Package ‘qwraps2’

December 2, 2019

Title Quick Wraps 2

Version 0.4.2

Description A collection of (wrapper) functions the creator found useful for quickly placing data summaries and formatted regression results into '.Rnw' or '.Rmd' files. Functions for generating commonly used graphics, such as receiver operating curves or Bland-Altman plots, are also provided by 'qwraps2'. 'qwraps2' is a updated version of a package 'qwraps'. The original version 'qwraps' was never submitted to CRAN but can be found at <https://github.com/dewittpe/qwraps/>. The implementation and limited scope of the functions within 'qwraps2' <https://github.com/dewittpe/qwraps2/> is fundamentally different from 'qwraps'.

Depends R (>= 3.0.2)

License GPL-2

Encoding UTF-8

URL https://github.com/dewittpe/qwraps2/

LazyData true

Imports dplyr, ggplot2, knitr, magrittr, Rcpp (>= 0.12.11), rlang, tidyr, utils

Suggests survival, testthat, covr, rbenchmark, rmarkdown

RoxygenNote 7.0.2

LinkingTo Rcpp (>= 0.12.11), RcppArmadillo

VignetteBuilder knitr

NeedsCompilation yes

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Repository CRAN

Date/Publication 2019-12-02 20:40:13 UTC
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backtick Backtick

Description

Encapsulate a string in backticks. Very helpful for in line code in knitr::spin scripts.

Usage

backtick(x, dequote = FALSE)

Arguments

x the thing to be deparsed and encapsulated in backticks
dequote remove the first and last double or signal quote form x
Confusion Matrices (Contingency Tables)

Description

Construction of confusion matrices, accuracy, sensitivity, specificity, confidence intervals (Wilson’s method and (optional bootstrapping)).

Usage

confusion_matrix(x, ...)

## Default S3 method:
confusion_matrix(
  x,
  y,
  positive,
  boot = FALSE,
  boot_samples = 1000L,
  alpha = 0.05,
  ...
)

## S3 method for class 'formula'
confusion_matrix(
  formula,
  data = parent.frame(),
  positive,
  boot = FALSE,
  boot_samples = 1000L,
  alpha = 0.05,
  ...
)

is.confusion_matrix(x)

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

Arguments

x prediction condition vector, a two level factor variable or a variable that can be converted to one.

... not currently used

y True Condition vector with the same possible values as x.
confusion_matrix

positive the level of x and y which is the positive outcome. If missing the first level of factor(y) will be used as the positive level.

boot boolean, should bootstrapped confidence intervals for the sensitivity and specificity be computed? Defaults to FALSE.

boot_samples number of bootstrapping sample to generate, defaults to 1000L. Ignored if boot == FALSE.

alpha 100(1-alpha) sensitivity. Ignored if boot == FALSE.

formula column (known) ~ row (test) for building the confusion matrix

data environment containing the variables listed in the formula

Details

Sensitivity and Specificity: For the sensitivity and specificity function we expect the 2-by-2 confusion matrix (contingency table) to be of the form:

<table>
<thead>
<tr>
<th>True Condition</th>
<th>+</th>
<th>-</th>
</tr>
</thead>
<tbody>
<tr>
<td>Predicted Condition</td>
<td>TP</td>
<td>FP</td>
</tr>
<tr>
<td>Predicted Condition</td>
<td>FN</td>
<td>TN</td>
</tr>
</tbody>
</table>

where

- FN: False Negative, and
- FP: False Positive,
- TN: True Negative,
- TP: True Positive.

Recall:

- sensitivity = TP / (TP + FN)
- specificity = TN / (TN + FP)
- positive predictive value (PPV) = TP / (TP + FP)
- negative predictive value (NPV) = TN / (TN + FN)

Value

The sensitivity and specificity functions return numeric values. confusion_matrix returns a list with elements:

- tab the confusion matrix,
- stats a matrix of summary statistics and confidence intervals.
Examples

# Example 1

test <- c(rep(1, 53), rep(0, 47))
truth <- c(rep(1, 20), rep(0, 33), rep(1, 10), rep(0, 37))
con_mat <- confusion_matrix(test, truth, positive = "1")
str(con_mat)
con_mat

# Example 2: based on an example from the wikipedia page:
# https://en.wikipedia.org/wiki/Confusion_matrix

animals <-
  data.frame(Predicted = c(rep("Cat", 5 + 2 + 0),
                           rep("Dog", 3 + 3 + 2),
                           rep("Rabbit", 0 + 1 + 11)),
             Actual = c(rep(c("Cat", "Dog", "Rabbit"), times = c(5, 2, 0)),
                        rep(c("Cat", "Dog", "Rabbit"), times = c(3, 3, 2)),
                        rep(c("Cat", "Dog", "Rabbit"), times = c(0, 1, 11)) ),
             stringsAsFactors = FALSE)
table(animals)
cats <- apply(animals, 1:2, function(x) ifelse(x == "Cat", "Cat", "Non-Cat"))

# Default calls, note the difference based on what is set as the 'positive'
# value.
confusion_matrix(cats[, "Predicted"], cats[, "Actual"], positive = "Cat")
confusion_matrix(cats[, "Predicted"], cats[, "Actual"], positive = "Non-Cat")

# Using a Formula
confusion_matrix(I(Actual == "Cat") ~ I(Predicted == "Cat"),
                  data = as.data.frame(animals),
                  positive = "TRUE")

# Example 3

russell <-
  data.frame(Pred = c(rep(0, 2295), rep(0, 118), rep(1, 1529), rep(1, 229)),
             Truth = c(rep(0, 2295), rep(1, 118), rep(0, 1529), rep(1, 229)))

# The values for Sensitivity, Specificity, PPV, and NPV are dependent on the
# "positive" level. By default, the first level of y is used.
confusion_matrix(x = russell$Pred, y = russell$Truth, positive = "0")
confusion_matrix(x = russell$Pred, y = russell$Truth, positive = "1")

---

**Extract Summary stats from regression objects**
Description

A collection of functions for extracting summary statistics and reporting regression results from `lm`, `glm` and other regression objects.

Usage

```r
extract_fstat(x)
extract_fpvalue(x)
```

## S3 method for class 'lm'
```r
extract_fpvalue(x)
```

Arguments

- `x` a `lm` object

Details

TO DO

Value

- a character vector of the formatted numbers
- formatted p-value from the F-test

See Also

`lm`

Examples

# TODO

---

file_check

File and Working Directory Check

Description

This check is three-fold: 1) verify the current working directory is as expected, 2) verify the user can access the file, and 3) verify the file contents are as expected (via md5sum).

