

# Package ‘Tplyr’

February 11, 2021

**Title** A Grammar of Clinical Data Summary

**Version** 0.4.0

**Description** A tool created to simplify the data manipulation necessary to create clinical reports.

**License** MIT + file LICENSE

**URL** <https://github.com/atorus-research/Tplyr>

**BugReports** <https://github.com/atorus-research/Tplyr/issues>

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.5.0)

**Imports** rlang (>= 0.4.6), assertthat (>= 0.2.1), magrittr (>= 1.5),  
dplyr (>= 1.0.0), purrr (>= 0.3.3), stringr (>= 1.4.0), tidyr  
(>= 1.0.2), tidyselect (>= 1.1.0), tibble (>= 3.0.1),  
lifecycle, forcats (>= 0.4.0)

**Suggests** testthat (>= 2.1.0), haven (>= 2.2.0), knitr, rmarkdown,  
huxtable, tidyverse, readr, kableExtra, pharmaRTF

**VignetteBuilder** knitr

**RoxygenNote** 7.1.1

**RdMacros** lifecycle

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2021-02-11 14:20:02 UTC

**R topics documented:**

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add\_column\_headers     *Attach column headers to a Tplyr output*

---

### Description

When working with 'huxtable' tables, column headers can be controlled as if they are rows in the data frame. add\_column\_headers eases the process of introducing these headers.

### Usage

```
add_column_headers(.data, s, header_n = NULL)
```

### Arguments

.data	The data.frame/tibble on which the headers shall be attached
s	The text containing the intended header string
header_n	A header_n or generic data.frame to use for binding count values. This is required if you are using the token replacement.

### Details

Headers are created by providing a single string. Columns are specified by delimitting each header with a '|' symbol. Instead of specifying the destination of each header, add\_column\_headers assumes that you have organized the columns of your data frame before hand. This means that after you use Tplyr::build(), if you'd like to reorganize the default column order (which is simply alphabetical), simply pass the build output to a dplyr::select or dplyr::relocate statement before passing into add\_column\_headers.

Spanning headers are also supported. A spanning header is an overarching header that sits across multiple columns. Spanning headers are introduced to add\_column\_header by providing the spanner text (i.e. the text that you'd like to sit in the top row), and then the spanned text (the bottom row) within curly brackets ('{}'). For example, take the iris dataset. We have the names:

```
"Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "Species"
```

If we wanted to provide a header string for this dataset, with spanners to help with categorization of the variables, we could provide the following string:

```
"Sepal {Length | Width} | Petal {Length | Width} | Species"
```

### Value

A data.frame with the processed header string elements attached as the top rows

### Important note

Make sure you are aware of the order of your variables prior to passing in to add\_column\_headers. The only requirement is that the number of column match. The rest is up to you.

### Development notes

There are a few features of `add_column_header` that are intended but not yet supported:

- Nested spanners are not yet supported. Only a spanning row and a bottom row can currently be created
- Different delimiters and indicators for a spanned group may be used in the future. The current choices were intuitive, but based on feedback it could be determined that less common characters may be necessary.

### Token Replacement

This function has support for reading values from the `header_n` object in a Tplyr table and adding them in the column headers. Note: The order of the parameters passed in the token is important. They should be first the treatment variable then any `cols` variables in the order they were passed in the table construction.

Use a double asterisk `**` at the beginning to start the token and another double asterisk to close it. You can separate column parameters in the token with a single underscore. For example, `**group1_flag2_param3**` will pull the count from the `header_n` binding for `group1` in the `treat_var`, `flag2` in the first `cols` argument, and `param3` in the second `cols` argument.

You can pass fewer arguments in the token to get the sum of multiple columns. For example, `**group1**` would get the sum of the `group1` `treat_var`, and all `cols` from the `header_n`.

### Examples

```
# Load in pipe
library(magrittr)
library(dplyr)
header_string <- "Sepal {Length | Width} | Petal {Length | Width} | Species"

iris2 <- iris %>%
  mutate_all(as.character)

iris2 %>% add_column_headers(header_string)

# Example with counts
mtcars2 <- mtcars %>%
  mutate_all(as.character)

t <- tplyr_table(mtcars2, vs, cols = am) %>%
  add_layer(
    group_count(cyl)
  )

b_t <- build(t) %>%
  mutate_all(as.character)

count_string <- paste0(" | V N=**0** {auto N=**0_0** | man N=**0_1**} |",
  " S N=**1** {auto N=**1_0** | man N=**1_1**} | | ")

add_column_headers(b_t, count_string, header_n(t))
```

---

 add\_layer

*Attach a layer to a tplyr\_table object*


---

### Description

add\_layer attaches a tplyr\_layer to a tplyr\_table object. This allows for a tidy style of programming (using magrittr piping, i.e. %>%) with a secondary advantage - the construction of the layer object may consist of a series of piped functions itself.

Tplyr encourages a user to view the construction of a table as a series of "layers". The construction of each of these layers are isolated and independent of one another - but each of these layers are children of the table itself. add\_layer isolates the construction of an individual layer and allows the user to construct that layer and insert it back into the parent. The syntax for this is intuitive and allows for tidy piping. Simply pipe the current table object in, and write the code to construct your layer within the layer parameter.

add\_layers is another approach to attaching layers to a tplyr\_table. Instead of constructing the entire table at once, add\_layers allows you to construct layers as different objects. These layers can then be attached into the tplyr\_table all at once.

add\_layer and add\_layers both additionally allow you to name the layers as you attach them. This is helpful when using functions like [get\\_numeric\\_data](#) or [get\\_stats\\_data](#) when you can access information from a layer directly. add\_layer has a name parameter, and layers can be named in add\_layers by submitting the layer as a named argument.

### Usage

```
add_layer(parent, layer, name = NULL)
```

```
add_layers(parent, ...)
```

### Arguments

parent	A tplyr_table or tplyr_layer/tplyr_subgroup_layer object
layer	A layer construction function and associated modifier functions
name	A name to provide the layer in the table layers container
...	Layers to be added

### Value

A tplyr\_table or tplyr\_layer/tplyr\_subgroup\_layer with a new layer inserted into the layer binding

### See Also

[[tplyr\\_table\(\)](#), [tplyr\\_layer\(\)](#), [group\\_count\(\)](#), [group\\_desc\(\)](#), [group\\_shift\(\)](#)]

**Examples**

```

# Load in pipe
library(magrittr)

## Single layer
t <- tplyr_table(mtcars, cyl) %>%
  add_layer(
    group_desc(target_var=mpg)
  )

## Single layer with name
t <- tplyr_table(mtcars, cyl) %>%
  add_layer(name='mpg',
    group_desc(target_var=mpg)
  )

# Using add_layers
t <- tplyr_table(mtcars, cyl)
l1 <- group_desc(t, target_var=mpg)
l2 <- group_count(t, target_var=cyl)

t <- add_layers(t, l1, 'cyl' = l2)

```

---

add\_risk\_diff

*Add risk difference to a count layer*


---

**Description**

A very common requirement for summary tables is to calculate the risk difference between treatment groups. `add_risk_diff` allows you to do this. The underlying risk difference calculations are performed using the Base R function [prop.test](#) - so prior to using this function, be sure to familiarize yourself with its functionality.

**Usage**

```
add_risk_diff(layer, ..., args = list(), distinct = TRUE)
```

**Arguments**

layer	Layer upon which the risk difference will be attached
...	Comparison groups, provided as character vectors where the first group is the comparison, and the second is the reference
args	Arguments passed directly into <a href="#">prop.test</a>
distinct	Logical - Use distinct counts (if available).

## Details

`add_risk_diff` can only be attached to a count layer, so the count layer must be constructed first. `add_risk_diff` allows you to compare the difference between treatment group, so all comparisons should be based upon the values within the specified `treat_var` in your `tplyr_table` object.

Comparisons are specified by providing two-element character vectors. You can provide as many of these groups as you want. You can also use groups that have been constructed using `add_treat_grps` or `add_total_group`. The first element provided will be considered the 'reference' group (i.e. the left side of the comparison), and the second group will be considered the 'comparison'. So if you'd like to see the risk difference of 'T1 - Placebo', you would specify this as `c('T1', 'Placebo')`.

