

# Package ‘poorman’

November 12, 2020

**Type** Package

**Title** A Poor Man's Dependency Free Recreation of 'dplyr'

**Version** 0.2.3

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**Description** A replication of key functionality from 'dplyr' and the wider 'tidyverse' using only 'base'.

**URL** <https://nathaneastwood.github.io/poorman/>,  
<https://github.com/nathaneastwood/poorman>

**BugReports** <https://github.com/nathaneastwood/poorman/issues>

**Depends** R (>= 3.5)

**Suggests** knitr, pkgdown, rmarkdown, roxygen2, tinytest

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2020-11-12 06:40:07 UTC

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---

across

*Apply a function (or functions) across multiple columns*

---

### Description

`across()` makes it easy to apply the same transformation to multiple columns, allowing you to use `select()` semantics inside in "data-masking" functions like `summarise()` and `mutate()`.

`across()` supersedes the family of dplyr "scoped variants" like `summarise_at()`, `summarise_if()`, and `summarise_all()` and therefore these functions will not be implemented in `poorman`.

**Usage**

```
across(.cols = everything(), .fns = NULL, ..., .names = NULL)
```

**Arguments**

<code>.fns</code>	Functions to apply to each of the selected columns. Possible values are: <ul style="list-style-type: none"> <li>• NULL, to returns the columns untransformed.</li> <li>• A function, e.g. <code>mean</code>.</li> <li>• A list of functions, e.g. <code>list(mean = mean, sum = sum)</code></li> </ul> Within these functions you can use <code>cur_group()</code> to access the current grouping keys.
<code>...</code>	Additional arguments for the function calls in <code>.fns</code> .
<code>.names</code>	character(n). Currently limited to specifying a vector of names to use for the outputs.
<code>cols, .cols</code>	<poor-select> Columns to transform. Because <code>across()</code> is used within functions like <code>summarise()</code> and <code>mutate()</code> , you can't select or compute upon grouping variables.

**Value**

A data.frame with one column for each column in `.cols` and each function in `.fns`.

**Examples**

```
# across() -----
iris %>%
  group_by(Species) %>%
  summarise(across(starts_with("Sepal"), mean))
iris %>%
  mutate(across(where(is.factor), as.character))

# Additional parameters can be passed to functions
iris %>%
  group_by(Species) %>%
  summarise(across(starts_with("Sepal"), mean, na.rm = TRUE))

# A named list of functions
iris %>%
  group_by(Species) %>%
  summarise(across(starts_with("Sepal"), list(mean = mean, sd = sd)))

# Use the .names argument to control the output names
iris %>%
  group_by(Species) %>%
  summarise(
    across(starts_with("Sepal"),
      mean,
      .names = c("mean_sepal_length", "mean_sepal_width"))
  )
```

arrange *Arrange rows by variables*

---

**Description**

Order rows of a `data.frame` by an expression involving its variables.

**Usage**

```
arrange(.data, ...)
```

**Arguments**

`.data` A `data.frame`.  
`...` A comma separated vector of unquoted name(s) to order the data by.

**Value**

A `data.frame`.

**Examples**

```
arrange(mtcars, mpg)
mtcars %>% arrange(mpg)
mtcars %>% arrange(cyl, mpg)
```

---

between *Do values in a numeric vector fall in specified range?*

---

**Description**

This is a shortcut for `x >= left & x <= right`.

**Usage**

```
between(x, left, right)
```

**Arguments**

`x` A numeric vector of values.  
`left, right` Boundary values.

**Value**

A logical vector the same length as `x`.

## Examples

```
between(1:12, 7, 9)

x <- rnorm(1e2)
x[between(x, -1, 1)]
```

---

bind

*Efficiently bind multiple data.frames by row and column*

---

## Description

Efficiently bind multiple data.frames by row and column

## Usage

```
bind_cols(...)

bind_rows(..., .id = NULL)
```

## Arguments

... data.frames to combine.  
Each argument can either be a data.frame, a list that could be a data.frame, or a list of data.frames.  
When row-binding, columns are matched by name, and any missing columns will be filled with NA.  
When column-binding, rows are matched by position, so all data.frames must have the same number of rows. To match by value, not position, see [mutate\\_joins](#).

.id character(1). data.frame identifier.  
When .id is supplied, a new column of identifiers is created to link each row to its original data.frame. The labels are taken from the named arguments to bind\_rows(). When a list of data.frames is supplied, the labels are taken from the names of the list. If no names are found a numeric sequence is used instead.

## Examples

```
one <- mtcars[1:4, ]
two <- mtcars[9:12, ]

# You can supply data frames as arguments:
bind_rows(one, two)

# The contents of lists are spliced automatically:
bind_rows(list(one, two))
```

```

bind_rows(split(mtcars, mtcars$cyl))
bind_rows(list(one, two), list(two, one))

# In addition to data frames, you can supply vectors. In the rows
# direction, the vectors represent rows and should have inner
# names:
bind_rows(
  c(a = 1, b = 2),
  c(a = 3, b = 4)
)

# You can mix vectors and data frames:
bind_rows(
  c(a = 1, b = 2),
  data.frame(a = 3:4, b = 5:6),
  c(a = 7, b = 8)
)

# When you supply a column name with the `.id` argument, a new
# column is created to link each row to its original data frame
bind_rows(list(one, two), .id = "id")
bind_rows(list(a = one, b = two), .id = "id")
bind_rows("group 1" = one, "group 2" = two, .id = "groups")

## Not run:
# Rows need to match when column-binding
bind_cols(data.frame(x = 1:3), data.frame(y = 1:2))

# even with 0 columns
bind_cols(data.frame(x = 1:3), data.frame())

## End(Not run)

bind_cols(one, two)
bind_cols(list(one, two))

```

---

case\_when

A General Vectorised if()

---

## Description

This function allows you to vectorise multiple `if_else()` statements. It is an R equivalent of the SQL CASE WHEN statement. If no cases match, NA is returned.

## Usage

```
case_when(...)
```

**Arguments**

... A sequence of two-sided formulas. The left hand side (LHS) determines which values match this case. The right hand side (RHS) provides the replacement value.

The LHS must evaluate to a logical vector. The RHS does not need to be logical, but all RHSs must evaluate to the same type of vector.

Both LHS and RHS may have the same length of either 1 or n. The value of n must be consistent across all cases. The case of  $n == 0$  is treated as a variant of  $n != 1$ .

NULL inputs are ignored.

**Value**

A vector of length 1 or n, matching the length of the logical input or output vectors, with the type (and attributes) of the first RHS. Inconsistent lengths or types will generate an error.

