

# Package ‘sjmisc’

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**Description** Collection of miscellaneous utility functions, supporting data transformation tasks like recoding, dichotomizing or grouping variables, setting and replacing missing values. The data transformation functions also support labelled data, and all integrate seamlessly into a 'tidyverse'-workflow.

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sjmisc-package	<i>Data and Variable Transformation Functions</i>
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## Description

### Purpose of this package

Collection of miscellaneous utility functions, supporting data transformation tasks like recoding, dichotomizing or grouping variables, setting and replacing missing values. The data transformation functions also support labelled data, and all integrate seamlessly into a 'tidyverse'-workflow.

### Design philosophy - consistent api

The design of this package follows, where appropriate, the *tidyverse-approach*, with the first argument of a function always being the data (either a data frame or vector), followed by variable names that should be processed by the function. If no variables are specified as argument, the function applies to the complete data that was indicated as first function argument.

There are two types of function designs:

***transformation/recoding functions*** Functions like `rec()` or `dicho()`, which transform or recode variables, typically return the complete data frame that was given as first argument, *additionally including* the transformed and recoded variables specified in the `...-ellipses` argument. The variables usually get a suffix, so original variables are preserved in the data.

***coercing/converting functions*** Functions like `to_factor()` or `to_label()`, which convert variables into other types or add additional information like variable or value labels as attribute, also typically return the complete data frame that was given as first argument. However, the variables specified in the `...-ellipses` argument are converted ("overwritten"), all other variables remain unchanged. Hence, these functions do not return any new, additional variables.

### Author(s)

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---

 add\_columns

*Add or replace data frame columns*


---

### Description

add\_columns() combines two or more data frames, but unlike `cbind` or `dplyr::bind_cols()`, this function binds data as last columns of a data frame (i.e., behind columns specified in `...`). This can be useful in a "pipe"-workflow, where a data frame returned by a previous function should be appended *at the end* of another data frame that is processed in `add_columns()`.

replace\_columns() replaces all columns in data with identically named columns in `...`, and adds remaining (non-duplicated) columns from `...` to data.

add\_id() simply adds an ID-column to the data frame, with values from 1 to `nrow(data)`, respectively for grouped data frames, values from 1 to group size. See 'Examples'.

### Usage

```
add_columns(data, ..., replace = TRUE)
```

```
replace_columns(data, ..., add.unique = TRUE)
```

```
add_id(data, var = "ID")
```

### Arguments

data	A data frame. For <code>add_columns()</code> , will be bound after data frames specified in <code>...</code> . For <code>replace_columns()</code> , duplicated columns in data will be replaced by columns in <code>...</code> .
...	More data frames to combine, resp. more data frames with columns that should replace columns in data.
replace	Logical, if TRUE (default), columns in <code>...</code> with identical names in data will replace the columns in data. The order of columns after replacing is preserved.
add.unique	Logical, if TRUE (default), remaining columns in <code>...</code> that did not replace any column in data, are appended as new columns to data.
var	Name of new the ID-variable.

### Value

For `add_columns()`, a data frame, where columns of data are appended after columns of `...`

For `replace_columns()`, a data frame where columns in data will be replaced by identically named columns in `...`, and remaining columns from `...` will be appended to data (if `add.unique = TRUE`).

For `add_id()`, a new column with ID numbers. This column is always the first column in the returned data frame.

**Note**

For `add_columns()`, by default, columns in data with identical names like columns in one of the data frames in `...` will be dropped (i.e. variables with identical names in `...` will replace existing variables in data). Use `replace = FALSE` to keep all columns. Identical column names will then be renamed, to ensure unique column names (which happens by default when using `dplyr::bind_cols()`). When replacing columns, replaced columns are not added to the end of the data frame. Rather, the original order of columns will be preserved.

**Examples**

```
data(efc)
d1 <- efc[, 1:3]
d2 <- efc[, 4:6]

library(dplyr)
head(bind_cols(d1, d2))
add_columns(d1, d2) %>% head()

d1 <- efc[, 1:3]
d2 <- efc[, 2:6]

add_columns(d1, d2, replace = TRUE) %>% head()
add_columns(d1, d2, replace = FALSE) %>% head()

# use case: we take the original data frame, select specific
# variables and do some transformations or recodings
# (standardization in this example) and add the new, transformed
# variables *to the end* of the original data frame
efc %>%
  select(e17age, c160age) %>%
  std() %>%
  add_columns(efc) %>%
  head()

# new variables with same name will overwrite old variables
# in "efc". order of columns is not changed.
efc %>%
  select(e16sex, e42dep) %>%
  to_factor() %>%
  add_columns(efc) %>%
  head()

# keep both old and new variables, automatically
# rename variables with identical name
efc %>%
  select(e16sex, e42dep) %>%
  to_factor() %>%
  add_columns(efc, replace = FALSE) %>%
  head()

# create sample data frames
d1 <- efc[, 1:10]
```

```

d2 <- efc[, 2:3]
d3 <- efc[, 7:8]
d4 <- efc[, 10:12]

# show original
head(d1)

library(sjlabelled)
# slightly change variables, to see effect
d2 <- as_label(d2)
d3 <- as_label(d3)

# replace duplicated columns, append remaining
replace_columns(d1, d2, d3, d4) %>% head()

# replace duplicated columns, omit remaining
replace_columns(d1, d2, d3, d4, add.unique = FALSE) %>% head()

# add ID to dataset
library(dplyr)
data(mtcars)
add_id(mtcars)

mtcars %>%
  group_by(gear) %>%
  add_id() %>%
  arrange(gear, ID) %>%
  print(n = 100)

```

---

add\_rows

---

*Merge labelled data frames*


---

### Description

Merges (full join) data frames and preserve value and variable labels.

### Usage

```
add_rows(..., id = NULL)
```

```
merge_df(..., id = NULL)
```

### Arguments

...	Two or more data frames to be merged.
id	Optional name for ID column that will be created to indicate the source data frames for appended rows.

## Details

This function works like `dplyr::bind_rows()`, but preserves variable and value label attributes. `add_rows()` row-binds all data frames in `...`, even if these have different numbers of columns. Non-matching columns will be column-bound and filled with NA-values for rows in those data frames that do not have this column.

Value and variable labels are preserved. If matching columns have different value label attributes, attributes from first data frame will be used.

`merge_df()` is an alias for `add_rows()`.

## Value

A full joined data frame.

## Examples

```
library(dplyr)
data(efc)
x1 <- efc %>% select(1:5) %>% slice(1:10)
x2 <- efc %>% select(3:7) %>% slice(11:20)

mydf <- add_rows(x1, x2)
mydf
str(mydf)

## Not run:
library(sjPlot)
view_df(mydf)
## End(Not run)

x3 <- efc %>% select(5:9) %>% slice(21:30)
x4 <- efc %>% select(11:14) %>% slice(31:40)

mydf <- add_rows(x1, x2, x3, x4, id = "subsets")
mydf
str(mydf)
```

## Description

`add_variables()` adds a new column to a data frame, while `add_case()` adds a new row to a data frame. These are convenient functions to add columns or rows not only at the end of a data frame, but at any column or row position. Furthermore, they allow easy integration into a pipe-workflow.

**Usage**

```
add_variables(data, ..., .after = Inf, .before = NULL)
```

```
add_case(data, ..., .after = Inf, .before = NULL)
```

**Arguments**

<code>data</code>	A data frame.
<code>...</code>	One or more named vectors that indicate the variables or values, which will be added as new column or row to data. For <code>add_case()</code> , non-matching columns in data will be filled with NA.
<code>.after</code> , <code>.before</code>	Numerical index of row or column, where after or before the new variable or case should be added. If <code>.after = -1</code> , variables or cases are added at the beginning; if <code>.after = Inf</code> , variables and cases are added at the end. In case of <code>add_variables()</code> , <code>.after</code> and <code>.before</code> may also be a character name indicating the column in data, after or in front of what <code>...</code> should be inserted.

**Value**

data, including the new variables or cases from `...`

**Note**

For `add_case()`, if variable does not exist, a new variable is created and existing cases for this new variable get the value NA. See 'Examples'.

**Examples**

```
d <- data.frame(
  a = c(1, 2, 3),
  b = c("a", "b", "c"),
  c = c(10, 20, 30),
  stringsAsFactors = FALSE
)

add_case(d, b = "d")
add_case(d, b = "d", a = 5, .before = 1)

# adding a new case for a new variable
add_case(d, e = "new case")

add_variables(d, new = 5)
add_variables(d, new = c(4, 4, 4), new2 = c(5, 5, 5), .after = "b")
```



---

all_na	<i>Check if vector only has NA values</i>
--------	---

---

**Description**

Check if all values in a vector are NA.

**Usage**

```
all_na(x)
```

**Arguments**

x                    A vector or data frame.

**Value**

Logical, TRUE if x has only NA values, FALSE if x has at least one non-missing value.

**Examples**

```
x <- c(NA, NA, NA)
y <- c(1, NA, NA)

all_na(x)
all_na(y)
all_na(data.frame(x, y))
all_na(list(x, y))
```

---

big_mark	<i>Format numbers</i>
----------	-----------------------

---

**Description**

big\_mark() formats large numbers with big marks, while prcn() converts a numeric scalar between 0 and 1 into a character vector, representing the percentage-value.

**Usage**

```
big_mark(x, big.mark = ",", ...)
```

```
prcn(x)
```

**Arguments**

x	A vector or data frame. All numeric inputs (including numeric character) vectors) will be prettified. For prcn(), a number between 0 and 1, or a vector or data frame with such numbers.
big.mark	Character, used as mark between every 3 decimals before the decimal point.
...	Other arguments passed down to the <code>prettyNum</code> -function.

**Value**

For `big_mark()`, a prettified x as character, with big marks. For `prcn`, a character vector with a percentage number.

**Examples**

```
# simple big mark
big_mark(1234567)

# big marks for several values at once, mixed numeric and character
big_mark(c(1234567, "55443322"))

# pre-defined width of character output
big_mark(c(1234567, 55443322), width = 15)

# convert numbers into percentage, as character
prcn(0.2389)
prcn(c(0.2143887, 0.55443, 0.12345))

dat <- data.frame(
  a = c(.321, .121, .64543),
  b = c("a", "b", "c"),
  c = c(.435, .54352, .234432)
)
prcn(dat)
```

---

count\_na

*Frequency table of tagged NA values*


---

**Description**

This method counts tagged NA values (see `tagged_na`) in a vector and prints a frequency table of counted tagged NAs.

**Usage**

```
count_na(x, ...)
```

**Arguments**

`x` A vector or data frame.

`...` Optional, unquoted names of variables that should be selected for further processing. Required, if `x` is a data frame (and no vector) and only selected variables from `x` should be processed. You may also use functions like `:` or `tidyselect`'s select-helpers. See 'Examples' or [package-vignette](#).

**Value**

A data frame with counted tagged NA values.

**Examples**

```
if (require("haven")) {
  x <- labelled(
    x = c(1:3, tagged_na("a", "c", "z"),
          4:1, tagged_na("a", "a", "c"),
          1:3, tagged_na("z", "c", "c"),
          1:4, tagged_na("a", "c", "z")),
    labels = c("Agreement" = 1, "Disagreement" = 4,
               "First" = tagged_na("c"), "Refused" = tagged_na("a"),
               "Not home" = tagged_na("z"))
  )
  count_na(x)

  y <- labelled(
    x = c(1:3, tagged_na("e", "d", "f"),
          4:1, tagged_na("f", "f", "d"),
          1:3, tagged_na("f", "d", "d"),
          1:4, tagged_na("f", "d", "f")),
    labels = c("Agreement" = 1, "Disagreement" = 4, "An E" = tagged_na("e"),
               "A D" = tagged_na("d"), "The eff" = tagged_na("f"))
  )

  # create data frame
  dat <- data.frame(x, y)

  # possible count()-function calls
  count_na(dat)
  count_na(dat$x)
  count_na(dat, x)
  count_na(dat, x, y)
}
```

**Description**

This function prints a basic descriptive statistic, including variable labels.

**Usage**

```
descr(
  x,
  ...,
  max.length = NULL,
  weights = NULL,
  show = "all",
  out = c("txt", "viewer", "browser"),
  encoding = "UTF-8",
  file = NULL
)
```

**Arguments**

<code>x</code>	A vector or a data frame. May also be a grouped data frame (see 'Note' and 'Examples').
<code>...</code>	Optional, unquoted names of variables that should be selected for further processing. Required, if <code>x</code> is a data frame (and no vector) and only selected variables from <code>x</code> should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's select-helpers. See 'Examples' or <a href="#">package-vignette</a> .
<code>max.length</code>	Numeric, indicating the maximum length of variable labels in the output. If variable names are longer than <code>max.length</code> , they will be shortened to the last whole word within the first <code>max.length</code> chars.
<code>weights</code>	Bare name, or name as string, of a variable in <code>x</code> that indicates the vector of weights, which will be applied to weight all observations. Default is <code>NULL</code> , so no weights are used.
<code>show</code>	Character vector, indicating which information (columns) that describe the data should be returned. May be one or more of <code>"type"</code> , <code>"label"</code> , <code>"n"</code> , <code>"NA.prc"</code> , <code>"mean"</code> , <code>"sd"</code> , <code>"se"</code> , <code>"md"</code> , <code>"trimmed"</code> , <code>"range"</code> , <code>"iqr"</code> , <code>"skew"</code> . There are two shortcuts: <code>show = "all"</code> (default) shows all information, <code>show = "short"</code> just shows <code>n</code> , missing percentage, mean and standard deviation.
<code>out</code>	Character vector, indicating whether the results should be printed to console ( <code>out = "txt"</code> ) or as HTML-table in the viewer-pane ( <code>out = "viewer"</code> ) or browser ( <code>out = "browser"</code> ).
<code>encoding</code>	Character vector, indicating the charset encoding used for variable and value labels. Default is <code>"UTF-8"</code> . Only used when <code>out</code> is not <code>"txt"</code> .
<code>file</code>	Destination file, if the output should be saved as file. Only used when <code>out</code> is not <code>"txt"</code> .

**Value**

A data frame with basic descriptive statistics.

**Note**

`data` may also be a grouped data frame (see [group\\_by](#)) with up to two grouping variables. Descriptive tables are created for each subgroup then.

**Examples**

```

data(efc)
descr(efc, e17age, c160age)

efc$weights <- abs(rnorm(nrow(efc), 1, .3))
descr(efc, c12hour, barthtot, weights = weights)

library(dplyr)
efc %>% select(e42dep, e15relat, c172code) %>% descr()

# show just a few elements
efc %>% select(e42dep, e15relat, c172code) %>% descr(show = "short")

# with grouped data frames
efc %>%
  group_by(e16sex) %>%
  select(e16sex, e42dep, e15relat, c172code) %>%
  descr()

# you can select variables also inside 'descr()'
efc %>%
  group_by(e16sex, c172code) %>%
  descr(e16sex, c172code, e17age, c160age)

# or even use select-helpers
descr(efc, contains("cop"), max.length = 20)

```

de\_mean

*Compute group-meaned and de-meaned variables***Description**

de\_mean() computes group- and de-meaned versions of a variable that can be used in regression analysis to model the between- and within-subject effect.

**Usage**

```
de_mean(x, ..., grp, append = TRUE, suffix.dm = "_dm", suffix.gm = "_gm")
```

**Arguments**

x	A data frame.
...	Names of variables that should be group- and de-meaned.
grp	Quoted or unquoted name of the variable that indicates the group- or cluster-ID.
append	Logical, if TRUE (the default) and x is a data frame, x including the new variables as additional columns is returned; if FALSE, only the new variables are returned.

suffix.dm, suffix.gm

String value, will be appended to the names of the group-meanded and de-meanded variables of `x`. By default, de-meanded variables will be suffixed with `"_dm"` and grouped-meanded variables with `"_gm"`.

