Description  The tidySummarizedExperiment package provides a set of tools for creating and manipulating tidy data representations of SummarizedExperiment objects. SummarizedExperiment is a widely used data structure in bioinformatics for storing high-throughput genomic data, such as gene expression or DNA sequencing data. The tidySummarizedExperiment package introduces a tidy framework for working with SummarizedExperiment objects. It allows users to convert their data into a tidy format, where each observation is a row and each variable is a column. This tidy representation simplifies data manipulation, integration with other tidyverse packages, and enables seamless integration with the broader ecosystem of tidy tools for data analysis.

License  GPL-3

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as_tibble  

Coerce lists, matrices, and more to data frames

Description

as_tibble() turns an existing object, such as a data frame or matrix, into a so-called tibble, a data frame with class tbl_df. This is in contrast with tibble(), which builds a tibble from individual columns. as_tibble() is to tibble() as base::as.data.frame() is to base::data.frame().

as_tibble() is an S3 generic, with methods for:

• data.frame: Thin wrapper around the list method that implements tibble’s treatment of rownames.
• matrix, poly, ts, table
• Default: Other inputs are first coerced with base::as.data.frame().

as_tibble_row() converts a vector to a tibble with one row. If the input is a list, all elements must have size one.

as_tibble_col() converts a vector to a tibble with one column.

Usage

## S3 method for class 'SummarizedExperiment'
as_tibble(
  x,
  ..., .name_repair = c("check_unique", "unique", "universal", "minimal"),
  rownames = pkgconfig::get_config("tibble::rownames", NULL)
)

Arguments

x  
A data frame, list, matrix, or other object that could reasonably be coerced to a tibble.

...  
Unused, for extensibility.

.name_repair  
Treatment of problematic column names:

• "minimal": No name repair or checks, beyond basic existence,
• "unique": Make sure names are unique and not empty,
• "check_unique": (default value), no name repair, but check they are unique,
• "universal": Make the names unique and syntactic
as_tibble

- a function: apply custom name repair (e.g., `.name_repair = make.names` for names in the style of base R).
- A purrr-style anonymous function, see `rlang::as_function()`

This argument is passed on as repair to `vctrs::vec_as_names()`. See there for more details on these terms and the strategies used to enforce them.

rownames

How to treat existing row names of a data frame or matrix:

- NULL: remove row names. This is the default.
- NA: keep row names.
- A string: the name of a new column. Existing rownames are transferred into this column and the `row.names` attribute is deleted. No name repair is applied to the new column name, even if `x` already contains a column of that name. Use `as_tibble(rownames_to_column(…))` to safeguard against this case.

Read more in `rownames`.

Value
tibble

Row names

The default behavior is to silently remove row names.

New code should explicitly convert row names to a new column using the `rownames` argument.

For existing code that relies on the retention of row names, call `pkgconfig::set_config("tibble::rownames" = NA)` in your script or in your package’s `.onLoad()` function.

Life cycle

Using `as_tibble()` for vectors is superseded as of version 3.0.0, prefer the more expressive `as_tibble_row()` and `as_tibble_col()` variants for new code.

See Also
tibble() constructs a tibble from individual columns. enframe() converts a named vector to a tibble with a column of names and column of values. Name repair is implemented using `vctrs::vec_as_names()`.

Examples

```r
tidySummarizedExperiment::pasilla %>%
  as_tibble()
```

```r
tidySummarizedExperiment::pasilla %>%
  as_tibble(.subset=-c(condition, type))
```
bind_rows

Efficiently bind multiple data frames by row and column

Description

This is an efficient implementation of the common pattern of `do.call(rbind, dfs)` or `do.call(cbind, dfs)` for binding many data frames into one.

This is an efficient implementation of the common pattern of `do.call(rbind, dfs)` or `do.call(cbind, dfs)` for binding many data frames into one.

Usage

```r
## S3 method for class 'SummarizedExperiment'
bind_rows(..., .id = NULL, add.cell.ids = NULL)

## S3 method for class 'SummarizedExperiment'
bind_cols(..., .id = NULL)

## S3 method for class 'RangedSummarizedExperiment'
bind_cols(..., .id = NULL)
```

Arguments

... Data frames to combine.

Each argument can either be a data frame, a list that could be a data frame, or a list of data frames.

When row-binding, columns are matched by name, and any missing columns will be filled with NA.

When column-binding, rows are matched by position, so all data frames must have the same number of rows. To match by value, not position, see mutate-joins.

.id Data frame identifier.

When `.id` is supplied, a new column of identifiers is created to link each row to its original data frame. The labels are taken from the named arguments to `bind_rows()`. When a list of data frames is supplied, the labels are taken from the names of the list. If no names are found a numeric sequence is used instead.

add.cell.ids Appends the corresponding values to

Details

The output of `bind_rows()` will contain a column if that column appears in any of the inputs.

The output of `bind_rows()` will contain a column if that column appears in any of the inputs.
Value

`bind_rows()` and `bind_cols()` return the same type as the first input, either a data frame, `tbl_df`, or `grouped_df`.

`bind_rows()` and `bind_cols()` return the same type as the first input, either a data frame, `tbl_df`, or `grouped_df`.

Examples

data(se)
ttservice::bind_rows(se, se)

se_bind <- se |> select(dex, albut)
se |> ttservice::bind_cols(se_bind)

count

Count the observations in each group

Description

count() lets you quickly count the unique values of one or more variables: `df %>% count(a, b)` is roughly equivalent to `df %>% group_by(a, b) %>% summarise(n = n())`. `count()` is paired with `tally()`, a lower-level helper that is equivalent to `df %>% summarise(n = n())`. Supply `wt` to perform weighted counts, switching the summary from `n = n()` to `n = sum(wt)`.

`add_count()` and `add_tally()` are equivalents to `count()` and `tally()` but use `mutate()` instead of `summarise()` so that they add a new column with group-wise counts.

Usage

```r
## S3 method for class 'SummarizedExperiment'
count(
x, ...
wt = NULL,
sort = FALSE,
name = NULL,
.drop = group_by_drop_default(x)
)
```

Arguments

- **x** A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from dbplyr or dplyr).
- **...** <data-masking> Variables to group by.
- **wt** <data-masking> Frequency weights. Can be NULL or a variable:
  - If NULL (the default), counts the number of rows in each group.
distinct

- If a variable, computes $\sum(wt)$ for each group.

`sort` If TRUE, will show the largest groups at the top.

`name` The name of the new column in the output.

If omitted, it will default to $n$. If there’s already a column called $n$, it will use $nn$. If there’s a column called $n$ and $nn$, it’ll use $nnn$, and so on, adding ns until it gets a new name.

`.drop` Handling of factor levels that don’t appear in the data, passed on to `group_by()`. For `count()`: if FALSE will include counts for empty groups (i.e. for levels of factors that don’t exist in the data).

[Deprecated] For `add_count()`: deprecated since it can’t actually affect the output.

Value

An object of the same type as `.data`. `count()` and `add_count()` group transiently, so the output has the same groups as the input.

Examples

data(se)
se |> count(dex)

---

**Description**

Keep only unique/distinct rows from a data frame. This is similar to `unique.data.frame()` but considerably faster.

**Usage**

```r
## S3 method for class 'SummarizedExperiment'
distinct(.data, ..., .keep_all = FALSE)
```

**Arguments**

- `.data` A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from dbplyr or dtplyr). See `Methods`, below, for more details.
- `...` Optional variables to use when determining uniqueness. If there are multiple rows for a given combination of inputs, only the first row will be preserved. If omitted, will use all variables in the data frame.
- `.keep_all` If TRUE, keep all variables in `.data`. If a combination of `...` is not distinct, this keeps the first row of values.
Value

An object of the same type as .data. The output has the following properties:

- Rows are a subset of the input but appear in the same order.
- Columns are not modified if ... is empty or .keep_all is TRUE. Otherwise, distinct() first calls mutate() to create new columns.
- Groups are not modified.
- Data frame attributes are preserved.

Methods

This function is a generic, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

The following methods are currently available in loaded packages: no methods found.

Examples

data(pasilla)
pasilla |> distinct(.sample)

---

extract

Extract a character column into multiple columns using regular expression groups

Description

[Superseded]

extract() has been superseded in favour of separate_wider_regex() because it has a more polished API and better handling of problems. Superseded functions will not go away, but will only receive critical bug fixes.

Given a regular expression with capturing groups, extract() turns each group into a new column. If the groups don’t match, or the input is NA, the output will be NA.

Usage

## S3 method for class 'SummarizedExperiment'
extract(
data,
col,
into,
regex = "(([[:alnum:]][:\]])+",
remove = TRUE,
convert = FALSE,
...
)


Arguments

- **data**: A data frame.
- **col**: `<tidy-select>` Column to expand.
- **into**: Names of new variables to create as character vector. Use `NA` to omit the variable in the output.
- **regex**: A string representing a regular expression used to extract the desired values. There should be one group (defined by `()` for each element of `into`.
- **remove**: If `TRUE`, remove input column from output data frame.
- **convert**: If `TRUE`, will run `type.convert()` with `as.is = TRUE` on new columns. This is useful if the component columns are integer, numeric or logical. `NB`: this will cause string "NA"s to be converted to NAs.
- **...**: Additional arguments passed on to methods.

Value

tidySummarizedExperiment

See Also

- `separate()` to split up by a separator.

Examples

tidySummarizedExperiment::pasilla |> 
extract(type, into="sequencing", regex="([a-z]*)_end", convert=TRUE)

Description

The `filter()` function is used to subset a data frame, retaining all rows that satisfy your conditions. To be retained, the row must produce a value of `TRUE` for all conditions. Note that when a condition evaluates to `NA` the row will be dropped, unlike base subsetting with `[

Usage

```r
## S3 method for class 'SummarizedExperiment'
filter(.data, ..., .preserve = FALSE)
```
Arguments

.data A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from dbplyr or dtplyr). See Methods, below, for more details.

... <data-masking> Expressions that return a logical value, and are defined in terms of the variables in .data. If multiple expressions are included, they are combined with the & operator. Only rows for which all conditions evaluate to TRUE are kept.

.preserve Relevant when the .data input is grouped. If .preserve = FALSE (the default), the grouping structure is recalculated based on the resulting data, otherwise the grouping is kept as is.