**Examples**

```
x <- 1:50
case_when(
  x %% 35 == 0 ~ "fizz buzz",
  x %% 5 == 0 ~ "fizz",
  x %% 7 == 0 ~ "buzz",
  TRUE ~ as.character(x)
)

# Like an if statement, the arguments are evaluated in order, so you must
# proceed from the most specific to the most general. This won't work:
case_when(
  TRUE ~ as.character(x),
  x %% 5 == 0 ~ "fizz",
  x %% 7 == 0 ~ "buzz",
  x %% 35 == 0 ~ "fizz buzz"
)

# If none of the cases match, NA is used:
case_when(
  x %% 5 == 0 ~ "fizz",
  x %% 7 == 0 ~ "buzz",
  x %% 35 == 0 ~ "fizz buzz"
)

# Note that NA values in the vector x do not get special treatment. If you want
# to explicitly handle NA values you can use the `is.na` function:
x[2:4] <- NA_real_
case_when(
  x %% 35 == 0 ~ "fizz buzz",
  x %% 5 == 0 ~ "fizz",
  x %% 7 == 0 ~ "buzz",
  is.na(x) ~ "nope",
  TRUE ~ as.character(x)
)
```

```

)

# All RHS values need to be of the same type. Inconsistent types will throw an error.
# This applies also to NA values used in RHS: NA is logical, use
# typed values like NA_real_, NA_complex, NA_character_, NA_integer_ as appropriate.
case_when(
  x %% 35 == 0 ~ NA_character_,
  x %% 5 == 0 ~ "fizz",
  x %% 7 == 0 ~ "buzz",
  TRUE ~ as.character(x)
)
case_when(
  x %% 35 == 0 ~ 35,
  x %% 5 == 0 ~ 5,
  x %% 7 == 0 ~ 7,
  TRUE ~ NA_real_
)

# case_when() evaluates all RHS expressions, and then constructs its
# result by extracting the selected (via the LHS expressions) parts.
# In particular NaN are produced in this case:
y <- seq(-2, 2, by = .5)
case_when(
  y >= 0 ~ sqrt(y),
  TRUE ~ y
)

## Not run:
case_when(
  x %% 35 == 0 ~ 35,
  x %% 5 == 0 ~ 5,
  x %% 7 == 0 ~ 7,
  TRUE ~ NA
)

## End(Not run)

# case_when is particularly useful inside mutate when you want to
# create a new variable that relies on a complex combination of existing
# variables
mtcars %>%
  mutate(
    efficient = case_when(
      mpg > 25 ~ TRUE,
      TRUE ~ FALSE
    )
  )

```



**Description**

Given a set of vectors, `coalesce()` finds the first non-missing value at each position. This is inspired by the SQL COALESCE function which does the same thing for NULLs.

**Usage**

```
coalesce(...)
```

**Arguments**

... Vectors. Inputs should be recyclable (either be length 1L or n) and coercible to a common type.

**Details**

Currently, `coalesce()` type checking does not take place.

**See Also**

[na\\_if\(\)](#) to replace specified values to a NA.

[replace\\_na\(\)](#) to replace a NA with a value.

**Examples**

```
# Use a single value to replace all missing vectors
x <- sample(c(1:5, NA, NA, NA))
coalesce(x, 0L)

# Or match together a complete vector from missing pieces
y <- c(1, 2, NA, NA, 5)
z <- c(NA, NA, 3, 4, 5)
coalesce(y, z)
```

---

context

*Context dependent expressions*

---

**Description**

These functions return information about the "current" group or "current" variable, so only work inside specific contexts like [summarise\(\)](#) and [mutate\(\)](#).

- `n()` gives the number of observations in the current group.
- `cur_data()` gives the current data for the current group (excluding grouping variables).
- `cur_data_all()` gives the current data for the current group (including grouping variables).

- `cur_group()` gives the group keys, a single row `data.frame` containing a column for each grouping variable and its value.
- `cur_group_id()` gives a unique numeric identifier for the current group.
- `cur_group_rows()` gives the rows the groups appear in the data.

### Usage

```
n()
cur_data()
cur_data_all()
cur_group()
cur_group_id()
cur_group_rows()
```

### `data.table`

If you're familiar with `data.table`:

- `cur_data()`  $\leftrightarrow$  `.SD`
- `cur_group_id()`  $\leftrightarrow$  `.GRP`
- `cur_group()`  $\leftrightarrow$  `.BY`
- `cur_group_rows()`  $\leftrightarrow$  `.I`

### See Also

See [group\\_data\(\)](#) for equivalent functions that return values for all groups.

### Examples

```
df <- data.frame(
  g = sample(rep(letters[1:3], 1:3)),
  x = runif(6),
  y = runif(6),
  stringsAsFactors = FALSE
)
gf <- df %>% group_by(g)

gf %>% summarise(n = n())

gf %>% mutate(id = cur_group_id())
gf %>% summarise(row = cur_group_rows())
gf %>% summarise(data = list(cur_group()))
gf %>% summarise(data = list(cur_data()))
```

---

count	<i>Count observations by 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 equivalent to `count()` and `tally()` but use `mutate()` instead of `summarise()` so that they add a new column with group-wise counts.

### Usage

```
count(x, ..., wt = NULL, sort = FALSE, name = NULL)
```

```
tally(x, wt = NULL, sort = FALSE, name = NULL)
```

```
add_count(x, ..., wt = NULL, sort = FALSE, name = NULL)
```

```
add_tally(x, wt = NULL, sort = FALSE, name = NULL)
```

### Arguments

<code>x</code>	A data.frame.
<code>...</code>	Variables to group by.
<code>wt</code>	If omitted, will count the number of rows. If specified, will perform a "weighted" count by summing the (non-missing) values of variable <code>wt</code> . If omitted, and column <code>n</code> exists, it will automatically be used as a weighting variable, although you will have to specify <code>name</code> to provide a new name for the output.
<code>sort</code>	logical(1). If TRUE, will show the largest groups at the top.
<code>name</code>	character(1). The name of the new column in the output. If omitted, it will default to <code>n</code> . If there's already a column called <code>n</code> , it will error, and require you to specify the name.

### Value

A data.frame. `count()` and `add_count()` have the same groups as the input.

### Examples

```
# count() is a convenient way to get a sense of the distribution of
# values in a dataset
mtcars %>% count(cyl)
mtcars %>% count(cyl, sort = TRUE)
mtcars %>% count(cyl, am, sort = TRUE)
# Note that if the data are already grouped, count() adds an additional grouping variable
```

```
# which is removed afterwards
mtcars %>% group_by(gear) %>% count(cyl)

# tally() is a lower-level function that assumes you've done the grouping
mtcars %>% tally()
mtcars %>% group_by(cyl) %>% tally()

# both count() and tally() have add_ variants that work like mutate() instead of summarise
mtcars %>% add_count(cyl, wt = am)
mtcars %>% add_tally(wt = am)
```

---

desc	<i>Descending order</i>
------	-------------------------

---

## Description

Transform a vector into a format that will be sorted in descending order. This is useful within [arrange\(\)](#).

