

Package ‘subsets’

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Type Package

Title A Holistic Grammar of Subsets

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Description Subsetting methods for various data-types.

These methods have the following properties.

- 1) Programmatically friendly.
- 2) Beginner friendly.
- 3) Class consistent.
- 4) Careful handling of names and other attributes.
- 5) Performance aware.
- 6) Support atomic objects (vectors, matrices, arrays).
- 7) Support factors.
- 8) Support lists.
- 9) Support data.frame-like objects (data.frame, data.table, tibble, tidytable).
- 10) Support ggplot2 aesthetics.

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Description

subsets: an Easy Grammar of Subsets

Motivation

Among programming languages, 'R' has perhaps one of the most flexible and comprehensive sub-setting functionality. But with flexibility often comes confusion and (apparent) inconsistencies. And 'R' is no exception.

This becomes quite apparent when one reads (online) documents such as "The R Inferno" by Patrick Burns, and "Frustration: One Year With R" by Reece Goding. These documents point out many inconsistencies, and sub-setting related inconsistencies make up a good portion of these documents.

To my surprise, there is no comprehensive R-package

(as far as I could see at least) that actually attempts to "fix" the subset-related issues laid out in these and other such documents.

Famous subset-related R packages such as 'dplyr' and 'data.table' focus almost exclusive on data.frame-like objects, and occasionally even add more frustration in some aspects, like being not very programmatically friendly.

Thus, this R package was born.

Although this package was somewhat made for people who are new to 'R' (especially when coming from another programming language), and found themselves confused, I trust this package will be useful even for those who are quite experienced in 'R'.

Goal & Properties

The Goal of the 'subsets' package is not to replace the square-brackets operators per-sé, (see [Extract](#)), but to provide **alternative** sub-setting methods and functions, to be used in situations where the square-brackets operators are inconvenient.

These are (hopefully) easier sub-setting methods and functions with the following properties:

- **Programmatically friendly:**
 - Non-standard evaluation is quite controversial (and for good reasons), and therefore completely absent in this R package.
 - Name-based arguments instead of position-based arguments.
 - Missing arguments can be filled with NULL, instead of using dark magic like `base::quote(expr =)`.
 - Functions are pipe-friendly.
- **Beginner friendly:**
 - No (silent) vector recycling.
 - Extracting and removing subsets uses the same syntax.
 - All functions return a copy of the object, unless stated otherwise.
- **Class consistent:**
 - sub-setting of multi-dimensional objects by specifying dimensions (i.e. rows, columns, ...) use `drop = FALSE`. So matrix in, matrix out.
 - The functions deliver the same results for data.frames, data.tables, tibbles, and tidytables. No longer does one have to re-learn the different brackets-based sub-setting rules for different types of data.frame-like objects. Powered by the subclass agnostic 'C'-code from 'collapse' and 'data.table'.
- **Explicit copy semantics:**
 - Sub-set operations that change its memory allocations, always return a modified copy of the object.
 - For sub-set operations that just change values in-place (similar to the `[<-` and `[[<-` methods) the user can choose a method that modifies the object by **reference**, or choose a method that returns a **deep copy**.
- **Careful handling of names and other attributes:**
 - Sub-setting an object by index names returns ALL indices with that name, not just the first.

- Data.frame-like objects (see supported classes below) are forced to have unique column names.
- Attributes of data.frame-like objects (see supported classes below) are always preserved when sub-setting.
- For other object types, the user can specify whether to preserve Attributes, or use R's `[]` attribute behaviour (i.e. drop most attributes). This is to ensure compatibility with R-packages that create their own attribute behaviour for sub-setting.
- **Support a wide variety of S3 classes:**
 - Support atomic objects (vectors, matrices, arrays).
 - Support factors.
 - Support lists.
 - Support the following data.frame-like objects: `data.frame`, `data.table`, `tibble`, and `tidytable` class, and classes that are straight-forward inheritors from these classes (such as `sf-data.frames` or `sf-data.tables`).
 - Support for the column selection sub-setting used in `ggplot2`'s `aes` function.
 - Support for sub-setting characters in a single string.
 - Since the main functions are S3 methods, other packages may add functionality for additional S3 classes.
- **Concise function and argument names.**
- **Performance aware:**

Despite the many checks performed, the functions are kept reasonably speedy, through the use of the 'Rcpp', 'collapse', and 'data.table' R-packages. Most of the heavy lifting in this package is done by the 'collapse' package.

Methods and Functions

The main focus is on the following generic S3 methods:

- `sb_x`: S3 method to extract, exchange, or duplicate subsets.
- `sb_rm`: S3 method to un-select ("remove") subsets.
- `sb_set`: S3 method to modify (transform or replace values) subsets of an object by **reference**. Since it's by reference, it does not allow coercion.
- `sb_mod`: S3 method to return a **copy** of an object with modified (transformed or replaced values) subsets. Has auto-coercion to a certain extent.
- `sb_coe`: S3 method to coerce and transform a whole object, or a recursive subset of an object.
- `sb_before`, `sb_after`: S3 methods to insert new values before or after an index along a dimension of an object.
- `sb_rec`: a function to access recursive subsets. Can be combined with the above S3 methods, for recursive sub-setting operations.

Additional specialized sub-setting functions are provided:

- `aes_pro` and `with_pro`: programmatically friendly and stable version of the `with` and `ggplot2::aes` functions.
- `sb_str`: extract or replace a subset of characters of a single string (each single character is treated as a single element).

- [sb_a](#): extract multiple attributes from an object.

And finally, a couple of helper functions for creating ranges, sequences, and indices (often needed in sub-setting) are provided:

- [n](#): Nested version of [c](#), and short-hand for [list](#).
- [idx_by](#): Compute grouped indices.
- [seq_rec](#): Recursive sequence generator (for example to generate a Fibonacci sequence).
- [seq_names](#): create a range of indices from a specified starting and ending name.
- [sub2coord](#), [coord2ind](#): Convert subscripts (array indices) to coordinates, coordinates to flat indices, and vice-versa.

Help pages

For an explanation of the classes, and how each class is treated by 'subsets', see [subsets_classes](#).

For an explanation of the common indexing arguments in the generic methods, see [subsets_idx_args](#).

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References

The badges shown in the documentation of this R-package were made using the services of: <https://shields.io/>

See Also

'subsets' relies on the 'Rcpp', 'collapse' and 'data.table' R-packages to ensure an acceptable performance of its functions despite the many checks that these functions perform. I also recommend using these packages for other sub-setting and data wrangling functionalities.

'subsets' uses a modified version of the [abind](#) function from the 'abind' R-package; the 'abind' package is recommended for binding and sub-filling arrays of arbitrary dimensions.

Besides these package, the following R packages work very nicely together with 'subsets':

- 'stringi':
The primary R package for fast and concise string manipulation - an essential part of any programming language.
- 'tinycodet':
Helps the user with their coding etiquette. Focuses on 4 aspects: (1) safe functionalities; (2) an import system that combines benefits of using a package without attaching, and attaching a package; (3) extending the capabilities of the 'stringi' package; (4) functions to reduce repetitive code.

aaa1_subsets_classes *Supported S3 classes, With Important Comments*

Description

The `sb_` generic methods support the following categories of S3 classes:

- atomic vector classes (vectors, matrices, arrays);
- factors;
- lists;
- the data.frame-like classes `data.frames`, `data.tables`, `tibbles`, `tidytables`, and classes that are straight-forward inheritors from these classes (such as `sf-data.frames` or `sf-data.tables`).

These categories of classes are quite different from each other. It is vital to understand their differences, in order to use the 'subsets' package properly.

