Package 'clinpubr'

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Description Accelerate the process from clinical data to medical publication, including clinical data cleaning, significant result screening, and the generation of publish-ready tables and figures.

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`add_lists` *Adding lists element-wise*

Description

Combine lists by adding element-wise.

Usage

```
add_lists(l1, l2)
```

Arguments

`l1, l2`	A pair of lists.

Value

A list.

Examples

```
l1 <- list(a = 1, b = 2)
l2 <- list(a = 3, b = 4, c = 5)
add_lists(l1, l2)
```

`answer_check` *Check answers of multiple choice questions*

Description

Check answers of multiple choice questions by matching the answers with the correct sequence.

Usage

```
answer_check(dat, seq, multi_column = FALSE)
```

Arguments

`dat`	A data frame of answers.
`seq`	A vector of correct answers, one element for each question.
`multi_column`	Logical, whether the multi-answers are in multiple columns.

Details

If `multi_column` is TRUE, the answers for Multiple-Answer Questions should be in multiple columns of logicals, with each column representing a choice. The `seq` should be a string of `"T"` and `"F"`. If `multi_column` is `FALSE`, the answers for Multiple-Answer Questions should be in one column, and the function would expect an exact match of `seq`.

Value

A data frame of boolean values, with ncol equals the number of questions.

Examples

```
dat <- data.frame(Q1 = c("A", "B", "C"), Q2 = c("AD", "AE", "ABF"))
seq <- c("A", "AE")
answer_check(dat, seq)
dat <- data.frame(
  Q1 = c("A", "B", "C"), Q2.A = c(TRUE, TRUE, FALSE),
  Q2.B = c(TRUE, FALSE, TRUE), Q2.C = c(FALSE, TRUE, FALSE)
)
seq <- c("A", "TFT")
answer_check(dat, seq, multi_column = TRUE)
```

baseline_table *Create a baseline table for a dataset.*

Description

Create a baseline table and a table of missing values. If the strata variable has more than 2 levels, a pairwise comparison table will also be created.

Usage

```
baseline_table(
  data,
  var_types = NULL,
  strata = NULL,
  vars = NULL,
  factor_vars = NULL,
  exact_vars = NULL,
  nonnormal_vars = NULL,
  seed = NULL,
  omit_missing_strata = FALSE,
  save_table = FALSE,
  filename = NULL,
  multiple_comparison_test = TRUE,
  p_adjust_method = "BH",
  smd = FALSE,
  ...
)
```

Arguments

data	A data frame.
var_types	An object from class var_types returned by get_var_types function.
strata	A variable to stratify the table. Overwrites the strata variable in var_types.
vars	A vector of variables to include in the table.
factor_vars	A vector of factor variables. Overwrites the factor variables in var_types.
exact_vars	A vector of variables to test for exactness. Overwrites the exact variables in var_types.
nonnormal_vars	A vector of variables to test for normality. Overwrites the nonnormal variables in var_types.
seed	A seed for the random number generator. This seed can be set for consistent simulation when performing fisher exact tests.
omit_missing_strata	A logical value indicating whether to omit missing values in the strata variable.
save_table	A logical value indicating whether to save the result tables.

filename — The name of the file to save the table. The file names for accompanying tables will be the same as the main table, but with "_missing" and "_pairwise" appended.

multiple_comparison_test — A logical value indicating whether to perform multiple comparison tests. Variables in factor_vars and exact_vars are tested with pairwise chisq.test or fisher.test, and other variables are tested with rstatix::dunn_test() or rstatix::games_howell_test().

p_adjust_method — The method to use for p-value adjustment for pairwise comparison. Default is "BH". See ?p.adjust.methods.

smd — A logical value indicating whether to include SMD in the table. Passed to tableone::print.TableOne().

... — Additional arguments passed to tableone::print.TableOne().

Value

A list containing the baseline table and accompanying tables.

Examples

```
withr::with_tempdir(
  {
    data(cancer, package = "survival")
    var_types <- get_var_types(cancer, strata = "sex")
    baseline_table(cancer, var_types = var_types, filename = "baseline.csv")

    # baseline table with pairwise comparison
    cancer$ph.ecog_cat <- factor(cancer$ph.ecog,
      levels = c(0:3),
      labels = c("0", "1", ">=2", ">=2")
    )
    var_types <- get_var_types(cancer, strata = "ph.ecog_cat")
   baseline_table(cancer, var_types = var_types, save_table = TRUE, filename = "baseline.csv")
    print(paste0("files saved to: ", getwd()))
  },
  clean = FALSE
)
```

---

break_at *Generate breaks for histogram*

Description

Generate breaks for histogram that covers xlim and includes a ref_val.

Usage

```
break_at(xlim, breaks, ref_val = NULL)
```

Arguments

xlim	A vector of length 2.
breaks	The number of breaks.
ref_val	The reference value to include in breaks.

Value

A vector of breaks of length breaks + 1.

Examples

```
break_at(xlim = c(0, 10), breaks = 12, ref_val = 3.12)
```

---

calculate_index *Calculate index based on conditions*

Description

Calculate an index based on multiple conditions. Each condition is evaluated and the result is weighted and summed to produce the final index.

Usage

```
calculate_index(.df, ..., .weight = 1, .na_replace = 0)
```

Arguments

.df	A data frame
...	Conditions to evaluate. See examples for more details.
.weight	Weight for each condition, should be of length 1 or equal to the number of conditions.
.na_replace	Value to replace NA, should be of length 1 or equal to the number of conditions.

Value

A numeric vector of index scores

Examples

```
df <- data.frame(x = c(1, 2, 3, 4, 5), y = c(1, 2, NA, 4, NA))
calculate_index(df, x > 3, y < 3, .weight = c(1, 2), .na_replace = 0)
```

calc_cindex *Calculate C-index for survival data*

Description

Calculate C-index for survival data. It's a wrapper function for `Hmisc::rcorr.cens()`.

Usage

```
calc_cindex(data, time_var, event_var, marker_var)
```

Arguments

`data`	A data frame containing the survival time, event indicator, and marker variable.
`time_var`	A string specifying the name of the survival time variable in the data frame.
`event_var`	A string specifying the name of the event indicator variable in the data frame.
`marker_var`	A string specifying the name of the marker variable in the data frame.

Value

The C-index value.

Examples

```
# Calculate C-index using lung dataset from survival package
data(cancer, package = "survival")
# Use age as the marker variable
calc_cindex(lung, "time", "status", "age")
```

check_nonnum *Check elements that are not numeric*

Description

Finds the elements that cannot be converted to numeric in a character vector. Useful when setting the strategy to clean numeric values.

Usage

```
check_nonnum(
  x,
  return_idx = FALSE,
  show_unique = TRUE,
  max_count = NULL,
  random_sample = FALSE,
  fix_len = FALSE
)
```

Arguments

x	A string vector that stores numerical values.
return_idx	A logical value. If TRUE, return the index of the elements that are not numeric.
show_unique	A logical value. If TRUE, return the unique elements that are not numeric. Omitted if return_idx is TRUE.
max_count	An integer. The maximum number of elements to show. If NULL or 0, show all elements. Omitted if return_idx is TRUE.
random_sample	A logical value. If TRUE, randomly sample the elements to show. Only works if max_count is not NULL or 0.
fix_len	A logical value. If TRUE, fill the vector with NA to fix the length to max_count.

Details

The function uses the as.numeric() function to try to convert the elements to numeric. If the conversion fails, the element is considered non-numeric.

Value

The (unique) elements that cannot be converted to numeric, and their indexes if return_idx is TRUE.

Examples

```
check_nonnum(c("\uFF11\uFF12\uFF13", "11..23", "3.14", "2.131", "35.2."))
```

---

classif_model_compare *Performance comparison of classification models*

Description

Compare the performance of classification models by commonly used metrics, and generate commonly used plots including receiver operating characteristic curve plot, decision curve analysis plot, and calibration plot.

Usage

```
classif_model_compare(
  data,
  target_var,
  model_names,
  colors = NULL,
  save_output = FALSE,
  figure_type = "png",
  output_prefix = "model_compare",
  as_probability = FALSE,
  auto_order = TRUE
)
```

Arguments

`data`	A data frame containing the target variable and the predicted values.
`target_var`	A string specifying the name of the target variable in the data frame.
`model_names`	A vector of strings specifying the names of the models to compare.
`colors`	A vector of colors to use for the plots. The last 2 colors are used for the "Treat all" and "Treat none" lines in the DCA plot.
`save_output`	A logical value indicating whether to output the results to files.
`figure_type`	A character string of the figure type. Can be `"png"`, `"pdf"`, and other types that `ggplot2::ggsave()` support.
`output_prefix`	A string specifying the prefix for the output files.
`as_probability`	A logical or a vector of variable names. The logical value indicates whether to convert variables not in range 0 to 1 into this range. The vector of variable names means to convert these variables to the range of 0 to 1.
`auto_order`	A logical value indicating whether to automatically order the models by their AUCs. If `TRUE`, the models will be ordered by their AUCs in descending order. If `FALSE`, the order in `model_names` will be retained.

Value

A list of various results. If the output files are not in desired format, these results can be modified for further use.

- metric_table: A data frame containing the performance metrics for each model.
- roc_plot: A `ggplot` object of Receiver Operating Characteristic curves.
- pr_plot: A `ggplot` object of Precision-Recall curves.
- dca_plot: A `ggplot` object of decision curve analysis plots.
- calibration_plot: A `ggplot` object of calibration plots.

Metrics

- AUC: Area Under the Receiver Operating Characteristic Curve
- PRAUC: Area Under the Precision-Recall Curve
- Accuracy: Overall accuracy
- Sensitivity: True positive rate
- Specificity: True negative rate
- Pos Pred Value: Positive predictive value
- Neg Pred Value: Negative predictive value
- F1: F1 score
- Kappa: Cohen's kappa
- Brier: Brier score
- cutoff: Optimal cutoff for classification, metrics that require a cutoff are based on this value.
- Youden: Youden's J statistic
- HosLem: Hosmer-Lemeshow test p-value

Examples

```
data(cancer, package = "survival")
df <- kidney
df$dead <- ifelse(df$time <= 100 & df$status == 0, NA, df$time <= 100)
df <- na.omit(df[, -c(1:3)])

model0 <- glm(dead ~ age + frail, family = binomial(), data = df)
model <- glm(dead ~ ., family = binomial(), data = df)
df$base_pred <- predict(model0, type = "response")
df$full_pred <- predict(model, type = "response")

classif_model_compare(df, "dead", c("base_pred", "full_pred"), save_output = FALSE)
```

`combine_files` *combine multiple data files into a single data frame*

Description

combine multiple data files into a single data frame

Usage

```
combine_files(
  path = ".",
  pattern = NULL,
  recursive = FALSE,
  add_file_name = FALSE,
  unique_only = TRUE,
  reader_fun = read.csv,
  ...
)
```

Arguments

`path`	A string as the path to find the data files.
`pattern`	A file pattern to filter the required data files.
`recursive`	A logical value to indicate whether to search files recursively in subdirectories.
`add_file_name`	A logical value to indicate whether to add the file name as a column. Note that the added file name will affect the uniqueness of the data.
`unique_only`	A logical value to indicate whether to remove the duplicated rows.
`reader_fun`	A function to read the data files. Can be `read.csv`, `openxlsx::read.xlsx`, etc.
`...`	Other parameters passed to the `reader_fun`.

Value

A data frame. If no data files found, return `NULL`.

Examples

```
library(withr)
with_tempdir({
  write.csv(data.frame(x = 1:3, y = 4:6), "file1.csv", row.names = FALSE)
  write.csv(data.frame(x = 7:9, y = 10:12), "file2.csv", row.names = FALSE)
  dat <- combine_files(pattern = "file")
})
print(dat)
```

---

combine_multichoice *Combine multi-choice columns into one*

Description

Combine multi-choice columns into one, each column consists of booleans whether a choice is presented.