Usage

```r
file_check(paths, md5sums = NULL, stop = FALSE)
```
Arguments

paths a character path to the target file
md5sums a character string for the expected md5sum of the target file. If NULL then only a file.exists check will be done.
stop if TRUE then an error is thrown if any of the checks fail. If FALSE (default) a logical is returned.

Details

The test for the file access is done to verify the file can be read by the current user.

The return of the function is TRUE if all the files in paths are accessible and all of requested md5sum checks pass. FALSE is any file is not accessible or any md5sum check fails. By default, if the return is TRUE then only TRUE will be printed to the console. If the return is FALSE then the attr(,"checks") is printed by default as well.

Good practice would be to use relative paths, a warning will be given if any of the paths are determined to be absolute paths.

Value

The function will return a single TRUE/FALSE value with attributes attr(,"checks").

Examples

## Not run:
# create two example files in the working directory:
cat("example file.", file = "QWRAPS2_EXAMPLE_1.txt")
cat("Another example file.", file = "QWRAPS2_EXAMPLE_2.txt")

# Check that you have access to these files: (Should return TRUE)
test1 <- file_check(c("QWRAPS2_EXAMPLE_1.txt", "QWRAPS2_EXAMPLE_2.txt"))
test1

# By default, when the checks return TRUE the details of the checks are not printed. You can view the details of the checks as follows:
attr(test1, "checks")

# If one or more files is not accessable then return is FALSE and the meta data is printed by default.
test2 <- file_check(c("UNLIKELYFILENAME", "QWRAPS2_EXAMPLE_1.txt", "QWRAPS2_EXAMPLE_2.txt"))
test2

# Or have an error thrown:
file_check(c("UNLIKELYFILENAME", "QWRAPS2_EXAMPLE_1.txt", "QWRAPS2_EXAMPLE_2.txt"), stop = TRUE)

# Verify the md5sums as well as file access:
file_check("QWRAPS2_EXAMPLE_1.txt", "7a3409e17f9de67740e64448a86e708")

# If you only need to verify a subset of md5sums then use an NA in the md5sums argument:
```r
file_check(c("QWRAPS2_EXAMPLE_1.txt", "QWRAPS2_EXAMPLE_2.txt"),
c("7a3409e17f9de067740e64448a86e708", NA))

# Verify all the md5sums
file_check(c("QWRAPS2_EXAMPLE_1.txt", "QWRAPS2_EXAMPLE_2.txt"),
c("7a3409e17f9de067740e64448a86e708", "798e52b92e0ae0e60f3f3db1273235d0"))

# clean up working directory
unlink("QWRAPS2_EXAMPLE_1.txt")
unlink("QWRAPS2_EXAMPLE_2.txt")

## End(Not run)
```

---

**frmt Format Wrappers**

**Description**

Functions for formating numeric values for consistent display in reports.

**Usage**

```r
frmt(x, digits = getOption("qwraps2_frmt_digits", 2))

frmtup(
  x,
  style = getOption("qwraps2_journal", "default"),
  digits = getOption("qwraps2_frmtp_digits", 4),
  markup = getOption("qwraps2_markup", "latex"),
  case = getOption("qwraps2_frmtp_case", "upper"),
  leading0 = getOption("qwraps2_frmtp_leading0", TRUE)
)

frmtci(
  x,
  est = 1,
  lcl = 2,
  ucl = 3,
  format = "est (lcl, ucl)",
  show_level = FALSE,
  ...
)
```
Arguments

x
a vector of numbers or a numeric matrix to format.
digits
number of digits, including trailing zeros, to the right of the decimal point. This option is ignored if is.integer(x) == TRUE.
style
a character string indicating a specific journal requirements for p-value formatting.
markup
a character string indicating if the output should be latex or markup.
case
a character string indicating if the output should be upper case or lower case.
leading0
boolean, whether or not the p-value should be reported as 0.0123 (TRUE, default), or .0123 (FALSE).
est
the numeric index of the vector element or the matrix column containing the point estimate.
lcl
the numeric index of the vector element or the matrix column containing the lower confidence limit.
ucl
the numeric index of the vector element or the matrix column containing the upper confidence limit.
format
a string with "est", "lcl", and "ucl" to denote the location of the estimate, lower confidence limit, and upper confidence limit for the formatted string. Defaults to "est (lcl, ucl)".
show_level
defaults to FALSE. If TRUE and format is the default, then "100*(1-options()$qwraps2_alpha) parenthesis and the lcl. If set to a string, then the given string will be placed between the left parenthesis and the lcl. If the format is not the default, then this argument is ignored.
...
args passed to frmt

Details

'frmt' is really just a wrapper for the formatC.
'frmt' formats P-values per journal requirements. As I work on papers aimed at different journals, the formatting functions will be extended to match.

Default settings are controlled through the function arguments but should be set via options().

Default settings report the P-value exactly if P > getOptions("qwraps2_frmtp_digits",4) and reports P < 10^-(getOptions("qwraps2_frmtp_digits",2)) otherwise. By the leading zero is controlled via getOptions("qwraps2_frmtp_leading0",TRUE) and a upper or lower case P is controlled by getOptions("qwraps2_frmtp_case","upper"). These options are ignored if style != "default".

Journals with predefined P-value formatting are noted in the qwraps2 documentation.

'frmtci' takes a matrix, or data.frame, with a point estimate and the lcl and ucl and formats a string for reporting. est (lcl, ucl) is the default. The confidence level can be added to the string, e.g., "est (95 format.

'frmtcip' expects four values, est, lcl, ucl, and p-value. The resulting sting will be of the form "est (lcl, ucl; p-value)".
The `Rpkg`, `CRANpkg`, and `Githubpkg` functions are used to help make documenting packages stylistically consistent and with valid urls. These functions were inspired by similar ones found in BioConductor’s BiocStyle package.

Value

a character vector of the formatted numbers

See Also

`formatC`

Examples

# Formatting numbers
integers <- c(1234L, 9861230L)
numbers <- c(1234, 9861230)
frmt(integers) # no decimal point
frmt(numbers) # decimal point and zeros to the right

numbers <- c(0.1234, 0.1, 1234.4321, 0.365, 0.375)
frmt(numbers)

# Formatting p-values
ps <- c(0.2, 0.001, 0.00092, 0.047, 0.034781, 0.0000872, 0.787, 0.05, 0.043)
# LaTeX is the default markup language
cbind("raw" = ps,
   "default" = frmtp(ps),
   "3lower" = frmtp(ps, digits = 3, case = "lower"),
   "PediDent" = frmtp(ps, style = "pediatric_dentistry"))

# Using markdown
cbind("raw" = ps,
   "default" = frmtp(ps, markup = "markdown"),
   "3lower" = frmtp(ps, digits = 3, case = "lower", markup = "markdown"),
   "PediDent" = frmtp(ps, style = "pediatric_dentistry", markup = "markdown"))

# Formatting the point estimate and confidence interval
# for a set of three values
temp <- c(a = 1.23, b = .32, CC = 1.78)
frmtci(temp)
frmtci(temp, show_level = TRUE)

# note that the show_level will be ignored in the following
frmtci(temp, format = "est ***lcl, ucl***", show_level = TRUE)

# show_level as a character
frmtci(temp, show_level = "confidence between: ")

# For a matrix: the numbers in this example don't mean anything, but the
# formatting should.
temp2 <- matrix(rnorm(12), nrow = 4, 
    dimnames = list(c("A", "B", "C", "D"), c("EST", "LOW", "HIGH")))
temp2
frmtci(temp2)

geometric_mean_var_sd  Geometric Mean, Variance, and Standard Deviation

Description
Return the geometric mean, variance, and standard deviation.