Thus this help page will explain their important properties and important differences.

Atomic Vector Classes

[require unique names: NO](#)

The atomic vector is the most basic class type.

Matrices and Arrays are just atomic vectors with dimension attributes.

All elements in an atomic vector class must have the same atomic type ("logical", "integer", "numeric", "complex", "character" and "raw").

Therefore, the [sb_coe](#) method will coerce the entirety of an atomic vector, NOT just a subset of it.

Factor Class

[require unique names: NO](#)

Factors have the property that they can only store values that are defined in their "levels" attribute; other values are not allowed, and thus result in NAs.

Thus And [sb_mod](#) does NOT coerce replacement values for factors! This is quite different from the atomic vector classes, which can store an infinite variety of values (provided they are of the same atomic type).

Due to these properties, there is NO `sb_set()` method for factors.

List Class

[require unique names: NO](#)

Lists are recursive objects (i.e. they can be nested), and they do not actually store values but rather store reference to other objects.

Therefore [sb_rec](#) method can be used to access recursive subsets of a list, no matter how deep/low in hierarchy it is in the list.

Data.frame-like classes

require unique names: YES

The data.frame-like objects quite different from the previously named classes.

And the different data.frame-like classes also differ from each other quite a bit - especially in terms of sub-setting.

The 'subsets' R-package attempts to keep the data.frame methods as class agnostic as possible, through the class agnostic functionality of the 'collapse' and 'data.table' R-packages.

These 3 things cause some **important** oddities in how data.frame-like classes are treated differently from the other classes:

- Whole-columns will be auto-coerced when replaced/transformed by `sb_mod()`, but partial columns will NOT be auto-coerced.
- The `sb_x` and `sb_rm` methods always automatically conserve all attributes (though names are adjusted accordingly, of course), they are never stripped, unlike the other classes.
- Giving a data.frame-like object with non-unique column names to the `sb_`-methods returns an error. Also, duplicating columns with `sb_x` will automatically adjust the column names to make them unique.

aaa2_subsets_idx_args

Index Arguments in the Generic Sub-setting Methods

Description

There are 6 types of arguments that can be used in the generic methods of 'subsets' to specify the indices to perform operations on:

- `i`: to specify flat (i.e. dimensionless) indices.
- `row`, `col`: to specify rows and/or columns in tabular objects.
- `idx`, `dims`: to specify indices of arbitrary dimensions in arrays.
- `rcl`: to specify rows (first dimension), columns (second dimension), and layers (third dimension), in arrays that have exactly 3 dimensions.
- `lvl`: specify levels, for factors only.
- `filter`, `vars`: to specify rows and/or columns specifically in data.frame-like objects.

Argument i

class: atomic

class: factor

class: list

Any of the following can be specified for argument `i`:

- NULL, only for multi-dimensional objects or factors, when specifying the other arguments (i.e. dimensional indices or factor levels.)
- a vector of length 0, in which case no indices are selected for the operation (i.e. empty selection).
- a **strictly positive integer** vector with indices.
- a **logical vector** (without NAs!), of the same length as x, giving the indices to select for the operation.
- a **character** vector of index names. If an object has multiple indices with the given name, ALL the corresponding indices will be selected for the operation.
- a **function** that returns a logical vector, giving the element indices to select for the operation.

Using the i arguments corresponds to doing something like the following:

```
sb_x(x, i = i) ==> x[i]
```

For a brief explanation of the relationship between flat indices (i), and the dimension indices (row, col, etc.), see the Details section in [sub2ind](#).

Arguments row, col

class: [matrix](#)
class: [data.frame-like](#)

Any of the following can be specified for the arguments row / col:

- NULL (default), corresponds to a missing argument, which results in ALL of the indices in this dimension being selected for the operation.
- a vector of length 0, in which case no indices are selected for the operation (i.e. empty selection).
- a **strictly positive integer** vector with dimension indices to select for the operation.
- a **logical** vector (without NAs!) of the same length as the corresponding dimension size, giving the indices of this dimension to select for the operation.
- a **character** vector of index names. If an object has multiple indices with the given name, ALL the corresponding indices will be selected for the operation.

NOTE: The arguments row and col will be ignored if i is specified.

Using the row, col arguments corresponds to doing something like the following:

```
sb_x(x, row = row, col = col) ==> x[row, col, drop = FALSE]
```

Arguments idx, dims

class: [array](#)

idx must be a list of indices.

dims must be an integer vector of the same length as idx, giving the dimensions to which the indices given in idx correspond to.

The elements of `idx` follow the same rules as the rules for `row` and `col`, EXCEPT one should not fill in `NULL`.

NOTE: The arguments `idx` and `dims` will be ignored if `i` is specified.

To keep the syntax short, the user can use the `n` function instead of `list()` to specify `idx`.

Using the `idx`, `dims` arguments, corresponds to doing something like the following, here using an example of a 4-dimensional array:

```
sb_x(x, n(1:10, 1:5), c(1, 3)) ==> x[1:10, , 1:5, , drop = FALSE]
```

Arguments `rc1`

class: array

The `rc1` argument is only applicable for arrays with exactly 3 dimensions.

If the user knows a-priori that an array has 3 dimensions, using `rc1` is more efficient than using the `idx`, `dims` arguments.

The `rc1` argument must be a list of exactly 3 elements, with the first element giving the indices of the first dimension (rows), the second element giving the indices of the second dimension (columns), and the third element giving the indices of the third and last dimension (layers); thus `rc1` stands for "rows, columns, layers" (i.e. the 3 dimensions of a 3-dimensional array).

For each of the aforementioned 3 elements of the list `rc1`, any of the following can be specified:

- `NULL`, corresponds to a missing argument, which results in ALL of the indices in this dimension being selected for the operation.
- a vector of length 0, in which case no indices are selected for the operation (i.e. empty selection).
- a **strictly positive integer** vector with dimension indices to select for the operation.
- a **logical** vector (without NAs!) of the same length as the corresponding dimension size, giving the indices of this dimension to select for the operation.
- a **character** vector of index names. If an object has multiple indices with the given name, ALL the corresponding indices will be selected for the operation.

By default `rc1` is not a list but simply `NULL`, to be used when specifying the other arguments (either `idx`, `dims` or `i`).

To keep the syntax short, the user can use the `n` function instead of `list()` to specify `rc1`.

Using the `rc1` argument corresponds to doing something like the following:

```
sb_x(x, rc1 = n(NULL, 1:10, 1:5)) ==> x[, 1:10, 1:5, drop = FALSE]
```

Argument `lvl`

class: factor

For this argument, the names of the levels of `x` can be given, selecting the corresponding indices for the operation.

Arguments filter, vars

class: data.frame-like

`filter` must be a one-sided formula with a single logical expression using the column names of the data.frame, giving the condition which observation/row indices should be selected for the operation. For example, to perform an operation on the rows for which column `height > 2` and for which column `sex != "female"`, specify the following formula:

```
~ (height > 2) & (sex != "female")
```

`vars` must be a function that returns a logical vector, giving the column indices to select for the operation.

For example, to select all numeric columns, specify `vars = is.numeric`.

Duplicates (for Names, Integers, and Levels)

Generally speaking, duplicate names, integers, or levels are NOT allowed in index selection. The exception is the `sb_x` method, as that method can be used for duplicating indices.

Disallowed Combinations of Index Arguments

One cannot specify `i` and the other indexing arguments simultaneously; it's either `i`, or the other arguments.

The arguments are evaluated in the following order:

1. Argument `i`
2. Argument `lvl` (for factors) or argument `rcl` (for 3-dimensional arrays)
3. The rest of the indexing arguments.