Usage

```
combine_multichoice(
  df,
  quest_cols,
  sep = ",",
  remove_cols = TRUE,
  remove_prefix = TRUE
)
```

Arguments

df	A data frame.
quest_cols	A named list where each element is a character vector of column names to combine, or a single character vector.
sep	A string to separate the data. Default is ",".
remove_cols	If TRUE, remove the original columns.
remove_prefix	If TRUE, automatically remove common prefix from column names when combining.

Value

A data frame with additional columns.

Examples

```
# Single group (backward compatibility)
df <- data.frame(q1 = c(TRUE, FALSE, TRUE), q2 = c(FALSE, TRUE, TRUE))
combine_multichoice(df, quest_cols = c("q1", "q2"))

# Multiple groups with named list
df <- data.frame(
  a1 = c(TRUE, FALSE, TRUE), a2 = c(FALSE, TRUE, TRUE),
  b1 = c(TRUE, TRUE, FALSE), b2 = c(FALSE, FALSE, TRUE)
)
combine_multichoice(df, quest_cols = list(groupA = c("a1", "a2"), groupB = c("b1", "b2")))
```

---

common_prefix *Get common prefix of a string vector*

Description

Get common prefix of a string vector

Usage

```
common_prefix(x)
```

Arguments

x	A string vector.

Value

A string that is the common prefix of the input vector.

Examples

```
common_prefix(c("Q1_a", "Q1_b", "Q1_c"))
```

---

cut_by *Convert Numeric to Factor*

Description

Divide numeric data into different groups. Easier to use than `base::cut()`.

Usage

```
cut_by(
  x,
  breaks,
  breaks_as_quantiles = FALSE,
  group = NULL,
  labels = NULL,
  label_type = "ori",
  right = FALSE,
  drop_empty = TRUE,
  verbose = FALSE,
  ...
)
```

Arguments

x	A numeric vector.
breaks	A numeric vector of internal cut points. If breaks_as_quantiles is TRUE, this is a proportion of the data. See Details.
breaks_as_quantiles	If TRUE, breaks is interpreted as a proportion of the data.
group	A character vector of the same length as x, used to group the data before cut. Only effective when breaks_as_quantiles is TRUE.
labels	A vector of labels for the resulting factor levels.
label_type	If labels is NULL, this sets the label type. "ori" for original labels, "LMH" for "Low Medium High" style. "combined" labels that combine "LMH" type or provided labels with the original range labels. Only "LMH" is supported when group is specified.
right	logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa. Note that the default is FALSE, which is different from base::cut().
drop_empty	If TRUE, drop empty levels.
verbose	If TRUE, print the cut points.
...	Other arguments passed to base::cut().

Details

cut_by() is a wrapper for base::cut(). Compared with the argument breaks in base::cut(), breaks here automatically sets the minimum and maximum. breaks outside the range of x are not allowed.

Value

A factor.

Note

The argument `right` in `base::cut()` is always set to `FALSE`, which means the levels follow the left closed right open convention.

Examples

```
set.seed(123)
cut_by(rnorm(100), c(0, 1, 2))
cut_by(rnorm(100), c(1 / 3, 2 / 3), breaks_as_quantiles = TRUE, label_type = "LMH")
```

---

data_overview *Data Overview and Quality Check*

Description

This function provides a comprehensive overview of a data.frame, including variable types, summary statistics, and potential data quality issues. It serves as a starting point for data cleaning by identifying problems that need attention.

Usage

```
data_overview(
  df,
  outlier_method = "iqr",
  outlier_threshold = NULL,
  verbose = TRUE,
  sample = 10000
)
```

Arguments

`df`	A data.frame to be analyzed
`outlier_method`	Method for detecting outliers, one of "iqr" (default), "zscore", or "mad"
`outlier_threshold`	Threshold value for detecting outliers. If NULL (default), uses method-specific defaults: • For MAD method: 1.4826 * 3 (approximately 3 standard deviations) • For IQR method: 1.5 (Tukey's rule) • For Z-score method: 3 (3 standard deviations)
`verbose`	If TRUE (default), prints result messages
`sample`	Maximum number of rows to sample for large datasets (default is 10000). Set to `NULL` `NA`, or `0` to disable sampling.

Value

A list containing:

- variable_types: Classification of variables by type
- summary_stats: Summary statistics for each variable
- quality_issues: Identified data quality problems
- recommendations: Suggestions for data cleaning

Examples

```
# Basic usage
data(mtcars)
overview <- data_overview(mtcars)
print(overview$variable_types)
print(overview$quality_issues)
```

---

detect_outliers *Detect outliers in a numeric vector.*

Description

Detect outliers in a numeric vector using various methods.

Usage

```
detect_outliers(x, method = "iqr", threshold = NULL)
```

Arguments

x	A numeric vector.
method	The method to use for outlier detection. One of "mad", "iqr", or "zscore".
threshold	The threshold value for detecting outliers. Defaults depend on the method.

Details

This function provides a unified interface for detecting outliers using different methods.

- "mad": Median absolute deviation method
- "iqr": Interquartile range method
- "zscore": Z-score method

Value

A list containing:

- outlier_mask: Logical vector indicating outliers, NA for missing values
- outlier_count: Number of outliers detected
- outlier_pct: Percentage of outliers in the data
- summary: Summary statistics including:
  - Before removing outliers: max, min, variance
  - After removing outliers: max, min, variance
  - Method-specific details

See Also

mad_outlier, iqr_outlier, zscore_outlier

Examples

```
x <- c(1, 2, 3, 4, 5, 100)
detect_outliers(x, method = "iqr")
```

---

df_view_nonnum *Show non-numeric elements in a data frame*

Description

Shows the non-numeric elements in a data frame. Only character columns are checked. Useful when setting the strategy to clean numeric values.

Usage

```
df_view_nonnum(
  df,
  max_count = 20,
  random_sample = FALSE,
  long_df = FALSE,
  subject_col = NULL,
  value_col = NULL
)
```

Arguments

df	A data frame.
max_count	An integer. The maximum number of elements to show for each column. If NULL or 0, show all elements, not recommended due to huge memory waste.
random_sample	A logical value. If TRUE, randomly sample the elements to show.

long_df	A logical value. If TRUE, the input df is provided in a long format.
subject_col	A character string. The name of the column that contains the subject identifier. Used when long_df is TRUE. If NULL, the subject column is assumed to be the first column.
value_col	A character string. The name of the column that contains the values. Used when long_df is TRUE. If NULL, the value column is assumed to be the second column.

Value

A data frame of the non-numeric elements.

Examples

```
df <- data.frame(
  x = c("1", "2", "3..3", "4", "6a"),
  y = c("1", "ss", "aa.a", "4", "xx"),
  z = c("1", "2", "3", "4", "6")
)
df_view_nonnum(df)
```

---

emp_colors *default color palette for* clinpubr *plots*

Description

default color palette for clinpubr plots

Usage

```
emp_colors
```

---

exclusion_count *Count the number of excluded samples at each step*

Description

This function sequentially applies exclusion criteria to a data frame and counts the number of samples removed at each step.

Usage

```
exclusion_count(.df, ..., .criteria_names = NULL, .na_exclude = TRUE)
```

Arguments

.df	A data frame.
...	Exclusion criteria. Logical expressions that define which rows to exclude.
.criteria_names	An optional character vector of names for the criteria. If NULL, the expressions themselves are used as names.
.na_exclude	A logical value. If TRUE, rows where the criterion evaluates to NA will be excluded, and a warning will be issued. Defaults to FALSE, where NA values are not excluded.

Value

A data frame with two columns: 'Criteria' and 'N', showing the number of samples at the start, the number excluded at each step, and the final number remaining.

Examples

```
cohort <- data.frame(
  age = c(17, 25, 30, NA, 50, 60),
  sex = c("M", "F", "F", "M", "F", "M"),
  value = c(1, NA, 3, 4, 5, NA),
  dementia = c(TRUE, FALSE, FALSE, FALSE, TRUE, FALSE)
)
exclusion_count(
  cohort,
  age < 18,
  is.na(value),
  dementia == TRUE,
  .criteria_names = c(
    "Age < 18 years",
    "Missing value",
    "History of dementia"
  )
)
```

---

extract_history *Extract Medical History from Clinical Text*

Description

Extract medical history information (disease, smoking, drinking, surgery, etc.) from clinical text records, supports Chinese text. The function uses vectorized string operations for high performance on large datasets.

Usage

```
extract_history(
  text,
  keywords,
  extract_duration = TRUE,
  duration_unit = c("original", "years", "days"),
  negation_window = 20,
  return_format = c("simple", "detailed", "data.frame")
)
```

Arguments

text	A character vector of clinical text records.
keywords	A character vector of keywords to search for. Can also be a named list where names are category names and values are keyword vectors.
extract_duration	Logical. If TRUE, extract duration information (years/months/days) when available. Default is TRUE.
duration_unit	Character. The unit for duration output. Can be "original" (keep as extracted), "years" (convert all to years), or "days" (convert all to days). Default is "original".
negation_window	Integer. The maximum character distance to look for negation words before the keyword. Default is 20.
return_format	Character. The format of return values. Can be "simple" (TRUE/FALSE/NA), "detailed" (duration strings like "5 years" when available, "yes"/"no" otherwise), or "data.frame" (separate columns for status and duration). Default is "simple".

Value

Depending on return_format:

- "simple": A logical vector with values TRUE, FALSE, or NA.
- "detailed": A character vector with duration strings (e.g., "5 years", "30 days") when available, otherwise TRUE, FALSE, or NA.
- "data.frame": A data frame with columns status (logical) and duration (character).

If keywords is a named list with multiple categories, returns a data frame with one column per category.

Examples

```
## Not run:
test_data <- c(
  "hypertension history 20 years",
  "appendectomy surgery history"
)
```

```
extract_history(test_data, "hypertension")

## End(Not run)
```

`extract_num` *Extract numbers from string.*

Description

Extract numerical values from strings. Can be used to filter out the unwanted information coming along with the numbers.

Usage

```
extract_num(
  x,
  res_type = c("first", "range"),
  multimatch2na = FALSE,
  leq_1 = FALSE,
  allow_neg = TRUE,
  zero_regexp = NULL,
  max_regexp = NULL,
  max_quantile = 0.95
)
```

Arguments

`x`	A character vector.
`res_type`	The type of the result. Can be `"first"` or `"range"`. If `"first"`, the first number in the string is extracted. If `"range"`, the mean of the range in the string is extracted.
`multimatch2na`	If `TRUE`, multiple matches will be converted to `NA`. Only works when `res_type` is `"first"`.
`leq_1`	If `TRUE`, numbers greater than 1 will be converted to `NA`. Only works when `res_type` is `"first"`.
`allow_neg`	If `TRUE`, negative numbers are allowed. Otherwise, only positive numbers are allowed.
`zero_regexp`	A regular expression to match the string that indicates zero.
`max_regexp`	A regular expression to match the string that indicates the maximum value.
`max_quantile`	The quantile of values to set the maximum value to.

Details

The function uses regular expressions to extract numbers from strings. The regular expression used is `"-?[0-9]+\\.?[0-9]*|-?\\.[0-9]+"`, which matches any number that may have a decimal point and may have a negative sign.

Value

A numeric vector.

Examples

```
x <- c("1.2(XXX)", "5-8POS", "NS", "FULL", "5.5", "4.2")
extract_num(x)
extract_num(x,
  res_type = "first", multimatch2na = TRUE, zero_regexp = "NEG|NS",
  max_regexp = "FULL"
)
extract_num(x, res_type = "range", allow_neg = FALSE, zero_regexp = "NEG|NS", max_regexp = "FULL")
```

---

fill_with_last *Fill NA values with the last valid value*

Description

Fill NA values with the last valid value. Can be used to fill excel combined cells.

Usage

```
fill_with_last(x)
```

Arguments

x	A vector.

Value

A vector.

Examples

```
fill_with_last(c(1, 2, NA, 4, NA, 6))
```

filter_rcs_predictors *Filter predictors for RCS*

Description

Filter predictors that can be used to fit for RCS models.

Usage

```
filter_rcs_predictors(data, predictors = NULL)
```

Arguments

data	A data frame.
predictors	A vector of predictor names to be filtered.

Value

A vector of predictor names. These variables are numeric and have more than 5 unique values.

