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Description Provides reusable building blocks for research packages across matrix representation, numerical computation, neighborhood evaluation, controlled execution, and runtime interoperability. Core tools preserve declared sparse semantics, expose dense-memory and output boundaries, standardize neighborhood and classification results, and align serial and parallel result and error behavior. Additional helpers support structured messages, optional dependency checks, and common statistical workflows.

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URL https://mengxu98.github.io/thisutils/

BugReports https://github.com/mengxu98/thisutils/issues

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`thisutils-package` *Reliable Utilities for Reusable Research Workflows*

Description

Reusable building blocks for matrix representation, numerically stable and resource-controlled computation, neighborhood and classification evaluation, consistent serial/parallel execution, structured messages, and research-package interoperability.

Author(s)

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Source

https://mengxu98.github.io/thisutils/

See Also

Useful links:

- https://mengxu98.github.io/thisutils/
- Report bugs at https://github.com/mengxu98/thisutils/issues

---

`%ss%` *Value selection operator*

Description

This operator returns the left side if it's not `NULL`, otherwise it returns the right side.

Usage

```
a %ss% b
```

Arguments

`a`	The left side value to check.
`b`	The right side value to use if `a` is `NULL`.

Value

`a` if it is not `NULL`, otherwise `b`.

Examples

```
NULL %ss% 10
5 %ss% 10
```

add_pkg_file *Add a package file and print package information*

Description

Add a package file and print package information

Usage

```
add_pkg_file(
  use_figlet = TRUE,
  figlet_font = "Slant",
 colors = c("red", "yellow", "green", "magenta", "cyan", "yellow", "green", "white",
    "magenta", "cyan"),
  verbose = TRUE
)
```

Arguments

use_figlet	Whether to use figlet for ASCII art generation. Default is TRUE. Details see figlet.
figlet_font	Character string, figlet font to use. Default is "Slant".
colors	Character vector, colors to use for the logo elements.
verbose	Whether to print the message. Default is TRUE.

Value

Creates a file named R/<pkg_name>-package.R.

aggregate_matrix *Aggregate matrix over groups*

Description

Aggregate matrix over groups

Usage

```
aggregate_matrix(x, groups = NULL, fun = "mean")
```

Arguments

x	A matrix.
groups	A character vector with the groups to aggregate over. Length must be ‘nrow(x)‘ or ‘1‘.
fun	Summary applied to each group: ‘"mean"‘, ‘"sum"‘, ‘"count"‘, ‘"max"‘, ‘"min"‘, or a function.

Value

A sparse summary matrix with groups in rows.

Examples

```
aggregate_matrix(
  matrix(1:6, nrow = 3),
  groups = c("a", "a", "b"),
  fun = "mean"
)
```

---

as_matrix *Convert matrix into dense/sparse matrix*

Description

Convert matrix into dense/sparse matrix

Usage

```
as_matrix(x, return_sparse = FALSE)
```

Arguments

x	A matrix.
return_sparse	Whether to output a sparse matrix. Default is FALSE.

Value

A dense or sparse matrix.

Examples

```
m <- simulate_sparse_matrix(
  1000, 1000,
  decimal = 3
)

a <- as_matrix(m)
a[1:5, 1:5]

b <- as_matrix(m, return_sparse = TRUE)
b[1:5, 1:5]
```

capitalize *Capitalize the first letter of each word*

Description

Capitalize the first letter of each word

Usage

```
capitalize(x, force_tolower = FALSE)
```

Arguments

x	A vector of character strings to be capitalized.
force_tolower	Whether to force the remaining letters to be lowercase.

Examples

```
x <- c(
  "hello world",
  "hello World"
)
capitalize(x)
```

check_ci_env *Check CI environment*

Description

Check CI environment

Usage

```
check_ci_env()
```

Value

A logical value.

check_pkg_status *Check if a package is installed with the specified version*

Description

Check if a package is installed with the specified version

Usage

```
check_pkg_status(pkg, version = NULL, lib = .libPaths()[1])
```

Arguments

pkg	Package name.
version	Package version to check. If NULL, only checks if the package is installed.
lib	The location of the library directories where to install the packages.

Value

TRUE if the package is installed with the specified version, FALSE otherwise.

check_r *Check and install R packages*

Description

Check and install R packages

Usage

```
check_r(
  packages,
  lib = .libPaths()[1],
  dependencies = NA,
  force = FALSE,
  install = TRUE,
  timeout = Inf,
  load = FALSE,
  cores = NULL,
  verbose = TRUE
)
```

Arguments

packages	Package to be installed. Package source can be *CRAN*, *Bioconductor* or *Github*. By default, the package name is extracted according to the packages parameter.
lib	The location of the library directories where to install the packages.
dependencies	Which dependencies to install. Passed to pak::pkg_install. Default is NA, auto install hard dependencies: *Depends*, *Imports*, and *LinkingTo*, excluding *Suggests*.
force	Whether to force the installation of packages. Default is FALSE.
install	Whether missing or outdated packages may be installed. Set to FALSE for read-only diagnostics. Default is TRUE for backward compatibility.
timeout	Maximum installation time in seconds. A finite timeout runs installation in a supervised R subprocess and terminates only that process tree on timeout. Default is Inf.
load	Whether to load packages after successful installation. Uses do.call dispatch to avoid CRAN static checks on base::library. Default is FALSE.
cores	Number of workers used by pak::pkg_install(). Use NULL (the default) to let pak select its worker count automatically.
verbose	Whether to print the message. Default is TRUE.

Details

GitHub packages are normally installed with pak. If pak cannot parse a GitHub package's DESCRIPTION file, check_r() retries that package with the optional remotes package. This preserves the fast dependency resolution path while supporting legacy repositories with malformed metadata. When PKG_SUBPROCESS_TIMEOUT is unset, the pak subprocess startup window is temporarily increased to 30 seconds and restored before returning.

Value

Package installation status.

---

check_sparsity *Check sparsity of matrix*

Description

Check sparsity of matrix

Usage

```
check_sparsity(x)
```

Arguments

x	A matrix.

Value

Sparsity of matrix.

`classification_metrics_compute` *Compute classification metrics*

Description

Compute multi-class classification metrics from predicted and true labels, including accuracy, macro-F1, purity, NMI, ARI, and rare-class recall.

Usage

```
classification_metrics_compute(predicted, truth, rare_threshold = 0.05)
```

Arguments

`predicted`	Character vector of predicted class labels.
`truth`	Character vector of true class labels (same length as `predicted`).
`rare_threshold`	Proportion threshold for rare-class recall. Classes with support proportion $<=$ this value contribute to the `rare_recall` metric. Default is `0.05`.

Value

A list with the following components:

accuracy Overall accuracy (scalar).

macro_f1 Macro-averaged F1 score (scalar).

purity Cluster purity (scalar).

nmi Normalized Mutual Information (scalar).

ari Adjusted Rand Index (scalar).

rare_recall Mean recall on rare classes (scalar, or `NA` if no rare classes).

class_table A data frame of per-class precision, recall, F1, and support.

Examples

```
predicted <- c("A", "A", "B", "B", "C")
truth <- c("A", "B", "B", "B", "C")
classification_metrics_compute(predicted, truth)
```

col_maxs *Column maxima*

Description

Column maxima

Usage

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

Arguments

x	A dense or sparse matrix.
na.rm	Whether to ignore ‘NA‘ values.

Value

A numeric vector of column maxima. Implicit sparse zeros are treated as zero.