One cannot specify `row` and `filter` simultaneously. It's either one or the other. Similarly, one cannot specify `col` and `vars` simultaneously.

In the above cases it holds that if one set is specified, the other is set is ignored.

First, Last, and Shuffle

The indices are counted forward. I.e. 1 is the first element, not the last.

One can use the `tail` function to get the last N indices.

One can use the `head` function to get the first N indices.

To shuffle elements of indices, use the `sample` function.

aaa3_subsets_NSE

*Controversy Surrounding Non-Standard Evaluation***Description**

Non-Standard Evaluation (sometimes abbreviated as "NSE"), is quite controversial. Consider the following example:

```
aplot <- "ggplot2"
library(aplot)
```

What package will be attached? It will not be 'ggplot2', nor will an error occur. Instead, the package 'aplot' will be attached.

This is due to evaluating the expression 'aplot' as a quoted expression, instead of evaluating the contents (i.e. string or formula) of the variable. In other words: Non-Standard Evaluation.

A standard evaluated expression works better.

Standard evaluation in 'R' is not limited to characters. Formulas can also be used. For example, if the `library()` function would support a formula input, the following would correctly load 'ggplot2':

```
aplot <- ~ ggplot2
library(aplot)
```

aes_pro

*Programmatically Friendly, Standard Evaluated Versions of with() and ggplot2::aes()***Description**

Programmatically friendly versions of the [with](#) and `ggplot2::aes` functions. These alternative functions are more programmatically friendly because it uses proper standard evaluation, instead of non-standard evaluation, tidy evaluation, or similar programmatically unfriendly evaluations.

Usage

```
aes_pro(...)

with_pro(data, form)
```

Arguments

... arguments to be passed to [aes](#), but given as one-sided formulas, rather than non-standard evaluated dark magic.

data a list, environment, or data.frame.

form a one-sided formula giving the expression to evaluate. Global variables are not allowed, only variables that are actually present in the data.

Details

Non-Standard Evaluation is quite controversial (see [subsets_NSE](#)).

Often standard-evaluated alternatives provided.

But in the case of the `aes()` function in 'ggplot2', the standard-evaluated alternative changes frequently, and the ones provided so far are rather clumsy.

The `aes_pro()` function is the standard evaluated alternative. Due to the way `aes_pro()` is programmed, it should work no matter how many times the standard evaluation techniques change in 'ggplot2'.

It should also work in older and newer versions of 'ggplot2'.

To support functions in combinations with references of the variables, the input used here are formula inputs, rather than character inputs.

See Examples section below.

Value

See [aes](#).

Examples

```
requireNamespace("ggplot2")

data("mpg", package = "ggplot2")
x <- ~ cty
y <- ~ sqrt(hwy)
color <- ~ drv

ggplot2::ggplot(mpg, aes_pro(x, y, color = color)) +
  ggplot2::geom_point()

myform <- ~ sqrt(hwy)
mpg$hwy_sqrt <- with_pro(mpg, myform)
summary(mpg)
```

dt

Functional forms of data.table Operations (also work on tidytables)

Description

Functional forms of special data.table operations - ALL programmatically friendly (no Non-Standard Evaluation).

`dt_aggregate()` aggregates a data.table or tidytable, and returns the aggregated copy.

`dt_setcoe()` coercively transforms columns of a data.table or tidytable BY REFERENCE.

Usage

```
dt_aggregate(x, SDcols = NULL, f, by, order_by = FALSE)
```

```
dt_setcoe(x, col = NULL, vars = NULL, f)
```

Arguments

<code>x</code>	a <code>data.table</code> or <code>tidytable</code> .
<code>SDcols</code>	atomic vector, giving the columns to which the aggregation function <code>f()</code> is to be applied on.
<code>f</code>	the aggregation function
<code>by</code>	atomic vector, giving the grouping columns.
<code>order_by</code>	logical (TRUE or FALSE), indicating if the aggregated result should be ordered by the columns specified in <code>by</code> .
<code>col, vars</code>	columns to select for coercion; see subsets_indx_args . Duplicates are not allowed.

Value

The sub-setted object.

Examples

```
requireNamespace("sf") && requireNamespace("ggplot2")

# dt_aggregate on sf-data.table ====

x <- sf::st_read(system.file("shape/nc.shp", package = "sf"))
x <- data.table::as.data.table(x)

x$region <- ifelse(x$CNTY_ID <= 2000, 'high', 'low')
plotdat <- dt_aggregate(
  x, SDcols = "geometry", f = sf::st_union, by = "region"
)

ggplot2::ggplot(plotdat, aes_pro(geometry = ~ geometry, fill = ~ region)) +
  ggplot2::geom_sf()

#####

# dt_setcoe ====

obj <- data.table::data.table(a = 1:10, b = letters[1:10], c = 11:20, d = factor(letters[1:10]))
str(obj) # notice that columns "a" and "c" are INTEGER (`int`)
sb_set(
  obj, filter = ~ (a >= 2) & (c <= 17), vars = is.numeric,
  tf = sqrt # WARNING: sqrt() results in `dbl`, but columns are `int`, so decimals lost
)
str(obj)
obj <- data.table::data.table(a = 1:10, b = letters[1:10], c = 11:20, d = factor(letters[1:10]))
dt_setcoe(obj, vars = is.numeric, f = as.numeric) # integers are now numeric
str(obj)
```

```
sb_set(obj,
  filter = ~ (a >= 2) & (c <= 17), vars = is.numeric,
  tf = sqrt # SAFE: coercion performed; so no warnings
)
str(obj)
```

idx_by

Compute Grouped Indices

Description

Given:

- a sub-set function `f`;
- the complete range of indices `r` of some object `x`;
- and a grouping factor `grp`;

the `idx_by()` function takes indices `f(r)` **per group** `grp`.

The result of `idx_by()` can be supplied to the indexing arguments (see [subsets_indx_args](#)) of: `sb_x`, `sb_rm`, `sb_mod`, `sb_set`, or `sb_coe`, to perform **grouped** subset operations.

Usage

```
idx_by(f, r, grp, parallel = FALSE, mc.cores = 1L)
```

Arguments

- | | |
|---|---|
| <code>f</code> | a subset function to be applied per group on <code>r</code> .
The function must accept a character or integer vector as input, and produce a character or integer vector as output.
For example, to subset the last element per group, specify:
<code>f = \(i) tail(i, 1)</code> |
| <code>r</code> | an integer or character vector, giving the complete range of indices of an object.
For example: <code>colnames(x)</code> , <code>1:nrow(x)</code> , etc. |
| <code>grp</code> | a factor giving the groups. Make sure its order corresponds to <code>i</code> and <code>r</code> , otherwise it makes no sense. |
| <code>parallel</code> , <code>mc.cores</code> | see BY . |

Value

A vector of indices of the same type as `r`.

Examples

```
# vectors ====
(a <- 1:20)
(grp <- factor(rep(letters[1:5], each = 4)))

# get the last element of `a` for each group in `grp`:
i <- indx_by(\(i)tail(i, 1), 1:length(a), grp)
sb_x(cbind(a, grp), row = i)

# data.frame ====
x <- data.frame(
  a = sample(1:20),
  b = letters[1:20],
  group = factor(rep(letters[1:5], each = 4))
)
print(x)
# get the first row for each group in data.frame `x`:
row <- indx_by(\(i)head(i, 1), 1:nrow(x), x$group)
sb_x(x, row)
# get the first row for each group for which a > 10:
x2 <- sb_x(x, filter = ~ a > 10)
row <- na.omit(indx_by(\(i)head(i, 1), 1:nrow(x2), x2$group))
sb_x(x2, row)
```

indx_x

Exported Utilities

Description

Exported utilities

Usage

```
indx_x(i, x, xnames, xsize)
```

```
indx_rm(i, x, xnames, xsize)
```

Arguments

i	See subsets_indx_args .
x	a vector, vector-like object, factor, data.frame, data.frame-like object, or a list.
xnames	names or dimension names
xsize	length or dimension size

Value

The subsetting object.

