TRUE, title, percentage, seed = 123, ...)
```

Arguments

<code>data</code>	a data frame
<code>response</code>	the response variable
<code>weights</code>	prior weights
<code>quan.val</code>	the quantile value to plot the line
<code>annotate</code>	whether to annotate the points
<code>line.col</code>	the colour of the horizontal line
<code>point.col</code>	the colour of the leverage points
<code>annot.col</code>	the colour of the annotated points
<code>plot</code>	whether to plot
<code>title</code>	whether to put a title
<code>percentage</code>	for very large data the percentage of points to use in the calculations
<code>seed</code>	the seed needed for selecting a subset of data if only a percentage of points are plotted
<code>...</code>	for extra argument

Details

The method used is as follows. Fit a linear model to all explanatory variables in the data and calculate the leverage points.

Value

The function plots the leverage points unless `plot=FALSE` is used where in this case the leverage points can be saved.

Author(s)

Mikis Stasinopoulos

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <https://www.jstatsoft.org/v23/i07/>.
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.
- Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.
- (see also <https://www.gamlss.com/>).

See Also

[data_outliers](#)

Examples

```
data_leverage(rent, response=R)
```

data_outliers	<i>Outlier identification</i>
---------------	-------------------------------

Description

Those two function identify outliers in variables in data

Usage

```
data_outliers(data, value = 4, min.distinct = 50, family = SHASHo)
```

```
y_outliers(var, value = 4, family = SHASH)
```

Arguments

data	a data frame
var	a continues variable
value	max value from which the absolute value of the z-scores should be greater to identify outliers
min.distinct	if a variable has less distinct values than min.distinct is excluded
family	the distribution family used for standardization

Details

the continuous variables are power transformed and then standardised

Value

return a list

Author(s)

Mikis Stasinopoulos

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <https://www.jstatsoft.org/v23/i07/>.

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[data_names](#)

Examples

```
da <- rent99[,-2]
data_outliers(da)
```

Description

The function `data_part()` takes a data set and creates a new identical data set with an extra factor called `partition` which can be used to allocate data in different data sets.

- i) if `partition=2` the factor has two levels `train`, and `test`.
- ii) if `partition=3` the factor has three levels `train`, for training data, `val` for validation data and `test` for test data.
- iii) if `partition > 4` say `K` then the levels are "1", "2"..."`K`". The factor then can be used for `K` cross validation sets.

the function `data_part_list()` in does similar things like the function `data_part()` but instead of adding a factor to the data creates a list with elements the training, test and validation data sets. Note that this function do not allow k-fold cross-validation or bootstrapping indexing.

The function `data_part_index()` takes a `data.frame` and produces a list of indices which then can be used to select different sections of the data.

The function `data_cut()` takes a `data.frame` and selects randomly specified % of the data. For `data.frames` with more than 50.000 observations is automatically select part of the data. The function `data_cut()` is used a lot in the plotting routines to make sure that plots are not take for ever.

Usage

```
data_part(data, partition = 2L, probs, setseed = 123, ...)
```

```
data_part_list(data, partition = 2, probs, setseed = 123, ...)
```

```
data_part_index(data, K = 2, bootstrap = FALSE)
```

```
data_cut(data, percentage, seed = 123)
```

Arguments

<code>data</code>	a <code>data.frame</code>
<code>partition</code>	2, 3 or a number less than 20
<code>K</code>	the number of partitions
<code>bootstrap</code>	whether bootstrap of k-fold cross validation samples
<code>probs</code>	probabilities for the random selection
<code>setseed</code>	setting the seed so the process can be repeated
<code>percentage</code>	The percentage of data to keep. If set, i.e. <code>percentage=0.5</code> only 50% are kept otherwise for large data set (more than 50.000) only percentage of data are kept.
<code>seed</code>	the <code>set.seed()</code> argument
<code>...</code>	extra arguments

Value

Both function produce a data frame. The function `data_part()` adds a factor partition while `data_rm1val()` removes variable with only one value.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <https://www.jstatsoft.org/v23/i07/>.

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[data_str](#)

Examples

