

# Package ‘pubh’

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**Title** A Toolbox for Public Health and Epidemiology

**Version** 1.3.7

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**Description** A toolbox for making R functions and capabilities more accessible to students and professionals from Epidemiology and Public Health related disciplines. Includes a function to report coefficients and confidence intervals from models using robust standard errors (when available), functions that expand 'ggplot2' plots and functions relevant for introductory papers in Epidemiology or Public Health. Please note that use of the provided data sets is for educational purposes only.

**Depends** R (>= 4.1.0), emmeans, ggformula, gtsummary (>= 1.9.9), huxtable, stats

**Imports** car, dplyr, Epi, epiR, epitools, ggplot2, jtools, lmtest, moonBook, performance, sandwich, sjlabelled, sjmisc, survival, tibble, tidyselect

**Suggests** broom, broom.helpers (>= 1.15.0), cardx, easystats, effectsize, ggeffects, ggsci, ISwR, knitr, lme4, MASS, nlme, nnet, report, rmarkdown, rstatix, sjPlot, see

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<code>axis_labs</code>	<i>Apply labels from variables to axis-labels in plots.</i>
------------------------	---

---

## Description

`axis_labs` takes labels from labelled data to use them as axis-labels for plots generated by `gformula` or `ggplot2`.

## Usage

```
axis_labs(object)
```

## Arguments

`object`            `ggplot2` object (see examples).

## Details

This functions is helpful when data has been already labelled by `sjlabelled`. It retrieves variable labels and use them for plotting.

## Value

A `ggplot2` object.

**Examples**

```

data(kfm, package = "ISwR")
require(sjlabelled, quietly = TRUE)
kfm <- kfm |>
  var_labels(
    dl.milk = "Breast-milk intake (dl/day)",
    sex = "Sex",
    weight = "Child weight (kg)",
    ml.suppl = "Milk substitute (ml/day)",
    mat.weight = "Maternal weight (kg)",
    mat.height = "Maternal height (cm)"
  )

kfm |>
  gf_point(weight ~ dl.milk) |>
  gf_lm(col = 2, interval = "confidence", col = 2) |>
  axis_labs()

kfm |>
  box_plot(dl.milk ~ sex, fill = "thistle", alpha = 0.8) |>
  axis_labs() |>
  gf_star(x1 = 1, y1 = 10.9, x2 = 2, y2 = 11, y3 = 11.2)

```

---

**bar\_error***Bar charts with error bars.*

---

**Description**

`bar_error` constructs bar charts in with error bars showing 95 confidence intervals around mean values. High of bars represent mean values.

**Usage**

```

bar_error(
  object = NULL,
  formula = NULL,
  data = NULL,
  fill = "indianred3",
  col = "black",
  alpha = 0.7,
  ...
)

```

**Arguments**

<code>object</code>	When chaining, this holds an object produced in the earlier portions of the chain. Most users can safely ignore this argument. See details and examples.
<code>formula</code>	A formula with shape: $y \sim x$ or $y \sim x   z$ where $y$ is a numerical variable and both $x$ and $z$ are factors.

<code>data</code>	A data frame where the variables in the formula can be found.
<code>fill</code>	Colour used to fill the bars.
<code>col</code>	Colour used for the borders of the bars.
<code>alpha</code>	Opacity of the colour fill (0 = invisible, 1 = opaque).
<code>...</code>	Additional information passed to <a href="#">gf_summary</a> .

### Examples

```
require(dplyr, quietly = TRUE)
require(sjlabelled, quietly = TRUE)
data(birthwt, package = "MASS")

birthwt <- birthwt |>
  mutate(
    smoke = factor(smoke, labels = c("Non-smoker", "Smoker")),
    Race = factor(race > 1, labels = c("White", "Non-white"))
  ) |>
  var_labels(
    bwt = "Birth weight (g)",
    smoke = "Smoking status"
  )

birthwt |>
  bar_error(bwt ~ smoke, fill = "plum3")

birthwt |>
  bar_error(bwt ~ smoke | Race, fill = "plum3")

birthwt |>
  bar_error(bwt ~ smoke, fill = ~Race)
```

---

 Bernard

*Survival of patients with sepsis.*


---

### Description

A randomised, double-blind, placebo-controlled trial of intravenous ibuprofen in 455 patients who had sepsis, defined as fever, tachycardia, tachypnea, and acute failure of at least one organ system.

### Usage

Bernard

### Format

A labelled tibble with 455 rows and 9 variables:

**id** Patient ID

**treat** Treatment, factor with levels "Placebo" and "Ibuprofen".  
**race** Race/ethnicity, factor with levels "White", "African American" and "Other".  
**fate** Mortality status at 30 days, factor with levels "Alive" and "Dead".  
**apache** Baseline APACHE score.  
**o2del** Oxygen delivery at baseline.  
**followup** Follow-up time in hours.  
**temp0** Baseline temperature in centigrades.  
**temp10** Temperature after 36 hr in centigrades.

### Source

Bernard, GR, et al. (1997) The effects of ibuprofen on the physiology and survival of patients with sepsis, *N Engl J Med* 336: 912–918.

### Examples

```
require(dplyr, quietly = TRUE)
data(Bernard)

Bernard |>
  select(fate, treat) |>
  cross_tbl(by = "fate")

contingency(fate ~ treat, data = Bernard)
```

---

bland\_altman

*Bland-Altman agreement plots.*

---

### Description

Bland-Altman agreement plots.

### Usage

```
bland_altman(  
  object = NULL,  
  formula = NULL,  
  data = NULL,  
  pch = 20,  
  size = 1,  
  col = "black",  
  transform = FALSE,  
  ...  
)
```

**Arguments**

object	When chaining, this holds an object produced in the earlier portions of the chain. Most users can safely ignore this argument. See details and examples.
formula	A formula with shape: $y \sim x$ (see details).
data	A data frame where the variables in the formula can be found.
pch	Symbol for plotting data.
size	Size of the symbol using to plot data.
col	Colour used for the symbol to plot data.
transform	Logical, should ratios instead of difference be used to construct the plot?
...	Further arguments passed to <code>gf_point</code> .

**Details**

`bland_altman` constructs Bland-Altman agreement plots.

Variables in formula are continuous paired observations. When the distribution of the outcome is not normal, but becomes normal with a log-transformation, `bland_altman` can plot the ratio between outcomes (difference in the log scale) by using option `transform = TRUE`.

**Examples**

```
data(wright, package = "ISwR")

wright |>
  bland_altman(mini.wright ~ std.wright,
    pch = 16,
    ylab = "Large-mini expiratory flow rate (l/min)",
    xlab = "Mean expiratory flow rate (l/min)"
  ) |>
  gf_labs(
    y = "Large-mini expiratory flow rate (l/min)",
    x = "Mean expiratory flow rate (l/min)"
  )

data(Sharples)

Sharples |>
  bland_altman(srweight ~ weight, transform = TRUE) |>
  gf_labs(x = "Mean of weights (kg)", y = "Measured weight / Self-reported weight")
```

---

 box\_plot

*Construct box plots.*


---

**Description**

`box_plot` is a wrap function that calls `gf_boxplot` to construct more aesthetic box plots.

**Usage**

```
box_plot(
  object = NULL,
  formula = NULL,
  data = NULL,
  fill = "indianred3",
  alpha = 0.7,
  outlier.shape = 20,
  outlier.size = 1,
  ...
)
```

**Arguments**

object	When chaining, this holds an object produced in the earlier portions of the chain. Most users can safely ignore this argument. See details and examples.
formula	A formula with shape: $y \sim x$ where $y$ is a numerical variable and $x$ is a factor.
data	A data frame where the variables in the formula can be found.
fill	Colour used for the box passed to <a href="#">gf_boxplot</a> .
alpha	Opacity (0 = invisible, 1 = opaque).
outlier.shape	Shape (pch) used as symbol for the outliers.
outlier.size	Size of the outlier symbol.
...	Further arguments passed to <a href="#">gf_boxplot</a> .

**Examples**

```
data(kfm, package = "ISwR")
require(sjlabelled, quietly = TRUE)
kfm <- kfm |>
  var_labels(
    dl.milk = "Breast-milk intake (dl/day)",
    sex = "Sex",
    weight = "Child weight (kg)",
    ml.suppl = "Milk substitute (ml/day)",
    mat.weight = "Maternal weight (kg)",
    mat.height = "Maternal height (cm)"
  )

kfm |>
  box_plot(dl.milk ~ sex, fill = "thistle", alpha = 0.8)

t.test(dl.milk ~ sex, data = kfm)

kfm |>
  box_plot(dl.milk ~ sex, fill = "thistle", alpha = 0.8) |>
  gf_star(1, 10.9, 2, 11, 11.4, legend = "p = 0.035", size = 2.5)
```

---

Brenner

*Prevalence of Helicobacter pylori infection in preschool children.*

---

### Description

A data set containing the prevalence of Helicobacter pylori infection in preschool children according to parental history of duodenal or gastric ulcer.