Examples

```
col_maxs(matrix(c(-2, 0, 3, 1), nrow = 2))
```

collapse_sparse_rows *Collapse sparse matrix rows by group*

Description

Collapse sparse matrix rows by group

Usage

```
collapse_sparse_rows(matrix, group)
```

Arguments

matrix	A sparse matrix.
group	A vector defining the output row groups.

Value

A sparse matrix with rows collapsed by ‘group‘.

Examples

```
mat <- Matrix::Matrix(
  matrix(c(1, 0, 2, 0, 3, 4), nrow = 3, byrow = TRUE),
  sparse = TRUE
)
collapse_sparse_rows(mat, c("g1", "g1", "g2"))
```

---

compute_lisi *Compute Local Inverse Simpson's Index (LISI)*

Description

Compute per-cell Local Inverse Simpson's Index (LISI) scores for one or more categorical variables. This is a clean-room reimplementation of the `immunogenomics/LISI`.

Usage

```
compute_lisi(
  X,
  meta_data,
  label_colnames,
  perplexity = 30,
  tol = 1e-05,
  max_iter = 50,
  knn_algorithm = c("auto", "brute_force", "clustered"),
  n_threads = NULL,
  max_dense_bytes = Inf
)
```

Arguments

`X`	A matrix-like object with cells in rows and embedding/features in columns.
`meta_data`	A data frame with one row per cell.
`label_colnames`	Character vector of column names in `meta_data` to evaluate.
`perplexity`	Effective neighborhood size. Defaults to `30`.
`tol`	Tolerance used in the binary search for the target perplexity. Defaults to `1e-5`.
`max_iter`	Maximum number of binary-search iterations. Defaults to `50`.
`knn_algorithm`	Exact nearest-neighbor search strategy. `"auto"` uses clustered exact search when there are at least 4096 observations and the requested neighborhood is less than one quarter of the data; otherwise it uses brute force. `"brute_force"` and `"clustered"` force either exact strategy.
`n_threads`	Number of C++ worker threads. `NULL` (the default) preserves the earlier automatic hardware-thread selection. Supply a positive integer to control CPU use explicitly.

max_dense_bytes
: Maximum estimated bytes allowed for the dense input and its C++ row-major copy. The default, `Inf`, preserves earlier behavior; supply a finite value to enable the guard.

Details

Both nearest-neighbor strategies are exact. Sparse `X` is converted to a dense matrix before neighbor search; this conversion is included in the `max_dense_bytes` check.

Value

A data frame with one row per cell and one column per label.

References

Korsunsky I, Millard N, Fan J, et al. Fast, sensitive and accurate integration of single-cell data with Harmony. *Nature Methods* (2019). https://www.nature.com/articles/s41592-019-0619-0

LISI reference implementation: https://github.com/immunogenomics/LISI

Examples

```
set.seed(1)
X <- rbind(
  matrix(stats::rnorm(100, mean = -1), ncol = 2),
  matrix(stats::rnorm(100, mean = 1), ncol = 2)
)
meta_data <- data.frame(
  batch = rep(c("A", "B"), each = 50),
  group = sample(c("g1", "g2"), 100, replace = TRUE)
)

res <- compute_lisi(
  X, meta_data,
  c("batch", "group"),
  perplexity = 10
)
head(res)
boxplot(res)
```

---

detect_cores *Detect the number of CPU cores*

Description

Detect the number of CPU cores

Usage

```
detect_cores(
  cores = NULL,
  num_session = NULL,
  max_threads = NULL,
  logical = FALSE
)
```

Arguments

cores	Requested number of workers. Only used when num_session is supplied; invalid values fall back to 1.
num_session	Number of tasks that can be scheduled concurrently. When supplied, the result is the usable worker count: the detected cores minus one reserved for the parent, capped by cores and num_session.
max_threads	Optional upper bound for the detected core count, e.g. the largest worker count a kernel can use. NULL leaves the detected value as is.
logical	Whether to report logical (hyper-threaded) cores, as parallel::detectCores() does.

Value

A single integer, at least 1. A failed or unusable probe falls back to 1 instead of propagating NA.

Examples

```
detect_cores()
detect_cores(max_threads = 2)
detect_cores(cores = 4, num_session = 8)
```

---

download *Download file from the Internet*

Description

Download file from the Internet

Usage

```
download(
  url,
  destfile,
  methods = c("auto", "wget", "libcurl", "curl", "wininet", "internal"),
  quiet = FALSE,
  ...,
  max_tries = 2
)
```

Arguments

url	a character string (or longer vector for the "libcurl" method) naming the URL of a resource to be downloaded.
destfile	a character string (or vector, see the url argument) with the file path where the downloaded file is to be saved. Tilde-expansion is performed.
methods	Methods to be used for downloading files. Can be "auto", "wget", "libcurl", "curl", "wininet", "internal". Default is "auto", which means to try different download methods.
quiet	If TRUE, suppress status messages (if any), and the progress bar.
...	Other arguments passed to utils::download.file.
max_tries	Number of tries for each download method. Default is 2.

---

fast_aggregate *Fast sparse aggregation*

Description

Fast sparse aggregation

Usage

```
fast_aggregate(x, groupings = NULL, form = NULL, fun = "sum", ...)
```

Arguments

x	A matrix. Dense inputs are coerced to a sparse matrix.
groupings	Group labels, recycled to a one-column data frame.
form	Optional model formula used to build the grouping design.
fun	Aggregation: ‘"sum"‘, ‘"mean"‘, or ‘"count"‘.
...	Unused.

Value

A sparse matrix with groups in rows.

Examples

```
fast_aggregate(
  matrix(1:6, nrow = 3),
  groupings = c("a", "a", "b"),
  fun = "sum"
)
```

fast_row_vars *Compute row variances*

Description

Compute sample or population variances for each row of a dense or sparse matrix without densifying sparse input.

Usage

```
fast_row_vars(x, unbiased = TRUE)
```

Arguments

x	A matrix or a 'Matrix' sparse matrix.
unbiased	Whether to compute the unbiased sample variance (the default) instead of the population variance.

Value

A numeric vector of row variances. Row names are retained when available. Matrices with zero columns return 'NA' for every row. A one-column matrix returns 'NA' for sample variance and '0' for population variance.

Examples

```
fast_row_vars(matrix(c(1, 2, 3, 4), nrow = 2))
```

figlet *The figlet function*

Description

Create ASCII art text using figlet.

Usage

```
figlet(
  text,
  font = "Slant",
  width = getOption("width", 80),
  justify = "left",
  absolute = FALSE,
  strip = TRUE
)
```

Arguments

text	Text to make bigger.
font	Name of font, path to font, or figlet_font object.
width	Width to use when justifying and breaking lines.
justify	Text justification to use in rendering ("left", "centre", "right").
absolute	Logical, indicating if alignment is absolute.
strip	Logical, indicating if whitespace should be removed.

Value

An object of class figlet_text which is a character vector with a handy print method.

References

https://github.com/richfitz/rfiglet, https://github.com/jbkunst/figletr, https://www.figlet.org/

Examples

```
figlet("thisutils")
```

---

figlet_font *Get a figlet font*

Description

Get a figlet font

Usage

```
figlet_font(font)
```

Arguments

font	Path or name of the font to load

Value

A ‘figlet_font‘ object for use with [figlet]

filter_nonzero_variance_features *Keep matrix rows with nonzero variance*

Description

Subset a matrix to selected rows and discard rows with missing or zero variance. Sparse input remains sparse.