Details

The filter() function is used to subset the rows of .data, applying the expressions in ... to the column values to determine which rows should be retained. It can be applied to both grouped and ungrouped data (see group_by() and ungroup()). However, dplyr is not yet smart enough to optimise the filtering operation on grouped datasets that do not need grouped calculations. For this reason, filtering is often considerably faster on ungrouped data.

Value

An object of the same type as .data. The output has the following properties:

- Rows are a subset of the input, but appear in the same order.
- Columns are not modified.
- The number of groups may be reduced (if .preserve is not TRUE).
- Data frame attributes are preserved.

Useful filter functions

There are many functions and operators that are useful when constructing the expressions used to filter the data:

- ==, >, >= etc
- &, |, !, xor()
- is.na()
- between(), near()

Grouped tibbles

Because filtering expressions are computed within groups, they may yield different results on grouped tibbles. This will be the case as soon as an aggregating, lagging, or ranking function is involved. Compare this ungrouped filtering:

starwars %>% filter(mass > mean(mass, na.rm = TRUE))

With the grouped equivalent:
starwars %>% group_by(gender) %>% filter(mass > mean(mass, na.rm = TRUE))

In the ungrouped version, `filter()` compares the value of `mass` in each row to the global average (taken over the whole data set), keeping only the rows with `mass` greater than this global average. In contrast, the grouped version calculates the average mass separately for each `gender` group, and keeps rows with `mass` greater than the relevant within-gender average.

Methods

This function is a **generic**, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

The following methods are currently available in loaded packages: no methods found.

See Also

Other single table verbs: `arrange()`, `mutate()`, `reframe()`, `rename()`, `select()`, `slice()`, `summarise()`

Examples

data(pasilla)
pasilla |> filter(.sample == "untrt1")

# Learn more in ?dplyr_tidy_eval

---

### Printing tibbles

One of the main features of the `tbl_df` class is the printing:

- Tibbles only print as many rows and columns as fit on one screen, supplemented by a summary of the remaining rows and columns.
- Tibble reveals the type of each column, which keeps the user informed about whether a variable is, e.g., `<chr>` or `<fct>` (character versus factor). See vignette("types") for an overview of common type abbreviations.

Printing can be tweaked for a one-off call by calling `print()` explicitly and setting arguments like `n` and `width`. More persistent control is available by setting the options described in `pillar::pillar_options`. See also vignette("digits") for a comparison to base options, and vignette("numbers") that showcases `num()` and `char()` for creating columns with custom formatting options.

As of tibble 3.1.0, printing is handled entirely by the `pillar` package. If you implement a package that extends tibble, the printed output can be customized in various ways. See vignette("extending", package = "pillar") for details, and `pillar::pillar_options` for options that control the display in the console.
Usage

```r
## S3 method for class 'SummarizedExperiment'
print(x, ..., n = NULL, width = NULL, n_extra = NULL)
```

Arguments

- `x`: Object to format or print.
- `...`: Passed on to `tbl_format_setup()`.
- `n`: Number of rows to show. If `NULL`, the default, will print all rows if less than the `print_max` option. Otherwise, will print as many rows as specified by the `print_min` option.
- `width`: Width of text output to generate. This defaults to `NULL`, which means use the `width` option.
- `n_extra`: Number of extra columns to print abbreviated information for, if the width is too small for the entire tibble. If `NULL`, the default, will print information about at most `tibble.max_extra_cols` extra columns.

Value

Prints a message to the console describing the contents of the `tidySummarizedExperiment`.

Examples

```r
data(pasilla)
print(pasilla)
```

---

### full_join

**Mutating joins**

Mutating joins add columns from `y` to `x`, matching observations based on the keys. There are four mutuating joins: the inner join, and the three outer joins.

**Inner join:**

An `inner_join()` only keeps observations from `x` that have a matching key in `y`. The most important property of an inner join is that unmatched rows in either input are not included in the result. This means that generally inner joins are not appropriate in most analyses, because it is too easy to lose observations.

**Outer joins:**

The three outer joins keep observations that appear in at least one of the data frames:

- A `left_join()` keeps all observations in `x`.
- A `right_join()` keeps all observations in `y`.
- A `full_join()` keeps all observations in `x` and `y`. 
Usage

## S3 method for class 'SummarizedExperiment'
full_join(x, y, by = NULL, copy = FALSE, suffix = c(".x", ".y"), ...)

Arguments

x, y
A pair of data frames, data frame extensions (e.g. a tibble), or lazy data frames (e.g. from dbplyr or dtplyr). See Methods, below, for more details.

by
A join specification created with join_by(), or a character vector of variables to join by.

If NULL, the default, *_join() will perform a natural join, using all variables in common across x and y. A message lists the variables so that you can check they’re correct; suppress the message by supplying by explicitly.

To join on different variables between x and y, use a join_by() specification. For example, join_by(a == b) will match x$a to y$b.

To join by multiple variables, use a join_by() specification with multiple expressions. For example, join_by(a == b, c == d) will match x$a to y$b and x$c to y$d. If the column names are the same between x and y, you can shorten this by listing only the variable names, like join_by(a, c).

join_by() can also be used to perform inequality, rolling, and overlap joins. See the documentation at ?join_by for details on these types of joins.

For simple equality joins, you can alternatively specify a character vector of variable names to join by. For example, by = c("a", "b") joins x$a to y$a and x$b to y$b. If variable names differ between x and y, use a named character vector like by = c("x_a" = "y_a", "x_b" = "y_b").

To perform a cross-join, generating all combinations of x and y, see cross_join().

copy
If x and y are not from the same data source, and copy is TRUE, then y will be copied into the same src as x. This allows you to join tables across srcs, but it is a potentially expensive operation so you must opt into it.

suffix
If there are non-joined duplicate variables in x and y, these suffixes will be added to the output to disambiguate them. Should be a character vector of length 2.

... Other parameters passed onto methods.

Value

An object of the same type as x (including the same groups). The order of the rows and columns of x is preserved as much as possible. The output has the following properties:

- The rows are affect by the join type.
  - inner_join() returns matched x rows.
  - left_join() returns all x rows.
  - right_join() returns matched of x rows, followed by unmatched y rows.
  - full_join() returns all x rows, followed by unmatched y rows.

- Output columns include all columns from x and all non-key columns from y. If keep = TRUE, the key columns from y are included as well.
If non-key columns in x and y have the same name, suffixes are added to disambiguate. If keep = TRUE and key columns in x and y have the same name, suffixes are added to disambiguate these as well.

If keep = FALSE, output columns included in by are coerced to their common type between x and y.

Many-to-many relationships

By default, dplyr guards against many-to-many relationships in equality joins by throwing a warning. These occur when both of the following are true:

- A row in x matches multiple rows in y.
- A row in y matches multiple rows in x.

This is typically surprising, as most joins involve a relationship of one-to-one, one-to-many, or many-to-one, and is often the result of an improperly specified join. Many-to-many relationships are particularly problematic because they can result in a Cartesian explosion of the number of rows returned from the join.

If a many-to-many relationship is expected, silence this warning by explicitly setting relationship = "many-to-many".

In production code, it is best to preemptively set relationship to whatever relationship you expect to exist between the keys of x and y, as this forces an error to occur immediately if the data doesn’t align with your expectations.

Inequality joins typically result in many-to-many relationships by nature, so they don’t warn on them by default, but you should still take extra care when specifying an inequality join, because they also have the capability to return a large number of rows.

Rolling joins don’t warn on many-to-many relationships either, but many rolling joins follow a many-to-one relationship, so it is often useful to set relationship = "many-to-one" to enforce this.

Note that in SQL, most database providers won’t let you specify a many-to-many relationship between two tables, instead requiring that you create a third junction table that results in two one-to-many relationships instead.

Methods

These functions are generics, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

Methods available in currently loaded packages:

- inner_join(): no methods found.
- left_join(): no methods found.
- right_join(): no methods found.
- full_join(): no methods found.

See Also

Other joins: cross_join(), filter-joins, nest_join()
Examples

```r
data(pasilla)

tt <- pasilla
tt |> full_join(tibble::tibble(condition="treated", dose=10))
```

Description

`ggplot()` initializes a ggplot object. It can be used to declare the input data frame for a graphic and to specify the set of plot aesthetics intended to be common throughout all subsequent layers unless specifically overridden.

Usage

```r
## S3 method for class 'SummarizedExperiment'
hhplot(data = NULL, mapping = aes(), ..., environment = parent.frame())
```

Arguments

- `data`: Default dataset to use for plot. If not already a data.frame, will be converted to one by `fortify()`. If not specified, must be supplied in each layer added to the plot.
- `mapping`: Default list of aesthetic mappings to use for plot. If not specified, must be supplied in each layer added to the plot.
- `...`: Other arguments passed on to methods. Not currently used.
- `environment`: [Deprecated] Used prior to tidy evaluation.

Details

`ggplot()` is used to construct the initial plot object, and is almost always followed by a plus sign (+) to add components to the plot.

There are three common patterns used to invoke `ggplot()`:

- `ggplot(data = df, mapping = aes(x, y, other aesthetics))`
- `ggplot(data = df)`
- `ggplot()`

The first pattern is recommended if all layers use the same data and the same set of aesthetics, although this method can also be used when adding a layer using data from another data frame.

The second pattern specifies the default data frame to use for the plot, but no aesthetics are defined up front. This is useful when one data frame is used predominantly for the plot, but the aesthetics vary from one layer to another.
group_by

The third pattern initializes a skeleton ggplot object, which is fleshed out as layers are added. This is useful when multiple data frames are used to produce different layers, as is often the case in complex graphics.

The data = and mapping = specifications in the arguments are optional (and are often omitted in practice), so long as the data and the mapping values are passed into the function in the right order. In the examples below, however, they are left in place for clarity.

Value

ggplot

Examples

library(ggplot2)
data(pasilla)
pasilla %>%
ggplot(aes(.sample, counts)) +
geom_boxplot()

---

Group by one or more variables

Description

Most data operations are done on groups defined by variables. group_by() takes an existing tbl and converts it into a grouped tbl where operations are performed "by group". ungroup() removes grouping.

Usage

## S3 method for class 'SummarizedExperiment'
group_by(.data, ..., .add = FALSE, .drop = group_by_drop_default(.data))

Arguments

.data A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from dbplyr or dtplyr). See Methods, below, for more details.