### Usage

Brenner

### Format

A labelled tibble with 863 rows and 2 variables:

**ulcer** History of duodenal or gastric ulcer, factor with levels "No" and "Yes".

**infected** Infected with Helicobacter pylori, factor with levels "No" and "Yes".

### Source

Brenner H, Rothenbacher D, Bode G, Adler G (1998) Parental history of gastric or duodenal ulcer and prevalence of Helicobacter pylori infection in preschool children: population based study. *BMJ* 316:665.

### Examples

```
require(dplyr, quietly = TRUE)
data(Brenner)
```

```
Brenner |>
  select(infected, ulcer) |>
  cross_tbl(by = "infected")
```

```
contingency(infected ~ ulcer, data = Brenner, method = "cross.sectional")
```

---

bst

*Bootstrap Confidence Intervals.*

---

### Description

bst estimates confidence intervals around the [mean](#), [median](#) or [geo\\_mean](#).

### Usage

```
bst(x, stat = "mean", n = 1000, CI = 95, digits = 2)
```

**Arguments**

x	A numerical variable. Missing observations are removed by default.
stat	Statistic, either "mean" (default), "median" or "gmean" (geometric mean).
n	Number of replicates for the bootstrap (n=1000 by default).
CI	Confidence intervals (CI=95 by default).
digits	Number of digits for rounding (default = 2).

**Value**

A data frame with the estimate and confidence intervals.

**Examples**

```
data(IgM, package = "ISwR")
bst(IgM, "median")

bst(IgM, "gmean")
```

---

chisq.fisher	<i>Internal test for chi-squared assumption. Fisher (2 by 2). If results = T, it fails</i>
--------------	--

---

**Description**

chisq.fisher is an internal function called by contingency and contingency2 that uses the Fisher exact test if results from the assumptions for the chi-squared test fail.

**Usage**

```
chisq.fisher(tab)
```

**Arguments**

tab	A numeric two by two table.
-----	-----------------------------

---

coef_det	<i>Coefficient of determination.</i>
----------	--------------------------------------

---

### Description

coef\_det estimates the coefficient of determination (r-squared) from fitted (predicted) and observed values. Outcome from the model is assumed to be numerical.

### Usage

```
coef_det(obs, fit)
```

### Arguments

obs	Vector with observed values (numerical outcome).
fit	Vector with fitted (predicted) values.

### Value

A scalar, the coefficient of determination (r-squared).

### Examples

```
## Linear regression:
Riboflavin <- seq(0, 80, 10)
OD <- 0.0125 * Riboflavin + rnorm(9, 0.6, 0.03)
titration <- data.frame(Riboflavin, OD)
model1 <- lm(OD ~ Riboflavin, data = titration)
summary(model1)
coef_det(titration$OD, fitted(model1))

## Non-linear regression:
library(nlme, quietly = TRUE)
data(Puromycin)
mm.tx <- gnls(rate ~ SSmicmen(conc, Vm, K),
  data = Puromycin,
  subset = state == "treated"
)
summary(mm.tx)
coef_det(Puromycin$rate[1:12], mm.tx$fitted)
```

---

`contingency`*Measures of association from two by two contingency tables (formula).*

---

### Description

`contingency` is a wrap that calls `epi.2by2` from package `epiR`.

### Usage

```
contingency(  
  object = NULL,  
  formula = NULL,  
  data = NULL,  
  method = "cohort.count",  
  ...  
)
```

### Arguments

<code>object</code>	When chaining, this holds an object produced in the earlier portions of the chain. Most users can safely ignore this argument. See details and examples.
<code>formula</code>	A formula with shape: <code>outcome ~ exposure</code> .
<code>data</code>	A data frame where the variables in the formula can be found.
<code>method</code>	A character string with options: <code>"cohort.count"</code> , <code>"cohort.time"</code> , <code>"case.control"</code> , or <code>"cross.sectional"</code> .
<code>...</code>	Further arguments passed to <code>epi.2by2</code> .

### Details

`contingency` uses a formula as a way to input variables.

`contingency` displays the contingency table as a way for the user to check that the reference levels in the categorical variables (outcome and exposure) are correct. Then displays measures of association (table from `epi.2by2`). It also reports either chi-squared test or exact Fisher's test; `contingency` checks which one of the tests two is appropriate.

### See Also

[epi.2by2](#).

### Examples

```
## A case-control study on the effect of alcohol on oesophageal cancer.  
Freq <- c(386, 29, 389, 171)  
status <- gl(2, 1, 4, labels = c("Control", "Case"))  
alcohol <- gl(2, 2, labels = c("0-39", "40+"))  
cancer <- data.frame(Freq, status, alcohol)
```

```
cancer <- expand_df(cancer)
contingency(status ~ alcohol, data = cancer, method = "case.control")

data(Oncho)
require(dplyr, quietly = TRUE)

Oncho |>
  select(mf, area) |>
  cross_tbl(by = "mf") |>
  theme_pubh(2)

Oncho |>
  contingency(mf ~ area)
```

---

contingency2	<i>Measures of association from two by two contingency tables (direct input).</i>
--------------	---

---

### Description

contingency2 is a wrap that calls `epi.2by2` from package `epiR`.

### Usage

```
contingency2(aa, bb, cc, dd, ...)
```

### Arguments

aa	Number of cases where both exposure and outcome are present.
bb	Number of cases where exposure is present but outcome is absent.
cc	Number of cases where exposure is absent but outcome is present.
dd	Number of cases where both exposure and outcome are absent.
...	Further arguments passed to <a href="#">epi.2by2</a> .

### See Also

[epi.2by2](#).

### Examples

```
## A case-control study on the effect of alcohol on oesophageal cancer.
Freq <- c(386, 29, 389, 171)
status <- gl(2, 1, 4, labels = c("Control", "Case"))
alcohol <- gl(2, 2, labels = c("0-39", "40+"))
cancer <- data.frame(Freq, status, alcohol)
cancer <- expand_df(cancer)

contingency2(171, 389, 29, 386, method = "case.control")
```

---

cosm_reg	<i>Cosmetics for tables of regression coefficients. Converts tables generated by <a href="#">tbl_regression</a> to <a href="#">huxtable</a> and adds some cosmetics.</i>
----------	--

---

### Description

Cosmetics for tables of regression coefficients. Converts tables generated by [tbl\\_regression](#) to [huxtable](#) and adds some cosmetics.

### Usage

```
cosm_reg(gt_tbl, pad = 3, type = 3, bold = TRUE, head_label = "**Variable**")
```

### Arguments

gt_tbl	A table object generated by <a href="#">tbl_regression</a> .
pad	Numerical, padding above and below rows.
type	Anova's type to calculate global p-values.
bold	Display labels in bold?
head_label	Character, label to be used as head for the variable's column.

### Value

A [huxtable](#).

### Examples

```
require(sjlabelled, quietly = TRUE)

data(diet, package = "Epi")
diet <- diet |>
  var_labels(
    chd = "Coronary Heart Disease",
    fibre = "Fibre intake (g/day)"
  )

model_binom <- glm(chd ~ fibre, data = diet, family = binomial)

model_binom |>
  tbl_regression(exponentiate = TRUE) |>
  cosm_reg(bold = TRUE) |>
  theme_pubh(1) |>
  add_footnote(get_r2(model_binom), font_size = 9)

data(birthwt, package = "MASS")
birthwt <- birthwt |>
  mutate(
    smoke = factor(smoke, labels = c("Non-smoker", "Smoker")),
```

```

    race = factor(race, labels = c("White", "African American", "Other"))
  ) |>
  var_labels(
    bwt = "Birth weight (g)",
    smoke = "Smoking status",
    race = "Race"
  )

model_norm <- lm(bwt ~ smoke + race, data = birthwt)

model_norm |>
  tbl_regression() |>
  cosm_reg(bold = TRUE) |>
  theme_pubh(1) |>
  add_footnote(get_r2(model_norm), font_size = 9)

```

---

cosm\_sum

*Cosmetics for summary tables Adds some cosmetics to tables of descriptive statistics generated by `tbl_summary`.*


---

## Description

Cosmetics for summary tables Adds some cosmetics to tables of descriptive statistics generated by `tbl_summary`.

## Usage

```
cosm_sum(gt_tbl, pad = 3, bold = FALSE, head_label = "**Variable**")
```

## Arguments

<code>gt_tbl</code>	A table object generated by <code>tbl_summary</code> .
<code>pad</code>	Numerical, padding above and below rows.
<code>bold</code>	Display labels in bold?
<code>head_label</code>	Character, label to be used as head for the variable's column.