```
da <- data_part(rent)
head(da)
mosaicplot(table(da$partition))

da.train <- subset(da, partition=="train")
da.test <- subset(da, partition=="test")
dim(da.train)
dim(da.test)

allda <- data_part_list(rent)
dim(allda[[1]]) # training data
dim(allda[[2]]) # test data

index <- data_part_index(rent)
trdata <- rent[index[[1]],]
tedata <- rent[index[[2]],]
dim(trdata)
dim(tedata)
dim(trdata)[1]+dim(tedata)[1]
dim(rent)
```

Description

There are several function operating on a data.frame and export a data.frame. The functions are

1) data_rm(): this function removes the variables specified by vars from the data.frame. Note that vars can take either character names or numbers.

2) data_rm1val(): This function looks for variables with a unique distinct value (most likely factors left from a previous subset() operation) and remove them form the data.

3) data_exclude_class(): This function looks for variable (columns) of a specified 'R' class and remove them from the data. The default class is "factor".

4) data_only_continuous(): This function pick up only the continuous variable in the data.frame.

5) data_select(): This function select only the variables in the vars list and save the data.

Usage

```
data_rm(data, vars)
```

```
data_rm1val(data)
```

```
data_exclude_class(data, class.out = "factor")
```

```
data_only_continuous(data)
```

```
data_select(data, vars)
```

```
data_rmNAvars(data)
```

Arguments

data	a data frame
vars	selected variables (columns from the data frame)
class.out	a specific variable class to be excluded form the data frame

Details

All the above functions can be used for piping i.e. da |> data_rm1val().

Value

return a data.frame

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

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(see also <https://www.gamlss.com/>).

See Also

data_cor

Examples

```
library(gamlss)
da <- rent |> data_rm( vars=c("Sp", "Sm"))
head(da)

da<- rent |> data_exclude_class()
head(da)

da<- data_only_continuous(rent)
head(da)

da <- rent |> data_select( vars=c("R", "F1", "A"))
head(da)
```

data_scale

Scaling Continuous Variables in Data

Description

The function `data_scale()` takes a data.frame and creates a new data set with all continuous variable standardised. The standardization can be

- i) scale 0 variance 1 which is equivalent to have the options `scale.to="z-scores"` and `family="NO"`. That is the z-scores after fitting a normal distribution to a continuous variable
- ii) A more general z-score using say `scale.to="z-scores"` and `family="SHASH"` in which case correction to the skewness and kurtosis is done to the specified variable or
- iii) the range is restricted from zero to one, i.e. `scale.to="0to1"`.

Usage

```
data_scale(data, response, position.response = NULL,
           scale.to = c("z-scores", "0to1"), family = "NO",
           scale.response = FALSE)
```

Arguments

data	A data frame
response	The name of the response variable
position.response	or the position of the response variable in the data.
scale.to	how to scape by normalization, scale.to="z-scores" or range 0 to 1 scale.to="0to1".
family	The family used in the standarization, defaul is family="NO" but any other continuous family from $-Inf$ to $+Inf$ will do i.e. family="SHASH".
scale.response	whether to scale also the response. The default value is scale.response=FALSE because in GAMLSS we are hoping to get the right family for the response.

Value

A data frame is return with all continous variables standarised.

Author(s)

Mikis Stasinopolos

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

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(see also <https://www.gamlss.com/>).

See Also

[data_zscores](#)

Examples

```
rent[, -c(4,5)] |> data_scale(, response=R)|> head()
```

data_str	<i>Function applied to data</i>
----------	---------------------------------

Description

his is a set of function are designed to help the user to deal with the structure of new data sets.

Usage

```
data_str(data, min.values = 100, min.levels = 10)

y_distinct(var)

data_distinct(data, get.distinct = FALSE, print=TRUE)

data_cha2fac(data, show.str = FALSE)

data_few2fac(data, min.levels = 10, show.str = FALSE)

data_int2num(data, min.values = 50, show.str = FALSE)

data_fac2num(data, vars)
```

Arguments

data	a data frame
min.values	the minimal value distinct values befor warning
min.levels	the minimal value distinct levels befor warning
var	a vector
vars	a character vector with names from the data
get.distinct	TRUE if you need to save the values FALSE if not not
show.str	whether to show the structure
print	TRUE or FALSE

Details

The function `data_str()` gives the structure of the data set.

The function `data_distinct()` gives the distinct values of the vectors in the data set

The function `y_distinct()` gives the distinct values of single vector

The function `data_cha2fac()` tranforms all character vectors to factors

The function `data_few2fac()` transform all vectors with fewer values than `min.levels` into factors

The function `data_int2num()` transform all integer vectors with more values than `min.values` into numeric

The function `data_fac2num()` transform selected variables factors into numeric vectors

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

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Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[data_dim](#)

Examples