... In group_by(), variables or computations to group by. Computations are always done on the ungrouped data frame. To perform computations on the grouped data, you need to use a separate mutate() step before the group_by(). Computations are not allowed in nest_by(). In ungroup(), variables to remove from the grouping.

.add When FALSE, the default, group_by() will override existing groups. To add to the existing groups, use .add = TRUE.

This argument was previously called add, but that prevented creating a new grouping variable called add, and conflicts with our naming conventions.
.drop

Drop groups formed by factor levels that don’t appear in the data? The default is TRUE except when .data has been previously grouped with .drop = FALSE. See `group_by_drop_default()` for details.

Value

A grouped data frame with class `grouped_df`, unless the combination of ... and add yields a empty set of grouping columns, in which case a tibble will be returned.

Methods

These function are generics, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

Methods available in currently loaded packages:

- `group_by()`: no methods found.
- `ungroup()`: no methods found.

Ordering

Currently, `group_by()` internally orders the groups in ascending order. This results in ordered output from functions that aggregate groups, such as `summarise()`.

When used as grouping columns, character vectors are ordered in the C locale for performance and reproducibility across R sessions. If the resulting ordering of your grouped operation matters and is dependent on the locale, you should follow up the grouped operation with an explicit call to `arrange()` and set the `.locale` argument. For example:

```r
data %>%
  group_by(chr) %>%
  summarise(avg = mean(x)) %>%
  arrange(chr, .locale = "en")
```

This is often useful as a preliminary step before generating content intended for humans, such as an HTML table.

Legacy behavior:

Prior to dplyr 1.1.0, character vector grouping columns were ordered in the system locale. If you need to temporarily revert to this behavior, you can set the global option `dplyr.legacy_locale` to TRUE, but this should be used sparingly and you should expect this option to be removed in a future version of dplyr. It is better to update existing code to explicitly call `arrange(.locale = )` instead. Note that setting `dplyr.legacy_locale` will also force calls to `arrange()` to use the system locale.

See Also

Other grouping functions: `group_map()`, `group_nest()`, `group_split()`, `group_trim()`
Examples

data(pasilla)
pasilla |> group_by(.sample)

---

group_split

Split data frame by groups

Description

[Experimental]

group_split() works like base::split() but:

- It uses the grouping structure from group_by() and therefore is subject to the data mask
- It does not name the elements of the list based on the grouping as this only works well for a single character grouping variable. Instead, use group_keys() to access a data frame that defines the groups.

group_split() is primarily designed to work with grouped data frames. You can pass ... to group and split an ungrouped data frame, but this is generally not very useful as you want have easy access to the group metadata.

Usage

### S3 method for class 'SummarizedExperiment'

group_split(.tbl, ..., .keep = TRUE)

Arguments

- `.tbl` A tbl.
- `...` If `.tbl` is an ungrouped data frame, a grouping specification, forwarded to group_by().
- `.keep` Should the grouping columns be kept?

Value

A list of tibbles. Each tibble contains the rows of `.tbl` for the associated group and all the columns, including the grouping variables. Note that this returns a list_of which is slightly stricter than a simple list but is useful for representing lists where every element has the same type.

Lifecycle

group_split() is not stable because you can achieve very similar results by manipulating the nested column returned from tidyr::nest(.by =). That also retains the group keys all within a single data structure. group_split() may be deprecated in the future.
inner_join

See Also

Other grouping functions: group_by(), group_map(), group_nest(), group_trim()

Examples

```r
data(pasilla, package = "tidySummarizedExperiment")
pasilla |> group_split(condition)
pasilla |> group_split(counts > 0)
pasilla |> group_split(condition, counts > 0)
```

---

### inner_join

#### Mutating joins

Description

Mutating joins add columns from y to x, matching observations based on the keys. There are four mutating joins: the inner join, and the three outer joins.

**Inner join:**

An inner_join() only keeps observations from x that have a matching key in y.

The most important property of an inner join is that unmatched rows in either input are not included in the result. This means that generally inner joins are not appropriate in most analyses, because it is too easy to lose observations.

**Outer joins:**

The three outer joins keep observations that appear in at least one of the data frames:

- A left_join() keeps all observations in x.
- A right_join() keeps all observations in y.
- A full_join() keeps all observations in x and y.

Usage

```r
## S3 method for class 'SummarizedExperiment'
inner_join(x, y, by = NULL, copy = FALSE, suffix = c(".x", ".y"), ...)
```

Arguments

- **x, y**
  
  A pair of data frames, data frame extensions (e.g. a tibble), or lazy data frames (e.g. from dbplyr or dtplyr). See Methods, below, for more details.

- **by**
  
  A join specification created with join_by(), or a character vector of variables to join by.

  If NULL, the default, *_join() will perform a natural join, using all variables in common across x and y. A message lists the variables so that you can check they're correct; suppress the message by supplying by explicitly.
To join on different variables between `x` and `y`, use a `join_by()` specification. For example, `join_by(a == b)` will match `x$a` to `y$b`.

To join by multiple variables, use a `join_by()` specification with multiple expressions. For example, `join_by(a == b, c == d)` will match `x$a` to `y$b` and `x$c` to `y$d`. If the column names are the same between `x` and `y`, you can shorten this by listing only the variable names, like `join_by(a, c)`.

`join_by()` can also be used to perform inequality, rolling, and overlap joins. See the documentation at `?join_by` for details on these types of joins.

For simple equality joins, you can alternatively specify a character vector of variable names to join by. For example, `by = c("a", "b")` joins `x$a` to `y$a` and `x$b` to `y$b`. If variable names differ between `x` and `y`, use a named character vector like `by = c("x_a" = "y_a", "x_b" = "y_b")`.

To perform a cross-join, generating all combinations of `x` and `y`, see `cross_join()`.

**copy**

If `x` and `y` are not from the same data source, and `copy` is `TRUE`, then `y` will be copied into the same src as `x`. This allows you to join tables across srcs, but it is a potentially expensive operation so you must opt into it.

**suffix**

If there are non-joined duplicate variables in `x` and `y`, these suffixes will be added to the output to disambiguate them. Should be a character vector of length 2.

... Other parameters passed onto methods.

### Value

An object of the same type as `x` (including the same groups). The order of the rows and columns of `x` is preserved as much as possible. The output has the following properties:

- The rows are affect by the join type.
  - `inner_join()` returns matched `x` rows.
  - `left_join()` returns all `x` rows.
  - `right_join()` returns matched of `x` rows, followed by unmatched `y` rows.
  - `full_join()` returns all `x` rows, followed by unmatched `y` rows.
- Output columns include all columns from `x` and all non-key columns from `y`. If `keep = TRUE`, the key columns from `y` are included as well.
- If non-key columns in `x` and `y` have the same name, suffixes are added to disambiguate. If `keep = TRUE` and key columns in `x` and `y` have the same name, suffixes are added to disambiguate these as well.
- If `keep = FALSE`, output columns included in `by` are coerced to their common type between `x` and `y`.

### Many-to-many relationships

By default, `dplyr` guards against many-to-many relationships in equality joins by throwing a warning. These occur when both of the following are true:

- A row in `x` matches multiple rows in `y`.
- A row in `y` matches multiple rows in `x`. 
inner_join

This is typically surprising, as most joins involve a relationship of one-to-one, one-to-many, or many-to-one, and is often the result of an improperly specified join. Many-to-many relationships are particularly problematic because they can result in a Cartesian explosion of the number of rows returned from the join.

If a many-to-many relationship is expected, silence this warning by explicitly setting `relationship = "many-to-many"`.

In production code, it is best to preemptively set `relationship` to whatever relationship you expect to exist between the keys of `x` and `y`, as this forces an error to occur immediately if the data doesn’t align with your expectations.

Inequality joins typically result in many-to-many relationships by nature, so they don’t warn on them by default, but you should still take extra care when specifying an inequality join, because they also have the capability to return a large number of rows.

Rolling joins don’t warn on many-to-many relationships either, but many rolling joins follow a many-to-one relationship, so it is often useful to set `relationship = "many-to-one"` to enforce this.

Note that in SQL, most database providers won’t let you specify a many-to-many relationship between two tables, instead requiring that you create a third junction table that results in two one-to-many relationships instead.

Methods

These functions are generics, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

Methods available in currently loaded packages:

- `inner_join()`: no methods found.
- `left_join()`: no methods found.
- `right_join()`: no methods found.
- `full_join()`: no methods found.

See Also

Other joins: `cross_join()`, `filter-joins`, `nest_join()`

Examples

data(pasilla)

```r
tt <- pasilla
tt |> inner_join(tt |
   distinct(condition) |>
   mutate(new_column=1:2) |>
   slice(1))
```
**left_join**

**Mutating joins**

**Description**

Mutating joins add columns from \(y\) to \(x\), matching observations based on the keys. There are four mutating joins: the inner join, and the three outer joins.

**Inner join:**

An `inner_join()` only keeps observations from \(x\) that have a matching key in \(y\).

The most important property of an inner join is that unmatched rows in either input are not included in the result. This means that generally inner joins are not appropriate in most analyses, because it is too easy to lose observations.

**Outer joins:**

The three outer joins keep observations that appear in at least one of the data frames:

- A `left_join()` keeps all observations in \(x\).
- A `right_join()` keeps all observations in \(y\).
- A `full_join()` keeps all observations in \(x\) and \(y\).

**Usage**

```r
## S3 method for class 'SummarizedExperiment'
left_join(x, y, by = NULL, copy = FALSE, suffix = c(".x", ".y"), ...)
```

**Arguments**

- `x, y` A pair of data frames, data frame extensions (e.g. a tibble), or lazy data frames (e.g. from dbplyr or dtplyr). See *Methods*, below, for more details.
- `by` A join specification created with `join_by()`, or a character vector of variables to join by.
  
  If NULL, the default, `*_join()` will perform a natural join, using all variables in common across \(x\) and \(y\). A message lists the variables so that you can check they're correct; suppress the message by supplying `by` explicitly.
  
  To join on different variables between \(x\) and \(y\), use a `join_by()` specification. For example, `join_by(a == b)` will match \(x\$a\) to \(y\$b\).
  
  To join by multiple variables, use a `join_by()` specification with multiple expressions. For example, `join_by(a == b, c == d)` will match \(x\$a\) to \(y\$b\) and \(x\$c\) to \(y\$d\). If the column names are the same between \(x\) and \(y\), you can shorten this by listing only the variable names, like `join_by(a, c)`.