Usage

gmean(x, na.rm = FALSE)
gvar(x, na.rm = FALSE)
gsd(x, na.rm = FALSE)

Arguments

x  a numeric vector
na_rm  a logical value indicating whether NA values should be stripped before the computation proceeds.

Value

a numeric value

ggplot2_extract_legend

ggplot2 tools

Description
A few handy tools for working with ggplot2.

Usage

ggplot2_extract_legend(x)

Arguments

x  a ggplot
Details

The `ggplot2_extract_legend` function returns a list with the first element being the legend and the second the original plot with the legend omitted.

Value

a list with each element a `ggplot`

Examples

```
# a simple plot
my_plot <-
  ggplot2::ggplot(mtcars) +
  ggplot2::aes(x = wt, y = mpg, color = wt, shape = factor(cyl)) +
  ggplot2::geom_point()

my_plot

# extract the legend. the return object is a list with two elements, the first
# element is the legend, the second is the original plot sans legend.
temp <- ggplot2_extract_legend(my_plot)

# view just the legend. This can be done via a call to the object or using
# plot or print.
temp
plot(temp[[1]])

# the original plot without the legend
plot(temp[[2]])
```

---

lazyload_cache_dir  Lazyload Cache

Description

Lazyload Cached label(s) or a whole directory.

Usage

```
lazyload_cache_dir(
  path = ".//cache",
  envir = parent.frame(),
  ask = FALSE,
  verbose = TRUE,
  full.names = TRUE,
  ...
)
```
lazyload_cache_labels(
  labels,
  path = "./cache/",
  envir = parent.frame(),
  verbose = TRUE,
  filter,
  full.names = TRUE,
  ...
)

**Arguments**

- **path**
  - the path to the cache directory.
- **envir**
  - the environment to load the objects into
- **ask**
  - if TRUE ask the user to confirm loading each database found in `path`
- **verbose**
  - if TRUE display the chunk labels being loaded
- **full.names**
  - use the full name, i.e., include the path, for the chunk label? This argument is passed to `list.files`.

... additional arguments passed to `list.files`.

- **labels**
  - a character vector of the chunk labels to load.
- **filter**
  - an optional function passed to `lazyLoad`. When called on a character vector of object names returns a logical vector: only objects for which this is true will be loaded.

**Details**

These functions helpful for loading cached chunks into an interactive R session. Consider the following scenario: you use knitr and have cached chunks for lazyloading. You’ve created the document, close up your IDE and move on to the next project. Later, you revisit the initial project and need to retrieve the objects created in the cached chunks. One option is to reevaluate all the code, but this could be time consuming. The other option is to use `lazyload_cache_labels` or `lazyload_cache_dir` to quickly (lazy)load the chunks into an active R session.

Use `lazyload_cache_dir` to load a whole directory of cached objects.

Use `lazyload_cache_labels` to load and explicit set of cached chunks.

---

**List Object Aliases**

**Description**

Aliases for `ls` providing additional details.
Usage

ll(pos = 1, pattern, order_by = "Size", decreasing = TRUE, head = FALSE, n = 5)

Arguments

pos specifies the environment as a position in the search list
pattern an optional regular expression. Only names matching pattern are returned. `glob2rx` can be used to convert wildcard patterns to regular expressions.
order_by a character, order the results by “Size” (default), “Type”, “Rows”, or “Columns”.
decreasing logical, defaults to `TRUE`, decreasing order? passed to `order`.
head logical, if `TRUE` then only return the first `n` objects per `order_by` and `decreasing`.
n number of rows to return, ignored if `head = FALSE`.

References

The basis for this work came from a Stack Overflow posting: http://stackoverflow.com/questions/1358003/tricks-to-manage-the-available-memory-in-an-r-session

See Also

`ls`

Examples

# View your current workspace
## Not run:
ls()
ll()

## End(Not run)

# View another environment
e <- new.env()
e$fit <- lm(mpg ~ wt, mtcars)
e$fit2 <- lm(mpg ~ wt + am + vs, data = mtcars)
e$x <- rnorm(1e5)
e$y <- runif(1e4)
e$z <- with(e, x * y)
e$w <- sum(e$z)
ls(e)
ll(e)
ll(e, head = TRUE)
Description
transform x either via the logit, or inverse logit.

Usage
logit(x)
invlogit(x)

Arguments
x a numeric vector

Details
The logit and inverse logit functions are part of R via the logistic distribution functions in the stats package. Quoting from the documentation for the logistic distribution
"qlogis(p) is the same as the logit function, logit(p) = log(p/1-p), and plogis(x) has consequently been called the 'inverse logit'."
See the examples for benchmarking these functions. The logit and invlogit functions are faster than the qlogis and plogis functions.

See Also
qlogis

Examples
library(qwraps2)
library(rbenchmark)

# compare logit to qlogis
p <- runif(1e5)
identical(logit(p), qlogis(p))
benchmark(logit(p), qlogis(p))

# compare invlogit to plogis
x <- runif(1e5, -1000, 1000)
identical(invlogit(x), plogis(x))
benchmark(invlogit(x), plogis(x))
mean_ci

Means and Confidence Intervals

Description

A function for calculating and formatting means and confidence interval.

Usage

```r
mean_ci(
  x,
  na_rm = FALSE,
  transform,
  alpha = getOption("qwraps2_alpha", 0.05),
  qdist = stats::qnorm,
  qdist.args = list()
)
```

## S3 method for class 'qwraps2_mean_ci'
print(x, ...)

Arguments

- **x** a numeric vector
- **na_rm** if true, omit NA values
- **transform** function transform to the mean and the confidence limits. See Details.
- **alpha** defaults to `getOption('qwraps2_alpha', 0.05)`. The symmetric 100(1-alpha)% CI will be determined.
- **qdist** defaults to `qnorm`. use `qt` for a Student t intervals.
- **qdist.args** list of arguments passed to `qdist`
- **...** arguments passed to `frmtci`.

