

# Package ‘papeR’

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**Title** A Toolbox for Writing Pretty Papers and Reports

**Version** 1.0-5

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**Description** A toolbox for writing 'knitr', 'Sweave' or other 'LaTeX'- or 'markdown'-based reports and to prettify the output of various estimated models.

**Depends** car, xtable

**Enhances** lme4, survival

**Imports** utils, gmodels, graphics, stats

**Suggests** nlme, knitr, rmarkdown, testthat (>= 0.10.0), foreign

**License** GPL-2

**URL** <https://github.com/hofnerb/papeR>

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**VignetteBuilder** knitr

**Collate** 'helpers.R' 'labels.R' 'summarize.R' 'plot.R' 'prettify.R'  
'toLatex.R'

**NeedsCompilation** no

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paper-package	<i>A Toolbox for Writing Pretty Papers and Reports</i>
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### Description

A toolbox for writing knitr, Sweave or other LaTeX- or markdown-based reports and to prettify the output of various estimated models.

### Details

Package: `paper`  
 Type: Package  
 Version: 1.0-5  
 Date: 2021-03-19  
 License: GPL-2

Version 1.0-0 is based on a completely refactored code base. Some functions from previous versions are deprecated. New functions to create summary tables exist (see [summarize](#)). The package now also provides a vignette and was extensively tested using `testthat`.

For news and changes see `news(package = "paper")`.

### Author(s)

Benjamin Hofner

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Anova.lme	<i>Anova Function for lme Models</i>
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---

### Description

This is a wrapper to [anova.lme](#) from package **nlme** and is coded similar to [Anova](#) from **car** as it produces marginal tests by default.

**Usage**

```
## S3 method for class 'lme'
Anova(mod, type = c("marginal", "sequential"), ...)
```

**Arguments**

```
mod          linear mixed model fitted with package nlme.
type         type of anova, either marginal (default) or sequential.
...          further arguments to be passed to anova.lme
```

**See Also**

[Anova](#) (package **car**)

**Examples**

```
## Example requires package nlme to be installed and loaded
if (require("nlme")) {
  ## Load data set Orthodont
  data(Orthodont, package = "nlme")

  ## Fit a model for distance with random intercept for Subject
  mod <- lme(distance ~ age + Sex, data = Orthodont, random = ~ 1 | Subject)

  Anova(mod)
}
```

---

confint.mer

*Confidence intervals for mixed models*

---

**Description**

Compute confidence intervals for mixed models from package **lme4** (prior to version 1.0). This function is only needed for backward compatibility.

**Usage**

```
## S3 method for class 'mer'
confint(object, parm, level = 0.95,
        simulate = c("ifneeded", TRUE, FALSE),
        B = 1000,...)
```

**Arguments**

object	Model of class mer.
parm	Parameters to be included in the confidence interval. See <a href="#">confint.default</a> for details.
level	the confidence level.
simulate	If <code>"ifneeded"</code> is specified (default), simulated confidence intervals are returned if (and only if) no z-value exists in the corresponding summary and asymptotic confidence intervals will be returned otherwise. If <code>TRUE</code> (or <code>"TRUE"</code> ) confidence intervals will be estimated using <a href="#">ci</a> from package <b>gmodels</b> which uses <a href="#">mcmc samp</a> internally. If <code>FALSE</code> (or <code>"FALSE"</code> ), asymptotic confidence intervals will be returned and an error is given if not possible.
B	number of samples to take in <a href="#">mcmc samp</a> . Per default 1000 samples are used.
...	Additional arguments. Currently not used.

**Value**

Matrix with confidence intervals.

**Author(s)**

Benjamin Hofner, partially based on code from package stats. See source code for documentation.

---

get\_option                      *Extract printing options from table.cont and table.fac objects*

---

**Description**

Helper function to extract printing options from `table.cont` and `table.fac` objects as produced by [latex.table.cont](#) and [latex.table.fac](#).

**Usage**

```
get_option(object, name)
```

**Arguments**

object	<code>table.cont</code> or <code>table.fac</code> object as produced by <a href="#">latex.table.cont</a> and <a href="#">latex.table.fac</a>
name	name of the option, e.g. <code>"table"</code> and <code>"align"</code> . See <a href="#">latex.table.cont</a> and <a href="#">latex.table.fac</a> for available options.

**Value**

Option.

**Author(s)**

Benjamin Hofner

**See Also**[latex.table.cont](#) and [latex.table.fac](#)

---

**labels***Extract labels from and set labels for data frames*

---

**Description**

Labels can be stored as an attribute "variable.label" for each variable in a data set using the assignment function. With the extractor function one can assess these labels.

**Usage**

```
## S3 method for class 'data.frame'
labels(object, which = NULL, abbreviate = FALSE, ...)

## assign labels
labels(data, which = NULL) <- value

## check if data.frame is a special labeled data.frame ('ldf')
is.ldf(object)

## convert object to labeled data.frame ('ldf')
convert.labels(object)
as.ldf(object, ...)

## special plotting function for labeled data.frames ('ldf')
## S3 method for class 'ldf'
plot(x, variables = names(x),
     labels = TRUE, by = NULL, with = NULL,
     regression.line = TRUE, line.col = "red", ...)
```

**Arguments**

object	a data.frame.
data	a data.frame.
which	either a number indicating the label to extract or a character string with the <i>variable name</i> for which the label should be extracted. One can also use a vector of numerics or character strings to extract mutiple labels. If which is NULL (default), all labels are returned.

