

Package ‘cheapr’

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Title Simple Functions to Save Time and Memory

Version 0.9.3

Maintainer Nick Christofides <nick.christofides.r@gmail.com>

Description Fast and memory-efficient (or 'cheap') tools to facilitate efficient programming, saving time and memory. It aims to provide 'cheaper' alternatives to common base R functions, as well as some additional functions.

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BugReports <https://github.com/NicChr/cheapr/issues>

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Author Nick Christofides [aut, cre] (<<https://orcid.org/0000-0002-9743-7342>>)

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cheapr-package	<i>cheapr: Simple Functions to Save Time and Memory</i>
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Description

In this package, 'cheap' means fast and efficient.

cheapr aims to provide a set of functions for programmers to write cheaper code, saving time and memory.

Author(s)

Maintainer: Nick Christofides <nick.christofides.r@gmail.com> ([ORCID](#))

See Also

Useful links:

- Report bugs at <https://github.com/NicChr/cheapr/issues>

count_val	<i>Count the number of occurrences of a value.</i>
-----------	--

Description

This is a programmer's version of `sum(x == value)` to count the number of occurrences of a value without creating a potentially large logical vector.

Usage

```
count_val(x, value, recursive = TRUE)
```

```
val_count(x, value, recursive = TRUE)
```

```
which_val(x, value, invert = FALSE)
```

Arguments

x	A vector, list, data frame or matrix.
value	A value with which to count the frequency of.
recursive	Should the function be applied recursively to lists?
invert	Should which_val find locations of everything except specified value? Default is FALSE.

Details

This is a generalisation of num_na() and as such the identity count_val(x, NA) == num_na(x) will always hold.

Value

A count of the number of times value appears in x.

factor_ *A faster version of factor()*

Description

A fast version of factor() using the collapse package. There are some additional utilities such as levels_factor() which returns the levels of a factor, as a factor, used_levels() which returns the used levels of a factor, and unused_levels() which returns the unused levels of a factor.

Usage

```
factor_(
  x = integer(),
  levels = NULL,
  order = TRUE,
  na_exclude = TRUE,
  ordered = is.ordered(x)
)
```

```
levels_factor(x)
```

```
used_levels(x)
```

```
unused_levels(x)
```

Arguments

x	A vector.
levels	Optional factor levels.
order	Should factor levels be sorted? Default is TRUE. It typically is faster to set this to FALSE, in which case the levels are sorted by order of first appearance.
na_exclude	Should NA values be excluded from the factor levels? Default is TRUE.
ordered	Should the result be an ordered factor?

Details

This operates similarly to `collapse::qF()`.

The main difference internally is that `collapse::funique()` is used and therefore s3 methods can be written for it.

Furthermore, for date-times `factor_` differs in that it differentiates all instances in time whereas `factor` differentiates calendar times. Using a daylight savings example where the clocks go back: `factor(as.POSIXct(1729984360, tz = "Europe/London") + 3600 *(1:5))` produces 4 levels whereas `factor_(as.POSIXct(1729984360, tz = "Europe/London") + 3600 *(1:5))` produces 5 levels.

Value

A factor or character in the case of `used_levels` and `unused_levels`.

gcd

Greatest common divisor and smallest common multiple

Description

Fast greatest common divisor and smallest common multiple using the Euclidean algorithm.

`gcd()` returns the greatest common divisor.

`scm()` returns the smallest common multiple.

`gcd2()` is a vectorised binary version of `gcd`.

`scm2()` is a vectorised binary version of `scm`.