## Details

Function `cosm_sum` adds some cosmetics to tables generated by `tbl_summary`, then converts the table as a `huxtable` and sets proper alignment.

## Value

A `huxtable`.

**Examples**

```
require(dplyr, quietly = TRUE)

data(Oncho)
Oncho |>
  select(-id) |>
  tbl_summary() |>
  cosm_sum(bold = TRUE) |>
  theme_pubh(1)
```

---

 cross\_tbl

*Table of descriptive statistics by categorical variable.*


---

**Description**

cross\_tbl is a wrapper to function from package [tbl\\_summary](#) that constructs tables of descriptive statistics stratified by levels of a categorical outcome.

**Usage**

```
cross_tbl(
  data,
  by,
  head_label = " ",
  bold = TRUE,
  show_total = TRUE,
  p_val = FALSE,
  pad = 3,
  method = 2,
  ...
)
```

**Arguments**

data	A data frame where the variables in the formula can be found.
by	The quoted name of the categorical variable (factor) used for the stratification.
head_label	Character, label to be used as head for the variable's column.
bold	Display labels in bold?
show_total	Logical, show column with totals?
p_val	Logical, show p-values?
pad	Numerical, padding above and bellow rows.
method	An integer indicating methods for continuous variables. 1 Reports means and standard deviations. 2 Reports medians and interquartile ranges.
...	Additional arguments passed to <a href="#">tbl_summary</a> .

## Details

Function `cross_tbl` is a relatively simple wrapper to function `tbl_summary`. It constructs contingency tables and can also be used to report a table with descriptives for all variables stratified by one of the variables. Please see examples to see how to list variables. If data is labelled, the label of the stratifying variable is used as part of the header.

## Value

A huxtable with descriptive statistics stratified by levels of the outcome.

## See Also

[tbl\\_summary](#)

## Examples

```
require(dplyr, quietly = TRUE)

#' data(Oncho)

## A two by two contingency table:
Oncho |>
  select(mf, area) |>
  cross_tbl(by = "mf", bold = TRUE) |>
  theme_pubh(2)

## Reporting prevalence:
Oncho |>
  select(mf, area) |>
  cross_tbl(by = "area", bold = TRUE) |>
  theme_pubh(2)

## Descriptive statistics for all variables in the \code{Oncho} data set except \code{id}.
Oncho |>
  select(-id) |>
  cross_tbl(by = "mf", bold = TRUE) |>
  theme_pubh(2)
```

---

diag\_test

*Diagnostic tests from variables.*

---

## Description

`diag_test` is a wrap function that calls `epi.tests` from package `epiR`. It computes sensitivity, specificity and other statistics related with screening tests.

## Usage

```
diag_test(object = NULL, formula = NULL, data = NULL, ...)
```

**Arguments**

object	When chaining, this holds an object produced in the earlier portions of the chain. Most users can safely ignore this argument. See details and examples.
formula	A formula with shape: outcome ~ predictor (see details).
data	A data frame where the variables in the formula can be found.
...	Further arguments passed to <code>epi.tests</code> .

**Details**

For the formula, the outcome is the gold standard and the explanatory variable is the new (screening) test. See examples.

**See Also**

[epi.tests](#).

**Examples**

```
## We compare the use of lung's X-rays on the screening of TB against the gold standard test.
Freq <- c(1739, 8, 51, 22)
BCG <- gl(2, 1, 4, labels = c("Negative", "Positive"))
Xray <- gl(2, 2, labels = c("Negative", "Positive"))
tb <- data.frame(Freq, BCG, Xray)
tb <- expand_df(tb)

tb |>
  diag_test2(BCG ~ Xray)
```

---

diag\_test2

*Diagnostic tests from direct input.*

---

**Description**

`diag_test2` is a wrap that calls `epi.tests` from package `epiR`. It computes sensitivity, specificity and other statistics related with screening tests.

**Usage**

```
diag_test2(aa, bb, cc, dd)
```

**Arguments**

aa	Number of cases where both screening test and the gold standard are positive.
bb	Number of cases where screening test is positive but gold standard is negative.
cc	Number of cases where screening test is negative but gold standard is positive.
dd	Number of cases where both screening test and the gold standard are negative.

**Details**

`diag.test` uses direct input variables.

**See Also**

[epi.tests](#).

**Examples**

```
## We compare the use of lung's X-rays on the screening of TB against the gold standard test.
diag_test2(22, 51, 8, 1739)
```

---

estat

*Descriptive statistics for continuous variables.*

---

**Description**

`estat` calculates descriptives of numerical variables.

**Usage**

```
estat(object = NULL, formula = NULL, data = NULL, digits = 2, label = NULL)
```

**Arguments**

<code>object</code>	When chaining, this holds an object produced in the earlier portions of the chain. Most users can safely ignore this argument. See details and examples.
<code>formula</code>	A formula with shape: <code>~ x</code> or <code>~ x z</code> (for groups).
<code>data</code>	A data frame where the variables in the formula can be found.
<code>digits</code>	Number of digits for rounding (default = 2).
<code>label</code>	Label used to display the name of the variable (see examples).

**Value**

A data frame with descriptive statistics.

**See Also**

[summary](#), [mytable](#).

**Examples**

```

data(kfm, package = "ISwR")
require(sjlabelled, quietly = TRUE)
kfm <- kfm |>
  var_labels(
    dl.milk = "Breast-milk intake (dl/day)",
    sex = "Sex",
    weight = "Child weight (kg)",
    ml.suppl = "Milk substitute (ml/day)",
    mat.weight = "Maternal weight (kg)",
    mat.height = "Maternal height (cm)"
  )

kfm |>
  estat(~dl.milk)

estat(~ dl.milk | sex, data = kfm)

kfm |>
  estat(~ weight | sex)

```

---

 expand\_df

*Expand a data frame.*


---

**Description**

expand\_df expands a data frame by a vector of frequencies.

**Usage**

```
expand_df(aggregate.data, index.var = "Freq", retain.freq = FALSE)
```

**Arguments**

aggregate.data A data frame.  
 index.var A numerical variable with the frequencies (counts).  
 retain.freq Logical expression indicating if frequencies should be kept.

**Details**

This is a generic function that resembles weighted frequencies in other statistical packages (for example, Stata). expand\_df was adapted from a function developed by deprecated package epicalc (now package epiDisplay).

**Value**

An expanded data frame with replicates given by the frequencies.

### Examples

```
Freq <- c(5032, 5095, 41, 204)
Mortality <- gl(2, 2, labels = c("No", "Yes"))
Calcium <- gl(2, 1, 4, labels = c("No", "Yes"))
anyca <- data.frame(Freq, Mortality, Calcium)
anyca
anyca.exp <- expand_df(anyca)
with(anyca.exp, table(Calcium, Mortality))
```

---

Fentress	<i>Migraine pain reduction.</i>
----------	---------------------------------

---

### Description

Randomised control trial on children suffering from frequent and severe migraine. Control group represents untreated children. The active treatments were either relaxation alone or relaxation with biofeedback.

### Usage

```
Fentress
```

### Format

A labelled tibble with 18 rows and 2 variables:

**pain** Reduction in weekly headache activity expressed as percentage of baseline data.

**group** Group, a factor with levels "Untreated", "Relaxation" (alone) and "Biofeedback" (relaxation and biofeedback).

### Source

Fentress, DW, et al. (1986) Biofeedback and relaxation-response in the treatment of pediatric migraine. *Dev Med Child Neurol* 28:1 39-46.

Altman, DA (1991) *Practical statistics for medical research*. Chapman & Hall/CRC.

### Examples

```
data(Fentress)

Fentress |>
  strip_error(pain ~ group)
```

---

freq_cont	<i>Relative and Cumulative Frequency.</i>
-----------	---

---

### Description

freq\_cont tabulates a continuous variable by given classes.

### Usage

```
freq_cont(x, bks, dg = 2)
```

### Arguments

x	A numerical (continuous) variable. Ideally, relatively long (greater than 100 observations).
bks	Breaks defining the classes (see example).
dg	Number of digits for rounding (default = 2).

### Value

A data frame with the classes, the mid-point, the frequencies, the relative and cumulative frequencies.

### Examples

```
data(IgM, package = "ISwR")
Ab <- data.frame(IgM)
estat(~IgM, data = Ab)
freq_cont(IgM, seq(0, 4.5, 0.5))
```

---

gen_bst_df	<i>Generate a data frame with estimate and bootstrap CIs.</i>
------------	---

---

### Description

gen\_bst\_df is a function called that generates a data frame with confidence intervals of a continuous variable by levels of one or two categorical ones (factors).