Usage

```
filter_nonzero_variance_features(x, features)
```

Arguments

x	A matrix or a ‘Matrix‘ sparse matrix.
features	Row names or indices to retain before variance filtering.

Value

‘x‘ restricted to selected rows whose variance is positive.

Examples

```
filter_nonzero_variance_features(
  matrix(c(1, 1, 1, 1, 1, 2), nrow = 2),
  features = 1:2
)
```

fit_trends *Fit feature trends*

Description

Fit feature trends

Usage

```
fit_trends(
  x,
  time,
  method = c("gam", "pretsa"),
  family = "gaussian",
  exposure = rep(1, ncol(x)),
  use_exposure = FALSE,
  reference_exposure = NULL,
```

```
  knot = 0,
  max_knot_allowed = 10,
  padjust_method = "fdr",
  return_fitted = TRUE,
  cores = 1,
  verbose = TRUE
)
```

Arguments

x	Numeric matrix with features in rows and observations in columns.
time	Finite numeric coordinate per observation. Named coordinates are aligned to column names; unnamed coordinates are positional.
method	Fitting method: "gam" or "pretsa".
family	GAM distribution, scalar or one named value per feature.
exposure	Positive observation exposures for GAM offsets.
use_exposure	Logical scalar or feature vector selecting which non-Gaussian fits use observation exposures.
reference_exposure	Positive scalar offset for other fits and reference scale for predictions. Defaults to the median positive finite exposure.
knot	Nonnegative number of interior knots or "auto" for BIC selection.
max_knot_allowed	Maximum interior knots in automatic selection.
padjust_method	Method passed to stats::p.adjust().
return_fitted	Include fitted, lower and upper matrices in the result.
cores	Number of GAM workers.
verbose	Report fitting failures and progress.

Details

Inputs are not transformed. PreTSA requires finite values; GAM omits unusable observations. Peak/valley times summarize the upper/lower 1% of fitted values, including ties for PreTSA.

Value

A list with statistics, time, and optional fitted, lower, and upper matrices, in input order. Statistics contain feature names, counts above each feature's minimum, fit scores, peak/valley times, P-values and adjusted P-values. Failed GAM fits return NA. GAM bounds use +/- 2 standard errors on the link scale; PreTSA bounds equal fitted values, not confidence intervals.

References

Zhuang and Ji, PreTSA, https://github.com/haotian-zhuang/PreTSA

Examples

```
t <- seq(0, 1, length.out = 40)
x <- rbind(a = sin(t * 5), b = cos(t * 3))
fit_trends(x, t, method = "pretsa")$statistics
```

`get_namespace_fun` *Get a function from a namespace*

Description

Get a function from a namespace

Usage

```
get_namespace_fun(pkg, fun)
```

Arguments

`pkg`	The name of the package.
`fun`	The name of the function.

Value

Function.

`get_verbose` *Get the verbose option*

Description

Resolve 'options(log_message.verbose)'. An explicit 'verbose' argument wins. Otherwise the option is used, and the default is 'TRUE'.

Usage

```
get_verbose(verbose = NULL)
```

Arguments

`verbose`	The verbose option. Default is 'NULL', which means to get the verbose option from the global options.

Value

The verbose option.

Examples

```
get_verbose()
get_verbose(verbose = FALSE)
get_verbose(verbose = TRUE)

options(log_message.verbose = FALSE)
get_verbose()
get_verbose(verbose = TRUE)

options(log_message.verbose = TRUE)
get_verbose()

options(log_message.verbose = NULL)
```

---

grapes-or-or-or-grapes

Empty-value selection operator

Description

Return the left side unless it is NULL or has length zero, otherwise return the right side. Use %ss% when only NULL should fall through; that matches the rlang %||% operator without masking it.

Usage

```
a %|||% b
```

Arguments

a	The left side value to check.
b	The right side value to use if a is NULL or length zero.

Value

a if it is not NULL and has length greater than zero, otherwise b.

Examples

```
NULL %|||% 10
character(0) %|||% "fallback"
5 %|||% 10
```

invoke_fun *Invoke a function with a list of arguments*

Description

Invoke a function with a list of arguments

Usage

```
invoke_fun(.fn, .args = list(), ..., .env = rlang::caller_env())
```

Arguments

.fn	A function, or function name as a string.
.args	A list or pairlist of argument values, or NULL.
...	Other arguments passed to the function.
.env	Evaluation environment for calls without arguments, or the parent of the temporary argument environment for calls with arguments. Captured expressions and caller-frame side effects use that temporary environment.

Examples

```
f <- function(x, y) {
  x + y
}
invoke_fun(f, list(x = 1, y = 2))
invoke_fun("f", list(x = 1, y = 2))
invoke_fun("f", x = 1, y = 2)
```

is_apple_silicon *Check if the system is running on Apple Silicon*

Description

Check if the system is running on Apple Silicon

Usage

```
is_apple_silicon()
```

Value

A logical value.

is_linux *Check if the operating system is Linux*

Description

Check if the operating system is Linux

Usage

```
is_linux()
```

Value

A logical value.

is_osx *Check if the operating system is macOS*

Description

Check if the operating system is macOS

Usage

```
is_osx()
```

Value

A logical value.

is_outlier *Detect outliers using MAD (Median Absolute Deviation)*

Description

Detect outliers using MAD (Median Absolute Deviation)

Usage

```
is_outlier(
  x,
  nmads = 2.5,
  constant = 1.4826,
  type = c("both", "lower", "higher")
)
```

Arguments

x	Numeric vector.
nmads	Number of MADs from the median to define the boundaries for outliers. Default is 2.5.
constant	Constant factor to convert the MAD to a standard deviation. Default is 1.4826, which is consistent with the MAD of a normal distribution.
type	Type of outliers to detect. Available options are "both", "lower", or "higher". If type is "both", it detects both lower and higher outliers. If type is "lower", it detects only lower outliers. If type is "higher", it detects only higher outliers.

Value

Numeric vector of indices indicating the positions of outliers in x.

Examples

```
x <- c(1, 2, 3, 4, 5, 100)
is_outlier(x) # returns 6

x <- c(3, 4, 5, NA, 6, 7)
is_outlier(x, nmads = 1.5, type = "lower") # returns 4

x <- c(10, 20, NA, 15, 35)
is_outlier(x, nmads = 2, type = "higher") # returns 3, 5
```

---

is_windows *Check if the operating system is Windows*

Description

Check if the operating system is Windows

Usage

```
is_windows()
```

Value

A logical value.

local_verbose *Temporarily set the shared verbose switch*

Description

Set ‘options(log_message.verbose)‘ for the calling frame, then restore the previous value. Nested ‘get_verbose()‘ calls, including compiled ‘log_message()‘ code, see the temporary value.

Usage

```
local_verbose(verbose)
```

Arguments

verbose	Single logical value.

Value

‘verbose‘, invisibly.

Examples

```
local({
  local_verbose(FALSE)
  get_verbose()
})
```

log_message *Print formatted message*

Description

Integrate the message printing function with the cli package, and the base::message function. The message could be suppressed by `base::suppressMessages`.

