

# Package ‘tidySingleCellExperiment’

May 18, 2024

**Type** Package

**Title** Brings SingleCellExperiment to the Tidyverse

**Version** 1.14.0

**Description** 'tidySingleCellExperiment' is an adapter that abstracts the 'SingleCellExperiment' container in the form of a 'tibble'. This allows \*tidy\* data manipulation, nesting, and plotting. For example, a 'tidySingleCellExperiment' is directly compatible with functions from 'tidyverse' packages `dplyr` and `tidyr`, as well as plotting with `ggplot2` and `plotly`. In addition, the package provides various utility functions specific to single-cell omics data analysis (e.g., aggregation of cell-level data to pseudobulks).

**License** GPL-3

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---

|                  |                            |
|------------------|----------------------------|
| <i>add_class</i> | <i>Add class to object</i> |
|------------------|----------------------------|

---

**Description**

Add class to object

**Usage**

`add_class(var, name)`

**Arguments**

|                   |                                   |
|-------------------|-----------------------------------|
| <code>var</code>  | A tibble                          |
| <code>name</code> | A character name of the attribute |

**Value**

A tibble with an additional attribute

---

|                        |                        |
|------------------------|------------------------|
| <i>aggregate_cells</i> | <i>Aggregate cells</i> |
|------------------------|------------------------|

---

**Description**

Combine cells into groups based on shared variables and aggregate feature counts.

**Usage**

```
## S4 method for signature 'SingleCellExperiment'
aggregate_cells(
  .data,
  .sample = NULL,
  slot = "data",
  assays = NULL,
  aggregation_function = Matrix::rowSums,
  ...
)
```

**Arguments**

|                                   |   |
|-----------------------------------|---|
| <code>.data</code>                | A <code>tidySingleCellExperiment</code> object      |
| <code>.sample</code>              | A vector of variables by which cells are aggregated |
| <code>slot</code>                 | The slot to which the function is applied           |
| <code>assays</code>               | The assay to which the function is applied          |
| <code>aggregation_function</code> | The method of cell-feature value aggregation        |
| <code>...</code>                  | Used for future extensibility                       |

**Value**

A tibble object

**Examples**

```
data(pbmc_small)
pbmc_small_pseudo_bulk <- pbmc_small |>
  aggregate_cells(c(groups, ident), assays="counts")
```

---

arrange

*Order rows using column values*

---

**Description**

`arrange()` orders the rows of a data frame by the values of selected columns.

Unlike other dplyr verbs, `arrange()` largely ignores grouping; you need to explicitly mention grouping variables (or use `.by_group = TRUE`) in order to group by them, and functions of variables are evaluated once per data frame, not once per group.

**Usage**

```
## S3 method for class 'SingleCellExperiment'
arrange(.data, ..., .by_group = FALSE)
```

## Arguments

|                        |   |
|------------------------|---|
| <code>.data</code>     | A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from <code>dbplyr</code> or <code>dtplyr</code> ). See <i>Methods</i> , below, for more details. |
| <code>...</code>       | <code>&lt;data-masking&gt;</code> Variables, or functions of variables. Use <code>desc()</code> to sort a variable in descending order.   |
| <code>.by_group</code> | If TRUE, will sort first by grouping variable. Applies to grouped data frames only.   |

## Details

### Missing values:

Unlike base sorting with `sort()`, NA are:

- always sorted to the end for local data, even when wrapped with `desc()`.
- treated differently for remote data, depending on the backend.

## Value

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

- All rows appear in the output, but (usually) in a different place.
- Columns are not modified.
- 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.

## See Also

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

## Examples

```
data(pbmc_small)
pbmc_small |>
  arrange(nFeature_RNA)
```

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 'SingleCellExperiment'
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: <ul style="list-style-type: none"> <li>• "minimal": No name repair or checks, beyond basic existence,</li> <li>• "unique": Make sure names are unique and not empty,</li> <li>• "check_unique": (default value), no name repair, but check they are unique,</li> <li>• "universal": Make the names unique and syntactic</li> <li>• a function: apply custom name repair (e.g., <code>.name_repair = make.names</code> for names in the style of base R).</li> <li>• A purrr-style anonymous function, see <code>rlang::as_function()</code></li> </ul> |

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

```
data(pbm_small)
pbm_small |> as_tibble()
```

---

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**

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

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

**Arguments**

|                           |  |
|---------------------------|--|
| <code>...</code>          | Data frames to combine.<br>Each argument can either be a data frame, a list that could be a data frame, or a list of data frames.<br>When row-binding, columns are matched by name, and any missing columns will be filled with NA.<br>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 <code>mutate_joins</code> . |
| <code>.id</code>          | Data frame identifier.<br>When <code>.id</code> 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 <code>'bind_rows()'</code> . 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.                                |
| <code>add.cell.ids</code> | from Seurat 3.0 A character vector of length( $x = c(x, y)$ ). Appends the corresponding values to the start of each objects' cell names.  |

**Details**

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

The output of `'bind_cols()'` 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(pbmc_small)
tt <- pbmc_small
bind_rows(tt, tt)

tt_bind <- tt |> select(nCount_RNA, nFeature_RNA)
tt |> bind_cols(tt_bind)
```



---

|              |   |
|--------------|---|
| cell_type_df | <i>Cell types of 80 PBMC single cells</i> |
|--------------|---|

---

### Description

A dataset containing the barcodes and cell types of 80 PBMC single cells.

### Usage