Details

Given a numeric vector, `mean_ci` will return a vector with the mean, LCL, and UCL. Using `frmtci` will be helpful for reporting the results in print.

The `transform` argument allows the use to transform the data. A common occurrence of using `mean_ci(log(x), transform = exp)` will return the geometric mean and confidence interval for x.

Value

a vector with the mean, lower confidence limit (LCL), and the upper confidence limit (UCL).

See Also

`frmtci`
mean_sd

Examples

# using the standard normal for the CI
mean_ci(mtcars$mpg)

# print it nicely
qwraps2::frmtci(mean_ci(mtcars$mpg))
qwraps2::frmtci(mean_ci(mtcars$mpg), show_level = TRUE)
qwraps2::frmtci(mean_ci(mtcars$mpg, alpha = 0.01), show_level = TRUE)

# Compare to the ci that comes form t.test
 t.test(mtcars$mpg)
t.test(mtcars$mpg)$conf.int
mean_ci(mtcars$mpg, qdist = stats::qt, qdist.args = list(df = 31))

# geometric version
mean_ci(log(mtcars$mpg), transform = exp, qdist = stats::qt, qdist.args = list(df = 31))

---

mean_sd  Mean and Standard deviation

Description

A function for calculating and formatting means and standard deviations.

Usage

mean_sd(
  x,
  digits = getOption("qwraps2_frmt_digits", 2),
  na_rm = FALSE,
  show_n = "ifNA",
  denote_sd = "pm",
  markup = getOption("qwraps2_markup", "latex")
)

gmean_sd(
  x,
  digits = getOption("qwraps2_frmt_digits", 2),
  na_rm = FALSE,
  show_n = "ifNA",
  denote_sd = "pm",
  markup = getOption("qwraps2_markup", "latex")
)
Arguments

- **x**: a numeric vector
- **digits**: digits to the right of the decimal point to return in the percentage estimate.
- **na_rm**: if true, omit NA values
- **show_n**: defaults to "ifNA". Other options are "always" or "never".
- **denote_sd**: a character string set to either "pm" or "paren" for reporting 'mean ± sd' or 'mean (sd)'
- **markup**: latex or markdown

Details

Given a numeric vector, `mean_sd` will return a character string with the mean and standard deviation. Formatting of the output will be extended in future versions.

`gmean_sd` returns the geometric mean and geometric standard deviation.

Value

a character vector of the formatted values

Examples

```r
set.seed(42)
x <- rnorm(1000, 3, 4)
mean(x)
sd(x)
mean_sd(x)
mean_sd(x, show_n = "always")
mean_sd(x, show_n = "always", denote_sd = "paren")
x[187] <- NA
mean_sd(x, na_rm = TRUE)
```

---

**median_iqr**

Median and Inner Quartile Range

Description

A function for calculating and formatting the median and inner quartile range of a data vector. 

@details Given a numeric vector, `median_iqr` will return a character string with the median and IQR. Formatting of the output will be extended in future versions.
Usage

\[
\text{median_iqr(} \ x, \\
\text{digits = getOption("qwraps2_frmtdigits", 2),} \\
\text{na.rm = FALSE,} \\
\text{show_n = "ifNA",} \\
\text{markup = getOption("qwraps2_markup", "latex")}\)
\]

Arguments

- **x**: a numeric vector
- **digits**: digits to the right of the decimal point to return.
- **na.rm**: if true, omit NA values
- **show_n**: defaults to "ifNA". Other options are "always" or "never".
- **markup**: latex or markdown

Value

a character vector of the formatted values

Examples

```r
set.seed(42)
x <- rnorm(1000, 3, 4)
median(x)
quantile(x, probs = c(1, 3)/4)
median_iqr(x)
median_iqr(x, show_n = "always")

x[187] <- NA
# median_iqr(x) ## Will error
median_iqr(x, na_rm = TRUE)
```

---

### n_perc

**Count and Percentage**

Description

A function for calculating and formatting counts and percentages.
Usage

```r
n_perc(
  x,
  digits = getOption("qwraps2_frmr_digits", 2),
  na.rm = FALSE,
  show_denom = "ifNA",
  show_symbol = TRUE,
  markup = getOption("qwraps2_markup", "latex")
)
```

```r
perc_n(
  x,
  digits = getOption("qwraps2_frmr_digits", 2),
  na.rm = FALSE,
  show_denom = "ifNA",
  markup = getOption("qwraps2_markup", "latex")
)
```

```r
n_perc0(
  x,
  digits = 0,
  na.rm = FALSE,
  show_denom = "never",
  show_symbol = FALSE,
  markup = getOption("qwraps2_markup", "latex")
)
```

Arguments

- **x**: a 0:1 or boolean vector
- **digits**: digits to the right of the decimal point to return in the percentage estimate.
- **na.rm**: if true, omit NA values
- **show_denom**: defaults to "ifNA". Other options are "always" or "never".
- **show_symbol**: if TRUE (default) the percent symbol is shown, else it is suppressed.
- **markup**: latex or markdown

Details

Default behavior will return the count of successes and the percentage as "N (pp can be controlled by setting na.rm = TRUE. In this case, the number of non-missing values will be reported by default. Omission of the non-missing values can be controlled by setting show_denom = "never".

The function n_perc0 uses a set of default arguments which may be advantageous for use in building tables.

Value

a character vector of the formatted values
pkg_check

Examples

n_perc(c(0, 1, 1, 1, 0, 0), show_denom = "always")
n_perc(c(0, 1, 1, 0, NA), na_rm = TRUE)

n_perc(mtcars$cyl == 6)

set.seed(42)
x <- rbinom(4269, 1, 0.314)
n_perc(x)
n_perc(x, show_denom = "always")
n_perc(x, show_symbol = FALSE)

# n_perc0 examples
n_perc0(c(0, 1, 1, 1, 0))
n_perc0(mtcars$cyl == 6)

pkg_check

Package Checks

Description

Check if a package is available on the local machine and optionally verify a version.

Usage

pkg_check(pkgs, versions, stop = FALSE)

Arguments

pkgs a character vector of package names to check for
versions an optional character vector, of the same length of pkgs for the minimum version of the packages.
stop if TRUE then an error is thrown if any of the checks fail. If FALSE (default) a logical is returned.

Details

When writing a script that will be shared it is very likely that the multiple authors/users will need to have a certain set of packages available to load. The pkg_check function will verify that the packages are available to load, this includes an optional version test, and attach the package to the search list if requested.

Testing for package versions will is done as packageVersion(x) >= version. If you need a specific version of a package you should explicitly use packageVersion(x) == version in your script.
qable: an extended version of knitr::kable

Description

Create a simple table via kable with row groups and rownames similar to those of hmisc::latex or htmlTable::htmlTable.