Usage

```
log_message(
  ...,
  expr = NULL,
  verbose = NULL,
  message_type = c("info", "success", "warning", "error", "running", "ask"),
  cli_model = TRUE,
  level = 1,
  symbol = "  ",
  text_color = NULL,
```

```
  back_color = NULL,
  text_style = NULL,
  multiline_indent = FALSE,
  timestamp = TRUE,
  timestamp_format = paste0("[", format(Sys.time(), "%Y-%m-%d %H:%M:%S"), "] "),
  timestamp_style = FALSE,
  plain_text = FALSE,
  .envir = parent.frame(),
  .frame = .envir
)
```

Arguments

`...`	The message to print.
`expr`	An optional expression to evaluate while capturing its standard output, messages, and warnings, then re-printing them with `log_message()` formatting. The evaluated result is returned invisibly unless it is visible by default.
`verbose`	Whether to print the message. Default is `TRUE`.
`message_type`	Type of message. Could be choose one of `"info"`, `"success"`, `"warning"`, `"error"`, `"running"`, and `"ask"`. When `"ask"` is used, the function will prompt the user for a Yes/No/Cancel response using utils::askYesNo, and returns `TRUE` for Yes, `FALSE` for No, and `NA` for Cancel. Default is `"info"`.
`cli_model`	Whether to use the `cli` package to print the message. Default is `TRUE`.
`level`	The level of the message, which affects the indentation. Level `1` has no indentation, higher levels add more indentation. Default is `1`.
`symbol`	The symbol used for indentation. When specified, it ignores the level parameter and uses the symbol directly. Default is `" "` (two spaces).
`text_color`	Color for the message text. Supports R color names (e.g., `"orange"`), hexadecimal colors (e.g., `"#000000"`), basic colors: `"red"`, `"green"`, `"blue"`, `"yellow"`, `"magenta"`, `"cyan"`, `"white"`, `"black"`, `"grey"`, `"silver"`, `"none"`, and bright colors: `"br_red"`, `"br_green"`, `"br_blue"`, `"br_yellow"`, `"br_magenta"`, `"br_cyan"`, `"br_white"`, `"br_black"`. Default is `NULL`.
`back_color`	Background color for the message text. Details see parameter `text_color`. Default is `NULL`.
`text_style`	Text styles to apply. Can be one or more of: `"bold"`, `"italic"`, `"underline"`, `"strikethrough"`, `"dim"`, `"inverse"`. Multiple styles can be combined (e.g., `c("bold", "underline")`). Default is `NULL`.
`multiline_indent`	Whether to apply consistent formatting (timestamp and indentation) to each line in multiline messages. When `TRUE`, each line gets the full formatting; when `FALSE`, only the first line gets the timestamp. Default is `FALSE`.
`timestamp`	Whether to show the current time in the message. Default is `TRUE`.
`timestamp_format`	Format string for timestamp display. Default is `"%Y-%m-%d %H:%M:%S"`.

timestamp_style
: Whether to apply the same text styling to the timestamp as the message text. When TRUE, timestamp formatting matches the message; when FALSE, timestamp keeps its default appearance. Default is FALSE.

plain_text
: Whether to print only the text content. When TRUE, level, symbol, timestamp, and message type formatting are suppressed, but color and multiline settings still apply.

.envir
: The environment to evaluate calls in. Default is parent.frame.

.frame
: The frame to use for error reporting. Default is .envir.

Value

Formated message, a logical value (TRUE/FALSE/NA) if message_type = "ask", or the evaluated result of expr if expr is supplied.

References

https://cli.r-lib.org/articles/index.html

Examples

```
# basic usage
log_message("Hello, ", "world!")

log_message("hello, world!")

log_message("Hello, world!", timestamp = FALSE)

log_message(
  "Hello, ", "world!",
  message_type = "success"
)

log_message(
  "Hello, world!",
  message_type = "warning"
)

log_message(
  "Processing data...",
  message_type = "running"
)

log_message(
  "Hello, ", "world!",
  cli_model = FALSE
)


# suppress messages
suppressMessages(log_message("Hello, world!"))
```

```
log_message("Hello, world!", verbose = FALSE)
options(log_message.verbose = FALSE)
log_message("Hello, world!")

# for global verbose option
options(log_message.verbose = TRUE)
log_message("Hello, world!", verbose = FALSE)
options(log_message.verbose = NULL)


# cli inline markup
log_message("{.arg abc} is a argument")

## 'message' can not deal with cli inline markup
message("hello, {.code world}!")

log_message("{.val list('abc')} is a {.cls {class(list('abc'))}}")

log_message("{.code lm(y ~ x)} is a code example")

log_message("{.dt List}list('abc')")

log_message("address: {.email example@example.com}")

log_message("{.emph R} is a programming language")

log_message("{.envvar R_HOME}")

log_message("{.file log_message.R} is a file")

log_message("{.fn lm} is a function")

log_message("{.fun lm} is a function")

log_message("{.help lm} to get help")

log_message("... see {.help [{.fun lm}](stats::lm)} to learn more")

log_message(
  "See the {.href [cli homepage](https://cli.r-lib.org)} for details"
)

log_message("press {.kbd ENTER}")

log_message("press {.key ENTER}")

log_message("URL: {.url https://cli.r-lib.org}")

log_message("Some {.field field}")

log_message("{.path /usr/bin/R} is a path")

log_message("{.pkg cli} is a package")
```

```
log_message("{.val object} is a variable")

log_message("{.run Rscript log_message.R} is a runnable file")

log_message("{.str object} is a string")

log_message("{.strong abc} is a strong string")

log_message("{.topic stats::lm} is a topic")

log_message("{.vignette cli} is a vignette")


# set indentation
log_message("Hello, world!", level = 2)

log_message("Hello, world!", symbol = "->")

log_message(
  "Hello, world!",
  symbol = "#####",
  level = 3
)

# color formatting
log_message(
  "This is a red message",
  text_color = "#ff9900"
)

log_message(
  "This is a message with background",
  back_color = "#EE4000"
)

log_message(
  "This is a message with both text and background",
  text_color = "white",
  back_color = "cyan"
)

log_message(
  "This is a message with background",
  back_color = "#EE4000",
  cli_model = FALSE
)

log_message(
  "This is a message with both text and background",
  text_color = "red",
  back_color = "cyan",
  cli_model = FALSE
```

```
)

log_message(
  "Hex color with {.arg cli_model = FALSE}",
  text_color = "#FF5733",
  cli_model = FALSE
)

log_message(
  "Bright red text",
  text_color = "br_red"
)

log_message(
  "Bright background",
  back_color = "br_yellow"
)

log_message(
  "Combined grey and style",
  text_color = "grey",
  text_style = "bold"
)

# text style formatting
log_message(
  "Bold message",
  text_style = "bold"
)

log_message(
  "Italic message",
  text_style = "italic"
)

log_message(
  "Underlined message",
  text_style = "underline"
)

log_message(
  "Combined styles",
  text_style = c("bold", "underline")
)

log_message(
  "Color and style",
  text_color = "blue",
  text_style = c("bold", "italic")
)

log_message(
  "Hex color and style",
```

```
  text_color = "#FF5733",
  text_style = c("bold", "underline")
)


# multiline message
log_message(
  "Line 1\nLine 2\nLine 3",
  multiline_indent = TRUE,
  text_style = "italic"
)

log_message(
  "Multi-line\ncolored\nmessage",
  text_color = "blue",
  text_style = "italic"
)

log_message(
  "Multi-line\ncolored\nmessage",
  text_color = "blue",
  timestamp = FALSE
)

# timestamp styling
log_message(
  "Multi-line message\nwith timestamp styling",
  text_color = "red",
  text_style = "bold",
  timestamp_style = TRUE
)

log_message(
  "Multi-line message\nwithout timestamp styling",
  text_color = "#669999",
  text_style = c("bold", "italic")
)


# combine cli package and log_message
log_message(
  cli::col_green(
    "I am a green line ",
    cli::col_blue(
      cli::style_underline(
        cli::style_bold("with a blue substring")
      )
    ),
    " that becomes green again!"
  )
)

# cli variables
```

```
fun <- function(x = 1) {
  log_message("{.val x}")
  log_message("{.val {x}}")
  log_message("{.val {x + 1}}")
}
fun()


# print objects directly
df <- data.frame(
  x = 1:3,
  y = letters[1:3],
  z = c(" a", "b  ", "c")
)
log_message("Content:\n", df)

# interactive prompt
if (interactive()) {
  log_message(
    "Do you want to continue?",
    message_type = "ask"
  )
}

# capture output from another expression
fun <- function() {
  cat("This is standard output\n")
  message("This is a message")
  return(1 + 1)
}
fun()

log_message(
  expr = fun(),
  message_type = "running"
)
```