## Usage

```
desc(x)
```

## Arguments

x                    A vector to transform.

## Value

A vector of the same length as x.

## Examples

```
desc(1:10)
desc(factor(letters))

first_day <- seq(as.Date("1910/1/1"), as.Date("1920/1/1"), "years")
desc(first_day)

mtcars %>% arrange(desc(mpg))
```

---

distinct	<i>Subset distinct/unique rows</i>
----------	------------------------------------

---

### Description

Select only distinct/unique rows from a data.frame.

### Usage

```
distinct(.data, ..., .keep_all = FALSE)
```

### Arguments

.data	A data.frame.
...	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.
.keep_all	logical(1). If TRUE, keep all variables in .data. If a combination of ... is not distinct, this keeps the first row of values.

### Value

A data.frame with 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.

### Examples

```
df <- data.frame(  
  x = sample(10, 100, rep = TRUE),  
  y = sample(10, 100, rep = TRUE)  
)  
nrow(df)  
nrow(distinct(df))  
nrow(distinct(df, x, y))  
  
distinct(df, x)  
distinct(df, y)  
  
# You can choose to keep all other variables as well  
distinct(df, x, .keep_all = TRUE)  
distinct(df, y, .keep_all = TRUE)
```

```
# You can also use distinct on computed variables
distinct(df, diff = abs(x - y))

# The same behaviour applies for grouped data frames,
# except that the grouping variables are always included
df <- data.frame(
  g = c(1, 1, 2, 2),
  x = c(1, 1, 2, 1)
) %>% group_by(g)
df %>% distinct(x)
```

---

 filter

*Return rows with matching conditions*


---

### Description

Use `filter()` to choose rows/cases where conditions are TRUE.

### Usage

```
filter(.data, ...)
```

### Arguments

<code>.data</code>	A data frame.
<code>...</code>	Logical predicated defined in terms of the variables in <code>.data</code> . Multiple conditions are combined with <code>&amp;</code> . Arguments within <code>...</code> are automatically quoted and evaluated within the context of the data frame.

### Value

A data frame.

### Useful filter functions

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

### Examples

```
filter(mtcars, am == 1)
mtcars %>% filter(cyl == 4)
mtcars %>% filter(cyl <= 5 & am > 0)
mtcars %>% filter(cyl == 4 | cyl == 8)
mtcars %>% filter(!(cyl %in% c(4, 6)), am != 0)
```

---

filter_joins	<i>Filtering joins filter rows from x based on the presence or absence of matches in y:</i>
--------------	---

---

### Description

- `semi_join()` return all rows from `x` with a match in `y`.
- `anti_join()` return all rows from `x` without a match in `y`.

### Usage

```
anti_join(x, y, by = NULL)
```

```
semi_join(x, y, by = NULL)
```

### Arguments

<code>x, y</code>	The <code>data.frames</code> to join.
<code>by</code>	A character vector of variables to join by. If <code>NULL</code> , the default, <code>*_join()</code> will do a natural join, using all variables with common names across the two tables. A message lists the variables so that you can check they're right (to suppress the message, simply explicitly list the variables that you want to join).

### Examples

```
table1 <- data.frame(
  pupil = rep(1:3, each = 2),
  test = rep(c("A", "B"), 3),
  score = c(60, 70, 65, 80, 85, 70),
  stringsAsFactors = FALSE
)
table2 <- table1[c(1, 3, 4), ]

table1 %>% anti_join(table2, by = c("pupil", "test"))
table1 %>% semi_join(table2, by = c("pupil", "test"))
```

---

glimpse	<i>Get a glimpse of your data</i>
---------	-----------------------------------

---

### 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 is no more than a wrapper around `utils::str()` only it returns the input (invisibly) meaning it can be used within a data pipeline.

**Usage**

```
glimpse(x, width = getOption("width"), ...)
```

**Arguments**

`x` An object to glimpse at.

`width` `integer(1)`. Width of the output.

`...` Additional parameters to pass to `utils::str()`.

**Value**

`x`, invisibly.

**Examples**

```
glimpse(mtcars)
```

---

group\_by

*Group by one or more variables*

---

**Description**

Determine the groups within a `data.frame` to perform operations on. `ungroup()` removes the grouping levels.

**Usage**

```
group_by(.data, ..., .add = FALSE)
```

```
ungroup(x, ...)
```

**Arguments**

`.data` `data.frame`. The data to group.

`...` One or more unquoted column names to group/ungroup the data by.

`.add` `logical(1)`. When `FALSE` (the default) `group_by()` will override existing groups. To add to existing groups, use `.add = TRUE`.

`x` A `data.frame`.

**Value**

When using `group_by()`, a `data.frame`, grouped by the grouping variables.

When using `ungroup()`, a `data.frame`.



**Examples**

```

group_by(mtcars, am, cyl)
ungroup(mutate(group_by(mtcars, am, cyl), sumMpg = sum(mpg)))
mtcars %>%
  group_by(am, cyl) %>%
  mutate(sumMpg = sum(mpg)) %>%
  ungroup()
mtcars %>%
  group_by(carb) %>%
  filter(any(gear == 5))

```

group\_cols

*Select Grouping Variables***Description**

This selection helper matches grouping variables. It can be used within [select\(\)](#) and [relocate\(\)](#) selections.

**Usage**

```
group_cols()
```

**See Also**

[groups\(\)](#) and [group\\_vars\(\)](#) for retrieving the grouping variables outside selection contexts.

**Examples**

```
mtcars %>% group_by(am, cyl) %>% select(group_cols())
```

group\_metadata

*Grouping metadata***Description**

- [group\\_data\(\)](#) returns a data frame that defines the grouping structure. The columns give the values of the grouping variables. The last column, always called `.rows`, is a list of integer vectors that gives the location of the rows in each group.
- [group\\_rows\(\)](#) returns the rows which each group contains.
- [group\\_indices\(\)](#) returns an integer vector the same length as `.data` that gives the group that each row belongs to.

- `group_vars()` gives names of grouping variables as character vector.
- `groups()` gives the names as a list of symbols.
- `group_size()` gives the size of each group.
- `n_groups()` gives the total number of groups.