```
data(cell_type_df)
```

### Format

A tibble containing 80 rows and 2 columns. Cells are a subsample of the Peripheral Blood Mononuclear Cells (PBMC) dataset of 2,700 single cell. Cell types were identified with SingleR.

**cell** cell identifier, barcode

**first.labels** cell type

### Value

‘tibble‘

### Source

[https://satijalab.org/seurat/v3.1/pbmc3k\\_tutorial.html](https://satijalab.org/seurat/v3.1/pbmc3k_tutorial.html)

---

|       |   |
|-------|---|
| count | <i>Count the observations in each group</i> |
|-------|---|

---

### 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**

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

## S3 method for class 'SingleCellExperiment'
add_count(x, ..., wt = NULL, sort = FALSE, name = NULL)
```

**Arguments**

|       |  |
|-------|--|
| x     | A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from dbplyr or dtplyr).   |
| ...   | <data-masking> Variables to group by.  |
| wt    | <data-masking> Frequency weights. Can be NULL or a variable: <ul style="list-style-type: none"> <li>• If NULL (the default), counts the number of rows in each group.</li> <li>• If a variable, computes <code>sum(wt)</code> for each group.</li> </ul>   |
| sort  | If TRUE, will show the largest groups at the top.  |
| name  | The name of the new column in the output.<br>If omitted, it will default to <code>n</code> . If there's already a column called <code>n</code> , it will use <code>nn</code> . If there's a column called <code>n</code> and <code>nn</code> , it'll use <code>nnn</code> , and so on, adding <code>ns</code> until it gets a new name.            |
| .drop | Handling of factor levels that don't appear in the data, passed on to <code>group_by()</code> .<br>For <code>count()</code> : if FALSE will include counts for empty groups (i.e. for levels of factors that don't exist in the data).<br><b>[Deprecated]</b> For <code>add_count()</code> : 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(pbmc_small)
pbmc_small |> count(groups)
```

---

|          |                                  |
|----------|----------------------------------|
| distinct | <i>Keep distinct/unique rows</i> |
|----------|----------------------------------|

---

### Description

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

### Usage

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

### Arguments

|                        |   |
|------------------------|---|
| <code>.data</code>     | A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from <code>dbplyr</code> or <code>dtplyr</code> ). See <i>Methods</i> , below, for more details.   |
| <code>...</code>       | <data-masking> 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. |
| <code>.keep_all</code> | If TRUE, keep all variables in <code>.data</code> . If a combination of <code>...</code> 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(pbmc_small)  
pbmc_small |> distinct(groups)
```

---

|            |                               |
|------------|-------------------------------|
| drop_class | <i>Remove class to abject</i> |
|------------|-------------------------------|

---

**Description**

Remove class to abject

**Usage**

```
drop_class(var, name)
```

**Arguments**

|      |                               |
|------|-------------------------------|
| var  | A tibble                      |
| name | A character name of the class |

**Value**

A tibble with an additional attribute

---

|         |   |
|---------|---|
| extract | <i>Extract a character column into multiple columns using regular expression groups</i> |
|---------|---|

---

**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 'SingleCellExperiment'
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 <code>type.convert()</code> with <code>as.is = TRUE</code> on new columns. This is useful if the component columns are integer, numeric or logical.<br>NB: this will cause string "NA"s to be converted to NAs. |
| ...     | Additional arguments passed on to methods.  |

**Value**

'tidySingleCellExperiment'

**See Also**

[separate\(\)](#) to split up by a separator.

**Examples**

```
data(pbmc_small)
pbmc_small |>
  extract(groups,
    into="g",
    regex="g([0-9])",
    convert=TRUE)
```

---

filter

*Keep rows that match a condition*

---

**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**

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

**Arguments**

|                        |  |
|------------------------|--|
| <code>.data</code>     | A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from <code>dbplyr</code> or <code>dtplyr</code> ). See <i>Methods</i> , below, for more details.  |
| <code>...</code>       | <data-masking> Expressions that return a logical value, and are defined in terms of the variables in <code>.data</code> . If multiple expressions are included, they are combined with the <code>&amp;</code> operator. Only rows for which all conditions evaluate to <code>TRUE</code> are kept. |
| <code>.preserve</code> | Relevant when the <code>.data</code> input is grouped. If <code>.preserve = FALSE</code> (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(pbm_small)
pbm_small |> filter(groups == "g1")

# Learn more in ?dplyr_tidy_eval
```

---

formatting

*Printing tibbles*

---

## Description

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**

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

**Arguments**

|       |   |
|-------|---|
| x     | Object to format or print.  |
| ...   | Passed on to <code>tbl_format_setup()</code> .  |
| n     | Number of rows to show. If NULL, the default, will print all rows if less than the <code>print_max</code> option. Otherwise, will print as many rows as specified by the <code>print_min</code> option. |
| width | Width of text output to generate. This defaults to NULL, which means use the <code>width</code> option.   |

**Value**

Prints a message to the console describing the contents of the ‘tidySingleCellExperiment’.

**Examples**

```
data(pbmc_small)
print(pbmc_small)
```

---

full\_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**

```
## S3 method for class 'SingleCellExperiment'
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 <i>Methods</i> , below, for more details.  |
| by     | A join specification created with <code>join_by()</code> , or a character vector of variables to join by.<br>If NULL, the default, <code>*_join()</code> 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.<br>To join on different variables between x and y, use a <code>join_by()</code> specification. For example, <code>join_by(a == b)</code> will match x\$a to y\$b.<br>To join by multiple variables, use a <code>join_by()</code> specification with multiple expressions. For example, <code>join_by(a == b, c == d)</code> 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 <code>join_by(a, c)</code> .<br><code>join_by()</code> can also be used to perform inequality, rolling, and overlap joins. See the documentation at <a href="#">?join_by</a> for details on these types of joins.<br>For simple equality joins, you can alternatively specify a character vector of variable names to join by. For example, <code>by = c("a", "b")</code> 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 <code>by = c("x_a" = "y_a", "x_b" = "y_b")</code> .<br>To perform a cross-join, generating all combinations of x and y, see <code>cross_join()</code> . |
| 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**

```
data(pbmc_small)
tt <- pbmc_small
tt |> full_join(tibble::tibble(groups="g1", other=1:4))
```