### Details

`de_mean()` is intended to create group- and de-meanded variables for complex random-effect-within-between models (see *Bell et al. 2018*), where group-effects (random effects) and fixed effects correlate (see *Bafumi and Gelman 2006*). This violation of one of the *Gauss-Markov-assumptions* can happen, for instance, when analysing panel data. To control for correlating predictors and group effects, it is recommended to include the group-meanded and de-meanded version of *time-varying covariates* in the model. By this, one can fit complex multilevel models for panel data, including time-varying, time-invariant predictors and random effects. This approach is superior to simple fixed-effects models, which lack information of variation in the group-effects or between-subject effects.

A description of how to translate the formulas described in *Bell et al. 2018* into R using `lmer()` from **lme4** or `glmmTMB()` from **glmmTMB** can be found here: [for lmer\(\)](#) and [for glmmTMB\(\)](#).

### Value

For `append = TRUE`, `x` including the group-/de-meanded variables as new columns is returned; if `append = FALSE`, only the group-/de-meanded variables will be returned.

### References

Bafumi J, Gelman A. 2006. Fitting Multilevel Models When Predictors and Group Effects Correlate. In. Philadelphia, PA: Annual meeting of the American Political Science Association.

Bell A, Fairbrother M, Jones K. 2018. Fixed and Random Effects Models: Making an Informed Choice. *Quality & Quantity*. doi: [10.1007/s111350180802x](https://doi.org/10.1007/s111350180802x)

### Examples

```
data(efc)
efc$ID <- sample(1:4, nrow(efc), replace = TRUE) # fake-ID
de_mean(efc, c12hour, barthtot, grp = ID, append = FALSE)
```

---

dicho

*Dichotomize variables*

---

### Description

Dichotomizes variables into dummy variables (0/1). Dichotomization is either done by median, mean or a specific value (see `dich.by`). `dicho_if()` is a scoped variant of `dicho()`, where recoding will be applied only to those variables that match the logical condition of `predicate`.

**Usage**

```
dicho(
  x,
  ...,
  dich.by = "median",
  as.num = FALSE,
  var.label = NULL,
  val.labels = NULL,
  append = TRUE,
  suffix = "_d"
)

dicho_if(
  x,
  predicate,
  dich.by = "median",
  as.num = FALSE,
  var.label = NULL,
  val.labels = NULL,
  append = TRUE,
  suffix = "_d"
)
```

**Arguments**

<code>x</code>	A vector or data frame.
<code>...</code>	Optional, unquoted names of variables that should be selected for further processing. Required, if <code>x</code> is a data frame (and no vector) and only selected variables from <code>x</code> should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's select-helpers. See 'Examples' or <a href="#">package-vignette</a> .
<code>dich.by</code>	Indicates the split criterion where a variable is dichotomized. Must be one of the following values (may be abbreviated): <p>"median" or "md" by default, <code>x</code> is split into two groups at the median.</p> <p>"mean" or "m" splits <code>x</code> into two groups at the mean of <code>x</code>.</p> <p><b>numeric value</b> splits <code>x</code> into two groups at the specific value. Note that the value is inclusive, i.e. <code>dich.by = 10</code> will split <code>x</code> into one group with values from lowest to 10 and another group with values greater than 10.</p>
<code>as.num</code>	Logical, if TRUE, return value will be numeric, not a factor.
<code>var.label</code>	Optional string, to set variable label attribute for the returned variable (see vignette <a href="#">Labelled Data and the sjlabelled-Package</a> ). If NULL (default), variable label attribute of <code>x</code> will be used (if present). If empty, variable label attributes will be removed.
<code>val.labels</code>	Optional character vector (of length two), to set value label attributes of dichotomized variable (see <a href="#">set_labels</a> ). If NULL (default), no value labels will be set.

append	Logical, if TRUE (the default) and x is a data frame, x including the new variables as additional columns is returned; if FALSE, only the new variables are returned.
suffix	Indicates which suffix will be added to each dummy variable. Use "numeric" to number dummy variables, e.g. <i>x_1</i> , <i>x_2</i> , <i>x_3</i> etc. Use "label" to add value label, e.g. <i>x_low</i> , <i>x_mid</i> , <i>x_high</i> . May be abbreviated.
predicate	A predicate function to be applied to the columns. The variables for which predicate returns TRUE are selected.

### Details

dicho() also works on grouped data frames (see [group\\_by](#)). In this case, dichotomization is applied to the subsets of variables in x. See 'Examples'.

### Value

x, dichotomized. If x is a data frame, for append = TRUE, x including the dichotomized variables as new columns is returned; if append = FALSE, only the dichotomized variables will be returned. If append = TRUE and suffix = "", recoded variables will replace (overwrite) existing variables.

### Note

Variable label attributes are preserved (unless changed via var.label-argument).

### Examples

```
data(efc)
summary(efc$c12hour)
# split at median
table(dicho(efc$c12hour))
# split at mean
table(dicho(efc$c12hour, dich.by = "mean"))
# split between value lowest to 30, and above 30
table(dicho(efc$c12hour, dich.by = 30))

# sample data frame, values from 1-4
head(efc[, 6:10])

# dichotomized values (1 to 2 = 0, 3 to 4 = 1)
library(dplyr)
efc %>%
  select(6:10) %>%
  dicho(dich.by = 2) %>%
  head()

# dichotomize several variables in a data frame
dicho(efc, c12hour, e17age, c160age, append = FALSE)

# dichotomize and set labels
frq(dicho(
  efc, e42dep,
  var.label = "Dependency (dichotomized)",
```



```

    val.labels = c("lower", "higher"),
    append = FALSE
  ))

# works also with grouped data frames
mtcars %>%
  dichotomize(disp, append = FALSE) %>%
  table()

mtcars %>%
  group_by(cyl) %>%
  dichotomize(disp, append = FALSE) %>%
  table()

# dichotomizing grouped data frames leads to different
# results for a dichotomized variable, because the split
# value is different for each group.
# compare:
mtcars %>%
  group_by(cyl) %>%
  summarise(median = median(disp))

median(mtcars$disp)

# dichotomize only variables with more than 10 unique values
p <- function(x) dplyr::n_distinct(x) > 10
dichotomize_if(mtcars, predicate = p, append = FALSE)

```

---

efc

*Sample dataset from the EUROFAMCARE project*


---

## Description

A SPSS sample data set, imported with the [read\\_spss](#) function.

## Examples

```

# Attach EFC-data
data(efc)

# Show structure
str(efc)

# show first rows
head(efc)

```

---

empty_cols	<i>Return or remove variables or observations that are completely missing</i>
------------	---

---

### Description

These functions check which rows or columns of a data frame completely contain missing values, i.e. which observations or variables completely have missing values, and either 1) returns their indices; or 2) removes them from the data frame.

### Usage

```
empty_cols(x)
empty_rows(x)
remove_empty_cols(x)
remove_empty_rows(x)
```

### Arguments

x                    A data frame.

### Value

For `empty_cols` and `empty_rows`, a numeric (named) vector with row or column indices of those variables that completely have missing values.

For `remove_empty_cols` and `remove_empty_rows`, a data frame with "empty" columns or rows removed.

### Examples

```
tmp <- data.frame(a = c(1, 2, 3, NA, 5),
                 b = c(1, NA, 3, NA, 5),
                 c = c(NA, NA, NA, NA, NA),
                 d = c(1, NA, 3, NA, 5))

tmp

empty_cols(tmp)
empty_rows(tmp)

remove_empty_cols(tmp)
remove_empty_rows(tmp)
```

---

find_var	<i>Find variable by name or label</i>
----------	---------------------------------------

---

### Description

This functions finds variables in a data frame, which variable names or variable (and value) label attribute match a specific pattern. Regular expression for the pattern is supported.

### Usage

```
find_var(
  data,
  pattern,
  ignore.case = TRUE,
  search = c("name_label", "name_value", "label_value", "name", "label", "value",
            "all"),
  out = c("table", "df", "index"),
  fuzzy = FALSE,
  regex = FALSE
)

find_in_data(
  data,
  pattern,
  ignore.case = TRUE,
  search = c("name_label", "name_value", "label_value", "name", "label", "value",
            "all"),
  out = c("table", "df", "index"),
  fuzzy = FALSE,
  regex = FALSE
)
```

### Arguments

data	A data frame.
pattern	Character string to be matched in data. May also be a character vector of length > 1 (see 'Examples'). pattern is searched for in column names and variable label attributes of data (see <a href="#">get_label</a> ). pattern might also be a regular-expression object, as returned by <code>stringr::regex()</code> . Alternatively, use <code>regex = TRUE</code> to treat pattern as a regular expression rather than a fixed string.
ignore.case	Logical, whether matching should be case sensitive or not. <code>ignore.case</code> is ignored when pattern is no regular expression or <code>regex = FALSE</code> .
search	Character string, indicating where pattern is sought. Use one of following options: " name_label " The default, searches for pattern in variable names and variable labels.

	"name_value" Searches for pattern in variable names and value labels.
	"label_value" Searches for pattern in variable and value labels.
	"name" Searches for pattern in variable names.
	"label" Searches for pattern in variable labels
	"value" Searches for pattern in value labels.
	"all" Searches for pattern in variable names, variable and value labels.
out	Output (return) format of the search results. May be abbreviated and must be one of: "table" A tabular overview (as data frame) with column indices, variable names and labels of matching variables. "df" A data frame with all matching variables. "index" A named vector with column indices of all matching variables.
fuzzy	Logical, if TRUE, "fuzzy matching" (partial and close distance matching) will be used to find pattern in data if no exact match was found.
regex	Logical, if TRUE, pattern is treated as a regular expression rather than a fixed string.

### Details

This function searches for pattern in data's column names and - for labelled data - in all variable and value labels of data's variables (see [get\\_label](#) for details on variable labels and labelled data). Regular expressions are supported as well, by simply using `pattern = stringr::regex(...)` or `regex = TRUE`.

### Value

By default (i.e. `out = "table"`), returns a data frame with three columns: column number, variable name and variable label. If `out = "index"`, returns a named vector with column indices of matching variables (variable names are used as names-attribute); if `out = "df"`, returns the matching variables as data frame

### Examples

```
data(efc)

# find variables with "cop" in variable name
find_var(efc, "cop")

# return data frame with matching variables
find_var(efc, "cop", out = "df")

# or return column numbers
find_var(efc, "cop", out = "index")

# find variables with "dependency" in names and variable labels
library(sjlabelled)
find_var(efc, "dependency")
get_label(efc$e42dep)
```

```

# find variables with "level" in names and value labels
res <- find_var(efc, "level", search = "name_value", out = "df")
res
get_labels(res, attr.only = FALSE)

# use sjPlot::view_df() to view results
## Not run:
library(sjPlot)
view_df(res)
## End(Not run)

```

---

flat\_table

*Flat (proportional) tables*


---

### Description

This function creates a labelled flat table or flat proportional (marginal) table.

### Usage

```

flat_table(
  data,
  ...,
  margin = c("counts", "cell", "row", "col"),
  digits = 2,
  show.values = FALSE,
  weights = NULL
)

```

### Arguments

data	A data frame. May also be a grouped data frame (see 'Note' and 'Examples').
...	One or more variables of data that should be printed as table.
margin	Specify the table margin that should be computed for proportional tables. By default, counts are printed. Use <code>margin = "cell"</code> , <code>margin = "col"</code> or <code>margin = "row"</code> to print cell, column or row percentages of the table margins.
digits	Numeric; for proportional tables, <code>digits</code> indicates the number of decimal places.
show.values	Logical, if TRUE, value labels are prefixed by the associated value.
weights	Bare name, or name as string, of a variable in <code>x</code> that indicates the vector of weights, which will be applied to weight all observations. Default is NULL, so no weights are used.

### Value

An object of class `ftable`.

**Note**

data may also be a grouped data frame (see [group\\_by](#)) with up to two grouping variables. Cross tables are created for each subgroup then.

**See Also**

[frq](#) for simple frequency table of labelled vectors.

**Examples**

```
data(efc)

# flat table with counts
flat_table(efc, e42dep, c172code, e16sex)

# flat table with proportions
flat_table(efc, e42dep, c172code, e16sex, margin = "row")

# flat table from grouped data frame. You need to select
# the grouping variables and at least two more variables for
# cross tabulation.
library(dplyr)
efc %>%
  group_by(e16sex) %>%
  select(e16sex, c172code, e42dep) %>%
  flat_table()

efc %>%
  group_by(e16sex, e42dep) %>%
  select(e16sex, e42dep, c172code, n4pstu) %>%
  flat_table()

# now it gets weird...
efc %>%
  group_by(e16sex, e42dep) %>%
  select(e16sex, e42dep, c172code, n4pstu, c161sex) %>%
  flat_table()
```

---

frq

*Frequency table of labelled variables*


---

**Description**

This function returns a frequency table of labelled vectors, as data frame.

**Usage**

```
frq(
  x,
  ...,
  sort.frq = c("none", "asc", "desc"),
  weights = NULL,
  auto.grp = NULL,
  show.strings = TRUE,
  show.na = TRUE,
  grp.strings = NULL,
  min.frq = 0,
  out = c("txt", "viewer", "browser"),
  title = NULL,
  encoding = "UTF-8",
  file = NULL
)
```

**Arguments**

x	A vector or a data frame. May also be a grouped data frame (see 'Note' and 'Examples').
...	Optional, unquoted names of variables that should be selected for further processing. Required, if x is a data frame (and no vector) and only selected variables from x should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's select-helpers. See 'Examples' or <a href="#">package-vignette</a> .
sort.frq	Determines whether categories should be sorted according to their frequencies or not. Default is "none", so categories are not sorted by frequency. Use "asc" or "desc" for sorting categories ascending or descending order.
weights	Bare name, or name as string, of a variable in x that indicates the vector of weights, which will be applied to weight all observations. Default is NULL, so no weights are used.
auto.grp	Numeric value, indicating the minimum amount of unique values in a variable, at which automatic grouping into smaller units is done (see <a href="#">group_var</a> ). Default value for <code>auto.group</code> is NULL, i.e. auto-grouping is off.
show.strings	Logical, if TRUE, frequency tables for character vectors will not be printed. This is useful when printing frequency tables of all variables from a data frame, and due to computational reasons character vectors should not be printed.
show.na	Logical, or "auto". If TRUE, the output always contains information on missing values, even if variables have no missing values. If FALSE, information on missing values are removed from the output. If <code>show.na = "auto"</code> , information on missing values is only shown when variables actually have missing values, else it's not shown.
grp.strings	Numeric, if not NULL, groups string values in character vectors, based on their similarity. See <a href="#">group_str</a> and <a href="#">str_find</a> for details on grouping, and their <code>precision</code> -argument to get more details on the distance of strings to be treated as equal.

<code>min.frq</code>	Numeric, indicating the minimum frequency for which a value will be shown in the output (except for the missing values, prevailing <code>show.na</code> ). Default value for <code>min.frq</code> is 0, so all value frequencies are shown. All values or categories that have less than <code>min.frq</code> occurrences in the data will be summarized in a " <code>n &lt; 100</code> " category.
<code>out</code>	Character vector, indicating whether the results should be printed to console ( <code>out = "txt"</code> ) or as HTML-table in the viewer-pane ( <code>out = "viewer"</code> ) or browser ( <code>out = "browser"</code> ).
<code>title</code>	String, will be used as alternative title to the variable label. If <code>x</code> is a grouped data frame, <code>title</code> must be a vector of same length as groups.
<code>encoding</code>	Character vector, indicating the charset encoding used for variable and value labels. Default is "UTF-8". Only used when <code>out</code> is not "txt".
<code>file</code>	Destination file, if the output should be saved as file. Only used when <code>out</code> is not "txt".

