Package ‘sjmisc’

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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.

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add_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 add_columns(), will be bound after data frames specified in .... For replace_columns(), duplicated columns in data will be replaced by columns in ....

...           More data frames to combine, resp. more data frames with columns that should replace columns in data.

replace       Logical, if TRUE (default), columns in ... 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 ... 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**

```r
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

```r
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)
```

add_variables

Add variables or cases to data frames

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

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

**Description**

Check if all values in a vector are NA.

**Usage**

```r
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**

```r
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**  
*Format numbers*

**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**

```r
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 prettyNum-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 \texttt{select_helpers}. See 'Examples' or package-vignette.

Value

A data frame with counted tagged NA values.

Examples

```r
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$x)
  count_na(dat$y)
  count_na(dat, x, y)
}
```

descr  Basic descriptive statistics

descr

Basic descriptive statistics

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

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 : or tidyselect’s select_helpers. See 'Examples' or package-vignette.
max.length Numeric, indicating the maximum length of variable labels in the output. If variable names are longer than max.length, they will be shortened to the last whole word within the first max.length chars.
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.
show Character vector, indicating which information (columns) that describe the data should be returned. May be one or more of "type", "label", "n", "NA.prc", "mean", "sd", "se", "md", "trimmed", "range", "iqr", "skew". There are two shortcuts: show = "all" (default) shows all information, show = "short" just shows n, missing percentage, mean and standard deviation.
out Character vector, indicating whether the results should be printed to console (out = "txt") or as HTML-table in the viewer-pane (out = "viewer") or browser (out = "browser").
encoding Character vector, indicating the charset encoding used for variable and value labels. Default is "UTF-8". Only used when out is not "txt".
file Destination file, if the output should be saved as file. Only used when out is not "txt".

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-meaned and de-meaned variables of \( x \). By default, de-meaned variables will be suffixed with "\_dm" and grouped-meaned variables with "\_gm".

Details

d\_mean() is intended to create group- and de-meaned 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-meaned and de-meaned 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-meaned variables as new columns is returned; if append = FALSE, only the group-/de-meaned variables will be returned.

References


Examples

data(efc)

\begin{verbatim}
/ecf$ID <- sample(1:4, nrow(efc), replace = TRUE) # fake-ID
de\_mean(ecf, c12hour, barthtot, grp = ID, append = FALSE)
\end{verbatim}

---

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

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.

dich.by Indicates the split criterion where a variable is dichotomized. Must be one of the following values (may be abbreviated):

"median" or "md" by default, x is split into two groups at the median.
"mean" or "m" splits x into two groups at the mean of x.

numeric value splits x into two groups at the specific value. Note that the value is inclusive, i.e. dich.by = 10 will split x into one group with values from lowest to 10 and another group with values greater than 10.

as.num Logical, if TRUE, return value will be numeric, not a factor.

var.label Optional string, to set variable label attribute for the returned variable (see vignette Labelled Data and the sjlabelled-Package). If NULL (default), variable label attribute of x will be used (if present). If empty, variable label attributes will be removed.

val.labels Optional character vector (of length two), to set value label attributes of dichotomized variable (see set_labels). 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 String value, will be appended to variable (column) names of x, if x is a data frame. If x 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:

- recoded variables (rec()) will be suffixed with "_r"
- recoded variables (recode_to()) will be suffixed with "_r0"
- dichotomized variables (dicho()) will be suffixed with "_d"
- grouped variables (split_var()) will be suffixed with "_g"
- grouped variables (group_var()) will be suffixed with "_gr"
- standardized variables (std()) will be suffixed with "_z"
- centered variables (center()) will be suffixed with "_c"
- de-meaned variables (de_mean()) will be suffixed with "_dm"
- group-meaned variables (de_mean()) will be suffixed with "_gm"

If suffix = "" and append = TRUE, existing variables that have been recoded/transformed will be overwritten.