<code>value</code>	a vector containing the labels (in the order of the variables). If which is given, only the corresponding subset is labeled. Note that all other labels contain the variable name as label afterwards.
<code>abbreviate</code>	logical (default: FALSE). If TRUE variable labels are abbreviated such that they remain unique. See <a href="#">abbreviate</a> for details. Further arguments to <a href="#">abbreviate</a> can be specified (see below).
<code>...</code>	further options passed to function <a href="#">abbreviate</a> if argument <code>abbreviate = TRUE</code> . In <code>x[...]</code> , <code>...</code> can be used to specify indices for extraction. See <a href="#">[</a> for details. In <code>plot</code> , <code>...</code> can be used to specify further graphical parameters.
<code>x</code>	a labeled data.frame with class 'ldf'.
<code>variables</code>	character vector or numeric vector defining (continuous) variables that should be included in the table. Per default, all numeric and factor variables of data are used.
<code>labels</code>	labels for the variables. If <code>labels = TRUE</code> (the default), <code>labels(data, which = variables)</code> is used as labels. If <code>labels = NULL</code> <code>variables</code> is used as label. Labels can also be specified as character vector.
<code>by</code>	a character or numeric value specifying a variable in the data set. This variable can be either a grouping factor or is used as numeric y-variable (see <code>with</code> for details). Per default no grouping is applied. See also 'Details' and 'Examples'.
<code>with</code>	a character or numeric value specifying a numeric variable with which to "correlate" all variables specified in <code>variables</code> . For numeric variables a scatterplot is plotted, for factor variables one gets a grouped boxplot. Per default no variable is given here. Instead of <code>with</code> one can also specify a numeric variable in <code>by</code> with the same results. See also 'Details' and 'Examples'.
<code>regression.line</code>	a logical argument specifying if a regression line should be added to scatter plots (which are plotted if both <code>variables</code> and <code>by</code> are numeric values).
<code>line.col</code>	the color of the regression line.

## Details

All labels are stored as attributes of the columns of the data frame, i.e., each variable has (up to) one attribute which contains the variable label.

One can set or extract labels from `data.frame` objects. If no labels are specified `labels(data)` returns the column names of the data frame.

Using `abbreviate = TRUE`, all labels are abbreviated to (at least) 4 characters such that they are unique. Other minimal lengths can be specified by setting `minlength` (see examples below).

Univariate plots can be easily obtained for all numeric and factor variables in a data set `data` by using `plot(data)`.

Bivariate plots can be obtained by specifying `by`. In case of a factor variable, grouped boxplots or spineplots are plotted depending on the class of the variable specified in `variables`. In case of a numeric variable, grouped boxplots or scatter plots are plotted depending on the class of the variable specified in `variables`. Note that one cannot specify `by` and `with` at the same time (as they are internally identical). Note that missings are excluded plot wise (also for bivariate plots).

**Value**

labels(data) returns a named vector of variable labels, where the names match the variable names and the values represent the labels.

**Note**

If a data set is generated by [read.spss](#) in package **foreign**, labels are stored in a single attribute of the data set. Assigning new labels, e.g. via labels(data) <- labels(data) removes this attribute and stores all labels as attributes of the variables. Alternatively one can use data <- convert.labels(data).

**Author(s)**

Benjamin Hofner

**See Also**

[read.spss](#) in package **foreign**

**Examples**

```
#####
### Basic labels manipulations

data <- data.frame(a = 1:10, b = 10:1, c = rep(1:2, 5))
labels(data) ## only the variable names
is.ldf(data) ## not yet

## now set labels
labels(data) <- c("my_a", "my_b", "my_c")
## one gets a named character vector of labels
labels(data)
## data is now a ldf:
is.ldf(data)

## Alternatively one could use as.ldf(data) or convert.labels(data);
## This would keep the default labels but set the class
## correctly.

## set labels for a and b only
## Note that which represents the variable names!
labels(data, which = c("a", "b")) <- c("x", "y")
labels(data)

## reset labels (to variable names):
labels(data) <- NULL
labels(data)

## set label for a only and use default for other labels:
labels(data, which = "a") <- "x"
labels(data)
```

```

## attach label for new variable:
data2 <- data
data2$z <- as.factor(rep(2:3, each = 5))
labels(data2) ## no real label for z, only variable name
labels(data2, which = "z") <- "new_label"
labels(data2)

#####
### Abbreviate labels

## attach long labels to data
labels(data) <- c("This is a long label", "This is another long label",
                 "This also")
labels(data)
labels(data, abbreviate = TRUE, minlength = 10)

#####
### Data manipulations

## reorder dataset:
tmp <- data2[, c(1, 4, 3, 2)]
labels(tmp)
## labels are kept and order is updated

## subsetting to single variables:
labels(tmp[, 2]) ## not working as tmp[, 2] drops to vector
## note that the label still exists but cannot be extracted
## using labels.default()
str(tmp[, 2])

labels(tmp[, 2, drop = FALSE]) ## prevent dropping

## one can also cbind labeled data.frame objects:
labels(cbind(data, tmp[, 2]))
## or better:
labels(cbind(data, tmp[, 2, drop = FALSE]))
## or rbind labeled.data.set objects:
labels(rbind(data, tmp[, -2]))

#####
### Plotting data sets

## plot the data auto"magically"; numerics as boxplot, factors as barplots
par(mfrow = c(2,2))
plot(data2)

## a single plot
plot(data2, variables = "a")
## grouped plot

```



```

plot(data2, variables = "a", by = "z")
## make "c" a factor and plot "c" vs. "z"
data2$c <- as.factor(data2$c)
plot(data2, variables = "c", by = "z")
## the same
plot(data2, variables = 3, by = 4)

## plot everything against "b"
## (grouped boxplots, stacked barplots or scatterplots)
plot(data2, with = "b")

```

---

latex.table.cont

*Produce (LaTeX) Summaries for Continuous Variables*


---

## Description

The function produces LaTeX tables with summary statistics for continuous variables. It makes use of the booktabs package in LaTeX to obtain tables with a nice layout.