### Details

The `...`-argument not only accepts variable names or expressions from `select`-helpers. You can also use logical conditions, math operations, or combining variables to produce "crosstables". See 'Examples' for more details.

### Value

A list of data frames with values, value labels, frequencies, raw, valid and cumulative percentages of `x`.

### Note

`x` may also be a grouped data frame (see [group\\_by](#)) with up to two grouping variables. Frequency tables are created for each subgroup then.

The `print()`-method adds a table header with information on the variable label, variable type, total and valid N, and mean and standard deviations. Mean and SD are *always* printed, even for categorical variables (factors) or character vectors. In this case, values are coerced into numeric vector to calculate the summary statistics.

To print tables in markdown or HTML format, use `print_md()` or `print_html()`.

### See Also

[flat\\_table](#) for labelled (proportional) tables.

### Examples

```
# simple vector
data(efc)
frq(efc$e42dep)

# with grouped data frames, in a pipe
```



```

library(dplyr)
efc %>%
  group_by(e16sex, c172code) %>%
  frq(e42dep)

# show only categories with a minimal amount of frequencies
frq(mtcars$gear)

frq(mtcars$gear, min.frq = 10)

frq(mtcars$gear, min.frq = 15)

# with select-helpers: all variables from the COPE-Index
# (which all have a "cop" in their name)
frq(efc, contains("cop"))

# all variables from column "c161sex" to column "c175empl"
frq(efc, c161sex:c175empl)

# for non-labelled data, variable name is printed,
# and "label" column is removed from output
data(iris)
frq(iris, Species)

# also works on grouped data frames
efc %>%
  group_by(c172code) %>%
  frq(is.na(nur_pst))

# group variables with large range and with weights
efc$weights <- abs(rnorm(n = nrow(efc), mean = 1, sd = .5))
frq(efc, c160age, auto.grp = 5, weights = weights)

# different weight options
frq(efc, c172code, weights = weights)
frq(efc, c172code, weights = "weights")
frq(efc, c172code, weights = efc$weights)
frq(efc$c172code, weights = efc$weights)

# group string values
dummy <- efc[1:50, 3, drop = FALSE]
dummy$words <- sample(
  c("Hello", "Helo", "Hole", "Apple", "Ape",
    "New", "Old", "System", "Systemic"),
  size = nrow(dummy),
  replace = TRUE
)

frq(dummy)
frq(dummy, grp.strings = 2)

#### other expressions than variables

```

```

# logical conditions
frq(mtcars, cyl ==6)

frq(efc, is.na(nur_pst), contains("cop"))

iris %>%
  frq(starts_with("Petal"), Sepal.Length > 5)

# computation of variables "on the fly"
frq(mtcars, (gear + carb) / cyl)

# crosstables
set.seed(123)
d <- data.frame(
  var_x = sample(letters[1:3], size = 30, replace = TRUE),
  var_y = sample(1:2, size = 30, replace = TRUE),
  var_z = sample(LETTERS[8:10], size = 30, replace = TRUE)
)
table(d$var_x, d$var_z)
frq(d, paste0(var_x, var_z))
frq(d, paste0(var_x, var_y, var_z))

```

---

group\_str

*Group near elements of string vectors*


---

### Description

This function groups elements of a string vector (character or string variable) according to the element's distance ('similarity'). The more similar two string elements are, the higher is the chance to be combined into a group.

### Usage

```

group_str(
  strings,
  precision = 2,
  strict = FALSE,
  trim.whitespace = TRUE,
  remove.empty = TRUE,
  verbose = FALSE,
  maxdist
)

```

### Arguments

strings	Character vector with string elements.
precision	Maximum distance ("precision") between two string elements, which is allowed to treat them as similar or equal. Smaller values mean less tolerance in matching.

strict	Logical; if TRUE, value matching is more strictly. See 'Examples'.
trim.whitespace	Logical; if TRUE (default), leading and trailing white spaces will be removed from string values.
remove.empty	Logical; if TRUE (default), empty string values will be removed from the character vector strings.
verbose	Logical; if TRUE, the progress bar is displayed when computing the distance matrix. Default in FALSE, hence the bar is hidden.
maxdist	Deprecated. Please use precision now.

### Value

A character vector where similar string elements (values) are recoded into a new, single value. The return value is of same length as `strings`, i.e. grouped elements appear multiple times, so the count for each grouped string is still available (see 'Examples').

### See Also

[str\\_find](#)

### Examples

```
oldstring <- c("Hello", "Helo", "Hole", "Apple",
              "Ape", "New", "Old", "System", "Systemic")
newstring <- group_str(oldstring)

# see result
newstring

# count for each groups
table(newstring)

# print table to compare original and grouped string
frq(oldstring)
frq(newstring)

# larger groups
newstring <- group_str(oldstring, precision = 3)
frq(oldstring)
frq(newstring)

# be more strict with matching pairs
newstring <- group_str(oldstring, precision = 3, strict = TRUE)
frq(oldstring)
frq(newstring)
```

---

`group_var`*Recode numeric variables into equal-ranged groups*

---

## Description

Recode numeric variables into equal ranged, grouped factors, i.e. a variable is cut into a smaller number of groups, where each group has the same value range. `group_labels()` creates the related value labels. `group_var_if()` and `group_labels_if()` are scoped variants of `group_var()` and `group_labels()`, where grouping will be applied only to those variables that match the logical condition of predicate.

## Usage

```
group_var(  
  x,  
  ...,  
  size = 5,  
  as.num = TRUE,  
  right.interval = FALSE,  
  n = 30,  
  append = TRUE,  
  suffix = "_gr"  
)
```

```
group_var_if(  
  x,  
  predicate,  
  size = 5,  
  as.num = TRUE,  
  right.interval = FALSE,  
  n = 30,  
  append = TRUE,  
  suffix = "_gr"  
)
```

```
group_labels(x, ..., size = 5, right.interval = FALSE, n = 30)
```

```
group_labels_if(x, predicate, size = 5, right.interval = FALSE, n = 30)
```

## Arguments

`x` A vector or data frame.

`...` Optional, unquoted names of variables that should be selected for further processing. Required, if `x` is a data frame (and no vector) and only selected variables from `x` should be processed. You may also use functions like `:` or `tidyselect`'s select-helpers. See 'Examples' or [package-vignette](#).

size	Numeric; group-size, i.e. the range for grouping. By default, for each 5 categories of $x$ a new group is defined, i.e. <code>size = 5</code> . Use <code>size = "auto"</code> to automatically resize a variable into a maximum of 30 groups (which is the ggplot-default grouping when plotting histograms). Use <code>n</code> to determine the amount of groups.
as.num	Logical, if TRUE, return value will be numeric, not a factor.
right.interval	Logical; if TRUE, grouping starts with the lower bound of size. See 'Details'.
n	Sets the maximum number of groups that are defined when auto-grouping is on ( <code>size = "auto"</code> ). Default is 30. If <code>size</code> is not set to "auto", this argument will be ignored.
append	Logical, if TRUE (the default) and $x$ is a data frame, $x$ including the new variables as additional columns is returned; if FALSE, only the new variables are returned.
suffix	Indicates which suffix will be added to each dummy variable. Use "numeric" to number dummy variables, e.g. $x_1, x_2, x_3$ etc. Use "label" to add value label, e.g. $x_{low}, x_{mid}, x_{high}$ . May be abbreviated.
predicate	A predicate function to be applied to the columns. The variables for which predicate returns TRUE are selected.

### Details

If `size` is set to a specific value, the variable is recoded into several groups, where each group has a maximum range of size. Hence, the amount of groups differ depending on the range of  $x$ .

If `size = "auto"`, the variable is recoded into a maximum of `n` groups. Hence, independent from the range of  $x$ , always the same amount of groups are created, so the range within each group differs (depending on  $x$ 's range).

`right.interval` determines which boundary values to include when grouping is done. If TRUE, grouping starts with the **lower bound** of size. For example, having a variable ranging from 50 to 80, groups cover the ranges from 50-54, 55-59, 60-64 etc. If FALSE (default), grouping starts with the upper bound of size. In this case, groups cover the ranges from 46-50, 51-55, 56-60, 61-65 etc. **Note:** This will cover a range from 46-50 as first group, even if values from 46 to 49 are not present. See 'Examples'.

If you want to split a variable into a certain amount of equal sized groups (instead of having groups where values have all the same range), use the `split_var` function!

`group_var()` also works on grouped data frames (see `group_by`). In this case, grouping is applied to the subsets of variables in  $x$ . See 'Examples'.

### Value

- For `group_var()`, a grouped variable, either as numeric or as factor (see parameter `as.num`). If  $x$  is a data frame, only the grouped variables will be returned.
- For `group_labels()`, a string vector or a list of string vectors containing labels based on the grouped categories of  $x$ , formatted as "from lower bound to upper bound", e.g. "10-19" "20-29" "30-39" etc. See 'Examples'.

**Note**

Variable label attributes (see, for instance, [set\\_label](#)) are preserved. Usually you should use the same values for `size` and `right.interval` in `group_labels()` as used in the `group_var` function if you want matching labels for the related recoded variable.

**See Also**

[split\\_var](#) to split variables into equal sized groups, [group\\_str](#) for grouping string vectors or [rec\\_pattern](#) and [rec](#) for another convenient way of recoding variables into smaller groups.

**Examples**

```
age <- abs(round(rnorm(100, 65, 20)))
age.grp <- group_var(age, size = 10)
hist(age)
hist(age.grp)

age.grpvar <- group_labels(age, size = 10)
table(age.grp)
print(age.grpvar)

# histogram with EUROFAMCARE sample dataset
# variable not grouped
library(sjlabelled)
data(efc)
hist(efc$e17age, main = get_label(efc$e17age))

# bar plot with EUROFAMCARE sample dataset
# grouped variable
ageGrp <- group_var(efc$e17age)
ageGrpLab <- group_labels(efc$e17age)
barplot(table(ageGrp), main = get_label(efc$e17age), names.arg = ageGrpLab)

# within a pipe-chain
library(dplyr)
efc %>%
  select(e17age, c12hour, c160age) %>%
  group_var(size = 20)

# create vector with values from 50 to 80
dummy <- round(runif(200, 50, 80))
# labels with grouping starting at lower bound
group_labels(dummy)
# labels with grouping startint at upper bound
group_labels(dummy, right.interval = TRUE)

# works also with gouped data frames
mtcars %>%
  group_var(displ, size = 4, append = FALSE) %>%
  table()

mtcars %>%
```

```
group_by(cyl) %>%
group_var(displ, size = 4, append = FALSE) %>%
table()
```

---

has_na	<i>Check if variables or cases have missing / infinite values</i>
--------	---

---

### Description

This functions checks if variables or observations in a data frame have NA, NaN or Inf values.

### Usage

```
has_na(x, ..., by = c("col", "row"), out = c("table", "df", "index"))
incomplete_cases(x, ...)
complete_cases(x, ...)
complete_vars(x, ...)
incomplete_vars(x, ...)
```

### Arguments

x	A data frame.
...	Optional, unquoted names of variables that should be selected for further processing. Required, if x is a data frame (and no vector) and only selected variables from x should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's <code>select</code> -helpers. See 'Examples' or <a href="#">package-vignette</a> .
by	Whether to check column- or row-wise for missing and infinite values. If <code>by = "col"</code> , <code>has_na()</code> checks for NA/NaN/Inf in <i>columns</i> ; If <code>by = "row"</code> , <code>has_na()</code> checks each row for these values.
out	Output (return) format of the results. May be abbreviated.

### Value

If x is a vector, returns TRUE if x has any missing or infinite values. If x is a data frame, returns TRUE for each variable (if `by = "col"`) or observation (if `by = "row"`) that has any missing or infinite values. If `out = "table"`, results are returned as data frame, with column number, variable name and label, and a logical vector indicating if a variable has missing values or not. However, it's printed in colors, with green rows indicating that a variable has no missings, while red rows indicate the presence of missings or infinite values. If `out = "index"`, a named vector is returned.

**Note**

`complete_cases()` and `incomplete_cases()` are convenient shortcuts for `has_na(by = "row", out = "index")`, where the first only returns case-id's for all complete cases, and the latter only for non-complete cases.

`complete_vars()` and `incomplete_vars()` are convenient shortcuts for `has_na(by = "col", out = "index")`, and again only return those column-id's for variables which are (in-)complete.

**Examples**

```
data(efc)
has_na(efc$e42dep)
has_na(efc, e42dep, tot_sc_e, c161sex)
has_na(efc)

has_na(efc, e42dep, tot_sc_e, c161sex, out = "index")
has_na(efc, out = "df")

has_na(efc, by = "row")
has_na(efc, e42dep, tot_sc_e, c161sex, by = "row", out = "index")
has_na(efc, by = "row", out = "df")

complete_cases(efc, e42dep, tot_sc_e, c161sex)
incomplete_cases(efc, e42dep, tot_sc_e, c161sex)
complete_vars(efc, e42dep, tot_sc_e, c161sex)
incomplete_vars(efc, e42dep, tot_sc_e, c161sex)
```

---

is\_crossed

*Check whether two factors are crossed or nested*


---

**Description**

These functions checks whether two factors are (fully) crossed or nested, i.e. if each level of one factor occurs in combination with each level of the other factor (`is_crossed()`) resp. if each category of the first factor co-occurs with only one category of the other (`is_nested()`). `is_cross_classified()` checks if one factor level occurs in some, but not all levels of another factor.

**Usage**

```
is_crossed(f1, f2)

is_nested(f1, f2)

is_cross_classified(f1, f2)
```



**Arguments**

f1                    Numeric vector or [factor](#).  
 f2                    Numeric vector or [factor](#).

**Value**

Logical. For `is_crossed()`, TRUE if factors are (fully) crossed, FALSE otherwise. For `is_nested()`, TRUE if factors are nested, FALSE otherwise. For `is_cross_classified()`, TRUE, if one factor level occurs in some, but not all levels of another factor.

**Note**

If factors are nested, a message is displayed to tell whether f1 is nested within f2 or vice versa.

**References**

Grace, K. The Difference Between Crossed and Nested Factors. ([web](#))

**Examples**

```
# crossed factors, each category of
# x appears in each category of y
x <- c(1,4,3,2,3,2,1,4)
y <- c(1,1,1,2,2,1,2,2)
# show distribution
table(x, y)
# check if crossed
is_crossed(x, y)

# not crossed factors
x <- c(1,4,3,2,3,2,1,4)
y <- c(1,1,1,2,1,1,2,2)
# show distribution
table(x, y)
# check if crossed
is_crossed(x, y)

# nested factors, each category of
# x appears in one category of y
x <- c(1,2,3,4,5,6,7,8,9)
y <- c(1,1,1,2,2,2,3,3,3)
# show distribution
table(x, y)
# check if nested
is_nested(x, y)
is_nested(y, x)

# not nested factors
x <- c(1,2,3,4,5,6,7,8,9,1,2)
y <- c(1,1,1,2,2,2,3,3,3,2,3)
```

```

# show distribution
table(x, y)
# check if nested
is_nested(x, y)
is_nested(y, x)

# also not fully crossed
is_crossed(x, y)

# but partially crossed
is_cross_classified(x, y)

```

---

is_empty	<i>Check whether string, list or vector is empty</i>
----------	--

---

### Description

This function checks whether a string or character vector (of length 1), a list or any vector (numeric, atomic) is empty or not.

### Usage

```
is_empty(x, first.only = TRUE, all.na.empty = TRUE)
```

### Arguments

x	String, character vector, list, data.frame or numeric vector or factor.
first.only	Logical, if FALSE and x is a character vector, each element of x will be checked if empty. If TRUE, only the first element of x will be checked.
all.na.empty	Logical, if x is a vector with NA-values only, is_empty will return FALSE if all.na.empty = FALSE, and will return TRUE if all.na.empty = TRUE (default).