`Tplyr` forms your two-way table in the background, and then runs `prop.test` appropriately. Similar to way that the display of layers are specified, the exact values and format of how you'd like the risk difference display are set using `set_format_strings`. This controls both the values and the format of how the risk difference is displayed. Risk difference formats are set within `set_format_strings` by using the name 'riskdiff'.

You have 5 variables to choose from in your data presentation:

**comp** Probability of the left hand side group (i.e. comparison)

**ref** Probability of the right hand side group (i.e. reference)

**dif** Difference of comparison - reference

**low** Lower end of the confidence interval (default is 95%, override with the `args` parameter)

**high** Upper end of the confidence interval (default is 95%, override with the `args` parameter)

Use these variable names when forming your `f_str` objects. The default presentation, if no string format is specified, will be:

```
f_str('xx.xxx (xx.xxx, xx.xxx)', dif, low, high)
```

Note - within `Tplyr`, you can account for negatives by allowing an extra space within your integer side settings. This will help with your alignment.

If columns are specified on a `Tplyr` table, risk difference comparisons still only take place between groups within the `treat_var` variable - but they are instead calculated treating the `cols` variables as by variables. Just like the `tplyr` layers themselves, the risk difference will then be transposed and display each risk difference as separate variables by each of the `cols` variables.

If `distinct` is `TRUE` (the default), all calculations will take place on the distinct counts, if they are available. Otherwise, non-distinct counts will be used.

One final note - `prop.test` may throw quite a few warnings. This is natural, because it alerts you when there's not enough data for the approximations to be correct. This may be unnerving coming from a SAS programming world, but this is R is trying to alert you that the values provided don't have enough data to truly be statistically accurate.

## Examples

```
library(magrittr)

## Two group comparisons with default options applied
t <- tplyr_table(mtcars, gear)
```

```

# Basic risk diff for two groups, using defaults
l1 <- group_count(t, carb) %>%
  # Compare 3 vs. 4, 3 vs. 5
  add_risk_diff(
    c('3', '4'),
    c('3', '5')
  )

# Build and show output
add_layers(t, l1) %>% build()

## Specify custom formats and display variables
t <- tplyr_table(mtcars, gear)

# Create the layer with custom formatting
l2 <- group_count(t, carb) %>%
  # Compare 3 vs. 4, 3 vs. 5
  add_risk_diff(
    c('3', '4'),
    c('3', '5')
  ) %>%
  set_format_strings(
    'n_counts' = f_str('xx (xx.x)', n, pct),
    'riskdiff' = f_str('xx.xxx, xx.xxx, xx.xxx, xx.xxx, xx.xxx', comp, ref, dif, low, high)
  )

# Build and show output
add_layers(t, l2) %>% build()

## Passing arguments to prop.test
t <- tplyr_table(mtcars, gear)

# Create the layer with args option
l3 <- group_count(t, carb) %>%
  # Compare 3 vs. 4, 4 vs. 5
  add_risk_diff(
    c('3', '4'),
    c('3', '5'),
    args = list(conf.level = 0.9, correct=FALSE, alternative='less')
  )

# Build and show output
add_layers(t, l3) %>% build()

```

---

add\_total\_row

*Add a Total row into a count summary.*


---

### Description

Adding a total row creates an additional observation in the count summary that presents the total counts (i.e. the n's that are summarized). The format of the total row will be formatted in the same



way as the other count strings.

### Usage

```
add_total_row(e, fmt = NULL, count_missings = TRUE, sort_value = NULL)
```

### Arguments

e	A count_layer object
fmt	An f_str object used to format the total row. If none is provided, display is based on the layer formatting.
count_missings	Whether or not to ignore the named arguments passed in 'set_count_missing()' when calculating counts total row. This is useful if you need to exclude/include the missing counts in your total row. Defaults to TRUE meaning total row will not ignore any values.
sort_value	The value that will appear in the ordering column for total rows. This must be a numeric value.

### Details

Totals are calculated using all grouping variables, including treat\_var and cols from the table level. If by variables are included, the grouping of the total and the application of denominators becomes ambiguous. You will be warned specifically if a percent is included in the format. To rectify this, use set\_denoms\_by(), and the grouping of add\_total\_row() will be updated accordingly.

### Examples

```
# Load in Pipe
library(magrittr)

tplyr_table(mtcars, gear) %>%
  add_layer(
    group_count(cyl) %>%
      add_total_row(f_str("xxxx", n))
  ) %>%
  build()
```

---

add\_treat\_grps

*Combine existing treatment groups for summary*

---

### Description

Summary tables often present individual treatment groups, but may additionally have a "Treatment vs. Placebo" or "Total" group added to show grouped summary statistics or counts. This set of functions offers an interface to add these groups at a table level and be consumed by subsequent layers.

**Usage**

```
add_treat_grps(table, ...)

add_total_group(table, group_name = "Total")

treat_grps(table)
```

**Arguments**

table	A tplyr_table object
...	A named vector where names will become the new treatment group names, and values will be used to construct those treatment groups
group_name	The treatment group name used for the constructed 'Total' group

**Details**

add\_treat\_grps allows you to specify specific groupings. This is done by supplying named arguments, where the name becomes the new treatment group's name, and those treatment groups are made up of the argument's values.

add\_total\_group is a simple wrapper around add\_treat\_grps. Instead of producing custom groupings, it produces a "Total" group by the supplied name, which defaults to "Total". This "Total" group is made up of all existing treatment groups within the population dataset.

The function treat\_grps allows you to see the custom treatment groups available in your tplyr\_table object

**Value**

The modified table object

**Examples**

```
tab <- tplyr_table(iris, Species)

# A custom group
add_treat_grps(tab, "Not Setosa" = c("versicolor", "virginica"))

# Add a total group
add_total_group(tab)

treat_grps(tab)
# Returns:
# $`Not Setosa`
#[1] "versicolor" "virginica"
#
# $Total
#[1] "setosa"      "versicolor" "virginica"
```

---

apply_row_masks	<i>Replace repeating row label variables with blanks in preparation for display.</i>
-----------------	--

---

### Description

Depending on the display package being used, row label values may need to be blanked out if they are repeating. This gives the data frame supporting the table the appearance of the grouping variables being grouped together in blocks. `apply_row_masks` does this work by blanking out the value of any `row_label` variable where the current value is equal to the value before it. Note - `apply_row_masks` assumes that the data frame has already be sorted and therefore should only be applied once the data frame is in its final sort sequence.

### Usage

```
apply_row_masks(dat, row_breaks = FALSE, ...)
```

### Arguments

<code>dat</code>	Data.frame / tibble to mask repeating row_labels
<code>row_breaks</code>	Boolean - set to TRUE to insert row breaks
<code>...</code>	Variable used to determine where row-breaks should be inserted. Breaks will be inserted when this group of variables changes values. This is determined by dataset order, so sorting should be done prior to using <code>apply_row_masks</code> . If left empty, <code>ord_layer_index</code> will be used.

### Details

Additionally, `apply_row_masks` can add row breaks for you between each layer. Row breaks are inserted as blank rows. This relies on the "break by" variables (submitted via `...`) constructed in `build` still being attached to the dataset. An additional order variable is attached named `ord_break`, but the output dataset is sorted to properly insert the row breaks between layers.

### Value

tibble with blanked out rows where values are repeating

---

build	<i>Trigger the execution of the tplyr_table</i>
-------	---

---

### Description

The functions used to assemble a `tplyr_table` object and each of the layers do not trigger the processing of any data. Rather, a lazy execution style is used to allow you to construct your table and then explicitly state when the data processing should happen. `build` triggers this event.

### Usage

```
build(x)
```

### Arguments

`x` A `tplyr_table` object

### Details

When the `build` command is executed, all of the data processing commences. Any preprocessing necessary within the table environment takes place first. Next, each of the layers begins executing. Once the layers complete executing, the output of each layer is stacked into the resulting data frame.