Usage

```r
qable(
  x,  
  rtitle, 
  rgroup, 
  rnames = rownames(x), 
  cnames = colnames(x), 
  markup = getOption("qwraps2_markup", "latex"), 
  ...  
)
```

Arguments

- `x` matrix or data.frame to be turned into a qable
- `rtitle` a row grouping title. See Details.
- `rgroup` a named numeric vector with the name of the row group and the number of rows within the group. `sum(rowgroup) == nrow(x)`.
- `rnames` a character vector of the row names
- `cnames` column names
- `markup` the markup language to use, passed to the `format` argument of `knitr::kable`.
- `...` additional arguments passed to `knitr::kable`

Details

`qable` is used as the printing method for `qwraps2_summary_table` objects. Check the vignettes for examples on building data summary tables.

`rtitle` can be used to add a title to the column constructed by the `rgroup` and `rnames`. The basic layout of a table generated by `qable` is:

```
  rgroup[1]  x[1, 1]    x[1, 2]
```
It should be noted that \( \text{escape} = \neg (\text{markup} == \text{"latex"}) \) is passed to \texttt{kable}.

**Value**

a character vector of the formatted numbers

**See Also**

\texttt{kable}

\texttt{summary_table}, for an example of build a data summary table, i.e., a “Table 1”.

For more detail on arguments you can pass to \ldots look at the non-exported functions form the \texttt{knitr} package \texttt{knitr:::kable_latex}, \texttt{knitr:::kable_markdown}, or others.

**Examples**

data(mtcars)
qable(mtcars)
qable(mtcars, markup = "markdown")

# by make
make <- sub("^([^w]+)\s?\([.\*]\)$", \"\1\", rownames(mtcars))
make <- c(table(make))

# A LaTeX table with a vertical bar between each column
qable(mtcars[sort(rownames(mtcars)), ], rgroup = make)

# A LaTeX table with no vertical bars between columns
qable(mtcars[sort(rownames(mtcars)), ], rgroup = make, vline = \"")

# a markdown table
qable(mtcars[sort(rownames(mtcars)), ], rgroup = make, markup = "markdown")

# define your own column names
qable(mtcars[sort(rownames(mtcars)), ],
    rgroup = make,
    cnames = toupper(colnames(mtcars)),
    markup = "markdown")

# define your own column names and add a title
qable(mtcars[sort(rownames(mtcars)), ],
    rtitle = "Make \& Model",
    rgroup = make,
    cnames = toupper(colnames(mtcars)),
    markup = "markdown")
Description

TO BE CONSTRUCTED

Usage

qacf(x, conf_level = 0.95, show_sig = FALSE, ...)

Arguments

- **x**: object
- **conf_level**: confidence level for determining ‘significant’ correlations.
- **show_sig**: logical, highlight significant correlations.
- **...**: Other arguments passed to stats::acf

Details

TO DO

Value

a ggplot.

Examples

```r
# Generate a random data set
set.seed(42)
n <- 250
x1 <- x2 <- x3 <- x4 <- vector('numeric', length = n)
x1[1] <- runif(1)
x2[1] <- runif(1)
x3[1] <- runif(1)
x4[1] <- runif(1)

# white noise
Z.1 <- rnorm(n, 0, 1)
Z.2 <- rnorm(n, 0, 2)
Z.3 <- rnorm(n, 0, 5)

for(i in 2:n)
{
x1[i] <- x1[i-1] + Z.1[i] - Z.1[i-1] + x4[i-1] - x2[i-1]
x2[i] <- x2[i-1] - 2 * Z.2[i] + Z.2[i-1] - x4[i-1]
x3[i] <- x3[i-1] + x2[i-1] + 0.2 * Z.3[i] + Z.3[i-1]
x4[i] <- x4[i-1] + runif(1, 0.5, 1.5) * x4[i-1]
}
```
qblandalman

Bland Altman Plots

Description

Construct and plot a Bland Altman plot in ggplot2.

Usage

qblandalman(x, alpha = getOption("qwraps2_alpha", 0.05), generate_data = TRUE)

qblandalman_build_data_frame(x, alpha = getOption("qwraps2_alpha", 0.05))

Arguments

x        a data.frame with two columns. If a data.frame with more than two columns is used only the first two columns will be used.
alpha    (Defaults to 0.05) place (1 - alpha)*100 place on the plot.
generate_data logical, defaults to TRUE. If TRUE, then the call to qblandalman_build_data_frame is done automatically for you. If FALSE, then you should explicitly call qblandalman_build_data_frame before calling qblandalman.

Details

Providing a data.frame with two columns, the function returns a ggplot version of a Bland Altman plot with the specified confidence intervals.

Two ways to call the plotting function. If you submit a data.frame qblandalman then the data needed to produce the Bland Altman plot is automatically generated by a call to qblandalman_build_data_frame. Alternatively, you may call qblandalman_build_data_frame directly and then call qblandalman. This might be helpful if you are putting multiple Bland Altman plots together into one ggplot object. See Examples.
Value

A ggplot. Minimal aesthetics have been used so that the user may modify the graphic as desired with ease.

References


Examples

## Not run:

# load ggplot2 and the diamonds data set
data(diamonds, package = "ggplot2")

# compare a simple regression to random noise
dat <-
  data.frame(fitted(lm(price ~ poly(carat, 4), data = diamonds)), # fitted values
diamonds$price + rnorm(nrow(diamonds), sd = 0.2), # observed with noise
pi) # extra column
qblandaltman(dat)

# simple example
dat <- data.frame(eval1 = rpois(100, 3), eval2 = rpois(100, 3.4))
qblandaltman(dat)

ggplot2::last_plot() + ggplot2::theme_bw()

# Two plots in one ggplot object
set.seed(42)
dat1 <- data.frame(eval1 = rnorm(100), eval2 = rt(100, df = 1))
dat2 <- data.frame(eval1 = rpois(50, 3), eval2 = rpois(50, 4))

# individual plots
qblandaltman(dat1)
qblandaltman(dat2)

# combined plots
dat <- rbind(cbind(set = "rnorm", qblandaltman_build_data_frame(dat1)),
cbind(set = "rpois", qblandaltman_build_data_frame(dat2)))
qblandaltman(dat, generate_data = FALSE) + ggplot2::facet_wrap(~ set)

## End(Not run)
qkmplot

Kaplan-Meier Plot

Description
A ggplot2 version of a Kaplan-Meier Plot

Usage
qkmplot(x, conf_int = FALSE, ...)
qkmplot_build_data_frame(x)

Arguments
x object
conf_int logical if TRUE show the CI
... Other arguments passed to survival::plot.survfit

Details
Functions to build, explicitly or implicitly, data.frames and then creating a ggplot2 KM plot.

Value
a ggplot.