Examples

```
filter_rcs_predictors(mtcars)
```

first_mode *Calculate the first mode*

Description

Calculate the first mode of a vector. Ignore NA values. Can be used if any mode is acceptable.

Usage

```
first_mode(x, empty_return)
```

Arguments

x	A vector.
empty_return	The value to return if the vector is empty.

Value

The first mode of the vector.

Examples

```
first_mode(c(1, 1, 2, 2, 3, 3, 3, NA, NA, NA))
```

format_pval *Format p-value for publication*

Description

Format p-value with modified default settings suitable for publication.

Usage

```
format_pval(
  p,
  text_ahead = NULL,
  digits = 1,
  nsmall = 2,
  eps = 0.001,
  na_empty = TRUE
)
```

Arguments

p	The numerical p values to be formatted.
text_ahead	A string to be added before the p value. If not NULL, this string will be connected to the formatted p value with "=" or "<".
digits	The number of digits to be used. Same as in base::format.pval.
nsmall	The number of digits after the decimal point. Same as in base::format.pval.
eps	The threshold for rounding p values to 0. Same as in base::format.pval.
na_empty	If TRUE, replace "NA" in result with an empty string.

Value

A string vector of formatted p values.

Examples

```
format_pval(c(0.001, 0.0001, 0.05, 0.1123456))
format_pval(c(0.001, 0.0001, 0.05, 0.1123456), text_ahead = "p value")
```

formula_add_covs *Add covariates to a formula*

Description

Add covariates to a formula. Support both formula and character string.

Usage

```
formula_add_covs(formula, covars)
```

Arguments

formula	A formula. Should be a formula or a character string of formula.
covars	A vector of covariates.

Value

A formula.

Examples

```
formula_add_covs("y ~ a + b", c("c", "d"))
```

get_samples *Generate a sample of values from a vector and collapse them.*

Description

Generate a string summary of a vector by picking samples.

Usage

```
get_samples(x, unique_only = FALSE, n_samples = 10, collapse = "\n")
```

Arguments

x	A vector of values.
unique_only	A logical value indicating whether to return unique values only.
n_samples	The number of samples to return.
collapse	The separator to use for collapsing the values.

Value

A character string.

Examples

```
get_samples(c(1, 2, 3, 4, 5))
get_samples(c(1, 2, 3, 4, 5), n_samples = 2)
get_samples(c(1, 2, 3, 3, 3), n_samples = 2, unique_only = TRUE)
get_samples(c(1, 2, 3, 4, 5), collapse = ", ")
```

---

get_valid *Get one valid value from vector.*

Description

Extract one valid (non-NA) value from a vector.

Usage

```
get_valid(x, mode = c("first", "mid", "last"), disjoint = FALSE)
```

Arguments

x	A vector.
mode	The mode of the valid value to extract. "first" extracts the first valid value, "last" extracts the last valid value, and "mid" extracts the middle valid value.
disjoint	If TRUE, the values extracted by the three modes are forced to be different. This behavior might be desired when trying to extract different values with different modes. The three modes extract values in the sequence: "first", "last", "mid".

Value

A single valid value from the vector. NA if all values are invalid.

Examples

```
get_valid(c(NA, 1, 2, NA, 3, NA, 4))
get_valid(c(NA, 1, NA), mode = "last", disjoint = TRUE)
```

`get_valid_subset` *Get the subset that satisfies the missing rate condition.*

Description

Get the subset of a data frame that satisfies the missing rate condition using a greedy algorithm.

Usage

```
get_valid_subset(
  df,
  row_na_ratio = 0.5,
  col_na_ratio = 0.2,
  row_priority = 1,
  adaptive_scoring = FALSE,
  speedup_ratio = 0,
  return_index = FALSE
)
```

Arguments

`df`	A data frame.
`row_na_ratio`	The maximum acceptable missing rate of rows. Should be in range of `[0, 1]`.
`col_na_ratio`	The maximum acceptable missing rate of columns. Should be in range of `[0, 1]`.
`row_priority`	A positive numerical, the priority to keep rows. The higher the value, the higher the priority, with `1` indicating equal priority for rows and columns.
`adaptive_scoring`	A logical, whether to use adaptive scoring that considers the improvement in missing rates for the other dimension. When TRUE, the score reflects how much removing a row/column helps the columns/rows get closer to their thresholds. Setting `adaptive_scoring = TRUE` would allow the algorithm to search in a wider range of candidates, but significantly increases the running time. Default is FALSE.
`speedup_ratio`	A numerical in `[0, 1]`. Controls how many rows/columns to remove per iteration. `0` removes one at a time (most precise), `1` removes all candidates at once (most aggressive).
`return_index`	A logical, whether to return only the row and column indices of the subset.

Details

The function is based on a greedy algorithm. It iteratively removes the row or column with the highest excessive missing rate weighted by the inverse of `row_priority` until the missing rates of all rows and columns are below the specified threshold. Then it reversely tries to add rows and columns that do not break the conditions back and finalize the subset. The result depends on the

row_priority parameter drastically, so it's recommended to try different row_priority values to find the most satisfying one.

When adaptive_scoring = TRUE, the scoring considers how much removing a row/column improves the missing rates of the other dimension. The score is calculated as:

- For rows: sum of improvements in column missing rates (how much closer columns get to col_na_ratio)
- For columns: sum of improvements in row missing rates (how much closer rows get to row_na_ratio) This allows the algorithm to consider removing rows/columns even if they don't exceed thresholds, if doing so helps other dimensions satisfy their thresholds.

Value

The subset data frame, or a list that contains the row and column indices of the subset.

Examples

```
data(cancer, package = "survival")
dim(cancer)
max_missing_rates(cancer)

cancer_valid <- get_valid_subset(cancer, row_na_ratio = 0.2, col_na_ratio = 0.1, row_priority = 1)
dim(cancer_valid)
max_missing_rates(cancer_valid)
```

---

get_var_types *Get variable types for baseline table*

Description

Automatic variable type and method determination for baseline table.

Usage

```
get_var_types(
  data,
  strata = NULL,
  norm_test_by_group = TRUE,
  omit_factor_above = 20,
  num_to_factor = 5,
  save_qqplots = FALSE,
  folder_name = "qqplots"
)
```

Arguments

data	A data frame.
strata	A character string indicating the column name of the strata variable.
norm_test_by_group	A logical value indicating whether to perform normality tests by group.
omit_factor_above	An integer indicating the maximum number of levels for a variable to be considered a factor.
num_to_factor	An integer. Numerical variables with number of unique values below or equal to this value would be considered a factor.
save_qqplots	A logical value indicating whether to save QQ plots. Sometimes the normality tests do not work well for some variables, and the QQ plots can be used to check the distribution.
folder_name	A character string indicating the folder name for saving QQ plots.

Value

An object from class var_types, which is just list containing the following elements:

factor_vars	A character vector of variables that are factors.
exact_vars	A character vector of variables that require fisher exact test.
nonnormal_vars	A character vector of variables that are nonnormal.
omit_vars	A character vector of variables that are excluded form the baseline table.
strata	A character vector of the strata variable.

Note

This function performs normality tests on the variables in the data frame and determines whether they are normal. This is done by performing Shapiro-Wilk, Lilliefors, Anderson-Darling, Jarque-Bera, and Shapiro-Francia tests. If at least two of these tests indicate that the variable is nonnormal, then it is considered nonnormal. To alleviate the problem that normality tests become too sensitive when sample size gets larger, the alpha level is determined by an experience formula that decrease with sample size.

This function also marks the factor variables that require fisher exact tests if any cell haves expected frequency less than or equal to 5. Note that this criterion less strict than the commonly used one.

Examples

```
data(cancer, package = "survival")
get_var_types(cancer, strata = "sex") # set save_qqplots = TRUE to check the QQ plots

var_types <- get_var_types(cancer, strata = "sex")
# for some reason we want the variable "pat.karno" ro be considered normal.
var_types$nonnormal_vars <- setdiff(var_types$nonnormal_vars, "pat.karno")
```

group_by_range *Group Sorted Vector by Range*

Description

Divide a numeric vector into groups such that the range (`max - min`) within each group does not exceed a given threshold. This is useful for clustering continuous values into contiguous bins controlled by a maximum span.

Usage

```
group_by_range(x, max_range)
```

Arguments

`x`	A sorted numeric vector, Date vector, or POSIXt vector.
`max_range`	A non-negative numeric threshold for the within-group range.

Value

An integer vector of group IDs (1-indexed).

Examples

```
group_by_range(c(1, 2, 5, 7, 10, 11, 11, 11), 3)
```

group_by_range_cpp *Group Sorted Vector by Range*

Description

Divide a sorted numeric vector into groups such that `max(x[group]) - min(x[group]) <= max_range`.

Usage

```
group_by_range_cpp(x, max_range)
```

Arguments

`x`	A sorted numeric vector, Date vector, or POSIXt vector.
`max_range`	A non-negative numeric threshold for the within-group range.

Value

An IntegerVector of group IDs (1-indexed).

`importance_plot` *Importance plot*

Description

Creates an importance plot from a named vector of values.

Usage

```
importance_plot(
  x,
  x_lab = "Importance",
  top_n = NULL,
  color = c("#56B1F7", "#132B43"),
  show_legend = FALSE,
  split_at = NULL,
  show_labels = TRUE,
  digits = 2,
  nsmall = 3,
  scientific = TRUE,
  label_color = "black",
  label_size = 3,
  label_hjust = max(x)/10,
  save_plot = FALSE,
  filename = "importance.png"
)
```

Arguments

`x`	A named vector of values, typically importance scores from models.
`x_lab`	A character string for the x-axis label.
`top_n`	The number of top values to show. If NULL, all values are shown.
`color`	A length-2 vector of low and high colors, or a single color for the bars.
`show_legend`	A logical value indicating whether to show the legend.
`split_at`	The index at which to split the plot into two halves, usually used to illustrate variable selection. If NULL, no split is made.
`show_labels`	A logical value indicating whether to show the value labels on the bars.
`digits`, `nsmall`, `scientific`	Controls the formatting of labels. Passed to `format()`.
`label_color`	The color of the labels.
`label_size`	The size of the labels.
`label_hjust`	The horizontal justification of the labels.
`save_plot`	A logical value indicating whether to save the plot.
`filename`	The filename to save the plot as.

Details

The importance plot is a bar plot that shows the importance of each variable in a model. The variables are sorted in descending order of importance, and the top_n variables are shown. If top_n is NULL, all variables are shown. The plot can be split into two halves at a specified index, which is useful for illustrating variable selection.

Value

A ggplot object

Examples

```
set.seed(1)
dummy_importance <- runif(20)^5
names(dummy_importance) <- paste0("var", 1:20)
importance_plot(dummy_importance, top_n = 15, split_at = 10, save_plot = FALSE)
```

---

indicate_duplicates *Determine duplicate elements including their first occurrence.*

Description

If an element is duplicated, all of its occurrence will be labeled TRUE. Useful to list and compare all duplicates.

Usage

```
indicate_duplicates(x)
```

Arguments

x	A vector.

Value

A logical vector.

Examples

```
indicate_duplicates(c(1, 2, NA, NA, 1))
indicate_duplicates(c(1, 2, 3, 4, 4))

# Useful to check duplicates in data frames.
df <- data.frame(
  id = c(1, 2, 1, 2, 3), year = c(2010, 2011, 2010, 2010, 2011),
  value = c(1, 2, 3, 4, 5)
)
df[indicate_duplicates(df[, c("id", "year")]), ]
```

`interaction_plot` *Plot interactions*

Description

Plot interactions between variables. Both logistic and Cox proportional hazards regression models are supported. The predictor variables in the model are can be used both in linear form or in restricted cubic spline form.