### Value

Logical, TRUE if x is a character vector or string and is empty, TRUE if x is a vector or list and of length 0, FALSE otherwise.

### Note

NULL- or NA-values are also considered as "empty" (see 'Examples') and will return TRUE, unless all.na.empty==FALSE.

**Examples**

```
is_empty("test")
is_empty("")
is_empty(NA)
is_empty(NULL)

# string is not empty
is_empty(" ")

# however, this trimmed string is
is_empty(trim(" "))

# numeric vector
x <- 1
is_empty(x)
x <- x[-1]
is_empty(x)

# check multiple elements of character vectors
is_empty(c("", "a"))
is_empty(c("", "a"), first.only = FALSE)

# empty data frame
d <- data.frame()
is_empty(d)

# empty list
is_empty(list(NULL))

# NA vector
x <- rep(NA,5)
is_empty(x)
is_empty(x, all.na.empty = FALSE)
```

---

is\_even

*Check whether value is even or odd*

---

**Description**

Checks whether x is an even or odd number. Only accepts numeric vectors.

**Usage**

```
is_even(x)
```

```
is_odd(x)
```

**Arguments**

x                    Numeric vector or single numeric value, or a data frame or list with such vectors.

**Value**

is\_even() returns TRUE for each even value of x, FALSE for odd values. is\_odd() returns TRUE for each odd value of x and FALSE for even values.

**Examples**

```
is_even(4)
is_even(5)
is_even(1:4)
```

```
is_odd(4)
is_odd(5)
is_odd(1:4)
```

---

is\_float

---

*Check if a variable is of (non-integer) double type or a whole number*


---

**Description**

is\_float() checks whether an input vector or value is a numeric non-integer (double), depending on fractional parts of the value(s). is\_whole() does the opposite and checks whether an input vector is a whole number (without fractional parts).

**Usage**

```
is_float(x)

is_whole(x)
```

**Arguments**

x                    A value, vector or data frame.

**Value**

For is\_float(), TRUE if x is a floating value (non-integer double), FALSE otherwise (also returns FALSE for character vectors and factors). For is\_whole(), TRUE if x is a vector with whole numbers only, FALSE otherwise (returns TRUE for character vectors and factors).

**Examples**

```
data(mtcars)
data(iris)
```

```
is.double(4)
is_float(4)
is_float(4.2)
```

```
is_float(iris)

is_whole(4)
is_whole(4.2)
is_whole(mtcars)
```

---

**is\_num\_fac***Check whether a factor has numeric levels only*

---

**Description**

is\_num\_fac() checks whether a factor has only numeric or any non-numeric factor levels, while is\_num\_chr() checks whether a character vector has only numeric strings.

**Usage**

```
is_num_fac(x)

is_num_chr(x)
```

**Arguments**

x                    A factor for is\_num\_fac() and a character vector for is\_num\_chr()

**Value**

Logical, TRUE if factor has numeric factor levels only, or if character vector has numeric strings only, FALSE otherwise.

**Examples**

```
# numeric factor levels
f1 <- factor(c(NA, 1, 3, NA, 2, 4))
is_num_fac(f1)

# not completely numeric factor levels
f2 <- factor(c(NA, "C", 1, 3, "A", NA, 2, 4))
is_num_fac(f2)

# not completely numeric factor levels
f3 <- factor(c("Justus", "Bob", "Peter"))
is_num_fac(f3)

is_num_chr(c("a", "1"))
is_num_chr(c("2", "1"))
```

---

merge\_imputations      *Merges multiple imputed data frames into a single data frame*

---

### Description

This function merges multiple imputed data frames from `mice::mids()`-objects into a single data frame by computing the mean or selecting the most likely imputed value.

### Usage

```
merge_imputations(
  dat,
  imp,
  ori = NULL,
  summary = c("none", "dens", "hist", "sd"),
  filter = NULL
)
```

### Arguments

<code>dat</code>	The data frame that was imputed and used as argument in the <code>mice</code> -function call.
<code>imp</code>	The <code>mice::mids()</code> -object with the imputed data frames from <code>dat</code> .
<code>ori</code>	Optional, if <code>ori</code> is specified, the imputed variables are appended to this data frame; else, a new data frame with the imputed variables is returned.
<code>summary</code>	After merging multiple imputed data, <code>summary</code> displays a graphical summary of the "quality" of the merged values, compared to the original imputed values. " <code>dens</code> " Creates a density plot, which shows the distribution of the mean of the imputed values for each variable at each observation. The larger the areas overlap, the better is the fit of the merged value compared to the imputed value. " <code>hist</code> " Similar to <code>summary = "dens"</code> , however, mean and merged values are shown as histogram. Bins should have almost equal height for both groups (mean and merged). " <code>sd</code> " Creates a dot plot, where data points indicate the standard deviation for all imputed values (y-axis) at each merged value (x-axis) for all imputed variables. The higher the standard deviation, the less precise is the imputation, and hence the merged value.
<code>filter</code>	A character vector with variable names that should be plotted. All non-defined variables will not be shown in the plot.

### Details

This method merges multiple imputations of variables into a single variable by computing the (rounded) mean of all imputed values of missing values. By this, each missing value is replaced by those values that have been imputed the most times.

`imp` must be a `mids`-object, which is returned by the `mice()`-function of the **mice**-package. `merge_imputations()` then creates a data frame for each imputed variable, by combining all imputations (as returned by the `complete`-function) of each variable, and computing the row means of this data frame. The mean value is then rounded for integer values (and not for numerical values with fractional part), which corresponds to the most frequent imputed value (mode) for a missing value. Missings in the original variable are replaced by the most frequent imputed value.

### Value

A data frame with (merged) imputed variables; or `ori` with appended imputed variables, if `ori` is specified. If `summary` is included, returns a list with the data frame data with (merged) imputed variables and some other summary information, including the plot as `ggplot`-object.

### Note

Typically, further analyses are conducted on pooled results of multiple imputed data sets (see `pool`), however, sometimes (in social sciences) it is also feasible to compute the mean or mode of multiple imputed variables (see *Burns et al. 2011*).

### References

Burns RA, Butterworth P, Kiely KM, Bielak AAM, Luszcz MA, Mitchell P, et al. 2011. Multiple imputation was an efficient method for harmonizing the Mini-Mental State Examination with missing item-level data. *Journal of Clinical Epidemiology*;64:787-93 doi: [10.1016/j.jclinepi.2010.10.011](https://doi.org/10.1016/j.jclinepi.2010.10.011)

### Examples

```
if (require("mice")) {
  imp <- mice(nhanes)

  # return data frame with imputed variables
  merge_imputations(nhanes, imp)

  # append imputed variables to original data frame
  merge_imputations(nhanes, imp, nhanes)

  # show summary of quality of merging imputations
  merge_imputations(nhanes, imp, summary = "dens", filter = c("chl", "hyp"))
}
```

---

move\_columns

*Move columns to other positions in a data frame*

---

### Description

`move_columns()` moves one or more columns in a data frame to another position.

**Usage**

```
move_columns(data, ..., .before, .after)
```

**Arguments**

<code>data</code>	A data frame.
<code>...</code>	Unquoted names or character vector with names of variables that should be moved to another position. You may also use functions like <code>:</code> or <code>tidyselect</code> 's <code>select</code> -helpers.
<code>.before</code>	Optional, column name or numeric index of the position where <code>col</code> should be moved to. If not missing, <code>col</code> is moved to the position <i>before</i> the column indicated by <code>.before</code> .
<code>.after</code>	Optional, column name or numeric index of the position where <code>col</code> should be moved to. If not missing, <code>col</code> is moved to the position <i>after</i> the column indicated by <code>.after</code> .

**Value**

`data`, with resorted columns.

**Note**

If neither `.before` nor `.after` are specified, the column is moved to the end of the data frame by default. `.before` and `.after` are evaluated in a non-standard fashion, so you need quasi-quotation when the value for `.before` or `.after` is a vector with the target-column value. See 'Examples'.

**Examples**

```
## Not run:
data(iris)

iris %>%
  move_columns(Sepal.Width, .after = "Species") %>%
  head()

iris %>%
  move_columns(Sepal.Width, .before = Sepal.Length) %>%
  head()

iris %>%
  move_columns(Species, .before = 1) %>%
  head()

iris %>%
  move_columns("Species", "Petal.Length", .after = 1) %>%
  head()

library(dplyr)
iris %>%
  move_columns(contains("Width"), .after = "Species") %>%
```



```
  head()
## End(Not run)

# using quasi-quotation
target <- "Petal.Width"
# does not work, column is moved to the end
iris %>%
  move_columns(Sepal.Width, .after = target) %>%
  head()

# using !! works
iris %>%
  move_columns(Sepal.Width, .after = !!target) %>%
  head()
```

---

numeric\_to\_factor      *Convert numeric vectors into factors associated value labels*

---

## Description

This function converts numeric variables into factors, and uses associated value labels as factor levels.

## Usage

```
numeric_to_factor(x, n = 4)
```

## Arguments

x	A data frame.
n	Numeric, indicating the maximum amount of unique values in x to be considered as "factor". Variables with more unique values than n are not converted to factor.

## Details

If x is a labelled vector, associated value labels will be used as level. Else, the numeric vector is simply coerced using `as.factor()`.

## Value

x, with numeric values with a maximum of n unique values being converted to factors.

## Examples

```
library(dplyr)
data(efc)
efc %>%
  select(e42dep, e16sex, c12hour, c160age, c172code) %>%
  numeric_to_factor()
```

---

rec	<i>Recode variables</i>
-----	-------------------------

---

### Description

`rec()` recodes values of variables, where variable selection is based on variable names or column position, or on select helpers (see documentation on `...`). `rec_if()` is a scoped variant of `rec()`, where recoding will be applied only to those variables that match the logical condition of predicate.

### Usage

```
rec(  
  x,  
  ...,  
  rec,  
  as.num = TRUE,  
  var.label = NULL,  
  val.labels = NULL,  
  append = TRUE,  
  suffix = "_r",  
  to.factor = !as.num  
)
```

```
rec_if(  
  x,  
  predicate,  
  rec,  
  as.num = TRUE,  
  var.label = NULL,  
  val.labels = NULL,  
  append = TRUE,  
  suffix = "_r",  
  to.factor = !as.num  
)
```

### Arguments

x	A vector or data frame.
...	Optional, unquoted names of variables that should be selected for further processing. Required, if x is a data frame (and no vector) and only selected variables from x should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's select-helpers. See 'Examples' or <a href="#">package-vignette</a> .
rec	String with recode pairs of old and new values. See 'Details' for examples. <a href="#">rec_pattern</a> is a convenient function to create recode strings for grouping variables.

<code>as.num</code>	Logical, if TRUE, return value will be numeric, not a factor.
<code>var.label</code>	Optional string, to set variable label attribute for the returned variable (see vignette <a href="#">Labelled Data and the sjlabelled-Package</a> ). If NULL (default), variable label attribute of <code>x</code> will be used (if present). If empty, variable label attributes will be removed.
<code>val.labels</code>	Optional character vector, to set value label attributes of recoded variable (see vignette <a href="#">Labelled Data and the sjlabelled-Package</a> ). If NULL (default), no value labels will be set. Value labels can also be directly defined in the <code>rec</code> -syntax, see 'Details'.
<code>append</code>	Logical, if TRUE (the default) and <code>x</code> is a data frame, <code>x</code> including the new variables as additional columns is returned; if FALSE, only the new variables are returned.
<code>suffix</code>	String value, will be appended to variable (column) names of <code>x</code> , if <code>x</code> is a data frame. If <code>x</code> is not a data frame, this argument will be ignored. The default value to suffix column names in a data frame depends on the function call: <ul style="list-style-type: none"> <li>• recoded variables (<code>rec()</code>) will be suffixed with <code>"_r"</code></li> <li>• recoded variables (<code>recode_to()</code>) will be suffixed with <code>"_r0"</code></li> <li>• dichotomized variables (<code>dicho()</code>) will be suffixed with <code>"_d"</code></li> <li>• grouped variables (<code>split_var()</code>) will be suffixed with <code>"_g"</code></li> <li>• grouped variables (<code>group_var()</code>) will be suffixed with <code>"_gr"</code></li> <li>• standardized variables (<code>std()</code>) will be suffixed with <code>"_z"</code></li> <li>• centered variables (<code>center()</code>) will be suffixed with <code>"_c"</code></li> </ul> <p>If <code>suffix = ""</code> and <code>append = TRUE</code>, existing variables that have been recoded/transformed will be overwritten.</p>
<code>to.factor</code>	Logical, alias for <code>as.num</code> . If TRUE, return value will be a factor, not numeric.
<code>predicate</code>	A predicate function to be applied to the columns. The variables for which predicate returns TRUE are selected.

## Details

The `rec` string has following syntax:

**recode pairs** each recode pair has to be separated by a `;`, e.g. `rec = "1=1; 2=4; 3=2; 4=3"`

**multiple values** multiple old values that should be recoded into a new single value may be separated with comma, e.g. `"1,2=1; 3,4=2"`

**value range** a value range is indicated by a colon, e.g. `"1:4=1; 5:8=2"` (recodes all values from 1 to 4 into 1, and from 5 to 8 into 2)

**value range for doubles** for double vectors (with fractional part), all values within the specified range are recoded; e.g. `1:2.5=1; 2.6:3=2` recodes 1 to 2.5 into 1 and 2.6 to 3 into 2, but 2.55 would not be recoded (since it's not included in any of the specified ranges)

**"min" and "max"** minimum and maximum values are indicated by *min* (or *lo*) and *max* (or *hi*), e.g. `"min:4=1; 5:max=2"` (recodes all values from minimum values of `x` to 4 into 1, and from 5 to maximum values of `x` into 2)

**"else"** all other values, which have not been specified yet, are indicated by *else*, e.g. `"3=1; 1=2; else=3"` (recodes 3 into 1, 1 into 2 and all other values into 3)

"copy" the "else"-token can be combined with *copy*, indicating that all remaining, not yet recoded values should stay the same (are copied from the original value), e.g. "3=1; 1=2; else=copy" (recodes 3 into 1, 1 into 2 and all other values like 2, 4 or 5 etc. will not be recoded, but copied, see 'Examples')

NA's NA values are allowed both as old and new value, e.g. "NA=1; 3:5=NA" (recodes all NA into 1, and all values from 3 to 5 into NA in the new variable)

"rev" "rev" is a special token that reverses the value order (see 'Examples')

**direct value labelling** value labels for new values can be assigned inside the recode pattern by writing the value label in square brackets after defining the new value in a recode pair, e.g. "15:30=1 [young aged]; 31:55=2 [middle aged]; 56:max=3 [old aged]". See 'Examples'.

## Value

x with recoded categories. If x is a data frame, for `append = TRUE`, x including the recoded variables as new columns is returned; if `append = FALSE`, only the recoded variables will be returned. If `append = TRUE` and `suffix = ""`, recoded variables will replace (overwrite) existing variables.

## Note

Please note following behaviours of the function:

- the "else"-token should always be the last argument in the rec-string.
- Non-matching values will be set to NA, unless captured by the "else"-token.
- Tagged NA values (see [tagged\\_na](#)) and their value labels will be preserved when copying NA values to the recoded vector with "else=copy".
- Variable label attributes (see, for instance, [get\\_label](#)) are preserved (unless changed via `var.label`-argument), however, value label attributes are removed (except for "rev", where present value labels will be automatically reversed as well). Use `val.labels`-argument to add labels for recoded values.
- If x is a data frame, all variables should have the same categories resp. value range (else, see second bullet, NAs are produced).

## See Also

[set\\_na](#) for setting NA values, [replace\\_na](#) to replace NA's with specific value, [recode\\_to](#) for re-shifting value ranges and [ref\\_lvl](#) to change the reference level of (numeric) factors.