Once this process is complete, any post-processing necessary within the table environment takes place, and the final output can be delivered. Metadata and traceability information are kept within each of the layer environments, which allows an investigation into the source of the resulting data-points. For example, numeric data from any summaries performed is maintained and accessible within a layer using `get_numeric_data`.

### Value

An executed `tplyr_table`

### See Also

`tplyr_table`, `tplyr_layer`, `add_layer`, `add_layers`, `layer_constructors`

### Examples

```
# Load in Pipe
library(magrittr)

tplyr_table(iris, Species) %>%
  add_layer(
    group_desc(Sepal.Length, by = "Sepal Length")
  ) %>%
  add_layer(
    group_desc(Sepal.Width, by = "Sepal Width")
  ) %>%
```

```
build()
```

---

f\_str *Create a f\_str object*

---

### Description

f\_str objects are intended to be used within the function `set_format_strings`. The f\_str object carries information that powers a significant amount of layer processing. The `format_string` parameter is capable of controlling the display of a data point and decimal precision. The variables provided in ... control which data points are used to populate the string formatted output.

### Usage

```
f_str(format_string, ..., empty = c(.overall = ""))
```

### Arguments

<code>format_string</code>	The desired display format. X's indicate digits. On the left, the number of x's indicates the integer length. On the right, the number of x's controls decimal precision and rounding. Variables are inferred by any separation of the 'x' values other than a decimal.
<code>...</code>	The variables to be formatted using the format specified in <code>format_string</code> .
<code>empty</code>	The string to display when the numeric data is not available. For desc layers, an unnamed character vector will populate within the provided format string, set to the same width as the fitted numbers. Use a single element character vector, with the element named <code>'.overall'</code> to instead replace the whole string.

### Details

Format strings are one of the most powerful components of 'Tplyr'. Traditionally, converting numeric values into strings for presentation can consume a good deal of time. Values and decimals need to align between rows, rounding before trimming is sometimes forgotten - it can become a tedious mess that is realistically not an important part of the analysis being performed. 'Tplyr' makes this process as simple as we can, while still allowing flexibility to the user.

Tplyr provides both manual and automatic decimal precision formatting. The display of the numbers in the resulting data frame is controlled by the `format_string` parameter. For manual precision, just like dummy values may be presented on your mocks, integer and decimal precision is specified by the user providing a string of 'x's for how you'd like your numbers formatted. If you'd like 2 integers with 3 decimal places, you specify your string as `'xx.xxx'`. 'Tplyr' does the work to get the numbers in the right place.

To take this a step further, automatic decimal precision can also be obtained based on the collected precision within the data. When creating tables where results vary by some parameter, different results may call for different degrees of precision. To use automatic precision, use a single 'a' on either the integer and decimal side. If you'd like to use increased precision (i.e. you'd like mean to

be collected precision +1), use 'a+1'. So if you'd like both integer and decimal precision to be based on the data as collected, you can use a format like 'a.a' - or for collected+1 decimal precision, 'a.a+1'. You can mix and match this with manual formats as well, making format strings such as 'xx.a+1'.

If you want two numbers on the same line, you provide two sets of x's. For example, if you're presenting a value like "mean (sd)" - you could provide the string 'xx.xx (xx.xxx)', or perhaps 'a.a+1 (a.a+2). Note that you're able to provide different integer lengths and different decimal precision for the two values. Each format string is independent and relates only to the format specified.

The other parameters of the `f_str` call specify what values should fill the x's. `f_str` objects are used slightly differently between different layers. When declaring a format string within a count layer, `f_str` expects to see the values `n` and (if desired) `pct`, which specifies the formatting for your n's and percent values. But in descriptive statistic layers, `f_str` parameters refer to the names of the summaries being performed, either by built in defaults, or custom summaries declared using [set\\_custom\\_summaries](#). See [set\\_format\\_strings](#) for some more notes about layers specific implementation.

Count and shift layers frequencies and percentages can be specified with 'n' and 'pct' respectively. Distinct values can also be presented in count layers with the arguments 'distinct' and 'distinct\_total'.

### Value

A `f_str` object

### Examples

```
f_str("xx.x (xx.x)", mean, sd)
f_str("a.a+1 (a.a+2)", mean, sd)
f_str("xx.a (xx.a+1)", mean, sd)
f_str("xx.x, xx.x, xx.x", q1, median, q3)
```

---

get\_by

*Set or return by layer binding*

---

### Description

Set or return by layer binding

### Usage

```
get_by(layer)
set_by(layer, by)
```

**Arguments**

layer            A tplyr\_layer object  
 by                A string, a variable name, or a list of variable names supplied using `dplyr::vars`.

**Value**

For `get_by`, the `by` binding of the supplied layer. For `set_by` the modified layer environment.

**Examples**

```
# Load in pipe
library(magrittr)
iris$Species2 <- iris$Species
lay <- tplyr_table(iris, Species) %>%
  group_count(Species) %>%
  set_by(vars(Species2, Sepal.Width))
```

---

get\_desc\_layer\_formats

*Get or set the default format strings for descriptive statistics layers*

---

**Description**

Tplyr provides you with the ability to set table-wide defaults of format strings. You may wish to reuse the same format strings across numerous layers. `set_desc_layer_formats` and `set_count_layer_formats` allow you to apply your desired format strings within the entire scope of the table.

**Usage**

```
get_desc_layer_formats(obj)

set_desc_layer_formats(obj, ...)

get_count_layer_formats(obj)

set_count_layer_formats(obj, ...)

get_shift_layer_formats(obj)

set_shift_layer_formats(obj, ...)
```

**Arguments**

obj                A tplyr\_table object  
 ...                formats to pass forward

**Details**

For descriptive statistic layers, you can also use `set_format_strings` and `set_desc_layer_formats` together within a table, but not within the same layer. In the absence of specified format strings, first the table will be checked for any available defaults, and otherwise the `tplyr.desc_layer_default_formats` option will be used. `set_format_strings` will always take precedence over either. Defaults cannot be combined between `set_format_strings`, `set_desc_layer_formats`, and the `tplyr.desc_layer_default_formats` because the order of presentation of results is controlled by the format strings, so relying on combinations of these setting would not be intuitive.

For count layers, you can override the `n_counts` or `riskdiff` format strings separately, and the narrowest scope available will be used from layer, to table, to default options.

---

<code>get_numeric_data</code>	<i>Retrieve the numeric data from a tplyr objects</i>
-------------------------------	---

---

**Description**

`get_numeric_data` provides access to the un-formatted numeric data for each of the layers within a `tplyr_table`, with options to allow you to extract distinct layers and filter as desired.

**Usage**

```
get_numeric_data(x, layer = NULL, where = TRUE, ...)
```

**Arguments**

<code>x</code>	A <code>tplyr_table</code> or <code>tplyr_layer</code> object
<code>layer</code>	Layer name or index to select out specifically
<code>where</code>	Subset criteria passed to <code>dplyr::filter</code>
<code>...</code>	Additional arguments to pass forward

**Details**

When used on a `tplyr_table` object, this method will aggregate the numeric data from all Tplyr layers. The data will be returned to the user in a list of data frames. If the data has already been processed (i.e. `build` has been run), the numeric data is already available and will be returned without reprocessing. Otherwise, the numeric portion of the layer will be processed.

Using the `layer` and `where` parameters, data for a specific layer can be extracted and subset. This is most clear when layers are given text names instead of using a layer index, but a numeric index works as well.

**Value**

Numeric data from the Tplyr layer



## Examples

```
# Load in pipe
library(magrittr)

t <- tplyr_table(mtcars, gear) %>%
  add_layer(name='drat',
            group_desc(drat)
  ) %>%
  add_layer(name='cyl',
            group_count(cyl)
  )

# Return a list of the numeric data frames
get_numeric_data(t)

# Get the data from a specific layer
get_numeric_data(t, layer='drat')
get_numeric_data(t, layer=1)

# Choose multiple layers by name or index
get_numeric_data(t, layer=c('cyl', 'drat'))
get_numeric_data(t, layer=c(2, 1))

# Get the data and filter it
get_numeric_data(t, layer='drat', where = gear==3)
```

---

get\_precision\_by      *Set or return precision\_by layer binding*

---

## Description

The precision\_by variables are used to collect the integer and decimal precision when auto-precision is used. These by variables are used to group the input data and identify the maximum precision available within the dataset for each by group. The precision\_by variables must be a subset of the by variables

## Usage

```
get_precision_by(layer)

set_precision_by(layer, precision_by)
```

## Arguments

layer            A tplyr\_layer object  
precision\_by    A string, a variable name, or a list of variable names supplied using dplyr::vars.