**Usage**

```
group_data(.data)
```

```
group_rows(.data)
```

```
group_indices(.data)
```

```
group_vars(x)
```

```
groups(x)
```

```
group_size(x)
```

```
n_groups(x)
```

**Arguments**

```
.data, x      A data.frame.
```

**See Also**

See [context](#) for equivalent functions that return values for the current group.

**Examples**

```
df <- data.frame(x = c(1,1,2,2))
group_vars(df)
group_rows(df)
group_data(df)

gf <- group_by(df, x)
group_vars(gf)
group_rows(gf)
group_data(gf)
```

---

`group_split`*Split data.frame by groups*

---

## Description

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

- it uses the grouping structure from `group_by()` and is therefore subject to the data mask
- it does not name the elements of the list based on the grouping as this typically loses information and is confusing

## Usage

```
group_split(.data, ..., .keep = TRUE)
```

```
group_keys(.data)
```

## Arguments

<code>.data</code>	A <code>data.frame</code> .
<code>...</code>	Grouping specification, forwarded to <code>group_by()</code> .
<code>.keep</code>	<code>logical(1)</code> . Should the grouping columns be kept (default: <code>TRUE</code> )?

## Details

### Grouped `data.frames`:

The primary use case for `group_split()` is with already grouped `data.frames`, typically a result of `group_by()`. In this case, `group_split()` only uses the first argument, the grouped `data.frame`, and warns when `...` is used.

Because some of these groups may be empty, it is best paired with `group_keys()` which identifies the representatives of each grouping variable for the group.

### Ungrouped `data.frames`:

When used on ungrouped `data.frames`, `group_split()` forwards the `...` to `group_by()` before the split, therefore the `...` are subject to the data mask.

## Value

- `group_split()` returns a list of `data.frames`. Each `data.frame` contains the rows of `.data` with the associated group and all the columns, including the grouping variables.
- `group_keys()` returns a `data.frame` with one row per group, and one column per grouping variable

## See Also

[group\\_by\(\)](#)

**Examples**

```
# Grouped data.frames:
mtcars %>% group_by(cyl, am) %>% group_split()
mtcars %>% group_by(cyl, am) %>% group_split(.keep = FALSE)
mtcars %>% group_by(cyl, am) %>% group_keys()

# Ungrouped data.frames:
mtcars %>% group_split(am, cyl)
```

---

if_else	<i>Vectorised if</i>
---------	----------------------

---

**Description**

This is a wrapper around `ifelse()` which checks that `true` and `false` are of the same type, making the output more predictable.

**Usage**

```
if_else(condition, true, false, missing = NULL)
```

**Arguments**

<code>condition</code>	A logical(n) vector.
<code>true, false</code>	Values to use for TRUE and FALSE in condition. They must either be the same length as <code>condition</code> or be length 1. They must also be the same type.
<code>missing</code>	If not NULL (the default), this will replace any missing values.

**Value**

A vector the same length as `condition` with values for TRUE and FALSE replaced by those specified in `true` and `false`, respectively.

**Examples**

```
x <- c(-5:5, NA)
if_else(x < 0, NA_integer_, x)
if_else(x < 0, "negative", "positive", "missing")

# Unlike ifelse, if_else preserves types
x <- factor(sample(letters[1:5], 10, replace = TRUE))
ifelse(x %in% c("a", "b", "c"), x, factor(NA))
# Attributes are taken from the `true` vector
if_else(x %in% c("a", "b", "c"), x, factor(NA))
```

---

lag *Compute lagged or leading values*

---

### Description

Find the "previous" (`lag()`) or "next" (`lead()`) values in a vector. Useful for comparing values behind of or ahead of the current values.

### Usage

```
lag(x, n = 1L, default = NA)
```

```
lead(x, n = 1L, default = NA)
```

### Arguments

x	A vector of values
n	A positive integer(1), giving the number of positions to lead or lag by.
default	The value used for non-existent rows (default: NA).

### Examples

```
lag(1:5)
lead(1:5)

x <- 1:5
data.frame(behind = lag(x), x, ahead = lead(x))

# If you want to look more rows behind or ahead, use `n`
lag(1:5, n = 1)
lag(1:5, n = 2)

lead(1:5, n = 1)
lead(1:5, n = 2)

# If you want to define a value for non-existing rows, use `default`
lag(1:5)
lag(1:5, default = 0)

lead(1:5)
lead(1:5, default = 6)
```

---

mutate	<i>Create or transform variables</i>
--------	--------------------------------------

---

### Description

mutate() adds new variables and preserves existing ones; transmute() adds new variables and drops existing ones. Both functions preserve the number of rows of the input. New variables overwrite existing variables of the same name.

### Usage

```
mutate(.data, ...)
```

```
transmute(.data, ...)
```

### Arguments

.data	A data.frame.
...	Name-value pairs of expressions, each with length 1L. The name of each argument will be the name of a new column and the value will be its corresponding value. Use a NULL value in mutate to drop a variable. New variables overwrite existing variables of the same name.

### Examples

```
mutate(mtcars, mpg2 = mpg * 2)
mtcars %>% mutate(mpg2 = mpg * 2)
mtcars %>% mutate(mpg2 = mpg * 2, cyl2 = cyl * 2)

# Newly created variables are available immediately
mtcars %>% mutate(mpg2 = mpg * 2, mpg4 = mpg2 * 2)

# You can also use mutate() to remove variables and modify existing variables
mtcars %>% mutate(
  mpg = NULL,
  disp = disp * 0.0163871 # convert to litres
)

# mutate() vs transmute -----
# mutate() keeps all existing variables
mtcars %>%
  mutate(displ_l = disp / 61.0237)

# transmute keeps only the variables you create
mtcars %>%
  transmute(displ_l = disp / 61.0237)
```

---

mutate_joins	<i>Mutating Joins</i>
--------------	-----------------------

---

**Description**

The mutating joins add columns from *y* to *x*, matching rows based on the keys:

- `inner_join()`: includes all rows in *x* and *y*.
- `left_join()`: includes all rows in *x*.
- `right_join()`: includes all rows in *y*.
- `full_join()`: includes all rows in *x* or *y*.

If a row in *x* matches multiple rows in *y*, all the rows in *y* will be returned once for each matching row in *x*.