---

**ggplot***Create a new ggplot from a tidySingleCellExperiment*

---

**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**

```
## S3 method for class 'SingleCellExperiment'
ggplot(data = NULL, mapping = aes(), ..., environment = parent.frame())
```

**Arguments**

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

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(pbmc_small)
pbmc_small |>
  ggplot(aes(groups, nCount_RNA)) +
  geom_boxplot()
```

---

glimpse

*Get a glimpse of your data*

---

### Description

`glimpse()` is like a transposed version of `print()`: columns run down the page, and data runs across. This makes it possible to see every column in a data frame. It's a little like `str()` applied to a data frame but it tries to show you as much data as possible. (And it always shows the underlying data, even when applied to a remote data source.)

See `format_glimpse()` for details on the formatting.

### Usage

```
## S3 method for class 'tidySingleCellExperiment'
glimpse(x, width = NULL, ...)
```

### Arguments

|                    |  |
|--------------------|--|
| <code>x</code>     | An object to glimpse at.   |
| <code>width</code> | Width of output: defaults to the setting of the <code>width</code> option (if finite) or the width of the console. |
| <code>...</code>   | Unused, for extensibility.   |

### Value

`x` original `x` is (invisibly) returned, allowing `glimpse()` to be used within a data pipe line.

**S3 methods**

glimpse is an S3 generic with a customised method for tbls and data.frames, and a default method that calls `str()`.

**Examples**

```
data(pbmc_small)
pbmc_small |> glimpse()
```

---

|          |                                       |
|----------|---------------------------------------|
| group_by | <i>Group by one or more variables</i> |
|----------|---------------------------------------|

---

**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 'SingleCellExperiment'
group_by(.data, ..., .add = FALSE, .drop = group_by_drop_default(.data))
```

**Arguments**

|                    |   |
|--------------------|---|
| <code>.data</code> | A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from <code>dbplyr</code> or <code>dtplyr</code> ). See <i>Methods</i> , below, for more details.   |
| <code>...</code>   | In <code>group_by()</code> , 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 <code>mutate()</code> step before the <code>group_by()</code> . Computations are not allowed in <code>nest_by()</code> . In <code>ungroup()</code> , variables to remove from the grouping. |
| <code>.add</code>  | When <code>FALSE</code> , the default, <code>group_by()</code> will override existing groups. To add to the existing groups, use <code>.add = TRUE</code> .<br>This argument was previously called <code>add</code> , but that prevented creating a new grouping variable called <code>add</code> , and conflicts with our naming conventions.  |
| <code>.drop</code> | Drop groups formed by factor levels that don't appear in the data? The default is <code>TRUE</code> except when <code>.data</code> has been previously grouped with <code>.drop = FALSE</code> . See <code>group_by_drop_default()</code> 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 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:

- `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:

```
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.

## Examples

```
data(pbmc_small)
pbmc_small |> group_by(groups)
```

---

`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 'SingleCellExperiment'  
group_split(.tbl, ..., .keep = TRUE)
```

## Arguments

|                    |   |
|--------------------|---|
| <code>.tbl</code>  | A tbl.  |
| <code>...</code>   | If <code>.tbl</code> is an ungrouped data frame, a grouping specification, forwarded to <code>group_by()</code> . |
| <code>.keep</code> | 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.

## See Also

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

**Examples**

```
data(pbmc_small)
pbmc_small |> group_split(groups)
```

---

 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**

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

**Arguments**

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



`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 <code>x</code> and <code>y</code> are not from the same data source, and <code>copy</code> is <code>TRUE</code> , then <code>y</code> will be copied into the same <code>src</code> as <code>x</code> . This allows you to join tables across <code>srcs</code> , but it is a potentially expensive operation so you must opt into it. |
| suffix | If there are non-joined duplicate variables in <code>x</code> and <code>y</code> , 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

```
data(pbmc_small)
tt <- pbmc_small
tt |> inner_join(tt |>
  distinct(groups) |>
  mutate(new_column=1:2) |>
  slice(1))
```

---

join\_features

*join\_features*

---

## Description

`join_features()` extracts and joins information for specific features

**Usage**

```
## S4 method for signature 'SingleCellExperiment'
join_features(
  .data,
  features = NULL,
  all = FALSE,
  exclude_zeros = FALSE,
  shape = "long",
  ...
)
```

**Arguments**

|               |  |
|---------------|--|
| .data         | A tidy SingleCellExperiment object   |
| features      | A vector of feature identifiers to join  |
| all           | If TRUE return all   |
| exclude_zeros | If TRUE exclude zero values  |
| shape         | Format of the returned table "long" or "wide"  |
| ...           | Parameters to pass to join wide, i.e. assay name to extract feature abundance from and gene prefix, for shape="wide" |

**Details**

This function extracts information for specified features and returns the information in either long or wide format.

**Value**

A ‘tidySingleCellExperiment’ object containing information for the specified features.