**Value**

For `get_precision_by`, the `precision_by` binding of the supplied layer. For `set_precision_by` the modified layer environment.

**Examples**

```
# Load in pipe
library(magrittr)
lay <- tplyr_table(mtcars, gear) %>%
  add_layer(
    group_desc(mpg, by=vars(carb, am)) %>%
    set_precision_by(carb)
  )
```

---

<code>get_precision_on</code>	<i>Set or return precision_on layer binding</i>
-------------------------------	---

---

**Description**

The `precision_on` variable is the variable used to establish numeric precision. This variable must be included in the list of `target_var` variables.

**Usage**

```
get_precision_on(layer)

set_precision_on(layer, precision_on)
```

**Arguments**

`layer`            A `tplyr_layer` object  
`precision_on`    A string, a variable name, or a list of variable names supplied using `dplyr::vars`.

**Value**

For `get_precision_on`, the `precision_on` binding of the supplied layer. For `set_precision_on` the modified layer environment.

**Examples**

```
# Load in pipe
library(magrittr)
lay <- tplyr_table(mtcars, gear) %>%
  add_layer(
    group_desc(vars(mpg, disp), by=vars(carb, am)) %>%
    set_precision_on(disp)
  )
```

---

get_stats_data	<i>Get statistics data</i>
----------------	----------------------------

---

**Description**

Like the layer numeric data, Tplyr also stores the numeric data produced from statistics like risk difference. This helper function gives you access to obtain that data from the environment

**Usage**

```
get_stats_data(x, layer = NULL, statistic = NULL, where = TRUE, ...)
```

**Arguments**

x	A tplyr_table or tplyr_layer object
layer	Layer name or index to select out specifically
statistic	Statistic name or index to select
where	Subset criteria passed to dplyr::filter
...	Additional arguments passed to dispatch

**Details**

When used on a tplyr\_table object, this method will aggregate the numeric data from all Tplyr layers and calculate all statistics. The data will be returned to the user in a list of data frames. If the data has already been processed (i.e. build has been run), the numeric data is already available and the statistic data will simply be returned. Otherwise, the numeric portion of the layer will be processed.

Using the layer, where, and statistic parameters, data for a specific layer statistic can be extracted and subset, allowing you to directly access data of interest. This is most clear when layers are given text names instead of using a layer index, but a numeric index works as well. If just a statistic is specified, that statistic will be collected and returned in a list of data frames, allowing you to grab, for example, just the risk difference statistics across all layers.

**Value**

The statistics data of the supplied layer

**Examples**

```
library(magrittr)

t <- tplyr_table(mtcars, gear) %>%
  add_layer(name='drat',
            group_desc(drat)
  ) %>%
  add_layer(name="cyl",
            group_count(cyl))
```

```

) %>%
add_layer(name="am",
           group_count(am) %>%
           add_risk_diff(c('4', '3')))
) %>%
add_layer(name="carb",
           group_count(carb) %>%
           add_risk_diff(c('4', '3')))
)

# Returns a list of lists, containing stats data from each layer
get_stats_data(t)

# Returns just the riskdiff statistics from each layer - NULL
# for layers without riskdiff
get_stats_data(t, statistic="riskdiff")

# Return the statistic data for just the "am" layer - a list
get_stats_data(t, layer="am")
get_stats_data(t, layer=3)

# Return the statistic data for just the "am" and "cyl", layer - a
# list of lists
get_stats_data(t, layer=c("am", "cyl"))
get_stats_data(t, layer=c(3, 2))

# Return just the statistic data for "am" and "cyl" - a list
get_stats_data(t, layer=c("am", "cyl"), statistic="riskdiff")
get_stats_data(t, layer=c(3, 2), statistic="riskdiff")

# Return the riskdiff for the "am" layer - a data frame
get_stats_data(t, layer="am", statistic="riskdiff")

# Return and filter the riskdiff for the am layer - a data frame
get_stats_data(t, layer="am", statistic="riskdiff", where = summary_var==1)

```

---

get_target_var	<i>Set or return treat_var binding</i>
----------------	--

---

## Description

Set or return treat\_var binding

## Usage

```
get_target_var(layer)
```

```
set_target_var(layer, target_var)
```

**Arguments**

layer            A tplyr\_layer object  
 target\_var      A symbol to perform the analysis on

**Value**

For treat\_var, the treatment variable binding of the layer object. For set\_treat\_var, the modified layer environment.

**Examples**

```
# Load in pipe
library(magrittr)
iris$Species2 <- iris$Species
lay <- tplyr_table(iris, Species) %>%
  group_count(Species) %>%
  set_target_var(Species2)
```

---

get\_where.tplyr\_layer *Set or return where binding for layer or table*

---

**Description**

Set or return where binding for layer or table

**Usage**

```
## S3 method for class 'tplyr_layer'
get_where(obj)

## S3 method for class 'tplyr_layer'
set_where(obj, where)

get_where(obj)

## S3 method for class 'tplyr_table'
get_where(obj)

set_where(obj, where)

## S3 method for class 'tplyr_table'
set_where(obj, where)

set_pop_where(obj, where)

get_pop_where(obj)
```

**Arguments**

`obj` A `tplyr_layer` or `tplyr_table` object.

`where` An expression (i.e. syntax) to be used to subset the data. Supply as programming logic (i.e. `x < 5 & y == 10`)

**Value**

For `where`, the `where` binding of the supplied object. For `set_where`, the modified object

**Examples**

```
# Load in pipe
library(magrittr)

iris$Species2 <- iris$Species
lay <- tplyr_table(iris, Species) %>%
  group_count(Species) %>%
  set_where(Petal.Length > 3) %>%
  # Set logic for pop_data as well
  set_pop_where(Petal.Length > 3)
```

---

<code>group_count</code>	<i>Create a count, desc, or shift layer for discrete count based summaries, descriptive statistics summaries, or shift count summaries</i>
--------------------------	--

---

**Description**

This family of functions specifies the type of summary that is to be performed within a layer. `count` layers are used to create summary counts of some discrete variable. `desc` layers create summary statistics, and `shift` layers summaries the counts of different changes in states. See the "details" section below for more information.

**Usage**

```
group_count(parent, target_var, by = vars(), where = TRUE, ...)
```

```
group_desc(parent, target_var, by = vars(), where = TRUE, ...)
```

```
group_shift(parent, target_var, by = vars(), where = TRUE, ...)
```

**Arguments**

`parent` Required. The parent environment of the layer. This must be the `tplyr_table` object that the layer is contained within.

`target_var` Symbol. Required, The variable name(s) on which the summary is to be performed. Must be a variable within the target dataset. Enter unquoted - i.e. `target_var = AEBODSYS`. You may also provide multiple variables with `vars`.

by	A string, a variable name, or a list of variable names supplied using <code>vars</code>
where	Call. Filter logic used to subset the target data when performing a summary.
...	Additional arguments to pass forward

## Details

**Count Layers** Count layers allow you to create summaries based on counting values with a variable. Additionally, this layer allows you to create n (%) summaries where you're also summarizing the proportion of instances a value occurs compared to some denominator. Count layers are also capable of producing counts of nested relationships. For example, if you want to produce counts of an overall outside group, and then the subgroup counts within that group, you can specify the target variable as `vars(OutsideVariable, InsideVariable)`. This allows you to do tables like Adverse Events where you want to see the Preferred Terms within Body Systems, all in one layer. Further control over denominators is available using the function `set_denoms_by` and distinct counts can be set using `set_distinct_by`

**Descriptive Statistics Layers** Descriptive statistics layers perform summaries on continuous variables. There are a number of summaries built into Tplyr already that you can perform, including n, mean, median, standard deviation, variance, min, max, inter-quartile range, Q1, Q3, and missing value counts. From these available summaries, the default presentation of a descriptive statistic layer will output 'n', 'Mean (SD)', 'Median', 'Q1, Q3', 'Min, Max', and 'Missing'. You can change these summaries using `set_format_strings`, and you can also add your own summaries using `set_custom_summaries`. This allows you to implement any additional summary statistics you want presented.