## Usage

```

latex.table.cont(..., caption = NULL, label = NULL,
  table = c("tabular", "longtable"), align = NULL,
  floating = FALSE, center = TRUE)

```

## Arguments

...	arguments for <a href="#">summarize</a> . See there for details.
caption	(optional) character string. Caption of LaTeX table. Note that captions are supported for all tables (see also details below).
label	(optional) character string. Label of LaTeX table specified as <code>\label{"label"}</code> .
table	character string. LaTeX table format, currently either "tabular" (default) or "longtable".
align	character string. LaTeX alignment of table rows, per default "l r . . . r", where "r" is repeated <code>ncol - 1</code> times.
floating	logical (default: FALSE). Determines whether the table is a floating object (i.e. use a table environment or not). Note that a longtable cannot be a floating object but captions can be used.
center	logical (default: TRUE). Determines if table should be centered.

## Details

This function is deprecated and only available for backward compatibility. Use [summarize](#) for more flexibility.

The output requires `\usepackage{booktabs}` in the LaTeX file.

Captions can be added to both, longtables and tabulars. In the latter case, captions are also supported if the table is no floating object. In this case, the LaTeX package `capt-of` is required.

**Value**

The output is printed with LaTeX style syntax highlighting to be used e.g. in Sweave chunks with `results=tex`.

**Author(s)**

Benjamin Hofner

**See Also**

[latex.table.fac](#) and [get\\_option](#)

**Examples**

```
## Example requires package nlme to be installed and loaded
if (require("nlme")) {
  ## Use dataset Orthodont
  data(Orthodont, package = "nlme")

  ## Get summary for continuous variables
  latex.table.cont(Orthodont)

  ## Change statistics to display
  latex.table.cont(Orthodont, quantiles = FALSE)
  latex.table.cont(Orthodont, count = FALSE, quantiles = FALSE)
  latex.table.cont(Orthodont, mean_sd = FALSE)

  ## Show column 'Missing' even if no missings are present
  latex.table.cont(Orthodont, show.NAs = TRUE)

  ## Change variables to display
  latex.table.cont(Orthodont, variables = "age")

  ## What happens in the display if we introduce some missing values:
  set.seed(1907)
  Orthodont$age[sample(nrow(Orthodont), 20)] <- NA
  latex.table.cont(Orthodont)
}
```

---

latex.table.fac

*Produce (LaTeX) Summaries for Factor Variables*

---

**Description**

The function produces LaTeX tables with summary statistics for factor variables. It makes use of the `booktabs` package in LaTeX to obtain tables with a nice layout.

**Usage**

```
latex.table.fac(..., caption = NULL, label = NULL,
  table = c("tabular", "longtable"), align = NULL,
  floating = FALSE, center = TRUE)
```

**Arguments**

...	arguments for <a href="#">summarize</a> . See there for details.
caption	(optional) character string. Caption of LaTeX table. Note that captions are supported for all tables (see also details below).
label	(optional) character string. Label of LaTeX table specified as <code>\label{"label"}</code> .
table	character string. LaTeX table format, currently either "tabular" (default) or "longtable".
align	character string. LaTeX alignment of table rows, per default "l1l r . . . r", where "r" is repeated <code>ncol - 2</code> times.
floating	logical (default: FALSE). Determines whether the table is a floating object (i.e. use a table environment or not). Note that a longtable cannot be a floating object but captions can be used.
center	logical (default: TRUE). Determines if table should be centered.

**Details**

This function is deprecated and only available for backward compatibility. Use [summarize](#) for more flexibility.

The output requires `\usepackage{booktabs}` in the LaTeX file.

Captions can be added to both, longtables and tabulars. In the latter case, captions are also supported if the table is no floating object. In this case, the LaTeX package `capt-of` is required.

**Value**

The output is printed with LaTeX style syntax highlighting to be used e.g. in Sweave chunks with `results=tex`.

**Author(s)**

Benjamin Hofner

**See Also**

[latex.table.cont](#) and [get\\_option](#)

**Examples**

```
## Example requires package nlme to be installed and loaded
if (require("nlme")) {
  ## Use dataset Orthodont
  data(Orthodont, package = "nlme")
}
```

```

## Get summary for continuous variables
latex.table.fac(Orthodont)

## Reorder data for table:
latex.table.fac(Orthodont, variables = c("Sex", "Subject"))

## What happens in the display if we introduce some missing values:
set.seed(1907)
Orthodont$Sex[sample(nrow(Orthodont), 20)] <- NA
latex.table.fac(Orthodont)
latex.table.fac(Orthodont, variables = "Sex")
## do not show statistics on missing values
latex.table.fac(Orthodont, variables = "Sex", show.NAs = FALSE)
}

```

---

prettify

---

*Make Pretty Summary and Anova Tables*


---

## Description

Improve summary tables by replacing variable names with labels and separating variable names and value labels of factor variables. Additionally, confidence intervals are added to summaries per default and p-values are formatted for pretty printing.

## Usage

```

## generic function called by all prettify.summary.xxx functions
## S3 method for class 'data.frame'
prettify(object, labels = NULL, sep = ": ", extra.column = FALSE,
         smallest.pval = 0.001, digits = NULL, scientific = FALSE,
         signif.stars = getOption("show.signif.stars"), ...)

## S3 method for class 'summary.lm'
prettify(object, labels = NULL, sep = ": ", extra.column = FALSE,
         confint = TRUE, level = 0.95,
         smallest.pval = 0.001, digits = NULL, scientific = FALSE,
         signif.stars = getOption("show.signif.stars"), ...)

## S3 method for class 'summary.glm'
prettify(object, labels = NULL, sep = ": ", extra.column = FALSE,
         confint = TRUE, level = 0.95, OR = TRUE,
         smallest.pval = 0.001, digits = NULL, scientific = FALSE,
         signif.stars = getOption("show.signif.stars"), ...)

## S3 method for class 'summary.coxph'
prettify(object, labels = NULL, sep = ": ", extra.column = FALSE,
         confint = TRUE, level = 0.95, HR = TRUE,