**Usage**

```
inner_join(  
  x,  
  y,  
  by = NULL,  
  suffix = c(".x", ".y"),  
  ...,  
  na_matches = c("na", "never")  
)
```

```
left_join(  
  x,  
  y,  
  by = NULL,  
  suffix = c(".x", ".y"),  
  ...,  
  keep = FALSE,  
  na_matches = c("na", "never")  
)
```

```
right_join(  
  x,  
  y,  
  by = NULL,  
  suffix = c(".x", ".y"),  
  ...,  
  keep = FALSE,  
  na_matches = c("na", "never")  
)
```

```
full_join(  
  x,  
  y,  
  by = NULL,  
  suffix = c(".x", ".y"),  
  ...,  
  keep = FALSE,  
  na_matches = c("na", "never")  
)
```

```

x,
y,
by = NULL,
suffix = c(".x", ".y"),
...,
keep = FALSE,
na_matches = c("na", "never")
)

```

## Arguments

x, y	The data.frames to join.
by	<p>A character vector of variables to join by. If NULL, the default, <code>*_join()</code> will do a natural join, using all variables with common names across the two tables. A message lists the variables so that you can check they're right (to suppress the message, simply explicitly list the variables that you want to join).</p> <p>To join by different variables on x and y use a named vector. For example, <code>by = c("a" = "b")</code> will match <code>x.a</code> to <code>y.b</code>.</p> <p>To join by multiple variables, use a vector with length &gt; 1. For example, <code>by = c("a", "b")</code> will match <code>x\$a</code> to <code>y\$a</code> and <code>x\$b</code> to <code>y\$b</code>. Use a named vector to match different variables in x and y. For example, <code>by = c("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>.</p> <p>To perform a cross-join, generating all combinations of x and y, use <code>by = character()</code>.</p>
suffix	character(2). If there are non-joined duplicate variables in x and y, these suffixes will be added to the output to disambiguate them.
...	Additional arguments to pass to <code>merge()</code>
na_matches	<p>Should NA and NaN values match one another?</p> <p>The default, "na", treats two NA or NaN values as equal, like <code>%in%</code>, <code>match()</code>, <code>merge()</code>.</p> <p>Use "never" to always treat two NA or NaN values as different, like joins for database sources, similarly to <code>merge(incomparables = FALSE)</code>.</p>
keep	<p>logical(1). Should the join keys from both x and y be preserved in the output?</p> <p>Only applies to <code>left_join()</code>, <code>right_join()</code>, and <code>full_join()</code>.</p>

## Value

A data.frame. The order of the rows and columns of x is preserved as much as possible. The output has the following properties:

- For `inner_join()`, a subset of x rows. For `left_join()`, all x rows. For `right_join()`, a subset of x rows, followed by unmatched y rows. For `full_join()`, all x rows, followed by unmatched y rows.
- For all joins, rows will be duplicated if one or more rows in x matches multiple rows in y.
- Output columns include all x columns and all y columns. If columns in x and y have the same name (and aren't included in `by`), suffixes are added to disambiguate.
- Output columns included in `by` are coerced to common type across x and y.
- Groups are taken from x.



## Examples

```
# If a row in `x` matches multiple rows in `y`, all the rows in `y` will be
# returned once for each matching row in `x`
df1 <- data.frame(x = 1:3)
df2 <- data.frame(x = c(1, 1, 2), y = c("first", "second", "third"))
df1 %>% left_join(df2)

# By default, NAs match other NAs so that there are two
# rows in the output of this join:
df1 <- data.frame(x = c(1, NA), y = 2)
df2 <- data.frame(x = c(1, NA), z = 3)
left_join(df1, df2)

# You can optionally request that NAs don't match, giving a
# a result that more closely resembles SQL joins
left_join(df1, df2, na_matches = "never")
```

---

na_if	<i>Convert values to NA</i>
-------	-----------------------------

---

## Description

This is a translation of the SQL command NULLIF. It is useful if you want to convert an annoying value to NA.

## Usage

```
na_if(x, y)
```

## Arguments

x	The vector to modify.
y	The value to replace with NA.

## Value

A modified version of x that replaces any values that are equal to y with NA.

## See Also

[coalesce\(\)](#) to replace missing values within subsequent vector(s) of value(s). [replace\\_na\(\)](#) to replace NA with a value.

[replace\\_na\(\)](#) to replace NA with a value.

[recode\(\)](#) to more generally replace values.

**Examples**

```
na_if(1:5, 5:1)

x <- c(1, -1, 0, 10)
100 / x
100 / na_if(x, 0)

y <- c("abc", "def", "", "ghi")
na_if(y, "")

# na_if() is particularly useful inside mutate(),
# and is meant for use with vectors rather than entire data.frames
mtcars %>%
  mutate(cyl = na_if(cyl, 6))
```

---

near *Compare two numeric vectors*

---

**Description**

This is a safe way of comparing if two vectors of floating point numbers are (pairwise) equal. This is safer than using `==`, because it has a built in tolerance.

**Usage**

```
near(x, y, tol = .Machine$double.eps^0.5)
```

**Arguments**

x, y	Numeric vectors to compare
tol	Tolerance of comparison.

**Examples**

```
sqrt(2) ^ 2 == 2
near(sqrt(2) ^ 2, 2)
```

---

nest_by	<i>Nest By</i>
---------	----------------

---

### Description

`nest_by()` is similar to `group_by()` however instead of storing the group structure in the metadata, it is made explicit in the data. Each group key is given a single row within the `data.frame` and the group's data is stored within a list-column of the `data.frame`.

### Usage

```
nest_by(.data, ..., .key = "data", .keep = FALSE)
```

### Arguments

<code>.data</code>	A <code>data.frame</code> .
<code>...</code>	Grouping specification, forwarded to <code>group_by()</code> .
<code>.key</code>	<code>character(1)</code> . The name of the column in which to nest the data (default: "data").
<code>.keep</code>	<code>logical(1)</code> . Should the grouping columns be kept (default: TRUE)?

### Details

Currently there is no pretty-printing provided for the results of `nest_by()` and they are not useble with other functions such as `mutate()`.

### Examples

```
mtcars %>% nest_by(am, cyl)
# Or equivalently
mtcars %>% group_by(am, cyl) %>% nest_by()
```

---

n_distinct	<i>Count the number of unique values in a set of vectors</i>
------------	--

---

### Description

This is the equivalent of `length(unique(x))` for multiple vectors.

### Usage

```
n_distinct(..., na.rm = FALSE)
```

**Arguments**

...                    Vectors of values.  
 na.rm                logical(1). If TRUE missing values don't count.

**Examples**

```
x <- sample(1:10, 1e5, rep = TRUE)
length(unique(x))
n_distinct(x)
```

---

peek_vars	<i>Peek at variables in the selection context</i>
-----------	---

---

**Description**

Return the vector of column names of the data currently available for selection.

**Usage**

```
peek_vars()
```

**Value**

A vector of column names.

---

pipe	<i>Forward-pipe operator</i>
------	------------------------------

---

**Description**

Pipe an object forward into a function or call expression.