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

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

# dichtomize 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 %>%
  dicho(disp, append = FALSE) %>%
  table()

mtcars %>%
  group_by(cyl) %>%
  dicho(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
dicho_if(efc, predicate = p, append = FALSE)

---

**efc**

Sample dataset from the EUROFAMCARE project

---

**Description**

A SPSS sample data set, imported with the `read_spss` function.
Examples

```r
# Attach EFC-data
data(efc)

# Show structure
str(efc)

# show first rows
head(efc)
```

<table>
<thead>
<tr>
<th>empty_cols</th>
<th>Return or remove variables or observations that are completely missing</th>
</tr>
</thead>
</table>

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

```r
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

```r
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))
```
find_var

```r
tmp
drop_empty_cols(tmp)
drop_empty_rows(tmp)
```

---

**find_var**  
*Find variable by name or label*

**Description**

This function 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**

```r
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
)
```

```r
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
find_var

label attributes of data (see get_label). pattern might also be a regular-expression object, as returned by stringr::regex(). Alternatively, use regex = TRUE to treat pattern as a regular expression rather than a fixed string.

ignore.case Logical, whether matching should be case sensitive or not. ignore.case is ignored when pattern is no regular expression or regex = FALSE.

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**

```r
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 `margin = "cell"`, `margin = "col"` or `margin = "row"` to print cell, column or row percentages of the table margins.
digits
show.values
weights

Array
Numeric; for proportional tables, digits indicates the number of decimal places.

Logical, if TRUE, value labels are prefixed by the associated value.

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.

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
```r
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 `%>%` or tidyselect’s `select_helpers`. See 'Examples' or package-vignette.
- **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 `group_var`). Default value for `auto.group` 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 show.na = "auto", 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 group_str and str_find for details on grouping, and their precision-argument to get more details on the distance of strings to be treated as equal.

min.frq Numeric, indicating the minimum frequency for which a value will be shown in the output (except for the missing values, prevailing show.na). Default value for min.frq is 0, so all value frequencies are shown. All values or categories that have less than min.frq occurrences in the data will be summarized in a "n < 100" category.

out Character vector, indicating whether the results should be printed to console (out = "txt") or as HTML-table in the viewer-pane (out = "viewer") or browser (out = "browser").

title String, will be used as alternative title to the variable label. If x is a grouped data frame, title must be a vector of same length as groups.

encoding Character vector, indicating the charset encoding used for variable and value labels. Default is "UTF-8". Only used when out is not "txt".

file Destination file, if the output should be saved as file. Only used when out 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.

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(
  "New", "Old", "System", "Systemic"),
  size = nrow(dummy),
  replace = TRUE,
  )
#### 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**

```r
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

```r
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)
```
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

```r
# Example usage to recode numeric variable
x <- c(1, 2, 3, 4, 5)
result <- group_var(x, size = 2)
```

```r
# Example use of scoped group_var_if
x <- c(1, 2, 3, 4, 5)
predicate <- x > 3
result <- group_var_if(x, predicate, size = 2)
```

```r
# Related value labels
result_labels <- group_labels(x, size = 2)
```

```r
# Related value labels with scoped version
result_labels_if <- group_labels_if(x, predicate, size = 2)
```

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`. 
group_var

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. size = 5. Use size = "auto" to automatically resize a variable into a maximum of 30 groups (which is the ggplot-default grouping when plotting histograms). Use n 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 (size = "auto"). Default is 30. If size 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      String value, will be appended to variable (column) names of x, if x is a data frame. If x 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:

  • recoded variables (rec()) will be suffixed with "_r"
  • recoded variables (recode_to()) will be suffixed with "_r0"
  • dichotomized variables (dicho()) will be suffixed with "_d"
  • grouped variables (split_var()) will be suffixed with "_g"
  • grouped variables (group_var()) will be suffixed with "_gr"
  • standardized variables (std()) will be suffixed with "_z"
  • centered variables (center()) will be suffixed with "_c"
  • de-meaned variables (de_mean()) will be suffixed with "_dm"
  • grouped-meaned variables (de_mean()) will be suffixed with "_gm"

If suffix = "" and append = TRUE, existing variables that have been recoded/transformed will be overwritten.

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**