**Examples**

```
data(pbmc_small)
pbmc_small %>% join_features(
  features=c("HLA-DRA", "LYZ"))
```

---

join\_transcripts      *(DEPRECATED) Extract and join information for transcripts.*

---

**Description**

join\_transcripts() extracts and joins information for specified transcripts

**Usage**

```
join_transcripts(
  .data,
  transcripts = NULL,
  all = FALSE,
  exclude_zeros = FALSE,
  shape = "long",
  ...
)
```

**Arguments**

|               |   |
|---------------|---|
| .data         | A tidySingleCellExperiment object   |
| transcripts   | A vector of transcript identifiers to join  |
| all           | If TRUE return all  |
| exclude_zeros | If TRUE exclude zero values   |
| shape         | Format of the returned table "long" or "wide"   |
| ...           | Parameters to pass to join wide, i.e. assay name to extract transcript abundance from |

**Details**

DEPRECATED, please use join\_features()

**Value**

A 'tbl' containing the information for the specified transcripts

**Examples**

```
print("DEPRECATED")
```

---

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**

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

**Arguments**

|                     |   |
|---------------------|---|
| <code>x, y</code>   | A pair of data frames, data frame extensions (e.g. a tibble), or lazy data frames (e.g. from <code>dbplyr</code> or <code>dtplyr</code> ). See <i>Methods</i> , below, for more details.  |
| <code>by</code>     | <p>A join specification created with <code>join_by()</code>, or a character vector of variables to join by.</p> <p>If <code>NULL</code>, the default, <code>*_join()</code> will perform a natural join, using all variables in common across <code>x</code> and <code>y</code>. A message lists the variables so that you can check they're correct; suppress the message by supplying <code>by</code> explicitly.</p> <p>To join on different variables between <code>x</code> and <code>y</code>, use a <code>join_by()</code> specification. For example, <code>join_by(a == b)</code> will match <code>x\$a</code> to <code>y\$b</code>.</p> <p>To join by multiple variables, use a <code>join_by()</code> specification with multiple expressions. For example, <code>join_by(a == b, c == d)</code> will match <code>x\$a</code> to <code>y\$b</code> and <code>x\$c</code> to <code>y\$d</code>. If the column names are the same between <code>x</code> and <code>y</code>, you can shorten this by listing only the variable names, like <code>join_by(a, c)</code>.</p> <p><code>join_by()</code> can also be used to perform inequality, rolling, and overlap joins. See the documentation at <a href="#">?join_by</a> for details on these types of joins.</p> <p>For simple equality joins, you can alternatively specify a character vector of variable names to join by. For example, <code>by = c("a", "b")</code> joins <code>x\$a</code> to <code>y\$a</code> and <code>x\$b</code> to <code>y\$b</code>. If variable names differ between <code>x</code> and <code>y</code>, use a named character vector like <code>by = c("x_a" = "y_a", "x_b" = "y_b")</code>.</p> <p>To perform a cross-join, generating all combinations of <code>x</code> and <code>y</code>, see <code>cross_join()</code>.</p> |
| <code>copy</code>   | If <code>x</code> and <code>y</code> are not from the same data source, and <code>copy</code> is <code>TRUE</code> , then <code>y</code> will be copied into the same <code>src</code> as <code>x</code> . This allows you to join tables across <code>srcs</code> , but it is a potentially expensive operation so you must opt into it.   |
| <code>suffix</code> | If there are non-joined duplicate variables in <code>x</code> and <code>y</code> , these suffixes will be added to the output to disambiguate them. Should be a character vector of length 2.   |
| <code>...</code>    | 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

```
data(pbmc_small)
tt <- pbmc_small
tt |> left_join(tt |>
  distinct(groups) |>
  mutate(new_column=1:2))

library(S4Vectors)
# y can be S4 DataFrame for *_join, though not tested on list columns
DF <- tt |>
  distinct(groups) |>
  mutate(new_column=1:2) |> DataFrame()
tt |> left_join(DF)
```

---

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

```
## S3 method for class 'SingleCellExperiment'
mutate(.data, ...)
```

### Arguments

|                    |  |
|--------------------|--|
| <code>.data</code> | A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from <code>dbplyr</code> or <code>dtplyr</code> ). See <i>Methods</i> , below, for more details.  |
| <code>...</code>   | <a href="#">&lt;data-masking&gt;</a> Name-value pairs. The name gives the name of the column in the output.<br>The value can be: <ul style="list-style-type: none"> <li>• A vector of length 1, which will be recycled to the correct length.</li> <li>• A vector the same length as the current group (or the whole data frame if ungrouped).</li> <li>• <code>NULL</code>, to remove the column.</li> <li>• A data frame or tibble, to create multiple columns in the output.</li> </ul> |

**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:

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

With the grouped equivalent:

```
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: [arrange\(\)](#), [rename\(\)](#), [slice\(\)](#), [summarise\(\)](#)

**Examples**

```
data(pbmc_small)
pbmc_small |> mutate(nFeature_RNA=1)
```

---

 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**

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

**Arguments**

|                         |   |
|-------------------------|---|
| <code>.data</code>      | A data frame.   |
| <code>...</code>        | <p><code>&lt;tidy-select&gt;</code> Columns to nest; these will appear in the inner data frames.</p> <p>Specified using name-variable pairs of the form <code>new_col = c(col1, col2, col3)</code>. The right hand side can be any valid tidyselect expression.</p> <p>If not supplied, then <code>...</code> is derived as all columns <i>not</i> selected by <code>.by</code>, and will use the column name from <code>.key</code>.</p> <p><b>[Deprecated]:</b> previously you could write <code>df %&gt;% nest(x, y, z)</code>. Convert to <code>df %&gt;% nest(data = c(x, y, z))</code>.</p> |
| <code>.names_sep</code> | <p>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 <code>names_sep</code> automatically stripped. This makes <code>names_sep</code> roughly symmetric between nesting and unnesting.</p>  |

**Details**

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

**Value**

'tidySingleCellExperiment\_nested'

**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(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**

```
data(pbmc_small)
pbmc_small |>
  nest(data=-groups) |>
  unnest(data)
```

---

pbmc\_small

*pbmc\_small*

---

**Description**

PBMC single cell RNA-seq data in 'SingleCellExperiment' format.

**Usage**