Examples

```
x <- 1:10
names(x) <- letters[1:10]
indx_x(1:5, x, names(x), length(x))
indx_rm(1:5, x, names(x), length(x))
```

n	<i>Nest</i>
---	-------------

Description

The `c()` function concatenates vectors or lists into a vector (if possible) or else a list.

In analogy to that function, the `n()` function **ne**sts objects into a list (not into an atomic vector, as atomic vectors cannot be nested).

It is a short-hand version of the [list](#) function.

This is handy because lists are often needed in 'subsets', especially for arrays.

Usage

```
n()
```

Value

The list.

Examples

```
obj <- array(1:64, c(4,4,3))
print(obj)
sb_x(obj, n(1:3, 1:2), c(1,3))
# above is equivalent to obj[1:3, , 1:2, drop = FALSE]
```

safer_partialmatch	<i>Set safer dollar, arguments, and attribute matching</i>
--------------------	--

Description

This function simply calls the following:

```
options(
  warnPartialMatchDollar = TRUE,
  warnPartialMatchArgs = TRUE,
  warnPartialMatchAttr = TRUE
)
```

Thus it forces 'R' to give a warning when partial matching occurs when using the dollar (\$) operator, or when other forms of partial matching occurs.

Usage

```
safer_partialmatch()
```

Value

Sets the options. Returns nothing.

Examples

```
interactive()

safer_partialmatch()
data(iris)
head(iris)
iris$Sepal.Length <- iris$Sepal.Length^2
head(iris)
```

sb_before

Methods to Insert New Values Before or After an Index Along a Dimension

Description

The `sb_before()` method inserts new values before some position along a dimension.
The `sb_after()` method inserts new values after some position along a dimension.

These functions use a modified version of `abind::abind` (see reference below).

Usage

```
sb_before(x, ...)

sb_after(x, ...)

## Default S3 method:
sb_before(x, new, pos = 1, .attr = NULL, ...)

## Default S3 method:
sb_after(x, new, pos = length(x), .attr = NULL, ...)

## S3 method for class 'array'
sb_before(x, new, margin, pos = 1, .attr = NULL, ...)

## S3 method for class 'array'
sb_after(x, new, margin, pos = dim(x)[margin], .attr = NULL, ...)

## S3 method for class 'factor'
sb_before(x, new, pos = 1, .attr = NULL, ...)

## S3 method for class 'factor'
```

```

sb_after(x, new, pos = length(x), .attr = NULL, ...)

## S3 method for class 'list'
sb_before(x, new, pos = 1, .attr = NULL, ...)

## S3 method for class 'list'
sb_after(x, new, pos = length(x), .attr = NULL, ...)

## S3 method for class 'data.frame'
sb_before(x, new, margin, pos = 1, .attr = NULL, ...)

## S3 method for class 'data.frame'
sb_after(x, new, margin, pos = collapse::fdim(x)[margin], .attr = NULL, ...)

```

Arguments

x	see subsets_classes .
...	further arguments passed to or from other methods.
new	the new value(s). The type of object depends on x: <ul style="list-style-type: none"> • For atomic objects, new can be any atomic object. However, if one wished the added values in new to be named, ensure new is the same type of object as x. For example: use matrix with column names for new when appending/inserting columns to matrix x. • For factors, new must be a factor. • For lists, new must be a (possible named) list. • For data.frame-like objects, new must be a data.frame.
pos	a strictly positive single integer scalar (so no duplicates), giving the position along the dimension (specified in margin), before or after which the new values are added.
.attr	a list, giving additional potentially missing attributes to be added to the returned object. By default, concatenation strips attributes, since the attributes of x and new may not be equal or even compatible. In the attr argument, the attributes of the merged object can be specified. Only attributes that are actually missing AFTER insertion will be added, thus preventing overwriting existing attributes like names. One may, for example, specify .attr = sb_a(x) or .attr = sb_a(new). If NULL (the default), no attributes will be added post-insert. If speed is important, NULL is the best option (but then attributes won't be preserved).
margin	a single scalar, giving the dimension along which to add new values.

Value

Returns a copy of the appended object.

References

Plate T, Heiberger R (2016). *abind: Combine Multidimensional Arrays*. R package version 1.4-5, <https://CRAN.R-project.org/package=abind>.

Examples

```
# atomic objects ====

x <- matrix(1:20 , ncol = 4)
print(x)
new <- -1 * x
sb_before(x, new, 1)
sb_before(x, new, 2)
sb_after(x, new, 1)
sb_after(x, new, 2)

#####

# factors ====

x <- factor(letters)
new <- factor("foo")
sb_before(x, new)
sb_after(x, new)

#####

# lists ====

x <- as.list(1:5)
new <- lapply(x, \(x)x*-1)
print(x)
sb_before(x, new)
sb_after(x, new)

#####

# data.frame-like objects ====

x <- data.frame(a = 1:10, b = letters[1:10], c = 11:20, d = factor(letters[1:10]))
new <- data.frame(e = 101:110)
sb_before(x, new, 2)
sb_after(x, new, 2)
new <- x[, ]
sb_before(x, new, 1)
sb_after(x, new, 1)
```

Description

This is an S3 Method to completely transform (a recursive subsets of) an object with explicit coercion.

Given some coercing function `v()`, the following can be stated about this method.

(1) For atomic objects (vectors, matrices, arrays), this method is equivalent to:

```
x[] <- v(x)
```

(2) For factors, this method is equivalent to:

```
x <- v(x)
```

(3) For lists, with one or multiple elements specified by argument `i`, this method is equivalent to:

```
x[i] <- lapply(x[i], v)
```

(4) And for data.frame-like objects, with one or multiple columns specified by argument `col`, this method is equivalent to:

```
collapse::ftransformv(x, col, v)
```

Note that when `x` is a `data.table`, one can coercively transform columns BY REFERENCE (which is more memory efficient), using the following code (again with columns specified by `col`, and some coercive transformation function `v`):

```
col <- ... # some integer/character vector of column indices/names
x[, (col) := lapply(.SD, v), .SDcols = col]
```

Usage

```
sb_coe(x, ...)

## Default S3 method:
sb_coe(x, v, ...)

## S3 method for class 'factor'
sb_coe(x, v, ...)

## S3 method for class 'list'
sb_coe(x, i, v, ...)

## S3 method for class 'data.frame'
sb_coe(x, col = NULL, vars = NULL, v, ...)
```

Arguments

<code>x</code>	see subsets_classes .
<code>...</code>	further arguments passed to or from other methods.
<code>v</code>	the coercive transformation function to use.
<code>i, col, vars</code>	See subsets_idx_args . An empty index selection returns the original object unchanged.

Details

When replacing values by reference, the (recursive subset of the) object is never coerced, as that requires making a deep copy; instead, the replacement value is coerced.

For example:

Using `sb_set()` to replacing/transform one or more values of an integer type (`int`) object / list element / data.frame column, to become 1.5, will NOT coerce the object / list element / data.frame column to a decimal type (`dbl`); instead, the replacement 1.5 is coerced to the integer 1.