Usage

```
gcd(
  x,
  tol = sqrt(.Machine$double.eps),
  na_rm = TRUE,
  round = TRUE,
  break_early = TRUE
)
```

```
scm(x, tol = sqrt(.Machine$double.eps), na_rm = TRUE)
```

```
gcd2(x, y, tol = sqrt(.Machine$double.eps), na_rm = TRUE)
```

```
scm2(x, y, tol = sqrt(.Machine$double.eps), na_rm = TRUE)
```

Arguments

x	A numeric vector.
tol	Tolerance. This must be a single positive number strictly less than 1.
na_rm	If TRUE the default, NA values are ignored.
round	If TRUE the output is rounded as <code>round(gcd, digits)</code> where <code>digits</code> is <code>ceiling(abs(log10(tol))) + 1</code> . This can potentially reduce floating point errors on further calculations. The default is TRUE.
break_early	This is experimental and applies only to floating-point numbers. When TRUE the algorithm will end once <code>gcd > 0 && gcd < 2 * tol</code> . This can offer a tremendous speed improvement. If FALSE the algorithm finishes once it has gone through all elements of x. The default is TRUE. For integers, the algorithm always breaks early once <code>gcd > 0 && gcd <= 1</code> .
y	A numeric vector.

Details

Method:

GCD:

The GCD is calculated using a binary function that takes input `GCD(gcd, x[i + 1])` where the output of this function is passed as input back into the same function iteratively along the length of x. The first gcd value is `x[1]`.

Zeroes are handled in the following way:

$$\text{GCD}(0, 0) = 0$$

$$\text{GCD}(a, 0) = a$$

This has the nice property that zeroes are essentially ignored.

SCM:

This is calculated using the GCD and the formula is:

$$\text{SCM}(x, y) = (\text{abs}(x) / \text{GCD}(x, y)) * \text{abs}(y)$$

If you want to calculate the gcd & lcm for 2 values or across 2 vectors of values, use `gcd2` and `scm2`.

Value

A number representing the GCD or SCM.

Examples

```
library(cheapr)
library(bench)
```

```

# Binary versions
gcd2(15, 25)
gcd2(15, seq(5, 25, 5))
scm2(15, seq(5, 25, 5))
scm2(15, 25)

# GCD across a vector
gcd(c(0, 5, 25))
mark(gcd(c(0, 5, 25)))

x <- rnorm(10^5)
gcd(x)
gcd(x, round = FALSE)
mark(gcd(x))

```

is_na

Efficient functions for dealing with missing values.

Description

is_na() is a parallelised alternative to is.na().
 num_na(x) is a faster and more efficient sum(is.na(x)).
 which_na(x) is a more efficient which(is.na(x))
 which_not_na(x) is a more efficient which(!is.na(x))
 row_na_counts(x) is a more efficient rowSums(is.na(x))
 row_all_na() returns a logical vector indicating which rows are empty and have only NA values.
 row_any_na() returns a logical vector indicating which rows have at least 1 NA value.
 The col_ variants are the same, but operate by-column.

Usage

```

is_na(x)

## Default S3 method:
is_na(x)

## S3 method for class 'POSIXlt'
is_na(x)

## S3 method for class 'vctrs_rcrd'
is_na(x)

## S3 method for class 'data.frame'
is_na(x)

num_na(x, recursive = TRUE)

which_na(x)

```

```

which_not_na(x)

any_na(x, recursive = TRUE)

all_na(x, recursive = TRUE)

row_na_counts(x, names = FALSE)

col_na_counts(x, names = FALSE)

row_all_na(x, names = FALSE)

col_all_na(x, names = FALSE)

row_any_na(x, names = FALSE)

col_any_na(x, names = FALSE)

```

Arguments

x	A vector, list, data frame or matrix.
recursive	Should the function be applied recursively to lists? The default is TRUE. Setting this to TRUE is actually much cheaper because when FALSE, the other NA functions rely on calling <code>is_na()</code> , therefore allocating a vector. This is so that alternative objects with <code>is.na</code> methods can be supported.
names	Should row/col names be added?

Details

These functions are designed primarily for programmers, to increase the speed and memory-efficiency of NA handling.

Most of these functions can be parallelised through `options(cheapr.cores)`.

Common use-cases:

To replicate `complete.cases(x)`, use `!row_any_na(x)`.

To find rows with any empty values, use `which_(row_any_na(df))`.