```

```

    smallest.pval = 0.001, digits = NULL, scientific = FALSE,
    signif.stars = getOption("show.signif.stars"),
    env = parent.frame(), ...)

## S3 method for class 'summary.lme'
prettify(object, labels = NULL, sep = ": ", extra.column = FALSE,
         confint = TRUE, level = 0.95,
         smallest.pval = 0.001, digits = NULL, scientific = FALSE,
         signif.stars = getOption("show.signif.stars"), ...)

## method for mixed models fitted with lme4 (vers. < 1.0)
## S3 method for class 'summary.mer'
prettify(object, labels = NULL, sep = ": ", extra.column = FALSE,
         confint = TRUE, level = 0.95,
         smallest.pval = 0.001, digits = NULL, scientific = FALSE,
         signif.stars = getOption("show.signif.stars"),
         simulate = c("ifneeded", TRUE, FALSE), B = 1000, ...)

## method for mixed models fitted with lme4 (vers. >= 1.0)
## S3 method for class 'summary.merMod'
prettify(object, labels = NULL, sep = ": ", extra.column = FALSE,
         confint = TRUE, level = 0.95,
         smallest.pval = 0.001, digits = NULL, scientific = FALSE,
         signif.stars = getOption("show.signif.stars"),
         method = c("profile", "Wald", "boot"), B = 1000, env = parent.frame(), ...)

## S3 method for class 'anova'
prettify(object, labels,
         smallest.pval = 0.001, digits = NULL, scientific = FALSE,
         signif.stars = getOption("show.signif.stars"), ...)

## helper function for pretty p-values
prettifyPValue(object, smallest.pval = 0.001, digits = NULL,
               scientific = FALSE,
               signif.stars = getOption("show.signif.stars"), ...)

```

## Arguments

object	object of class <code>data.frame</code> resulting (most likely) from a call to <code>summary</code> or directly the output from <code>summary</code> , <code>anova</code> or <code>Anova</code> (the latter from package <code>car</code> ).
labels	specify labels here. For the format see <code>labels</code> .
sep	separator between variable label and value label of a factor variable (default: <code>": "</code> ).
extra.column	logical: provide an extra column for the value labels of factors (default: <code>FALSE</code> ).
confint	logical value indicating if confidence intervals could be added or the confidence intervals themselves. Using <code>confint = TRUE</code> is experimental only and special care needs to be taken

	that the data set used for fitting is neither changed nor deleted. See ‘Details’ and ‘Examples’.
level	confidence level; Per default 0.95% confidence intervals are returned
OR	logical. Should odds ratios be added? Only applicable if a logistic regression model was fitted (i.e., with family = "binomial").
HR	logical. Should hazard ratios be added?
smallest.pval	determines the smallest p-value to be printed exactly. Smaller values are given as "< smallest.pval". This argument is passed to the eps argument of <code>format.pval</code> . See there for details.
digits	number of significant digits. The default, NULL, uses <code>getOption("digits")</code> for formatting p-values and leaves all other columns unchanged. If digits are specified, all columns use this number of significant digits (columnwise). See also argument digits in <code>format</code> .
scientific	specifies if numbers should be printed in scientific format. For details and possible values see <code>format</code> .
signif.stars	logical (default = TRUE). Should significance stars be added? Per default system options are used. See <code>getOption("show.signif.stars")</code> .
simulate	should the asymptotic or simulated confidence intervals be used? See <code>confint.mer</code> for details.
B	number of samples to take in <code>mcmcSamp</code> . See <code>confint.mer</code> for details.
method	Determines the method for computing confidence intervals; One of "profile" (default), "Wald", "boot". For details see <code>confint.merMod</code> in package <b>lme4</b> .
...	further options. Currently not applicable.
env	specify environment in which the model was fitted. Needed to find the correct data for refitting the model in order to obtain confidence intervals.

## Details

Specialized functions that `prettify` summary tables of various models exist. For the `data.frame` method, `extra.column` and `sep` can only be used if labels are specified as variable names need to be known in order to split variable name and factor level. For `summary` objects, variable names can be extracted from the objects.

To compute confidence intervals, the model is refitted internally extracting the call and environment from the model summary. All functions then use `confint` on the refitted model. For `mer` models special `confint` functions are defined in this package (for backward compatibility). For details see there. Note that it is highly important **not** to modify or delete the data in the fitting environment if one wants to obtain correct confidence intervals. See examples for what might happen. We try our best to find changes of the data and to warn the user (but without any warranty).

Alternatively, one can directly specify the confidence intervals using e.g. `confint = confint(model)`, where `model` is the fitted model. This does not rely on refitting of the model and should always work as expected. In this case, arguments `level`, `simulate` and `B` are ignored. Note that in this case it is advised to also specify the labels by hand!

`prettifyPValue` is a helper function used within the `prettify` functions but can also be used directly on a `data.frame` object. The function tries to (cleverly) “guess” the column of p-values (based on the column names) and formats them nicely. Additionally, significance stars are added if requested.

**Value**

data.frame with prettier variable labels. For summary functions additionally confidence intervals (if requested), odds ratio (for logistic regression models, if requested), p-values formatted for pretty printing and significance stars (if requested) are attached.

**Author(s)**

Benjamin Hofner

**See Also**

[summary](#), [summary.lm](#), [summary.glm](#), [summary.lme](#), [summary.merMod](#) (or [summary.mer-class](#) in `lme4 < 1.0`) and [summary.coxph](#) for summary functions.

[anova](#) and [Anova](#) for ANOVA functions.

[confint](#) and [ci](#) for confidence intervals. Special functions are implemented for mixed models: [confint.mer](#).