**Usage**

```
lhs %>% rhs
```

**Arguments**

lhs                    The result you are piping.  
 rhs                    Where you are piping the result to.

**Author(s)**

Nathan Eastwood and Antoine Fabri <antoine.fabri@gmail.com>.

**Examples**

```

# Basic use:
iris %>% head

# Use with lhs as first argument
iris %>% head(10)

# Using the dot place-holder
"Ceci n'est pas une pipe" %>% gsub("une", "un", .)

# When dot is nested, lhs is still placed first:
sample(1:10) %>% paste0(LETTERS[.])

# This can be avoided:
rnorm(100) %>% {c(min(.), mean(.), max(.))} %>% floor

# Lambda expressions:
iris %>%
{
  size <- sample(1:10, size = 1)
  rbind(head(., size), tail(., size))
}

# renaming in lambdas:
iris %>%
{
  my_data <- .
  size <- sample(1:10, size = 1)
  rbind(head(my_data, size), tail(my_data, size))
}

```

---

pull

*Pull out a single variable*


---

**Description**

This is a direct replacement for `[[.data.frame`.

**Usage**

```
pull(.data, var = -1)
```

**Arguments**

<code>.data</code>	A data.frame.
<code>var</code>	A variable specified as: <ul style="list-style-type: none"> <li>a literal variable name</li> </ul>

- a positive integer, giving the position counting from the left
- a negative integer, giving the position counting from the right

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

### Examples

```
mtcars %>% pull(-1)
mtcars %>% pull(1)
mtcars %>% pull(cyl)
mtcars %>% pull("cyl")
```

---

recode

*Recode values*

---

### Description

This is a vectorised version of `switch()`: you can replace numeric values based on their position or their name, and character or factor values only by their name. This is an S3 generic: `{poorman}` provides methods for numeric, character, and factors. For logical vectors, use `if_else()`. For more complicated criteria, use `case_when()`.

You can use `recode()` directly with factors; it will preserve the existing order of levels while changing the values. Alternatively, you can use `recode_factor()`, which will change the order of levels to match the order of replacements.

This is a direct port of the `dplyr::recode()` function.

### Usage

```
recode(.x, ..., .default = NULL, .missing = NULL)
```

```
recode_factor(.x, ..., .default = NULL, .missing = NULL, .ordered = FALSE)
```

### Arguments

<code>.x</code>	A vector to modify
<code>...</code>	Replacements. For character and factor <code>.x</code> , these should be named and replacement is based only on their name. For numeric <code>.x</code> , these can be named or not. If not named, the replacement is done based on position i.e. <code>.x</code> represents positions to look for in replacements. See examples. When named, the argument names should be the current values to be replaced, and the argument values should be the new (replacement) values. All replacements must be the same type, and must have either length one or the same length as <code>.x</code> .

<code>.default</code>	If supplied, all values not otherwise matched will be given this value. If not supplied and if the replacements are the same type as the original values in <code>.x</code> , unmatched values are not changed. If not supplied and if the replacements are not compatible, unmatched values are replaced with NA. <code>.default</code> must be either length 1 or the same length as <code>.x</code> .
<code>.missing</code>	If supplied, any missing values in <code>.x</code> will be replaced by this value. Must be either length 1 or the same length as <code>.x</code> .
<code>.ordered</code>	<code>logical(1)</code> . If TRUE, <code>recode_factor()</code> creates an ordered factor.

### Value

A vector the same length as `.x`, and the same type as the first of `...`, `.default`, or `.missing`. `recode_factor()` returns a factor whose levels are in the same order as in `...`. The levels in `.default` and `.missing` come last.

### See Also

[na\\_if\(\)](#) to replace specified values with a NA.  
[coalesce\(\)](#) to replace missing values with a specified value.  
[replace\\_na\(\)](#) to replace NA with a value.

### Examples

```
# For character values, recode values with named arguments only. Unmatched
# values are unchanged.
char_vec <- sample(c("a", "b", "c"), 10, replace = TRUE)
recode(char_vec, a = "Apple")
recode(char_vec, a = "Apple", b = "Banana")

# Use .default as replacement for unmatched values. Note that NA and
# replacement values need to be of the same type.
recode(char_vec, a = "Apple", b = "Banana", .default = NA_character_)

# Throws an error as NA is logical, not character.
## Not run:
recode(char_vec, a = "Apple", b = "Banana", .default = NA)

## End(Not run)

# For numeric values, named arguments can also be used
num_vec <- c(1:4, NA)
recode(num_vec, `2` = 20L, `4` = 40L)

# Or if you don't name the arguments, recode() matches by position.
# (Only works for numeric vector)
recode(num_vec, "a", "b", "c", "d")
# .x (position given) looks in (...), then grabs (... value at position)
# so if nothing at position (here 5), it uses .default or NA.
recode(c(1, 5, 3), "a", "b", "c", "d", .default = "nothing")
```

```

# Note that if the replacements are not compatible with .x,
# unmatched values are replaced by NA and a warning is issued.
recode(num_vec, `2` = "b", `4` = "d")
# use .default to change the replacement value
recode(num_vec, "a", "b", "c", .default = "other")
# use .missing to replace missing values in .x
recode(num_vec, "a", "b", "c", .default = "other", .missing = "missing")

# For factor values, use only named replacements
# and supply default with levels()
factor_vec <- factor(c("a", "b", "c"))
recode(factor_vec, a = "Apple", .default = levels(factor_vec))

# Use recode_factor() to create factors with levels ordered as they
# appear in the recode call. The levels in .default and .missing
# come last.
recode_factor(num_vec, `1` = "z", `2` = "y", `3` = "x")
recode_factor(num_vec, `1` = "z", `2` = "y", `3` = "x", .default = "D")
recode_factor(num_vec, `1` = "z", `2` = "y", `3` = "x", .default = "D", .missing = "M")

# When the input vector is a compatible vector (character vector or
# factor), it is reused as default.
recode_factor(letters[1:3], b = "z", c = "y")
recode_factor(factor(letters[1:3]), b = "z", c = "y")

```

---

relocate

*Change column order*


---

## Description

Use `relocate()` to change column positions, using the same syntax as `select()` to make it easy to move blocks of columns at once.

## Usage

```
relocate(.data, ..., .before = NULL, .after = NULL)
```

## Arguments

<code>.data</code>	A data frame.
<code>...</code>	<poor-select> Columns to move.
<code>.before, .after</code>	<poor-select> Destination of columns selected by <code>...</code> . Supplying neither will move columns to the left-hand side; specifying both will result in an error.



**Value**

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

- Rows are not affected.
- The same columns appear in the output, but (usually) in a different place.
- Data frame attributes are preserved.
- Groups are not affected.