Usage

```
interaction_plot(
  data,
  y,
  predictor,
  group_var,
  time = NULL,
  time2 = NULL,
  covars = NULL,
  cluster = NULL,
  group_colors = NULL,
  save_plot = FALSE,
  filename = NULL,
  height = 4,
  width = 4,
  xlab = predictor,
  ylab = NULL,
  show_n = TRUE,
  group_title = group_var,
  ...
)
```

Arguments

`data`	A data frame.
`y`	A character string of the outcome variable.
`predictor`	A character string of the predictor variable.
`group_var`	A character string of the group variable. The variable should be categorical. If a numeric variable is provided, it will be split by the median value.
`time`	A character string of the time variable. If `NULL`, logistic regression is used. Otherwise, Cox proportional hazards regression is used.
`time2`	A character string of the ending time of the interval for interval censored or counting process data only.
`covars`	A character vector of covariate names.

cluster	A character string of the cluster variable. If set, correct for heteroscedasticity and for correlated responses from cluster samples using `rms::robcov()`.
group_colors	A character vector of colors for the plot. If `NULL`, the default colors are used.
save_plot	A logical value indicating whether to save the plot.
filename	The name of the file to save the plot. Support both `.png` and `.pdf` formats.
height	The height of the saved plot.
width	The width of the saved plot.
xlab	The label of the x-axis.
ylab	The label of the y-axis.
show_n	A logical value indicating whether to show the number of observations in the plot.
group_title	The title of the group variable.
...	Additional arguments passed to the `ggplot` function.

Value

A `ggplot` object.

Examples

```
data(cancer, package = "survival")
interaction_plot(cancer,
  y = "status", time = "time", predictor = "age", group_var = "sex",
  save_plot = FALSE
)
interaction_plot(cancer,
  y = "status", predictor = "age", group_var = "sex",
  save_plot = FALSE
)
interaction_plot(cancer,
  y = "wt.loss", predictor = "age", group_var = "sex",
  save_plot = FALSE
)
```

---

interaction_p_value *Calculate interaction p-value*

Description

This function calculates the interaction p-value between a predictor and a group variable in a linear, logistic, or Cox proportional hazards model.

Usage

```
interaction_p_value(
  data,
  y,
  predictor,
  group_var,
  time = NULL,
  time2 = NULL,
  covars = NULL,
  cluster = NULL,
  rcs_knots = NULL
)
```

Arguments

data	A data frame.
y	A character string of the outcome variable. The variable should be binary or numeric and determines the type of model to be used. If the variable is binary, logistic or Cox regression is used. If the variable is numeric, linear regression is used.
predictor	A character string of the predictor variable.
group_var	A character string of the group variable. The variable should be categorical. If a numeric variable is provided, it will be split by the median value.
time	A character string of the time variable. If NULL, linear or logistic regression is used. Otherwise, Cox proportional hazards regression is used.
time2	A character string of the ending time of the interval for interval censored or counting process data only.
covars	A character vector of covariate names.
cluster	A character string of the cluster variable. If set, correct for heteroscedasticity and for correlated responses from cluster samples using rms::robcov().
rcs_knots	The number of rcs knots. If NULL, a linear model would be fitted instead.

Value

A numerical, the interaction p-value

Examples

```
data(cancer, package = "survival")
interaction_p_value(
  data = cancer, y = "status", predictor = "age", group_var = "sex",
  time = "time", rcs_knots = 4
)
```

`interaction_scan` *Scan for interactions between variables*

Description

Scan for interactions between variables and output results. Both logistic and Cox proportional hazards regression models are supported. The predictor variables in the model are can be used both in linear form or in restricted cubic spline form.

Usage

```
interaction_scan(
  data,
  y,
  time = NULL,
  time2 = NULL,
  predictors = NULL,
  group_vars = NULL,
  covars = NULL,
  cluster = NULL,
  try_rcs = TRUE,
  p_adjust_method = "BH",
  save_table = FALSE,
  filename = NULL
)
```

Arguments

`data`	A data frame.
`y`	A character string of the outcome variable.
`time`	A character string of the time variable. If `NULL`, logistic regression is used. Otherwise, Cox proportional hazards regression is used.
`time2`	A character string of the ending time of the interval for interval censored or counting process data only.
`predictors`	The predictor variables to be scanned for interactions. If `NULL`, all variables except `y` and `time` are taken as predictors.
`group_vars`	The group variables to be scanned for interactions. If `NULL`, all variables except `y` and `time` are taken as group variables. The group variables should be categorical. If a numeric variable is included, it will be split by the median value.
`covars`	A character vector of covariate names.
`cluster`	A character string of the cluster variable. If set, correct for heteroscedasticity and for correlated responses from cluster samples using `rms::robcov()`.
`try_rcs`	A logical value indicating whether to perform restricted cubic spline interaction analysis.

p_adjust_method
: The method to use for p-value adjustment for pairwise comparison. Default is "BH". See ?p.adjust.methods.

save_table
: A logical value indicating whether to save the results as a table.

filename
: The name of the file to save the results. File will be saved in .csv format.

Value

A data frame containing the results of the interaction analysis.

Examples

```
data(cancer, package = "survival")
interaction_scan(cancer, y = "status", time = "time", save_table = FALSE)
```

---

keep_by_keyword *Keep string segment by regex keyword position*

Description

Desensitize a character vector by removing the unneeded part of each string. The retained part is determined by keyword matches from a regular expression.

Usage

```
keep_by_keyword(
  x,
  keyword,
  from = c("start", "first", "last"),
  to = c("first", "last", "end"),
  include_keyword = TRUE
)
```

Arguments

x
: A character vector.

keyword
: A regular expression keyword pattern.

from
: Left boundary of retained text:
  - "start": start of the string.
  - "first": first keyword match.
  - "last": last keyword match.

to
: Right boundary of retained text:
  - "first": first keyword match.
  - "last": last keyword match.
  - "end": end of the string.

include_keyword
: Logical. Whether to include the keyword match used as split point in output.

Value

A character vector with retained text only.

Examples

```
urls <- c(
  "https://hospital.example.com/patient/123?token=abc",
  "https://trial.example.org/visit/456"
)
# Keep domain only
keep_by_keyword(urls, "com|org|net", from = "start", to = "last", include_keyword = TRUE)

ids <- c("SITE-2026-0001", "CTR-2025-0912")
# Keep site prefix before first '-'
keep_by_keyword(ids, "-", from = "start", to = "first", include_keyword = FALSE)
```

---

mad_outlier *Mark possible outliers using different methods.*

Description

Mark possible outliers in a numeric vector using various methods. These functions return a logical vector indicating which values are outliers.

Usage

```
mad_outlier(x, threshold = 1.4826 * 3)

iqr_outlier(x, threshold = 1.5)

zscore_outlier(x, threshold = 3)
```

Arguments

x	A numeric vector.
threshold	The threshold value for detecting outliers. Defaults depend on the method: • For MAD method: 1.4826 * 3 (approximately 3 standard deviations) • For IQR method: 1.5 (Tukey's rule) • For Z-score method: 3 (3 standard deviations)

Details

- **MAD method**: Uses median absolute deviation to identify outliers. Values with absolute deviation from the median greater than the threshold are considered outliers.
- **IQR method**: Uses interquartile range to identify outliers. Values below Q1 - threshold * IQR or above Q3 + threshold * IQR are considered outliers.
- **Z-score method**: Uses standardized Z-scores to identify outliers. Values with an absolute Z-score greater than the threshold are considered outliers.

Value

A logical vector indicating which values are outliers.

Examples

```
x <- c(1, 2, 3, 4, 5, 100, NA)
mad_outlier(x)
iqr_outlier(x, threshold = 2.0)
zscore_outlier(x, threshold = 2.5)
```

---

max_missing_rates *Get the maximum missing rate of rows and columns.*

Description

Get the maximum missing rate of rows and columns.

Usage

```
max_missing_rates(df)
```

Arguments

df	A data frame.

Value

A list that contains the maximum missing rate of rows and columns.

Examples

```
data(cancer, package = "survival")
max_missing_rates(cancer)
```

`merge_by_range` *Merge Data Frames by Exact Keys and Value Range*

Description

Merge two data frames where shared keys in `by` must match exactly and the value in `y[[y_val]]` must fall within the range defined by `x[[x_start]]` and `x[[x_end]]`.

This function is particularly useful for date-based matching scenarios, where you need to match events (e.g., examinations, treatments) to time intervals (e.g., hospital admissions, visits). While the function accepts any ordered values (numeric, Date, POSIXt), date matching is the primary use case.

This avoids constructing the full Cartesian product that would be produced by a regular equality join followed by range filtering.

Merge two data frames where shared keys in `by` must match exactly and the value in `y[[y_val]]` must fall within the range defined by `x[[x_start]]` and `x[[x_end]]`.

This function is particularly useful for date-based matching scenarios, where you need to match events (e.g., examinations, treatments) to time intervals (e.g., hospital admissions, visits). While the function accepts any ordered values (numeric, Date, POSIXt), date matching is the primary use case.

This avoids constructing the full Cartesian product that would be produced by a regular equality join followed by range filtering.

Usage

```
merge_by_range(
  x,
  y,
  by,
  x_start,
  x_end = NULL,
  y_val,
  range_relax = c(0, 0),
  all_y = TRUE,
  suffixes = c(".x", ".y")
)

merge_by_range(
  x,
  y,
  by,
  x_start,
  x_end = NULL,
  y_val,
  range_relax = c(0, 0),
  all_y = TRUE,
```

```
  suffixes = c(".x", ".y")
)
```

Arguments

x	A data frame containing the range columns.
y	A data frame containing the point-in-time value column.
by	Either a character vector of column names that must match exactly in both data frames, or a named list with elements x and y specifying different column names in each data frame (e.g., `list(x = c("id1", "id2"), y = c("ID1", "ID2"))`). The two vectors must have the same length and are matched by position. Use `character(0)` when no exact-match keys are needed.
x_start	Column name in x containing the range start.
x_end	Column name in x containing the range end. If NULL, defaults to x_start (treating the range as a single point).
y_val	Column name in y containing the value to be matched.
range_relax	A numeric vector of length 2 specifying how to extend the matching range. The first element extends backwards from x_start, the second extends forwards from x_end. Default is `c(0, 0)` (no extension). Both values must be >= 0.
all_y	Logical, whether to keep rows from y that have no match.
suffixes	Character vector of length 2 used for duplicated non-key column names from x and y.

Details

Matching proceeds in three stages:

1. Rows in x and y are first grouped by the exact-match keys in by.
2. Within each group, `y[[y_val]]` is matched against the interval defined by `x[[x_start]]` and `x[[x_end]]`, optionally extended by range_relax.
3. When range_relax is non-zero, the relaxed intervals are clipped against neighboring core intervals before matching, but never clipped further than the original core interval.

If any row from y still matches multiple clipped ranges in x, a warning is issued and `.cp_y_row_id` is retained in the output so duplicate matches can be identified downstream.

When `all_y = TRUE`, rows from y with no match are appended to the result with NA values for columns coming from x and for since_start.

Matching proceeds in three stages:

1. Rows in x and y are first grouped by the exact-match keys in by.
2. Within each group, `y[[y_val]]` is matched against the interval defined by `x[[x_start]]` and `x[[x_end]]`, optionally extended by range_relax.
3. When range_relax is non-zero, the relaxed intervals are clipped against neighboring core intervals before matching, but never clipped further than the original core interval.

If any row from y still matches multiple clipped ranges in x, a warning is issued and .cp_y_row_id is retained in the output so duplicate matches can be identified downstream.

When all_y = TRUE, rows from y with no match are appended to the result with NA values for columns coming from x and for since_start.

Value

A data frame containing matched rows from x and y. The output includes a since_start column indicating the numeric difference between y_val and x_start (in the units of the values, e.g., days for Date objects).

A data frame containing matched rows from x and y. The output includes a since_start column indicating the numeric difference between y_val and x_start (in the units of the values, e.g., days for Date objects).