**Shift Layers** A shift layer displays an endpoint's 'shift' throughout the duration of the study. It is an abstraction over the count layer, however we have provided an interface that is more efficient and intuitive. Targets are passed as named symbols using `dplyr::vars`. Generally the baseline is passed with the name 'row' and the shift is passed with the name 'column'. Both counts (n) and percentages (pct) are supported and can be specified with the `set_format_strings` function. To allow for flexibility when defining percentages, you can define the denominator using the `set_denoms_by` function. This function takes variable names and uses those to determine the denominator for the counts.

## Value

An `tplyr_layer` environment that is a child of the specified parent. The environment contains the object as listed below.

A `tplyr_layer` object

## See Also

[[add\\_layer](#), [add\\_layers](#), [tplyr\\_table](#), [tplyr\\_layer](#)]

## Examples

```
# Load in pipe
library(magrittr)

t <- tplyr_table(iris, Species) %>%
```

```

add_layer(
  group_desc(target_var=Sepal.Width)
)

t <- tplyr_table(iris, Species) %>%
  add_layer(
    group_desc(target_var=Sepal.Width)
  )

t <- tplyr_table(mtcars, am) %>%
  add_layer(
    group_shift(vars(row=gear, column=carb), by=cyl)
  )

```

---

header_n	<i>Return or set header_n binding</i>
----------	---------------------------------------

---

### Description

The ‘header\_n()’ functions can be used to automatically pull the header\_n derivations from the table or change them for future use.

### Usage

```
header_n(table)
```

```
header_n(x) <- value
```

```
set_header_n(table, value)
```

### Arguments

table	A tplyr_table object
x	A tplyr_table object
value	A data.frame with columns with the treatment variable, column variabes, and a variable with counts named ‘n’.
header_n	A data.frame with columns with the treatment variable, column variabes, and a variable with counts named ‘n’.

### Details

The ‘header\_n’ object is created by Tplyr when a table is built and intended to be used by the ‘add\_column\_headers()’ function when displaying table level population totals. These methods are intended to be used for calling the population totals calculated by Tplyr, and to overwrite them if a user chooses to.

If you have a need to change the header Ns that appear in your table headers, say you know you are working with a subset of the data that doesn’t represent the totals, you can replace the data used with ‘set\_header\_n()’.



**Value**

For `tplyr_header_n` the `header_n` binding of the `tplyr_table` object. For `tplyr_header_n<-` and `set_tplyr_header_n` the modified object.

**Examples**

```
tab <- tplyr_table(mtcars, gear)

header_n(tab) <- data.frame(
  gear = c(3, 4, 5),
  n = c(10, 15, 45)
)
```

---

keep_levels	<i>Select levels to keep in a count layer</i>
-------------	---

---

**Description**

In certain cases you only want a layer to include certain values of a factor. The `'keep_levels()'` function allows you to pass character values to be included in the layer. The others are ignored. **\*\*NOTE: Denominator calculation is unaffected by this function, see the examples on how to include this logic in your percentages\*\***

**Usage**

```
keep_levels(e, ...)
```

**Arguments**

e	A <code>count_layer</code> object
...	Character values to count into the layer

**Value**

The modified Tplyr layer object

**Examples**

```
library(dplyr)
mtcars <- mtcars %>%
  mutate_all(as.character)

t <- tplyr_table(mtcars, gear) %>%
  add_layer(
    group_count(cyl) %>%
```

```

      keep_levels("4", "8") %>%
      set_denom_where(cyl %in% c("4", "8"))
    ) %>%
    build()

```

---

pop\_data

*Return or set population data bindings*

---

### Description

The population data is used to gather information that may not be available from the target dataset. For example, missing treatment groups, population N counts, and proper N counts for denominators will be provided through the population dataset. The population dataset defaults to the target dataset unless otherwise specified using `set_pop_data`.

### Usage

```

pop_data(table)

pop_data(x) <- value

set_pop_data(table, pop_data)

```

### Arguments

table	A <code>tplyr_table</code> object
x	A <code>tplyr_table</code> object
value	A <code>data.frame</code> with population level information
pop_data	A <code>data.frame</code> with population level information

### Value

For `tplyr_pop_data` the `pop_data` binding of the `tplyr_table` object. For `tplyr_pop_data<-` nothing is returned, the `pop_data` binding is set silently. For `set_tplyr_pop_data` the modified object.

### Examples

```

tab <- tplyr_table(iris, Species)

pop_data(tab) <- mtcars

```

---

pop_treat_var	<i>Return or set pop_treat_var binding</i>
---------------	--

---

**Description**

The treatment variable used in the target data may be different than the variable within the population dataset. `set_pop_treat_var` allows you to change this.

**Usage**

```
pop_treat_var(table)

set_pop_treat_var(table, pop_treat_var)
```

**Arguments**

table	A <code>tplyr_table</code> object
pop_treat_var	Variable containing treatment group assignments within the <code>pop_data</code> binding. Supply unquoted.

**Value**

For `tplyr_pop_treat_var` the `pop_treat_var` binding of the `tplyr_table` object. For `set_tplyr_pop_treat_var` the modified object.

**Examples**

```
tab <- tplyr_table(iris, Species)

pop_data(tab) <- mtcars
set_pop_treat_var(tab, mpg)
```

---

process_formatting	<i>Process layers to get formatted and pivoted tables.</i>
--------------------	--

---

**Description**

This is an internal method, but is exported to support S3 dispatch. Not intended for direct use by a user.

**Usage**

```
process_formatting(x, ...)
```

**Arguments**

x                    A tplyr\_layer object  
 ...                  arguments passed to dispatch

**Value**

The formatted\_table object that is binded to the layer

---

process\_statistic\_data

*Process a tplyr\_statistic object*

---

**Description**

This is an internal function that is not meant for use externally, but must be exported. Use with caution.

**Usage**

process\_statistic\_data(x, ...)

**Arguments**

x                    A tplyr\_statistic environment  
 ...                  Additional pass through parameters

**Value**

Numeric statistic data from a tplyr statistic

---

process\_statistic\_formatting

*Process string formatting on a tplyr\_statistic object*

---

**Description**

This is an internal function that is not meant for use externally, but must be exported. Use with caution.

**Usage**

process\_statistic\_formatting(x, ...)

**Arguments**

x                    A tplyr\_statistic environment  
 ...                  Additional pass through parameters

**Value**

Formatted tplyr\_statistic data

---

process\_summaries      *Process layers to get numeric results of layer*

---

**Description**

This is an internal method, but is exported to support S3 dispatch. Not intended for direct use by a user.

**Usage**

```
process_summaries(x, ...)
```

**Arguments**

x                    a tplyr\_layer object  
 ...                  arguments passed to dispatch

**Value**

The tplyr\_layer object with a 'built\_table' binding

---

set\_custom\_summaries    *Set custom summaries to be performed within a descriptive statistics layer*

---

**Description**

This function allows a user to define custom summaries to be performed in a call to `dplyr::summarize()`. A custom summary by the same name as a default summary will override the default. This allows the user to override the default behavior of summaries built into 'Tplyr', while also adding new desired summary functions.

**Usage**

```
set_custom_summaries(e, ...)
```

**Arguments**

e desc layer on which the summaries should be bound

... Named parameters containing syntax to be used in a call to `dplyr::summarize()`

**Details**

When programming the logic of the summary function, use the variable name `.var` to within your summary functions. This allows you apply the summary function to each variable when multiple target variables are declared.