For this reason, the `sb_coe()` method can be used to coercively transform an object BEFORE replacing or transforming values by reference.

See also the Examples section below.

Value

A copy of the coercively transformed object.

Examples

```
obj <- data.frame(a = 1:10, b = letters[1:10], c = 11:20, d = factor(letters[1:10]))
str(obj) # notice that columns "a" and "c" are INTEGER (`int`)
sb_set(
  obj, filter = ~ (a >= 2) & (c <= 17), vars = is.numeric,
  tf = sqrt # WARNING: sqrt() results in `dbl`, but columns are `int`, so decimals lost
)
print(obj)
obj <- data.frame(a = 1:10, b = letters[1:10], c = 11:20, d = factor(letters[1:10]))
obj <- sb_coe(obj, vars = is.numeric, v = as.numeric)
str(obj)
sb_set(obj,
  filter = ~ (a >= 2) & (c <= 17), vars = is.numeric,
  tf = sqrt # SAFE: coercion performed; so no warnings
)
print(obj)
```

sb_mod

Method to Return a Copy of an Object With Modified Subsets

Description

This is an S3 Method to return a copy of an object with modified subsets.

Usage

```
sb_mod(x, ...)
```

```
## Default S3 method:
```

```
sb_mod(x, i, ..., rp, tf)
```

```
## S3 method for class 'matrix'
```

```
sb_mod(x, row = NULL, col = NULL, i = NULL, ..., rp, tf)
```

```

## S3 method for class 'array'
sb_mod(x, idx = NULL, dims = NULL, rcl = NULL, i = NULL, ..., rp, tf)

## S3 method for class 'factor'
sb_mod(x, i = NULL, lvl = NULL, ..., rp)

## S3 method for class 'list'
sb_mod(x, i, ..., rp, tf)

## S3 method for class 'data.frame'
sb_mod(
  x,
  row = NULL,
  col = NULL,
  filter = NULL,
  vars = NULL,
  coe = NULL,
  ...,
  rp,
  tf
)

```

Arguments

x	see subsets_classes .
...	further arguments passed to or from other methods.
i, lvl, row, col, idx, dims, rcl, filter, vars	See subsets_idx_args . An empty index selection returns the original object unchanged.
rp	an object of somewhat the same type as the selected subset of x, and the same same length as the selected subset of x or a length of 1.
tf	the transformation function.
coe	For data.frame-like objects, sb_mod() can only coerce whole columns, not subsets of columns. So it does not automatically coerce column types when row or filter is also specified. Therefore, the user can specify a coercion function, to be applied on the entirety of every column specified in col or vars; columns outside this subset are not affected. This coercion function is, of course, applied before replacement (rp) or transformation (tf()). By default, coe = NULL which means no columns are coercively transformed. See also the Auto-Coercion Rules and Examples sections below, and also see sb_coe .

Details

Transform or Replace

Specifying argument tf will transform the subset.

Specifying `rp` will replace the subset.

One cannot specify both `tf` and `rp`. It's either one set or the other.

Note that the `tf` argument is not available for factors: this is intentional.

Value

A copy of the object with replaced/transformed values.

Auto-Coercion Rules

Atomic objects

auto-coercion: YES

Atomic objects are automatically coerced to fit the replaced values.

For example, replacing one or multiple values in an integer vector (type `int`) with a decimal number (type `dbl`) will coerce the entire vector to type `dbl`.

Factors

auto-coercion: NO

Factors only accept values that are part of their levels, and thus do NOT support coercion.

Replacing a value with a new value not part of its levels, will result in the replacement value being `NA`.

Data.frame-like objects when replacing/transforming whole columns

auto-coercion: depends

When replacing whole columns, so `row = NULL` and `filter = NULL`, coercion takes place according to the contents of the column.

I.e. if the column is atomic, it follows the atomic rules, if it is a factor, it follows the rules of the factor, etc.

Note that coercion of columns needs `row = NULL` and `filter = NULL`; NO auto-coercion will take place when specifying something like `row = 1:nrow(x)` (see next section).

Data.frame-like objects when partially replacing/transforming columns

auto-coercion: NO

If rows are specified, and thus not whole columns but parts of columns are replaced or transformed, NO auto-coercion takes place.

I.e.: replacing/transforming a value in an integer (`int`) column to become `1.5`, will NOT coerce the column to the decimal type (`dbl`); instead, the replacement value `1.5` is coerced to integer `1`.

The `coe` argument allows the user to enforce coercion, even if subsets of columns are replaced/transformed instead of whole columns.

Specifically, the `coe` arguments allows the user to specify a coercive function to be applied on the entirety of every column specified in `col` or `vars`; columns outside this subset are not affected.

This coercion function is, of course, applied before replacement (`rp`) or transformation (`tf()`).

Lists

auto-coercion: depends

Lists themselves allow complete change of their elements, since lists are merely pointers.

However, a recursive subset of a list which itself is not a list, follows the coercion rules of whatever class the recursive subset is.

Examples

```
# atomic objects ====

obj <- matrix(1:16, ncol = 4)
colnames(obj) <- c("a", "b", "c", "a")
print(obj)
rp <- -1:-9
sb_mod(obj, 1:3, 1:3, rp = rp)
# above is equivalent to obj[1:3, 1:3] <- -1:-9; obj
sb_mod(obj, i = \(\x)x<=5, rp = -1:-5)
# above is equivalent to obj[obj <= 5] <- -1:-5; obj
sb_mod(obj, col = "a", rp = -1:-8)
# above is equivalent to obj[, which(colnames(obj) %in% "a")] <- -1:-8; obj
sb_mod(obj, 1:3, 1:3, tf = \(\x) -x)
# above is equivalent to obj[1:3, 1:3] <- (-1 * obj[1:3, 1:3]); obj
sb_mod(obj, i = \(\x)x<=5, tf = \(\x) -x)
# above is equivalent to obj[obj <= 5] <- (-1 * obj[obj <= 5]); obj

obj <- matrix(1:16, ncol = 4)
colnames(obj) <- c("a", "b", "c", "a")
print(obj)
sb_mod(obj, 1:3, 1:3, tf = \(\x) -x)
# above is equivalent to obj[1:3, 1:3] <- -1 * obj[1:3, 1:3]
sb_mod(obj, i = \(\x)x<=5, tf = \(\x) -x)
# above is equivalent to obj[obj <= 5] <- -1:-5; obj
sb_mod(obj, col = "a", tf = \(\x) -x)
# above is equivalent to obj[, which(colnames(obj) %in% "a")] <- -1:-8; obj

obj <- array(1:64, c(4,4,3))
print(obj)
sb_mod(obj, list(1:3, 1:2), c(1,3), rp = -1:-24)
# above is equivalent to obj[1:3, , 1:2] <- -1:-24
sb_mod(obj, i = \(\x)x<=5, rp = -1:-5)
# above is equivalent to obj[obj <= 5] <- -1:-5

#####

# lists ====

obj <- list(a = 1:10, b = letters[1:11], c = 11:20)
print(obj)
sb_mod(obj, "a", rp = list(1L))
# above is equivalent to obj[["a"]] <- 1L; obj
sb_mod(obj, is.numeric, rp = list(-1:-10, -11:-20))
# above is equivalent to obj[which(sapply(obj, is.numeric))] <- list(-1:-10, -11:-20); obj

#####

# data.frame-like objects ====

obj <- data.frame(a = 1:10, b = letters[1:10], c = 11:20, d = factor(letters[1:10]))
str(obj) # notice that columns "a" and "c" are INTEGER (`int`)

sb_mod(
  obj, filter = ~ (a >= 2) & (c <= 17), vars = is.numeric,
```



```

    tf = sqrt # WARNING: sqrt() results in `dbl`, but columns are `int`, so decimals lost
  )
  sb_mod(
    obj, filter = ~ (a >= 2) & (c <= 17), vars = is.numeric,
    coe = as.double, tf = sqrt # SAFE: coercion performed
  )

obj <- data.frame(a = 1:10, b = letters[1:10], c = 11:20, d = factor(letters[1:10]))
str(obj) # notice that columns "a" and "c" are INTEGER (`int`)
sb_mod(
  obj, vars = is.numeric,
  tf = sqrt # SAFE: row=NULL & filter = NULL, so regular auto-coercion
)

```

sb_rec

Access Recursive Subsets

Description

The `sb_rec()` method allows the user to access recursive subsets of lists, and can be combined (i.e. piped) with the generic methods provided by 'subsets'.