### Usage

```
gen_bst_df(object = NULL, formula = NULL, data = NULL, stat = "mean", ...)
```

**Arguments**

object	When chaining, this holds an object produced in the earlier portions of the chain. Most users can safely ignore this argument. See details and examples.
formula	A formula with shape: $y \sim x$ or $y \sim x   z$ where $y$ is a numerical variable and both $x$ and $z$ are factors.
data	A data frame where the variables in the formula can be found.
stat	Statistic used for <a href="#">bst</a> .
...	Passes optional arguments to <a href="#">bst</a> .

**Value**

A data frame with the confidence intervals by level.

**Examples**

```
data(kfm, package = "ISwR")
require(sjlabelled, quietly = TRUE)
kfm <- kfm |>
  var_labels(
    dl.milk = "Breast-milk intake (dl/day)",
    sex = "Sex",
    weight = "Child weight (kg)",
    ml.suppl = "Milk substitute (ml/day)",
    mat.weight = "Maternal weight (kg)",
    mat.height = "Maternal height (cm)"
  )

kfm |>
  gen_bst_df(dl.milk ~ sex)

data(birthwt, package = "MASS")
require(dplyr, quietly = TRUE)
birthwt <- mutate(birthwt,
  smoke = factor(smoke, labels = c("Non-smoker", "Smoker")),
  Race = factor(race > 1, labels = c("White", "Non-white"))
)

birthwt <- birthwt |>
  var_labels(
    bwt = "Birth weight (g)",
    smoke = "Smoking status"
  )

gen_bst_df(bwt ~ smoke | Race, data = birthwt)
```

---

geo_mean	<i>Geometric mean.</i>
----------	------------------------

---

**Description**

Geometric mean.

**Usage**

```
geo_mean(x)
```

**Arguments**

x                    A numeric variable with no negative values.

**Value**

A scalar, the calculated geometric mean.

**Examples**

```
data(IgM, package = "ISwR")
Ab <- data.frame(IgM)
estat(~IgM, data = Ab)
geo_mean(IgM)
```

---

get_r2	<i>Estimate R2 or Pseudo-R2 from regression models</i>
--------	--

---

**Description**

get\_r2 is a is a wrap function that calls r2 from package performance. Calculates the R2 or pseudo-R2 value for different regression model objects, returning a character object for easy printing in tables of coefficients.

**Usage**

```
get_r2(model, ...)
```

**Arguments**

model                A statistical regression model.  
...                    Additional arguments passed to r2.

## Details

The main purpose of `get_r2` is to allow easy printing of R2 value in tables of coefficients (see examples).

## See Also

[r2](#).

## Examples

```
require(dplyr, quietly = TRUE)
require(sjlabelled, quietly = TRUE)

data(birthwt, package = "MASS")
birthwt <- birthwt |>
  mutate(
    smoke = factor(smoke, labels = c("Non-smoker", "Smoker")),
    race = factor(race, labels = c("White", "African American", "Other"))
  ) |>
  var_labels(
    bwt = "Birth weight (g)",
    smoke = "Smoking status",
    race = "Race"
  )

model_norm <- lm(bwt ~ smoke + race, data = birthwt)

model_norm |>
  glm_coef(labels = model_labels(model_norm)) |>
  as_hux() |>
  set_align(everywhere, 2:3, "right") |>
  theme_pubh() |>
  add_footnote(get_r2(model_norm), font_size = 9)
```

---

gf\_star

*Annotating a plot to display differences between groups.*

---

## Description

`gf_star` Is a function used to display differences between groups (see details).

## Usage

```
gf_star(fig, x1, y1, x2, y2, y3, legend = "*", ...)
```

**Arguments**

fig	A gformula object.
x1	Position in x for the start of the horizontal line.
y1	Position in y for the start of the vertical line, below to the horizontal line.
x2	Position in x for the end of the horizontal line.
y2	Position in y where the horizontal line is drawn.
y3	Position in y where the text is added.
legend	Character text used for annotating the plot.
...	Additional information passed to <code>gf_text</code> .

**Details**

This function draws an horizontal line from coordinate (x1, y2) to coordinate (x2, y2). Draws vertical lines below the horizontal line, towards data, from (x1, y1) to (x1, y2) and from (x2, y1) to (x2, y2). Finally, adds text above the horizontal line, at the mid point between x1 and x2. See examples.

**Examples**

```
data(kfm, package = "ISwR")
require(sjlabelled, quietly = TRUE)
kfm <- kfm |>
  var_labels(
    dl.milk = "Breast-milk intake (dl/day)",
    sex = "Sex",
    weight = "Child weight (kg)",
    ml.suppl = "Milk substitute (ml/day)",
    mat.weight = "Maternal weight (kg)",
    mat.height = "Maternal height (cm)"
  )

kfm |>
  box_plot(dl.milk ~ sex, fill = "thistle", alpha = 0.8) |>
  gf_star(x1 = 1, y1 = 10.9, x2 = 2, y2 = 11, y3 = 11.2)

kfm |>
  box_plot(dl.milk ~ sex, fill = "thistle", alpha = 0.8) |>
  gf_star(1, 10.9, 2, 11, 11.4, legend = "p = 0.035", size = 2.5)

data(energy, package = "ISwR")
energy <- energy |>
  var_labels(
    expend = "Energy expenditure (MJ/day)",
    stature = "Stature"
  )

energy |>
  strip_error(expend ~ stature, col = "red") |>
  gf_star(1, 13, 2, 13.2, 13.4, "**")
```

glm\_coef

*Table of coefficients from generalised linear models.***Description**

glm\_coef displays estimates with confidence intervals and p-values from generalised linear models (see Details).

**Usage**

```
glm_coef(
  model,
  digits = 2,
  alpha = 0.05,
  labels = NULL,
  se_rob = FALSE,
  type = "cond",
  exp_norm = FALSE
)
```

**Arguments**

model	A model from any of the classes listed in the details section.
digits	A scalar, number of digits for rounding the results (default = 2).
alpha	Significant level (default = 0.05) used to calculate confidence intervals.
labels	An optional character vector with the names of the coefficients (including intercept).
se_rob	Logical, should robust errors be used to calculate confidence intervals? (default = FALSE).
type	Character, either "cond" (condensed) or "ext" (extended). See details.
exp_norm	Logical, should estimates and confidence intervals should be exponentiated? (for family == "gaussian").

**Details**

glm\_coef recognises objects (models) from the following classes: clm, clogit, coxph, gee, glm, glmerMod, lm, lme, lmerMod, multinom, negbin, polr and survreg

For models from logistic regression (including conditional logistic, ordinal and multinomial), Poisson or survival analysis, coefficient estimates and corresponding confidence intervals are automatically exponentiated (back-transformed).

By default, glm\_coef uses naive standard errors for calculating confidence intervals but has the option of using robust standard errors instead.

glm\_coef can display two different data frames depending on the option of type, for type type = "cond" (the default), glm\_coef displays the standard table of coefficients with confidence intervals and p-values; for type = "ext", glm\_coef displays additional statistics including standard errors.

Please read the Vignette on Regression for more details.

**Value**

A data frame with estimates, confidence intervals and p-values from glm objects.

**Examples**

```
require(dplyr, quietly = TRUE)
require(sjlabelled, quietly = TRUE)

## Continuous outcome.
data(birthwt, package = "MASS")
birthwt <- birthwt |>
  mutate(
    smoke = factor(smoke, labels = c("Non-smoker", "Smoker")),
    race = factor(race, labels = c("White", "African American", "Other"))
  ) |>
  var_labels(
    bwt = "Birth weight (g)",
    smoke = "Smoking status",
    race = "Race"
  )

model_norm <- lm(bwt ~ smoke + race, data = birthwt)

glm_coef(model_norm, labels = model_labels(model_norm))

## Logistic regression.
data(diet, package = "Epi")
model_binom <- glm(chd ~ fibre, data = diet, family = binomial)
model_binom |>
  glm_coef(labels = c("Constant", "Fibre intake (g/day)"))

model_binom |>
  glm_coef(labels = c("Constant", "Fibre intake (g/day)"), type = "ext")
```

---

harm\_mean

*Harmonic mean.*

---

**Description**

Harmonic mean.

**Usage**

```
harm_mean(x)
```

**Arguments**

x                    A numeric variable with no zero values.

**Value**

A scalar, the calculated harmonic mean.

**Examples**

```
data(IgM, package = "ISwR")
Ab <- data.frame(IgM)
estat(~IgM, data = Ab)
harm_mean(IgM)
```

---

 hist\_norm

*Histogram with Normal density curve.*


---

**Description**

hist\_norm constructs histograms and adds corresponding Normal density curve.