```r
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 starting at upper bound
group_labels(dummy, right.interval = TRUE)

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

mtcars %>%
  group_by(cyl) %>%
  group_var(disp, size = 4, append = FALSE) %>%
  table()

---

**has_na**

*Check if variables or cases have missing / infinite values*

**Description**

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

**Usage**

```r
has_na(x, ..., by = c("col", "row"), out = c("table", "df", "index"))
```

```r
incomplete_cases(x, ...)
```

```r
complete_cases(x, ...)
```

```r
complete_vars(x, ...)
```

```r
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 `:` or tidyselect's `select_helpers`. See 'Examples' or package-vignette.

- `by`  
  Whether to check column- or row-wise for missing and infinite values. If `by = "col"`, `has_na()` checks for `NA/NaN/Inf` in columns; If `by = "row"`, `has_na()` 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

\texttt{complete\_cases()} and \texttt{incomplete\_cases()} are convenient shortcuts for \texttt{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.

\texttt{complete\_vars()} and \texttt{incomplete\_vars()} are convenient shortcuts for \texttt{has\_na(by = \"col\", out = \"index\")}, and again only return those column-id's for variables which are (in-)complete.

Examples

```r
data(efc)
has_na(efc$e42dep)
has_na(efc, e42dep, tot_sc_e, c161sex)
has_na(efc, c161sex)
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 (\texttt{is\_crossed()}) resp. if each category of the first factor co-occurs with only one category of the other (\texttt{is\_nested()}). \texttt{is\_cross\_classified()} checks if one factor level occurs in some, but not all levels of another factor.
is_crossed

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(1,4,3,2,3,1,4)
y <- c(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(1,1,2,1,1,2,2)
# 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(1,1,2,2,3,3,3)
# show distribution
is_empty

Check whether string, list or vector is empty

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.
is_even

Examples

```r
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**

```r
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

```r
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**

```r
is_num_fac(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**

```r
# 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)
```

```r
# not completely numeric factor levels
```
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

- **dat**
  The data frame that was imputed and used as argument in the `mice`-function call.

- **imp**
  The `mice::mids()`-object with the imputed data frames from `dat`.

- **ori**
  Optional, if `ori` is specified, the imputed variables are appended to this data frame; else, a new data frame with the imputed variables is returned.

- **summary**
  After merging multiple imputed data, `summary` displays a graphical summary of the "quality" of the merged values, compared to the original imputed values.

  - "dens" 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.

  - "hist" Similar to `summary = "dens"`, however, mean and merged values are shown as histogram. Bins should have almost equal height for both groups (mean and merged).

  - "sd" 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.

- **filter**
  A character vector with variable names that should be plotted. All non-defined variables will not be shown in the plot.
merge_imputations

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() than 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 was 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


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

data A data frame.

... Unquoted names or character vector with names of variables that should be
 moved to another position. You may also use functions like : or tidyselect’s
 select_helpers.

.before Optional, column name or numeric index of the position where col should be
 moved to. If not missing, col is moved to the position before the column indi-
cated by .before.

.after Optional, column name or numeric index of the position where col should be
 moved to. If not missing, col is moved to the position after the column indicated
 by .after.

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.

Examples

## Not run:
data(iris)

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

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

iris %>
move_columns(Species, .before = 1) %>>%
```r
library(dplyr)
iris %>%
  move_columns("Species", "Petal.Length", .after = 1) %>%
  head()
```