`matrix_process` *Process matrix*

Description

Process matrix

Usage

```
matrix_process(
  matrix,
  method = c("raw", "zscore", "fc", "log2fc", "log1p"),
  ...
)
```

Arguments

matrix	A matrix.
method	Method to use for processing the matrix.
...	Other arguments passed to the method.

Value

A processed matrix.

Examples

```
m <- simulate_sparse_matrix(10, 10)
matrix_process(m, method = "raw")
matrix_process(m, method = "zscore")
matrix_process(m, method = "fc")
matrix_process(m, method = "log2fc")
matrix_process(m, method = "log1p")
m <- as_matrix(m)
matrix_process(m, method = function(x) x / rowMeans(x))
```

---

matrix_to_table *Switch matrix to table*

Description

Switch matrix to table

Usage

```
matrix_to_table(
  matrix,
  row_names = NULL,
  col_names = NULL,
  threshold = 0,
  keep_zero = TRUE
)
```

Arguments

matrix	A matrix.
row_names	Character vector of row names to filter by.
col_names	Character vector of column names to filter by.
threshold	The threshold for filtering values based on absolute values. Defaults to 0.
keep_zero	Whether to keep zero values in the table. Defaults to true for backward compatibility.

Details

With `keep_zero = FALSE`, sparse input is traversed through its stored entries and implicit zeros are not materialized. The backward-compatible default, `keep_zero = TRUE`, emits every selected matrix position, including implicit sparse zeros, and therefore requires time and output memory proportional to the selected `nrow * ncol`. When zeros are omitted, an all-zero row or column is absent from the table and cannot be reconstructed by `table_to_matrix()` without separate dimension metadata.

Value

A table with three columns: `row`, `col`, and `value`.

See Also

table_to_matrix

Examples

```
test_matrix <- simulate_sparse_matrix(10, 10)
colnames(test_matrix) <- paste0("c", 1:10)
rownames(test_matrix) <- paste0("r", 1:10)
table <- matrix_to_table(test_matrix)
matrix_new <- table_to_matrix(table)
test_matrix <- test_matrix[rownames(matrix_new), colnames(matrix_new)] |>
  as_matrix()
identical(test_matrix, matrix_new)

matrix_to_table(
  test_matrix,
  threshold = 2
)

matrix_to_table(
  test_matrix,
  row_names = c("r1", "r2"),
  col_names = c("c1", "c2")
)
```

---

max_depth *Maximum depth of a list*

Description

Maximum depth of a list

Usage

```
max_depth(x, depth = 0)
```

Arguments

x	A list.
depth	The depth of the list.

Examples

```
x <- list(
  a = list(b = list(c = 1)),
  d = list(e = list(f = 2))
)
max_depth(x)
```

---

maximump *Maximum P-value*

Description

Maximum P-value

Usage

```
maximump(p, alpha = 0.05, log.p = FALSE)
```

Arguments

p	A vector of P-values.
alpha	The significance level.
log.p	Whether to return the log of the P-value.

Examples

```
p <- c(0.01, 0.02, 0.03, 0.04, 0.05)
maximump(p)
maximump(p, alpha = 0.01)
maximump(p, log.p = TRUE)
```

meanp *Mean P-value*

Description

Mean P-value

Usage

```
meanp(p)
```

Arguments

p	A vector of P-values.

Examples

```
p <- c(0.01, 0.02, 0.03, 0.04, 0.05)
meanp(p)
```

minimump *Minimum P-value*

Description

Minimum P-value

Usage

```
minimump(p, alpha = 0.05, log.p = FALSE)
```

Arguments

p	A vector of P-values.
alpha	The significance level.
log.p	Whether to return the log of the P-value.

Examples

```
p <- c(0.01, 0.02, 0.03, 0.04, 0.05)
minimump(p)
minimump(p, alpha = 0.01)
minimump(p, log.p = TRUE)
```

normalization *Normalize numeric vector*

Description

Normalize numeric vector

Usage

```
normalization(x, method = "max_min", na_rm = TRUE, ...)
```

Arguments

x	Input numeric vector.
method	Method used for normalization.
na_rm	Whether to remove NA values, and if setting TRUE, using 0 instead. Default is TRUE.
...	Parameters for other methods.

Value

Normalized numeric vector.

Examples

```
x <- c(runif(2), NA, -runif(2))
x
normalization(x, method = "max_min")
normalization(x, method = "maximum")
normalization(x, method = "sum")
normalization(x, method = "softmax")
normalization(x, method = "z_score")
normalization(x, method = "mad")
normalization(x, method = "unit_vector")
normalization(x, method = "unit_vector", na_rm = FALSE)
```

parallelize_fun *Parallelize a function*

Description

Parallelize a function

Usage

```
parallelize_fun(
  x,
  fun,
  cores = 1,
  export_fun = NULL,
  clean_result = FALSE,
  throw_error = TRUE,
  progress_bar_width = 10L,
  timestamp_format = paste0("[", format(Sys.time(), "%Y-%m-%d %H:%M:%S"), "] "),
  verbose = TRUE,
  backend = c("auto", "fork", "psock"),
  timeout = Inf,
  total_timeout = Inf,
  seed = NULL,
  progress = verbose
)
```

Arguments

x	A vector or list to apply over.
fun	The function to be applied to each element.
cores	The number of worker processes to use for parallelization. Default is 1.
export_fun	Character vector naming functions or other objects from the environment of fun that PSOCK workers need. Objects referenced from a global environment are not discovered automatically; list them here or include them in each element of x.
clean_result	Whether to remove failed results from output. If FALSE, failed results are kept as error objects. Default is FALSE.
throw_error	Whether to print detailed error information for failed results. Default is TRUE.
progress_bar_width	Width of the verbose progress bar in characters. Default is 10L.
timestamp_format	Format string for timestamp display. Default is "%Y-%m-%d %H:%M:%S".
verbose	Whether to print the message. Default is TRUE.
backend	Parallel backend. "auto" uses PSOCK on every platform. Use "fork" to opt in to forked workers on supported systems. "fork" is unavailable on Windows. Prefer PSOCK in long-lived sessions that also use child-process managers such as callr or processx, because they can compete with R's fork-worker signal handler.
timeout	Maximum number of seconds that a parallel worker task may run. Inf disables task timeouts. This is ignored when execution uses one core.
total_timeout	Maximum number of seconds allowed for the complete call. Inf disables the overall deadline. In single-core mode the deadline is checked between inputs but cannot interrupt a function that is already running.

`seed` Optional integer seed. When supplied, every input receives a deterministic independent L'Ecuyer-CMRG random-number stream, making results reproducible across worker counts and scheduling order. The caller's random number state is restored when the call finishes.