Usage

```
sb_rec(lst, rec)
```

Arguments

<code>lst</code>	a list, or list-like object.
<code>rec</code>	a vector of length <code>p</code> , such that <code>lst[[rec]]</code> is equivalent to <code>lst[[rec[1]]]</code> ... <code>[[rec[p]]]</code> , providing all but the final indexing results in a list. When on a certain subset level of a nested list, multiple subsets with the same name exist, only the first one will be selected when performing recursive indexing by name, due to the recursive nature of this type of subsetting.

Value

The sub-setted object.

Examples

```

lst <- list(
  A = list(
    A = list(A = "AAA", B = "AAB"),
    A = list(A = "AA2A", B = "AA2B"),
    B = list(A = "ABA", B = "ABB")
  ),
  B = list(
    A = list(A = "BAA", B = "BAB"),

```

```

      B = list(A = "BBA", B = "BBB")
    )
  )
  sb_rec(lst, c(1,2,2)) # this gives "AA2B"
  sb_rec(lst, c("A", "B", "B")) # this gives "ABB"
  sb_rec(lst, c(2,2,1)) # this gives "BBA"
  sb_rec(lst, c("B", "B", "A")) # this gives "BBA"

  # return a modified copy of the second-lowest level,
  # where replace "ABB" is replaced with -1:
  sb_rec(lst, c("A", "B")) |> sb_coe(i = "B", v = as.double) |> sb_mod(i = "B", rp = list(-1))

  # replace "AAA" with -1 BY REFERENCE:
  sb_rec(lst, c("A", "A")) |> sb_set(i = "A", rp = list(-1))
  lst # notice the first element is replaced by -1

```

sb_rm

Method to Un-Select Subsets of an Object

Description

This is an S3 Method to un-select subsets from an object.

Usage

```

sb_rm(x, ...)

## Default S3 method:
sb_rm(x, i, ..., rat = FALSE)

## S3 method for class 'matrix'
sb_rm(x, row = NULL, col = NULL, i = NULL, ..., rat = FALSE)

## S3 method for class 'array'
sb_rm(x, idx = NULL, dims = NULL, rcl = NULL, i = NULL, ..., rat = FALSE)

## S3 method for class 'factor'
sb_rm(x, i = NULL, lvl = NULL, drop = FALSE, ..., rat = FALSE)

## S3 method for class 'list'
sb_rm(x, i, drop = FALSE, ..., rat = FALSE)

## S3 method for class 'data.frame'
sb_rm(x, row = NULL, col = NULL, filter = NULL, vars = NULL, ...)

```

Arguments

x	see subsets_classes .
...	further arguments passed to or from other methods.

i, lvl, row, col, idx, dims, rcl, filter, vars	See subsets_indx_args . An empty index selection results in nothing being removed, and the entire object is returned.
rat	logical, indicating if attributes should be returned with the sub-setted object. See Details section for more info.
drop	logical. <ul style="list-style-type: none"> • For factors: If drop = TRUE, unused levels are dropped, if drop = FALSE they are not dropped. • For lists: if drop = TRUE, selecting a single element will give the simplified result, like using <code>[[]]</code>. If drop = FALSE, a list is always returned regardless of the number of elements.

Details

One the rat argument

Most `[]` - methods strip most (but not all) attributes.

If `rat = FALSE`, this default behaviour is preserved, for compatibility with special classes. This is the fastest option.

If `rat = TRUE`, attributes from `x` missing after sub-setting are re-assigned to `x`. Already existing attributes after sub-setting will not be overwritten.

There is no `rat` argument for data.frame-like object: their attributes will always be preserved.

NOTE: In the following situations, the `rat` argument will be ignored, as the attributes necessarily have to be dropped:

- when `x` is a list, AND `drop = TRUE`, AND a single element is selected.
- when `x` is a matrix or array, and sub-setting is done through the `i` argument.

Value

A copy of the sub-setted object.

Examples

```
# atomic objects ====

obj <- matrix(1:16, ncol = 4)
colnames(obj) <- c("a", "b", "c", "a")
print(obj)
sb_rm(obj, 1:3, 1:3)
# above is equivalent to obj[-1:-3, -1:-3, drop = FALSE]
sb_rm(obj, i = \ (x)x>5)
# above is equivalent to obj[!obj > 5]
sb_rm(obj, col = "a")
# above is equivalent to obj[, which(!colnames(obj) %in% "a")]

obj <- array(1:64, c(4,4,3))
print(obj)
sb_rm(obj, n(1, c(1, 3)), c(1, 3))
sb_rm(obj, rcl = n(1, NULL, c(1, 3)))
# above 2 lines are equivalent to obj[-1, c(-1, -3), drop = FALSE]
sb_rm(obj, i = \ (x)x>5)
# above is equivalent to obj[!obj > 5]
```

```
#####

# lists ====

obj <- list(a = 1:10, b = letters[1:11], c = 11:20)
print(obj)
sb_rm(obj, "a")
# above is equivalent to obj[which(!names(obj) %in% "a")]
sb_rm(obj, 1) # obj[-1]
sb_rm(obj, 1:2)
# above is equivalent to obj[seq_len(length(obj))[-1:-2]]
sb_rm(obj, is.numeric, drop = TRUE)
# above is equivalent to obj[!sapply(obj, is.numeric)] IF this returns a single element
obj <- list(a = 1:10, b = letters[1:11], c = letters)
sb_rm(obj, is.numeric)
# above is equivalent to obj[!sapply(obj, is.numeric)] # this time singular brackets?
# for recursive indexing, see sb_rec()

#####

# factors ====

obj <- factor(rep(letters[1:5], 2))
sb_rm(obj, lvl = "a")
# above is equivalent to obj[which(!obj %in% "a")]

#####

# data.frame-like objects ====

obj <- data.frame(a = 1:10, b = letters[1:10], c = 11:20, d = factor(letters[1:10]))
print(obj)
sb_rm(obj, 1:3, 1:3)
# above is equivalent to obj[-1:-3, -1:-3, drop = FALSE]
sb_rm(obj, filter = ~ (a > 5) & (c < 19), vars = is.numeric)
```

sb_set

Method to Modify Subsets of an Object By Reference

Description

This is an S3 Method to replace or transform a subset of an object BY REFERENCE.