Examples

```
admissions <- data.frame(
  patient_id = c(1, 1, 2),
  date_start = as.Date(c("2024-01-01", "2024-02-01", "2024-03-01")),
  date_end = as.Date(c("2024-01-10", "2024-02-10", "2024-03-05")),
  ward = c("A", "B", "C")
)
examinations <- data.frame(
  patient_id = c(1, 1, 2, 3),
  exam_date = as.Date(c("2024-01-05", "2024-02-10", "2024-03-07", "2024-01-01")),
  exam_name = c("CT", "MRI", "XR", "US")
)

merge_by_range(
  x = admissions,
  y = examinations,
  by = "patient_id",
  x_start = "date_start",
  x_end = "date_end",
  y_val = "exam_date"
)

admissions <- data.frame(
  patient_id = c(1, 1, 2),
  date_start = as.Date(c("2024-01-01", "2024-02-01", "2024-03-01")),
  date_end = as.Date(c("2024-01-10", "2024-02-10", "2024-03-05")),
  ward = c("A", "B", "C")
)
examinations <- data.frame(
  patient_id = c(1, 1, 2, 3),
  exam_date = as.Date(c("2024-01-05", "2024-02-10", "2024-03-07", "2024-01-01")),
  exam_name = c("CT", "MRI", "XR", "US")
)

merge_by_range(
  x = admissions,
```

```
  y = examinations,
  by = "patient_id",
  x_start = "date_start",
  x_end = "date_end",
  y_val = "exam_date"
)
```

`merge_by_substring` *Merge Data Frame by String Key Matching*

Description

This function merges two data frames based on string key matching. It searches for keys from `key_df[[key_col]]` in `data[[search_col]]` and adds corresponding columns from `key_df` to `data`.

Usage

```
merge_by_substring(
  data,
  key_df,
  search_col,
  key_col,
  value_cols,
  case_insensitive = TRUE,
  ...
)
```

Arguments

`data`	The primary data frame to be enhanced with additional columns
`key_df`	A data frame containing string keys and their corresponding values
`search_col`	Column name in `data` to search for keys (default: "name")
`key_col`	Column name in `key_df` containing keys to match (default: "key")
`value_cols`	Column name(s) in `key_df` to add to `data` (default: "value") Can be a single column name or a character vector of column names. Defaults to "value" if not provided.
`case_insensitive`	Whether to perform case-insensitive matching (default: TRUE) Defaults to TRUE if not provided.
`...`	Additional arguments passed to `stringi::stri_detect_regex()`.

Value

A data frame with all columns from `data` plus matched columns from `key_df`. Unmatched rows will have NA values in the added columns.

Examples

```
# Basic usage
main_data <- data.frame(
  name = c("AB", "B,C", "A..", "ACD"),
  value = c(1, 2, 3, 4)
)
key_lookup <- data.frame(
  key = c("A", "B", "C", "ACD", "AB"),
  category = c("cat1", "cat2", "cat3", "cat4", "cat1"),
  code = c("001", "002", "003", "004", "001")
)
result <- merge_by_substring(main_data, key_lookup,
  search_col = "name",
  key_col = "key", value_cols = c("category", "code")
)
print(result)
```

`merge_ordered_vectors` *Merging vectors while maintaining order*

Description

Merge multiple vectors into one while trying to maintain the order of elements in each vector. The relative order of elements is compared by their first occurrence in the vectors in the list. This function is useful when merging slightly different vectors, such as questionnaires of different versions.

Usage

```
merge_ordered_vectors(vectors)
```

Arguments

`vectors`	A list of vectors to be merged.

Value

A vector.

Examples

```
merge_ordered_vectors(list(c(1, 3, 4, 5, 7, 10), c(2, 5, 6, 7, 8), c(1, 7, 5, 10)))
```

na2false *Replace NA values with FALSE*

Description

Replace NA values with FALSE in logical vectors. For other vectors, the behavior relies on R's automatic conversion rules.

Usage

```
na2false(x)
```

Arguments

x	A vector.

Value

A vector with NA values replaced by FALSE.

Examples

```
na2false(c(TRUE, FALSE, NA, TRUE, NA))
na2false(c(1, 2, NA))
```

na_max *Safe min and max functions that return NA if all values are NA*

Description

Instead of returning -Inf or Inf, returns NA if all values are NA. It also ignores NA values by default, which is different from base R functions. This is useful when summarizing data frames with dplyr::summarise().

Usage

```
na_max(x, na.rm = TRUE)

na_min(x, na.rm = TRUE)
```

Arguments

x	A numeric vector.
na.rm	A logical value indicating whether to remove NA values before computation. Defaults to TRUE instead of FALSE in base R functions.

Value

The minimum or maximum value of the vector or NA if all values are NA.

Examples

```
na_max(c(1, 2, 3, NA))
na_min(c(NA, NA, NA))
```

---

predictor_effect_plot *Plot the effect of a predictor variable*

Description

This is a versatile function to plot the relationship between a predictor variable and the outcome. It supports numeric (linear or RCS) and categorical predictors for logistic, linear, and Cox models. It can display the distribution of the predictor variable as a histogram (for numeric) or bar plot (for categorical).

Usage

```
predictor_effect_plot(
  data,
  x,
  y,
  time = NULL,
  time2 = NULL,
  covars = NULL,
  cluster = NULL,
  method = "auto",
  knot = 4,
  add_hist = TRUE,
  ref = "x_median",
  ref_digits = 3,
  show_total_n = TRUE,
  group_by_ref = TRUE,
  group_title = NULL,
  group_labels = NULL,
  group_colors = NULL,
  breaks = 20,
  line_color = "#e23e57",
  print_p_ph = TRUE,
  trans = "identity",
  save_plot = FALSE,
  create_dir = FALSE,
  filename = NULL,
  y_lim = NULL,
  hist_max = NULL,
```

```
  xlim = NULL,
  height = 6,
  width = 6,
  return_details = FALSE
)
```

Arguments

data	A data frame.
x	A character string of the predictor variable.
y	A character string of the outcome variable.
time	A character string of the time variable for Cox models. If NULL, logistic or linear regression is used.
time2	A character string of the ending time for interval-censored or counting process data.
covars	A character vector of covariate names.
cluster	A character string of the cluster variable for robust variance estimation.
method	A character string specifying the method for handling the predictor x. Can be "auto", "rcs", "linear", or "categorical". If "auto", the function decides based on the type of x.
knot	The number of knots for RCS. If NULL, AIC is used to find the optimal number.
add_hist	A logical value. If TRUE, add a distribution plot (histogram or bar plot).
ref	The reference value for numeric predictors, or the reference level for categorical predictors. For numeric x, can be "x_median", "x_mean", "ratio_min", or a numeric value.
ref_digits	The number of digits for the reference value label.
show_total_n	A logical value. If TRUE, show the total number of samples.
group_by_ref	A logical value. If TRUE and x is numeric, split the histogram at the reference value.
group_title	A character string for the group legend title.
group_labels	A character vector for group labels.
group_colors	A character vector of colors for the distribution plot. If NULL, the default colors are used. If group_by_ref is FALSE, the first color is used as fill color.
breaks	The number of breaks for the histogram.
line_color	The color for the effect line/points.
print_p_ph	A logical value. If TRUE (and model is Cox), print the p-value for the proportional hazards test.
trans	The transformation for the y-axis. Passed to ggplot2::scale_y_continuous(transform = trans).
save_plot	A logical value indicating whether to save the plot.
create_dir	A logical value for creating the save directory.
filename	A character string for the saved plot filename.

y_lim	The y-axis limits.
hist_max	The maximum value for the histogram y-axis.
xlim	The x-axis limits for numeric predictors. If NULL, the limits are the 0.025 and 0.975 quantiles. The actual plot range might be slightly larger than this range to fit the histogram.
height	The height of the saved plot.
width	The width of the saved plot.
return_details	A logical value indicating whether to return plot details.

Value

A ggplot object, or a list with the plot and details if return_details is TRUE.

Examples

```
data(cancer, package = "survival")
cancer$dead <- cancer$status == 2
cancer <- cancer[!is.na(cancer$inst), ]
predictor_effect_plot(
  data = cancer,
  x = "age",
  y = "dead",
  method = "linear",
  covars = "ph.karno",
  add_hist = FALSE,
  trans = "log2",
  save_plot = FALSE,
  cluster = "inst"
)
```

---

qq_show *QQ plot*

Description

QQ plot for a sample.

Usage

```
qq_show(
  x,
  title = NULL,
  save = FALSE,
  filename = "QQplot.png",
  width = 2,
  height = 2
)
```

Arguments

x	A sample.
title	Title of the plot.
save	If TRUE, save the plot.
filename	Filename of the plot.
width	Width of the plot.
height	Height of the plot.

Value

A plot.

Examples

```
qq_show(rnorm(100))
```

---

rcs_plot *Plot restricted cubic spline*

Description

This function is a wrapper for `predictor_effect_plot` with `method = "rcs"`. It plots a restricted cubic spline for a predictor in a regression model.

Usage

```
rcs_plot(
  data,
  x,
  y,
  time = NULL,
  time2 = NULL,
  covars = NULL,
  cluster = NULL,
  knot = 4,
  add_hist = TRUE,
  ref = "x_median",
  ref_digits = 3,
  show_total_n = TRUE,
  group_by_ref = TRUE,
  group_title = NULL,
  group_labels = NULL,
  group_colors = NULL,
  breaks = 20,
  rcs_color = "#e23e57",
```

```
  print_p_ph = TRUE,
  trans = "identity",
  save_plot = FALSE,
  create_dir = FALSE,
  filename = NULL,
  y_lim = NULL,
  hist_max = NULL,
  xlim = NULL,
  height = 6,
  width = 6,
  return_details = FALSE
)
```

Arguments

data	A data frame.
x	A character string of the predictor variable.
y	A character string of the outcome variable.
time	A character string of the time variable for Cox models. If NULL, logistic or linear regression is used.
time2	A character string of the ending time for interval-censored or counting process data.
covars	A character vector of covariate names.
cluster	A character string of the cluster variable for robust variance estimation.
knot	The number of knots for RCS. If NULL, AIC is used to find the optimal number.
add_hist	A logical value. If TRUE, add a distribution plot (histogram or bar plot).
ref	The reference value for numeric predictors, or the reference level for categorical predictors. For numeric x, can be "x_median", "x_mean", "ratio_min", or a numeric value.
ref_digits	The number of digits for the reference value label.
show_total_n	A logical value. If TRUE, show the total number of samples.
group_by_ref	A logical value. If TRUE and x is numeric, split the histogram at the reference value.
group_title	A character string for the group legend title.
group_labels	A character vector for group labels.
group_colors	A character vector of colors for the distribution plot. If NULL, the default colors are used. If group_by_ref is FALSE, the first color is used as fill color.
breaks	The number of breaks for the histogram.
rcs_color	The color for the restricted cubic spline. This is passed to line_color in predictor_effect_plot.
print_p_ph	A logical value. If TRUE (and model is Cox), print the p-value for the proportional hazards test.

trans	The transformation for the y-axis. Passed to ggplot2::scale_y_continuous(transform = trans).
save_plot	A logical value indicating whether to save the plot.
create_dir	A logical value for creating the save directory.
filename	A character string for the saved plot filename.
y_lim	The y-axis limits.
hist_max	The maximum value for the histogram y-axis.
xlim	The x-axis limits for numeric predictors. If NULL, the limits are the 0.025 and 0.975 quantiles. The actual plot range might be slightly larger than this range to fit the histogram.
height	The height of the saved plot.
width	The width of the saved plot.
return_details	A logical value indicating whether to return plot details.

Value

A ggplot object, or a list containing the ggplot object and other details if return_details is TRUE.

Examples

```
data(cancer, package = "survival")
# coxph model with time assigned
rcs_plot(cancer, x = "age", y = "status", time = "time", covars = "ph.karno", save_plot = FALSE)

# logistic model with time not assigned
cancer$dead <- cancer$status == 2
rcs_plot(cancer, x = "age", y = "dead", covars = "ph.karno", save_plot = FALSE)
```

---

regression_basic_results

Basic results of logistic or Cox regression.

Description

Generate the result table of logistic or Cox regression with different settings of the predictor variable and covariates. Also generate KM curves for Cox regression.