`progress` Whether to draw a dynamic terminal progress bar. The default follows `verbose`. Set this to `FALSE` while keeping `verbose = TRUE` to emit concise lifecycle messages through `log_message()` without terminal timing output, for example in reports and persistent logs.

Value

A list of computed results. If `clean_result = FALSE`, failed results are included as error objects. If `clean_result = TRUE`, only successful results are returned.

Examples

```
parallelize_fun(1:3, function(x) {
  Sys.sleep(0.2)
  x^2
})

parallelize_fun(list(1, 2, 3), function(x) {
  Sys.sleep(0.2)
  x^2
}, cores = 2)

# Examples with error handling
parallelize_fun(1:5, function(x) {
  if (x == 3) stop("Error on element 3")
  x^2
}, clean_result = FALSE)

parallelize_fun(1:5, function(x) {
  if (x == 3) stop("Error on element 3")
  x^2
}, clean_result = TRUE)

# Control error printing
parallelize_fun(1:5, function(x) {
  if (x == 2) stop("Error on element 3")
  if (x == 4) stop("Error on element 4")
  x^2
})

parallelize_fun(1:5, function(x) {
  if (x == 3) stop("Error on element 3")
  x^2
}, throw_error = FALSE)
```

parse_inline_expressions *Parse inline expressions*

Description

Parse “ inline expressions and evaluate them in the current environment, while preserving outer formatting markers like ‘{.val ...}‘.

Usage

```
parse_inline_expressions(text, env = parent.frame())
```

Arguments

text	A character string containing inline expressions to parse.
env	Environment in which to evaluate expressions. Defaults to the calling environment.

Value

A character string with expressions evaluated but formatting preserved.

Examples

```
i <- 1
parse_inline_expressions(
  "{.val {i}}"
)

x <- 5
y <- 10
parse_inline_expressions(
  "{.pkg {x + y}}"
)

name <- "testing"
name <- parse_inline_expressions(
  "{.pkg {name}}"
)
name

log_message(name)
```

`pearson_correlation` *Correlation and covariance calculation for sparse matrix*

Description

Correlation and covariance calculation for sparse matrix

Usage

```
pearson_correlation(x, y = NULL, max_dense_bytes = Inf)
```

Arguments

`x`	A numeric matrix or sparse `Matrix` with observations in rows.
`y`	An optional numeric matrix or sparse `Matrix` with the same number of rows as `x`.
`max_dense_bytes`	Maximum estimated bytes allowed for the dense covariance, correlation, and cross-product matrices. The default is 'Inf' for backward compatibility. Supply a finite value to enable the guard.

Details

This lower-level helper deliberately returns dense covariance and correlation matrices and therefore requires memory proportional to 'ncol(x) * ncol(y)'. Prefer [sparse_cor()] when a sparse, blockwise result is sufficient.

Value

A list with covariance and correlation matrices.

Examples

```
m1 <- simulate_sparse_matrix(
  100, 100
)
m2 <- simulate_sparse_matrix(
  100, 100,
  sparsity = 0.05
)
a <- pearson_correlation(m1, m2)
a$cov[1:5, 1:5]
a$cor[1:5, 1:5]
```

print.thisutils_logo *Print logo*

Description

Print logo

Usage

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

Arguments

x	Input information.
...	Other parameters.

Value

Print the ASCII logo

r_square *Coefficient of determination (R^2)*

Description

Coefficient of determination (R^2)

Usage

```
r_square(y_true, y_pred)
```

Arguments

y_true	A numeric vector with ground truth values.
y_pred	A numeric vector with predicted values.

Value

The R^2 value.

Examples

```
y <- rnorm(100)
y_pred <- y + rnorm(100, sd = 0.5)
r_square(y, y_pred)
```

remove_r *Check and remove R packages*

Description

Check and remove R packages

Usage

```
remove_r(packages, lib = .libPaths()[1], verbose = TRUE)
```

Arguments

packages	Package to be removed.
lib	The location of the library directories where to remove the packages.
verbose	Whether to print the message. Default is TRUE.

remove_space *Remove and normalize spaces*

Description

Remove and normalize spaces

Usage

```
remove_space(
  x,
  trim_start = TRUE,
  trim_end = FALSE,
  collapse_multiple = TRUE,
  preserve_newlines = TRUE
)
```

Arguments

x	A vector of character strings.
trim_start	Whether to remove leading spaces before the first word. Default is TRUE.
trim_end	Whether to remove trailing spaces after the last word. Default is FALSE.
collapse_multiple	Whether to collapse multiple consecutive spaces between words into a single space. Default is TRUE.
preserve_newlines	Whether to preserve newline characters when collapsing spaces. Default is TRUE.

Value

A character vector with spaces normalized according to the specified parameters.

Examples

```
x <- c(
  " hello  world ",
  "  test   case  ",
  "no space",
  "   multiple   spaces   "
)
remove_space(x)
remove_space(x, trim_start = FALSE)
remove_space(x, trim_end = TRUE)
remove_space(x, collapse_multiple = FALSE)
remove_space(
  x,
  trim_start = FALSE,
  trim_end = FALSE,
  collapse_multiple = FALSE
)

# with newlines
multiline <- c(
  "hello\n\n  world  ",
  "  first  \n  second  "
)
remove_space(multiline)
remove_space(multiline, preserve_newlines = FALSE)
```

---

row_maxs *Row maxima*

Description

Row maxima

Usage

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

Arguments

x	A dense or sparse matrix.
na.rm	Whether to ignore ‘NA‘ values.

Value

A numeric vector of row maxima. Implicit sparse zeros are treated as zero.

Examples

```
row_maxs(matrix(c(-2, 0, 3, 1), nrow = 2))
```

`run_biocneighbors_knn` *Find nearest neighbors with BiocNeighbors*

Description

Find nearest neighbors within a reference matrix or from a query matrix to a reference matrix. The wrapper standardizes matrix coercion, distance metric, and self-neighbor removal across consumers.

Usage

```
run_biocneighbors_knn(
  reference,
  query = NULL,
  k,
  metric = c("euclidean", "cosine"),
  exclude_self = FALSE,
  n_threads = 1L
)
```

Arguments

`reference`	Numeric reference matrix with observations in rows.
`query`	Optional numeric query matrix with the same number of columns.
`k`	Number of nearest neighbors to return.
`metric`	Distance metric: ‘"euclidean"‘ or ‘"cosine"‘.
`exclude_self`	Whether to remove self-neighbors when ‘query‘ is ‘NULL‘.
`n_threads`	Number of BiocNeighbors threads.

Value

A list with integer matrix ‘idx‘ and numeric matrix ‘dist‘.

Examples

```
if (nzchar(system.file(package = "BiocNeighbors"))) {
  run_biocneighbors_knn(matrix(rnorm(20), ncol = 2), k = 2)
}
```

`run_dense_topk` *Dense matrix top-k selection*

Description

For each column or row of a dense numeric matrix, extract the top `k` elements and their indices. The default returns the largest values; set `decreasing = FALSE` to retain the smallest values, as in nearest-neighbor selection from a distance matrix.

Usage

```
run_dense_topk(x, k, by = c("col", "row"), decreasing = TRUE)
```

Arguments

`x`	A numeric matrix (or something coercible to one).
`k`	Number of entries to retain per column or row. Must be a positive integer.
`by`	Direction of selection: `"col"` ranks row entries independently within each column, while `"row"` ranks column entries independently within each row.
`decreasing`	Whether to sort in decreasing order (largest values first). Default is `TRUE`.