## Examples

```
data(efc)
table(efc$e42dep, useNA = "always")

# replace NA with 5
table(rec(efc$e42dep, rec = "1=1;2=2;3=3;4=4;NA=5"), useNA = "always")

# recode 1 to 2 into 1 and 3 to 4 into 2
table(rec(efc$e42dep, rec = "1,2=1; 3,4=2"), useNA = "always")
```

```

# keep value labels. variable label is automatically preserved
library(dplyr)
efc %>%
  select(e42dep) %>%
  rec(rec = "1,2=1; 3,4=2",
      val.labels = c("low dependency", "high dependency")) %>%
  frq()

# works with mutate
efc %>%
  select(e42dep, e17age) %>%
  mutate(dependency_rev = rec(e42dep, rec = "rev")) %>%
  head()

# recode 1 to 3 into 1 and 4 into 2
table(rec(efc$e42dep, rec = "min:3=1; 4=2"), useNA = "always")

# recode 2 to 1 and all others into 2
table(rec(efc$e42dep, rec = "2=1; else=2"), useNA = "always")

# reverse value order
table(rec(efc$e42dep, rec = "rev"), useNA = "always")

# recode only selected values, copy remaining
table(efc$e15relat)
table(rec(efc$e15relat, rec = "1,2,4=1; else=copy"))

# recode variables with same category in a data frame
head(efc[, 6:9])
head(rec(efc[, 6:9], rec = "1=10;2=20;3=30;4=40"))

# recode multiple variables and set value labels via recode-syntax
dummy <- rec(
  efc, c160age, e17age,
  rec = "15:30=1 [young]; 31:55=2 [middle]; 56:max=3 [old]",
  append = FALSE
)
frq(dummy)

# recode variables with same value-range
lapply(
  rec(
    efc, c82cop1, c83cop2, c84cop3,
    rec = "1,2=1; NA=9; else=copy",
    append = FALSE
  ),
  table,
  useNA = "always"
)

# recode character vector
dummy <- c("M", "F", "F", "X")
rec(dummy, rec = "M=Male; F=Female; X=Refused")

```

```

# recode numeric to character
rec(efc$e42dep, rec = "1=first;2=2nd;3=third;else=hi") %>% head()

# recode non-numeric factors
data(iris)
table(rec(iris, Species, rec = "setosa=huhu; else=copy", append = FALSE))

# recode floating points
table(rec(
  iris, Sepal.Length, rec = "lo:5=1;5.01:6.5=2;6.501:max=3", append = FALSE
))

# preserve tagged NAs
if (require("haven")) {
  x <- labelled(c(1:3, tagged_na("a", "c", "z"), 4:1),
               c("Agreement" = 1, "Disagreement" = 4, "First" = tagged_na("c"),
                 "Refused" = tagged_na("a"), "Not home" = tagged_na("z")))
  # get current value labels
  x
  # recode 2 into 5; Values of tagged NAs are preserved
  rec(x, rec = "2=5;else=copy")
}

# use select-helpers from dplyr-package
out <- rec(
  efc, contains("cop"), c161sex:c175empl,
  rec = "0,1=0; else=1",
  append = FALSE
)
head(out)

# recode only variables that have a value range from 1-4
p <- function(x) min(x, na.rm = TRUE) > 0 && max(x, na.rm = TRUE) < 5
out <- rec_if(efc, predicate = p, rec = "1:3=1;4=2;else=copy")
head(out)

```

---

recode\_to

*Recode variable categories into new values*


---

### Description

Recodes (or "renumbers") the categories of variables into new category values, beginning with the lowest value specified by lowest. Useful when recoding dummy variables with 1/2 values to 0/1 values, or recoding scales from 1-4 to 0-3 etc. `recode_to_if()` is a scoped variant of `recode_to()`, where recoding will be applied only to those variables that match the logical condition of predicate.

**Usage**

```
recode_to(x, ..., lowest = 0, highest = -1, append = TRUE, suffix = "_r0")

recode_to_if(
  x,
  predicate,
  lowest = 0,
  highest = -1,
  append = TRUE,
  suffix = "_r0"
)
```

**Arguments**

<code>x</code>	A vector or data frame.
<code>...</code>	Optional, unquoted names of variables that should be selected for further processing. Required, if <code>x</code> is a data frame (and no vector) and only selected variables from <code>x</code> should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's select-helpers. See 'Examples' or <a href="#">package-vignette</a> .
<code>lowest</code>	Indicating the lowest category value for recoding. Default is 0, so the new variable starts with value 0.
<code>highest</code>	If specified and greater than <code>lowest</code> , all category values larger than <code>highest</code> will be set to NA. Default is -1, i.e. this argument is ignored and no NA's will be produced.
<code>append</code>	Logical, if TRUE (the default) and <code>x</code> is a data frame, <code>x</code> including the new variables as additional columns is returned; if FALSE, only the new variables are returned.
<code>suffix</code>	Indicates which suffix will be added to each dummy variable. Use "numeric" to number dummy variables, e.g. <code>x_1</code> , <code>x_2</code> , <code>x_3</code> etc. Use "label" to add value label, e.g. <code>x_low</code> , <code>x_mid</code> , <code>x_high</code> . May be abbreviated.
<code>predicate</code>	A predicate function to be applied to the columns. The variables for which predicate returns TRUE are selected.

**Value**

`x` with recoded category values, where `lowest` indicates the lowest value; If `x` is a data frame, for `append = TRUE`, `x` including the recoded variables as new columns is returned; if `append = FALSE`, only the recoded variables will be returned. If `append = TRUE` and `suffix = ""`, recoded variables will replace (overwrite) existing variables.

**Note**

Value and variable label attributes are preserved.

**See Also**

[rec](#) for general recoding of variables and [set\\_na](#) for setting NA values.





to	Maximum value that should be recoded.
width	Numeric, indicating the range of each group.
other	String token, indicating how to deal with all other values that have not been captured by the recode pattern. See 'Details' on the else-token in <a href="#">rec</a> .

**Value**

A list with two values:

pattern string pattern that can be used as rec argument for the [rec](#)-function.

labels the associated values labels that can be used with [set\\_labels](#).

**See Also**

[group\\_var](#) for recoding variables into smaller groups, and [group\\_labels](#) to create the associated value labels.

**Examples**

```
rp <- rec_pattern(1, 100)
rp

# sample data, inspect age of carers
data(efc)
table(efc$c160age, exclude = NULL)
table(rec(efc$c160age, rec = rp$pattern), exclude = NULL)

# recode carers age into groups of width 5
x <- rec(
  efc$c160age,
  rec = rp$pattern,
  val.labels = rp$labels
)
# watch result
frq(x)
```

---

ref\_lvl

---

*Change reference level of (numeric) factors*


---

**Description**

Changes the reference level of (numeric) factor.

**Usage**

```
ref_lvl(x, ..., lvl = NULL)
```

**Arguments**

x	A vector or data frame.
...	Optional, unquoted names of variables that should be selected for further processing. Required, if x is a data frame (and no vector) and only selected variables from x should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's select-helpers. See 'Examples' or <a href="#">package-vignette</a> .
lvl	Either numeric, indicating the new reference level, or a string, indicating the value label from the new reference level. If x is a factor with non-numeric factor levels, <code>relevel(x, ref = lvl)</code> is returned. See 'Examples'.

**Details**

Unlike [relevel](#), this function behaves differently for factor with numeric factor levels or for labelled data, i.e. factors with value labels for the values. `ref_lvl()` changes the reference level by recoding the factor's values using the [rec](#) function. Hence, all values from lowest up to the reference level indicated by `lvl` are recoded, with `lvl` starting as lowest factor value. For factors with non-numeric factor levels, the function simply returns `relevel(x, ref = lvl)`. See 'Examples'.

**Value**

x with new reference level. If x is a data frame, the complete data frame x will be returned, where variables specified in ... will be re-leveled; if ... is not specified, applies to all variables in the data frame.

**See Also**

[to\\_factor](#) to convert numeric vectors into factors; [rec](#) to recode variables.

**Examples**

```
data(efc)
x <- to_factor(efc$e42dep)
str(x)
frq(x)

# see column "val" in frq()-output, which indicates
# how values/labels were recoded after using ref_lvl()
x <- ref_lvl(x, lvl = 3)
str(x)
frq(x)

library(dplyr)
dat <- efc %>%
  select(c82cop1, c83cop2, c84cop3) %>%
  to_factor()

frq(dat)
ref_lvl(dat, c82cop1, c83cop2, lvl = 2) %>% frq()

# compare numeric and string value for "lvl"-argument
```

```
x <- to_factor(efc$e42dep)
frq(x)
ref_lvl(x, lvl = 2) %>% frq()
ref_lvl(x, lvl = "slightly dependent") %>% frq()

# factors with non-numeric factor levels
data(iris)
levels(iris$Species)
levels(ref_lvl(iris$Species, lvl = 3))
levels(ref_lvl(iris$Species, lvl = "versicolor"))
```

---

remove_var	<i>Remove variables from a data frame</i>
------------	---

---

## Description

This function removes variables from a data frame, and is intended to use within a pipe-workflow. `remove_cols()` is an alias for `remove_var()`.

## Usage

```
remove_var(x, ...)

remove_cols(x, ...)
```

## Arguments

<code>x</code>	A vector or data frame.
<code>...</code>	Character vector with variable names, or unquoted names of variables that should be removed from the data frame. You may also use functions like <code>:</code> or <code>tidyselect</code> 's select-helpers.

## Value

`x`, with variables specified in `...` removed.

## Examples

```
mtcars %>% remove_var("disp", "cyl")
mtcars %>% remove_var(c("wt", "vs"))
mtcars %>% remove_var(drat:am)
```

---

replace_na	<i>Replace NA with specific values</i>
------------	--

---

### Description

This function replaces (tagged) NA's of a variable, data frame or list of variables with value.

### Usage

```
replace_na(x, ..., value, na.label = NULL, tagged.na = NULL)
```

### Arguments

x	A vector or data frame.
...	Optional, unquoted names of variables that should be selected for further processing. Required, if x is a data frame (and no vector) and only selected variables from x should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's <code>select</code> -helpers. See 'Examples' or <a href="#">package-vignette</a> .
value	Value that will replace the NA's.
na.label	Optional character vector, used to label the the former NA-value (i.e. adding a <code>labels</code> attribute for value to x).
tagged.na	Optional single character, specifies a <a href="#">tagged_na</a> value that will be replaced by value. Herewith it is possible to replace only specific NA values of x.

### Details

While regular NA values can only be *completely* replaced with a single value, [tagged\\_na](#) allows to differentiate between different qualitative values of NAs. Tagged NAs work exactly like regular R missing values except that they store one additional byte of information: a tag, which is usually a letter ("a" to "z") or character number ("0" to "9"). Therewith it is possible to replace only specific NA values, while other NA values are preserved.

### Value

x, where NA's are replaced with value. If x is a data frame, the complete data frame x will be returned, with replaced NA's for variables specified in `...`; if `...` is not specified, applies to all variables in the data frame.

### Note

Value and variable label attributes are preserved.

### See Also

[set\\_na](#) for setting NA values, [rec](#) for general recoding of variables and [recode\\_to](#) for re-shifting value ranges.

**Examples**

```

library(sjlabelled)
data(efc)
table(efc$e42dep, useNA = "always")
table(replace_na(efc$e42dep, value = 99), useNA = "always")

# the original labels
get_labels(replace_na(efc$e42dep, value = 99))
# NA becomes "99", and is labelled as "former NA"
get_labels(
  replace_na(efc$e42dep, value = 99, na.label = "former NA"),
  values = "p"
)

dummy <- data.frame(
  v1 = efc$c82cop1,
  v2 = efc$c83cop2,
  v3 = efc$c84cop3
)
# show original distribution
lapply(dummy, table, useNA = "always")
# show variables, NA's replaced with 99
lapply(replace_na(dummy, v2, v3, value = 99), table, useNA = "always")

if (require("haven")) {
  x <- labelled(c(1:3, tagged_na("a", "c", "z"), 4:1),
               c("Agreement" = 1, "Disagreement" = 4, "First" = tagged_na("c"),
                 "Refused" = tagged_na("a"), "Not home" = tagged_na("z")))
  # get current NA values
  x
  get_na(x)

  # replace only the NA, which is tagged as NA(c)
  replace_na(x, value = 2, tagged.na = "c")
  get_na(replace_na(x, value = 2, tagged.na = "c"))

  table(x)
  table(replace_na(x, value = 2, tagged.na = "c"))

  # tagged NA also works for non-labelled class
  # init vector
  x <- c(1, 2, 3, 4)
  # set values 2 and 3 as tagged NA
  x <- set_na(x, na = c(2, 3), as.tag = TRUE)
  # see result
  x
  # now replace only NA tagged with 2 with value 5
  replace_na(x, value = 5, tagged.na = "2")
}

```

---

reshape_longer	<i>Reshape data into long format</i>
----------------	--------------------------------------

---

### Description

reshape\_longer() reshapes one or more columns from wide into long format.

### Usage

```
reshape_longer(  
  x,  
  columns = colnames(x),  
  names.to = "key",  
  values.to = "value",  
  labels = NULL,  
  numeric.timevar = FALSE,  
  id = ".id"  
)
```

### Arguments

x	A data frame.
columns	Names of variables (as character vector), or column index of variables, that should be reshaped. If multiple column groups should be reshaped, use a list of vectors (see 'Examples').
names.to	Character vector with name(s) of key column(s) to create in output. Either one name per column group that should be gathered, or a single string. In the latter case, this name will be used as key column, and only one key column is created.
values.to	Character vector with names of value columns (variable names) to create in output. Must be of same length as number of column groups that should be gathered. See 'Examples'.
labels	Character vector of same length as values.to with variable labels for the new variables created from gathered columns. See 'Examples'.
numeric.timevar	Logical, if TRUE, the values of the names.to column will be recoded to numeric values, in sequential ascending order.
id	Name of ID-variable.

### Value

A reshaped data frame.

### See Also

[to\\_long](#)

**Examples**

```
# Reshape one column group into long format
mydat <- data.frame(
  age = c(20, 30, 40),
  sex = c("Female", "Male", "Male"),
  score_t1 = c(30, 35, 32),
  score_t2 = c(33, 34, 37),
  score_t3 = c(36, 35, 38)
)

reshape_longer(
  mydat,
  columns = c("score_t1", "score_t2", "score_t3"),
  names.to = "time",
  values.to = "score"
)

# Reshape multiple column groups into long format
mydat <- data.frame(
  age = c(20, 30, 40),
  sex = c("Female", "Male", "Male"),
  score_t1 = c(30, 35, 32),
  score_t2 = c(33, 34, 37),
  score_t3 = c(36, 35, 38),
  speed_t1 = c(2, 3, 1),
  speed_t2 = c(3, 4, 5),
  speed_t3 = c(1, 8, 6)
)

reshape_longer(
  mydat,
  columns = list(
    c("score_t1", "score_t2", "score_t3"),
    c("speed_t1", "speed_t2", "speed_t3")
  ),
  names.to = "time",
  values.to = c("score", "speed")
)

# or ...
reshape_longer(
  mydat,
  list(3:5, 6:8),
  names.to = "time",
  values.to = c("score", "speed")
)

# gather multiple columns, label columns
x <- reshape_longer(
  mydat,
  list(3:5, 6:8),
```

```

names.to = "time",
values.to = c("score", "speed"),
labels = c("Test Score", "Time needed to finish")
)

library(sjlabelled)
str(x$score)
get_label(x$speed)

```

---

rotate\_df

*Rotate a data frame*


---

## Description

This function rotates a data frame, i.e. columns become rows and vice versa.

## Usage

```
rotate_df(x, rn = NULL, cn = FALSE)
```

## Arguments

x	A data frame.
rn	Character vector (optional). If not NULL, the data frame's rownames will be added as (first) column to the output, with rn being the name of this column.
cn	Logical (optional), if TRUE, the values of the first column in x will be used as column names in the rotated data frame.