Usage

```
regression_basic_results(
  data,
  x,
  y,
  time = NULL,
```

```
  time2 = NULL,
  model_covs = NULL,
  cluster = NULL,
  pers = c(0.1, 10, 100),
  factor_breaks = NULL,
  factor_labels = NULL,
  quantile_breaks = NULL,
  quantile_labels = NULL,
  label_with_range = FALSE,
  save_output = FALSE,
  figure_type = "png",
  ref_levels = "lowest",
  est_nsmall = 2,
  p_nsmall = 3,
  pval_eps = 0.001,
  median_nsmall = 0,
  colors = NULL,
  xlab = NULL,
  legend_title = x,
  legend_pos = c(0.8, 0.8),
  pval_pos = NULL,
  n_y_pos = 0.9,
  height = 6,
  width = 6,
  ...
)
```

Arguments

data	A data frame.
x	A character string of the predictor variable.
y	A character string of the outcome variable.
time	A character string of the time variable. If NULL, logistic regression is used. Otherwise, Cox proportional hazards regression is used.
time2	A character string of the ending time of the interval for interval censored or counting process data only.
model_covs	A character vector or a named list of covariates for different models. If NULL, only the crude model is used.
cluster	A character string of the cluster variable. If set, correct for heteroscedasticity and for correlated responses from cluster samples using rms::robcov().
pers	A numeric vector of the denominators of variable x. Set this denominator to obtain a reasonable OR or HR.
factor_breaks	A numeric vector of the breaks to factorize the x variable.
factor_labels	A character vector of the labels for the factor levels.
quantile_breaks	A numeric vector of the quantile breaks to factorize the x variable.

quantile_labels
: A character vector of the labels for the quantile levels.

label_with_range
: A logical value indicating whether to add the range of the levels to the labels.

save_output
: A logical value indicating whether to save the results.

figure_type
: A character string of the figure type. Can be "png", "pdf", and other types that ggplot2::ggsave() support.

ref_levels
: A vector of strings of the reference levels of the factor variable. You can use "lowest" or "highest" to select the lowest or highest level as the reference level. Otherwise, any level that matches the provided strings will be used as the reference level.

est_nsmall
: An integer specifying the precision for the estimates in the plot.

p_nsmall
: An integer specifying the number of decimal places for the p-values.

pval_eps
: The threshold for rounding p values to 0.

median_nsmall
: The minimum number of digits to the right of the decimal point for the median survival time.

colors
: A vector of colors for the KM curves.

xlab
: A character string of the x-axis label of the survival plot.

legend_title
: A character string of the title of the legend.

legend_pos
: A numeric vector of the position of the legend.

pval_pos
: A numeric vector of the position of the p-value.

n_y_pos
: A numerical of range 0 to 1 to assign the y position of total sample count. NULL to hide.

height
: The height of the plot.

width
: The width of the plot.

...
: Additional arguments passed to the survminer::ggsurvplot function for KM curve.

Details

The function regression_basic_results generates the result table of logistic or Cox regression with different settings of the predictor variable and covariates. The setting of the predictor variable includes the original x, the standardized x, the log of x, and x divided by denominators in pers as continuous variables, and the factorization of the variable including split by median, by quartiles, and by factor_breaks and quantile_breaks. The setting of the covariates includes different models with different covariates.

Value

A list of results, including the regression table and the KM curve plots.

Note

For factor variables with more than 2 levels, p value for trend is also calculated.

Examples

```
data(cancer, package = "survival")
# coxph model with time assigned
res1 <- regression_basic_results(cancer,
  x = "age", y = "status", time = "time",
  model_covs = list(Crude = c(), Model1 = c("ph.karno"), Model2 = c("ph.karno", "sex")),
  save_output = FALSE,
 ggtheme = survminer::theme_survminer(font.legend = c(14, "plain", "black")) # theme for KM
)

# logistic model with time not assigned
cancer$dead <- cancer$status == 2
res2 <- regression_basic_results(cancer,
  x = "age", y = "dead", ref_levels = c("Q3", "High"),
  model_covs = list(Crude = c(), Model1 = c("ph.karno"), Model2 = c("ph.karno", "sex")),
  save_output = FALSE
)
```

---

regression_fit *Obtain regression results*

Description

This function fit the regression of a predictor in a linear, logistic, or Cox proportional hazards model.

Usage

```
regression_fit(
  data,
  y,
  predictor,
  time = NULL,
  time2 = NULL,
  covars = NULL,
  cluster = NULL,
  rcs_knots = NULL,
  returned = c("full", "predictor_split", "predictor_combined")
)
```

Arguments

data	A data frame.
y	A character string of the outcome variable. The variable should be binary or numeric and determines the type of model to be used. If the variable is binary, logistic or cox regression is used. If the variable is numeric, linear regression is used.
predictor	A character string of the predictor variable.

time — A character string of the time variable. If NULL, linear or logistic regression is used. Otherwise, Cox proportional hazards regression is used.

time2 — A character string of the ending time of the interval for interval censored or counting process data only.

covars — A character vector of covariate names.

cluster — A character string of the cluster variable. If set, correct for heteroscedasticity and for correlated responses from cluster samples using rms::robcov().

rcs_knots — The number of rcs knots. If NULL, a linear model would be fitted instead.

returned — The return mode of this function.

- "full": return the full regression result.
- "predictor_split": return the regression parameter of the predictor, could have multiple lines.
- "predictor_combined": return the regression parameter of the predictor, test the predictor as a whole and takes only one line.

Value

A list containing the regression ratio and p-value of the predictor. If rcs_knots is not NULL, the list contains the overall p-value and the nonlinear p-value of the rcs model. If return_full_result is TRUE, the complete result of the regression model is returned.

Examples

```
data(cancer, package = "survival")
regression_fit(data = cancer, y = "status", predictor = "age", time = "time", rcs_knots = 4)
```

---

regression_forest *Forest plot of regression results*

Description

Generate the forest plot of logistic or Cox regression with different models.

Usage

```
regression_forest(
  data,
  model_vars,
  y,
  time = NULL,
  time2 = NULL,
  cluster = NULL,
  as_univariate = FALSE,
  est_nsmall = 2,
  p_nsmall = 3,
```

```
  show_vars = NULL,
  save_plot = FALSE,
  filename = NULL,
  ...
)
```

Arguments

data	A data frame.
model_vars	A character vector or a named list of predictor variables for different models.
y	A character string of the outcome variable.
time	A character string of the time variable. If NULL, logistic regression is used. Otherwise, Cox proportional hazards regression is used.
time2	A character string of the ending time of the interval for interval censored or counting process data only.
cluster	A character string of the cluster variable. If set, correct for heteroscedasticity and for correlated responses from cluster samples using rms::robcov().
as_univariate	A logical value indicating whether to treat the model_vars as univariate.
est_nsmall	An integer specifying the precision for the estimates in the plot.
p_nsmall	An integer specifying the number of decimal places for the p-values.
show_vars	A character vector of variable names to be shown in the plot. If NULL, all variables are shown.
save_plot	A logical value indicating whether to save the plot.
filename	A character string specifying the filename for the plot. If NULL, a default filename is used.
...	Additional arguments passed to the forestploter::forest function.

Value

A gtable object.

Examples

```
data(cancer, package = "survival")
cancer$ph.ecog_cat <- factor(cancer$ph.ecog, levels = c(0:3), labels = c("0", "1", ">=2", ">=2"))
regression_forest(cancer,
 model_vars = c("age", "sex", "wt.loss", "ph.ecog_cat", "meal.cal"), y = "status", time = "time",
  as_univariate = TRUE, save_plot = FALSE
)

regression_forest(cancer,
 model_vars = c("age", "sex", "wt.loss", "ph.ecog_cat", "meal.cal"), y = "status", time = "time",
  show_vars = c("age", "sex", "ph.ecog_cat", "meal.cal"), save_plot = FALSE
)

regression_forest(cancer,
  model_vars = list(
```

```
    M0 = c("age"),
    M1 = c("age", "sex", "wt.loss", "ph.ecog_cat", "meal.cal"),
    M2 = c("age", "sex", "wt.loss", "ph.ecog_cat", "meal.cal", "pat.karno")
  ),
  y = "status", time = "time",
  show_vars = c("age", "sex", "ph.ecog_cat", "meal.cal"), save_plot = FALSE
)
```

`regression_scan` *Scan for significant regression predictors*

Description

Scan for significant regression predictors and output results. Both logistic and Cox proportional hazards regression models are supported. The predictor variables in the model are can be used both in linear form or in restricted cubic spline form.

Usage

```
regression_scan(
  data,
  y,
  time = NULL,
  time2 = NULL,
  predictors = NULL,
  covars = NULL,
  cluster = NULL,
  num_to_factor = 5,
  p_adjust_method = "BH",
  save_table = FALSE,
  filename = NULL
)
```

Arguments

`data`	A data frame.
`y`	A character string of the outcome variable.
`time`	A character string of the time variable. If `NULL`, logistic regression is used. Otherwise, Cox proportional hazards regression is used.
`time2`	A character string of the ending time of the interval for interval censored or counting process data only.
`predictors`	The predictor variables to be scanned for relationships. If `NULL`, all variables except `y` and `time` are taken as predictors.
`covars`	A character vector of covariate names.
`cluster`	A character string of the cluster variable. If set, correct for heteroscedasticity and for correlated responses from cluster samples using `rms::robcov()`.

num_to_factor An integer. Numerical variables with number of unique values below or equal to this value would be considered a factor.

p_adjust_method
The method to use for p-value adjustment. Default is "BH". See `?p.adjust.methods`. Note that the p-value adjustment is only applied column wise, not applied among all available p-values in the table.

save_table A logical value indicating whether to save the results as a table.

filename The name of the file to save the results. File will be saved in `.csv` format.

Details

The function first determines the type of each predictor variable (`numerical`, `factor`, `num_factor` (numerical but with less unique values than or equal to `num_to_factor`), or `other`). Then, it performs regression analysis for available transforms of each predictor variable and saves the results.

Value

A data frame containing the results of the regression analysis.

The available transforms for each predictor type are

- `numerical`: `original`, `logarithm`, `categorized`, `rcs`
- `num_factor`: `original`, `categorized`
- `factor`: `original`
- `other`: none

The transforms are applied as follows

- `original`: Fit the regression model with the original variable. Provide HR/OR and p-values in results.
- `logarithm`: If the `numerical` variable is all greater than 0, fit the regression model with the log-transformed variable. Provide HR/OR and p-values in results.
- `categorized`: For `numerical` variables, fit the regression model with the binarized variable split at the median value. For `num_factor` variables, fit the regression model with the variable after `as.factor()`. Provide HR/OR and p-values in results. If the number of levels is greater than 2, no single HR/OR is provided, but the p-value of the overall test can be provided with TYPE-2 ANOVA from `car::Anova()`.
- `rcs`: Fit the regression model with the restricted cubic spline variable. The overall and nonlinear p-values are provided in results. These p-vals are calculated by `anova()` of `rms::cph()` or `rms::Glm`.

Examples

```
data(cancer, package = "survival")
regression_scan(cancer, y = "status", time = "time", save_table = FALSE)
```

replace_elements *Replacing elements in a vector*

Description

Replacing elements in a vector

Usage

```
replace_elements(x, from, to)
```

Arguments

x	A vector.
from	A vector of elements to be replaced.
to	A vector of elements to replace the original ones.

Value

A vector.

Examples

```
replace_elements(c("a", "x", "1", NA, "a"), c("a", "b", NA), c("A", "B", "XX"))
```

screen_data_list *Screen and Join Multi-Table Clinical Data by Expression*

Description

One-call cohort screening pipeline with expression stages:

1. entry stage: evaluate `entry_expr` and decide which keys enter downstream;
2. anchor stage (optional): evaluate `anchor_expr` and keep records from first anchor onward;
3. optional follow-up visit filtering;
4. optional outer-join integration.

`entry_expr` and `anchor_expr` support boolean combinations of grouped terms, for example: `any(Hb > 10) & all(icd != "J18")` or `mean(Hb, na.rm = TRUE) > 10 & any(icd == "I10")`. `&` is applied as set intersection and `|` as set union on keys defined by level.