Value

A list with two components:

idx Integer matrix of 1-based indices into the opposite dimension.

value Numeric matrix of corresponding values.

Both matrices have `ncol(x)` rows when `by = "col"` and `nrow(x)` rows when `by = "row"`.

Examples

```
m <- matrix(rnorm(100), nrow = 10)
run_dense_topk(m, k = 3, by = "col")
run_dense_topk(m, k = 3, by = "row")
run_dense_topk(m, k = 3, by = "col", decreasing = FALSE)
```

run_sparse_stored_topk_by_column

Compatibility wrapper for stored column-wise sparse top-k selection

Description

`run_sparse_stored_topk_by_column()` preserves the stored-entry column-wise interface used in earlier releases. New code should call `run_sparse_topk_stored()` with `by = "col"`.

Usage

```
run_sparse_stored_topk_by_column(x, k, decreasing = TRUE)
```

Arguments

`x`	A `dgCMatrix` (or something coercible to one).
`k`	Number of top entries to retain per column or row. Must be a positive integer.
`decreasing`	Whether to sort in decreasing order (largest values first). Default is `TRUE`.

Value

A list with `idx` and `value` matrices as described in `run_sparse_topk_stored()`.

run_sparse_topk

Sparse matrix top-k selection

Description

For each column or row of a sparse `dgCMatrix`, extract the top `k` matrix elements and their indices. By default, unstored positions participate with their matrix value of zero. For column-wise selection, this gives the same semantics as `run_dense_topk()`.

Usage

```
run_sparse_topk(
  x,
  k,
  by = c("col", "row"),
  decreasing = TRUE,
  include_implicit_zeros = TRUE
)
```

Arguments

x	A dgCMatrix (or something coercible to one).
k	Number of top entries to retain per column or row. Must be a positive integer.
by	Direction of selection: "col" ranks row entries independently within each column, while "row" ranks column entries independently within each row.
decreasing	Whether to sort in decreasing order (largest values first). Default is TRUE.
include_implicit_zeros	Whether unstored sparse positions participate as zeros. The default, TRUE, gives ordinary matrix semantics. Set to FALSE to rank only stored entries; for that use case, prefer the more explicit run_sparse_topk_stored().

Value

A list with two components:

idx Integer matrix of 1-based indices into the opposite dimension.

value Numeric matrix of corresponding values.

Both matrices have ncol(x) rows when by = "col" and nrow(x) rows when by = "row".

Examples

```
m <- Matrix::rsparsematrix(10, 20, density = 0.3)
run_sparse_topk(m, k = 3, by = "col")
run_sparse_topk(m, k = 3, by = "row")
```

---

run_sparse_topk_by_column

Compatibility wrapper for column-wise sparse top-k selection

Description

run_sparse_topk_by_column() preserves the column-wise interface used in earlier releases: only explicitly stored entries participate, and missing ranks are padded with NA indices and zero values. New code should call run_sparse_topk() or run_sparse_topk_stored() to select the intended sparse-zero semantics explicitly.

Usage

```
run_sparse_topk_by_column(x, k, decreasing = TRUE)
```

Arguments

x	A dgCMatrix (or something coercible to one).
k	Number of stored entries to retain per column.
decreasing	Whether to sort in decreasing order. Defaults to TRUE.

Value

A list with `idx` and `value` matrices. Columns with fewer than `k` stored entries use `NA` indices and zero values for the remaining ranks.

`run_sparse_topk_stored`

Stored sparse entries top-k selection

Description

For each column or row of a sparse `dgCMatrix`, rank only explicitly stored entries. Unstored zeros never become candidates. This is useful for sparse adjacency matrices, where stored entries represent graph edges rather than samples from a full numeric matrix.

Usage

```
run_sparse_topk_stored(x, k, by = c("col", "row"), decreasing = TRUE)
```

Arguments

`x`	A `dgCMatrix` (or something coercible to one).
`k`	Number of top entries to retain per column or row. Must be a positive integer.
`by`	Direction of selection: `"col"` ranks row entries independently within each column, while `"row"` ranks column entries independently within each row.
`decreasing`	Whether to sort in decreasing order (largest values first). Default is `TRUE`.

Value

A list with `idx` and `value` matrices as described in `run_sparse_topk()`. Groups with fewer than `k` stored entries are padded with `NA` in both matrices.

Examples

```
graph <- Matrix::sparseMatrix(
  i = c(1, 3, 2), j = c(1, 1, 2), x = c(1, 3, -2),
  dims = c(3, 2)
)
run_sparse_topk_stored(graph, k = 2, by = "col")
```

`simulate_sparse_matrix` *Generate a simulated sparse matrix*

Description

This function generates a sparse matrix with a specified number of rows and columns, a given sparsity level, and a distribution function for the non-zero values.

Usage

```
simulate_sparse_matrix(
  nrow,
  ncol,
  sparsity = 0.95,
  distribution_fun = function(n) stats::rpois(n, lambda = 0.5) + 1,
  decimal = 0,
  seed = 1
)
```

Arguments

`nrow`	Number of rows in the matrix.
`ncol`	Number of columns in the matrix.
`sparsity`	Proportion of zero elements (sparsity level). Default is `0.95`, meaning 95% of elements are zero (5% are non-zero).
`distribution_fun`	Function to generate non-zero values.
`decimal`	Controls the number of decimal places in the generated values. If set to `0`, values will be integers. When `decimal` > 0, random decimal parts are uniformly distributed across the full range. Default is `0`.
`seed`	Random seed for reproducibility.

Value

A sparse matrix of class "dgCMatrix".

Examples

```
simulate_sparse_matrix(1000, 500) |>
  check_sparsity()

simulate_sparse_matrix(10, 10, decimal = 1)
simulate_sparse_matrix(10, 10, decimal = 5)
```

sparse_cor *Resource-controlled sparse correlation*

Description

Compute correlations from matrix-like input and return a sparse matrix. Pearson cross-products remain sparse and correlations are evaluated in column blocks so block-local working memory is bounded independently of the full output dimensions.

Usage

```
sparse_cor(
  x,
  y = NULL,
  method = c("pearson", "spearman", "kendall"),
  allow_neg = TRUE,
  remove_na = TRUE,
  remove_inf = TRUE,
  threshold = 0,
  block_size = 256L,
  max_dense_bytes = Inf,
  max_output_entries = Inf,
  ...
)
```

Arguments

x	A numeric matrix or sparse Matrix with observations in rows.
y	An optional numeric matrix or sparse Matrix with the same number of rows as x.
method	Correlation coefficient: "pearson", "spearman", or "kendall".
allow_neg	Logical. Whether to allow negative values or set them to 0.
remove_na	Logical. Whether to replace NA values with 0.
remove_inf	Logical. Whether to replace infinite values with 0.
threshold	Non-negative absolute correlation threshold. Values with absolute magnitude below this threshold are omitted from the sparse output.
block_size	Maximum number of target columns in each Pearson working block. The effective size may be reduced to honor max_dense_bytes.
max_dense_bytes	Maximum estimated bytes allowed for block-local Pearson working arrays or dense rank-correlation arrays. The default is Inf for backward compatibility. Supply a finite value to enable this guard.
max_output_entries	Maximum number of stored values allowed in the sparse result. The default, Inf, preserves the historical unbounded output behavior; set a finite value to fail before returning an output that exceeds the workflow's storage budget.

... Other arguments passed to stats::cor() for Spearman and Kendall correlations.