```
data(pbmc_small)
```

**Format**

A ‘SingleCellExperiment’ object containing 80 Peripheral Blood Mononuclear Cells (PBMC) from 10x Genomics. Generated by subsampling the PBMC dataset of 2,700 single cells.

**Value**

‘tidySingleCellExperiment’

**Source**

[https://satijalab.org/seurat/v3.1/pbmc3k\\_tutorial.html](https://satijalab.org/seurat/v3.1/pbmc3k_tutorial.html)

---

pbmc\_small\_nested\_interactions

*Intercellular ligand-receptor interactions for 38 ligands from a single cell RNA-seq cluster.*

---

**Description**

A dataset containing ligand-receptor interactions within a sample. There are 38 ligands from a single cell cluster versus 35 receptors in 6 other clusters.

**Usage**

```
data(pbmc_small_nested_interactions)
```

**Format**

A ‘tibble’ containing 100 rows and 9 columns. Cells are a subsample of the PBMC dataset of 2,700 single cells. Cell interactions were identified with ‘SingleCellSignalR’.

**sample** sample identifier

**ligand** cluster and ligand identifier

**receptor** cluster and receptor identifier

**ligand.name** ligand name

**receptor.name** receptor name

**origin** cluster containing ligand

**destination** cluster containing receptor

**interaction.type** type of interaction, paracrine or autocrine

**LRscore** interaction score

**Value**

‘tibble’

**Source**

[https://satijalab.org/seurat/v3.1/pbmc3k\\_tutorial.html](https://satijalab.org/seurat/v3.1/pbmc3k_tutorial.html)

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**

```
## S3 method for class 'SingleCellExperiment'
pivot_longer(
  data,
  cols,
  ...,
  cols_vary = "fastest",
  names_to = "name",
  names_prefix = NULL,
  names_sep = NULL,
  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      | <a href="#">&lt;tidy-select&gt;</a> 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? <ul style="list-style-type: none"> <li>• "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.</li> <li>• "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.</li> </ul> |
| 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()` or `numeric()`) 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

'tidySingleCellExperiment'

### Examples

```
data(pbmc_small)
pbmc_small |> pivot_longer(
  cols=c(orig.ident, groups),
  names_to="name", values_to="value")
```

---

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 `ggplot2::qplot()`).

### Usage

```
## S3 method for class 'SingleCellExperiment'
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"
)

```

## Arguments

|              |  |
|--------------|--|
| data         | A data frame (optional) or <a href="#">crosstalk::SharedData</a> object.   |
| ...          | Arguments (i.e., attributes) passed along to the trace type. See <a href="#">schema()</a> for a list of acceptable attributes for a given trace type (by going to <code>traces -&gt; type -&gt; attributes</code> ). Note that attributes provided at this level may override other arguments (e.g. <code>plot_ly(x = 1:10, y = 1:10, color = I("red"), marker = list(color = "blue"))</code> ).   |
| type         | A character string specifying the trace type (e.g. "scatter", "bar", "box", etc). If specified, it <i>always</i> 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 <code>split</code> in that it creates one trace for every unique value.   |
| color        | Values mapped to relevant 'fill-color' attribute(s) (e.g. <code>fillcolor</code> , <code>marker.color</code> , <code>textfont.color</code> , etc.). The mapping from data values to color codes may be controlled using <code>colors</code> and <code>alpha</code> , or avoided altogether via <code>I()</code> (e.g., <code>color = I("red")</code> ). Any color understood by <code>grDevices::col2rgb()</code> may be used in this way. |
| colors       | Either a <a href="#">colorbrewer2.org</a> palette name (e.g. "YlOrRd" or "Blues"), or a vector of colors to interpolate in hexadecimal "#RRGGBB" format, or a color interpolation function like <code>colorRamp()</code> .   |
| alpha        | A number between 0 and 1 specifying the alpha channel applied to color. Defaults to 0.5 when mapping to <code>fillcolor</code> and 1 otherwise.  |
| stroke       | Similar to <code>color</code> , but values are mapped to relevant 'stroke-color' attribute(s) (e.g., <code>marker.line.color</code> and <code>line.color</code> for filled polygons). If not specified, stroke inherits from <code>color</code> .  |
| strokes      | Similar to <code>colors</code> , but controls the stroke mapping.  |
| alpha_stroke | Similar to <code>alpha</code> , but applied to stroke.   |
| size         | (Numeric) values mapped to relevant 'fill-size' attribute(s) (e.g., <code>marker.size</code> , <code>textfont.size</code> , and <code>error_x.width</code> ). The mapping from data values to symbols may be controlled using <code>sizes</code> , or avoided altogether via <code>I()</code> (e.g., <code>size = I(30)</code> ).  |

|           |  |
|-----------|--|
| 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., <code>marker.line.width</code> , <code>line.width</code> for filled polygons, and <code>error_x.thickness</code> ) The mapping from data values to symbols may be controlled using spans, or avoided altogether via <code>I()</code> (e.g., <code>span = I(30)</code> ). |
| spans     | A numeric vector of length 2 used to scale span to pixels.   |
| symbol    | (Discrete) values mapped to <code>marker.symbol</code> . The mapping from data values to symbols may be controlled using symbols, or avoided altogether via <code>I()</code> (e.g., <code>symbol = I("pentagon")</code> ). Any <code>pch</code> value or <code>symbol name</code> may be used in this way.                                     |
| symbols   | A character vector of <code>pch</code> values or <code>symbol names</code> .   |
| linetype  | (Discrete) values mapped to <code>line.dash</code> . The mapping from data values to symbols may be controlled using linetypes, or avoided altogether via <code>I()</code> (e.g., <code>linetype = I("dash")</code> ). Any <code>lty</code> (see <code>par</code> ) value or <code>dash name</code> may be used in this way.                   |
| linetypes | A character vector of <code>lty</code> values or <code>dash names</code>   |
| 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 <code>event_data()</code> 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'