## Value

A (rotated) data frame.

## Examples

```

x <- mtcars[1:3, 1:4]
rotate_df(x)
rotate_df(x, rn = "property")

# use values in 1. column as column name
rotate_df(x, cn = TRUE)
rotate_df(x, rn = "property", cn = TRUE)

# also works on list-results
library(purrr)

dat <- mtcars[1:3, 1:4]
tmp <- purrr::map(dat, function(x) {
  sdev <- stats::sd(x, na.rm = TRUE)
  ulsdev <- mean(x, na.rm = TRUE) + c(-sdev, sdev)
})

```



```
names(ulsdev) <- c("lower_sd", "upper_sd")
ulsdev
})
tmp
as.data.frame(tmp)
rotate_df(tmp)

tmp <- purrr::map_df(dat, function(x) {
  sdev <- stats::sd(x, na.rm = TRUE)
  ulsdev <- mean(x, na.rm = TRUE) + c(-sdev, sdev)
  names(ulsdev) <- c("lower_sd", "upper_sd")
  ulsdev
})
tmp
rotate_df(tmp)
```

---

round\_num

*Round numeric variables in a data frame*

---

### Description

round\_num() rounds numeric variables in a data frame that also contains non-numeric variables. Non-numeric variables are ignored.

### Usage

```
round_num(x, digits = 0)
```

### Arguments

x                    A vector or data frame.  
digits                Numeric, number of decimals to round to.

### Value

x with all numeric variables rounded.

### Examples

```
data(iris)
round_num(iris)
```

---

row_count	<i>Count row or column indices</i>
-----------	------------------------------------

---

### Description

`row_count()` mimics base R's `rowSums()`, with sums for a specific value indicated by `count`. Hence, it is equivalent to `rowSums(x == count, na.rm = TRUE)`. However, this function is designed to work nicely within a pipe-workflow and allows select-helpers for selecting variables and the return value is always a data frame (with one variable).

`col_count()` does the same for columns. The return value is a data frame with one row (the column counts) and the same number of columns as `x`.

### Usage

```
row_count(x, ..., count, var = "rowcount", append = TRUE)
```

```
col_count(x, ..., count, var = "colcount", append = TRUE)
```

### Arguments

<code>x</code>	A vector or data frame.
<code>...</code>	Optional, unquoted names of variables that should be selected for further processing. Required, if <code>x</code> is a data frame (and no vector) and only selected variables from <code>x</code> should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's select-helpers. See 'Examples' or <a href="#">package-vignette</a> .
<code>count</code>	The value for which the row or column sum should be computed. May be a numeric value, a character string (for factors or character vectors), <code>NA</code> , <code>Inf</code> or <code>NULL</code> to count missing or infinite values, or null-values.
<code>var</code>	Name of new the variable with the row or column counts.
<code>append</code>	Logical, if <code>TRUE</code> (the default) and <code>x</code> is a data frame, <code>x</code> including the new variables as additional columns is returned; if <code>FALSE</code> , only the new variables are returned.

### Value

For `row_count()`, a data frame with one variable: the sum of `count` appearing in each row of `x`; for `col_count()`, a data frame with one row and the same number of variables as in `x`: each variable holds the sum of `count` appearing in each variable of `x`. If `append = TRUE`, `x` including this variable will be returned.

### Examples

```
dat <- data.frame(
  c1 = c(1, 2, 3, 1, 3, NA),
  c2 = c(3, 2, 1, 2, NA, 3),
  c3 = c(1, 1, 2, 1, 3, NA),
  c4 = c(1, 1, 3, 2, 1, 2)
```

```

)

row_count(dat, count = 1, append = FALSE)
row_count(dat, count = NA, append = FALSE)
row_count(dat, c1:c3, count = 2, append = TRUE)

col_count(dat, count = 1, append = FALSE)
col_count(dat, count = NA, append = FALSE)
col_count(dat, c1:c3, count = 2, append = TRUE)

```

---

row\_sums

*Row sums and means for data frames*


---

## Description

`row_sums()` and `row_means()` compute row sums or means for at least `n` valid values per row. The functions are designed to work nicely within a pipe-workflow and allow select-helpers for selecting variables.

## Usage

```

row_sums(x, ...)

## Default S3 method:
row_sums(x, ..., n, var = "rowsums", append = TRUE)

## S3 method for class 'mids'
row_sums(x, ..., var = "rowsums", append = TRUE)

row_means(x, ...)

total_mean(x, ...)

## Default S3 method:
row_means(x, ..., n, var = "rowmeans", append = TRUE)

## S3 method for class 'mids'
row_means(x, ..., var = "rowmeans", append = TRUE)

```

## Arguments

`x` A vector or data frame.

`...` Optional, unquoted names of variables that should be selected for further processing. Required, if `x` is a data frame (and no vector) and only selected variables from `x` should be processed. You may also use functions like `:` or `tidyselect`'s select-helpers. See 'Examples' or [package-vignette](#).

n	<p>May either be</p> <ul style="list-style-type: none"> <li>• a numeric value that indicates the amount of valid values per row to calculate the row mean or sum;</li> <li>• a value between 0 and 1, indicating a proportion of valid values per row to calculate the row mean or sum (see 'Details').</li> <li>• or Inf. If <math>n = \text{Inf}</math>, all values per row must be non-missing to compute row mean or sum.</li> </ul> <p>If a row's sum of valid (i.e. non-NA) values is less than <math>n</math>, NA will be returned as value for the row mean or sum.</p>
var	Name of new the variable with the row sums or means.
append	Logical, if TRUE (the default) and $x$ is a data frame, $x$ including the new variables as additional columns is returned; if FALSE, only the new variables are returned.

### Details

For  $n$ , must be a numeric value from 0 to  $\text{ncol}(x)$ . If a row in  $x$  has at least  $n$  non-missing values, the row mean or sum is returned. If  $n$  is a non-integer value from 0 to 1,  $n$  is considered to indicate the proportion of necessary non-missing values per row. E.g., if  $n = .75$ , a row must have at least  $\text{ncol}(x) * n$  non-missing values for the row mean or sum to be calculated. See 'Examples'.

### Value

For `row_sums()`, a data frame with a new variable: the row sums from  $x$ ; for `row_means()`, a data frame with a new variable: the row means from  $x$ . If `append = FALSE`, only the new variable with row sums resp. row means is returned. `total_mean()` returns the mean of all values from all specified columns in a data frame.

### Examples

```
data(efc)
efc %>% row_sums(c82cop1:c90cop9, n = 3, append = FALSE)

library(dplyr)
row_sums(efc, contains("cop"), n = 2, append = FALSE)

dat <- data.frame(
  c1 = c(1,2,NA,4),
  c2 = c(NA,2,NA,5),
  c3 = c(NA,4,NA,NA),
  c4 = c(2,3,7,8),
  c5 = c(1,7,5,3)
)
dat

row_means(dat, n = 4)
row_sums(dat, n = 4)

row_means(dat, c1:c4, n = 4)
# at least 40% non-missing
```

```
row_means(dat, c1:c4, n = .4)
row_sums(dat, c1:c4, n = .4)

# total mean of all values in the data frame
total_mean(dat)

# create sum-score of COPE-Index, and append to data
efc %>%
  select(c82cop1:c90cop9) %>%
  row_sums(n = 1)

# if data frame has only one column, this column is returned
row_sums(dat[, 1, drop = FALSE], n = 0)
```

---

seq\_col

*Sequence generation for column or row counts of data frames*

---

### Description

seq\_col(x) is a convenient wrapper for seq\_len(ncol(x)), while seq\_row(x) is a convenient wrapper for seq\_len(nrow(x)).

### Usage

```
seq_col(x)
```

```
seq_row(x)
```

### Arguments

x                    A data frame.

### Value

A numeric sequence from 1 to number of columns or rows.

### Examples

```
data(iris)
seq_col(iris)
seq_row(iris)
```

---

set_na_if	<i>Replace specific values in vector with NA</i>
-----------	--

---

### Description

set\_na\_if() is a scoped variant of [set\\_na](#), where values will be replaced only with NA's for those variables that match the logical condition of predicate.

### Usage

```
set_na_if(x, predicate, na, drop.levels = TRUE, as.tag = FALSE)
```

### Arguments

x	A vector or data frame.
predicate	A predicate function to be applied to the columns. The variables for which predicate returns TRUE are selected.
na	Numeric vector with values that should be replaced with NA values, or a character vector if values of factors or character vectors should be replaced. For labelled vectors, may also be the name of a value label. In this case, the associated values for the value labels in each vector will be replaced with NA. na can also be a named vector. If as.tag = FALSE, values will be replaced only in those variables that are indicated by the value names (see 'Examples').
drop.levels	Logical, if TRUE, factor levels of values that have been replaced with NA are dropped. See 'Examples'.
as.tag	Logical, if TRUE, values in x will be replaced by tagged_na, else by usual NA values. Use a named vector to assign the value label to the tagged NA value (see 'Examples').

### Value

x, with all values in na being replaced by NA. If x is a data frame, the complete data frame x will be returned, with NA's set for variables specified in ...; if ... is not specified, applies to all variables in the data frame.

### See Also

[replace\\_na](#) to replace NA's with specific values, [rec](#) for general recoding of variables and [recode\\_to](#) for re-shifting value ranges. See [get\\_na](#) to get values of missing values in labelled vectors.

### Examples

```
dummy <- data.frame(var1 = sample(1:8, 100, replace = TRUE),
                    var2 = sample(1:10, 100, replace = TRUE),
                    var3 = sample(1:6, 100, replace = TRUE))
```

```
p <- function(x) max(x, na.rm = TRUE) > 7
```

```
tmp <- set_na_if(dummy, predicate = p, na = 8:9)
head(tmp)
```

---

shorten_string	<i>Shorten character strings</i>
----------------	----------------------------------

---

## Description

This function shortens strings that are longer than `max.length` chars, without cropping words.

## Usage

```
shorten_string(s, max.length = NULL, abbr = "...")
```

## Arguments

<code>s</code>	A string.
<code>max.length</code>	Maximum length of chars for the string.
<code>abbr</code>	String that will be used as suffix, if <code>s</code> was shortened.

## Details

If the string length defined in `max.length` happens to be inside a word, this word is removed from the returned string (see 'Examples'), so the returned string has a *maximum length* of `max.length`, but might be shorter.

## Value

A shortened string.

## Examples

```
s <- "This can be considered as very long string!"

# string is shorter than max.length, so returned as is
shorten_string(s, 60)

# string is shortened to as many words that result in
# a string of maximum 20 chars
shorten_string(s, 20)

# string including "considered" is exactly of length 22 chars
shorten_string(s, 22)
```

---

split\_var

*Split numeric variables into smaller groups*


---

## Description

Recode numeric variables into equal sized groups, i.e. a variable is cut into a smaller number of groups at specific cut points. `split_var_if()` is a scoped variant of `split_var()`, where transformation will be applied only to those variables that match the logical condition of predicate.

## Usage

```
split_var(
  x,
  ...,
  n,
  as.num = FALSE,
  val.labels = NULL,
  var.label = NULL,
  inclusive = FALSE,
  append = TRUE,
  suffix = "_g"
)
```

```
split_var_if(
  x,
  predicate,
  n,
  as.num = FALSE,
  val.labels = NULL,
  var.label = NULL,
  inclusive = FALSE,
  append = TRUE,
  suffix = "_g"
)
```

## Arguments

x	A vector or data frame.
...	Optional, unquoted names of variables that should be selected for further processing. Required, if x is a data frame (and no vector) and only selected variables from x should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's select-helpers. See 'Examples' or <a href="#">package-vignette</a> .
n	The new number of groups that x should be split into.
as.num	Logical, if TRUE, return value will be numeric, not a factor.



val.labels	Optional character vector, to set value label attributes of recoded variable (see vignette <a href="#">Labelled Data and the sjlabelled-Package</a> ). If NULL (default), no value labels will be set. Value labels can also be directly defined in the rec-syntax, see 'Details'.
var.label	Optional string, to set variable label attribute for the returned variable (see vignette <a href="#">Labelled Data and the sjlabelled-Package</a> ). If NULL (default), variable label attribute of x will be used (if present). If empty, variable label attributes will be removed.
inclusive	Logical; if TRUE, cut point value are included in the preceding group. This may be necessary if cutting a vector into groups does not define proper ("equal sized") group sizes. See 'Note' and 'Examples'.
append	Logical, if TRUE (the default) and x is a data frame, x including the new variables as additional columns is returned; if FALSE, only the new variables are returned.
suffix	Indicates which suffix will be added to each dummy variable. Use "numeric" to number dummy variables, e.g. x_1, x_2, x_3 etc. Use "label" to add value label, e.g. x_low, x_mid, x_high. May be abbreviated.
predicate	A predicate function to be applied to the columns. The variables for which predicate returns TRUE are selected.

### Details

split\_var() splits a variable into equal sized groups, where the amount of groups depends on the n-argument. Thus, this functions [cuts](#) a variable into groups at the specified [quantiles](#).

By contrast, [group\\_var](#) recodes a variable into groups, where groups have the same value range (e.g., from 1-5, 6-10, 11-15 etc.).

split\_var() also works on grouped data frames (see [group\\_by](#)). In this case, splitting is applied to the subsets of variables in x. See 'Examples'.

### Value

A grouped variable with equal sized groups. If x is a data frame, for append = TRUE, x including the grouped variables as new columns is returned; if append = FALSE, only the grouped variables will be returned. If append = TRUE and suffix = "", recoded variables will replace (overwrite) existing variables.

### Note

In case a vector has only few number of unique values, splitting into equal sized groups may fail. In this case, use the inclusive-argument to shift a value at the cut point into the lower, preceding group to get equal sized groups. See 'Examples'.

### See Also

[group\\_var](#) to group variables into equal ranged groups, or [rec](#) to recode variables.

**Examples**

```

data(efc)
# non-grouped
table(efc$neg_c_7)

# split into 3 groups
table(split_var(efc$neg_c_7, n = 3))

# split multiple variables into 3 groups
split_var(efc, neg_c_7, pos_v_4, e17age, n = 3, append = FALSE)
frq(split_var(efc, neg_c_7, pos_v_4, e17age, n = 3, append = FALSE))

# original
table(efc$e42dep)

# two groups, non-inclusive cut-point
# vector split leads to unequal group sizes
table(split_var(efc$e42dep, n = 2))

# two groups, inclusive cut-point
# group sizes are equal
table(split_var(efc$e42dep, n = 2, inclusive = TRUE))

# Unlike dplyr's ntile(), split_var() never splits a value
# into two different categories, i.e. you always get a clean
# separation of original categories
library(dplyr)

x <- dplyr::ntile(efc$neg_c_7, n = 3)
table(efc$neg_c_7, x)

x <- split_var(efc$neg_c_7, n = 3)
table(efc$neg_c_7, x)

# works also with grouped data frames
mtcars %>%
  split_var(displ, n = 3, append = FALSE) %>%
  table()

mtcars %>%
  group_by(cyl) %>%
  split_var(displ, n = 3, append = FALSE) %>%
  table()

```

---

spread\_coef

*Spread model coefficients of list-variables into columns*


---

**Description**

This function extracts coefficients (and standard error and p-values) of fitted model objects from (nested) data frames, which are saved in a list-variable, and spreads the coefficients into new

columns.

## Usage

```
spread_coef(data, model.column, model.term, se, p.val, append = TRUE)
```

## Arguments

<code>data</code>	A (nested) data frame with a list-variable that contains fitted model objects (see 'Details').
<code>model.column</code>	Name or index of the list-variable that contains the fitted model objects.
<code>model.term</code>	Optional, name of a model term. If specified, only this model term (including p-value) will be extracted from each model and added as new column.
<code>se</code>	Logical, if TRUE, standard errors for estimates will also be extracted.
<code>p.val</code>	Logical, if TRUE, p-values for estimates will also be extracted.
<code>append</code>	Logical, if TRUE (default), this function returns data with new columns for the model coefficients; else, a new data frame with model coefficients only are returned.