  `join_by()` can also be used to perform inequality, rolling, and overlap joins. See the documentation at `?join_by` for details on these types of joins.

  For simple equality joins, you can alternatively specify a character vector of variable names to join by. For example, `by = c("a", "b")` joins `x$a` to `y$a` and `x$b` to `y$b`. If variable names differ between \(x\) and \(y\), use a named character vector like `by = c("x_a" = "y_a", "x_b" = "y_b")`.

  To perform a cross-join, generating all combinations of \(x\) and \(y\), see `cross_join()`.
**left_join**

- **copy**: If x and y are not from the same data source, and copy is TRUE, then y will be copied into the same src as x. This allows you to join tables across srcs, but it is a potentially expensive operation so you must opt into it.

- **suffix**: If there are non-joined duplicate variables in x and y, these suffixes will be added to the output to disambiguate them. Should be a character vector of length 2.

... Other parameters passed onto methods.

**Value**

An object of the same type as x (including the same groups). The order of the rows and columns of x is preserved as much as possible. The output has the following properties:

- The rows are affected by the join type.
  - `inner_join()` returns matched x rows.
  - `left_join()` returns all x rows.
  - `right_join()` returns matched of x rows, followed by unmatched y rows.
  - `full_join()` returns all x rows, followed by unmatched y rows.

- Output columns include all columns from x and all non-key columns from y. If keep = TRUE, the key columns from y are included as well.

- If non-key columns in x and y have the same name, suffixes are added to disambiguate. If keep = TRUE and key columns in x and y have the same name, suffixes are added to disambiguate these as well.

- If keep = FALSE, output columns included in by are coerced to their common type between x and y.

**Many-to-many relationships**

By default, dplyr guards against many-to-many relationships in equality joins by throwing a warning. These occur when both of the following are true:

- A row in x matches multiple rows in y.
- A row in y matches multiple rows in x.

This is typically surprising, as most joins involve a relationship of one-to-one, one-to-many, or many-to-one, and is often the result of an improperly specified join. Many-to-many relationships are particularly problematic because they can result in a Cartesian explosion of the number of rows returned from the join.

If a many-to-many relationship is expected, silence this warning by explicitly setting relationship = "many-to-many".

In production code, it is best to preemptively set relationship to whatever relationship you expect to exist between the keys of x and y, as this forces an error to occur immediately if the data doesn't align with your expectations.

Inequality joins typically result in many-to-many relationships by nature, so they don't warn on them by default, but you should still take extra care when specifying an inequality join, because they also have the capability to return a large number of rows.
Rolling joins don’t warn on many-to-many relationships either, but many rolling joins follow a many-to-one relationship, so it is often useful to set `relationship = "many-to-one"` to enforce this.

Note that in SQL, most database providers won’t let you specify a many-to-many relationship between two tables, instead requiring that you create a third junction table that results in two one-to-many relationships instead.

Methods

These functions are generics, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

Methods available in currently loaded packages:

- `inner_join()`: no methods found.
- `left_join()`: no methods found.
- `right_join()`: no methods found.
- `full_join()`: no methods found.

See Also

Other joins: `cross_join()`, `filter-joins`, `nest_join()`

Examples

```r
data(pasilla)

tt <- pasilla

# Merging the left table with a distinct condition
# and creating a new column

tt |> left_join(tt |> distinct(condition) |> mutate(new_column=1:2))
```

mutate

Create, modify, and delete columns

Description

`mutate()` creates new columns that are functions of existing variables. It can also modify (if the name is the same as an existing column) and delete columns (by setting their value to NULL).

Usage

```r
## S3 method for class 'SummarizedExperiment'
mutate(.data, ...)
```
Arguments

- `.data` A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from dbplyr or dtplyr). See Methods, below, for more details.

- `<data-masking>` Name-value pairs. The name gives the name of the column in the output.
  
  The value can be:
  - A vector of length 1, which will be recycled to the correct length.
  - A vector the same length as the current group (or the whole data frame if ungrouped).
  - NULL, to remove the column.
  - A data frame or tibble, to create multiple columns in the output.

Value

An object of the same type as `.data`. The output has the following properties:

- Columns from `.data` will be preserved according to the `.keep` argument.
- Existing columns that are modified by `...` will always be returned in their original location.
- New columns created through `...` will be placed according to the `.before` and `.after` arguments.
- The number of rows is not affected.
- Columns given the value NULL will be removed.
- Groups will be recomputed if a grouping variable is mutated.
- Data frame attributes are preserved.

Useful mutate functions

- `+`, `-`, `log()`, etc., for their usual mathematical meanings
- `lead()`, `lag()`
- `dense_rank()`, `min_rank()`, `percent_rank()`, `row_number()`, `cume_dist()`, `ntile()`
- `cumsum()`, `cummean()`, `cummin()`, `cummax()`, `cumany()`, `cumall()`
- `na_if()`, `coalesce()`
- `if_else()`, `recode()`, `case_when()`

Grouped tibbles

Because mutating expressions are computed within groups, they may yield different results on grouped tibbles. This will be the case as soon as an aggregating, lagging, or ranking function is involved. Compare this ungrouped mutate:

```r
starwars %>%
  select(name, mass, species) %>%
  mutate(mass_norm = mass / mean(mass, na.rm = TRUE))
```
With the grouped equivalent:

```r
starwars %>%
  select(name, mass, species) %>%
  group_by(species) %>%
  mutate(mass_norm = mass / mean(mass, na.rm = TRUE))
```

The former normalises mass by the global average whereas the latter normalises by the averages within species levels.

**Methods**

This function is a **generic**, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

Methods available in currently loaded packages: no methods found.

**See Also**

Other single table verbs: `rename()`, `slice()`, `summarise()`

**Examples**

```r
data(pasilla)
pasilla |> mutate(logcounts=log2(counts))
```

---

**nest**

*Nest rows into a list-column of data frames*

**Description**

Nesting creates a list-column of data frames; unnesting flattens it back out into regular columns. Nesting is implicitly a summarising operation: you get one row for each group defined by the non-nested columns. This is useful in conjunction with other summaries that work with whole datasets, most notably models.

Learn more in vignette("nest").

**Usage**

```r
# S3 method for class 'SummarizedExperiment'
nest(.data, ..., .names_sep = NULL)
```
Arguments

.data A data frame.

... <tidy-select> Columns to nest; these will appear in the inner data frames. Specified using name-variable pairs of the form new_col = c(col1, col2, col3). The right hand side can be any valid tidyselect expression. If not supplied, then ... is derived as all columns not selected by .by, and will use the column name from .key. [Deprecated]: previously you could write df %>% nest(x, y, z). Convert to df %>% nest(data = c(x, y, z)).

.names_sep If NULL, the default, the inner names will come from the former outer names. If a string, the new inner names will use the outer names with names_sep automatically stripped. This makes names_sep roughly symmetric between nesting and unnesting.

Details

If neither ... nor .by are supplied, nest() will nest all variables, and will use the column name supplied through .key.

Value

tidySummarizedExperiment_nested

New syntax

tidy 1.0.0 introduced a new syntax for nest() and unnest() that’s designed to be more similar to other functions. Converting to the new syntax should be straightforward (guided by the message you’ll receive) but if you just need to run an old analysis, you can easily revert to the previous behaviour using nest_legacy() and unnest_legacy() as follows:

```
library(tidyr)
nest <- nest_legacy
unnest <- unnest_legacy
```

Grouped data frames

df %>% nest(data = c(x, y)) specifies the columns to be nested; i.e. the columns that will appear in the inner data frame. df %>% nest(.by = c(x, y)) specifies the columns to nest by; i.e. the columns that will remain in the outer data frame. An alternative way to achieve the latter is to nest() a grouped data frame created by dplyr::group_by(). The grouping variables remain in the outer data frame and the others are nested. The result preserves the grouping of the input. Variables supplied to nest() will override grouping variables so that df %>% group_by(x, y) %>% nest(data = !z) will be equivalent to df %>% nest(data = !z).

You can’t supply .by with a grouped data frame, as the groups already represent what you are nesting by.
Examples

```r
 tidySummarizedExperiment::pasilla |> 
   nest(data=-condition)
```

### pasilla

**Read counts of RNA-seq samples of Pasilla knock-down by Brooks et al.**

**Description**

A SummarizedExperiment dataset containing the transcriptome information for Drosophila Melanogaster.

**Usage**

```r
 data(pasilla)
```

**Format**

containing 14599 features and 7 biological replicates.

**Source**


---

### pivot_longer

**Pivot data from wide to long**

**Description**

`pivot_longer()` "lengthens" data, increasing the number of rows and decreasing the number of columns. The inverse transformation is `pivot_wider()`

Learn more in vignette("pivot").

**Usage**

```r
 ## S3 method for class 'SummarizedExperiment'
pivot_longer( 
   data, 
   cols, 
   ..., 
   cols_vary = "fastest", 
   names_to = "name", 
   names_prefix = NULL, 
   names_sep = NULL, 
```
pivot_longer

names_pattern = NULL,
names_ptypes = NULL,
names_transform = NULL,
names_repair = "check_unique",
values_to = "value",
values_drop_na = FALSE,
values_ptypes = NULL,
values_transform = NULL
)

Arguments

data A data frame to pivot.
cols <tidy-select> Columns to pivot into longer format.
... Additional arguments passed on to methods.
cols_vary When pivoting cols into longer format, how should the output rows be arranged relative to their original row number?
  • "fastest", the default, keeps individual rows from cols close together in the output. This often produces intuitively ordered output when you have at least one key column from data that is not involved in the pivoting process.
  • "slowest" keeps individual columns from cols close together in the output. This often produces intuitively ordered output when you utilize all of the columns from data in the pivoting process.

names_to A character vector specifying the new column or columns to create from the information stored in the column names of data specified by cols.
  • If length 0, or if NULL is supplied, no columns will be created.
  • If length 1, a single column will be created which will contain the column names specified by cols.
  • If length >1, multiple columns will be created. In this case, one of names_sep or names_pattern must be supplied to specify how the column names should be split. There are also two additional character values you can take advantage of:
    – NA will discard the corresponding component of the column name.
    – ".value" indicates that the corresponding component of the column name defines the name of the output column containing the cell values, overriding values_to entirely.

names_prefix A regular expression used to remove matching text from the start of each variable name.
names_sep, names_pattern If names_to contains multiple values, these arguments control how the column name is broken up.
  names_sep takes the same specification as separate(), and can either be a numeric vector (specifying positions to break on), or a single string (specifying a regular expression to split on).
  names_pattern takes the same specification as extract(), a regular expression containing matching groups (()).
If these arguments do not give you enough control, use `pivot_longer_spec()` to create a spec object and process manually as needed.