Usage

```
sb_set(x, ...)
```

```
## Default S3 method:
sb_set(x, i, ..., rp, tf)

## S3 method for class 'matrix'
sb_set(x, row = NULL, col = NULL, i = NULL, ..., rp, tf)

## S3 method for class 'array'
sb_set(x, idx = NULL, dims = NULL, rcl = NULL, i = NULL, ..., rp, tf)

## S3 method for class 'list'
sb_set(x, i, ..., rp, tf)

## S3 method for class 'data.frame'
sb_set(x, row = NULL, col = NULL, filter = NULL, vars = NULL, ..., rp, tf)
```

Arguments

x	see subsets_classes .
...	further arguments passed to or from other methods.
i, row, col, idx, dims, rcl, filter, vars	See subsets_idx_args . An empty index selection returns the original object unchanged.
rp	an object of somewhat the same type as the selected subset of x, and the same same length as the selected subset of x or a length of 1.
tf	the transformation function.

Details

Transform or Replace

Specifying argument tf will transform the subset. Specifying rp will replace the subset. One cannot specify both tf and rp. It's either one set or the other.
Note that there is not sb_set() method for factors: this is intentional.

Value

Returns: VOID. This method modifies the object by REFERENCE.
Do NOT use assignment like x <- sb_set(x, ...).
Since this function returns void, you'll just get NULL.

Warning

Due to the way replacement or transformation by reference works, types (see [typeof](#)) CANNOT be coerced to another type. Thus, for example, the following code:

```
x <- 1:16
sb_set(x, i = 1:8, rp = 8.5)
x
```

gives `c(rep(8, 8) 9:16)` instead of `c(rep(8.5, 8), 9:16)`, because `x` is of type integer, so `rp` is interpreted as type integer also.

Examples

```
gen_mat <- function() {
  obj <- matrix(1:16, ncol = 4)
  colnames(obj) <- c("a", "b", "c", "a")
  return(obj)
}

# atomic objects ====

obj <- obj2 <- gen_mat()
obj
sb_set(obj, 1:3, 1:3, rp = -1:-9)
obj2
obj <- obj2 <- gen_mat()
obj
sb_set(obj, i = \(\x)x<=5, rp = -1:-5)
obj2
obj <- obj2 <- gen_mat()
obj
sb_set(obj, col = "a", rp = cbind(-1:-4, -5:-8))
obj2

obj <- obj2 <- gen_mat()
obj
sb_set(obj, 1:3, 1:3, tf = \(\x) -x)
obj2
obj <- obj2 <- gen_mat()
obj
sb_set(obj, i = \(\x)x<=5, tf = \(\x) -x)
obj2
obj <- obj2 <- gen_mat()
obj
sb_set(obj, col = "a", tf = \(\x) -x)
obj2

gen_array <- function() {
  array(1:64, c(4,4,3))
}
obj <- gen_array()
obj
sb_set(obj, list(1:3, 1:2, c(1, 3)), 1:3, rp = -1:-12)
obj
obj <- gen_array()
obj
sb_set(obj, i = \(\x)x<=5, rp = -1:-5)
obj
```

Description

The `sb_a()` function subsets extracts one or more attributes from an object.

The `sb_str()` function subsets characters of single string, or replace a subset of the characters of a single string with the subsets of the characters of another string. In both cases, a single string is treated as a iterable vector, where each single character in a string is a single element. The `sb_str()` function is considerably faster than doing the equivalent operation in base 'R' or even 'stringi'.

Usage

```
sb_str(str, ind, rp.str, rp.ind)
```

```
sb_a(x, a = NULL)
```

Arguments

<code>str</code>	a single string.
<code>ind</code>	an integer vector, giving the positions of the string to subset.
<code>rp.str, rp.ind</code>	similar to <code>str</code> and <code>ind</code> , respectively. If not specified, <code>sb_str()</code> will perform something like <code>str[ind]</code> treating <code>str</code> as an iterable vector. If these ARE specified, <code>sb_str()</code> will perform something like <code>str[ind] <- rp.str[rp.ind]</code> treating <code>str</code> and <code>rp.str</code> as iterable vectors.
<code>x</code>	an object
<code>a</code>	a character vector of attribute names. If <code>NULL</code> (default), ALL attributes are returned.

Value

The sub-setted object.

Examples

```
x <- matrix(1:10, ncol = 2)
colnames(x) <- c("a", "b")
attr(x, "test") <- "test"
sb_a(x, "test")
sb_a(x)
```

```
x <- "hello"
sb_str(x, 5:1) # this gives "olleh"
```

```

sb_str(x, c(1:5, 5)) # this gives "helloo"
sb_str(x, c(2:5)) # this gives "ello"
sb_str(x, seq(1, 5, by = 2)) # this gives "hlo"
sb_str(x, 1:4, "world", 1:4) # this gives "worlo"

```

sb_x

Method to Extract, Exchange, or Duplicate Subsets of an Object

Description

This is an S3 Method to extract, exchange, or duplicate (i.e. replicate indices x times) indices of an object.

Usage

```

sb_x(x, ...)

## Default S3 method:
sb_x(x, i, ..., rat = FALSE)

## S3 method for class 'matrix'
sb_x(x, row = NULL, col = NULL, i = NULL, ..., rat = FALSE)

## S3 method for class 'array'
sb_x(x, idx = NULL, dims = NULL, rcl = NULL, i = NULL, ..., rat = FALSE)

## S3 method for class 'factor'
sb_x(x, i = NULL, lvl = NULL, drop = FALSE, ..., rat = FALSE)

## S3 method for class 'list'
sb_x(x, i, drop = FALSE, ..., rat = FALSE)

## S3 method for class 'data.frame'
sb_x(x, row = NULL, col = NULL, filter = NULL, vars = NULL, ...)

```

Arguments

x	see subsets_classes .
...	further arguments passed to or from other methods.
i, lvl, row, col, idx, dims, rcl, filter, vars	See subsets_indx_args . Duplicates are allowed, resulting in duplicated indices. An empty index selection results in an empty object of length 0.
rat	logical, indicating if attributes should be returned with the sub-setted object. See Details section for more info.
drop	logical. <ul style="list-style-type: none"> For factors: If drop = TRUE, unused levels are dropped, if drop = FALSE they are not dropped.

- For lists: if drop = TRUE, selecting a single element will give the simplified result, like using [[]]. If drop = FALSE, a list is always returned regardless of the number of elements.

Details

One the rat argument

Most [- methods strip most (but not all) attributes.

If rat = FALSE, this default behaviour is preserved, for compatibility with special classes. This is the fastest option.

If rat = TRUE, attributes from x missing after sub-setting are re-assigned to x. Already existing attributes after sub-setting will not be overwritten.

There is no rat argument for data.frame-like object: their attributes will always be preserved.

NOTE: In the following situations, the rat argument will be ignored, as the attributes necessarily have to be dropped:

- when x is a list, AND drop = TRUE, AND a single element is selected.
- when x is a matrix or array, and sub-setting is done through the i argument.

Value

Returns a copy of the sub-setted object.