An important, yet not immediately obvious, part of using `set_custom_summaries` is to understand the link between the named parameters you set in `set_custom_summaries` and the names called in `f_str` objects within `set_format_strings`. In `f_str`, after you supply the string format you'd like your numbers to take, you specify the summaries that fill those strings.

When you go to set your format strings, the name you use to declare a summary in `set_custom_summaries` is the same name that you use in your `f_str` call. This is necessary because `set_format_strings` needs some means of putting two summaries in the same value, and setting a row label for the summary being performed.

Review the examples to see this put into practice. Note the relationship between the name created in `set_custom_summaries` and the name used in `set_format_strings` within the `f_str` call

**Value**

Binds a variable `custom_summaries` to the specified layer

**Examples**

```
#Load in pipe
library(magrittr)

tplyr_table(iris, Species) %>%
  add_layer(
    group_desc(Sepal.Length, by = "Sepal Length") %>%
    set_custom_summaries(
      geometric_mean = exp(sum(log(.var[.var > 0]),
                             na.rm=TRUE) / length(.var))
    ) %>%
    set_format_strings(
      'Geometric Mean' = f_str('xx.xx', geometric_mean)
    )
  ) %>%
  build()
```

---

set_denoms_by	<i>Set variables used in pct denominator calculation</i>
---------------	--

---

### Description

This function is used when calculating pct in count or shift layers. The percentages default to the treatment variable and any column variables but can be calculated on any variables passed to target\_var, treat\_var, by, or cols.

### Usage

```
set_denoms_by(e, ...)
```

### Arguments

e	A count/shift layer object
...	Unquoted variable names

### Value

The modified layer object

### Examples

```
library(magrittr)

# Default has matrix of treatment group, additional columns,
# and by variables sum to 1
tplyr_table(mtcars, am) %>%
  add_layer(
    group_shift(vars(row=gear, column=carb), by=cyl) %>%
      set_format_strings(f_str("xxx (xx.xx%)", n, pct)) %>%
  ) %>%
  build()

tplyr_table(mtcars, am) %>%
  add_layer(
    group_shift(vars(row=gear, column=carb), by=cyl) %>%
      set_format_strings(f_str("xxx (xx.xx%)", n, pct)) %>%
      set_denoms_by(cyl, gear) # Row % sums to 1
  ) %>%
  build()

tplyr_table(mtcars, am) %>%
  add_layer(
    group_shift(vars(row=gear, column=carb), by=cyl) %>%
      set_format_strings(f_str("xxx (xx.xx%)", n, pct)) %>%
      set_denoms_by(cyl, gear, am) # % within treatment group sums to 1
  ) %>%
  build()
```

---

set_denom_ignore	<i>Set values the denominator calculation will ignore</i>
------------------	---

---

### Description

```
‘r lifecycle::badge("defunct")‘
```

This is generally used for missing values. Values like "", NA, "NA" are common ways missing values are presented in a data frame. In certain cases, percentages do not use "missing" values in the denominator. This function notes different values as "missing" and excludes them from the denominators.

### Usage

```
set_denom_ignore(e, ...)
```

### Arguments

e	A count_layer object
...	Values to exclude from the percentage calculation. If you use ‘set_missing_counts()‘ this should be the name of the parameters instead of the values, see the example below.

### Value

The modified layer object

### Examples

```
library(magrittr)
mtcars2 <- mtcars
mtcars2[mtcars$cyl == 6, "cyl"] <- NA
mtcars2[mtcars$cyl == 8, "cyl"] <- "Not Found"

tplyr_table(mtcars2, gear) %>%
  add_layer(
    group_count(cyl) %>%
      set_missing_count(f_str("xx ", n), Missing = c(NA, "Not Found"))
      # This function is currently deprecated. It was replaced with an
      # argument in set_missing_count
      # set_denom_ignore("Missing")
  ) %>%
  build()
```



---

set_denom_where	<i>Set Logic for denominator subsetting</i>
-----------------	---

---

### Description

By default, denominators in count layers are subset based on the layer level where logic. In some cases this might not be correct. This functions allows the user to override this behavior and pass custom logic that will be used to subset the target dataset when calculating denominators for the layer.

### Usage

```
set_denom_where(e, denom_where)
```

### Arguments

e	A count_layer/shift_layer object
denom_where	An expression (i.e. syntax) to be used to subset the target dataset for calculating layer denominators. Supply as programming logic (i.e. $x < 5$ & $y == 10$ ). To remove the layer where parameter subsetting for the total row and thus the percentage denominators, pass 'TRUE' to this function.

### Value

The modified Tplyr layer object

### Examples

```
library(magrittr)
t10 <- tplyr_table(mtcars, gear) %>%
  add_layer(
    group_count(cyl, where = cyl != 6) %>%
    set_denom_where(TRUE)
    # The denominators will be based on all of the values, including 6
  ) %>%
  build()
```

---

set_distinct_by	<i>Set counts to be distinct by some grouping variable.</i>
-----------------	---

---

### Description

In some situations, count summaries may want to see distinct counts by a variable like subject. For example, the number of subjects in a population who had a particular adverse event. set\_distinct\_by allows you to set the by variables used to determine a distinct count.

**Usage**

```
set_distinct_by(e, distinct_by)
```

**Arguments**

e                    A count\_layer/shift\_layer object  
distinct\_by        Variable(s) to get the distinct data.

**Details**

When a distinct\_by value is set, distinct counts will be used by default. If you wish to combine distinct and not distinct counts, you can choose which to display in your `f_str` objects using `n`, `pct`, `distinct`, and `distinct_pct`.

**Value**

The layer object with

**Examples**

```
#Load in pipe
library(magrittr)

tplyr_table(mtcars, gear) %>%
  add_layer(
    group_count(cyl) %>%
      set_distinct_by(carb)
  ) %>%
  build()
```

---

set\_format\_strings     *Set the format strings and associated summaries to be performed in a layer*

---

**Description**

'Tplyr' gives you extensive control over how strings are presented. `set_format_strings` allows you to apply these string formats to your layer. This behaves slightly differently between layers.

**Usage**

```
set_format_strings(e, ...)

## S3 method for class 'desc_layer'
set_format_strings(e, ..., cap = getOption("tplyr.precision_cap"))

## S3 method for class 'count_layer'
set_format_strings(e, ...)
```

**Arguments**

e	Layer on which to bind format strings
...	Named parameters containing calls to <code>f_str</code> to set the format strings
cap	A named character vector containing an 'int' element for the cap on integer precision, and a 'dec' element for the cap on decimal precision.

**Details**

Format strings are one of the most powerful components of 'Tplyr'. Traditionally, converting numeric values into strings for presentation can consume a good deal of time. Values and decimals need to align between rows, rounding before trimming is sometimes forgotten - it can become a tedious mess that, in the grand scheme of things, is not an important part of the analysis being performed. 'Tplyr' makes this process as simple as we can, while still allowing flexibility to the user.

In a count layer, you can simply provide a single `f_str` object to specify how you want your n's (and possibly percents) formatted. If you are additionally supplying a statistic, like risk difference using `add_risk_diff`, you specify the count formats using the name 'n\_counts'. The risk difference formats would then be specified using the name 'riskdiff'. In a descriptive statistic layer, `set_format_strings` allows you to do a couple more things:

- By naming parameters with character strings, those character strings become a row label in the resulting data frame
- The actual summaries that are performed come from the variable names used within the `f_str` calls
- Using multiple summaries (declared by your `f_str` calls), multiple summary values can appear within the same line. For example, to present "Mean (SD)" like displays.
- Format strings in the desc layer also allow you to configure how empty values should be presented. In the `f_str` call, use the `empty` parameter to specify how missing values should present. A single element character vector should be provided. If the vector is unnamed, that value will be used in the format string and fill the space similar to how the numbers will display. Meaning - if your empty string is 'NA' and your format string is 'xx (xxx)', the empty values will populate as 'NA ( NA)'. If you name the character vector in the 'empty' parameter 'overall', like `empty = c(overall='')`, then that exact string will fill the value instead. For example, providing 'NA' will instead create the formatted string as 'NA' exactly.

See the `f_str` documentation for more details about how this implementation works.