`names_ptypes, values_ptypes`

Optionally, a list of column name-prototype pairs. Alternatively, a single empty prototype can be supplied, which will be applied to all columns. A prototype (or ptype for short) is a zero-length vector (like `integer()`) that defines the type, class, and attributes of a vector. Use these arguments if you want to confirm that the created columns are the types that you expect. Note that if you want to change (instead of confirm) the types of specific columns, you should use `names_transform` or `values_transform` instead.

`names_transform, values_transform`

Optionally, a list of column name-function pairs. Alternatively, a single function can be supplied, which will be applied to all columns. Use these arguments if you need to change the types of specific columns. For example, `names_transform = list(week = as.integer)` would convert a character variable called `week` to an integer.

If not specified, the type of the columns generated from `names_to` will be character, and the type of the variables generated from `values_to` will be the common type of the input columns used to generate them.

`names_repair` What happens if the output has invalid column names? The default, "check_unique" is to error if the columns are duplicated. Use "minimal" to allow duplicates in the output, or "unique" to de-duplicated by adding numeric suffixes. See `vctrs::vec_as_names()` for more options.

`values_to` A string specifying the name of the column to create from the data stored in cell values. If `names_to` is a character containing the special `.value` sentinel, this value will be ignored, and the name of the value column will be derived from part of the existing column names.

`values_drop_na` If TRUE, will drop rows that contain only NAs in the `value_to` column. This effectively converts explicit missing values to implicit missing values, and should generally be used only when missing values in data were created by its structure.

**Details**

`pivot_longer()` is an updated approach to `gather()`, designed to be both simpler to use and to handle more use cases. We recommend you use `pivot_longer()` for new code; `gather()` isn’t going away but is no longer under active development.

**Value**

`tidySummarizedExperiment`

**Examples**

```
# See vignette("pivot") for examples and explanation
library(dplyr)
tidySummarizedExperiment::pasilla %>%
  pivot_longer(c(condition, type),
```
pivot_wider

names_to="name", values_to="value")

pivot_wider  Pivot data from long to wide

Description

pivot_wider() "widens" data, increasing the number of columns and decreasing the number of rows. The inverse transformation is pivot_longer().

Learn more in vignette("pivot").

Usage

## S3 method for class 'SummarizedExperiment'
pivot_wider(
data,
...,
id_cols = NULL,
id_expand = FALSE,
names_from = name,
names_prefix = "",
names_sep = "_",
names_glue = NULL,
names_sort = FALSE,
names_vary = "fastest",
names_expand = FALSE,
names_repair = "check_unique",
values_from = value,
values_fill = NULL,
values_fn = NULL,
unused_fn = NULL
)

Arguments

data  A data frame to pivot.

...  Additional arguments passed on to methods.

id_cols  <tidy-select> A set of columns that uniquely identify each observation. Typically used when you have redundant variables, i.e. variables whose values are perfectly correlated with existing variables.

Defaults to all columns in data except for the columns specified through names_from and values_from. If a tidyselect expression is supplied, it will be evaluated on data after removing the columns specified through names_from and values_from.
id Expand Should the values in the id_cols columns be expanded by expand() before pivoting? This results in more rows, the output will contain a complete expansion of all possible values in id_cols. Implicit factor levels that aren’t represented in the data will become explicit. Additionally, the row values corresponding to the expanded id_cols will be sorted.

names_from, values_from
<tidy-select> A pair of arguments describing which column (or columns) to get the name of the output column (names_from), and which column (or columns) to get the cell values from (values_from). If values_from contains multiple values, the value will be added to the front of the output column.

names_prefix String added to the start of every variable name. This is particularly useful if names_from is a numeric vector and you want to create syntactic variable names.

names_sep If names_from or values_from contains multiple variables, this will be used to join their values together into a single string to use as a column name.

names_glue Instead of names_sep and names_prefix, you can supply a glue specification that uses the names_from columns (and special .value) to create custom column names.

names_sort Should the column names be sorted? If FALSE, the default, column names are ordered by first appearance.

names_vary When names_from identifies a column (or columns) with multiple unique values, and multiple values_from columns are provided, in what order should the resulting column names be combined?
  * "fastest" varies names_from values fastest, resulting in a column naming scheme of the form: value1_name1, value1_name2, value2_name1, value2_name2. This is the default.
  * "slowest" varies names_from values slowest, resulting in a column naming scheme of the form: value1_name1, value2_name1, value1_name2, value2_name2.

names_expand Should the values in the names_from columns be expanded by expand() before pivoting? This results in more columns, the output will contain column names corresponding to a complete expansion of all possible values in names_from. Implicit factor levels that aren’t represented in the data will become explicit. Additionally, the column names will be sorted, identical to what names_sort would produce.

names_repair What happens if the output has invalid column names? The default, "check_unique" is to error if the columns are duplicated. Use "minimal" to allow duplicates in the output, or "unique" to de-duplicated by adding numeric suffixes. See vctrs::vec_as_names() for more options.

values_fill Optionally, a (scalar) value that specifies what each value should be filled in with when missing.

This can be a named list if you want to apply different fill values to different value columns.

values_fn Optionally, a function applied to the value in each cell in the output. You will typically use this when the combination of id_cols and names_from columns does not uniquely identify an observation.
This can be a named list if you want to apply different aggregations to different values_from columns.

 unused_fn  

 Optionally, a function applied to summarize the values from the unused columns (i.e. columns not identified by id_cols, names_from, or values_from). The default drops all unused columns from the result. This can be a named list if you want to apply different aggregations to different unused columns. id_cols must be supplied for unused_fn to be useful, since otherwise all unspecifed columns will be considered id_cols. This is similar to grouping by the id_cols then summarizing the unused columns using unused_fn.

Details

pivot_wider() is an updated approach to spread(), designed to be both simpler to use and to handle more use cases. We recommend you use pivot_wider() for new code; spread() isn't going away but is no longer under active development.

Value

tidySummarizedExperiment

See Also

pivot_wider_spec() to pivot "by hand" with a data frame that defines a pivoting specification.

Examples

# See vignette("pivot") for examples and explanation
library(dplyr)
tidySummarizedExperiment::pasilla %>%
  pivot_wider(names_from=feature, values_from=counts)

plot_ly

*Initiate a plotly visualization*

Description

This function maps R objects to plotly.js, an (MIT licensed) web-based interactive charting library. It provides abstractions for doing common things (e.g. mapping data values to fill colors (via color) or creating animations (via frame)) and sets some different defaults to make the interface feel more 'R-like' (i.e., closer to plot() and ggplot::qplot()).
Usage

```r
## S3 method for class 'tbl_df'
plot_ly(
  data = data.frame(),
  ..., 
  type = NULL,
  name = NULL,
  color = NULL,
  colors = NULL,
  alpha = NULL,
  stroke = NULL,
  strokes = NULL,
  alpha_stroke = 1,
  size = NULL,
  sizes = c(10, 100),
  span = NULL,
  spans = c(1, 20),
  symbol = NULL,
  symbols = NULL,
  linetype = NULL,
  linetypes = NULL,
  split = NULL,
  frame = NULL,
  width = NULL,
  height = NULL,
  source = "A"
)
```

```r
## S3 method for class 'SummarizedExperiment'
plot_ly(
  data = data.frame(),
  ..., 
  type = NULL,
  name = NULL,
  color = NULL,
  colors = NULL,
  alpha = NULL,
  stroke = NULL,
  strokes = NULL,
  alpha_stroke = 1,
  size = NULL,
  sizes = c(10, 100),
  span = NULL,
  spans = c(1, 20),
  symbol = NULL,
  symbols = NULL,
  linetype = NULL,
  linetypes = NULL,
  split = NULL,
  frame = NULL,
  width = NULL,
  height = NULL,
  source = "A"
)
```
split = NULL,
frame = NULL,
width = NULL,
height = NULL,
source = "A"
)

Arguments

data A data frame (optional) or crosstalk::SharedData object.

... Arguments (i.e., attributes) passed along to the trace type. See schema() for a list of acceptable attributes for a given trace type (by going to traces -> type -> attributes). Note that attributes provided at this level may override other arguments (e.g. plot_ly(x = 1:10, y = 1:10, color = I("red"), marker = list(color = "blue"))).

type A character string specifying the trace type (e.g. "scatter", "bar", "box", etc). If specified, it always creates a trace, otherwise

name Values mapped to the trace’s name attribute. Since a trace can only have one name, this argument acts very much like split in that it creates one trace for every unique value.

color Values mapped to relevant ‘fill-color’ attribute(s) (e.g. fillcolor, marker.color, textfont.color, etc.). The mapping from data values to color codes may be controlled using colors and alpha, or avoided altogether via I() (e.g., color = I("red")). Any color understood by grDevices::col2rgb() may be used in this way.

colors Either a colorbrewer2.org palette name (e.g. "YlOrRd" or "Blues"), or a vector of colors to interpolate in hexadecimal "#RRGGBB" format, or a color interpolation function like colorRamp().

alpha A number between 0 and 1 specifying the alpha channel applied to color. Defaults to 0.5 when mapping to fillcolor and 1 otherwise.

stroke Similar to color, but values are mapped to relevant ‘stroke-color’ attribute(s) (e.g., marker.line.color and line.color for filled polygons). If not specified, stroke inherits from color.

strokes Similar to colors, but controls the stroke mapping.

alpha_stroke Similar to alpha, but applied to stroke.

size (Numeric) values mapped to relevant ‘fill-size’ attribute(s) (e.g., marker.size, textfont.size, and error_x.width). The mapping from data values to symbols may be controlled using sizes, or avoided altogether via I() (e.g., size = I(30)).

sizes A numeric vector of length 2 used to scale size to pixels.

span (Numeric) values mapped to relevant ‘stroke-size’ attribute(s) (e.g., marker.line.width, line.width for filled polygons, and error_x.thickness) The mapping from data values to symbols may be controlled using spans, or avoided altogether via I() (e.g., span = I(30)).

spans A numeric vector of length 2 used to scale span to pixels.
symbol (Discrete) values mapped to marker.symbol. The mapping from data values to symbols may be controlled using symbols, or avoided altogether via I() (e.g., symbol = I("pentagon")). Any pch value or symbol name may be used in this way.

symbols A character vector of pch values or symbol names.

linetype (Discrete) values mapped to line.dash. The mapping from data values to symbols may be controlled using linetypes, or avoided altogether via I() (e.g., linetype = I("dash")). Any lty (see par) value or dash name may be used in this way.

linetypes A character vector of lty values or dash names

split (Discrete) values used to create multiple traces (one trace per value).

frame (Discrete) values used to create animation frames.

width Width in pixels (optional, defaults to automatic sizing).

height Height in pixels (optional, defaults to automatic sizing).

source a character string of length 1. Match the value of this string with the source argument in event_data() to retrieve the event data corresponding to a specific plot (shiny apps can have multiple plots).