**Usage**

```
hist_norm(
  object = NULL,
  formula = NULL,
  data = NULL,
  bins = 20,
  fill = "indianred3",
  color = "black",
  alpha = 0.4,
  ...
)
```

**Arguments**

object	When chaining, this holds an object produced in the earlier portions of the chain. Most users can safely ignore this argument. See details and examples.
formula	A formula with shape: $\sim y$ or $\sim y x$ where $y$ is a numerical variable and $x$ is a factor.
data	A data frame where the variables in the formula can be found.
bins	Number of bins of the histogram.
fill	Colour to fill the bars of the histogram.
color	Colour used for the border of the bars.
alpha	Opacity (0 = invisible, 1 = opaque).
...	Further arguments passed to <a href="#">gf_dhistogram</a> .

**Examples**

```

require(dplyr, quietly = TRUE)
require(sjlabelled, quietly = TRUE)
data(birthwt, package = "MASS")
birthwt <- birthwt |>
  mutate(
    smoke = factor(smoke, labels = c("Non-smoker", "Smoker")),
    Race = factor(race > 1, labels = c("White", "Non-white"))
  ) |>
  var_labels(
    bwt = "Birth weight (g)",
    smoke = "Smoking status"
  )

birthwt |>
  hist_norm(~bwt, alpha = 0.7, bins = 20, fill = "cadetblue")

birthwt |>
  hist_norm(~ bwt | smoke, alpha = 0.7, bins = 20, fill = "cadetblue")

```

---

Hodgkin

*T-cell counts from Hodgkin's disease patients.*


---

**Description**

Number of CD4+ T-cells and CD8+ T-cells in blood samples from patients in remission from Hodgkin's disease or in remission from disseminated malignancies.

**Usage**

Hodgkin

**Format**

A labelled tibble with 40 rows and 3 variables:

**CD4** Concentration of CD4+ T-cells (cells / mm<sup>3</sup>).

**CD8** Concentration of CD8+ T-cells (cells / mm<sup>3</sup>).

**Group** Group, factor with levels "Non-Hodgkin" and "Hodgkin".

**Source**

Shapiro, CM, et al (1986) Immunologic status of patients in remission from Hodgkin's disease and disseminated malignancies. *Am J Med Sci* 293:366-370.

Altman, DA (1991) *Practical statistics for medical research*. Chapman & Hall/CRC.

**Examples**

```

data(Hodgkin)
require(dplyr, quietly = TRUE)
require(sjlabelled, quietly = TRUE)

Hodgkin <- Hodgkin |>
  mutate(
    Ratio = CD4 / CD8
  ) |>
  var_labels(
    Ratio = "CD4+ / CD8+ T-cells"
  )

estat(~ Ratio | Group, data = Hodgkin)

Hodgkin |>
  qq_plot(~ Ratio | Group)

Hodgkin$Ratio <- Hodgkin$CD4 / Hodgkin$CD8
estat(~ Ratio | Group, data = Hodgkin)

qq_plot(~ Ratio | Group, data = Hodgkin)

```

---

 inv\_logit

*Inverse of the logit*


---

**Description**

inv\_logit Calculates the inverse of the logit (probability in logistic regression)

**Usage**

```
inv_logit(x)
```

**Arguments**

x Numerical value used to compute the inverse of the logit.

---

 jack\_knife

*Ranks leverage observations from Jackknife method.*


---

**Description**

jack\_knife Ranks the squared differences between mean values from Jackknife analysis (arithmetic mean estimated by removing one observation at a time) and the original mean value.

**Usage**

```
jack_knife(x)
```

**Arguments**

`x` A numeric variable. Missing values are removed by default.

**Value**

Data frame with the ranked squared differences.

**See Also**

[rank\\_leverage](#).

**Examples**

```
x <- rnorm(10, 170, 8)
x
mean(x)
jack_knife(x)

x <- rnorm(100, 170, 8)
mean(x)
head(jack_knife(x))
```

---

Kirkwood

*Body weight and plasma volume.*

---

**Description**

Body weight and plasma volume in eight healthy men.

**Usage**

```
Kirkwood
```

**Format**

A labelled data frame with 8 rows and 3 variables:

**subject** Subject ID.

**weight** Body weight in kg.

**volume** Plasma volume in litres.

**Source**

Kirkwood, BR and Sterne, JAC (2003) Essential Medical Statistics. Second Edition. Blackwell.

**Examples**

```
data(Kirkwood)

Kirkwood |>
  gf_point(volume ~ weight) |>
  gf_lm(col = "indianred3", interval = "confidence", fill = "indianred3")
```

---

knife_mean	<i>Jackknife for means.</i>
------------	-----------------------------

---

**Description**

knife\_mean is an internal function. Calculates arithmetic means by removing one observation at a time.

**Usage**

```
knife_mean(x)
```

**Arguments**

x                    A numerical variable. Missing values are removed for the mean calculation.

**Value**

A vector with the mean calculations.

**Examples**

```
x <- rnorm(10, 170, 8)
x
mean(x)
knife_mean(x)
```

---

leverage	<i>Leverage.</i>
----------	------------------

---

**Description**

leverage is an internal function called by [rank\\_leverage](#).

**Usage**

```
leverage(x)
```

**Arguments**

x                    A numeric variable. Missing values are removed by default.

**Details**

Estimates the leverage of each observation around the arithmetic mean.

**Value**

Variable with corresponding leverage estimations

**Examples**

```
x <- rnorm(10, 170, 8)
x
mean(x)
leverage(x)
rank_leverage(x)
```

---

logistic\_gof                    *Goodness of fit for Logistic Regression.*

---

**Description**

logistic\_gof performs the Hosmer and Lemeshow test to test the goodness of fit of a logistic regression model. This function is part of `residuals.lrm` from package `rms`.

**Usage**

```
logistic_gof(model)
```

**Arguments**

model                    A logistic regression model object.

**Author(s)**

Frank Harrell, Vanderbilt University <f.harrell@vanderbilt.edu>

**References**

Hosmer DW, Hosmer T, Lemeshow S, le Cessie S, Lemeshow S. A comparison of goodness-of-fit tests for the logistic regression model. *Stat in Med* 16:965–980, 1997.

**Examples**

```
data(diet, package = "Epi")
model <- glm(chd ~ fibre, data = diet, family = binomial)
glm_coef(model, labels = c("Constant", "Fibre intake (g/day)"))
logistic_gof(model)
```

---

Macmahon

*Breast cancer and age of childbirth.*

---

### Description

An international case-control study to test the hypothesis that breast cancer is related to the age that a woman gives childbirth.

### Usage

Macmahon

### Format

A labelled tibble with 185 rows and 2 variables:

**cancer** Diagnosed with breast cancer, a factor with levels "No" and "Yes".

**age** Age mother gives childbirth, factor with levels "<20", "20-24", "25-29", "30-34" and ">34".

### Source

Macmahon, B. et al. (1970). Age at first birth and breast cancer risk. Bull WHO 43, 209-221.

### Examples

```
require(dplyr, quietly = TRUE)
data(Macmahon)
```

```
Macmahon |>
  select(cancer, age) |>
  cross_tbl(by = "cancer")
```

---

mhor

*Mantel-Haenszel odds ratio.*

---

### Description

mhor computes odds ratios by levels of the stratum variable as well as the Mantel-Haenszel pooled odds ratio. The test for effect modification (test for interaction) is also displayed.

### Usage

```
mhor(object = NULL, formula = NULL, data = NULL)
```

**Arguments**

object	When chaining, this holds an object produced in the earlier portions of the chain. Most users can safely ignore this argument. See details and examples.
formula	A formula with shape: outcome ~ stratum/exposure.
data	A data frame containing the variables used in formula.

**Value**

Odds ratios with 95 outcome by levels of stratum. The Mantel-Haenszel pooled OR and the test for effect modification is also reported.

**Examples**

```
data(oswego, package = "epitools")
require(dplyr, quietly = TRUE)
require(sjlabelled, quietly = TRUE)
oswego <- oswego |>
  mutate(
    ill = factor(ill, labels = c("No", "Yes")),
    sex = factor(sex, labels = c("Female", "Male")),
    chocolate.ice.cream = factor(chocolate.ice.cream, labels = c("No", "Yes"))
  ) |>
  var_labels(
    ill = "Developed illness",
    sex = "Sex",
    chocolate.ice.cream = "Consumed chocolate ice cream"
  )

oswego |>
  select(ill, sex, chocolate.ice.cream) |>
  tbl_summary() |>
  cosm_sum() |>
  theme_pubh()

oswego |>
  mhor(ill ~ sex / chocolate.ice.cream)
```

---

 model\_labels

*Using labels as coefficient names in tables of coefficients.*


---

**Description**

model\_labels replaces row names in glm\_coef with labels from the original data frame.

**Usage**

```
model_labels(model, intercept = TRUE)
```

**Arguments**

`model`            A generalised linear model.  
`intercept`        Logical, should the intercept be added to the list of coefficients?

**Details**

`model_labels` does not handle yet interaction terms, see examples.

Please read the Vignette on Regression for more examples.