To find empty rows use `which_(row_all_na(df))` or `which_na(df)`. To drop empty rows use `na_rm(df)` or `sset(df, which_(row_all_na(df), TRUE))`.

is_na:

`is_na` is an S3 generic function. It will internally fall back on using `is.na` if it can't find a suitable method. Alternatively you can write your own `is_na` method. For example there is a method for `vctrs_rcrd` objects that simply converts it to a data frame and then calls `row_all_na()`. There is also a POSIX1t method for `is_na` that is much faster than `is.na`.

Lists:

When `x` is a list, `num_na`, `any_na` and `all_na` will recursively search the list for NA values. If `recursive = F` then `is_na()` is used to find NA values.

`is_na` differs to `is.na` in 2 ways:

- List elements are counted as NA if either that value is NA, or if it's a list, then all values of that list are NA.
- When called on a data frame, it returns TRUE for empty rows that contain only NA values.

Value

Number or location of NA values.

Examples

```
library(cheapr)
library(bench)

x <- 1:10
x[c(1, 5, 10)] <- NA
num_na(x)
which_na(x)
which_not_na(x)

row_nas <- row_na_counts(airquality, names = TRUE)
col_nas <- col_na_counts(airquality, names = TRUE)
row_nas
col_nas

df <- sset(airquality, j = 1:2)

# Number of NAs in data
num_na(df)
# Which rows are empty?
row_na <- row_all_na(df)
sset(df, row_na)

# Removing the empty rows
sset(df, which_(row_na, invert = TRUE))
# Or
na_rm(df)
# Or
sset(df, row_na_counts(df) < ncol(df))
```

lag_

Lagged operations.

Description

Fast lags and leads optionally using dynamic vectorised lags, ordering and run lengths.

Usage

```
lag_(x, n = 1L, fill = NULL, set = FALSE, recursive = TRUE)
```

```
lag2_(
  x,
  n = 1L,
  order = NULL,
  run_lengths = NULL,
  fill = NULL,
  recursive = TRUE
)
```

Arguments

x	A vector or data frame.
n	Number of lags. Negative values are accepted. lag2_ accepts a vector of dynamic lags and leads which gets recycled to the length of x.
fill	Value used to fill first n values. Default is NA.
set	Should x be updated by reference? If TRUE no copy is made and x is updated in place. The default is FALSE.
recursive	Should list elements be lagged as well? If TRUE, this is useful for data frames and will return row lags. If FALSE this will return a plain lagged list.
order	Optionally specify an ordering with which to apply the lags. This is useful for example when applying lags chronologically using an unsorted time variable.
run_lengths	Optional integer vector of run lengths that defines the size of each lag run. For example, supplying c(5, 5) applies lags to the first 5 elements and then essentially resets the bounds and applies lags to the next 5 elements as if they were an entirely separate and standalone vector. This is particularly useful in conjunction with the order argument to perform a by-group lag. See the examples for details.

Details

For most applications, it is more efficient and recommended to use lag_(). For anything that requires dynamic lags, lag by order of another variable, or by-group lags, one can use lag2_(). To do cyclic lags, see the examples below for an implementation.

lag2_:

lag2_ is a generalised form of lag_ that by default performs simple lags and leads. It has 3 additional features but does not support updating by reference or long vectors.

These extra features include:

- n - This shares the same name as the n argument in lag_ for consistency. The difference is that lag_ accepts a lag vector of length 1 whereas this accepts a vector of dynamic lags allowing for flexible combinations of variable sized lags and leads. These are recycled to the length

of the data and will always align with the data, meaning that if you supply a custom order argument, this ordering is applied both to `x` and the recycled lag vector `n` simultaneously.

- `order` - Apply lags in any order you wish. This can be useful for reverse order lags, lags against unsorted time variables, and by-group lags.
- `run_lengths` - Specify the size of individual lag runs. For example, if you specify `run_lengths = c(3, 4, 2)`, this will apply your lags to the first 3 elements and then reset, applying lags to the next 4 elements, to reset again and apply lags to the final 2 elements. Each time the reset occurs, it treats each run length sized 'chunk' as a unique and separate vector. See the examples for a showcase.