Details
Unless type is specified, this function just initiates a plotly object with 'global' attributes that are passed onto downstream uses of add_trace() (or similar). A formula must always be used when referencing column name(s) in data (e.g. plot_ly(mtcars, x = ~wt)). Formulas are optional when supplying values directly, but they do help inform default axis/scale titles (e.g., plot_ly(x = mtcars$wt) vs plot_ly(x = ~mtcars$wt))

Value
plotly
plotly

Author(s)
Carson Sievert

References
https://plotly-r.com/overview.html

See Also
• For initializing a plotly-geo object: plot_geo()
• For initializing a plotly-mapbox object: plot_mapbox()
• For translating a ggplot2 object to a plotly object: ggplotly()
• For modifying any plotly object: layout(), add_trace(), style()
• For linked brushing: highlight()
For arranging multiple plots: `subplot()`, `crosstalk::bscols()`
- For inspecting plotly objects: `plotly_json()`
- For quick, accurate, and searchable plotly.js reference: `schema()`

Examples

```r
data(se)
se |>
    plot_ly(x = ~counts)

data(se)
se |>
    plot_ly(x = ~counts)
```

---

**pull**  
*Extract a single column*

Description

`pull()` is similar to $. It’s mostly useful because it looks a little nicer in pipes, it also works with remote data frames, and it can optionally name the output.

Usage

```r
## S3 method for class 'SummarizedExperiment'
pull(.data, var = -1, name = NULL, ...)
```

Arguments

- `.data`  
  A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from `dbplyr` or `dplyr`). See Methods, below, for more details.

- `var`  
  A variable specified as:
  - a literal variable name
  - a positive integer, giving the position counting from the left
  - a negative integer, giving the position counting from the right.

  The default returns the last column (on the assumption that’s the column you’ve created most recently).

  This argument is taken by expression and supports quasiquotation (you can unquote column names and column locations).

- `name`  
  An optional parameter that specifies the column to be used as names for a named vector. Specified in a similar manner as `var`.

- `...`  
  For use by methods.
Value

A vector the same size as \texttt{.data}.

Methods

This function is a \texttt{generic}, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

The following methods are currently available in loaded packages: no methods found.

Examples

\begin{verbatim}
data(pasilla)
pasilla |> pull(feature)
\end{verbatim}

\begin{verbatim}
rename |> pull(feature)
\end{verbatim}

\begin{verbatim}
rename_with |> pull(feature)
\end{verbatim}

\begin{verbatim}
rename_with |> pull(feature)
\end{verbatim}

Description

\texttt{rename()} changes the names of individual variables using \texttt{new\_name = old\_name} syntax; \texttt{rename\_with()} renames columns using a function.

Usage

\begin{verbatim}
## S3 method for class 'SummarizedExperiment'
rename(.data, ...)
\end{verbatim}

Arguments

\begin{verbatim}
.data
\end{verbatim}

A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from \texttt{dbplyr} or \texttt{dplyr}). See \texttt{Methods}, below, for more details.

\begin{verbatim}
...
\end{verbatim}

For \texttt{rename(): <tidy-select>} Use \texttt{new\_name = old\_name} to rename selected variables.

For \texttt{rename\_with(): additional arguments passed onto .fn}.

Value

An object of the same type as \texttt{.data}. The output has the following properties:

\begin{itemize}
  \item Rows are not affected.
  \item Column names are changed; column order is preserved.
  \item Data frame attributes are preserved.
  \item Groups are updated to reflect new names.
\end{itemize}
Methods

This function is a generic, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

The following methods are currently available in loaded packages: no methods found.

See Also

Other single table verbs: mutate(), slice(), summarise()

Examples

data(pasilla)
pasilla |> rename(cond=condition)

Description

Mutating joins add columns from y to x, matching observations based on the keys. There are four mutating joins: the inner join, and the three outer joins.

Inner join:

An inner_join() only keeps observations from x that have a matching key in y.

The most important property of an inner join is that unmatched rows in either input are not included in the result. This means that generally inner joins are not appropriate in most analyses, because it is too easy to lose observations.

Outer joins:

The three outer joins keep observations that appear in at least one of the data frames:

• A left_join() keeps all observations in x.
• A right_join() keeps all observations in y.
• A full_join() keeps all observations in x and y.

Usage

```r
## S3 method for class 'SummarizedExperiment'
right_join(x, y, by = NULL, copy = FALSE, suffix = c(".x", ".y"), ...)
```
Arguments

- **x, y** A pair of data frames, data frame extensions (e.g. a tibble), or lazy data frames (e.g. from dbplyr or dtplyr). See Methods, below, for more details.

- **by** A join specification created with `join_by()`, or a character vector of variables to join by.
  
  If NULL, the default, `*_join()` will perform a natural join, using all variables in common across x and y. A message lists the variables so that you can check they’re correct; suppress the message by supplying by explicitly.
  
  To join on different variables between x and y, use a `join_by()` specification. For example, `join_by(a == b)` will match `x$a` to `y$b`.
  
  To join by multiple variables, use a `join_by()` specification with multiple expressions. For example, `join_by(a == b, c == d)` will match `x$a` to `y$b` and `x$c` to `y$d`. If the column names are the same between x and y, you can shorten this by listing only the variable names, like `join_by(a, c)`.

- **copy** If x and y are not from the same data source, and `copy` is TRUE, then y will be copied into the same src as x. This allows you to join tables across srcs, but it is a potentially expensive operation so you must opt into it.

- **suffix** If there are non-joined duplicate variables in x and y, these suffixes will be added to the output to disambiguate them. Should be a character vector of length 2.

- **...** Other parameters passed onto methods.

Value

An object of the same type as x (including the same groups). The order of the rows and columns of x is preserved as much as possible. The output has the following properties:

- The rows are affect by the join type.
  - `inner_join()` returns matched x rows.
  - `left_join()` returns all x rows.
  - `right_join()` returns matched of x rows, followed by unmatched y rows.
  - `full_join()` returns all x rows, followed by unmatched y rows.

- Output columns include all columns from x and all non-key columns from y. If `keep` = TRUE, the key columns from y are included as well.

- If non-key columns in x and y have the same name, suffixes are added to disambiguate. If `keep` = TRUE and key columns in x and y have the same name, suffixes are added to disambiguate these as well.

- If `keep` = FALSE, output columns included in by are coerced to their common type between x and y.
Many-to-many relationships

By default, dplyr guards against many-to-many relationships in equality joins by throwing a warning. These occur when both of the following are true:

- A row in x matches multiple rows in y.
- A row in y matches multiple rows in x.

This is typically surprising, as most joins involve a relationship of one-to-one, one-to-many, or many-to-one, and is often the result of an improperly specified join. Many-to-many relationships are particularly problematic because they can result in a Cartesian explosion of the number of rows returned from the join.

If a many-to-many relationship is expected, silence this warning by explicitly setting relationship = "many-to-many".

In production code, it is best to preemptively set relationship to whatever relationship you expect to exist between the keys of x and y, as this forces an error to occur immediately if the data doesn't align with your expectations.

Inequality joins typically result in many-to-many relationships by nature, so they don't warn on them by default, but you should still take extra care when specifying an inequality join, because they also have the capability to return a large number of rows.

Rolling joins don't warn on many-to-many relationships either, but many rolling joins follow a many-to-one relationship, so it is often useful to set relationship = "many-to-one" to enforce this.

Note that in SQL, most database providers won't let you specify a many-to-many relationship between two tables, instead requiring that you create a third junction table that results in two one-to-many relationships instead.

Methods

These functions are generics, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

Methods available in currently loaded packages:

- inner_join(): no methods found.
- left_join(): no methods found.
- right_join(): no methods found.
- full_join(): no methods found.

See Also

Other joins: cross_join(), filter-joins, nest_join()
Examples

data(pasilla)

tt <- pasilla
tt |> right_join(tt |>
  distinct(condition) |>
  mutate(new_column=1:2) |>
  slice(1))

Description

rowwise() allows you to compute on a data frame a row-at-a-time. This is most useful when a vectorised function doesn’t exist.

Most dplyr verbs preserve row-wise grouping. The exception is summarise(), which return a grouped_df. You can explicitly ungroup with ungroup() or as_tibble(), or convert to a grouped_df with group_by().

Usage

## S3 method for class 'SummarizedExperiment'
rowwise(data, ...)

Arguments

  data Input data frame.

  ... <tidy-select> Variables to be preserved when calling summarise(). This is typically a set of variables whose combination uniquely identify each row.

  NB: unlike group_by() you can not create new variables here but instead you can select multiple variables with (e.g.) everything().

Value

A row-wise data frame with class rowwise_df. Note that a rowwise_df is implicitly grouped by row, but is not a grouped_df.

List-columns

Because a rowwise has exactly one row per group it offers a small convenience for working with list-columns. Normally, summarise() and mutate() extract a groups worth of data with [. But when you index a list in this way, you get back another list. When you’re working with a rowwise tibble, then dplyr will use [[ instead of [ to make your life a little easier.
sample_n

See Also

`nest_by()` for a convenient way of creating rowwise data frames with nested data.

Examples

# TODO

---

**sample_n**  
*Sample n rows from a table*

Description

[Superseded] `sample_n()` and `sample_frac()` have been superseded in favour of `slice_sample()`. While they will not be deprecated in the near future, retirement means that we will only perform critical bug fixes, so we recommend moving to the newer alternative.