Examples
require(survival)
leukemia.surv <- survival::survfit(survival::Surv(time, status) ~ x, data = survival::aml)
survival:::plot.survfit(leukemia.surv, conf.int = TRUE, lty = 2:3, col = 1:2)

qkmplot_build_data_frame(leukemia.surv)
qkmplot(leukemia.surv, conf_int = TRUE)

intonly_fit <- survival::survfit(survival::Surv(time, status) ~ 1, data = survival::aml)
survival:::plot.survfit(intonly_fit, conf.int = TRUE)

qkmplot_build_data_frame(intonly_fit)
qkmplot(intonly_fit, conf_int = TRUE)
qroc

Receiver Operator Curves

Description

Construction of ROC curves.

Usage

qroc(x, ...)

qroc_build_data_frame(fit, n_threshold = 200)

auc(.data)

Arguments

  x  a glm fit or data.frame generated by qroc_build_data_frame.
  ... Ignored
  fit a glm fit with family = binomial().
  n_threshold number of thresholds to test against.
  .data    a data.frame generated by qroc_build_data_frame.

Details

Given a glm fit with family = "binomial" (either a log-link or logit-link should be fine, a data set will be constructed and ROC plots generated.

The area under the curve (AUC) is determined by a trapezoid approximation.

Value

a ggplot. Minimal aesthetics have been used so that the user may modify the graphic as desired with ease.

AUC for the data set generated by

Examples

## Not run:
# load ggplot2 and the diamonds data set
library(ggplot2)
data(diamonds, package = "ggplot2")

# Create two logistic regression models
fit1 <- glm(I(price > 2800) ~ cut * color, data = diamonds, family = binomial())
fit2 <- glm(I(price > 2800) ~ cut + color + clarity, data = diamonds, family = binomial())
# Easiest way to get an ROC plot:
qroc(fit1)
qroc(fit2)

# Create two data sets, this will also let you get the AUC out
data1 <- qroc_build_data_frame(fit1)
data2 <- qroc_build_data_frame(fit2)
auc(data1)
auc(data2)

# Plotting the ROC from the data set can be done too
qroc(data1)

# Add the AUC value to the plot title
qroc(data2) + ggtitle(paste("Fit 2\nAUC =", round(auc(data2), 2)))

# build a data set for plotting to ROCs on one plot
plot_data <- rbind(cbind(Model = "fit1", data1),
                   cbind(Model = "fit2", data2))
qroc(plot_data) + aes(color = Model)

# with AUC in the legend
plot_data <- rbind(cbind(Model = paste("Fit1\nauc =", round(auc(data1), 3)), data1),
                   cbind(Model = paste("Fit2\nauc =", round(auc(data2), 3)), data2))
qroc(plot_data) +
  theme_bw() +
  aes(color = Model, linetype = Model) +
  theme(legend.position = "bottom",
        legend.text.align = 0.5)

## End(Not run)

---

qwraps2

A collection of wrapper functions aimed at aiding the authoring of reproducible reports.

Description

qwraps2 is a collection of helpful functions when working on a varied collection of different analysis reports. There are two types of functions, helpful data summary functions, formatting results from regression models, and ggplot2 wrappers.

Details

Several wrappers for ggplot2 style graphics, such as ROC, AUC, Bland-Altman, and KM plots are provided. Named as qroc, qacf, qblandaltman and qkmplot to pay homage to qplot form ggplot2 and the standard names for such plots.

Other functions are used to quickly generate meaningful character strings for outputting results in .Rnw, .Rmd, or other similar functions.
Options

There are several options which can be set via `options` and will be used via `getOption`. The following lists, in alphabetical order the different options which are available and what they control.

- `getOptions("qwraps2_alpha",0.05)` significance level, used for generating \((1 - \text{getOptions("qwraps2_alpha",0.05)}) \times 100\%\) confidence intervals, and determining significance for p-value < `getOptions("qwraps2_alpha",0.05)`.  
- `getOptions("qwraps2_frmt_digits",2)` Number of digits to the right of the decimal point for any value other than p-values.  
- `getOptions("qwraps2_frmtp_case","upper")` set to either 'upper' or 'lower' for the case of the 'P' for reporting p-values.  
- `getOptions("qwraps2_frmtp_digits",4)` Number of digits to the right of the decimal point to report p-values too. If \(\log_{10}(p\text{-value}) < \text{getOptions("qwraps2_frmtp_digits",4)}\) then the output will be "P < 0.01", to however many digits are correct. Other options control other parts of the output p-value format.  
- `getOptions("qwraps2_frmtp_leading0",TRUE)` to display or not to display the leading zero in p-values, i.e., if TRUE p-values are reported as 0.02 versus when FALSE p-values are reported as .02.  
- `getOptions("qwraps2_journal","default")` if a journal has specific formatting for p-values or other statistics, this option will control the output. Many other options are ignored if this is any other than default. Check the github wiki, or this file, for current lists of implemented journal style methods.  
- `getOptions("qwraps2_markup","latex")` value set to 'latex' or to 'markdown'. Output is formatted to meet requirements of either markup language.  
- `getOptions("qwraps2_style","default")` By setting this option to a specific journal, p-values and other output, will be formatted to meet journal requirements.

Journals with predefined formatting

- Obstetrics \& Gynecology  
  - `options(qwraps2_journal = "obstetrics_gynecology")`  
  - P-value formatting as of April 2015:  
    Express P values to no more than three decimal places.  
    Based on observations of published work, leading 0 will be omitted.

- Pediatric Dentistry:  
  - `options(qwraps2_journal = "pediatric_dentistry")`  
  - P-value formatting as of March 2015.  
    If \(P > .01\), the actual value for P should be expressed to 2 digits. Non-significant values should not be expressed as "NS" whether or note P is significant, unless rounding a significant P-value expressed to 3 digits would make it non significant (ie P=.049, not P=.05). If \(P < .01\), it should be express to 3 digits (eg, P=.003, not P<.05). Actual P-values should be expressed unless \(P < .001\), in which case they should be so designated.
Rpkg

Formatting Style on URLs for packages on CRAN, Github, and Gitlab.

Description

Functions for controlling the look of package names in markdown created vignettes and easy curating of URLs for the packages.