**Value**

The layer environment with the format string binding added

Returns the modified layer object.

**Examples**

```
# Load in pipe
library(magrittr)
```

```

# In a count layer
tplyr_table(mtcars, gear) %>%
  add_layer(
    group_count(cyl) %>%
      set_format_strings(f_str('xx (xx%)', n, pct))
  ) %>%
  build()

# In a descriptive statistics layer
tplyr_table(mtcars, gear) %>%
  add_layer(
    group_desc(mpg) %>%
      set_format_strings(
        "n" = f_str("xx", n),
        "Mean (SD)" = f_str("xx.x", mean, empty='NA'),
        "SD" = f_str("xx.xx", sd),
        "Median" = f_str("xx.x", median),
        "Q1, Q3" = f_str("xx, xx", q1, q3, empty=c(.overall='NA')),
        "Min, Max" = f_str("xx, xx", min, max),
        "Missing" = f_str("xx", missing)
      )
  ) %>%
  build()

# In a shift layer
tplyr_table(mtcars, am) %>%
  add_layer(
    group_shift(vars(row=gear, column=carb), by=cyl) %>%
      set_format_strings(f_str("xxx (xx.xx%)", n, pct))
  ) %>%
  build()

```

---

set\_indentation      *Set the option to prefix the row\_labels in the inner count\_layer*

---

### Description

When a count layer uses nesting (i.e. triggered by [set\\_nest\\_count](#)), the indentation argument's value will be used as a prefix for the inner layer's records

### Usage

```
set_indentation(e, indentation)
```

### Arguments

e                    A count\_layer object

indentation        A character to prefix the row labels in an inner count layer

**Value**

The modified count\_layer environment

---

set_missing_count	<i>Set the display for missing strings</i>
-------------------	--

---

**Description**

Controls how missing counts are handled and displayed in the layer

**Usage**

```
set_missing_count(e, fmt = NULL, sort_value = NULL, denom_ignore = FALSE, ...)
```

**Arguments**

e	A count_layer object
fmt	An f_str object to change the display of the missing counts
sort_value	A numeric value that will be used in the ordering column. This should be numeric. If it is not supplied the ordering column will be the maximum value of what appears in the table plus one.
denom_ignore	A boolean. Specifies Whether or not to include the missing counts specified within the ... parameter within denominators. If set to TRUE, the values specified within ... will be ignored.
...	Parameters used to note which values to describe as missing. Generally NA and "Missing" would be used here. Parameters can be named character vectors where the names become the row label.

**Value**

The modified layer

**Examples**

```
library(magrittr)
library(dplyr)
mtcars2 <- mtcars %>%
  mutate_all(as.character)
mtcars2[mtcars$cyl == 6, "cyl"] <- NA

tplyr_table(mtcars2, gear) %>%
  add_layer(
    group_count(cyl) %>%
      set_missing_count(f_str("xx ", n), Missing = NA)
  ) %>%
  build()
```

---

set_nest_count	<i>Set the option to nest count layers</i>
----------------	--

---

### Description

If set to TRUE, the second variable specified in `target_var` will be nested inside of the first variable. This allows you to create displays like those commonly used in adverse event tables, where one column holds both the labels of the outer categorical variable and the inside event variable (i.e. AEBODSYS and AEDECOD).

### Usage

```
set_nest_count(e, nest_count)
```

### Arguments

<code>e</code>	A <code>count_layer</code> object
<code>nest_count</code>	A logical value to set the nest option

### Value

The modified layer

---

set_order_count_method	<i>Set the ordering logic for the count layer</i>
------------------------	---

---

### Description

The sorting of a table can greatly vary depending on the situation at hand. For count layers, when creating tables like adverse event summaries, you may wish to order the table by descending occurrence within a particular treatment group. But in other situations, such as AEs of special interest, or subject disposition, there may be a specific order you wish to display values. Tplyr offers solutions to each of these situations.

Instead of allowing you to specify a custom sort order, Tplyr instead provides you with order variables that can be used to sort your table after the data are summarized. Tplyr has a default order in which the table will be returned, but the order variables will always persist. This allows you to use powerful sorting functions like [arrange](#) to get your desired order, and in double programming situations, helps your validator understand the how you achieved a particular sort order and where discrepancies may be coming from.

When creating order variables for a layer, for each 'by' variable Tplyr will search for a <VAR>N version of that variable (i.e. VISIT <-> VISITN, PARAM <-> PARAMN). If available, this variable will be used for sorting. If not available, Tplyr will created a new ordered factor version of that variable to use in alphanumeric sorting. This allows the user to control a custom sorting order by

leaving an existing <VAR>N variable in your dataset if it exists, or create one based on the order in which you wish to sort - no custom functions in Tplyr required.

Ordering of results is where things start to differ. Different situations call for different methods. Descriptive statistics layers keep it simple - the order in which you input your formats using `set_format_strings` is the order in which the results will appear (with an order variable added). For count layers, Tplyr offers three solutions: If there is a <VAR>N version of your target variable, use that. If not, if the target variable is a factor, use the factor orders. Finally, you can use a specific data point from your results columns. The result column can often have multiple data points, between the n counts, percent, distinct n, and distinct percent. Tplyr allows you to choose which of these values will be used when creating the order columns for a specified result column (i.e. based on the `treat_var` and `cols` arguments). See the 'Sorting a Table' section for more information.

Shift layers sort very similarly to count layers, but to order your row shift variable, use an ordered factor.

### Usage

```
set_order_count_method(e, order_count_method)

set_ordering_cols(e, ...)

set_result_order_var(e, result_order_var)
```

### Arguments

<code>e</code>	A <code>count_layer</code> object
<code>order_count_method</code>	The logic determining how the rows in the final layer output will be indexed. Options are 'bycount', 'byfactor', and 'byvarn'.
<code>...</code>	Unquoted variables used to select the columns whose values will be extracted for ordering.
<code>result_order_var</code>	The numeric value the ordering will be done on. This can be either n, <code>distinct_n</code> , <code>pct</code> , or <code>distinct_pct</code> . Due to the evaluation of the layer you can add a value that isn't actually being evaluated, if this happens this will only error out in the ordering.

### Value

Returns the modified layer object. The 'ord\_' columns are added during the build process.

### Sorting a Table

When a table is built, the output has several `ordering(ord_)` columns that are appended. The first represents the layer index. The index is determined by the order the layer was added to the table. Following are the indices for the by variables and the target variable. The by variables are ordered based on:

1. The 'by' variable is a factor in the target dataset

2. If the variable isn't a factor, but has a <VAR>N variable (i.e. VISIT -> VISITN, TRT -> TRTN)
3. If the variable is not a factor in the target dataset, it is coerced to one and ordered alphabetically.

The target variable is ordered depending on the type of layer. See more below.

### Ordering a Count Layer

There are many ways to order a count layer depending on the preferences of the table programmer. Tplyr supports sorting by a descending amount in a column in the table, sorting by a <VAR>N variable, and sorting by a custom order. These can be set using the 'set\_order\_count\_method' function.

**Sorting by a numeric count** A selected numeric value from a selected column will be indexed based on the descending numeric value. The numeric value extracted defaults to 'n' but can be changed with 'set\_result\_order\_var'. The column selected for sorting defaults to the first value in the treatment group variable. If there were arguments passed to the 'cols' argument in the table those must be specified with 'set\_ordering\_columns'.

**Sorting by a 'varn' variable** If the treatment variable has a <VAR>N variable. It can be indexed to that variable.

**Sorting by a factor(Default)** If a factor is found for the target variable in the target dataset that is used to order, if no factor is found it is coerced to a factor and sorted alphabetically.

**Sorting a nested count layer** If two variables are targeted by a count layer, two methods can be passed to 'set\_order\_count'. If two are passed, the first is used to sort the blocks, the second is used to sort the "inside" of the blocks. If one method is passed, that will be used to sort both.

### Ordering a Desc Layer

The order of a desc layer is mostly set during the object construction. The by variables are resolved and index with the same logic as the count layers. The target variable is ordered based on the format strings that were used when the layer was created.