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

```r
## End(Not run)
```

---

### 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**

```r
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**

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

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

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

### 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`.

- **`rec`**  
  
  String with recode pairs of old and new values. See 'Details' for examples. `rec_pattern` is a convenient function to create recode strings for grouping variables.

- **`as.num`**  
  
  Logical, if TRUE, return value will be numeric, not a factor.
Optional string, to set variable label attribute for the returned variable (see vignette Labelled Data and the sjlabelled-Package). If NULL (default), variable label attribute of x will be used (if present). If empty, variable label attributes will be removed.

Optional character vector, to set value label attributes of recoded variable (see vignette Labelled Data and the sjlabelled-Package). If NULL (default), no value labels will be set. Value labels can also be directly defined in the rec-syntax, see 'Details'.

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.

String value, will be appended to variable (column) names of x, if x is a data frame. If x 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:

- recoded variables (rec()) will be suffixed with "_r"
- recoded variables (recode_to()) will be suffixed with "_r0"
- dichotomized variables (dicho()) will be suffixed with "_d"
- grouped variables (split_var()) will be suffixed with "_g"
- grouped variables (group_var()) will be suffixed with "_gr"
- standardized variables (sd()) will be suffixed with "_z"
- centered variables (center()) will be suffixed with "_c"
- de-meaned variables (de_mean()) will be suffixed with "_dm"
- grouped-meaned variables (de_mean()) will be suffixed with "_gm"

If suffix = "" and append = TRUE, existing variables that have been recoded/transformed will be overwritten.

A predicate function to be applied to the columns. The variables for which predicate returns TRUE are selected.

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:max=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 indicates 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")
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

- **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.
- **lowest**: Indicating the lowest category value for recoding. Default is 0, so the new variable starts with value 0.
- **highest**: If specified and greater than lowest, all category values larger than highest will be set to NA. Default is -1, i.e. this argument is ignored and no NA's will be produced.
- **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**: String value, will be appended to variable (column) names of x, if x is a data frame. If x 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:
  - recoded variables (rec()) will be suffixed with "_r"
  - recoded variables (recode_to()) will be suffixed with "_r0"
  - dichotomized variables (dicho()) will be suffixed with "_d"
  - grouped variables (split_var()) will be suffixed with "_g"
  - grouped variables (group_var()) will be suffixed with "_gr"
  - standardized variables (std()) will be suffixed with "_z"
  - centered variables (center()) will be suffixed with "_c"
  - de-meaned variables (de_mean()) will be suffixed with "_dm"
  - grouped-meaned variables (de_mean()) will be suffixed with "_gm"

  If suffix = "" and append = TRUE, existing variables that have been recoded/transformed will be overwritten.

- **predicate**: A predicate function to be applied to the columns. The variables for which predicate returns TRUE are selected.
recode_to

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.

Examples

# recode 1-4 to 0-3
dummy <- sample(1:4, 10, replace = TRUE)
recode_to(dummy)

# recode 3-6 to 0-3
# note that numeric type is returned
dummy <- as.factor(3:6)
recode_to(dummy)

# lowest value starting with 1
dummy <- sample(11:15, 10, replace = TRUE)
recode_to(dummy, lowest = 1)

# lowest value starting with 1, highest with 3
# all others set to NA
dummy <- sample(11:15, 10, replace = TRUE)
recode_to(dummy, lowest = 1, highest = 3)

# recode multiple variables at once
data(efc)
recode_to(efc, c82cop1, c83cop2, c84cop3, append = FALSE)

library(dplyr)

efc %>%
  select(c82cop1, c83cop2, c84cop3) %>%
  mutate(
    c82new = recode_to(c83cop2, lowest = 5),
    c83new = recode_to(c84cop3, lowest = 3)
  ) %>%
  head()
Create recode pattern for 'rec' function

Description

Convenient function to create a recode pattern for the rec function, which recodes (numeric) vectors into smaller groups.

Usage

rec_pattern(from, to, width = 5, other = NULL)

Arguments

- from: Minimum value that should be recoded.
- 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 rec.

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

```r
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 `:` or tidyselect’s `select_helpers`. See 'Examples' or package-vignette.

- **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, `relevel(x, ref = lvl)` 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  

Remove variables from a data frame

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

- **x**: A vector or data frame.
- **...**: Character vector with variable names, or unquoted names of variables that should be removed from the data frame. You may also use functions like : or tidyselect's `select_helpers`.