Table of differences between `lag_` and `lag2_`:

Description	<code>lag_</code>	<code>lag2_</code>
Lags	Yes	Yes
Leads	Yes	Yes
Long vector support	Yes	No
Lag by reference	Yes	No
Dynamic vectorised lags	No	Yes
Data frame row lags	Yes	Yes
Alternative order lags	No	Yes

Value

A lagged object the same size as `x`.

Examples

```
library(cheapr)
library(bench)

# A use-case for data.table
# Adding 0 because can't update ALTREP by reference
df <- data.frame(x = 1:10^5 + 0L)

# Normal data frame lag
sset(lag_(df), 1:10)

# Lag these behind by 3 rows
sset(lag_(df, 3, set = TRUE), 1:10)

df$x[1:10] # x variable was updated by reference!

# The above can be used naturally in data.table to lag data
# without any copies

# To perform regular R row lags, just make sure set is `FALSE`
sset(lag_(as.data.frame(EuStockMarkets), 5), 1:10)

# lag2_ is a generalised version of lag_ that allows
```

```
# for much more complex lags

x <- 1:10

# lag every 2nd element
lag2_(x, n = c(1, 0)) # lag vector is recycled

# Explicit Lag(3) using a vector of lags
lags <- lag_sequence(length(x), 3, partial = FALSE)
lag2_(x, n = lags)

# Alternating lags and leads
lag2_(x, c(1, -1))

# Lag only the 3rd element
lags <- integer(length(x))
lags[3] <- 1L
lag2_(x, lags)

# lag in descending order (same as a lead)

lag2_(x, order = 10:1)

# lag that resets after index 5
lag2_(x, run_lengths = c(5, 5))

# lag with a time index
years <- sample(2011:2020)
lag2_(x, order = order(years))

# Example of how to do a cyclical lag
n <- length(x)

# When k >= 0
k <- min(3, n)
lag2_(x, c(rep(-n + k, k), rep(k, n - k)))
# When k < 0
k <- max(-3, -n)
lag2_(x, c(rep(k, n + k), rep(n + k, -k)))

# As it turns out, we can do a grouped lag
# by supplying group sizes as run lengths and group order as the order

set.seed(45)
g <- sample(c("a", "b"), 10, TRUE)

# NOTE: collapse::flag will not work unless g is already sorted!
# This is not an issue with lag2_()
collapse::flag(x, g = g)
lag2_(x, order = order(g), run_lengths = collapse::GRP(g)$group.sizes)

# For production code, we can of course make
# this more optimised by using collapse::radixorderv()
```

```

# Which calculates the order and group sizes all at once

o <- collapse::radixorderv(g, group.sizes = TRUE)
lag2_(x, order = o, run_lengths = attr(o, "group.sizes"))

# Let's finally wrap this up in a nice grouped-lag function

grouped_lag <- function(x, n = 1, g = integer(length(x))){
  o <- collapse::radixorderv(g, group.sizes = TRUE, sort = FALSE)
  lag2_(x, n, order = o, run_lengths = attr(o, "group.sizes"))
}

# And voila!
grouped_lag(x, g = g)

# A method to extract this information from dplyr

## We can actually get this information easily from a `grouped_df` object
## Uncomment the below code to run the implementation
# library(dplyr)
# library(timeplyr)
# eu_stock <- EuStockMarkets |>
#   ts_as_tibble() |>
#   group_by(stock_index = group)
# groups <- group_data(eu_stock) # Group information
# group_order <- unlist(groups$.rows) # Order of groups
# group_sizes <- lengths_(groups$.rows) # Group sizes
#
# # by-stock index lag
# lag2_(eu_stock$value, order = group_order, run_lengths = group_sizes)
#
# # Verifying this output is correct
# eu_stock |>
#   ungroup() |>
#   mutate(lag1 = lag_(value), .by = stock_index) |>
#   mutate(lag2 = lag2_(value, order = group_order, run_lengths = group_sizes)) |>
#   summarise(lags_are_equal = identical(lag1, lag2))

# Let's compare this to data.table

library(data.table)
default_threads <- getDTthreads()
setDTthreads(1)
dt <- data.table(x = 1:10^5,
                 g = sample.int(10^4, 10^5, TRUE))

bench::mark(dt[, y := shift(x), by = g][[["y"]],
             grouped_lag(dt$x, g = dt$g),
             iterations = 10)
setDTthreads(default_threads)

```

lengths_ *List utilities*

Description

Functions to help work with lists.