These functions were superseded because we realised it was more convenient to have two mutually exclusive arguments to one function, rather than two separate functions. This also made it to clean up a few other smaller design issues with `sample_n()`/`sample_frac`:

- The connection to `slice()` was not obvious.
- The name of the first argument, `tbl`, is inconsistent with other single table verbs which use `.data`.
- The `size` argument uses tidy evaluation, which is surprising and undocumented.
- It was easier to remove the deprecated `.env` argument.
- ... was in a suboptimal position.

Usage

```r
## S3 method for class 'SummarizedExperiment'
sample_n(tbl, size, replace = FALSE, weight = NULL, .env = NULL, ...)

## S3 method for class 'SummarizedExperiment'
sample_frac(tbl, size = 1, replace = FALSE, weight = NULL, .env = NULL, ...)
```

Arguments

- `tbl`  
  A data.frame.
- `size`  
  `<tidy-select>` For `sample_n()`, the number of rows to select. For `sample_frac()`, the fraction of rows to select. If `tbl` is grouped, `size` applies to each group.
- `replace`  
  Sample with or without replacement?
- `weight`  
  `<tidy-select>` Sampling weights. This must evaluate to a vector of non-negative numbers the same length as the input. Weights are automatically standardised to sum to 1.
- `.env`  
  DEPRECATED.
- `...`  
  ignored
select

Value

tidySummarizedExperiment

Examples

data(pasilla)
pasilla |> sample_n(50)
pasilla |> sample_frac(0.1)

---

se

Read counts of RNA-seq samples derived from Pasilla knock-down by Brooks et al.

---

Description

A SummarizedExperiment dataset containing the transcriptome information for Drosophila Melanogaster.

Usage

data(se)

Format

containing 14599 features and 7 biological replicates.

Source


---

select

Keep or drop columns using their names and types

---

Description

Select (and optionally rename) variables in a data frame, using a concise mini-language that makes it easy to refer to variables based on their name (e.g. a:f selects all columns from a on the left to f on the right) or type (e.g. where(is.numeric) selects all numeric columns).

Overview of selection features:
Tidyverse selections implement a dialect of R where operators make it easy to select variables:

- : for selecting a range of consecutive variables.
- ! for taking the complement of a set of variables.
- & and | for selecting the intersection or the union of two sets of variables.
- c() for combining selections.
In addition, you can use **selection helpers**. Some helpers select specific columns:

- **everything()**: Matches all variables.
- **last_col()**: Select last variable, possibly with an offset.
- **group_cols()**: Select all grouping columns.

Other helpers select variables by matching patterns in their names:

- **starts_with()**: Starts with a prefix.
- **ends_with()**: Ends with a suffix.
- **contains()**: Contains a literal string.
- **matches()**: Matches a regular expression.
- **num_range()**: Matches a numerical range like x01, x02, x03.

Or from variables stored in a character vector:

- **all_of()**: Matches variable names in a character vector. All names must be present, otherwise an out-of-bounds error is thrown.
- **any_of()**: Same as all_of(), except that no error is thrown for names that don’t exist.

Or using a predicate function:

- **where()**: Applies a function to all variables and selects those for which the function returns TRUE.

**Usage**

```r
## S3 method for class 'SummarizedExperiment'
select(.data, ...)
```

**Arguments**

- `.data`: A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from dbplyr or dtplyr). See **Methods**, below, for more details.
- `...`: One or more unquoted expressions separated by commas. Variable names can be used as if they were positions in the data frame, so expressions like `x:y` can be used to select a range of variables.

**Value**

An object of the same type as `.data`. The output has the following properties:

- Rows are not affected.
- Output columns are a subset of input columns, potentially with a different order. Columns will be renamed if `new_name = old_name` form is used.
- Data frame attributes are preserved.
- Groups are maintained; you can’t select off grouping variables.

**Methods**

This function is a **generic**, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

The following methods are currently available in loaded packages: no methods found.
Examples

Here we show the usage for the basic selection operators. See the specific help pages to learn about helpers like starts_with().

The selection language can be used in functions like dplyr::select() or tidyr::pivot_longer(). Let’s first attach the tidyverse:

library(tidyverse)

# For better printing
iris <- as_tibble(iris)

Select variables by name:

starwars %>% select(height)
#> # A tibble: 87 x 1
#>    height
#>      <int>
#> 1      172
#> 2      167
#> 3       96
#> 4      202
#> # i 83 more rows

iris %>% pivot_longer(Sepal.Length)
#> # A tibble: 150 x 6
#>   Sepal.Width Petal.Length Petal.Width Species name   value
#>       <dbl>       <dbl>       <dbl> <fct>   <chr>   <dbl>
#> 1       3.5        1.4         0.2 setosa Sepal.Length 5.1
#> 2       3           1.4         0.2 setosa Sepal.Length 4.9
#> 3       3.2         1.3         0.2 setosa Sepal.Length 4.7
#> 4       3.1         1.5         0.2 setosa Sepal.Length 4.6
#> # i 146 more rows

Select multiple variables by separating them with commas. Note how the order of columns is determined by the order of inputs:

starwars %>% select(homeworld, height, mass)
#> # A tibble: 87 x 3
#>   homeworld height mass
#>      <chr> <int> <dbl>
#> 1    Tatooine 172  77
#> 2    Tatooine 167  75
#> 3    Naboo    96   32
#> 4    Tatooine 202 136
#> # i 83 more rows

Functions like tidyr::pivot_longer() don’t take variables with dots. In this case use c() to select multiple variables:
iris %>% pivot_longer(c(Sepal.Length, Petal.Length))
#> # A tibble: 300 x 5
#>   Sepal.Width Petal.Width Species name     value
#>       <dbl>     <dbl> <fct> <chr>     <dbl>
#> 1       3.5       0.2  setosa Sepal.Length 5.1
#> 2       3.5       0.2  setosa Petal.Length 1.4
#> 3        3        0.2  setosa Sepal.Length 4.9
#> 4        3        0.2  setosa Petal.Length 1.4
#> # i 296 more rows

**Operators:**

The : operator selects a range of consecutive variables:

starwars %>% select(name:mass)
#> # A tibble: 87 x 3
#>   name     height mass
#>   <chr>    <int> <dbl>
#> 1 Luke Skywalker 172   77
#> 2 C-3PO        167   75
#> 3 R2-D2         96   32
#> 4 Darth Vader  202  136
#> # i 83 more rows

The ! operator negates a selection:

starwars %>% select(!(name:mass))
#> # A tibble: 87 x 11
#>    hair_color skin_color eye_color birth_year sex gender homeworld species
#> <chr>        <chr>      <chr>         <dbl> <chr>   <chr>      <chr>     <chr>
#> 1 blond       fair       blue           19 male masculine Tatooine Human
#> 2 <NA>        gold       yellow         112 none masculine Tatooine Droid
#> 3 <NA>        white, blue red            33 none masculine Naboo Droid
#> 4 none        white       yellow         41.9 male masculine Tatooine Human
#> # i 83 more rows
#> # i 3 more variables: films <list>, vehicles <list>, starships <list>

iris %>% select(!c(Sepal.Length, Petal.Length))
#> # A tibble: 150 x 3
#>   Sepal.Width Petal.Width Species
#>       <dbl>     <dbl> <fct>
#> 1       3.5       0.2  setosa
#> 2        3        0.2  setosa
#> 3        3.2       0.2  setosa
#> 4        3.1       0.2  setosa
#> # i 146 more rows

iris %>% select(lends_with("Width"))
#> # A tibble: 150 x 3
#>   Sepal.Length Petal.Length Species
#>       <dbl>     <dbl> <fct>
# select

```r
#> 1  5.1  1.4 setosa
#> 2  4.9  1.4 setosa
#> 3  4.7  1.3 setosa
#> 4  4.6  1.5 setosa
#> # i 146 more rows
```

& and | take the intersection or the union of two selections:

```r
inger %>% select(starts_with("Petal") & ends_with("Width"))
#> # A tibble: 150 x 1
#> Petal.Width
#> <dbl>
#> 1 0.2
#> 2 0.2
#> 3 0.2
#> 4 0.2
#> # i 146 more rows

nger %>% select(starts_with("Petal") | ends_with("Width"))
#> # A tibble: 150 x 3
#> Petal.Length Petal.Width Sepal.Width
#> <dbl> <dbl> <dbl>
#> 1  1.4  0.2  3.5
#> 2  1.4  0.2  3.0
#> 3  1.3  0.2  3.2
#> 4  1.5  0.2  3.1
#> # i 146 more rows
```

To take the difference between two selections, combine the & and ! operators:

```r
nger %>% select(starts_with("Petal") & !ends_with("Width"))
#> # A tibble: 150 x 1
#> Petal.Length
#> <dbl>
#> 1 1.4
#> 2 1.4
#> 3 1.3
#> 4 1.5
#> # i 146 more rows
```

See Also

Other single table verbs: `arrange()`, `filter()`, `mutate()`, `reframe()`, `rename()`, `slice()`, `summarise()`

Examples

data(pasilla)
pasilla | select(.sample, .feature, counts)
separate

Separate a character column into multiple columns with a regular expression or numeric locations

Description

[Superseded]

`separate()` has been superseded in favour of `separate_wider_position()` and `separate_wider_delim()` because the two functions make the two uses more obvious, the API is more polished, and the handling of problems is better. Superseded functions will not go away, but will only receive critical bug fixes.

Given either a regular expression or a vector of character positions, `separate()` turns a single character column into multiple columns.

Usage

```r
## S3 method for class 'SummarizedExperiment'
separate(
  data, 
  col, 
  into, 
  sep = "[^[:alnum:]]+", 
  remove = TRUE, 
  convert = FALSE, 
  extra = "warn", 
  fill = "warn", 
  ... 
)
```

Arguments

data A data frame.

col <tidy-select> Column to expand.

into Names of new variables to create as character vector. Use NA to omit the variable in the output.

sep Separator between columns.

If character, sep is interpreted as a regular expression. The default value is a regular expression that matches any sequence of non-alphanumeric values.

If numeric, sep is interpreted as character positions to split at. Positive values start at 1 at the far-left of the string; negative value start at -1 at the far-right of the string. The length of sep should be one less than into.

remove If TRUE, remove input column from output data frame.

convert If TRUE, will run `type.convert()` with as.is = TRUE on new columns. This is useful if the component columns are integer, numeric or logical.