## 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**

```
data(pbmc_small)
pbmc_small |>
  plot_ly(x = ~ nCount_RNA, y = ~ nFeature_RNA)
```

---

|      |                                |
|------|--------------------------------|
| pull | <i>Extract a single column</i> |
|------|--------------------------------|

---

**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**

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

**Arguments**

|                    |  |
|--------------------|--|
| <code>.data</code> | A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from <i>dbplyr</i> or <i>dtplyr</i> ). See <i>Methods</i> , below, for more details.  |
| <code>var</code>   | A variable specified as: <ul style="list-style-type: none"> <li>• a literal variable name</li> <li>• a positive integer, giving the position counting from the left</li> <li>• a negative integer, giving the position counting from the right.</li> </ul> <p>The default returns the last column (on the assumption that's the column you've created most recently).</p> <p>This argument is taken by expression and supports <a href="#">quasiquotation</a> (you can unquote column names and column locations).</p> |
| <code>name</code>  | An optional parameter that specifies the column to be used as names for a named vector. Specified in a similar manner as <code>var</code> .  |
| <code>...</code>   | For use by methods.  |

**Value**

A vector the same size as `.data`.

**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(pbmc_small)
pbmc_small |> pull(groups)
```

---

|           |  |
|-----------|--|
| quo_names | <i>Convert array of quosure (e.g. c(col_a, col_b)) into character vector</i> |
|-----------|--|

---

**Description**

Convert array of quosure (e.g. `c(col_a, col_b)`) into character vector

**Usage**

```
quo_names(v)
```

**Arguments**

`v` A array of quosures (e.g. `c(col_a, col_b)`)

**Value**

A character vector

---

|        |                       |
|--------|-----------------------|
| rename | <i>Rename columns</i> |
|--------|-----------------------|

---

## Description

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

## Usage

```
## S3 method for class 'SingleCellExperiment'  
rename(.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 <i>Methods</i> , below, for more details.             |
| ...   | For rename(): <code>&lt;tidy-select&gt;</code> Use new_name = old_name to rename selected variables.<br>For rename_with(): additional arguments passed onto .fn. |

## Value

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

- Rows are not affected.
- Column names are changed; column order is preserved.
- Data frame attributes are preserved.
- Groups are updated to reflect new names.

## 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\(\)](#), [slice\(\)](#), [summarise\(\)](#)

## Examples

```
data(pbmc_small)  
pbmc_small |> rename(s_score=nFeature_RNA)
```

---

return\_arguments\_of     *returns variables from an expression*

---

### Description

returns variables from an expression

### Usage

```
return_arguments_of(expression)
```

### Arguments

expression     an expression

### Value

list of symbols

---

right\_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

```
## S3 method for class 'SingleCellExperiment'
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 <i>Methods</i> , below, for more details.   |
| by     | <p>A join specification created with <code>join_by()</code>, or a character vector of variables to join by.</p> <p>If NULL, the default, <code>*_join()</code> 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.</p> <p>To join on different variables between x and y, use a <code>join_by()</code> specification. For example, <code>join_by(a == b)</code> will match x\$a to y\$b.</p> <p>To join by multiple variables, use a <code>join_by()</code> specification with multiple expressions. For example, <code>join_by(a == b, c == d)</code> 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 <code>join_by(a, c)</code>.</p> <p><code>join_by()</code> can also be used to perform inequality, rolling, and overlap joins. See the documentation at <a href="#">?join_by</a> for details on these types of joins.</p> <p>For simple equality joins, you can alternatively specify a character vector of variable names to join by. For example, <code>by = c("a", "b")</code> 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 <code>by = c("x_a" = "y_a", "x_b" = "y_b")</code>.</p> <p>To perform a cross-join, generating all combinations of x and y, see <code>cross_join()</code>.</p> |
| 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**

```
data(pbmc_small)
tt <- pbmc_small
tt |> right_join(tt |>
  distinct(groups) |>
  mutate(new_column=1:2) |>
  slice(1))
```

rowwise

*Group input by rows***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 'SingleCellExperiment'
rowwise(data, ...)
```

**Arguments**

|                   |  |
|-------------------|--|
| <code>data</code> | Input data frame.  |
| <code>...</code>  | <code>&lt;tidy-select&gt;</code> Variables to be preserved when calling <code>summarise()</code> . This is typically a set of variables whose combination uniquely identify each row.<br><b>NB:</b> unlike <code>group_by()</code> you can not create new variables here but instead you can select multiple variables with (e.g.) <code>everything()</code> . |

**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.

**See Also**

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

**Examples**

```
# TODO
```

---

|          |                                   |
|----------|-----------------------------------|
| sample_n | <i>Sample n rows from a table</i> |
|----------|-----------------------------------|

---

**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**

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

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

**Arguments**

|                      |   |
|----------------------|---|
| <code>tbl</code>     | A data.frame.   |
| <code>size</code>    | <tidy-select> For <code>sample_n()</code> , the number of rows to select. For <code>sample_frac()</code> , the fraction of rows to select. If <code>tbl</code> is grouped, <code>size</code> applies to each group. |
| <code>replace</code> | Sample with or without replacement?   |
| <code>weight</code>  | <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.  |
| <code>.env</code>    | DEPRECATED.   |
| <code>...</code>     | ignored   |



**Value**

'tidySingleCellExperiment'