Value

- **x**, with variables specified in **...** removed.

Examples

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

```r
replace_na
Replace NA with specific values
```

Description

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

Usage

```r
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 : or tidyselect’s `select_helpers`. See ‘Examples’ or package-vignette.
- **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 labels attribute for value to `x`).
- **tagged.na**: Optional single character, specifies a `tagged_na` 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 NA’s. Tagged NA’s 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

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

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

```r
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**  
*Reshape data into long format*

**Description**

*reshape_longer()* reshapes one or more columns from wide into long format.

**Usage**

```r
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'.
reshape_longer

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")
)


### rotate_df

**Rotate a data frame**

**Description**

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

**Usage**

```r
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

```r
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  Count row or column indices

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

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.
count  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), NA, Inf or NULL to count missing or infinite values, or null-values.
var  Name of new the variable with the row or column counts.
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.

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

May either be

- a numeric value that indicates the amount of valid values per row to calculate the row mean or sum;
- a value between 0 and 1, indicating a proportion of valid values per row to calculate the row mean or sum (see ’Details’).
- or Inf. If n = Inf, all values per row must be non-missing to compute row mean or sum.

If a row’s sum of valid (i.e. non-NA) values is less than n, NA will be returned as value for the row mean or sum.

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 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 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**

```r
seq_col(x)
seq_row(x)
```

**Arguments**

- `x`  
  A data frame.

**Value**

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

**Examples**

```r
data(iris)
seq_col(iris)
seq_row(iris)
```
**set_na_if**

*Replace specific values in vector with NA*

**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**

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

---

**shorten_string**

**Shorten character strings**

**Description**

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

**Usage**

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

**Arguments**

- `s` A string.
- `max.length` Maximum length of chars for the string.
- `abbr` String that will be used as suffix, if `s` 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**

```r
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

```r
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 `:` or `tidyselect`'s `select_helpers`. See 'Examples' or package-vignette.
- **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.
split_var

val.labels  Optional character vector, to set value label attributes of recoded variable (see vignette Labelled Data and the sjlabelled-Package). 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 Labelled Data and the sjlabelled-Package). 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 preceeding 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 String value, will be appended to variable (column) names of x, if x is a data frame. If x 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:

- recoded variables (rec()) will be suffixed with "_r"
- recoded variables (recode_to()) will be suffixed with "_r0"
- dichotomized variables (dicho()) will be suffixed with "_d"
- grouped variables (split_var()) will be suffixed with "_g"
- grouped variables (group_var()) will be suffixed with "_gr"
- standardized variables (std()) will be suffixed with "_z"
- centered variables (center()) will be suffixed with "_c"
- de-meaned variables (de_mean()) will be suffixed with "_dm"
- grouped-meaned variables (de_mean()) will be suffixed with "_gm"

If suffix = "" and append = TRUE, existing variables that have been recoded/transformed will be overwritten.

candidate A predicate function to be applied to the columns. The variables for which candidate 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 function 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 a 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(disp, n = 3, append = FALSE) %>%
table()

mtcars %>%
  group_by(cyl) %>%
  split_var(disp, n = 3, append = FALSE) %>%
spread_coef

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

data A (nested) data frame with a list-variable that contains fitted model objects (see 'Details').
model.column Name or index of the list-variable that contains the fitted model objects.
model.term 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.
se Logical, if TRUE, standard errors for estimates will also be extracted.
p.val Logical, if TRUE, p-values for estimates will also be extracted.
append 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

```r
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
  library(sjstats)
  efc %>%
    bootstrap(100) %>%
    mutate(
      models = map(strap, ~lm(neg_c_7 ~ e42dep + c161sex + c172code, data = .x))
    ) %>%
    spread_coef(models, se = FALSE, p.val = FALSE)
    boot_ci(e42dep, c161sex, c172code)
}
```
Standardize and center variables

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

```r
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

- **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.
- **robust** Character vector, indicating the method applied when standardizing variables with `std()`. By default, standardization is achieved by dividing the centered variables by their standard deviation (`robust = "sd"`). However, for skewed distributions, the median absolute deviation (MAD, `robust = "mad"`) or Gini’s mean difference (`robust = "gmd"`) might be more robust measures of dispersion. For the latter option, `sjstats` needs to be installed. `robust = "2sd"` divides
the centered variables by two standard deviations, following a suggestion by Gelman (2008), so the rescaled input is comparable to binary variables.

include.fac Logical, if TRUE, factors will be converted to numeric vectors and also standardized or centered.