**Examples**

```
## Example requires package nlme to be installed and loaded
if (require("nlme")) {
  ## Load data set Orthodont
  data(Orthodont, package = "nlme")

  #####
  # Linear model
  #####

  ## Fit a linear model
  linmod <- lm(distance ~ age + Sex, data = Orthodont)
  ## Extract pretty summary
  prettify(summary(linmod))

  ## Extract anova (sequential tests)
  anova(linmod)
  ## now prettify it
  prettify(anova(linmod))

  #####
  # Random effects model (nlme)
  #####

  ### (fit a more suitable model with random effects)
  ## With package nlme:
  require("nlme")
  ## Fit a model for distance with random intercept for Subject
  mod <- lme(distance ~ age + Sex, data = Orthodont, random = ~ 1 | Subject)
  summary(mod)
  ## Extract fixed effects table, add confidence interval and make it pretty
  prettify(summary(mod))
  ## Extract fixed effects table only and make it pretty
```

```

prettify(summary(mod), confint = FALSE)

#####
# Random effects model (lme4)
#####

set.seed(130913)

## With package lme4:
if (require("lme4") && require("car")) {
  ## Fit a model for distance with random intercept for Subject
  mod4 <- lmer(distance ~ age + Sex + (1|Subject), data = Orthodont)
  summary(mod4)
  ## Extract fixed effects table and make it pretty
  prettify(summary(mod4))

  ## Extract and prettify anova (sequential tests)
  prettify(anova(mod4))

  ## Better: extract Anova (partial instead of sequential tests)
  library("car")
  Anova(mod4)
  ## now prettify it
  prettify(Anova(mod4))
}

#####
# Cox model
#####

## survival models
if (require("survival")) {
  ## Load data set ovarian (now part of cancer)
  data(cancer, package = "survival")

  ## fit a Cox model
  mod5 <- coxph(Surv(futime, fustat) ~ age, data=ovarian)
  summary(mod5)
  ## Make pretty summary
  prettify(summary(mod5))

  ## Make pretty summary
  prettify(Anova(mod5))
}

#####
# ATTENTION when confint = TRUE: Do not modify or delete data
#####

## Fit a linear model (same as above)
linmod <- lm(distance ~ age + Sex, data = Orthodont)
## Extract pretty summary

```



```

    prettify(summary(linmod))

    ## Change the data (age in month instead of years)
    Orthodont$age <- Orthodont$age * 12
    prettify(summary(linmod)) ## confidence intervals for age have changed
                             ## but coefficients stayed the same; a
                             ## warning is issued

    ## Remove data in fitting environment
    rm(Orthodont)
    prettify(summary(linmod)) ## confidence intervals are missing as no
                             ## data set was available to refit the model

#####
# Use confint to specify confidence interval without refitting
#####

    ## make labels without using the data set
    labels <- c("distance", "age", "Subject", "Sex")
    names(labels) <- labels

    ## usually easier via: labels(Orthodont)

    prettify(summary(linmod), confint = confint(linmod),
               labels = labels)
}

```

---

summarize

---

*Produce Summary Tables for Data Sets*


---

## Description

The function produces summary tables for factors and continuous variables. The obtained tables can be used directly in R, with LaTeX and HTML (by using the [xtable](#) function) or Markdown (e.g. by using the function [kable](#)).

## Usage

```

summarize(data, type = c("numeric", "factor"),
          variables = names(data), variable.labels = labels, labels = NULL,
          group = NULL, test = !is.null(group), colnames = NULL,
          digits = NULL, digits.pval = 3, smallest.pval = 0.001,
          sep = NULL, sanitize = TRUE, drop = TRUE,
          show.NAs = any(is.na(data[, variables])), ...)

```

**Arguments**

<code>data</code>	data set to be used.
<code>type</code>	print summary table for either numeric or factor variables.
<code>variables</code>	character vector defining variables that should be included in the table. Per default, all numeric or factor variables of data are used, depending on type.
<code>variable.labels</code> , <code>labels</code>	labels for the variables. If <code>variable.labels = NULL</code> (default) <code>variables</code> is used as label. If <code>variable.labels = TRUE</code> , <code>labels(data, which = variables)</code> is used as labels. Instead of <code>variable.labels</code> one can also use <code>labels</code> .
<code>group</code>	character specifying a grouping factor. Per default no grouping is applied.
<code>test</code>	logical or character string. If a group is given, this argument determines whether a test for group differences is computed. For details see <a href="#">summarize_numeric</a> and <a href="#">summarize_factor</a> .
<code>colnames</code>	a vector of character strings of appropriate length. The vector supplies alternative column names for the resulting table. If <code>NULL</code> default names are used.
<code>digits</code>	number of digits to round to. For defaults see <a href="#">summarize_numeric</a> and <a href="#">summarize_factor</a> .
<code>digits.pval</code>	number of significant digits used for p-values.
<code>smallest.pval</code>	determines the smallest p-value to be printed exactly. Smaller values are given as “< smallest.pval”. This argument is passed to the <code>eps</code> argument of <code>format.pval</code> . See there for details.
<code>sep</code>	logical. Determines whether separators (lines) should be added after each variable. For defaults see <a href="#">summarize_numeric</a> and <a href="#">summarize_factor</a> .
<code>sanitize</code>	logical (default: <code>TRUE</code> ) or a sanitizing function used to clean the input in order to be useable in LaTeX environments. Per default <code>toLatex.character</code> is used.
<code>drop</code>	logical (default: <code>TRUE</code> ). Determines whether variables, which contain only missing values are dropped from the table.
<code>show.NAs</code>	logical. Determines if NAs are displayed. Per default, <code>show.NAs</code> is <code>TRUE</code> if there are any missings in the variables to be displayed (and <code>FALSE</code> if not). For details see <a href="#">summarize_numeric</a> and <a href="#">summarize_factor</a> .
<code>...</code>	additional arguments for <a href="#">summarize_numeric</a> and <a href="#">summarize_factor</a> . See there for details.