Details

Pearson input and cross-products remain sparse. Centering, scaling, and thresholding are fused in a column-block scan rather than materializing a dense correlation block. The final sparse result can nevertheless contain up to `ncol(x) * ncol(y)` stored values when `threshold = 0`; use `threshold` and `max_output_entries` to make this boundary explicit.

Spearman and Kendall correlation require ranking and currently densify the input and full correlation result. Their estimated peak working size is checked against `max_dense_bytes` before conversion.

Value

A sparse correlation matrix.

Examples

```
m1 <- simulate_sparse_matrix(
  500, 100
)
m2 <- simulate_sparse_matrix(
  500, 100,
  seed = 2025
)
a <- sparse_cor(m1)
b <- sparse_cor(m1, m2)
c <- as_matrix(
  cor(as_matrix(m1)),
  return_sparse = TRUE
)
d <- as_matrix(
  cor(as_matrix(m1), as_matrix(m2)),
  return_sparse = TRUE
)

a[1:5, 1:5]
c[1:5, 1:5]
all.equal(a, c)

b[1:5, 1:5]
d[1:5, 1:5]
all.equal(b, d)

m1[sample(1:500, 10)] <- NA
m2[sample(1:500, 10)] <- NA

sparse_cor(m1, m2)[1:5, 1:5]

system.time(
  sparse_cor(m1)
```

```
)
system.time(
  cor(as_matrix(m1))
)

system.time(
  sparse_cor(m1, m2)
)
system.time(
  cor(as_matrix(m1), as_matrix(m2))
)
```

`split_indices` *Split indices.*

Description

An optimised version of split for the special case of splitting row indices into groups.

Usage

```
split_indices(group, n = 0L)
```

Arguments

`group`	Integer indices
`n`	The largest integer (may not appear in index). This is hint: if the largest value of `group` is bigger than `n`, the output will silently expand.

Value

A list of vectors of indices.

References

https://github.com/hadley/plyr/blob/d57f9377eb5d56107ba3136775f2f0f005f33aa3/src/split-numeric.cpp#L20

Examples

```
split_indices(sample(10, 100, rep = TRUE))
split_indices(sample(10, 100, rep = TRUE), 10)
```

sump *Sum P-value*

Description

Sum P-value

Usage

```
sump(p)
```

Arguments

p	A vector of P-values.

Examples

```
p <- c(0.01, 0.02, 0.03, 0.04, 0.05)
sump(p)
```

table_to_matrix *Switch table to matrix*

Description

Switch table to matrix

Usage

```
table_to_matrix(
  table,
  row_names = NULL,
  col_names = NULL,
  threshold = 0,
  return_sparse = FALSE
)
```

Arguments

table	A table with three columns: row, col, and value.
row_names	Character vector of row names to filter by.
col_names	Character vector of column names to filter by.
threshold	The threshold for filtering values based on absolute values. Defaults to 0.
return_sparse	Whether to return a sparse matrix. Defaults to false.

Value

A matrix.

See Also

matrix_to_table

Examples

```
table <- data.frame(
  row = c("r1", "r2", "r3", "r4", "r5", "r6"),
  col = c("c4", "c5", "c6", "c1", "c2", "c3"),
  value = c(0.6, -0.5, -0.4, 0.3, 0.2, 0.1)
)
matrix <- table_to_matrix(table)
table_new <- matrix_to_table(matrix)
identical(table, table_new)

table_to_matrix(table, threshold = 0.3)

table_to_matrix(
  table,
  row_names = c("r1", "r2"),
  col_names = c("c4", "c5")
)

sparse_matrix <- simulate_sparse_matrix(10, 10)
table_sparse <- matrix_to_table(
  sparse_matrix
)
sparse_matrix_new <- table_to_matrix(
  table_sparse,
  return_sparse = TRUE
)
identical(sparse_matrix, sparse_matrix_new)
```

---

thisutils_logo *The logo of thisutils*

Description

The thisutils logo, using ASCII or Unicode characters Use cli::ansi_strip to get rid of the colors.

Usage

```
thisutils_logo(unicode = cli::is_utf8_output())
```

Arguments

unicode	Unicode symbols on UTF-8 platforms. Default is cli::is_utf8_output.

Value

A character vector with class `thisutils_logo`.

References

https://github.com/tidyverse/tidyverse/blob/main/R/logo.R

Examples

```
thisutils_logo()
```

---

try_get *Try to evaluate an expression a set number of times before failing*

Description

The function is used as a fail-safe if code sometimes works and sometimes doesn't, usually because it depends on a resource that may be temporarily unavailable. It tries to evaluate the expression `max_tries` times. If all the attempts fail, it throws an error; if not, the evaluated expression is returned.

Usage

```
try_get(expr, max_tries = 5, error_message = "", retry_message = "Retrying...")
```

Arguments

`expr`	The expression to be evaluated.
`max_tries`	The maximum number of attempts to evaluate the expression before giving up. Default is 5.
`error_message`	Additional custom error message to be displayed when an error occurs.
`retry_message`	Message displayed when a new try to evaluate the expression would be attempted.

Value

The evaluated expression if successful, otherwise it throws an error if all attempts are unsuccessful.

Examples

```
f <- function() {
  value <- runif(1, min = 0, max = 1)
  if (value > 0.5) {
    log_message("value is larger than 0.5")
    return(value)
  } else {
    log_message(
```

```
      "value is smaller than 0.5",
      message_type = "error"
    )
  }
}
f_evaluated <- try_get(expr = f())
print(f_evaluated)
```

---

unnest_fun *Unnest a list-column*

Description

Implement similar functions to the `tidyr::unnest` function.

Usage

```
unnest_fun(data, cols, keep_empty = FALSE)
```

Arguments

data	A data frame.
cols	Columns to unnest.
keep_empty	By default, you get one row of output for each element of the list your unchopping/unnesting. This means that if there's a size-0 element (like `NULL` or an empty data frame), that entire row will be dropped from the output. If you want to preserve all rows, use `keep_empty = TRUE` to replace size-0 elements with a single row of missing values.

Examples

```
data <- data.frame(
  id = 1:3,
  x = c("a", "b", "c"),
  stringsAsFactors = FALSE
)
data$data <- list(
  c(1, 2),
  c(3, 4, 5),
  c(6)
)
unnest_fun(data, cols = "data")

data2 <- data.frame(
  id = 1:3,
  x = c("a", "b", "c"),
  stringsAsFactors = FALSE
)
data2$data <- list(
```

```
  c(1, 2),
  numeric(0),
  c(6)
)
unnest_fun(data2, cols = "data")
unnest_fun(data2, cols = "data", keep_empty = TRUE)
```

---

votep *Vote P-value*

Description

Vote P-value

Usage

```
votep(p, alpha = 0.5)
```

Arguments

p	A vector of P-values.
alpha	The significance level.

Examples

```
p <- c(0.01, 0.02, 0.03, 0.04, 0.05)
votep(p)
votep(p, alpha = 0.01)
```

---

wilkinsonp *Wilkinson's P-value*

Description

Wilkinson's P-value

Usage

```
wilkinsonp(p, r = 1, alpha = 0.05, log.p = FALSE)
```

Arguments

p	A vector of P-values.
r	The number of studies to include in the P-value calculation.
alpha	The significance level.
log.p	Whether to return the log of the P-value.

Examples

```
p <- c(0.01, 0.02, 0.03, 0.04, 0.05)
wilkinsonp(p)
wilkinsonp(p, r = 2)
wilkinsonp(p, alpha = 0.01)
wilkinsonp(p, log.p = TRUE)
```

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