Usage

```
screen_data_list(
  data_list,
  entry_expr,
  entry_level = c("patient_id", "visit_id", "date"),
  anchor_expr = NULL,
  anchor_level = c("date", "visit_id"),
  anchor_window = c("from_first_anchor", "none"),
  patient_id_map,
  visit_id_map = NULL,
  date_map = NULL,
  followup_min_visits = NULL,
  followup_table = NULL,
  output = c("list", "joined"),
  return_audit = FALSE,
  verbose = FALSE
)
```

Arguments

`data_list`	A named list of data frames. If `output = "joined"`, all tables will be outer-joined in the order of `data_list` after filtering. If `output = "list"`, tables are filtered but not joined.
`entry_expr`	Entry expression for key selection. Supports grouped terminal expressions combined by `&`, `|`, and parentheses.
`entry_level`	Granularity used to build entry keys: `"patient_id"`, `"visit_id"`, or `"date"`.
`anchor_expr`	Optional anchor expression. Same grammar as `entry_expr`.
`anchor_level`	Granularity used for anchor order: `"date"` or `"visit_id"`.
`anchor_window`	Anchor window strategy: `"none"` or `"from_first_anchor"`.
`patient_id_map, visit_id_map, date_map`	Join key column mappings. Each can be either: • a single column name (character of length 1) that is used as the patient/visit/date ID column for all tables that contain it, or • a named vector where names are table names and values are column names specific to each table.
`followup_min_visits`	Optional minimum number of distinct visits per patient.
`followup_table`	Table used to count follow-up visits. Only used when `followup_min_visits` is not `NULL`. If missing, defaults to the first table that has both `patient_id` and `visit_id` mappings.
`output`	Output format: `"list"` or `"joined"`. If `"joined"`, all tables will be outer-joined after filtering, which works best when join keys are unique and tables are in "wide" format.
`return_audit`	Logical, whether to return audit logs.
`verbose`	Logical, whether to print progress messages.

Value

If `return_audit = FALSE`, returns filtered list or joined data frame. If `return_audit = TRUE`, returns a list with:

- `data`: filtered list or joined data frame
- `audit$entry_scope`: entry key scope application log
- `audit$anchor_scope`: anchor window application log
- `audit$followup`: follow-up filtering log
- `audit$join`: join step log

Examples

```
patient <- data.frame(pid = 1:3)
admission <- data.frame(
  pid = c(1, 1, 2, 2, 3),
  vid = c(11, 12, 21, 22, 31),
  admit_day = c(1, 5, 2, 8, 3)
)
diagnosis <- data.frame(
  pid = c(1, 1, 2, 3),
  vid = c(11, 12, 21, 31),
  dx_day = c(1, 5, 2, 3),
  icd = c("I10", "I11", "I10", "J18")
)
lab <- data.frame(
  pid = c(1, 1, 2, 2, 3),
  vid = c(11, 12, 21, 22, 31),
  lab_day = c(1, 5, 2, 8, 3),
  Hb = c(9.8, 11.3, 10.8, 9.2, 8.6)
)

# Scenario 1: any target diagnosis, keep all records of matched patients.
res_s1 <- screen_data_list(
 data_list = list(patient = patient, admission = admission, diagnosis = diagnosis, lab = lab),
  entry_expr = any(icd == "I10"),
  entry_level = "patient_id",
  patient_id_map = "pid",
  output = "list"
)

# Scenario 2: any target diagnosis, keep diagnosis-index admission and after.
res_s2 <- screen_data_list(
 data_list = list(patient = patient, admission = admission, diagnosis = diagnosis, lab = lab),
  entry_expr = any(icd == "I10"),
  entry_level = "patient_id",
  anchor_expr = icd == "I10",
  anchor_level = "date",
  anchor_window = "from_first_anchor",
  patient_id_map = "pid",
  visit_id_map = c(admission = "vid", diagnosis = "vid", lab = "vid"),
  date_map = c(admission = "admit_day", diagnosis = "dx_day", lab = "lab_day"),
```

```
  output = "list"
)

# Scenario 3: target diagnosis patients, then abnormal indicator visit and after.
res_s3 <- screen_data_list(
 data_list = list(patient = patient, admission = admission, diagnosis = diagnosis, lab = lab),
  entry_expr = any(icd == "I10"),
  entry_level = "patient_id",
  anchor_expr = Hb > 10,
  anchor_level = "date",
  anchor_window = "from_first_anchor",
  patient_id_map = "pid",
  visit_id_map = c(admission = "vid", diagnosis = "vid", lab = "vid"),
  date_map = c(admission = "admit_day", diagnosis = "dx_day", lab = "lab_day"),
  output = "list"
)
```

`split_multichoice` *Split multi-choice data into columns*

Description

Split multi-choice data into columns, each new column consists of booleans whether a choice is presented.

Usage

```
split_multichoice(
  df,
  quest_cols,
  split = "",
  remove_space = TRUE,
  link = "_",
  remove_cols = TRUE
)
```

Arguments

`df`	A data frame.
`quest_cols`	A vector of column names that contain multi-choice data.
`split`	A string to split the data. Default is `""`.
`remove_space`	If `TRUE`, remove space in the data.
`link`	A string to link the column name and the option. Default is `"_"`.
`remove_cols`	If `TRUE`, remove the original columns.

Value

A data frame with additional columns.

Examples

```
df <- data.frame(q1 = c("ab", "c da", "b a", NA), q2 = c("a b", "a c", "d", "ab"))
split_multichoice(df, quest_cols = c("q1", "q2"))
```

`str_match_replace` *Match string and replace with corresponding value*

Description

Partially match a string and replace with corresponding value. This function is useful to recover the original names of variables after legalized using `make.names` or modified by other functions.

Usage

```
str_match_replace(x, to_match, to_replace)
```

Arguments

`x`	A vector.
`to_match`	A vector of strings to be matched.
`to_replace`	A vector of strings to replace the matched ones, must have the same length as `to_match`.

Value

A vector.

Examples

```
ori_names <- c("xx (mg/dl)", "b*x", "Covid-19")
modified_names <- c("v1", "v2", "v3")
x <- c("v1.v2", "v3.yy", "v4")
str_match_replace(x, modified_names, ori_names)
```

subgroup_forest *Create subgroup forest plot.*

Description

Create subgroup forest plot with `glm` or `coxph` models. The interaction p-values are calculated using likelihood ratio tests.

Usage

```
subgroup_forest(
  data,
  subgroup_vars,
  x,
  y,
  time = NULL,
  time2 = NULL,
  standardize_x = FALSE,
  covars = NULL,
  cluster = NULL,
  est_nsmall = 2,
  p_nsmall = 3,
  group_cut_quantiles = 0.5,
  save_plot = FALSE,
  filename = NULL,
  ...
)
```

Arguments

`data`	A data frame.
`subgroup_vars`	A character vector of variable names to be used as subgroups. It's recommended that the variables are categorical. If the variables are continuous, they will be cut into groups.
`x`	A character string of the predictor variable.
`y`	A character string of the outcome variable.
`time`	A character string of the time variable. If `NULL`, logistic regression is used. Otherwise, Cox proportional hazards regression is used.
`time2`	A character string of the ending time of the interval for interval censored or counting process data only.
`standardize_x`	A logical value. If `TRUE`, the predictor variable will be standardized.
`covars`	A character vector of covariate names.
`cluster`	A character string of the cluster variable. If set, correct for heteroscedasticity and for correlated responses from cluster samples using `rms::robcov()`.

est_nsmall	An integer specifying the precision for the estimates in the plot.
p_nsmall	An integer specifying the number of decimal places for the p-values.
group_cut_quantiles	A vector of numerical values between 0 and 1, specifying the quantile to use for cutting continuous subgroup variables.
save_plot	A logical value indicating whether to save the plot.
filename	A character string specifying the filename for the plot. If NULL, a default filename is used.
...	Additional arguments passed to the forestploter::forest function.

Value

A gtable object.

Examples

```
data(cancer, package = "survival")
# coxph model with time assigned
subgroup_forest(cancer,
  subgroup_vars = c("age", "sex", "wt.loss"), x = "ph.ecog", y = "status",
  time = "time", covars = "ph.karno", ticks_at = c(1, 2), save_plot = FALSE
)

# logistic model with time not assigned
cancer$dead <- cancer$status == 2
subgroup_forest(cancer,
  subgroup_vars = c("age", "sex", "wt.loss"), x = "ph.ecog", y = "dead",
  covars = "ph.karno", ticks_at = c(1, 2), save_plot = FALSE
)

cancer$ph.ecog_cat <- factor(cancer$ph.ecog, levels = c(0:3), labels = c("0", "1", ">=2", ">=2"))
subgroup_forest(cancer,
  subgroup_vars = c("sex", "wt.loss"), x = "ph.ecog_cat", y = "dead",
  covars = "ph.karno", ticks_at = c(1, 2), save_plot = FALSE
)
```

---

subject_view *Get an overview of different subjects in data.*

Description

Get a table of subject details for the clinical data. This table could be labeled and used for subject name standardization.

Usage

```
subject_view(
  df,
  subject_col,
  info_cols,
  value_col = NULL,
  info_n_samples = 10,
  info_collapse = "\n",
  info_unique = FALSE,
  save_table = FALSE,
  filename = NULL
)
```

Arguments

df	A data frame of medical records that contains test subject, value, and unit cols.
subject_col	The name of the subject column.
info_cols	The names of the columns to get detailed information.
value_col	The name of the column that contains values. This column must be numerical.
info_n_samples	The number of samples to show in the detailed information columns.
info_collapse	The separator to use for collapsing the detailed information.
info_unique	A logical value indicating whether to show unique values only.
save_table	A logical value indicating whether to save the table to a csv file.
filename	The name of the csv file to be saved.

Value

A data frame of subject details.

Examples

```
df <- data.frame(subject = sample(c("a", "b"), 1000, replace = TRUE), value = runif(1000))
df$unit <- NA
df$unit[df$subject == "a"] <- sample(c("mg/L", "g/l", "g/L"),
  sum(df$subject == "a"),
  replace = TRUE
)
df$value[df$subject == "a" & df$unit == "mg/L"] <-
  df$value[df$subject == "a" & df$unit == "mg/L"] * 1000
df$unit[df$subject == "b"] <- sample(c(NA, "g", "mg"), sum(df$subject == "b"), replace = TRUE)
df$value[df$subject == "b" & df$unit %in% "mg"] <-
  df$value[df$subject == "b" & df$unit %in% "mg"] * 1000
df$value[df$subject == "b" & is.na(df$unit)] <- df$value[df$subject == "b" & is.na(df$unit)] *
  sample(c(1, 1000), size = sum(df$subject == "b" & is.na(df$unit)), replace = TRUE)
subject_view(
  df = df, subject_col = "subject", info_cols = c("value", "unit"), value_col = "value",
  save_table = FALSE
)
```

`test_normality` *Test normality of a numeric variable*

Description

Perform multiple normality tests on a numeric variable and determine if it follows normal distribution.

Usage

```
test_normality(x, alpha = 0.05, all_positive = NULL)
```

Arguments

`x`	A numeric vector to test for normality.
`alpha`	The significance level for normality tests. Default is 0.05.
`all_positive`	A logical value indicating whether all values are non-negative. If TRUE and standard deviation is less than mean, the variable is considered non-normal (likely right-skewed).

Value

A logical value indicating whether the variable is normal (TRUE) or non-normal (FALSE).

Note

This function performs Shapiro-Wilk, Lilliefors, Anderson-Darling, Jarque-Bera, and Shapiro-Francia tests. If at least two of these tests indicate that the variable is nonnormal (p < alpha), then it is considered nonnormal. For positive variables, if SD < mean, it's also considered non-normal as it suggests right skewness.

Examples

```
# Test normal data
normal_data <- rnorm(100)
test_normality(normal_data)

# Test non-normal data
skewed_data <- rexp(100)
test_normality(skewed_data)
```

`time_roc_plot` *Calculate and plot time-dependent ROC curves*

Description

Calculate time-dependent ROC curves using the `timeROC` package and plot them using `ggplot2`.