Usage

```
lengths_(x, names = FALSE)

unlisted_length(x)

new_list(length = 0L, default = NULL)
```

Arguments

x	A list.
names	Should names of list elements be added? Default is FALSE.
length	Length of list.
default	Default value for each list element.

Value

`lengths_()` returns the list lengths.
`unlisted_length()` is an alternative to `length(unlist(x))`.
`new_list()` is like `vector("list", length)` but also allows you to specify a default value for each list element. This can be useful for initialising with a catch-all value so that when you unlist you're guaranteed a list of length \geq to the specified length.

Examples

```
library(cheapr)
l <- list(1:10,
         NULL,
         list(integer(), NA_integer_, 2:10))

lengths_(l) # Faster lengths()
unlisted_length(l) # length of vector if we unlist
paste0("length: ", length(print(unlist(l))))

unlisted_length(l) - num_na(l) # Number of non-NA elements

# We can create and initialise a new list with a default value
l <- new_list(20, 0L)
l[1:5]
# This works well with vctrs_list_of objects
vctrs::new_list_of(l, ptype = integer())[1:5]
```

Description

A cheaper summary() function, designed for larger data.

Usage

```
overview(x, hist = FALSE, digits = getOption("cheapr.digits", 2))

## Default S3 method:
overview(x, hist = FALSE, digits = getOption("cheapr.digits", 2))

## S3 method for class 'logical'
overview(x, hist = FALSE, digits = getOption("cheapr.digits", 2))

## S3 method for class 'numeric'
overview(x, hist = FALSE, digits = getOption("cheapr.digits", 2))

## S3 method for class 'character'
overview(x, hist = FALSE, digits = getOption("cheapr.digits", 2))

## S3 method for class 'factor'
overview(x, hist = FALSE, digits = getOption("cheapr.digits", 2))

## S3 method for class 'Date'
overview(x, hist = FALSE, digits = getOption("cheapr.digits", 2))

## S3 method for class 'POSIXt'
overview(x, hist = FALSE, digits = getOption("cheapr.digits", 2))

## S3 method for class 'ts'
overview(x, hist = FALSE, digits = getOption("cheapr.digits", 2))

## S3 method for class 'zoo'
overview(x, hist = FALSE, digits = getOption("cheapr.digits", 2))

## S3 method for class 'data.frame'
overview(x, hist = FALSE, digits = getOption("cheapr.digits", 2))
```

Arguments

x	A vector or data frame.
hist	Should in-line histograms be returned? Default is FALSE.
digits	How many decimal places should the summary statistics be printed as? Default is 2.

Details

No rounding of statistics is done except in printing which can be controlled either through the `digits` argument in `overview()`, or by setting the option `options(cheapr.digits)`.

To access the underlying data, for example the numeric summary, just use `$numeric`, e.g. `overview(rnorm(30))$numeric`.

Value

An object of class "overview". Under the hood this is just a list of data frames. Key summary statistics are reported in each data frame.

Examples

```
library(cheapr)
overview(iris)

# With histograms
overview(airquality, hist = TRUE)

# Round to 0 decimal places
overview(airquality, digits = 0)

# We can set an option for all overviews
options(cheapr.digits = 1)
overview(rnorm(100))
options(cheapr.digits = 2) # The default
```

 recycle

Recycle objects to a common size

Description

A convenience function to recycle R objects to either a common or specified size.

Usage

```
recycle(..., length = NULL)
```

Arguments

<code>...</code>	Objects to recycle.
<code>length</code>	Optional length to recycle objects to.