Usage

Rpkg(pkg)
CRANpkg(pkg)
Githubpkg(pkg, username)
Gitlabpkg(pkg, username)

Arguments

pkg The name of the package, will work as a quoted or raw name.
username username for Github.com or Gitlab.com

Examples

Rpkg(qwraps2)
Rpkg("qwraps2")

CRANpkg(qwraps2)
CRANpkg("qwraps2")

Githubpkg(qwraps2, "dewittpe")
Githubpkg("qwraps2", dewittpe)

Gitlabpkg(qwraps2, "dewittpe")
Gitlabpkg("qwraps2", dewittpe)

StatStepribbon Stat Step Ribbon

Description

Provides staiestep values for ribbon plots (Copied this from the https://github.com/hrbrmstr/ggalt version 0.6.0, which is not yet on CRAN. Some minor modifications to the file have been made).
References

https://groups.google.com/forum/?fromgroups#!topic/ggplot2/9cFWHaH1CPs

---

**stat_stepribbon**  Step ribbon statistic

**Description**

Provides stairstep values for ribbon plots (Copied this from the https://github.com/hrbrmstr/ggalt version 0.6.0, which is not yet on CRAN. Some minor modifications to the file have been made).

**Usage**

```r
stat_stepribbon(
  mapping = NULL,
  data = NULL,
  geom = "ribbon",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  direction = "hv",
  ...
)
```

**Arguments**

- **mapping**  Set of aesthetic mappings created by `aes()` or `aes()`. If specified and `inherit.aes` = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.
- **data**  The data to be displayed in this layer. There are three options:
  - If NULL, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x,10)`).
- **geom**  which geom to use; defaults to "ribbon"
- **position**  Position adjustment, either as a string, or the result of a call to a position adjustment function.
- **na.rm**  If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend  logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes  If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

direction  hv for horizontal-vertical steps, ‘vh” for vertical-horizontal steps

...  Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = ”red” or size = 3. They may also be parameters to the paired geom/stat.

References

https://groups.google.com/forum/?fromgroups#!topic/ggplot2/9cFWHaH1CPs

Examples

```r
x <- 1:10
df <- data.frame(x=x, y=x+10, ymin=x+7, ymax=x+12)

gg <- ggplot2::ggplot(df, ggplot2::aes(x, y))
gg <- gg + ggplot2::geom_ribbon(ggplot2::aes(ymin=ymin, ymax=ymax),
stat="stepribbon", fill="#b2b2b2")

gg <- gg + ggplot2::geom_step(color="#2b2b2b")

gg <- ggplot2::ggplot(df, ggplot2::aes(x, y))

gg <- gg + ggplot2::geom_ribbon(ggplot2::aes(ymin=ymin, ymax=ymax),
stat="stepribbon", fill="#b2b2b2",
direction="hv")

gg <- gg + ggplot2::geom_step(color="#2b2b2b")

```

---

**summary_table**  
*Data Summary Tables*

**Description**

Tools useful for building data summary tables.

Tool to quickly generate the code for summarizing the variables of a data.frame.

**Usage**

```r
summary_table(x, summaries = qsummary(x))
```

```
## S3 method for class 'qwraps2_summary_table'
cbind(..., deparse.level = 1)
```
summary_table

## S3 method for class 'qwraps2_summary_table'
rbind(..., deparse.level = 1)
qsummary(.data, numeric_summaries, n_perc_args, env)

### Arguments

- **x**: a data.frame or grouped_df.
- **summaries**: a list of lists of formulae for summarizing the data set. See Details and examples.
- **...**: qwraps2_summary_table objects to bind together
- **deparse.level**: integer controlling the construction of labels in the case of non-matrix-like arguments (for the default method): deparse.level = 0 constructs no labels; the default, deparse.level = 1 or deparse.level = 2 constructs labels from the argument names.
- **.data**: a data.frame
- **numeric_summaries**: a list of functions to use for summarizing numeric variables. The functions need to be provided as character strings with the single argument defined by the %s symbol.
- **n_perc_args**: a list of arguments to pass to n_perc to be used with character or factor variables in .data.
- **env**: environment to assign to the resulting formulae

### Details

summary_table can be used to generate good looking, simple tables in LaTeX or markdown. Functions like xtables::print.xtable and Hmisc::latex provide many more tools for formatting tables. The purpose of summary_table is to generate good looking tables quickly within workflow for summarizing a data set.

Creating a list-of-lists of summary functions to apply to a data set will allow the exploration of the whole data set and grouped data sets. In the example provided on this page we see a set of summary measures for the mtcars data set and the construction of a table for the whole data set and for a grouped data set. When working through the example pay attention to the use of group_by and ungroup from dplyr.

The list-of-lists should be thought of as follows: the outer list defines row groups, the inner lists define the rows within each row group.

More detailed use of these functions can be found the "summary-statistics" vignette.

The print method for the qwraps2_summary_table objects is just a simple wrapper for qable.

### Value

a qwraps2_summary_table object.
See Also

`qable` for marking up `qwraps2_data_summary` objects. `group_by` for `grouped_df` objects. The vignette("summary-statistics",package = "qwraps2") for detailed use of these functions and cavets.

cbind
rbind

Examples

# A list-of-lists for the summaries arg. This object is of the basic form:
# It is recommended that you use the .data pronoun in the functions, see
# help(topic = ".data", package = "rlang") for details on this pronoun.
# list("row group A" =
#    list("row 1A" = ~ <summary function>,
#          "row 2A" = ~ <summary function>),
#    "row group B" =
#    list("row 1B" = ~ <summary function>,
#          "row 2B" = ~ <summary function>,
#          "row 3B" = ~ <summary function>))

our_summaries <-
  list("Miles Per Gallon" =
      list("min" = ~ min(.data$mpg),
           "mean" = ~ mean(.data$mpg),
           "mean ± sd" = ~ qwraps2::mean_sd(.data$mpg),
           "max" = ~ max(.data$mpg)),
     "Weight" =
      list("median" = ~ median(.data$wt)),
     "Cylinders" =
      list("4 cyl: n (%)" = ~ qwraps2::n_perc0(.data$cyl == 4),
            "6 cyl: n (%)" = ~ qwraps2::n_perc0(.data$cyl == 6),
            "8 cyl: n (%)" = ~ qwraps2::n_perc0(.data$cyl == 8)))

# Going to use markdown for the markup language in this example, the original
# option will be reset at the end of the example.
orig_opt <- options()$qwraps2_markup
options(qwraps2_markup = "markdown")

# The summary table for the whole mtcars data set
whole_table <- summary_table(mtcars, our_summaries)
whole_table

# The summary table for mtcars grouped by am (automatic or manual transmission)
# This will generate one column for each level of mtcars$am
grouped_by_table <-
  summary_table(dplyr::group_by(mtcars, .data$am), our_summaries)
grouped_by_table

# To build a table with a column for the whole data set and each of the am
# levels
cbind(whole_table, grouped_by_table)
# Adding a caption for a LaTeX table

\begin{verbatim}
print(whole_table, caption = "Hello world", markup = "latex")
\end{verbatim}