**Value**

A special `data.frame` with additional class `summary` containing the computed statistics is returned from function `summarize`. Additional attributes required for the `xtable.summary` or `print.xtable.summary` function are contained as attributes. These are extracted using the function `get_option`.

**Author(s)**

Benjamin Hofner

**See Also**

For details see [summarize\\_numeric](#) and [summarize\\_factor](#).

Conversion to LaTeX tables can be done using [xtable.summary](#) and [print.xtable.summary](#).

[get\\_option](#)

**Examples**

```
if (require("nlme")) {
  ## Use dataset Orthodont
  data(Orthodont, package = "nlme")

  ## Get summary for continuous variables
  (tab1 <- summarize(Orthodont, type = "numeric"))

  ## Change statistics to display
  summarize(Orthodont, quantiles = FALSE, type = "numeric")
  summarize(Orthodont, quantiles = FALSE, count = FALSE, type = "numeric")
  summarize(Orthodont, mean_sd = FALSE, type = "numeric")

  ## Get summary for categorical variables
  (tab2 <- summarize(Orthodont, type = "fac"))

  ## use fraction instead of percentage
  summarize(Orthodont, percent = FALSE, type = "fac")

  ## Using the tables with Markdown
  if (require("knitr")) {
    kable(tab1)
    kable(tab2)
  }

  ## Using the tables with LaTeX
  if (require("xtable")) {
    xtable(tab1)
    ## grouped table
    xtable(summarize(Orthodont, group = "Sex"))
    xtable(tab2)
  }
}
```

---

summarize\_factor

*Produce Summary Tables for Data Sets*


---

**Description**

The function produces summary tables for factor variables. The obtained tables can be used directly in R, with LaTeX and HTML (by using the [xtable](#) function) or Markdown (e.g. by using the function [kable](#)).

**Usage**

```
summarize_factor(data,
  variables = names(data), variable.labels = labels, labels = NULL,
  group = NULL, test = !is.null(group), colnames = NULL,
  digits = 3, digits.pval = 3, smallest.pval = 0.001,
  sep = TRUE, sanitize = TRUE, drop = TRUE,
  show.NAs = any(is.na(data[, variables])),
  ## additional specific arguments
  percent = TRUE, cumulative = FALSE,
  na.lab = "<Missing>", ...)
```

**Arguments**

<code>data</code>	data set to be used.
<code>variables</code>	variables that should be included in the table. For details see <a href="#">summarize</a> .
<code>variable.labels, labels</code>	labels for the variables. For details see <a href="#">summarize</a> .
<code>group</code>	character specifying a grouping factor. For details see <a href="#">summarize</a> .
<code>test</code>	logical or character specifying test for group differences. For details see <a href="#">summarize</a> .
<code>colnames</code>	a vector of character strings of appropriate length. For details see <a href="#">summarize</a> .
<code>digits</code>	number of digits to round to (only used for fractions). Per default all values are rounded to three digits.
<code>digits.pval</code>	number of significant digits used for p-values.
<code>smallest.pval</code>	determines the smallest p-value to be printed exactly. For details see <a href="#">summarize</a> .
<code>sep</code>	logical (default: TRUE). Determines whether separators (lines) should be added after each variable.
<code>sanitize</code>	logical (default: TRUE) or a sanitizing function. For details see <a href="#">summarize</a> .
<code>drop</code>	logical (default: TRUE). Determines whether variables, which contain only missing values are dropped from the table.
<code>show.NAs</code>	logical. Determines if NAs are displayed as a separate category for each factor variable with missings. If TRUE, an additional statistic which includes the missings is displayed (see Examples). Per default, <code>show.NAs</code> is TRUE if there are any missings in the variables to be displayed (and FALSE if not).
<code>percent</code>	logical. Should the fractions be given as percent values? Otherwise, fractions are given as decimal numbers.
<code>cumulative</code>	logical. Should cumulative fractions be displayed?
<code>na.lab</code>	label for missing values (default: "<Missing>").
<code>...</code>	additional arguments. Currently not used.

**Value**

A special data.frame with additional class summary containing the computed statistics is returned from function `summarize`. Additional attributes required for the `xtable.summary` or `print.xtable.summary` function are contained as attributes. These are extracted using the function `get_option`.

**Author(s)**

Benjamin Hofner

**See Also**For details see [link{summarize}](#) and [link{summarize\\_factor}](#).Conversion to LaTeX tables can be done using [xtable.summary](#) and [print.xtable.summary.get\\_option](#)**Examples**

```
## Example requires package nlme to be installed and loaded
if (require("nlme")) {
  ## Use dataset Orthodont
  data(Orthodont, package = "nlme")

  ## Get summary for continuous variables
  summarize(Orthodont, type = "factor")

  ## Reorder data for table:
  summarize(Orthodont, variables = c("Sex", "Subject"), type = "factor")

  ## What happens in the display if we introduce some missing values:
  set.seed(1907)
  Orthodont$Sex[sample(nrow(Orthodont), 20)] <- NA
  summarize(Orthodont, type = "factor")
  summarize(Orthodont, variables = "Sex", type = "factor")
  ## do not show statistics on missing values
  summarize(Orthodont, variables = "Sex", show.NAs = FALSE, type = "factor")
}
```

---

summarize\_numeric

*Produce Summary Tables for Data Sets*


---

**Description**

The function produces summary tables for continuous variables. The obtained tables can be used directly in R, with LaTeX and HTML (by using the [xtable](#) function) or Markdown (e.g. by using the function [kable](#)).