**Examples**

```
df <- data.frame(
  a = 1, b = 1, c = 1, d = "a", e = "a", f = "a",
  stringsAsFactors = FALSE
)
df %>% relocate(f)
df %>% relocate(a, .after = c)
df %>% relocate(f, .before = b)
df %>% relocate(a, .after = last_col())

# Can also select variables based on their type
df %>% relocate(where(is.character))
df %>% relocate(where(is.numeric), .after = last_col())
# Or with any other select helper
df %>% relocate(any_of(c("a", "e", "i", "o", "u")))

# When .before or .after refers to multiple variables they will be
# moved to be immediately before/after the selected variables.
df2 <- data.frame(
  a = 1, b = "a", c = 1, d = "a",
  stringsAsFactors = FALSE
)
df2 %>% relocate(where(is.numeric), .after = where(is.character))
df2 %>% relocate(where(is.numeric), .before = where(is.character))
```

---

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**

```
rename(.data, ...)
```

```
rename_with(.data, .fn, .cols = everything(), ...)
```

**Arguments**

<code>.data</code>	A <code>data.frame</code>
<code>...</code>	For <code>rename()</code> : comma separated key-value pairs in the form of <code>new_name = old_name</code> to rename selected variables. For <code>rename_with()</code> : additional arguments passed onto <code>.fn</code> .
<code>.fn</code>	A function() used to transform the selected <code>.cols</code> . Should return a character vector the same length as the input.
<code>.cols</code>	Columns to rename; defaults to all columns.

**Value**

A `data.frame` with 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.

**Examples**

```
rename(mtcars, MilesPerGallon = mpg)
rename(mtcars, Cylinders = cyl, Gears = gear)
mtcars %>% rename(MilesPerGallon = mpg)

rename_with(mtcars, toupper)
rename_with(mtcars, toupper, starts_with("c"))
```

---

replace\_na

*Replace missing values*

---

**Description**

Replace missing values in a `data.frame` or vector.

**Usage**

```
replace_na(data, replace, ...)
```

**Arguments**

<code>data</code>	A <code>data.frame</code> or vector.
<code>replace</code>	If <code>data</code> is a <code>data.frame</code> , a named list giving the value to replace NA with for each column. If <code>data</code> is a vector, a single value used for replacement.
<code>...</code>	Additional arguments passed onto methods; not currently used.

**Value**

If data is a data.frame, `replace_na()` returns a data.frame. If data is a vector, `replace_na()` returns a vector of class determined by the union of data and replace.

**See Also**

[na\\_if\(\)](#) to replace specified values with a NA.

[coalesce\(\)](#) to replace missing values within subsequent vector(s) of value(s).

**Examples**

```
df <- data.frame(x = c(1, 2, NA), y = c("a", NA, "b"), stringsAsFactors = FALSE)
df %>% replace_na(list(x = 0, y = "unknown"))
df %>% mutate(x = replace_na(x, 0))

df$x %>% replace_na(0)
df$y %>% replace_na("unknown")
```

---

rownames

*Tools for working with row names*

---

**Description**

Tools for working with row names

**Usage**

```
rownames_to_column(.data, var = "rowname")
```

**Arguments**

`.data` A data.frame.

`var` character(1). The name of the column to use for row names.

**Value**

A data.frame

**Examples**

```
mtcars %>% rownames_to_column()
```

---

select	<i>Subset columns using their names and types</i>
--------	---

---

### 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). You can also use predicate functions like `is.numeric()` to select variables based on their properties.

### Usage

```
select(.data, ...)
```

### Arguments

<code>.data</code>	A <code>data.frame</code> .
<code>...</code>	<code>&lt;poor-select&gt;</code> 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.

### Details

#### Overview of selection features:

`poorman` 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.

These 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`.

These helpers select variables from 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.

This helper selects variables with a function:

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

**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.

**Examples**

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

# Select variables by name:
mtcars %>% select(mpg)

# Select multiple variables by separating them with commas. Note
# how the order of columns is determined by the order of inputs:
mtcars %>% select(displ, gear, am)

# Rename variables:
mtcars %>% select(MilesPerGallon = mpg, everything())

# The `:` operator selects a range of consecutive variables:
select(mtcars, mpg:cyl)

# The `!` operator negates a selection:
mtcars %>% select(!(mpg:qsec))
mtcars %>% select(!ends_with("p"))

# `&` and `|` take the intersection or the union of two selections:
iris %>% select(starts_with("Petal") & ends_with("Width"))
iris %>% select(starts_with("Petal") | ends_with("Width"))

# To take the difference between two selections, combine the `&` and
# `!` operators:
iris %>% select(starts_with("Petal") & !ends_with("Width"))
```

---

 select\_helpers

*Select Helpers*


---

**Description**

These functions allow you to select variables based on their names.

- `starts_with()`: Starts with a prefix.

- `ends_with()`: Ends with a prefix.
- `contains()`: Contains a literal string.
- `matches()`: Matches a regular expression.
- `all_of()`: Matches variable names in a character vector. All names must be present, otherwise an error is thrown.
- `any_of()`: The same as `all_of()` except it doesn't throw an error.
- `everything()`: Matches all variables.
- `last_col()`: Select the last variable, possibly with an offset.

### Usage

```
starts_with(match, ignore.case = TRUE, vars = peek_vars())
```

```
ends_with(match, ignore.case = TRUE, vars = peek_vars())
```

```
contains(match, ignore.case = TRUE, vars = peek_vars())
```

```
matches(match, ignore.case = TRUE, perl = FALSE, vars = peek_vars())
```

```
num_range(prefix, range, width = NULL, vars = peek_vars())
```

```
all_of(x, vars = peek_vars())
```

```
any_of(x, vars = peek_vars())
```

```
everything(vars = peek_vars())
```

```
last_col(offset = 0L, vars = peek_vars())
```

### Arguments

<code>match</code>	character(n). If length > 1, the union of the matches is taken.
<code>ignore.case</code>	logical(1). If TRUE, the default, ignores case when matching names.
<code>vars</code>	character(n). A character vector of variable names. When called from inside selecting functions such as <code>select()</code> , these are automatically set to the names of the table.
<code>perl</code>	logical(1). Should Perl-compatible regexps be used?
<code>prefix</code>	A prefix which starts the numeric range.
<code>range</code>	integer(n). A sequence of integers, e.g. 1:5.
<code>width</code>	numeric(1). Optionally, the "width" of the numeric range. For example, a range of 2 gives "01", a range of three "001", etc.
<code>x</code>	character(n). A vector of column names.
<code>offset</code>	integer(1). Select the nth variable from the end of the data.frame.

**Value**

An integer vector giving the position of the matched variables.

**See Also**

[select\(\)](#), [relocate\(\)](#), [where\(\)](#), [group\\_cols\(\)](#)

**Examples**