## Details

This function requires a (nested) data frame (e.g. created by the `nest`-function of the **tidyr**-package), where several fitted models are saved in a list-variable (see 'Examples'). Since nested data frames with fitted models stored as list-variable are typically fit with an identical formula, all models have the same dependent and independent variables and only differ in their subsets of data. The function then extracts all coefficients from each model and saves each estimate in a new column. The result is a data frame, where each *row* is a model with each model's coefficients in an own *column*.

## Value

A data frame with columns for each coefficient of the models that are stored in the list-variable of data; or, if `model.term` is given, a data frame with the term's estimate. If `se = TRUE` or `p.val = TRUE`, the returned data frame also contains columns for the coefficients' standard error and p-value. If `append = TRUE`, the columns are appended to data, i.e. data is also returned.

## Examples

```
if (require("dplyr") && require("tidyr") && require("purrr")) {
  data(efc)

  # create nested data frame, grouped by dependency (e42dep)
  # and fit linear model for each group. These models are
  # stored in the list variable "models".
  model.data <- efc %>%
    filter(!is.na(e42dep)) %>%
    group_by(e42dep) %>%
    nest() %>%
    mutate(
```

```

    models = map(data, ~lm(neg_c_7 ~ c12hour + c172code, data = .x))
  )

# spread coefficients, so we can easily access and compare the
# coefficients over all models. arguments `se` and `p.val` default
# to `FALSE`, when `model.term` is not specified
spread_coef(model.data, models)
spread_coef(model.data, models, se = TRUE)

# select only specific model term. `se` and `p.val` default to `TRUE`
spread_coef(model.data, models, c12hour)

# spread_coef can be used directly within a pipe-chain
efc %>%
  filter(!is.na(e42dep)) %>%
  group_by(e42dep) %>%
  nest() %>%
  mutate(
    models = map(data, ~lm(neg_c_7 ~ c12hour + c172code, data = .x))
  ) %>%
  spread_coef(models)

# spread_coef() makes it easy to generate bootstrapped
# confidence intervals, using the 'bootstrap()' and 'boot_ci()'
# functions from the 'sjstats' package, which creates nested
# data frames of bootstrap replicates
if (require("sjstats")) {
  efc %>%
    # generate bootstrap replicates
    bootstrap(100) %>%
    # apply lm to all bootstrapped data sets
    mutate(
      models = map(strap, ~lm(neg_c_7 ~ e42dep + c161sex + c172code, data = .x))
    ) %>%
    # spread model coefficient for all 100 models
    spread_coef(models, se = FALSE, p.val = FALSE) %>%
    # compute the CI for all bootstrapped model coefficients
    boot_ci(e42dep, c161sex, c172code)
}
}

```

**Description**

`std()` computes a z-transformation (standardized and centered) on the input. `center()` centers the input. `std_if()` and `center_if()` are scoped variants of `std()` and `center()`, where transformation will be applied only to those variables that match the logical condition of predicate.

**Usage**

```
std(
  x,
  ...,
  robust = c("sd", "2sd", "gmd", "mad"),
  include.fac = FALSE,
  append = TRUE,
  suffix = "_z"
)
```

```
std_if(
  x,
  predicate,
  robust = c("sd", "2sd", "gmd", "mad"),
  include.fac = FALSE,
  append = TRUE,
  suffix = "_z"
)
```

```
center(x, ..., include.fac = FALSE, append = TRUE, suffix = "_c")
```

```
center_if(x, predicate, include.fac = FALSE, append = TRUE, suffix = "_c")
```

**Arguments**

<code>x</code>	A vector or data frame.
<code>...</code>	Optional, unquoted names of variables that should be selected for further processing. Required, if <code>x</code> is a data frame (and no vector) and only selected variables from <code>x</code> should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's <code>select</code> -helpers. See 'Examples' or <a href="#">package-vignette</a> .
<code>robust</code>	Character vector, indicating the method applied when standardizing variables with <code>std()</code> . By default, standardization is achieved by dividing the centered variables by their standard deviation ( <code>robust = "sd"</code> ). However, for skewed distributions, the median absolute deviation (MAD, <code>robust = "mad"</code> ) or Gini's mean difference ( <code>robust = "gmd"</code> ) might be more robust measures of dispersion. For the latter option, <b><code>sjstats</code></b> needs to be installed. <code>robust = "2sd"</code> divides the centered variables by two standard deviations, following a suggestion by <i>Gelman (2008)</i> , so the rescaled input is comparable to binary variables.
<code>include.fac</code>	Logical, if TRUE, factors will be converted to numeric vectors and also standardized or centered.
<code>append</code>	Logical, if TRUE (the default) and <code>x</code> is a data frame, <code>x</code> including the new variables as additional columns is returned; if FALSE, only the new variables are returned.
<code>suffix</code>	Indicates which suffix will be added to each dummy variable. Use "numeric" to number dummy variables, e.g. <code>x_1</code> , <code>x_2</code> , <code>x_3</code> etc. Use "label" to add value label, e.g. <code>x_low</code> , <code>x_mid</code> , <code>x_high</code> . May be abbreviated.
<code>predicate</code>	A predicate function to be applied to the columns. The variables for which predicate returns TRUE are selected.

## Details

`std()` and `center()` also work on grouped data frames (see [group\\_by](#)). In this case, standardization or centering is applied to the subsets of variables in `x`. See 'Examples'.

For more complicated models with many predictors, Gelman and Hill (2007) suggest leaving binary inputs as is and only standardize continuous predictors by dividing by two standard deviations. This ensures a rough comparability in the coefficients.

## Value

If `x` is a vector, returns a vector with standardized or centered variables. If `x` is a data frame, for `append = TRUE`, `x` including the transformed variables as new columns is returned; if `append = FALSE`, only the transformed variables will be returned. If `append = TRUE` and `suffix = ""`, recoded variables will replace (overwrite) existing variables.

## Note

`std()` and `center()` only return a vector, if `x` is a vector. If `x` is a data frame and only one variable is specified in the `...-ellipses` argument, both functions do return a data frame (see 'Examples').

## References

Gelman A (2008) Scaling regression inputs by dividing by two standard deviations. *Statistics in Medicine* 27: 2865-2873. <http://www.stat.columbia.edu/~gelman/research/published/standardizing7.pdf>

Gelman A, Hill J (2007) *Data Analysis Using Regression and Multilevel/Hierarchical Models*. Cambridge, Cambridge University Press: 55-57

## Examples

```
data(efc)
std(efc$c160age) %>% head()
std(efc, e17age, c160age, append = FALSE) %>% head()

center(efc$c160age) %>% head()
center(efc, e17age, c160age, append = FALSE) %>% head()

# NOTE!
std(efc$e17age) # returns a vector
std(efc, e17age) # returns a data frame

# with quasi-quotation
x <- "e17age"
center(efc, !!x, append = FALSE) %>% head()

# works with mutate()
library(dplyr)
efc %>%
  select(e17age, neg_c_7) %>%
```

```

mutate(age_std = std(e17age), burden = center(neg_c_7)) %>%
  head()

# works also with grouped data frames
mtcars %>% std(displ)

# compare new column "disp_z" w/ output above
mtcars %>%
  group_by(cyl) %>%
  std(displ)

data(iris)
# also standardize factors
std(iris, include.fac = TRUE, append = FALSE)
# don't standardize factors
std(iris, include.fac = FALSE, append = FALSE)

# standardize only variables with more than 10 unique values
p <- function(x) dplyr::n_distinct(x) > 10
std_if(efc, predicate = p, append = FALSE)

```

---

str\_contains

*Check if string contains pattern*


---

## Description

This functions checks whether a string or character vector `x` contains the string `pattern`. By default, this function is case sensitive.

## Usage

```
str_contains(x, pattern, ignore.case = FALSE, logic = NULL, switch = FALSE)
```

## Arguments

- |                          |   |
|--------------------------|---|
| <code>x</code>           | Character string where matches are sought. May also be a character vector of length > 1 (see 'Examples').   |
| <code>pattern</code>     | Character string to be matched in <code>x</code> . May also be a character vector of length > 1 (see 'Examples').   |
| <code>ignore.case</code> | Logical, whether matching should be case sensitive or not.  |
| <code>logic</code>       | Indicates whether a logical combination of multiple search pattern should be made. <ul style="list-style-type: none"> <li>Use "or", "OR" or " " for a logical or-combination, i.e. at least one element of <code>pattern</code> is in <code>x</code>.</li> <li>Use "and", "AND" or "&amp;" for a logical AND-combination, i.e. all elements of <code>pattern</code> are in <code>x</code>.</li> </ul> |

- Use "not", "NOT" or "!" for a logical NOT-combination, i.e. no element of pattern is in x.
  - By default, logic = NULL, which means that TRUE or FALSE is returned for each element of pattern separately.
- switch            Logical, if TRUE, x will be sought in each element of pattern. If switch = TRUE, x needs to be of length 1.

### Details

This function iterates all elements in pattern and looks for each of these elements if it is found in *any* element of x, i.e. which elements of pattern are found in the vector x.

Technically, it iterates pattern and calls `grep(x, pattern[i], fixed = TRUE)` for each element of pattern. If `switch = TRUE`, it iterates pattern and calls `grep(pattern[i], x, fixed = TRUE)` for each element of pattern. Hence, in the latter case (if `switch = TRUE`), x must be of length 1.

### Value

TRUE if x contains pattern.

### Examples

```
str_contains("hello", "hel")
str_contains("hello", "hal")

str_contains("hello", "Hel")
str_contains("hello", "Hel", ignore.case = TRUE)

# which patterns are in "abc"?
str_contains("abc", c("a", "b", "e"))

# is pattern in any element of 'x'?
str_contains(c("def", "abc", "xyz"), "abc")
# is "abcde" in any element of 'x'?
str_contains(c("def", "abc", "xyz"), "abcde") # no...
# is "abc" in any of pattern?
str_contains("abc", c("defg", "abcde", "xyz12"), switch = TRUE)

str_contains(c("def", "abcde", "xyz"), c("abc", "123"))

# any pattern in "abc"?
str_contains("abc", c("a", "b", "e"), logic = "or")

# all patterns in "abc"?
str_contains("abc", c("a", "b", "e"), logic = "and")
str_contains("abc", c("a", "b"), logic = "and")

# no patterns in "abc"?
str_contains("abc", c("a", "b", "e"), logic = "not")
str_contains("abc", c("d", "e", "f"), logic = "not")
```



str\_find

*Find partial matching and close distance elements in strings***Description**

This function finds the element indices of partial matching or similar strings in a character vector. Can be used to find exact or slightly mistyped elements in a string vector.

**Usage**

```
str_find(string, pattern, precision = 2, partial = 0, verbose = FALSE)
```

**Arguments**

string	Character vector with string elements.
pattern	String that should be matched against the elements of string.
precision	Maximum distance ("precision") between two string elements, which is allowed to treat them as similar or equal. Smaller values mean less tolerance in matching.
partial	Activates similar matching (close distance strings) for parts (substrings) of the string. Following values are accepted: <ul style="list-style-type: none"> <li>• 0 for no partial distance matching</li> <li>• 1 for one-step matching, which means, only substrings of same length as pattern are extracted from string matching</li> <li>• 2 for two-step matching, which means, substrings of same length as pattern as well as strings with a slightly wider range are extracted from string matching</li> </ul>
	Default value is 0. See 'Details' for more information.
verbose	Logical; if TRUE, the progress bar is displayed when computing the distance matrix. Default in FALSE, hence the bar is hidden.

**Details****Computation Details**

Fuzzy string matching is based on regular expressions, in particular `grep(pattern = "(<pattern>){~<precision>}", x = string)`. This means, precision indicates the number of chars inside pattern that may differ in string to consider it as "matching". The higher precision is, the more tolerant is the search (i.e. yielding more possible matches). Furthermore, the higher the value for partial is, the more matches may be found.

**Partial Distance Matching**

For `partial = 1`, a substring of `length(pattern)` is extracted from string, starting at position 0 in string until the end of string is reached. Each substring is matched against pattern, and results with a maximum distance of precision are considered as "matching". If `partial = 2`, the range of the extracted substring is increased by 2, i.e. the extracted substring is two chars longer and so on.

**Value**

A numeric vector with index position of elements in string that partially match or are similar to pattern. Returns -1 if no match was found.

**Note**

This function does *not* return the position of a matching string *inside* another string, but the element's index of the string vector, where a (partial) match with pattern was found. Thus, searching for "abc" in a string "this is abc" will not return 9 (the start position of the substring), but 1 (the element index, which is always 1 if string only has one element).

**See Also**

[group\\_str](#)

**Examples**

```
string <- c("Hello", "Helo", "Hole", "Apple", "Ape", "New", "Old", "System", "Systemic")
str_find(string, "hel") # partial match
str_find(string, "stem") # partial match
str_find(string, "R") # no match
str_find(string, "saste") # similarity to "System"

# finds two indices, because partial matching now
# also applies to "Systemic"
str_find(string,
          "sytsme",
          partial = 1)

# finds partial matching of similarity
str_find("We are Sex Pistols!", "postils")
```

---

str\_start

*Find start and end index of pattern in string*

---

**Description**

str\_start() finds the beginning position of pattern in each element of x, while str\_end() finds the stopping position of pattern in each element of x.

**Usage**

```
str_start(x, pattern, ignore.case = TRUE, regex = FALSE)
```

```
str_end(x, pattern, ignore.case = TRUE, regex = FALSE)
```

**Arguments**

x	A character vector.
pattern	Character string to be matched in x. pattern might also be a regular-expression object, as returned by <code>stringr::regex()</code> . Alternatively, use <code>regex = TRUE</code> to treat pattern as a regular expression rather than a fixed string.
ignore.case	Logical, whether matching should be case sensitive or not. <code>ignore.case</code> is ignored when pattern is no regular expression or <code>regex = FALSE</code> .
regex	Logical, if TRUE, pattern is treated as a regular expression rather than a fixed string.

**Value**

A numeric vector with index of start/end position(s) of pattern found in x, or -1, if pattern was not found in x.

**Examples**

```
path <- "this/is/my/fileofinterest.csv"
str_start(path, "/")

path <- "this//is//my//fileofinterest.csv"
str_start(path, "//")
str_end(path, "//")

x <- c("my_friend_likes me", "your_friend likes_you")
str_start(x, "_")

# pattern "likes" starts at position 11 in first, and
# position 13 in second string
str_start(x, "likes")

# pattern "likes" ends at position 15 in first, and
# position 17 in second string
str_end(x, "likes")

x <- c("I like to move it, move it", "You like to move it")
str_start(x, "move")
str_end(x, "move")

x <- c("test1234testagain")
str_start(x, "\\d+4")
str_start(x, "\\d+4", regex = TRUE)
str_end(x, "\\d+4", regex = TRUE)
```

---

tidy_values	<i>Clean values of character vectors.</i>
-------------	---

---

### Description

This function "cleans" values of a character vector or levels of a factor by removing space and punctuation characters.

### Usage

```
tidy_values(x, ...)  
  
clean_values(x, ...)
```

### Arguments

x	A vector or data frame.
...	Optional, unquoted names of variables that should be selected for further processing. Required, if x is a data frame (and no vector) and only selected variables from x should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's select-helpers. See 'Examples' or <a href="#">package-vignette</a> .

### Value

x, with "cleaned" values or levels.