# A **warning** about grouped_df objects.
# If you use dplyr::group_by or
dplyr::rowwise to manipulate a data set and fail to use dplyr::ungroup you
# might find a table that takes a long time to create and does not summarize the
# data as expected. For example, let's build a data set with twenty subjects
# and injury severity scores for head and face injuries. We'll clean the data
# by finding the max ISS score for each subject and then reporting summary
# statistics there of.

set.seed(42)
library(magrittr)
adat <- dplyr::data_frame(id = letters[1:20],
                         head_iss = sample(1:6, 20, replace = TRUE, prob = 10 * (6:1)),
                         face_iss = sample(1:6, 20, replace = TRUE, prob = 10 * (6:1)))

iss_summary <-
  list("Head ISS" =
       list("min" = ~ min(.data$head_iss),
            "median" = ~ median(.data$head_iss),
            "max" = ~ max(.data$head_iss)),
      "Face ISS" =
       list("min" = ~ min(.data$face_iss),
            "median" = ~ median(.data$face_iss),
            "max" = ~ max(.data$face_iss)),
      "Max ISS" =
       list("min" = ~ min(.data$iss),
            "median" = ~ median(.data$iss),
            "max" = ~ max(.data$iss)))

subject_level_dat <-
  dat %>%
    dplyr::group_by(.data$id) %>%
    dplyr::mutate(iss = max(head_iss, face_iss))

# Want: a table with one column for all subjects with nine rows divided up into
# three row groups. However, this will create a table with 20 columns, one for
# each subject
summary_table(subject_level_dat, iss_summary)

# Ungroup the data.frame to get the correct output
subject_level_dat %>%
  dplyr::ungroup() %>%
  summary_table(iss_summary)

# The Default call will work with non-syntactically valid names and will
# generate a table with statistics defined by the qsummary call.
mtcars %>%
\end{verbatim}
```r
# Another example from the diamonds data
data("diamonds", package = "ggplot2")
diamonds["The Price"] <- diamonds$price
diamonds["A Logical"] <- sample(c(TRUE, FALSE), size = nrow(diamonds), replace = TRUE)
diamonds["badcol"] <- replicate(expr = list(c(1:34)), n = nrow(diamonds))

summary_table(diamonds)
summary_table(diamonds, qsummary(diamonds))
summary_table(dplyr::group_by(diamonds, .data$cut))
summary_table(dplyr::group_by(diamonds, .data$cut),
  list("My Summary of Price" =
    list("min price" = ~ min(.data$price),
      "IQR" = ~ stats::IQR(.data$price))))

# Data sets with missing values
temp <- mtcars
temp$cyl[5] <- NA
temp$am[c(1, 5, 10)] <- NA
temp$am <- factor(temp$am, levels = 0:1, labels = c("Automatic", "Manual"))
temp$vs <- as.logical(temp$vs)
temp$vs[c(2, 6)] <- NA
qsummary(dplyr::select(temp, .data$cyl, .data$am, .data$vs))
summary_table(dplyr::select(temp, .data$cyl, .data$am, .data$vs))

# binding tables together. The original design and expected use of
# summary_table did not require a rbind, as all rows are defined in the
# summaries argument. That said, here are examples of using cbind and rbind to
# build several different tables.
our_summary1 <-
  list("Miles Per Gallon" =
    list("min" = ~ min(.data$mpg),
      "max" = ~ max(.data$mpg),
      "mean (sd)" = ~ qwraps2::mean_sd(.data$mpg)),
    "Displacement" =
    list("min" = ~ min(.data$disp),
      "max" = ~ max(.data$disp),
      "mean (sd)" = ~ qwraps2::mean_sd(.data$disp)))

our_summary2 <-
  list("Weight (1000 lbs)" =
    list("min" = ~ min(.data$wt),
      "max" = ~ max(.data$wt),
      "mean (sd)" = ~ qwraps2::mean_sd(.data$wt)),
    "Forward Gears" =
    list("Three" = ~ qwraps2::n_perc0(.data$gear == 3),
      "Four" = ~ qwraps2::n_perc0(.data$gear == 4),
      "Five" = ~ qwraps2::n_perc0(.data$gear == 5),
      "Eight" = ~ qwraps2::n_perc0(.data$gear == 8),
      "Ten" = ~ qwraps2::n_perc0(.data$gear == 10)))
```
"Four" = ~ qwraps2::n_perc0(.data$gear == 4),
"Five" = ~ qwraps2::n_perc0(.data$gear == 5))

tab1 <- summary_table(mtcars, our_summary1)
tab2 <- summary_table(dplyr::group_by(mtcars, am), our_summary1)
tab3 <- summary_table(dplyr::group_by(mtcars, vs), our_summary1)

tab4 <- summary_table(mtcars, our_summary2)
tab5 <- summary_table(dplyr::group_by(mtcars, am), our_summary2)
tab6 <- summary_table(dplyr::group_by(mtcars, vs), our_summary2)

cbind(tab1, tab2, tab3)
cbind(tab4, tab5, tab6)

rbind(tab1, tab4)
all.equal(rbind(tab1, tab4), summary_table(mtcars, c(our_summary1, our_summary2)))

## Not run:
cbind(tab1, tab4) # error because rows are not the same
rbind(tab1, tab2) # error because columns are not the same

## End(Not run)

# reset the original markup option that was used before this example was
# evaluated.
options(qwraps2_markup = orig_opt)

# Detailed examples in the vignette
# vignette("summary-statistics", package = "qwraps2")

---

### tab_summary

#### Tabular Summaries

**Description**

Tool to quickly generate the code for summarizing a variable. To be used with summary_table. This function has been deprecated, see `qsummary` instead.

**Usage**

```r

tab_summary(
  x,
  n_perc_args = list(digits = 0, show_symbol = FALSE),
  envir = parent.frame()
)
```

---

### tab_summary

#### Tabular Summaries

**Description**

Tool to quickly generate the code for summarizing a variable. To be used with summary_table. This function has been deprecated, see `qsummary` instead.

**Usage**

```r

tab_summary(
  x,
  n_perc_args = list(digits = 0, show_symbol = FALSE),
  envir = parent.frame()
)
```
**Arguments**

- **x**: a variable to summarize
- **n_perc_args**: a list of arguments to pass to `n_perc`
- **envir**: the environment to attach to the resulting formulea

---

**Description**

Compute the integral of y with respect to x via trapezoid rule.

**Usage**

```r
traprule(x, y)
```

**Arguments**

- **x, y**: numeric vectors of equal length

**Value**

a numeric value, the estimated integral

**Examples**

```r
xvec <- seq(-2 * pi, 3 * pi, length = 560)
foo <- function(x) { sin(x) + x * cos(x) + 12 }
yvec <- foo(xvec)
plot(xvec, yvec, type = "l")

integrate(f = foo, lower = -2 * pi, upper = 3 * pi)
traprule(xvec, yvec)
```
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