Usage

```
time_roc_plot(
  data,
  time_var,
  event_var,
  marker_var,
  times = c(12, 36, 60),
  time_unit = "months",
  weighting = "marginal",
  cause = 1,
  colors = NULL,
  title = FALSE,
  save_plot = FALSE,
  filename = "time_roc.png"
)
```

Arguments

`data`	A data frame containing the survival time, event indicator, and marker variable.
`time_var`	A string specifying the name of the survival time variable in the data frame.
`event_var`	A string specifying the name of the event indicator variable in the data frame.
`marker_var`	A string specifying the name of the marker variable in the data frame.
`times`	A numeric vector of times at which to compute the time-dependent ROC curves.
`time_unit`	A character string specifying the unit of the time variable, recommended to be in plural form. Default is "months".
`weighting`	A character string specifying the weighting method. Default is "marginal". See `timeROC::timeROC()` for details.
`cause`	The value of the event indicator that denotes the event of interest. Default is `1`.
`colors`	A vector of colors to use for the ROC curves. If NULL, uses default colors.
`title`	A logical value indicating whether to include a title. Default is `FALSE`.
`save_plot`	A logical value indicating whether to save the plot to a file. Default is `FALSE`.
`filename`	A string specifying the filename to save the plot. Default is "time_roc.png".

Value

A list containing:

- time_roc: The timeROC result object.
- plot: A ggplot object of the time-dependent ROC curves.

Examples

```
# Plot time-dependent ROC curves using lung dataset from survival package
library(survival)
data(cancer, package = "survival")
# Use age as the marker variable, plot at 180, 365, and 730 days
lung$status <- lung$status == 2
result <- time_roc_plot(lung, "time", "status", "age", times = c(180, 365, 730), time_unit = "days")
result$plot

# Save the plot to a file
# time_roc_plot(lung, "time", "status", "age", times = c(180, 365, 730),
#               time_unit = "days", save_plot = TRUE)
```

---

to_date *Convert numerical or character date to date.*

Description

Convert numerical (especially Excel date) or character date to date. Can deal with common formats and allow different formats in one vector.

Usage

```
to_date(
  x,
  from_excel = TRUE,
  verbose = TRUE,
  try_formats = c("%Y-%m-%d", "%Y/%m/%d", "%Y%m%d", "%Y.%m.%d")
)
```

Arguments

x	A vector that stores dates in numerical or character types.
from_excel	If TRUE, treat numerical values as Excel dates.
verbose	If TRUE, print the values that cannot be converted.
try_formats	A character vector of date formats to try. Same as tryFormats in as.Date.

Value

A single valid value from the vector. NA if all values are invalid.

Examples

```
to_date(c(43562, "2020-01-01", "2020/01/01", "20200101", "2020.01.01"))
```

`to_wide` *Fast long-to-wide conversion with item selection*

Description

Convert long-format data to wide format by grouping keys, using one column as item names and one column as values. When there are multiple values under the same key-item combination, values are reduced by `agg_fun`. Designed to convert long-format clinical data in database to wide format for analysis and publication.

Usage

```
to_wide(df, keys, item_col, value_col, items = NULL, agg_fun = get_valid)
```

Arguments

`df`	A data frame in long format.
`keys`	A character vector of key column names.
`item_col`	A single column name that contains item names.
`value_col`	A single column name that contains values to spread.
`items`	Optional character vector of items to keep in wide format. If provided, output item columns follow this order and missing items are kept as `NA` columns.
`agg_fun`	Aggregation function used when key-item combinations have multiple values. Default is `get_valid()`.

Value

A wide-format data frame.

Examples

```
df <- data.frame(
  id = c(1, 1, 1, 2, 2),
  visit = c("v1", "v1", "v1", "v1", "v1"),
  item = c("A", "A", "B", "A", "C"),
  value = c(3, 5, 2, 1, 9)
)

to_wide(
  df,
  keys = c("id", "visit"),
  item_col = "item",
  value_col = "value",
  items = c("A", "B", "C"),
```

```
  agg_fun = max
)
```

`unit_standardize` *Standardize units of numeric data.*

Description

Standardize units of numeric data, especially for data of medical records with different units.

Usage

```
unit_standardize(
  df,
  subject_col,
  value_col,
  unit_col,
  change_rules,
  extract_numbers = FALSE,
  verbose = FALSE
)
```

Arguments

`df`	A data frame of medical records that contains test subject, value, and unit cols.
`subject_col`	The name of the subject column.
`value_col`	The name of the value column.
`unit_col`	The name of the unit column.
`change_rules`	A data frame or a list of lists. See details
`extract_numbers`	A logical value indicating whether to apply `extract_num` to extract numeric values from the value column.
`verbose`	A logical value indicating whether to print progress messages.

Details

`change_rules` can accept two formats: If a data frame, it must contain the following columns:

- `subject`: The subject to be standardized.
- `unit`: The units of the subject.
- `label`: The role of the unit, the rule is as follows:
  - `"t"`: the target unit to be standardized to. If not specified, the function will use the most common unit in the data (retrieved by `first_mode()`).
  - `"r"`: The units to be removed, and the corresponding values be set to `NA`. Set this when data with this unit cannot be used.

  - A number: Set the multiplier of this unit, the standardized value will be `value * multiplier`. And `NA` and `""` is considered the same as `1`.

If a list of lists, each list contains the following elements:

- `subject`: The subject to be standardized.
- `target_unit`: The target unit to be standardized to. If not specified, the function will use the most common unit in the data (retrieved by `first_mode()`).
- `units2change`: The units to be changed. If not specified, the function will use all units except the target unit. Must be specified to apply different `coeffs`.
- `coeffs`: The coefficients to be used for the conversion. If not specified, the function will use 1 for all units to be changed.
- `units2remove`: The units to be removed, and the corresponding values be set to `NA`. Set this when data with this unit cannot be used.

It's recommended to use the labeled result from `unit_view()` as the input.

Value

A data frame with subject units standardized.

Examples

```
# Example 1: Using the list as change_rules is more convenient for small datasets.
df <- data.frame(
  subject = c("a", "a", "b", "b", "b", "c", "c"), value = c(1, 2, 3, 4, 5, 6, 7),
  unit = c(NA, "x", "x", "x", "y", "a", "b")
)
change_rules <- list(
  list(subject = "a", target_unit = "x", units2change = c(NA), coeffs = c(20)),
  list(subject = "b"),
  list(subject = "c", target_unit = "b")
)
unit_standardize(df,
  subject_col = "subject", value_col = "value", unit_col = "unit",
  change_rules = change_rules
)

# Example 2: Using the labeled result from `unit_view()` as the input
# is more robust for large datasets.
df <- data.frame(subject = sample(c("a", "b"), 1000, replace = TRUE), value = runif(1000))
df$unit <- NA
df$unit[df$subject == "a"] <- sample(c("mg/L", "g/l", "g/L"),
  sum(df$subject == "a"),
  replace = TRUE
)
df$value[df$subject == "a" & df$unit == "mg/L"] <-
  df$value[df$subject == "a" & df$unit == "mg/L"] * 1000
df$unit[df$subject == "b"] <- sample(c(NA, "m.g", "mg"), sum(df$subject == "b"),
  prob = c(0.3, 0.05, 0.65), replace = TRUE
)
```

```
df$value[df$subject == "b" & df$unit %in% "mg"] <-
  df$value[df$subject == "b" & df$unit %in% "mg"] * 1000
df$value[df$subject == "b" & is.na(df$unit)] <- df$value[df$subject == "b" & is.na(df$unit)] *
  sample(c(1, 1000), size = sum(df$subject == "b" & is.na(df$unit)), replace = TRUE)

unit_table <- unit_view(
  df = df, subject_col = "subject",
  value_col = "value", unit_col = "unit", save_table = FALSE
)
unit_table$label <- c("t", NA, 1e-3, NA, NA, "r") # labeling the units

df_standardized <- unit_standardize(
  df = df, subject_col = "subject", value_col = "value",
  unit_col = "unit", change_rules = unit_table
)
unit_view(
  df = df_standardized, subject_col = "subject", value_col = "value", unit_col = "unit",
  save_table = FALSE, conflicts_only = FALSE
)
```

`unit_view` *Generate a table of conflicting units.*

Description

Get a table of conflicting units for the clinical data, along with the some useful information, this table could be labeled and used for unit standardization.

Usage

```
unit_view(
  df,
  subject_col,
  value_col,
  unit_col,
  quantiles = c(0.025, 0.975),
  save_table = FALSE,
  filename = NULL,
  conflicts_only = TRUE,
  verbose = FALSE
)
```

Arguments

`df`	A data frame of medical records that contains test subject, value, and unit cols.
`subject_col`	The name of the subject column.
`value_col`	The name of the value column.
`unit_col`	The name of the unit column.

quantiles	A vector of quantiles to be shown in the table.
save_table	A logical value indicating whether to save the table to a csv file.
filename	The name of the csv file to be saved.
conflicts_only	A logical value indicating whether to only show the conflicting units.
verbose	A logical value indicating whether to print progress messages.

Value

A data frame of conflicting units.

Examples

```
df <- data.frame(subject = sample(c("a", "b"), 1000, replace = TRUE), value = runif(1000))
df$unit <- NA
df$unit[df$subject == "a"] <- sample(c("mg/L", "g/l", "g/L"),
  sum(df$subject == "a"),
  replace = TRUE
)
df$value[df$subject == "a" & df$unit == "mg/L"] <-
  df$value[df$subject == "a" & df$unit == "mg/L"] * 1000
df$unit[df$subject == "b"] <- sample(c(NA, "g", "mg"), sum(df$subject == "b"), replace = TRUE)
df$value[df$subject == "b" & df$unit %in% "mg"] <-
  df$value[df$subject == "b" & df$unit %in% "mg"] * 1000
df$value[df$subject == "b" & is.na(df$unit)] <- df$value[df$subject == "b" & is.na(df$unit)] *
  sample(c(1, 1000), size = sum(df$subject == "b" & is.na(df$unit)), replace = TRUE)
unit_view(
  df = df, subject_col = "subject",
  value_col = "value", unit_col = "unit", save_table = FALSE
)
```

---

unmake_names *Unmake names*

Description

Inverse function of `make.names`. You can use `make.names` to make colnames legal for subsequent processing and analysis in R. Then use this function to switch back for publication.

Usage

```
unmake_names(x, ori_names)
```

Arguments

x	A vector of names generated by `base::make.names()`.
ori_names	A vector of original names.

Details

The function will try to match the names in `x` with the names in `ori_names`. If the names in `x` are not in `ori_names`, the function will return `NA`.

Value

A vector of original names.

Examples

```
ori_names <- c("xx (mg/dl)", "b*x", "Covid-19")
x <- c(make.names(ori_names), "aa")
unmake_names(x, ori_names)
```

---

value_initial_cleaning

Preliminarily cleaning string vectors

Description

Cleaning illegal characters in string vectors that store numerical values. The function is useful for cleaning electrical health records in Chinese.

`char_initial_cleaning()` will convert full-width characters to half-width characters, removes whitespace at the start and end, replaces all internal whitespace with a single space, and replace empty strings with `NA`.

`value_initial_cleaning()` will additionally remove all spaces and extra dots.

Usage

```
value_initial_cleaning(x, remove_inequal = FALSE, fix_encoding = TRUE)

char_initial_cleaning(x, fix_encoding = TRUE)
```

Arguments

`x`	A string vector.
`remove_inequal`	A logical value. If `TRUE`, remove comparison symbols such as <, > from the string
`fix_encoding`	Logical. If `TRUE`, automatically detect and repair non-UTF-8 encoding issues before cleaning. Default is `TRUE`.

Value

A string vector with less illegal characters.

Note

When `fix_encoding = TRUE`, a warning will be issued if encoding repairs are made.

Examples

```
x <- c("\uFF11\uFF12\uFF13", "11..23", "\uff41\uff42\uff41\uff4e\uff44\uff4f\uff4e",
       "hello world ")
value_initial_cleaning(x)
char_initial_cleaning(x)
```

`vec2code` *Generate code from string vector*

Description

Generate the code that can be used to generate the string vector. `name2code()` is a wrapper of `vec2code(names(x))` to generate code for names of a vector, list, data frame, or any object with names.

Usage

```
vec2code(x)

name2code(x)
```

Arguments

`x`	A string vector.

Value

A string that contains the code to generate the vector.

Examples

```
vec2code(colnames(mtcars))
name2code(mtcars)
```

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