**Examples**

```
require(dplyr, quietly = TRUE)
require(sjlabelled, quietly = TRUE)

data(birthwt, package = "MASS")
birthwt <- birthwt |>
  mutate(
    smoke = factor(smoke, labels = c("Non-smoker", "Smoker")),
    race = factor(race, labels = c("White", "African American", "Other"))
  ) |>
  var_labels(
    bwt = "Birth weight (g)",
    smoke = "Smoking status",
    race = "Race"
  )

model_norm <- lm(bwt ~ smoke + race, data = birthwt)

glm_coef(model_norm, labels = model_labels(model_norm))

model_int <- lm(formula = bwt ~ smoke * race, data = birthwt)

model_int |>
  glm_coef(labels = c(
    model_labels(model_int),
    "Smoker: African American",
    "Smoker: Other"
  ))
```

---

multiple

---

*Multiple comparisons with plot.*


---

**Description**

`multiple` displays results from post-doc analysis and constructs corresponding plot.

**Usage**

```
multiple(
  model,
  formula,
  adjust = "mvt",
  type = "response",
  reverse = TRUE,
  level = 0.95,
  digits = 2,
  ...
)
```

**Arguments**

model	A fitted model supported by <code>emmeans</code> , such as the result of a call to <code>aov</code> , <code>lm</code> , <code>glm</code> , etc.
formula	A formula with shape: <code>~ y</code> or <code>~ y   x</code> (for interactions). Where <code>y</code> is the term of the model on which comparisons are made and <code>x</code> is a term interacting with <code>y</code> .
adjust	Method to adjust CIs and p-values (see details).
type	Type of prediction (matching "linear.predictor", "link", or "response").
reverse	Logical argument. Determines the direction of comparisons.
level	Confidence interval significance level.
digits	Number of digits for rounding (default = 2).
...	Further arguments passed to <code>emmeans</code> .

**Details**

The default adjusting method is "mvt" which uses the multivariate t distribution. Other options are: "bonferroni", "holm", "hochberg", "tukey" and "none". The default option for argument `reverse` is to make reverse comparisons, i.e., against the reference level matching comparisons from `lm` and `glm`.

**Value**

A list with objects: `df` A data frame with adjusted p-values, `fig_ci` a plot with estimates and adjusted confidence intervals and `fig_pval` a plot comparing adjusted p-values.

**See Also**

[emmeans](#), [pwpp](#).

**Examples**

```
data(birthwt, package = "MASS")
birthwt$race <- factor(birthwt$race, labels = c("White", "African American", "Other"))

model_1 <- aov(bwt ~ race, data = birthwt)
```

```
multiple(model_1, ~race)$df

multiple(model_1, ~race)$fig_ci |>
  gf_labs(y = "Race", x = "Difference in birth weights (g)")

multiple(model_1, ~race)$fig_pval |>
  gf_labs(y = "Race")
```

---

odds\_trend

*Function to calculate OR using Wald CI, and plot trend.*

---

## Description

odds\_trend calculates the odds ratio with confidence intervals (Wald) for different levels (three or more) of the exposure variable, constructs the corresponding plot and calculates if the trend is significant or not.

## Usage

```
odds_trend(formula, data, angle = 45, hjust = 1, method = "wald", ...)
```

## Arguments

formula	A formula with shape: outcome ~ exposure.
data	A data frame where the variables in the formula can be found.
angle	Angle of for the x labels (default = 45).
hjust	Horizontal adjustment for x labels (default = 1).
method	Method for calculating confidence interval around odds ratio.
...	Passes optional arguments to oddsratio.

## Details

odds\_trend is a wrap function that calls oddsratio from package epitools.

Additional methods for confidence intervals include: "midp", "fisher", and "small".

## Value

A list with components df a data frame with the results and fig corresponding plot.

## See Also

[oddsratio](#).

**Examples**

```
## A cross-sectional study looked at the association between obesity and a biopsy resulting
## from mammography screening.

Freq <- c(3441, 34, 39137, 519, 20509, 280, 12149, 196, 11882, 199)
Biopsy <- gl(2, 1, 10, labels = c("No", "Yes"))
Weight <- gl(5, 2, 10, labels = c(
  "Underweight", "Normal", "Over (11-24%)",
  "Over (25-39%)", "Over (> 39%)"
))
breast <- data.frame(Freq, Biopsy, Weight)
breast

breast <- expand_df(breast)
require(sjlabelled, quietly = TRUE)

breast <- var_labels(breast,
  Weight = "Weight group"
)

odds_trend(Biopsy ~ Weight, data = breast)$df
odds_trend(Biopsy ~ Weight, data = breast)$fig
```

---

Oncho

*Onchocerciasis in Sierra Leone.*


---

**Description**

Study of onchocerciasis ("river blindness") in Sierra Leone, in which subjects were classified according to whether they lived in villages in savannah or rainforest area.

**Usage**

Oncho

**Format**

A labelled tibble with 1302 rows and 7 variables:

**id** Subject ID.

**mf** Infected with *Onchocerciasis volvulus*, factor with levels "Not-infected" and "Infected".

**area** Area of residence, factor with levels "Savannah" and "Rainforest".

**agegrp** Age group in years, factor with levels "5-9", "10-19", "20-39" and "40+".

**sex** Subject sex, factor with levels "Male" and "Female".

**mfload** Microfilariae load.

**lesions** Severe eye lesions, factor with levels "No" and "Yes".

**Source**

McMahon, JE, Sowa, SIC, Maude, GH and Kirkwood BR (1988) Onchocerciasis in Sierra Leone 2: a comparison of forest and savannah villages. *Trans Roy Soc Trop Med Hyg* 82: 595-600.  
 Kirkwood, BR and Sterne, JAC (2003) *Essential Medical Statistics*. Second Edition. Blackwell.

**Examples**

```
require(dplyr, quietly = TRUE)
data(Oncho)

Oncho |>
  select(mf, agegrp) |>
  cross_tbl(by = "mf")
```

---

predict\_inv

*Given y solve for x in a simple linear model.*

---

**Description**

predict\_inv Calculates the value the predictor x that generates value y with a simple linear model.

**Usage**

```
predict_inv(model, y)
```

**Arguments**

model	A simple linear model object (class lm).
y	A numerical scalar, the value of the outcome for which we want to calculate the predictor x.

**Value**

The estimated value of the predictor.

**Examples**

```
## Spectrophotometry example. Titration curve for riboflavin (nmol/ml). The sample has an absorbance
## of 1.15. Aim is to estimate the concentration of riboflavin in the sample.

Riboflavin <- seq(0, 80, 10)
OD <- 0.0125 * Riboflavin + rnorm(9, 0.6, 0.03)
titration <- data.frame(Riboflavin, OD)

require(sjlabelled, quietly = TRUE)
titration <- titration |>
  var_labels(
    Riboflavin = "Riboflavin (nmol/ml)",
```

```

    OD = "Optical density"
  )

titration |>
  gf_point(OD ~ Riboflavin) |>
  gf_smooth(col = "indianred3", se = TRUE, lwd = 0.5, method = "loess")

## Model with intercept different from zero:
model <- lm(OD ~ Riboflavin, data = titration)
glm_coef(model)

predict_inv(model, 1.15)

```

---

prop\_or

*Proportion, p1 from proportion p2 and OR.*


---

### Description

prop\_or is a simple function to calculate a proportion, from another proportion and the odds ratio between them.

### Usage

```
prop_or(p2, or)
```

### Arguments

p2                   The value of a proportion in the unexposed group (p2).  
or                     The odds ratio of p1/p2.

### Value

p1, the proportion in the exposed group (p1).

### Examples

```

flu <- matrix(c(20, 80, 220, 140), nrow = 2)
colnames(flu) <- c("Yes", "No")
rownames(flu) <- c("Vaccine", "Placebo")
flu

or <- (20 * 140) / (80 * 220)
p2 <- 80 / 220
prop_or(p2 = p2, or = or)
20 / 240

```

---

pseudo_r2	<i>Pseudo R2 (logistic regression) pseudo_r2 Calculates R2 analogues (pseudo R2) of logistic regression.</i>
-----------	--

---

**Description**

Pseudo R2 (logistic regression) pseudo\_r2 Calculates R2 analogues (pseudo R2) of logistic regression.

**Usage**

```
pseudo_r2(model)
```

**Arguments**

model            A logistic regression model.

**Details**

pseudo\_r2 calculates three pseudo R2 of logistic regression models: 1) Nagelkerke, 2) Cox and Snell, 3) Hosmer and Lemeshow.

**Value**

A data frame with the calculated pseudo R2 values.

**Examples**

```
data(Oncho)
model_oncho <- glm(mf ~ area, data = Oncho, binomial)
glm_coef(model_oncho, labels = c("Constant", "Area (rainforest/savannah)"))
pseudo_r2(model_oncho)
```

---

qq_plot	<i>Quantile-quantile plots against the standard Normal distribution.</i>
---------	--

---

**Description**

qq\_plot constructs quantile-quantile plots against the standard normal distribution (also known as quantile-normal plots).