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 String value, will be appended to variable (column) names of x, if x is a data frame. If x 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:

• recoded variables (rec()) will be suffixed with "_r"
• recoded variables (recode_to()) will be suffixed with "_r0"
• dichotomized variables (dicho()) will be suffixed with "_d"
• grouped variables (split_var()) will be suffixed with "_g"
• grouped variables (group_var()) will be suffixed with "_gr"
• standardized variables (std()) will be suffixed with "_z"
• centered variables (center()) will be suffixed with "_c"
• de-meaned variables (de_mean()) will be suffixed with "_dm"
• grouped-meaned variables (de_mean()) will be suffixed with "_gm"

If suffix = "" and append = TRUE, existing variables that have been recoded/transformed will be overwritten.

predicate 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


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(disp)

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

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 function checks whether a string or character vector \( x \) contains the string \( \text{pattern} \). By default, this function is case sensitive.

**Usage**

\[
\text{str\_contains}(x, \text{pattern}, \text{ignore\_case} = \text{FALSE}, \text{logic} = \text{NULL}, \text{switch} = \text{FALSE})
\]

**Arguments**

- **x**: Character string where matches are sought. May also be a character vector of length > 1 (see 'Examples').
- **pattern**: Character string to be matched in \( x \). May also be a character vector of length > 1 (see 'Examples').
- **ignore\_case**: Logical, whether matching should be case sensitive or not.
- **logic**: Indicates whether a logical combination of multiple search pattern should be made.
  - Use "or", "OR" or "|" for a logical or-combination, i.e. at least one element of \( \text{pattern} \) is in \( x \).
  - Use "and", "AND" or "&" for a logical AND-combination, i.e. all elements of \( \text{pattern} \) are in \( x \).
  - Use "not", "NOT" or "!" for a logical NOT-combination, i.e. no element of \( \text{pattern} \) is in \( x \).
  - By default, \( \text{logic} = \text{NULL} \), which means that \text{TRUE} or \text{FALSE} is returned for each element of \( \text{pattern} \) separately.
- **switch**: Logical, if \text{TRUE}, \( x \) will be sought in each element of \( \text{pattern} \). If \( \text{switch} = \text{TRUE} \), \( x \) needs to be of length 1.

**Details**

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

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

**Value**

\text{TRUE} if \( x \) contains \( \text{pattern} \).
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:

- 0 for no partial distance matching
- 1 for one-step matching, which means, only substrings of same length as pattern are extracted from string matching
- 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

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 \( \text{grep}(\text{pattern} = "(<\text{pattern}>){~<\text{precision}>}", x = \text{string}) \). This means, precision indicates the number of chars inside \text{pattern} that may differ in \text{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 \text{partial} = 1, a substring of \text{length(pattern)} is extracted from \text{string}, starting at position 0 in \text{string} until the end of \text{string} is reached. Each substring is matched against \text{pattern}, and results with a maximum distance of \text{precision} are considered as "matching". If \text{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 \text{string} that partially match or are similar to \text{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 \text{string} vector, where a (partial) match with \text{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 \text{string} only has one element).

See Also

\text{group_str}
Examples

```r
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 "System"
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**

```r
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 `stringr::regex()`. Alternatively, use `regex = TRUE` to treat `pattern` as a regular expression rather than a fixed string.
- `ignore.case` Logical, whether matching should be case sensitive or not. `ignore.case` is ignored when `pattern` is no regular expression or `regex = FALSE`.
- `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

```r
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

Clean values of character vectors.

Description

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

Usage

```r
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 `:` or tidyselect’s `select_helpers`. See ‘Examples’ or `package-vignette`. 
to_character

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_character

Convert variable into character vector and replace values with associated value labels

Description

This function converts (replaces) variable values (also of factors or character vectors) with their associated value labels and returns them as character vector. This is just a convenient wrapper for as.character(to_label(x)).