**Usage**

```
summarize_numeric(data,
  variables = names(data), variable.labels = labels, labels = NULL,
  group = NULL, test = !is.null(group), colnames = NULL,
  digits = 2, digits.pval = 3, smallest.pval = 0.001,
  sep = !is.null(group), sanitize = TRUE,
  drop = TRUE, show.NAs = any(is.na(data[, variables])),
```

```
## additional specific arguments
count = TRUE, mean_sd = TRUE, quantiles = TRUE,
incl_outliers = TRUE, ...)
```

### Arguments

<code>data</code>	data set to be used.
<code>variables</code>	variables that should be included in the table. For details see <a href="#">summarize</a> .
<code>variable.labels</code> , <code>labels</code>	labels for the variables. For details see <a href="#">summarize</a> .
<code>group</code>	character specifying a grouping factor. For details see <a href="#">summarize</a> .
<code>test</code>	logical or character specifying test for group differences. For details see <a href="#">summarize</a> .
<code>colnames</code>	a vector of character strings of appropriate length. For details see <a href="#">summarize</a> .
<code>digits</code>	number of digits to round to. Per default all values are rounded to two digits.
<code>digits.pval</code>	number of significant digits used for p-values.
<code>smallest.pval</code>	determines the smallest p-value to be printed exactly. For details see <a href="#">summarize</a> .
<code>sep</code>	logical (default: TRUE if grouping specified, FALSE otherwise). Determines whether separators (lines) should be added after each variable.
<code>sanitize</code>	logical (default: TRUE) or a sanitizing function. For details see <a href="#">summarize</a> .
<code>drop</code>	logical (default: TRUE). Determines whether variables, which contain only missing values are dropped from the table.
<code>show.NAs</code>	logical. Determines if the number of missings (NAs) is displayed as a separate column. Per default, <code>show.NAs</code> is TRUE if there are any missings in the variables to be displayed (and FALSE if not).
<code>count</code>	(logical) indicator if number of complete cases ("n") should be included in the table (default: TRUE).
<code>mean_sd</code>	(logical) indicator if mean and standard deviation should be included in the table (default: TRUE).
<code>quantiles</code>	(logical) indicator if quantiles (including min and max) should be included in the table (default: TRUE).
<code>incl_outliers</code>	Per default we use <a href="#">fivenum</a> to compute the quantiles (if <code>quantiles = TRUE</code> ). If extreme values should be excluded from min/max in the table, <code>boxplot( , plot = FALSE)\$stats</code> is used instead.
<code>...</code>	additional arguments. Currently not used.

### Value

A special data.frame with additional class `summary` containing the computed statistics is returned from function `summarize`. Additional attributes required for the `xtable.summary` or `print.xtable.summary` function are contained as attributes. These are extracted using the function `get_option`.

### Author(s)

Benjamin Hofner

**See Also**

For details see [link{summarize}](#) and [link{summarize\\_factor}](#).

Conversion to LaTeX tables can be done using [xtable.summary](#) and [print.xtable.summary](#).

[get\\_option](#)

**Examples**

```
if (require("nlme")) {
  ## Use dataset Orthodont
  data(Orthodont, package = "nlme")

  ## Get summary for continuous variables
  summarize(Orthodont, type = "numeric")

  ## Change statistics to display
  summarize(Orthodont, quantiles = FALSE, type = "numeric")
  summarize(Orthodont, quantiles = FALSE, count = FALSE, type = "numeric")
  summarize(Orthodont, mean_sd = FALSE, type = "numeric")

  ## for more examples see ?summarize
}
```

---

toLatex

*Cleaning R Code for printing in LaTeX environments*


---

**Description**

The function produces code that LaTeX is able to typeset.

**Usage**

```
## S3 method for class 'character'
toLatex(object, ...)

## S3 method for class 'sessionInfo'
toLatex(object, pkgs = NULL, locale = FALSE,
         base.pkgs = FALSE, other.pkgs = TRUE,
         namespace.pkgs = FALSE, citations = TRUE,
         citecommand = "\\citep", file = NULL,
         append = FALSE, ...)
```

**Arguments**

object	either an object of class <code>character</code> which should be cleaned for printing in LaTeX environments or an object of class <a href="#">sessionInfo</a> .
pkgs	character vector (optional). Specify specific packages here to show information on these (instead of all attached packages). See package in <a href="#">sessionInfo</a> .

locale	logical (default = FALSE). Show information on locale.
base.pkgs	logical (default = FALSE). Show information on base packages.
other.pkgs	logical (default = TRUE). Show information on currently attached packages. If pkgs is specified, information on these packages is given instead of all attached packages.
namespace.pkgs	logical (default = FALSE). Show information on packages whose namespaces are currently loaded but not attached.
citations	logical (default = TRUE). Should citations for all packages be added? BibTeX is used for storing the citations.
citecommand	Specify LaTeX-command for citation here. Curly brackets are added internally. Note that \ needs to be escaped, i.e., one needs to write \\ instead.
file	Specify path to BibTeX file where citations should be saved. If file = NULL is specified, the BibTeX entries are attached to the output as attribute "BibTeX". See examples for details.
append	logical (default = FALSE). Should citations be added to an existing BibTeX file (if existing) or should old BibTeX files be overwritten?
...	additional arguments. Currently not used.

### Value

A character string with special markup is returned: The output is printed with LaTeX style syntax highlighting to be used e.g. in Sweave chunks with `results=tex`.

### Author(s)

Benjamin Hofner, based on code from package `xtable`, `bibtex` and package `utils`. See source code for documentation.

### See Also

[toLatex](#). For details on `toLatex.sessionInfo` see also [sessionInfo](#).