Examples

```
# atomic objects ====

obj <- matrix(1:16, ncol = 4)
colnames(obj) <- c("a", "b", "c", "a")
print(obj)
sb_x(obj, 1:3, 1:3)
# above is equivalent to obj[1:3, 1:3, drop = FALSE]
sb_x(obj, i = \ (x)x>5)
# above is equivalent to obj[obj > 5]
sb_x(obj, col = c("a", "a"))
# above is equivalent to obj[, lapply(c("a", "a"), \ (i) which(colnames(obj) == i)) |> unlist()]

obj <- array(1:64, c(4,4,3))
print(obj)
sb_x(obj, n(1:3, 1:2), c(1,3))
sb_x(obj, rcl = n(1:3, NULL, 1:2))
# above 2 lines are equivalent to obj[1:3, , 1:2, drop = FALSE]
sb_x(obj, i = \ (x)x>5)
# above is equivalent to obj[obj > 5]

#####

# lists ====

obj <- list(a = 1:10, b = letters[1:11], c = 11:20)
print(obj)
sb_x(obj, 1) # obj[1]
sb_x(obj, 1, drop = TRUE) # obj[[1]]
sb_x(obj, 1:2) # obj[1:2]
sb_x(obj, is.numeric) # obj[sapply(obj, is.numeric)]
```

```
# for recursive indexing, see sb_rec()

#####

# factors ====

obj <- factor(rep(letters[1:5], 2))
sb_x(obj, lvl = c("a", "a"))
# above is equivalent to obj[lapply(c("a", "a"), \(i) which(obj == i)) |> unlist()]

#####

# data.frame-like objects ====

obj <- data.frame(a = 1:10, b = letters[1:10], c = 11:20, d = factor(letters[1:10]))
print(obj)
sb_x(obj, 1:3, 1:3) # obj[1:3, 1:3, drop = FALSE]
sb_x(obj, filter = ~ (a > 5) & (c < 19), vars = is.numeric)
```

seq_names

*Generate Integer Sequence From a Range of Names***Description**

Generate integer sequence from a range of names.

Usage

```
seq_names(names, start, end, inv = FALSE)
```

Arguments

names	a character vector of names. Duplicate names, empty names, or a character vector of length zero are not allowed.
start	the name giving the starting index of the sequence
end	the name giving the ending index of the sequence
inv	logical, if TRUE, the indices of all names EXCEPT the names of the specified sequence will be given.

Value

An integer vector.

Examples

```
x <- data.frame(a = 1:10, b = letters[1:10], c = factor(letters[1:10]), d = -1:-10)
ind <- seq_names(colnames(x), "b", "d")
sb_x(x, col = ind)
```

seq_rec

*Recursive Sequence Generator***Description**

This is a recursive sequence generator. The function is essentially a highly generalized version of a Fibonacci sequence generator. One can change the initial values, the window size, and even the window function used.

This function assumes only the following about the sequence being generated:

- The sequence consists of real numbers (i.e. class integer or class double).
- The window size is the same for all iterations.
- The window function is the same for all iterations.
- The sequence grows until a vector of length n is achieved.

Usage

```
seq_rec(inits = c(0, 1), n = 10L, f = sum)
```

Arguments

inits	<p>a numeric (double or integer) vector giving the initial values. Any numbers are allowed, even negative and/or fractional numbers. Note that numbers given must give valid results when passed to function f(). IMPORTANT: The length of inits determines the window size w. For a regular Fibonacci, inits = 0:1, which of course means a window size of w = 2.</p>
n	<p>a single integer, giving the size of the numeric vector to generate. NOTE: it must hold that n is larger than or equal to the window size w. The window size is equal to w = length(inits).</p>
f	<p>the function to be used on the last w numbers to generate the next number of the sequence at each iteration. This must be a function that takes as input a numeric vector, and returns a single numeric value. For a regular Fibonacci sequence, this would be either: f = sum, or (since window size is 2) $f = x[2] + x[1]$</p>

Details

The default values of the arguments give the first 10 numbers of a regular Fibonacci sequence.
See examples for several number series created with this function.
This function is written in C++ using Rcpp for better performance.

Value

A sequence of numbers.

Examples

```
seq_rec() # by default gives Fibonacci numbers
seq_rec(0:3, 10L, sum) # a weird shifted version of Fibonacci
seq_rec(inits=2:1) # Lucas numbers
c(1, seq_rec(c(1, 2), f=prod)) # Multiplicative Fibonacci
seq_rec(f=\(x)2*x[2]+x[1]) # Pell numbers
seq_rec(inits = c(1, 0), f=\(x)2*x[1]) # see https://oeis.org/A077957
seq_rec(f=\(x)x[2]+2*x[1]) # Jacobsthal numbers
seq_rec(c(1,1,1), f=\(x)x[1] + x[2]) # Padovan sequence
seq_rec(c(3,0,2), f=\(x)x[1] + x[2]) # Perrin numbers
seq_rec(c(0,1,3), f=\(x)3*x[3] - 3*x[2] + x[1]) # Triangular numbers
```

sub2ind

Convert Subscripts to Coordinates, Coordinates to Flat Indices, and Vice-Versa

Description

sub2coord() converts a list of integer subscripts to an integer matrix of coordinates.
 coord2ind() converts an integer matrix of coordinates to an integer vector of flat indices.
 ind2coord() converts an integer vector of flat indices to an integer matrix of coordinates.
 coord2sub() converts an integer matrix of coordinates to a list of integer subscripts. Note that the coord2sub() function performs a very simple (one might even say naive) conversion.

All of these functions are written to be memory-efficient.

The coord2ind() is thus the opposite of [arrayInd](#), and ind2coord is merely a convenient wrapper around [arrayInd](#).

Usage

```
sub2coord(sub, x.dim)

coord2sub(coord)

coord2ind(coord, x.dim, checks = TRUE)

ind2coord(ind, x.dim)
```

Arguments

sub	a list of integer subscripts. The first element of the list corresponds to the first dimension (rows), the second element to the second dimensions (columns), etc. The length of sub must be equal to the length of x.dim. One cannot give an empty subscript; instead fill in something like seq_len(dim(x)[margin]). NOTE: The coord2sub() function does not support duplicate subscripts.
x.dim	an integer vector giving the dimensions of the array in question. I.e. dim(x).

coord	<p>an integer matrix, giving the coordinate indices (subscripts) to convert. Each row is an index, and each column is the dimension. The first columns corresponds to the first dimension, the second column to the second dimensions, etc.</p> <p>The number of columns of coord must be equal to the length of <code>x.dim</code>.</p>
checks	<p>logical, indicating if arguments checks should be performed. Defaults to TRUE. Can be set to FALSE for minor speed improvements, but not recommended.</p>
ind	<p>an integer vector, giving the flat position indices to convert.</p>

Details

The S3 classes in 'R' use the standard Linear Algebraic convention, as in academic fields like Mathematics and Statistics, in the following sense:

- vectors are **column** vectors (i.e. vertically aligned vectors);
- index counting starts at 1;
- rows are the first dimension/subscript, columns are the second dimension/subscript, etc.

Thus, the orientation of flat indices in, for example, a 4 by 4 matrix, is as follows:

	[,1]	[,2]	[,3]	[,4]
[1,]	1	5	9	13
[2,]	2	6	10	14
[3,]	3	7	11	15
[4,]	4	8	12	16

The subscript `[1,2]` refers to the first row and the second column. In a 4 by 4 matrix, subscript `[1,2]` corresponds to flat index 5.

The functions described here thus follow also this convention.

Value

For `sub2coord()` and `ind2coord()`:

Returns an integer matrix of coordinates (with properties as described in argument `coord`).

For `coord2ind()`:

Returns an integer vector of flat indices (with properties as described in argument `ind`).

For `coord2sub()`:

Returns a list of integer subscripts (with properties as described in argument `sub`)

Examples

```
x.dim <- c(1000, 10, 4, 4)
x.len <- prod(x.dim)
x <- array(1:x.len, x.dim)
```

```
sub <- list(c(4,1), c(3,2), c(2,3), c(1,4))
coord <- sub2coord(sub, x.dim)
print(coord)
ind <- coord2ind(coord, x.dim)
print(ind)
all(x[ind] == c(x[c(4,1), c(3,2), c(2,3), c(1,4)])) # TRUE
coord2 <- ind2coord(ind, x.dim)
print(coord)
all(coord == coord2) # TRUE
sub2 <- coord2sub(coord2)
sapply(1:4, \(i) sub2[[i]] == sub[[i]]) |> all() # TRUE
```

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