**Usage**

```
qq_plot(
  object = NULL,
  formula = NULL,
  data = NULL,
  pch = 20,
  col = "indianred3",
  ylab = NULL,
  ...
)
```

**Arguments**

<code>object</code>	When chaining, this holds an object produced in the earlier portions of the chain. Most users can safely ignore this argument. See details and examples.
<code>formula</code>	A formula with shape: $\sim x$ or $\sim x z$ where $x$ is a numerical variable and $z$ is a factor.
<code>data</code>	A data frame where the variables in the formula can be found.
<code>pch</code>	Point character passed to <a href="#">gf_qq</a> .
<code>col</code>	Colour of the reference line, passed to <a href="#">gf_line</a> .
<code>ylab</code>	Optional character passed as label for the y-axis.
<code>...</code>	Further arguments passed to <a href="#">gf_qq</a> .

**Examples**

```
data(kfm, package = "ISwR")
require(sjlabelled, quietly = TRUE)
kfm <- kfm |>
  var_labels(
    dl.milk = "Breast-milk intake (dl/day)",
    sex = "Sex",
    weight = "Child weight (kg)",
    ml.suppl = "Milk substitute (ml/day)",
    mat.weight = "Maternal weight (kg)",
    mat.height = "Maternal height (cm)"
  )

kfm |>
  qq_plot(~dl.milk)

qq_plot(~ dl.milk | sex, data = kfm)
```

---

rank_influence	<i>Ranks observations based upon influence measures on models.</i>
----------------	--

---

**Description**

rank\_influence calculates influence measures of each data observation on models and then ranks them.

**Usage**

```
rank_influence(model)
```

**Arguments**

model            A generalised linear model object.

**Details**

rank\_influence is a wrap function that calls [influence.measures](#), ranks observations on their significance influence on the model and displays the 10 most influential observations (if they are significant).

**See Also**

[influence.measures](#).

**Examples**

```
data(diet, package = "Epi")
model <- glm(chd ~ fibre, data = diet, family = binomial)
rank_influence(model)
```

---

rank_leverage	<i>Ranks observations by leverage.</i>
---------------	--

---

**Description**

rank\_leverage ranks observations by their leverage (influence) on the arithmetic mean.

**Usage**

```
rank_leverage(x)
```

**Arguments**

x                A numeric variable. Missing values are removed by default.

**Value**

A data frame ranking observations by their leverage around the mean.

**See Also**

[jack\\_knife](#).

**Examples**

```
x <- rnorm(10, 170, 8)
x
mean(x)
rank_leverage(x)
```

```
x <- rnorm(100, 170, 8)
mean(x)
head(rank_leverage(x))
```

---

reference_range	<i>Reference range (reference interval).</i>
-----------------	--

---

**Description**

reference\_range estimates the reference range (reference interval) of a numerical variable.

**Usage**

```
reference_range(avg, std)
```

**Arguments**

avg	The arithmetic mean (a scalar numerical value).
std	The standard deviation (a scalar numerical value).

**Details**

The reference range assumes normality and represents the limits that would include 95 observations.

**Value**

A data frame with the reference range limits.

**Examples**

```
x <- rnorm(100, 170, 8)
round(mean(x), 2)
round(sd(x), 2)

round(reference_range(mean(x), sd(x)), 2)
```

---

rel_dis	<i>Relative Dispersion.</i>
---------	-----------------------------

---

**Description**

Calculates the coefficient of variation (relative dispersion) of a variable. The relative dispersion is defined as the standard deviation over the arithmetic mean.

**Usage**

```
rel_dis(x)
```

**Arguments**

x                    A numerical variable. NA's observations are removed by default.

**Value**

The coefficient of variation (relative dispersion).

**Examples**

```
height <- rnorm(100, 170, 8)
rel_dis(height)
```

---

Roberts	<i>Extracorporeal membrane oxygenation in neonates.</i>
---------	---

---

**Description**

A clinical trial on the value of extracorporeal membrane oxygenation for term neonates with severe respiratory failure. RCT compares active treatment against conventional management.

**Usage**

```
Roberts
```

**Format**

A labelled tibble with 185 rows and 2 variables:

**emo** Extracorporeal membrane oxygenation treatment, factor with levels "No" and "Yes".

**survived** One year survival, factor with levels "No" and "Yes".

**Source**

Roberts, TE (1998) Extracorporeal Membrane Oxygenation Economics Working Group. Economic evaluation and randomised controlled trial of extracorporeal membrane oxygenation: UK collaborative trial. *Brit Med J* 317:911-16.

**Examples**

```
require(dplyr, quietly = TRUE)
data(Roberts)
```

```
Roberts |>
  select(survived, emo) |>
  cross_ttbl(by = "survived")
```

---

 Rothman

---

*Oral contraceptives and stroke.*


---

**Description**

A case-control study of oral contraceptives and stroke in young women with presence or absence of hypertension. Cases represent thrombotic stroke and controls are hospital controls. The group of no hypertension includes normal blood pressure (<140/90 mm Hg) and borderline hypertension (140-159/90-94 mm Hg). Hypertension group includes moderate hypertension (160-179/95-109 mm Hg) and severe hypertension (180+/110+ mm Hg). This data has been used as an example of joint exposure by Rothman for measuring interactions (see examples).

**Usage**

Rothman

**Format**

A labelled tibble with 477 rows and 3 variables:

**stroke** Thrombotic stroke, factor with levels "No" and "Yes".

**oc** Current user of oral contraceptives, factor with levels "Non-user" and "User".

**ht** Hypertension, factor with levels "No" (<160/95 mm Hg) and "Yes".

**Source**

Collaborative Group for the Study of Stroke in Young Women (1975) Oral contraceptives and stroke in young women. *JAMA* 231:718-722.

Rothman, KJ (2002) *Epidemiology. An Introduction*. Oxford University Press.

**Examples**

```

require(dplyr, quietly = TRUE)
data(Rothman)

Rothman |>
  select(stroke, oc, ht) |>
  tbl_summary() |>
  cosm_sum()

mhor(stroke ~ ht / oc, data = Rothman)

## Model with standard interaction term:
model1 <- glm(stroke ~ ht * oc, data = Rothman, family = binomial)
glm_coef(model1)

## Model considering join exposure:
Rothman$join <- 0
Rothman$join[Rothman$oc == "Non-user" & Rothman$ht == "Yes"] <- 1
Rothman$join[Rothman$oc == "User" & Rothman$ht == "No"] <- 2
Rothman$join[Rothman$oc == "User" & Rothman$ht == "Yes"] <- 3
Rothman$join <- factor(Rothman$join, labels = c(
  "Unexposed", "Hypertension", "OC user",
  "OC and hypertension"
))

require(sjlabelled, quietly = TRUE)
Rothman$join <- set_label(Rothman$join, label = "Exposure")

Rothman |>
  select(stroke, join) |>
  cross_tbl(by = "stroke")

model2 <- glm(stroke ~ join, data = Rothman, family = binomial)
glm_coef(model2)

```

---

round\_pval

*Rounding p-values.*


---

**Description**

round\_pval is an internal function called by glm\_coef to round p-values from model coefficients.

**Usage**

```
round_pval(pval)
```

**Arguments**

pval                    vector of p-values, numeric.

---

Sandler

*Passive smoking in adulthood and cancer risk.*

---

### Description

A case-control study to investigate the effects of passive smoking on cancer. Passive smoking was defined as exposure to the cigarette smoke of a spouse who smoked at least one cigarette per day for at least 6 months.

### Usage

Sandler

### Format

A labelled tibble with 998 rows and 3 variables:

**passive** Passive smoker, factor with levels "No" and "Yes".

**cancer** Diagnosed with cancer, factor with levels "No" and "Yes".

**smoke** Active smoker, factor with levels "No" and "Yes".

### Source

Sandler, DP, Everson, RB, Wilcox, AJ (1985). Passive smoking in adulthood and cancer risk. *Amer J Epidem*, 121: 37-48.

### Examples

```
require(dplyr, quietly = TRUE)
data(Sandler)

Sandler |>
  select(cancer, passive) |>
  cross_tbl(by = "cancer")

mhor(cancer ~ smoke / passive, data = Sandler)
```

---

Sharples

*Measured and self-reported weight in New Zealand.*

---

### Description

Data on measured and self-reported weight from 40–50 year old participants in the 1989/1990 Life In New Zealand Survey.