### Examples

```
txt <- "Price: <= 500$ & additional goodies"
toLatex(txt)

#####
## session info for automatic inclusion in reports

info <- toLatex(sessionInfo())
info

## extract first part (the Latex part)
toLatex(info)
## extract second part (the BibTeX part)
toBibtex(info)
```



```
#####
## usual usage scenario

## Do not run the following code automatically as it needs
## write access to the current working directory.
## This code (without removing the file) could for example
## be included in a LaTeX chunk of your Sweave or knitr
## report.

## Not run: getwd()    ## location where write access is needed
toLatex(sessionInfo(), file = "packages.bib")
file.remove("packages.bib")

## End(Not run)
```

---

xtable.summary

*Create And Print Tables With Markup*


---

## Description

The function produces objects which can be printed to LaTeX and HTML code.

## Usage

```
## S3 method for class 'summary'
xtable(x, caption = NULL, label = NULL, align = NULL,
       digits = NULL, display = NULL, ...)

## S3 method for class 'xtable.summary'
print(x, rules = NULL, header = NULL,
      caption.placement = getOption("xtable.caption.placement", "top"),
      hline.after = getOption("xtable.hline.after", NULL),
      include.rownames = FALSE,
      add.to.row = getOption("xtable.add.to.row", NULL),
      booktabs = getOption("xtable.booktabs", TRUE),
      sanitize.text.function = get_option(x, "sanitize"),
      math.style.negative = getOption("xtable.math.style.negative", TRUE),
      math.style.exponents = getOption("xtable.math.style.exponents", TRUE),
      tabular.environment = getOption("xtable.tabular.environment", "tabular"),
      floating = getOption("xtable.floating", FALSE),
      latex.environments = getOption("xtable.latex.environments", c("center")),
      ...)
```

**Arguments**

x	object of class "summary", which is produced by the function <a href="#">summarize</a> or an object of class "xtable.summary" produced by <a href="#">xtable</a> .
caption	character vector specifying the table's caption; see <a href="#">xtable</a> for details.
label	character string specifying the LaTeX label or HTML anchor; see <a href="#">xtable</a> for details.
align	character string specifying the alignment of table columns; see <a href="#">xtable</a> for details.
digits	numeric vector specifying the number of digits to display in each column; see <a href="#">xtable</a> for details.
display	character string specifying the column types; see <a href="#">xtable</a> for details.
rules	character string specifying the rules to be used. Per default the rules are defined by <a href="#">summarize</a> and subsequently extracted from x via <code>get_option(x, "rules")</code> .
header	character string specifying the table header to be used. Per default the header is defined by <a href="#">summarize</a> and subsequently extracted from x via <code>get_option(x, "header")</code> .
caption.placement	can be either "bottom" or "top" (default). Note that the standard default of <a href="#">print.xtable</a> is "bottom".
hline.after	vector indicating the rows after which a horizontal line is printed. Here, the default is to not draw hlines (i.e. <code>hline.after = NULL</code> ) and horizontal lines are added via <code>add.to.row</code> (see there for details). Note that the standard default of <a href="#">print.xtable</a> is <code>c(-1, 0, nrow(x))</code> .
add.to.row	list of row numbers (pos) and text (command) to be added to the specified rows. Per default, top and bottom rules are added to the table and a rule specified in <code>rules</code> is added below the heading. If <code>sep = TRUE</code> in <a href="#">summarize</a> additional separators (as specified in <code>rules</code> ) are added after each variable.
include.rownames	logical. Always set to FALSE.
booktabs	logical. If TRUE (default), the <code>toprule</code> , <code>midrule</code> and <code>bottomrule</code> tags from the LaTeX package "booktabs" are used rather than <code>hline</code> for the horizontal line tags. Note that the standard default of <a href="#">print.xtable</a> is FALSE.
sanitize.text.function	All non-numeric entries (except row and column names) are sanitised in an attempt to remove characters which have special meaning for the output format. Per default the function <a href="#">toLatex</a> is used to sanitize the text. For more options see <a href="#">print.xtable</a> .
math.style.negative	logical. If TRUE (default) the negative sign is wrapped in dollar signs for LaTeX tables. Note that the standard default of <a href="#">print.xtable</a> is FALSE.
math.style.exponents	logical. If TRUE (default) scientific numbers are set as exponents. See <a href="#">print.xtable</a> for details. Note that the standard default of <a href="#">print.xtable</a> is FALSE.

tabular.environment	character string. Per default "tabular" is used. For long tables that span over more than one page, one can use "longtable". For more options see <a href="#">print.xtable</a> .
floating	logical. Determine if the table is printed in a floating environment. Note that the standard default of <a href="#">print.xtable</a> is TRUE. See there for details.
latex.environments	character string. Per default "center" is used. In contrast to the default behavior of <a href="#">print.xtable</a> , tables are also centered if no floating environment is used. For details and more options see <a href="#">print.xtable</a> .
...	additional arguments passed to <a href="#">xtable</a> or <a href="#">print.xtable</a> . See there for details.

### Details

We use the standard xtable function but add a special class that allows different defaults in the print.xtable function.

In general, all options of print.xtable can be used as well as global options set via options(). E.g. options(xtable.booktabs = FALSE will set the argument booktabs per default to FALSE for all calls to print.xtable.

### Value

After printing, a table with LaTeX markup is returned.

### Author(s)

Benjamin Hofner

### See Also

For details see [xtable](#) and [print.xtable](#).  
[summarize](#), [get\\_option](#)

### Examples

```
if (require("nlme")) {
  ## Use dataset Orthodont
  data(Orthodont, package = "nlme")

  ## Get summary for continuous variables
  (tab1 <- summarize(Orthodont, type = "numeric"))

  ## Get summary for categorical variables
  (tab2 <- summarize(Orthodont, type = "fac"))

  ## Using the tables with LaTeX
  if (require("xtable")) {
    xtable(tab1)
    ## grouped table
    xtable(summarize(Orthodont, group = "Sex"))
  }
}
```

```
    xtable(tab2)  
  }  
}
```

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