**Examples**

```
data(pbmc_small)
pbmc_small |> sample_n(50)
pbmc_small |> sample_frac(0.1)
```

---

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**

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

**Arguments**

|                    |  |
|--------------------|--|
| <code>.data</code> | A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from dbplyr or dtplyr). See <i>Methods</i> , below, for more details.   |
| <code>...</code>   | <tidy-select> 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 <code>x:y</code> 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(!ends_with("Width"))
#> # A tibble: 150 x 3
#>   Sepal.Length Petal.Length Species
#>   <dbl>      <dbl> <fct>
#> 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:

```
iris %>% 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
```

```
iris %>% 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
#> 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:

```
iris %>% 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(pbm_small)
pbm_small |> select(cell, orig.ident)
```

---

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**

```
## S3 method for class 'SingleCellExperiment'
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.<br>If character, sep is interpreted as a regular expression. The default value is a regular expression that matches any sequence of non-alphanumeric values.<br>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 <code>type.convert()</code> with <code>as.is = TRUE</code> on new columns. This is useful if the component columns are integer, numeric or logical.<br>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: <ul style="list-style-type: none"> <li>• "warn" (the default): emit a warning and drop extra values.</li> <li>• "drop": drop any extra values without a warning.</li> <li>• "merge": only splits at most <code>length(into)</code> times</li> </ul>  |
| fill    | If sep is a character vector, this controls what happens when there are not enough pieces. There are three valid options: <ul style="list-style-type: none"> <li>• "warn" (the default): emit a warning and fill from the right</li> <li>• "right": fill with missing values on the right</li> <li>• "left": fill with missing values on the left</li> </ul>   |
| ...     | Additional arguments passed on to methods.   |

**Value**

'tidySingleCellExperiment'

**See Also**

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

**Examples**

```
data(pbmc_small)
un <- pbmc_small |> unite("new_col", c(orig.ident, groups))
un |> separate(new_col, c("orig.ident", "groups"))
```

---

|       |  |
|-------|--|
| slice | <i>Subset rows using their positions</i> |
|-------|--|

---

**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 'SingleCellExperiment'
slice(.data, ..., .by = NULL, .preserve = FALSE)

## S3 method for class 'SingleCellExperiment'
slice_sample(
  .data,
  ...,
  n = NULL,
  prop = NULL,
  by = NULL,
  weight_by = NULL,
  replace = FALSE
)

## S3 method for class 'SingleCellExperiment'
slice_head(.data, ..., n, prop, by = NULL)

## S3 method for class 'SingleCellExperiment'
slice_tail(.data, ..., n, prop, by = NULL)
```

```

## S3 method for class 'SingleCellExperiment'
slice_min(
  .data,
  order_by,
  ...,
  n,
  prop,
  by = NULL,
  with_ties = TRUE,
  na_rm = FALSE
)

## S3 method for class 'SingleCellExperiment'
slice_max(
  .data,
  order_by,
  ...,
  n,
  prop,
  by = NULL,
  with_ties = TRUE,
  na_rm = FALSE
)

```

### Arguments

|                        |   |
|------------------------|---|
| <code>.data</code>     | A data frame, data frame extension (e.g. a tibble), or a lazy data frame (e.g. from <code>dbplyr</code> or <code>dtplyr</code> ). See <i>Methods</i> , below, for more details.   |
| <code>...</code>       | For <code>slice()</code> : <a href="#">&lt;data-masking&gt;</a> Integer row values.<br>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.<br>For <code>slice_*()</code> , these arguments are passed on to methods.  |
| <code>.by, by</code>   | <b>[Experimental]</b><br><a href="#">&lt;tidy-select&gt;</a> Optionally, a selection of columns to group by for just this operation, functioning as an alternative to <code>group_by()</code> . For details and examples, see <code>?dplyr_by</code> .  |
| <code>.preserve</code> | Relevant when the <code>.data</code> input is grouped. If <code>.preserve = FALSE</code> (the default), the grouping structure is recalculated based on the resulting data, otherwise the grouping is kept as is.   |
| <code>n, prop</code>   | Provide either <code>n</code> , the number of rows, or <code>prop</code> , the proportion of rows to select. If neither are supplied, <code>n = 1</code> will be used. If <code>n</code> is greater than the number of rows in the group (or <code>prop &gt; 1</code> ), the result will be silently truncated to the group size. <code>prop</code> will be rounded towards zero to generate an integer number of rows.<br>A negative value of <code>n</code> or <code>prop</code> will be subtracted from the group size. For example, <code>n = -2</code> with a group of 5 rows will select $5 - 2 = 3$ rows; <code>prop = -0.25</code> with 8 rows will select $8 * (1 - 0.25) = 6$ rows. |



|           |  |
|-----------|--|
| weight_by | <data-masking> 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.  |
| replace   | Should sampling be performed with (TRUE) or without (FALSE, the default) replacement.  |
| order_by  | <data-masking> Variable or function of variables to order by. To order by multiple variables, wrap them in a data frame or tibble.   |
| with_ties | Should ties be kept together? The default, TRUE, may return more rows than you request. Use FALSE to ignore ties, and return the first n rows.   |
| na_rm     | Should missing values in order_by be removed from the result? If FALSE, NA values are sorted to the end (like in <code>arrange()</code> ), so they will only be included if there are insufficient non-missing values to reach n/prop. |

### 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.

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- `slice_max()`: no methods found.
- `slice_sample()`: no methods found.

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:

- `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: [arrange\(\)](#), [mutate\(\)](#), [rename\(\)](#), [summarise\(\)](#)

### Examples

```
data(pbmc_small)
pbmc_small |> slice(1)

data(pbmc_small)
pbmc_small |> slice_sample(n=1)
pbmc_small |> slice_sample(prop=0.1)

data(pbmc_small)
# First rows based on existing order
pbmc_small |> slice_head(n=5)

data(pbmc_small)
# First rows based on existing order
pbmc_small |> slice_tail(n=5)

data(pbmc_small)