**Usage**

Sharples

**Format**

A tibble with 343 rows and 4 variables:

**srweight** Self-reported weight in kg.

**weight** Measured weight in kg.

**srbmi** Body mass index calculated from self-reported weight and self-reported height in kg/m<sup>2</sup>.

**mbmi** Body mass index calculated from measured weight and measured height in kg/m<sup>2</sup>.

**Source**

Sharples, H, et al. (2012) Agreement between measured and self-reported height, weight and BMI in predominantly European middle-aged New Zealanders: findings from a nationwide 1989 survey. *New Zealand Med J* 125: 60-69.

**Examples**

```
Sharples |>
  bland_altman(srweight ~ weight, transform = TRUE) |>
  gf_labs(x = "Mean of weights (kg)", y = "Measured weight / Self-reported weight")
```

---

 ss\_jk

*Sum of squares for Jackknife.*

---

**Description**

ss\_jk is an internal function called by [jack\\_knife](#). It calculates the squared difference of a numerical variable around a given value (for example, the mean).

**Usage**

```
ss_jk(obs, stat)
```

**Arguments**

obs                    A numerical vector with no missing values (NA's).

stat                   The value of the statistic that is used as a reference.

**Value**

The squared difference between a variable and a given value.

**Examples**

```
x <- rnorm(10, 170, 8)
x
mean(x)
ss_jk(x, mean(x))
jack_knife(x)
```

---

stats_quotes	<i>Internal function to calculate descriptive statistics.</i>
--------------	---

---

**Description**

stats\_quotes is an internal function called by estat.

**Usage**

```
stats_quotes(x, data2, digits = 2)
```

**Arguments**

x	a numeric variable
data2	A data frame where x can be found.
digits	Number of digits for rounding.

---

strip_error	<i>Strip plots with error bars.</i>
-------------	-------------------------------------

---

**Description**

strip\_error constructs strip plots with error bars showing 95 confidence intervals around mean values.

**Usage**

```
strip_error(
  object = NULL,
  formula = NULL,
  data = NULL,
  pch = 20,
  size = 1,
  alpha = 0.7,
  col = "indianred3",
  ...
)
```

**Arguments**

object	When chaining, this holds an object produced in the earlier portions of the chain. Most users can safely ignore this argument. See details and examples.
formula	A formula with shape: $y \sim x$ or $y \sim x z$ where $y$ is a numerical variable and both $x$ and $z$ are factors.
data	A data frame where the variables in the formula can be found.
pch	Point character passed to <a href="#">gf_point</a> or <a href="#">gf_jitter</a> .
size	Size of the symbol (pch) for representing data values.
alpha	Opacity of the symbol (0 = invisible, 1 = opaque).
col	A colour or formula used for mapping colour.
...	Additional information passed to <a href="#">gf_jitter</a> or <a href="#">gf_point</a> .

**Examples**

```

data(energy, package = "ISwR")
require(sjlabelled, quietly = TRUE)
energy <- energy |>
  var_labels(
    expend = "Energy expenditure (MJ/day)",
    stature = "Stature"
  )

energy |>
  strip_error(expend ~ stature, col = "red")

t.test(expend ~ stature, data = energy)

## Adding an horizontal line to show significant difference:
energy |>
  strip_error(expend ~ stature, col = "red") |>
  gf_star(1, 13, 2, 13.2, 13.4, "**")

data(birthwt, package = "MASS")
require(dplyr, quietly = TRUE)
birthwt <- birthwt |>
  mutate(
    smoke = factor(smoke, labels = c("Non-smoker", "Smoker")),
    Race = factor(race > 1, labels = c("White", "Non-white"))
  ) |>
  var_labels(
    bwt = "Birth weight (g)",
    smoke = "Smoking status"
  )

birthwt |>
  strip_error(bwt ~ smoke | Race, col = "darksalmon")

birthwt |>
  strip_error(bwt ~ smoke, col = ~Race)

```

```

birthwt |>
  strip_error(bwt ~ smoke, pch = ~Race, col = ~Race)

birthwt |>
  strip_error(bwt ~ smoke | Race)

```

---

Thall	<i>RCT on the treatment of epilepsy.</i>
-------	--

---

### Description

Randomised control trial of an antiepileptic drug (prograbide), in which the number of seizures of 59 patients at baseline and other four follow-up visits were recorded.

### Usage

Thall

### Format

A tibble with 59 rows and 8 variables:

**id** Subject ID.

**treat** Treatment, factor with levels "Control" and "Prograbide".

**base** Number of seizures at baseline.

**age** Age in years at baseline.

**y1** Number of seizures at year one follow-up.

**y2** Number of seizures at year two follow-up.

**y3** Number of seizures at year three follow-up.

**y4** Number of seizures at year four follow-up.

### Source

Thall, PF and Vail, SC (1990) Some covariance models for longitudinal count data with over-dispersion. *Biometrics*, 46: 657-671.

Stukel, TA (1993) Comparison of methods for the analysis of longitudinal data. *Statistics Med* 12: 1339-1351.

Shoukri, MM and Chaudhary, MA (2007) *Analysis of correlated data with SAS and R*. Third Edition. Chapman & Hall/CRC.

**Examples**

```

data(Thall)

c1 <- cbind(Thall[, c(1:5)], count = Thall$y1)[, c(1:4, 6)]
c2 <- cbind(Thall[, c(1:4, 6)], count = Thall$y2)[, c(1:4, 6)]
c3 <- cbind(Thall[, c(1:4, 7)], count = Thall$y3)[, c(1:4, 6)]
c4 <- cbind(Thall[, c(1:4, 8)], count = Thall$y3)[, c(1:4, 6)]
epilepsy <- rbind(c1, c2, c3, c4)

require(lme4, quietly = TRUE)
model_glmmer <- glmer(count ~ treat + base + I(age - mean(age, na.rm = TRUE)) +
  (1 | id), data = epilepsy, family = poisson)
glm_coef(model_glmmer, labels = c(
  "Treatment (Prograbide/Control)",
  "Baseline count", "Age (years)"
))

```

---

theme_pubh	<i>A theme for huxtables This function quickly set a default style for a huxtable.</i>
------------	--

---

**Description**

A theme for huxtables This function quickly set a default style for a huxtable.

**Usage**

```
theme_pubh(ht, rw = 1)
```

**Arguments**

ht	A huxtable object.
rw	A numeric vector with the rows on which a bottom border is desired.

**Details**

theme\_pubh is a variation of theme\_article with the added flexibility of adding a bottom border line at desired row numbers.

**Examples**

```

require(dplyr, quietly = TRUE)
data(Oncho)

Oncho |>
  select(area, mf) |>
  cross_tbl(by = "area") |>
  theme_pubh(2)

```

```
data(Bernard)

t1 <- estat(~ apache | fate, data = Bernard)
t2 <- estat(~ o2del | fate, data = Bernard)
rbind(t1, t2) |>
  as_hux() |>
  theme_pubh(c(1, 3))
```

---

Tuzson

*Peak knee velocity in walking at flexion and extension.*

---

### Description

Data of peak knee velocity in walking at flexion and extension in studies about functional performance in cerebral palsy.

### Usage

Tuzson

### Format

A labelled tibble with 18 rows and 2 variables:

**flexion** Peak knee velocity in gait: flexion (degree/s).

**extension** Peak knee velocity in gait: extension (degree/s).

### Source

Tuzson, AE, Granata, KP, and Abel, MF (2003) Spastic velocity threshold constrains functional performance in cerebral palsy. Arch Phys Med Rehabil 84: 1363-1368.

### Examples

```
data(Tuzson)

Tuzson |>
  gf_point(flexion ~ extension)

cor.test(~ flexion + extension, data = Tuzson)
```

---

Vanderpump

*Smoking and mortality in Whickham, England.*

---

### Description

Data represents women participating in a health survey in Whickham, England in 1972-1974.

### Usage

Vanderpump

### Format

A labelled tibble with 1314 rows and 3 variables:

**vstatus** Vitality status, factor with levels "Alive" and "Death".

**smoker** Smoking status, factor with levels "Non-smoker" and "Smoker".

**agegrp** Age group, factor with levels "18-44", "45-64" and "64+".

### Source

Vanderpump, MP, et al (1996) *Thyroid*, 6:155-160.

Appleton, DR, French, JM and Vanderpump, PJ (1996) Ignoring a covariate: An example of Simpson's paradox. *The American Statistician* 50:340-341.

Vittinghoff, E, Glidden, DV, Shiboski, SC and McCulloh, CE (2005) *Regression methods in Biostatistics*. Springer.

### Examples

```
require(dplyr, quietly = TRUE)
data(Vanderpump)

Vanderpump |>
  select(vstatus, agegrp, smoker) |>
  tbl_strata(
    strata = smoker,
    .tbl_fun = ~ .x |>
      tbl_summary(by = agegrp)
  ) |>
  cosm_sum(bold = TRUE, head_label = " ")

mhor(vstatus ~ agegrp / smoker, data = Vanderpump)
```

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