```
data_str(rent)
data_distinct(rent)
data_cha2fac(rent)
data_few2fac(rent)
data_int2num(rent)
```

data_void

Finding the Percentage of Empty Spaces

Description

The function `void()` is looking for the % of empty spaces in the direction of two variables `x` and `y`.

The function `data_void()` is looking pair-wise for empty spaces in all the continuous variables in the data set.

Usage

```
data_void(data, digits = 3, plot = TRUE, diag.off = TRUE,
          lower.tri.off = FALSE,
          method = c("square", "circle"),
          outline.color = "gray", colors = c("blue", "white", "red"),
          legend.title = "Void", title, ggtheme = ggplot2::theme_minimal(),
          tl.cex = 12, tl.col = "black", tl.srt = 45, lab = TRUE,
          lab_col = "black", lab_size = 3, circle.size = 20, seed = 123,
          percentage)
```

```
void(x, y, plot = TRUE, print = TRUE, table.length)
```

Arguments

data	A data frame
digits	the digits for printing the correlation coefficients
plot	whether to plot or not
diag.off	whether to show the diagonal elements
lower.tri.off	whether to show the lower part of the matrix
method	plotting in "square" or "circle"
outline.color	the outline colour
colors	the range of colours
legend.title	title for the legend
title	the main title
ggtheme	the theme for the plot, see package ggthemes for more themes
tl.cex	the text size for the marginal labels
tl.col	the colour of the marginal labels
tl.srt	the angle of the text in the bottom labels of the table
lab	whether to show the correlation coefficients in the table
lab_col	the colour of the lettering of the correlation coefficients
lab_size	the size of the lettering of the correlation coefficients, increase (or decrease) if the default 3 is not appropriate
circle.size	the size of the circles, increase (or decrease) if the default 20 is not appropriate
seed	the <code>set.seed()</code> value
percentage	the percentage of data to show if the observation number is too big
x	the first variable in <code>void()</code>
y	the second variable in <code>void()</code>
print	whether to print the results
table.length	the table length (if signing is calculated automatically)

Details

The functions `void()` and `data_void()` work with discretising the data in the x and y direction and then calculate the % of zeros. By discretising the data we mean cut both variable x variables and y, at an equal spaced grid of k points and create a (k x k) dimensional matrix containing the number of data points in the grid. The problem thought, with any attempt to calculate the % of empty spaces is that by increasing k in the x and y directions would result more zeros cells and therefore more % empty spaces. To avoid this we need a way to stop the discretization at a stage before the data become too sparse. The way this is done in the current function is the following;

i) If the n points (x, y) are randomly allocated we would expect the number of counts in the cells of the matrix of a discretised two dimensional data set to be Poisson distributed with a probability for zeros equal to $\exp(-\mu)$ where μ is the mean of the Poisson distribution. That is, under the null hypothesis that the n points are spread randomly we expect some of the cell to be zero with probability $\exp(-\mu)$. Given n the number of observations, we can use this information to find out at which discretation point k we should stop.

ii) To identify at which stage k we should stop for given number of observations say n, we have generated randomly from a uniform distribution n values for x and y. We use those values to calculate at which point k this will give a probability of zero close to 0.05. We calculate those probabilities using $\exp(-xbar)$ where xbar is the mean of the cells. By doing this we found that the following is holding; $\log k = -0.516 + 0.498 \log n$. This equation provide us with an easy way to calculate k given n.

Value

It produce a value between zero and 1.

Author(s)

Mikis Stasinopoulos

References

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. doi:10.1201/9780429298547.

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(see also <https://www.gamlss.com/>).

See Also

[data_cor](#)

Examples

```
void(rent$A, rent$F1)
data_void(rent)
```

data_xyplot

Plotting the response against the explanatory variables

Description

The function `data_xyplot()` plots the response against all other variables in a given data set.

The function `data_plot()` plots all variables individually.

The function `data_bucket()` plots the bucket plot for all continuous variables.

The function `data_zscores()` calculates and plots the z-scores (obtained after fitting the SHASHO distribution) for all continuous variables.

The function `y_zscores()` calculates and plots the z-scores (obtained after fitting the SHASHO distribution) for a single variable.

The function `data_response()` calculates and plots the z-scores (obtained after fitting the SHASHO distribution) for the response variable.

Usage

```
data_xyplot(data, response, point.size = 0.5, nrow = NULL,
            ncol = NULL, percentage, seed = 123,
            max.levels = 10, plots.per.page = 9, one.by.one = FALSE, title, ...)
```

```
data_plot(data, value = 3, hist.col = "black", hist.fill = "white",
          dens.fill = "#FF6666", nrow = NULL, ncol = NULL,
          percentage, seed = 123,
          plot.hist = TRUE, plots.per.page = 9,
          one.by.one = FALSE,
          title, ...)
```