Details

Data frames are recycled by recycling their rows.

`recycle()` is optimised to only recycle objects that need recycling.

NULL objects are ignored and not recycled or returned.

Value

A list of recycled R objects.

Examples

```
library(cheapr)

recycle(Sys.Date(), 1:10)

# Any vectors of zero-length are all recycled to zero-length
recycle(integer(), 1:10)

# Data frame rows are recycled
recycle(sset(iris, 1:3), length = 3 * 3)

# To recycle list items, use `do.call()`
my_list <- list(from = 1L, to = 10L, by = seq(0.1, 1, 0.1))
do.call(recycle, my_list)
```

sequence_

Utilities for creating many sequences

Description

sequence_ is an extension to [sequence](#) which accepts decimal number increments.
seq_id can be paired with sequence_ to group individual sequences.
seq_ is a vectorised version of [seq](#).
window_sequence creates a vector of window sizes for rolling calculations.
lag_sequence creates a vector of lags for rolling calculations.
lead_sequence creates a vector of leads for rolling calculations.

Usage

```
sequence_(size, from = 1L, by = 1L, add_id = FALSE)

seq_id(size)

seq_(from = 1L, to = 1L, by = 1L, add_id = FALSE)

seq_size(from, to, by = 1L)

window_sequence(size, k, partial = TRUE, ascending = TRUE, add_id = FALSE)

lag_sequence(size, k, partial = TRUE, add_id = FALSE)

lead_sequence(size, k, partial = TRUE, add_id = FALSE)
```


Arguments

size	Vector of sequence lengths.
from	Start of sequence(s).
by	Unit increment of sequence(s).
add_id	Should the ID numbers of the sequences be added as names? Default is FALSE.
to	End of sequence(s).
k	Window/lag size.
partial	Should partial windows/lags be returned? Default is TRUE.
ascending	Should window sequence be ascending? Default is TRUE.

Details

sequence_() works in the same way as sequence() but can accept non-integer by values. It also recycles from and to, in the same way as sequence().

If any of the sequences contain values > .Machine\$integer.max, then the result will always be a double vector.

from can be also be a date, date-time, or any object that supports addition and multiplication.

seq_() is a vectorised version of seq() that strictly accepts only the arguments from, to and by.

Value

A vector of length sum(size) except for seq_ which returns a vector of size sum((to - from) / (by + 1))

Examples

```
library(cheapr)
sequence(1:3)
sequence_(1:3)

sequence(1:3, by = 0.1)
sequence_(1:3, by = 0.1)

# Add IDs to the sequences
sequence_(1:3, by = 0.1, add_id = TRUE)
# Turn this quickly into a data frame
enframe_(sequence_(1:3, by = 0.1, add_id = TRUE))

sequence(c(3, 2), by = c(-0.1, 0.1))
sequence_(c(3, 2), by = c(-0.1, 0.1))

# Vectorised version of seq()
seq_(1, 10, by = c(1, 0.5))
# Same as below
c(seq(1, 10, 1), seq(1, 10, 0.5))
```

```

# Programmers may use seq_size() to determine final sequence lengths

sizes <- seq_size(1, 10, by = c(1, 0.5))
print(paste(c("sequence sizes: (", sizes, ") total size:", sum(sizes)),
           collapse = " "))

# We can group sequences using seq_id

from <- Sys.Date()
to <- from + 10
by <- c(1, 2, 3)
x <- seq_(from, to, by, add_id = TRUE)
class(x) <- "Date"
x

# Utilities for rolling calculations

window_sequence(c(3, 5), 3)
window_sequence(c(3, 5), 3, partial = FALSE)
window_sequence(c(3, 5), 3, partial = TRUE, ascending = FALSE)
# One can for example use these in data.table::frollsum