Usage

```r
to_character(
  x,
  ..., 
  add.non.labelled = FALSE,
  prefix = FALSE,
  var.label = NULL,
  drop.na = TRUE,
  drop.levels = FALSE
)
```

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.

add.non.labelled

Logical, if TRUE, values without associated value label will also be converted to labels (as is). See ‘Examples’.
prefix Logical, if TRUE, the value labels used as factor levels or character values will be prefixed with their associated values. See 'Examples'.

var.label Optional string, to set variable label attribute for the returned variable (see vignette Labelled Data and the sjlabelled-Package). If NULL (default), variable label attribute of x will be used (if present). If empty, variable label attributes will be removed.

drop.na Logical, if TRUE, tagged NA values with value labels will be converted to regular NA's. Else, tagged NA values will be replaced with their value labels. See 'Examples' and get_na.

drop.levels Logical, if TRUE, unused factor levels will be dropped (i.e. droplevels will be applied before returning the result).

Value
A character vector with the associated value labels as values. If x is a data frame, the complete data frame x will be returned, where variables specified in ... are coerced to character variables; if ... is not specified, applies to all variables in the data frame.

Note
Value labels will be removed when converting variables to factors, variable labels, however, are preserved.

This function is kept for backwards-compatibility. It is preferred to use sjlabelled::as_character().

Examples

```r
library(sjlabelled)
data(efc)
print(get_labels(efc)["c161sex"])
head(efc$c161sex)
head(to_character(efc$c161sex))

# Find more examples at '?sjlabelled::as_label'
```
to_dummy

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.

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. x_1, x_2, x_3 etc. Use "label" to add value label, e.g. x_low, x_mid, x_high. 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_factor**  
*Convert variable into factor and keep value labels*

**Description**

This function converts a variable into a factor, but preserves variable and value label attributes. See 'Examples'.

**Usage**

```r
to_factor(x, ..., add.non.labelled = FALSE, ref.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 : or tidyselect’s `select_helpers`. See 'Examples' or package-vignette.
- `add.non.labelled` Logical, if `TRUE`, non-labelled values also get value labels.
- `ref.lvl` Numeric, specifies the reference level for the new factor. Use this parameter if a different factor level than the lowest value should be used as reference level. If `NULL`, lowest value will become the reference level. See `ref_lvl` for details.

**Details**

`to_factor` converts numeric values into a factor with numeric levels. `as_label`, however, converts a vector into a factor and uses value labels as factor levels.

**Value**

A factor, including variable and value labels. If `x` is a data frame, the complete data frame `x` will be returned, where variables specified in `...` are coerced to factors (including variable and value labels); if `...` is not specified, applies to all variables in the data frame.

**Note**

This function is intended for use with vectors that have value and variable label attributes. Unlike `as.factor`, `to_factor` converts a variable into a factor and preserves the value and variable label attributes.

Adding label attributes is automatically done by importing data sets with one of the `read_*`-functions, like `read_spss`. Else, value and variable labels can be manually added to vectors with `set_labels` and `set_label`.

This function is kept for backwards-compatibility. It is preferred to use `as_factor`.
See Also

- `as_numeric` to convert a factor into a numeric vector and `as_label` to convert a vector into a factor with labelled factor levels.

Examples

```r
library(sjlabelled)
data(efc)
# normal factor conversion, loses value attributes
x <- as.factor(efc$e42dep)
frq(x)

# factor conversion, which keeps value attributes
x <- to_factor(efc$e42dep)
frq(x)

# create partially labelled vector
x <- set_labels(efc$e42dep,
    labels = c(`1` = "independent", `4` = "severe dependency",
    `9` = "missing value"))