```
data_bucket(data, value = 3, max.levels = 20,
            nrow = NULL, ncol = NULL, plots.per.page = 9,
            one.by.one = FALSE, title, percentage, seed = 123,
            ...)
```

```
y_zscores(x, family = SHASHO, plot = TRUE, hist = FALSE, ...)
```

```
data_zscores(data, plot = TRUE, hist=FALSE, value = 3, family = SHASHO,
            max.levels = 10, hist.col = "black", hist.fill = "white",
            dens.fill = "#FF6666", nrow = NULL, ncol = NULL,
            plots.per.page = 9, one.by.one = FALSE, title, percentage,
            seed = 123,...)
```

```
data_response(data, response, plot = TRUE, percentage, seed = 123)
```

Arguments

data	a data frame
x	a single variable
family	a gamlss distribution family (continuous)
response	the response variable should be in the data
point.size	the size of points in scatter plots
nrow	the number of rows in the plot
ncol	the number of columns in the plot
plots.per.page	maximu plots per page
one.by.one	whether plotted individually
value	value to identify outliers if y_dots is used i.e. for upper tail an outliers is if it is greater than $Q_3 + value * IQ$
hist.col	the colour of lines of the histogram, if plot.hist=TRUE
hist.fill	the colour of the histogram, if plot.hist=TRUE
dens.fill	the color of the density plot, if plot.hist=TRUE
plot.hist	whether to use y_dots() or y_hist() for the continuous variables
plot	whether to plot
hist	whether histogram or dot plot
max.levels	excludes from plotting bucket plots for variables with less than max.levels, distinct values
title	title of the plot
percentage	if set, i.e. 0.50, plots a portotion of data otherwise for big data sets greater than 50.000 observartions it plots a porpotion
seed	the set.seed() argument
...	other arguments

Details

The function `data_xyplot()` it takes a data frame and plot all the explanarory variables against the response.

The function `data_plot()` it takes a data frame and plot all variables against the response. The continuous are plotted using `y_dots()` or `y_hist()` while the factors and integer as bar plots.

Value

Plots of the data

Author(s)

Mikis Stasinopoulos

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

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(see also <https://www.gamlss.com/>).

See Also

[data_names](#)

Examples

```
da <- rent99[,-2]
data_xyplot(da, rent)
data_plot(da)
y_zscores(da$rent)
data_response(da, response=rent)
```

Index

- * **diagnostic**
 - data_void, 19
- * **leverage**
 - data_leverage, 10
- * **package**
 - gamlss.prepdata-package, 2
- * **regression**
 - data_cor, 3
 - data_dim, 6
 - data_inter, 8
 - data_leverage, 10
 - data_part, 12
 - data_rm, 15
 - data_scale, 16
 - data_str, 18
 - data_void, 19
 - data_xyplot, 22
- data_association (data_cor), 3
- data_bucket (data_xyplot), 22
- data_cha2fac (data_str), 18
- data_cor, 3, 7, 9, 21
- data_cut (data_part), 12
- data_dim, 6, 19
- data_distinct (data_str), 18
- data_exclude_class (data_rm), 15
- data_fac2num (data_str), 18
- data_few2fac (data_str), 18
- data_int2num (data_str), 18
- data_inter, 8
- data_leverage, 10
- data_names, 12, 24
- data_names (data_dim), 6
- data_omit (data_dim), 6
- data_only_continuous (data_rm), 15
- data_outliers, 11, 11
- data_part, 12
- data_part_index (data_part), 12
- data_part_list (data_part), 12
- data_pcor (data_cor), 3
- data_plot (data_xyplot), 22
- data_rename (data_dim), 6
- data_response (data_xyplot), 22
- data_rm, 15
- data_rm1val (data_rm), 15
- data_rmNAvars (data_rm), 15
- data_scale, 16
- data_select (data_rm), 15
- data_shorter_names (data_dim), 6
- data_str, 14, 18
- data_void, 19
- data_which_na (data_dim), 6
- data_xyplot, 22
- data_zscores, 17
- data_zscores (data_xyplot), 22
- gamlss, 3
- gamlss.family, 3
- gamlss.prepdata
 - (gamlss.prepdata-package), 2
- gamlss.prepdata-package, 2
- high_val (data_cor), 3
- low_val (data_cor), 3
- void (data_void), 19
- y_distinct (data_str), 18
- y_outliers (data_outliers), 11
- y_zscores (data_xyplot), 22