```

setdiff_

Extra utilities

Description

Extra utilities

Usage

```
setdiff_(x, y, dups = TRUE)
```

```
intersect_(x, y, dups = TRUE)
```

```
cut_numeric(
  x,
  breaks,
  labels = NULL,
  include.lowest = FALSE,
  right = TRUE,
  dig.lab = 3L,
  ordered_result = FALSE,
  ...
)
```

```
x %in_% table
```

```

x %!in% table

enframe_(x, name = "name", value = "value")

deframe_(x)

na_rm(x)

sample_(x, size = cpp_vec_length(x), replace = FALSE, prob = NULL)

```

Arguments

x	A vector or data frame.
y	A vector or data frame.
dups	Should duplicates be kept? Default is TRUE.
breaks	See ?cut.
labels	See ?cut.
include.lowest	See ?cut.
right	See ?cut.
dig.lab	See ?cut.
ordered_result	See ?cut.
...	Further arguments passed onto cut or set.seed.
table	See ?collapse::fmatch
name	The column name to assign the names of a vector.
value	The column name to assign the values of a vector.
size	See ?sample.
replace	See ?sample.
prob	See ?sample.

Details

intersect_() and setdiff_() are faster and more efficient alternatives to intersect() and setdiff() respectively.

enframe_() and deframe_() are faster alternatives to tibble::enframe() and tibble::deframe() respectively.

cut_numeric() is a faster and more efficient alternative to cut.default().

Value

enframe()_ converts a vector to a data frame.

deframe()_ converts a 1-2 column data frame to a vector.

intersect_() returns a vector of common values between x and y.

setdiff_() returns a vector of values in x but not y.

cut_numeric() places values of a numeric vector into buckets, defined through the breaks argument and returns a factor unless labels = FALSE, in which case an integer vector of break indices

is returned.

`%in_%` and `%!in_%` both return a logical vector signifying if the values of `x` exist or don't exist in `table` respectively.

`na_rm()` is a convenience function that removes NA values and empty rows in the case of data frames. For more advanced NA handling, see `?is_na`.

`sample_()` is an alternative to `sample()` that natively samples data frame rows through `sset()`. It also does not have a special case when `length(x)` is 1.

`set_abs`*Math operations by reference - Experimental*

Description

These functions transform your variable by reference, with no copies being made. It is advisable to only use these if you know what you are doing.

Usage

```
set_abs(x)
```

```
set_floor(x)
```

```
set_ceiling(x)
```

```
set_trunc(x)
```

```
set_exp(x)
```

```
set_sqrt(x)
```

```
set_change_sign(x)
```

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

```
set_log(x, base = exp(1))
```

```
set_pow(x, y)
```

```
set_add(x, y)
```

```
set_subtract(x, y)
```

```
set_multiply(x, y)
```

```
set_divide(x, y)
```

Arguments

x	A numeric vector.
digits	Number of digits to round to.
base	Logarithm base.
y	A numeric vector.

Details

These functions are particularly useful for situations where you have made a copy and then wish to perform further operations without creating more copies.

NA and NaN values are ignored though in some instances NaN values may be replaced with NA. These functions will **not work** on **any** classed objects, meaning they only work on standard integer and numeric vectors and matrices.

When a copy has to be made:

A copy is only made in certain instances, e.g. when passing an integer vector to set_log(). A warning will always be thrown in this instance alerting the user to assign the output to an object because x has not been updated by reference.

To ensure consistent and expected outputs, always assign the output to the same object,

e.g. x <- set_log(x) (**do this**)

set_log(x) (**don't do this**)

x2 <- set_log(x) (Don't do this either)

No copy is made here unless x is an integer vector.

Value

The exact same object with no copy made, just transformed.

Examples

```
library(cheapr)
library(bench)

x <- rnorm(2e05)
options(cheapr.cores = 2)
mark(
  base = exp(log(abs(x))),
  cheapr = set_exp(set_log(set_abs(x)))
)
options(cheapr.cores = 1)
```

`sset`*Cheaper subset*

Description

Cheaper alternative to `[]` that consistently subsets data frame rows, always returning a data frame. There are explicit methods for enhanced data frames like tibbles, `data.tables` and `sf`.