NB: this will cause string "NA"s to be converted to NAs.
extra

If sep is a character vector, this controls what happens when there are too many pieces. There are three valid options:

- "warn" (the default): emit a warning and drop extra values.
- "drop": drop any extra values without a warning.
- "merge": only splits at most length(into) times

fill

If sep is a character vector, this controls what happens when there are not enough pieces. There are three valid options:

- "warn" (the default): emit a warning and fill from the right
- "right": fill with missing values on the right
- "left": fill with missing values on the left

Value

tidySummarizedExperiment

See Also

unite(), the complement, extract() which uses regular expression capturing groups.

Examples

un <- tidySummarizedExperiment::pasilla |> unite("group", c(condition, type))
un |> separate(col=group, into=c("condition", "type"))

Description
	slice() lets you index rows by their (integer) locations. It allows you to select, remove, and duplicate rows. It is accompanied by a number of helpers for common use cases:

- slice_head() and slice_tail() select the first or last rows.
- slice_sample() randomly selects rows.
- slice_min() and slice_max() select rows with the smallest or largest values of a variable.

If .data is a grouped_df, the operation will be performed on each group, so that (e.g.) slice_head(df, n = 5) will select the first five rows in each group.

Usage

## S3 method for class 'SummarizedExperiment'
slice(.data, ..., .preserve = FALSE)
Arguments

.data A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from dbplyr or dtplyr). See Methods, below, for more details.

... For slice(): <data-masking> Integer row values.

Provide either positive values to keep, or negative values to drop. The values provided must be either all positive or all negative. Indices beyond the number of rows in the input are silently ignored.

For slice_*(), these arguments are passed on to methods.

.preserve Relevant when the .data input is grouped. If .preserve = FALSE (the default), the grouping structure is recalculated based on the resulting data, otherwise the grouping is kept as is.

Details

Slice does not work with relational databases because they have no intrinsic notion of row order. If you want to perform the equivalent operation, use filter() and row_number().

Value

An object of the same type as .data. The output has the following properties:

- Each row may appear 0, 1, or many times in the output.
- Columns are not modified.
- Groups are not modified.
- Data frame attributes are preserved.

Methods

These function are generics, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

Methods available in currently loaded packages:

- slice(): no methods found.
- slice_head(): no methods found.
- slice_tail(): no methods found.
- slice_min(): no methods found.
- slice_max(): no methods found.
- slice_sample(): no methods found.

See Also

Other single table verbs: mutate(), rename(), summarise()
Examples

```r
data(pasilla)
pasilla |> slice(1)
```

---

**summarise**  
_Summarise each group down to one row_

**Description**

`summarise()` creates a new data frame. It returns one row for each combination of grouping variables; if there are no grouping variables, the output will have a single row summarising all observations in the input. It will contain one column for each grouping variable and one column for each of the summary statistics that you have specified. `summarise()` and `summarize()` are synonyms.

**Usage**

```r
## S3 method for class 'SummarizedExperiment'
summarise(.data, ...)

## S3 method for class 'SummarizedExperiment'
summarize(.data, ...)
```

**Arguments**

- `.data`  
  A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from dbplyr or dplyr). See _Methods_, below, for more details.

- `...`  
  `<data-masking>` Name-value pairs of summary functions. The name will be the name of the variable in the result. The value can be:
  - A vector of length 1, e.g. `min(x), n()`, or `sum(is.na(y))`.
  - A data frame, to add multiple columns from a single expression.

[Deprecated] Returning values with size 0 or >1 was deprecated as of 1.1.0. Please use `reframe()` for this instead.

**Value**

An object _usually_ of the same type as `.data`.

- The rows come from the underlying `group_keys()`.
- The columns are a combination of the grouping keys and the summary expressions that you provide.
- The grouping structure is controlled by the `.groups=` argument, the output may be another grouped_df, a tibble or a rowwise data frame.
- Data frame attributes are not preserved, because `summarise()` fundamentally creates a new data frame.
Useful functions

- Center: mean(), median()
- Spread: sd(), IQR(), mad()
- Range: min(), max().
- Position: first(), last(), nth().
- Count: n(), n_distinct()
- Logical: any(), all()

Backend variations

The data frame backend supports creating a variable and using it in the same summary. This means that previously created summary variables can be further transformed or combined within the summary, as in mutate(). However, it also means that summary variables with the same names as previous variables overwrite them, making those variables unavailable to later summary variables. This behaviour may not be supported in other backends. To avoid unexpected results, consider using new names for your summary variables, especially when creating multiple summaries.

Methods

This function is a generic, which means that packages can provide implementations (methods) for other classes. See the documentation of individual methods for extra arguments and differences in behaviour.

The following methods are currently available in loaded packages: no methods found.

See Also

Other single table verbs: mutate(), rename(), slice()

Examples

data(pasilla)
pasilla |> summarise(mean(counts))

Description

[Experimental]

For easier customization, the formatting of a tibble is split into three components: header, body, and footer. The tbl_format_header() method is responsible for formatting the header of a tibble. Override this method if you need to change the appearance of the entire header. If you only need to change or extend the components shown in the header, override or extend tbl_sum() for your class which is called by the default method.
## S3 method for class 'tidySummarizedExperiment'

```r
tbl_format_header(x, setup, ...)
```

### Arguments

- **x**: A tibble-like object.
- **setup**: A setup object returned from `tbl_format_setup()`.
- **...**: These dots are for future extensions and must be empty.

### Value

A character vector.

### Examples

```r
# TODO
```

---

**Description**

`tidySeurat` for Seurat

### Usage

```r
 tidy(object)
```

### Arguments

- **object**: A `SummarizedExperiment` object

### Value

A `tidyseurat` object.

### Examples

```r
 data(pasilla)
pasilla %>% tidy()
```
unite

Unite multiple columns into one by pasting strings together

Description

Convenience function to paste together multiple columns into one.

Usage

```r
## S3 method for class 'SummarizedExperiment'
unite(data, col, ..., sep = "_", remove = TRUE, na.rm = FALSE)
```

Arguments

- **data**: A data frame.
- **col**: The name of the new column, as a string or symbol. This argument is passed by expression and supports quasiquotation (you can unquote strings and symbols). The name is captured from the expression with `rlang::ensym()` (note that this kind of interface where symbols do not represent actual objects is now discouraged in the tidyverse; we support it here for backward compatibility).
- **...**: `<tidy-select>` Columns to unite
- **sep**: Separator to use between values.
- **remove**: If TRUE, remove input columns from output data frame.
- **na.rm**: If TRUE, missing values will be removed prior to uniting each value.

Value

`tidySummarizedExperiment`

See Also

- `separate()`, the complement.

Examples

```r
tidySummarizedExperiment::pasilla |> 
  unite("group", c(condition, type))
```
unnest

Unnest a list-column of data frames into rows and columns

Description

Unnest expands a list-column containing data frames into rows and columns.

Usage

```r
## S3 method for class 'tidySummarizedExperiment_nested'
unnest(
data,
cols,
..., 
keep_empty = FALSE,
ptype = NULL,
names_sep = NULL,
names_repair = "check_unique",
.drop,
.id,
.sep,
.preserve
)
```

```r
unnest_summarized_experiment(
data,
cols,
..., 
keep_empty = FALSE,
ptype = NULL,
names_sep = NULL,
names_repair = "check_unique",
.drop,
.id,
.sep,
.preserve
)
```

Arguments

data A data frame.
cols <tidy-select> List-columns to unnest.

When selecting multiple columns, values from the same row will be recycled to their common size.

... [Deprecated]: previously you could write `df %>% unnest(x, y, z)`. Convert to `df %>% unnest(c(x, y, z))`. If you previously created a new variable in
unnest() you’ll now need to do it explicitly with mutate(). Convert df %>% unnest(y = fun(x, y, z)) to df %>% mutate(y = fun(x, y, z)) %>% unnest(y).

keep_empty
By default, you get one row of output for each element of the list that you are unchopping/unnesting. This means that if there’s a size-0 element (like NULL or an empty data frame or vector), then 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.

ptype
Optionally, a named list of column name-prototype pairs to coerce cols to, overriding the default that will be guessed from combining the individual values. Alternatively, a single empty ptype can be supplied, which will be applied to all cols.

names_sep
If NULL, the default, the outer names will come from the inner names. If a string, the outer names will be formed by pasting together the outer and the inner column names, separated by names_sep.

names_repair
Used to check that output data frame has valid names. Must be one of the following options:
- "minimal": no name repair or checks, beyond basic existence,
- "unique": make sure names are unique and not empty,
- "check_unique": (the default), no name repair, but check they are unique,
- "universal": make the names unique and syntactic
- a function: apply custom name repair.
- tidyr_legacy: use the name repair from tidyr 0.8.
- a formula: a purrr-style anonymous function (see rlang::as_function())
See vctrs::vec_as_names() for more details on these terms and the strategies used to enforce them.

.drop, .preserve
[Deprecated]: all list-columns are now preserved; If there are any that you don’t want in the output use select() to remove them prior to unnesting.

.id
[Deprecated]: convert df %>% unnest(x, .id = "id") to df %>% mutate(id = names(x)) %>% unnest(x)

.sep
[Deprecated]: use names_sep instead.

Value
tidySummarizedExperiment

New syntax
tidyr 1.0.0 introduced a new syntax for nest() and unnest() that’s designed to be more similar to other functions. Converting to the new syntax should be straightforward (guided by the message you’ll receive) but if you just need to run an old analysis, you can easily revert to the previous behaviour using nest_legacy() and unnest_legacy() as follows:

library(tidyrr)
nest <- nest_legacy
unnest <- unnest_legacy
See Also

Other rectangling: hoist(), unnest_longer(), unnest_wider()

Examples

```r
library(tidySummarizedExperiment)
tidySummarizedExperiment::pasilla |> nest(data=-condition) |> unnest(data)
tidySummarizedExperiment::pasilla |> nest(data=-condition) |> unnest_summarized_experiment(data)
```

Description

See magrittr::%>% for details.

Usage

```r
lhs %>% rhs
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>lhs</td>
<td>A value or the magrittr placeholder.</td>
</tr>
<tr>
<td>rhs</td>
<td>A function call using the magrittr semantics.</td>
</tr>
</tbody>
</table>

Value

The result of calling rhs(lhs).

Examples

```r
library(magrittr)
1 %>% sum(2)
```
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