### Examples

```
f1 <- sprintf("Char %s", sample(LETTERS[1:5], size = 10, replace = TRUE))  
f2 <- as.factor(sprintf("F / %s", sample(letters[1:5], size = 10, replace = TRUE)))  
f3 <- sample(1:5, size = 10, replace = TRUE)  
  
x <- data.frame(f1, f2, f3, stringsAsFactors = FALSE)  
  
clean_values(f1)  
clean_values(f2)  
clean_values(x)
```

---

to_dummy	<i>Split (categorical) vectors into dummy variables</i>
----------	---

---

### Description

This function splits categorical or numeric vectors with more than two categories into 0/1-coded dummy variables.

**Usage**

```
to_dummy(x, ..., var.name = "name", suffix = c("numeric", "label"))
```

**Arguments**

x	A vector or data frame.
...	Optional, unquoted names of variables that should be selected for further processing. Required, if x is a data frame (and no vector) and only selected variables from x should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's select-helpers. See 'Examples' or <a href="#">package-vignette</a> .
var.name	Indicates how the new dummy variables are named. Use "name" to use the variable name or any other string that will be used as is. Only applies, if x is a vector. See 'Examples'.
suffix	Indicates which suffix will be added to each dummy variable. Use "numeric" to number dummy variables, e.g. <code>x_1</code> , <code>x_2</code> , <code>x_3</code> etc. Use "label" to add value label, e.g. <code>x_low</code> , <code>x_mid</code> , <code>x_high</code> . May be abbreviated.

**Value**

A data frame with dummy variables for each category of x. The dummy coded variables are of type `atomic`.

**Note**

NA values will be copied from x, so each dummy variable has the same amount of NA's at the same position as x.

**Examples**

```
data(efc)
head(to_dummy(efc$e42dep))

# add value label as suffix to new variable name
head(to_dummy(efc$e42dep, suffix = "label"))

# use "dummy" as new variable name
head(to_dummy(efc$e42dep, var.name = "dummy"))

# create multiple dummies, append to data frame
to_dummy(efc, c172code, e42dep)

# pipe-workflow
library(dplyr)
efc %>%
  select(e42dep, e16sex, c172code) %>%
  to_dummy()
```

---

to\_long *Convert wide data to long format*

---

### Description

This function converts wide data into long format. It allows to transform multiple key-value pairs to be transformed from wide to long format in one single step.

### Usage

```
to_long(data, keys, values, ..., labels = NULL, recode.key = FALSE)
```

### Arguments

data	A data.frame that should be transformed from wide to long format.
keys	Character vector with name(s) of key column(s) to create in output. Either one key value per column group that should be gathered, or a single string. In the latter case, this name will be used as key column, and only one key column is created. See 'Examples'.
values	Character vector with names of value columns (variable names) to create in output. Must be of same length as number of column groups that should be gathered. See 'Examples'.
...	Specification of columns that should be gathered. Must be one character vector with variable names per column group, or a numeric vector with column indices indicating those columns that should be gathered. See 'Examples'.
labels	Character vector of same length as values with variable labels for the new variables created from gathered columns. See 'Examples' and 'Details'.
recode.key	Logical, if TRUE, the values of the key column will be recoded to numeric values, in sequential ascending order.

### Details

This function reshapes data from wide to long format, however, you can gather multiple column groups at once. Value and variable labels for non-gathered variables are preserved. Attributes from gathered variables, such as information about the variable labels, are lost during reshaping. Hence, the new created variables from gathered columns don't have any variable label attributes. In such cases, use labels argument to set back variable label attributes.

### See Also

[reshape\\_longer](#)

**Examples**

```
# create sample
mydat <- data.frame(age = c(20, 30, 40),
                    sex = c("Female", "Male", "Male"),
                    score_t1 = c(30, 35, 32),
                    score_t2 = c(33, 34, 37),
                    score_t3 = c(36, 35, 38),
                    speed_t1 = c(2, 3, 1),
                    speed_t2 = c(3, 4, 5),
                    speed_t3 = c(1, 8, 6))

# gather multiple columns. both time and speed are gathered.
to_long(
  data = mydat,
  keys = "time",
  values = c("score", "speed"),
  c("score_t1", "score_t2", "score_t3"),
  c("speed_t1", "speed_t2", "speed_t3")
)

# alternative syntax, using "reshape_longer()"
reshape_longer(
  mydat,
  columns = list(
    c("score_t1", "score_t2", "score_t3"),
    c("speed_t1", "speed_t2", "speed_t3")
  ),
  names.to = "time",
  values.to = c("score", "speed")
)

# or ...
reshape_longer(
  mydat,
  list(3:5, 6:8),
  names.to = "time",
  values.to = c("score", "speed")
)

# gather multiple columns, use numeric key-value
to_long(
  data = mydat,
  keys = "time",
  values = c("score", "speed"),
  c("score_t1", "score_t2", "score_t3"),
  c("speed_t1", "speed_t2", "speed_t3"),
  recode.key = TRUE
)

# gather multiple columns by column names and column indices
to_long(
  data = mydat,
```

```

    keys = "time",
    values = c("score", "speed"),
    c("score_t1", "score_t2", "score_t3"),
    6:8,
    recode.key = TRUE
  )

# gather multiple columns, use separate key-columns
# for each value-vector
to_long(
  data = mydat,
  keys = c("time_score", "time_speed"),
  values = c("score", "speed"),
  c("score_t1", "score_t2", "score_t3"),
  c("speed_t1", "speed_t2", "speed_t3")
)

# gather multiple columns, label columns
mydat <- to_long(
  data = mydat,
  keys = "time",
  values = c("score", "speed"),
  c("score_t1", "score_t2", "score_t3"),
  c("speed_t1", "speed_t2", "speed_t3"),
  labels = c("Test Score", "Time needed to finish")
)

library(sjlabelled)
str(mydat$score)
get_label(mydat$speed)

```

---

to\_value

*Convert factors to numeric variables*


---

### Description

This function converts (replaces) factor levels with the related factor level index number, thus the factor is converted to a numeric variable. `to_value()` and `to_numeric()` are aliases.

### Usage

```
to_value(x, ..., start.at = NULL, keep.labels = TRUE, use.labels = FALSE)
```

### Arguments

`x` A vector or data frame.



...	Optional, unquoted names of variables that should be selected for further processing. Required, if <code>x</code> is a data frame (and no vector) and only selected variables from <code>x</code> should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's select-helpers. See 'Examples' or <a href="#">package-vignette</a> .
<code>start.at</code>	Starting index, i.e. the lowest numeric value of the variable's value range. By default, this argument is <code>NULL</code> , hence the lowest value of the returned numeric variable corresponds to the lowest factor level (if factor levels are numeric) or to 1 (if factor levels are not numeric).
<code>keep.labels</code>	Logical, if <code>TRUE</code> , former factor levels will be added as value labels. For numeric factor levels, values labels will be used, if present. See 'Examples' and <a href="#">set_labels</a> for more details.
<code>use.labels</code>	Logical, if <code>TRUE</code> and <code>x</code> has numeric value labels, these value labels will be set as numeric values.

### Value

A numeric variable with values ranging either from `start.at` to `start.at + length` of factor levels, or to the corresponding factor levels (if these were numeric). If `x` is a data frame, the complete data frame `x` will be returned, where variables specified in `...` are coerced to numeric; if `...` is not specified, applies to all variables in the data frame.

### Note

This function is kept for backwards-compatibility. It is preferred to use [as\\_numeric](#).

### Examples

```
library(sjlabelled)
data(efc)
test <- as_label(efc$e42dep)
table(test)
table(to_value(test))

# Find more examples at '?sjlabelled::as_numeric'
```

---

trim

*Trim leading and trailing whitespaces from strings*

---

### Description

Trims leading and trailing whitespaces from strings or character vectors.

### Usage

```
trim(x)
```

**Arguments**

`x` Character vector or string, or a list or data frame with such vectors. Function is vectorized, i.e. vector may have a length greater than 1. See 'Examples'.

**Value**

Trimmed `x`, i.e. with leading and trailing spaces removed.

**Examples**

```
trim("white space at end ")
trim(" white space at start and end ")
trim(c(" string1 ", " string2", "string 3 "))

tmp <- data.frame(a = c(" string1 ", " string2", "string 3 "),
                 b = c(" strong one ", " string two", " third string "),
                 c = c(" str1 ", " str2", "str3 "))

tmp
trim(tmp)
```

---

typical\_value

*Return the typical value of a vector*

---

**Description**

This function returns the "typical" value of a variable.

**Usage**

```
typical_value(x, fun = "mean", weights = NULL, ...)
```

**Arguments**

`x` A variable.

`fun` Character vector, naming the function to be applied to `x`. Currently, "mean", "weighted.mean", "median" and "mode" are supported, which call the corresponding R functions (except "mode", which calls an internal function to compute the most common value). "zero" simply returns 0. **Note:** By default, if `x` is a factor, only `fun = "mode"` is applicable; for all other functions (including the default, "mean") the reference level of `x` is returned. For character vectors, only the mode is returned. You can use a named vector to apply other different functions to integer, numeric and categorical `x`, where factors are first converted to numeric vectors, e.g. `fun = c(numeric = "median", factor = "mean")`. See 'Examples'.

`weights` Name of variable in `x` that indicated the vector of weights that will be applied to weight all observations. Default is `NULL`, so no weights are used.

`...` Further arguments, passed down to `fun`.

**Details**

By default, for numeric variables, `typical_value()` returns the mean value of `x` (unless changed with the `fun`-argument).

For factors, the reference level is returned or the most common value (if `fun = "mode"`), unless `fun` is a named vector. If `fun` is a named vector, specify the function for integer, numeric and categorical variables as element names, e.g. `fun = c(integer = "median", factor = "mean")`. In this case, factors are converted to numeric values (using `to_value`) and the related function is applied. You may abbreviate the names `fun = c(i = "median", f = "mean")`. See also 'Examples'.

For character vectors the most common value (mode) is returned.

**Value**

The "typical" value of `x`.

**Examples**

```
data(iris)
typical_value(iris$Sepal.Length)

library(purrr)
map(iris, ~ typical_value(.x))

# example from ?stats::weighted.mean
wt <- c(5, 5, 4, 1) / 15
x <- c(3.7, 3.3, 3.5, 2.8)

typical_value(x, fun = "weighted.mean")
typical_value(x, fun = "weighted.mean", weights = wt)

# for factors, return either reference level or mode value
set.seed(123)
x <- sample(iris$Species, size = 30, replace = TRUE)
typical_value(x)
typical_value(x, fun = "mode")

# for factors, use a named vector to apply other functions than "mode"
map(iris, ~ typical_value(.x, fun = c(n = "median", f = "mean")))
```

---

var\_rename

*Rename variables*


---

**Description**

This function renames variables in a data frame, i.e. it renames the columns of the data frame.

**Usage**

```
var_rename(x, ..., verbose = TRUE)

rename_variables(x, ..., verbose = TRUE)

rename_columns(x, ..., verbose = TRUE)
```

**Arguments**

x	A data frame.
...	A named vector, or pairs of named vectors, where the name (lhs) equals the column name that should be renamed, and the value (rhs) is the new column name.
verbose	Logical, if TRUE, a warning is displayed when variable names do not exist in x.

**Value**

x, with new column names for those variables specified in ...

**Examples**

```
dummy <- data.frame(
  a = sample(1:4, 10, replace = TRUE),
  b = sample(1:4, 10, replace = TRUE),
  c = sample(1:4, 10, replace = TRUE)
)

rename_variables(dummy, a = "first.col", c = "3rd.col")

# using quasi-quotation
library(rlang)
v1 <- "first.col"
v2 <- "3rd.col"
rename_variables(dummy, a = !!v1, c = !!v2)

x1 <- "a"
x2 <- "b"
rename_variables(dummy, !!x1 := !!v1, !!x2 := !!v2)

# using a named vector
new_names <- c(a = "first.col", c = "3rd.col")
rename_variables(dummy, new_names)
```

**Description**

This function returns the type of a variable as character. It is similar to `pillar::type_sum()`, however, the return value is not truncated, and `var_type()` works on data frames and within pipe-chains.

**Usage**

```
var_type(x, ..., abbr = FALSE)
```

**Arguments**

<code>x</code>	A vector or data frame.
<code>...</code>	Optional, unquoted names of variables that should be selected for further processing. Required, if <code>x</code> is a data frame (and no vector) and only selected variables from <code>x</code> should be processed. You may also use functions like <code>:</code> or <code>tidyselect</code> 's <code>select-helpers</code> . See 'Examples' or <a href="#">package-vignette</a> .
<code>abbr</code>	Logical, if TRUE, returns a shortened, abbreviated value for the variable type (as returned by <code>pillar::type_sum()</code> ). If FALSE (default), a longer "description" is returned.

**Value**

The variable type of `x`, as character.

**Examples**

```
data(efc)

var_type(1)
var_type(1L)
var_type("a")

var_type(efc$e42dep)
var_type(to_factor(efc$e42dep))

library(dplyr)
var_type(efc, contains("cop"))
```

---

word\_wrap

---

*Insert line breaks in long labels*


---

**Description**

Insert line breaks in long character strings. Useful if you want to wordwrap labels / titles for plots or tables.

**Usage**

```
word_wrap(labels, wrap, linesep = NULL)
```

**Arguments**

**labels** Label(s) as character string, where a line break should be inserted. Several strings may be passed as vector (see 'Examples').

**wrap** Maximum amount of chars per line (i.e. line length). If `wrap = Inf` or `wrap = 0`, no word wrap will be performed (i.e. labels will be returned as is).

**linesep** By default, this argument is `NULL` and a regular new line string ("`\n`") is used. For HTML-purposes, for instance, `linesep` could be "`<br>`".

**Value**

New label(s) with line breaks inserted at every `wrap`'s position.

**Examples**

```
word_wrap(c("A very long string", "And another even longer string!"), 10)
message(word_wrap("Much too long string for just one line!", 15))
```

---

zap_inf	<i>Convert infite or NaN values into regular NA</i>
---------	---

---

**Description**

Replaces all infinite (`Inf` and `-Inf`) or `NaN` values with regular `NA`.

**Usage**

```
zap_inf(x, ...)
```

**Arguments**

**x** A vector or a data frame.

**...** Optional, unquoted names of variables that should be selected for further processing. Required, if `x` is a data frame (and no vector) and only selected variables from `x` should be processed. You may also use functions like `:` or `tidyselect`'s select-helpers. See 'Examples' or [package-vignette](#).

**Value**

`x`, where all `Inf`, `-Inf` and `NaN` are converted to `NA`.

## Examples

```
x <- c(1, 2, NA, 3, NaN, 4, NA, 5, Inf, -Inf, 6, 7)
zap_inf(x)

data(efc)
# produce some NA and NaN values
efc$e42dep[1] <- NaN
efc$e42dep[2] <- NA
efc$c12hour[1] <- NaN
efc$c12hour[2] <- NA
efc$e17age[2] <- NaN
efc$e17age[1] <- NA

# only zap NaN for c12hour
zap_inf(efc$c12hour)

# only zap NaN for c12hour and e17age, not for e42dep,
# but return complete data framee
zap_inf(efc, c12hour, e17age)

# zap NaN for complete data frame
zap_inf(efc)
```

---

%nin%

*Value matching*

---

## Description

`%nin%` is the complement to `%in%`. It looks which values in `x` do *not* match (hence, are *not in*) values in `y`.

## Usage

```
x %nin% y
```

## Arguments

`x`                    Vector with values to be matched.  
`y`                    Vector with values to be matched against.

## Details

See 'Details' in [match](#).

## Value

A logical vector, indicating if a match was *not* located for each element of `x`, thus the values are TRUE or FALSE and never NA.

**Examples**

```
c("a", "B", "c") %in% letters  
c("a", "B", "c") %nin% letters
```

```
c(1, 2, 3, 4) %in% c(3, 4, 5, 6)  
c(1, 2, 3, 4) %nin% c(3, 4, 5, 6)
```



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