Usage

```
sset(x, ...)  
  
## S3 method for class 'Date'  
sset(x, i, ...)  
  
## S3 method for class 'POSIXct'  
sset(x, i, ...)  
  
## S3 method for class 'factor'  
sset(x, i, ...)  
  
## S3 method for class 'data.frame'  
sset(x, i, j, ...)  
  
## S3 method for class 'tbl_df'  
sset(x, i, j, ...)  
  
## S3 method for class 'POSIXlt'  
sset(x, i, j, ...)  
  
## S3 method for class 'data.table'  
sset(x, i, j, ...)  
  
## S3 method for class 'sf'  
sset(x, i, j, ...)
```

Arguments

<code>x</code>	Vector or data frame.
<code>...</code>	Further parameters passed to <code>[]</code> .
<code>i</code>	A logical or vector of indices.
<code>j</code>	Column indices, names or logical vector.

Details

sset is an S3 generic. You can either write methods for sset or [. sset will fall back on using [when no suitable method is found.

To get into more detail, using sset() on a data frame, a new list is always allocated through new_list().

Difference to base R:

When i is a logical vector, it is passed directly to which_().

This means that NA values are ignored and this also means that i is not recycled, so it is good practice to make sure the logical vector matches the length of x. To return NA values, use sset(x, NA_integer_).

ALTREP range subsetting:

When i is an ALTREP compact sequence which can be commonly created using e.g. 1:10 or using seq_len, seq_along and seq.int, sset internally uses a range-based subsetting method which is faster and doesn't allocate i into memory.

Value

A new vector, data frame, list, matrix or other R object.

Examples

```
library(cheapr)
library(bench)

# Selecting columns
sset(airquality, j = "Temp")
sset(airquality, j = 1:2)

# Selecting rows
sset(iris, 1:5)

# Rows and columns
sset(iris, 1:5, 1:5)
sset(iris, iris$Sepal.Length > 7, c("Species", "Sepal.Length"))

# Comparison against base
x <- rnorm(10^4)

mark(x[1:10^3], sset(x, 1:10^3))
mark(x[x > 0], sset(x, x > 0))

df <- data.frame(x = x)

mark(df[df$x > 0, , drop = FALSE],
      sset(df, df$x > 0),
      check = FALSE) # Row names are different

## EXTRA: An easy way to incorporate cheaper into dplyr's filter()
```

```
# cheapr_filter <- function(.data, ..., .by = NULL, .preserve = FALSE){
#   filter_df <- .data |>
#     dplyr::mutate(..., .by = {{ .by }}, .keep = "none")
#   groups <- dplyr::group_vars(filter_df)
#   filter_df <- cheapr::sset(filter_df, j = setdiff(names(filter_df), groups))
#   n_filters <- ncol(filter_df)
#   if (n_filters < 1){
#     .data
#   } else {
#     dplyr::dplyr_row_slice(.data, cheapr::which_(Reduce(`&`, filter_df)),
#                           preserve = .preserve)
#   }
# }
```

which_ *Memory-efficient alternative to which()*

Description

Exactly the same as `which()` but more memory efficient.

Usage

```
which_(x, invert = FALSE)
```

Arguments

<code>x</code>	A logical vector.
<code>invert</code>	If TRUE, indices of values that are not TRUE are returned (including NA). If FALSE (the default), only TRUE indices are returned.

Details

This implementation is similar in speed to `which()` but usually more memory efficient.

Value

An unnamed integer vector.

Examples

```
library(cheapr)
library(bench)
x <- sample(c(TRUE, FALSE), 1e05, TRUE)
x[sample.int(1e05, round(1e05/3))] <- NA

mark(which_(TRUE), which(TRUE))
mark(which_(FALSE), which(FALSE))
mark(which_(logical()), which(logical()))
```



```
mark(which_(x), which(x), iterations = 20)
mark(base = which(is.na(match(x, TRUE))),
      collapse = collapse::whichv(x, TRUE, invert = TRUE),
      cheapr = which_(x, invert = TRUE),
      iterations = 20)
```

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