# only copy existing value labels
to_factor(x)
get_labels(to_factor(x), values = "p")

# also add labels to non-labelled values
to_factor(x, add.non.labelled = TRUE)
get_labels(to_factor(x, add.non.labelled = TRUE), values = "p")

# Convert to factor, using different reference level
x <- to_factor(efc$e42dep)
str(x)
table(x)

x <- to_factor(efc$e42dep, ref.lvl = 3)
str(x)
table(x)

# easily coerce specific variables in a data frame to factor
# and keep other variables, with their class preserved
to_factor(efc, e42dep, e16sex, c172code)

# use select-helpers from dplyr-package
library(dplyr)
to_factor(efc, contains("cop"), c161sex:c175empl)
```
to_label

Convert variable into factor with associated value labels

Description

This function converts (replaces) values of a variable (also of factors or character vectors) with their associated value labels. Might be helpful for factor variables. For instance, if you have a Gender variable with 0/1 value, and associated labels are male/female, this function would convert all 0 to male and all 1 to female and returns the new variable as factor.

Usage

```r
to_label(
  x,
  ..., 
  add.non.labelled = FALSE,
  prefix = FALSE,
  var.label = NULL,
  drop.na = TRUE,
  drop.levels = FALSE
)
```

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.
- `add.non.labelled` Logical, if TRUE, values without associated value label will also be converted to labels (as is). See ‘Examples’.
- `prefix` Logical, if TRUE, the value labels used as factor levels or character values will be prefixed with their associated values. See ‘Examples’.
- `var.label` Optional string, to set variable label attribute for the returned variable (see vignette Labelled Data and the sjlabelled-Package). If NULL (default), variable label attribute of `x` will be used (if present). If empty, variable label attributes will be removed.
- `drop.na` Logical, if TRUE, tagged NA values with value labels will be converted to regular NA's. Else, tagged NA values will be replaced with their value labels. See ‘Examples’ and `get_na`.
- `drop.levels` Logical, if TRUE, unused factor levels will be dropped (i.e. `droplevels` will be applied before returning the result).
to_long

Value
A factor with the associated value labels as factor levels. If x is a data frame, the complete data frame x will be returned, where variables specified in ... are coerced to factors; if ... is not specified, applies to all variables in the data frame.

Note
Value label attributes will be removed when converting variables to factors.

This function is kept for backwards-compatibility. It is preferred to use as_label.

Examples
library(sjlabelled)
data(efc)
print(get_labels(efc)['c161sex'])
head(efc$c161sex)
head(to_label(efc$c161sex))

# Find more examples at '?sjlabelled::as_label'

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))

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,
to_value

```r
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)
to_numeric(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 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.
start.at Starting index, i.e. the lowest numeric value of the variable's value range. By default, this argument is NULL, 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).
keep.labels Logical, if TRUE, former factor levels will be added as value labels. For numeric factor levels, values labels will be used, if present. See 'Examples' and set_labels for more details.
use.labels Logical, if TRUE and x 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**

```r
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**

```r
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**

```r
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")))

---

**Description**

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

**Usage**

```r
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**

```r
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)

---

### var_type

**Determine variable type**

#### Description

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

#### Usage

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

#### 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.
- **abbr**: Logical, if TRUE, returns a shortened, abbreviated value for the variable type (as returned by `type_sum`). If FALSE (default), a longer “description” is returned.

#### Value

The variable type of `x`, as character.

#### Examples

```r
data(efc)
var_type(1)
var_type(1L)
var_type("a")

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

library(dplyr)
```
word_wrap

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 Convert infinite or NaN values into regular NA

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 frame
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

\[
\begin{align*}
c("a", "B", "c") \%in\% letters \\
c("a", "B", "c") \%nin\% letters \\
c(1, 2, 3, 4) \%in\% c(3, 4, 5, 6) \\
c(1, 2, 3, 4) \%nin\% c(3, 4, 5, 6)
\end{align*}
\]
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