```
mtcars %>% select(starts_with("c"))
mtcars %>% select(starts_with(c("c", "h")))
mtcars %>% select(ends_with("b"))
mtcars %>% relocate(contains("a"), .before = mpg)
iris %>% select(matches(".t."))
mtcars %>% select(last_col())

# `all_of()` selects the variables in a character vector:
iris %>% select(all_of(c("Petal.Length", "Petal.Width")))
# `all_of()` is strict and will throw an error if the column name isn't found
try({iris %>% select(all_of(c("Species", "Genres")))})
# However `any_of()` allows missing variables
iris %>% select(any_of(c("Species", "Genres")))
```

---

slice

*Subset rows by position*

---

**Description**

Subset rows by their original position in the data.frame. Grouped data.frames use the position within each group.

**Usage**

```
slice(.data, ...)

slice_head(.data, ..., n, prop)

slice_tail(.data, ..., n, prop)

slice_min(.data, order_by, ..., n, prop, with_ties = TRUE)

slice_max(.data, order_by, ..., n, prop, with_ties = TRUE)

slice_sample(.data, ..., n, prop, weight_by = NULL, replace = FALSE)
```

**Arguments**

<code>.data</code>	A <code>data.frame</code> .
<code>...</code>	For <code>slice()</code> : integer row values. Provide either positive values to keep, or negative values to drop. The values provided must be either all positive or negative. Indices beyond the number of rows in the input are silently ignored.
<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. If the proportion of a group size is not an integer, it is rounded down.
<code>order_by</code>	The variable to order by.
<code>with_ties</code>	<code>logical(1)</code> . Should ties be kept together? The default, <code>TRUE</code> , may return more rows than you request. Use <code>FALSE</code> to ignore ties, and return the first <code>n</code> rows.
<code>weight_by</code>	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>replace</code>	<code>logical(1)</code> . Should sampling be performed with ( <code>TRUE</code> ) or without ( <code>FALSE</code> , the default) replacement.

**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.

**Examples**

```
slice(mtcars, c(1, 2, 3))
mtcars %>% slice(1:3)

# Similar to head(mtcars, 1)
mtcars %>% slice(1L)

# Similar to tail(mtcars, 1):
mtcars %>% slice(n())
mtcars %>% slice(5:n())
# Rows can be dropped with negative indices:
slice(mtcars, -(1:4))

# First and last rows based on existing order
mtcars %>% slice_head(n = 5)
mtcars %>% slice_tail(n = 5)

# Grouped operations:
```



```
mtcars %>% group_by(am, cyl, gear) %>% slice_head(n = 2)
```

---

**summarise***Reduce multiple values down to a single value*

---

## Description

Create one or more scalar variables summarising the variables of an existing data.frame. Grouped data.frames will result in one row in the output for each group.

## Usage

```
summarise(.data, ...)
```

```
summarize(.data, ...)
```

## Arguments

`.data` A data.frame.

`...` 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 vector of length n, e.g. `quantile()`.

## Details

`summarise()` and `summarize()` are synonyms.

## Examples

```
summarise(mtcars, mean(mpg))
summarise(mtcars, meanMpg = mean(mpg), sumMpg = sum(mpg))
mtcars %>% summarise(mean(mpg))
```

---

unite	<i>Unite Multiple Columns Into One</i>
-------	--

---

**Description**

Convenience function to paste together multiple columns.

**Usage**

```
unite(data, col, ..., sep = "_", remove = TRUE, na.rm = FALSE)
```

**Arguments**

data	A data.frame.
col	character(1) or symbol(1). The name of the new column.
...	The columns to unite.
sep	character(1). Separator to use between the values.
remove	logical(1). If TRUE, remove the input columns from the output data.frame.
na.rm	logical(1). If TRUE, missing values will be remove prior to uniting each value.

**Value**

A data.frame with the columns passed via ... pasted together in a new column.

**Examples**

```
df <- data.frame(x = c("a", "a", NA, NA), y = c("b", NA, "b", NA))
df

df %>% unite("z", x:y, remove = FALSE)
# To remove missing values:
df %>% unite("z", x:y, na.rm = TRUE, remove = FALSE)
```

---

where	<i>Select variables with a function</i>
-------	---

---

**Description**

This selection helper selects the variables for which a function returns TRUE.

**Usage**

```
where(fn)
```

**Arguments**

fn                    A function that returns TRUE or FALSE.

**Value**

A vector of integer column positions which are the result of the fn evaluation.

**See Also**

[select\\_helpers](#)

**Examples**

```
iris %>% select(where(is.numeric))
iris %>% select(where(function(x) is.numeric(x)))
iris %>% select(where(function(x) is.numeric(x) && mean(x) > 3.5))
```

---

window\_rank

*Windowed Rank Functions*

---

**Description**

Six variations on ranking functions, mimicking the ranking functions described in SQL2003. They are currently implemented using the built in [rank\(\)](#) function. All ranking functions map smallest inputs to smallest outputs. Use `desc()` to reverse the direction.

**Usage**

`cume_dist(x)`

`dense_rank(x)`

`min_rank(x)`

`ntile(x = row_number(), n)`

`percent_rank(x)`

`row_number(x)`

**Arguments**

x                    A vector of values to rank. Missing values are left as is. If you want to treat them as the smallest or largest values, replace with `Inf` or `-Inf` before ranking.

n                    `integer(1)`. The number of groups to split up into.

### Details

- `cume_dist()`: a cumulative distribution function. Proportion of all values less than or equal to the current rank.
- `dense_rank()`: like `min_rank()`, but with no gaps between ranks
- `min_rank()`: equivalent to `rank(ties.method = "min")`
- `ntile()`: a rough rank, which breaks the input vector into `n` buckets. The size of the buckets may differ by up to one, larger buckets have lower rank.
- `percent_rank()`: a number between 0 and 1 computed by rescaling `min_rank` to [0, 1]
- `row_number()`: equivalent to `rank(ties.method = "first")`

### Examples

```
x <- c(5, 1, 3, 2, 2, NA)
row_number(x)
min_rank(x)
dense_rank(x)
percent_rank(x)
cume_dist(x)
```

```
ntile(x, 2)
ntile(1:8, 3)
```

```
# row_number can be used with single table verbs without specifying x
# (for data frames and databases that support windowing)
mutate(mtcars, row_number() == 1L)
mtcars %>% filter(between(row_number(), 1, 10))
```

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