# Rows with minimum and maximum values of a metadata variable
pbmc_small |> slice_min(nFeature_RNA, n=5)

# slice_min() and slice_max() may return more rows than requested
# in the presence of ties.
pbmc_small |> slice_min(nFeature_RNA, n=2)

# Use with_ties=FALSE to return exactly n matches
pbmc_small |> slice_min(nFeature_RNA, n=2, with_ties=FALSE)

# Or use additional variables to break the tie:
pbmc_small |> slice_min(tibble::tibble(nFeature_RNA, nCount_RNA), n=2)

# Use by for group-wise operations
pbmc_small |> slice_min(nFeature_RNA, n=5, by=groups)
```

```
data(pbmc_small)
# Rows with minimum and maximum values of a metadata variable
pbmc_small |> slice_max(nFeature_RNA, n=5)
```

---

|           |   |
|-----------|---|
| summarise | <i>Summarise each group down to one row</i> |
|-----------|---|

---

## 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

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

```
## S3 method for class 'SingleCellExperiment'
summarize(.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 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: `arrange()`, `mutate()`, `rename()`, `slice()`

### Examples

```
data(pbmc_small)
pbmc_small |> summarise(mean(nCount_RNA))
```

---

|                   |                                      |
|-------------------|--------------------------------------|
| tbl_format_header | <i>Format the header of a tibble</i> |
|-------------------|--------------------------------------|

---

### 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.

**Usage**

```
## S3 method for class 'tidySingleCellExperiment'  
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**

```
# TODO
```

---

tidy                                    *tidy for 'SingleCellExperiment'*

---

**Description**

tidy for 'SingleCellExperiment'

**Usage**

```
tidy(object)  
  
## S3 method for class 'SingleCellExperiment'  
tidy(object)
```

**Arguments**

object              A 'SingleCellExperiment' object.

**Value**

A 'tidySingleCellExperiment' object.

**Examples**

```
data(pbmc_small)  
pbmc_small
```

---

`unite`*Unite multiple columns into one by pasting strings together*

---

## Description

Convenience function to paste together multiple columns into one.

## Usage

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

## Arguments

|                     |  |
|---------------------|--|
| <code>data</code>   | A data frame.  |
| <code>col</code>    | The name of the new column, as a string or symbol.<br>This argument is passed by expression and supports <a href="#">quasiquote</a> (you can unquote strings and symbols). The name is captured from the expression with <a href="#">rlang::ensym()</a> (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). |
| <code>...</code>    | <a href="#">&lt;tidy-select&gt;</a> Columns to unite   |
| <code>sep</code>    | Separator to use between values.   |
| <code>remove</code> | If TRUE, remove input columns from output data frame.  |
| <code>na.rm</code>  | If TRUE, missing values will be removed prior to uniting each value.   |

## Value

‘tidySingleCellExperiment’

## See Also

[separate\(\)](#), the complement.

## Examples

```
data(pbmc_small)  
pbmc_small |> unite(  
  col="new_col",  
  c("orig.ident", "groups"))
```

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**

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

unnest_single_cell_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 | <code>&lt;tidy-select&gt;</code> List-columns to unnest.<br>When selecting multiple columns, values from the same row will be recycled to their common size.                                |
| ...  | <b>[Deprecated]:</b> previously you could write <code>df %&gt;% unnest(x, y, z)</code> . Convert to <code>df %&gt;% unnest(c(x, y, z))</code> . 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 <code>keep_empty = TRUE</code> 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 <code>names_sep</code> .  |
| names_repair     | Used to check that output data frame has valid names. Must be one of the following options: <ul style="list-style-type: none"> <li>• "minimal": no name repair or checks, beyond basic existence,</li> <li>• "unique": make sure names are unique and not empty,</li> <li>• "check_unique": (the default), no name repair, but check they are unique,</li> <li>• "universal": make the names unique and syntactic</li> <li>• a function: apply custom name repair.</li> <li>• <a href="#">tidyr_legacy</a>: use the name repair from tidyr 0.8.</li> <li>• a formula: a purrr-style anonymous function (see <a href="#">rlang::as_function()</a>)</li> </ul> <p>See <a href="#">vctrs::vec_as_names()</a> for more details on these terms and the strategies used to enforce them.</p> |
| .drop, .preserve | <b>[Deprecated]:</b> all list-columns are now preserved; If there are any that you don't want in the output use <code>select()</code> to remove them prior to unnesting.   |
| .id              | <b>[Deprecated]:</b> convert <code>df %&gt;% unnest(x, .id = "id")</code> to <code>df %&gt;% mutate(id = names(x)) %&gt;% unnest(x)</code>   |
| .sep             | <b>[Deprecated]:</b> use <code>names_sep</code> instead.   |

**Value**

‘tidySingleCellExperiment’

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

**See Also**

Other rectangling: [hoist\(\)](#), [unnest\\_longer\(\)](#), [unnest\\_wider\(\)](#)

**Examples**

```
data(pbmc_small)
pbmc_small |>
  nest(data=-groups) |>
  unnest(data)
```

---

%>%

*Pipe operator*

---

**Description**

See [magrittr::%>%](#) for details.

**Usage**

```
lhs %>% rhs
```

**Arguments**

|     |   |
|-----|---|
| lhs | A value or the ‘magrittr’ placeholder.          |
| rhs | A function call using the ‘magrittr’ semantics. |

**Value**

The result of calling ‘rhs(lhs)’.

**Examples**

```
`%>%` <- magrittr::`%>%`
letters %>% head(n=3)
```

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