### Examples

```
library(dplyr)

# Default sorting by factor
t <- tplyr_table(mtcars, gear) %>%
  add_layer(
    group_count(cyl)
  )
build(t)

# Sorting by <VAR>N
mtcars$cylN <- mtcars$cyl
t <- tplyr_table(mtcars, gear) %>%
  add_layer(
    group_count(cyl) %>%
      set_order_count_method("byvarn")
  )
```



```

)

# Sorting by row count
t <- tplyr_table(mtcars, gear) %>%
  add_layer(
    group_count(cyl) %>%
      set_order_count_method("bycount") %>%
      # Orders based on the 6 gear group
      set_ordering_cols(6)
  )

# Sorting by row count by percentages
t <- tplyr_table(mtcars, gear) %>%
  add_layer(
    group_count(cyl) %>%
      set_order_count_method("bycount") %>%
      set_result_order_var(pct)
  )

# Sorting when you have column arguments in the table
t <- tplyr_table(mtcars, gear, cols = vs) %>%
  add_layer(
    group_count(cyl) %>%
      # Uses the fourth gear group and the 0 vs group in ordering
      set_ordering_cols(4, 0)
  )

# Using a custom factor to order
mtcars$cyl <- factor(mtcars$cyl, c(6, 4, 8))
t <- tplyr_table(mtcars, gear) %>%
  add_layer(
    group_count(cyl) %>%
      # This is the default but can be used to change the setting if it is
      # set at the table level.
      set_order_count_method("byfactor")
  )

```

---

set\_outer\_sort\_position

*Set the value of a outer nested count layer to Inf or -Inf*

---

## Description

Set the value of a outer nested count layer to Inf or -Inf

## Usage

```
set_outer_sort_position(e, outer_sort_position)
```

**Arguments**

`e` A `count_layer` object

`outer_sort_position` Either 'asc' or 'desc'. If desc the final ordering helper will be set to Inf, if 'asc' the ordering helper is set to -Inf.

**Value**

The modified count layer.

---

`set_total_row_label` *Set the label for the total row*

---

**Description**

The row label for a total row defaults to "Total", however this can be overridden using this function.

**Usage**

```
set_total_row_label(e, total_row_label)
```

**Arguments**

`e` A `count_layer` object

`total_row_label` A character to label the total row

**Value**

The modified `count_layer` object

**Examples**

```
# Load in pipe
library(magrittr)

t <- tplyr_table(mtcars, gear) %>%
  add_layer(
    group_count(cyl) %>%
      add_total_row() %>%
      set_total_row_label("Total Cyl")
  )
build(t)
```

## Description

```
'r lifecycle::badge("experimental")'
```

## Details

'Tplyr' is a package dedicated to simplifying the data manipulation necessary to create clinical reports. Clinical data summaries can often be broken down into two factors - counting discrete variables (or counting shifts in state), and descriptive statistics around a continuous variable. Many of the reports that go into a clinical report are made up of these two scenarios. By abstracting this process away, 'Tplyr' allows you to rapidly build these tables without worrying about the underlying data manipulation.

'Tplyr' takes this process a few steps further by abstracting away most of the programming that goes into proper presentation, which is where a great deal of programming time is spent. For example, 'Tplyr' allows you to easily control:

**String formatting** Different reports warrant different presentation of your strings. Programming this can get tedious, as you typically want to make sure that your decimals properly align. 'Tplyr' abstracts this process away and provides you with a simple interface to specify how you want your data presented

**Treatment groups** Need a total column? Need to group summaries of multiple treatments? 'Tplyr' makes it simple to add additional treatment groups into your report

**Denominators** n (%) counts often vary based on the summary being performed. 'Tplyr' allows you to easily control what denominators are used based on a few common scenarios

**Sorting** Summarizing data is one thing, but ordering it for presentation. Tplyr automatically derives sorting variable to give you the data you need to order your table properly. This process is flexible so you can easily get what you want by leveraging your data or characteristics of R.

Another powerful aspect of 'Tplyr' are the objects themselves. 'Tplyr' does more than format your data. Metadata about your table is kept under the hood, and functions allow you to access information that you need. For example, 'Tplyr' allows you to calculate and access the raw numeric data of calculations as well, and easily pick out just the pieces of information that you need.

Lastly, 'Tplyr' was built to be flexible, yet intuitive. A common pitfall of building tools like this is over automation. By doing too much, you end up not doing enough. 'Tplyr' aims to hit the sweet spot in between. Additionally, we designed our function interfaces to be clean. Modifier functions offer you flexibility when you need it, but defaults can be set to keep the code concise. This allows you to quickly assemble your table, and easily make changes where necessary.

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## See Also

Useful links:

- <https://github.com/atorus-research/Tplyr>
- Report bugs at <https://github.com/atorus-research/Tplyr/issues>

## Examples

```
# Load in pipe
library(magrittr)

# Use just the defaults
tplyr_table(mtcars, gear) %>%
  add_layer(
    group_desc(mpg, by=cyl)
  ) %>%
  add_layer(
    group_count(carb, by=cyl)
  ) %>%
  build()

# Customize and modify
tplyr_table(mtcars, gear) %>%
  add_layer(
    group_desc(mpg, by=cyl) %>%
    set_format_strings(
      "n" = f_str("xx", n),
      "Mean (SD)" = f_str("a.a+1 (a.a+2)", mean, sd, empty='NA'),
      "Median" = f_str("a.a+1", median),
      "Q1, Q3" = f_str("a, a", q1, q3, empty=c(.overall='NA')),
      "Min, Max" = f_str("a, a", min, max),
      "Missing" = f_str("xx", missing)
    )
  ) %>%
  add_layer(
    group_count(carb, by=cyl) %>%
    add_risk_diff(
      c('5', '3'),
      c('4', '3')
    ) %>%
    set_format_strings(
      n_counts = f_str('xx (xx%)', n, pct),
      riskdiff = f_str('xx.xxx (xx.xxx, xx.xxx)', dif, low, high)
    )
  )
```

```

    ) %>%
    set_order_count_method("bycount") %>%
    set_ordering_cols('4') %>%
    set_result_order_var(pct)
  ) %>%
  build()

# A Shift Table
tplyr_table(mtcars, am) %>%
  add_layer(
    group_shift(vars(row=gear, column=carb), by=cyl) %>%
    set_format_strings(f_str("xxx (xx.xx%)", n, pct))
  ) %>%
  build()

```

---

tplyr\_layer

*Create a tplyr\_layer object*


---

## Description

This object is the workhorse of the tplyr package. A tplyr\_layer can be thought of as a block, or "layer" of a table. Summary tables typically consist of different sections that require different summaries. When programming these section, your code will create different layers that need to be stacked or merged together. A tplyr\_layer is the container for those isolated building blocks.

When building the tplyr\_table, each layer will execute independently. When all of the data processing has completed, the layers are brought together to construct the output.

tplyr\_layer objects are not created directly, but are rather created using the layer constructor functions [group\\_count](#), [group\\_desc](#), and [group\\_shift](#).

## Usage

```
tplyr_layer(parent, target_var, by, where, type, ...)
```

## Arguments

parent	tplyr_table or tplyr_layer. Required. The parent environment of the layer. This must be either the tplyr_table object that the layer is contained within, or another tplyr_layer object of which the layer is a subgroup.
target_var	Symbol. Required, The variable name on which the summary is to be performed. Must be a variable within the target dataset. Enter unquoted - i.e. target_var = AEBODSYS.
by	A string, a variable name, or a list of variable names supplied using <code>dplyr::vars</code>
where	Call. Filter logic used to subset the target data when performing a summary.
type	"count", "desc", or "shift". Required. The category of layer - either "counts" for categorical counts, "desc" for descriptive statistics, or "shift" for shift table counts
...	Additional arguments

**Value**

A tplyr\_layer environment that is a child of the specified parent. The environment contains the object as listed below.

**tplyr\_layer Core Object Structure**

`type` This is an attribute. A string indicating the layer type, which controls the summary that will be performed.

`target_var` A quosure of a name, which is the variable on which a summary will be performed.

`by` A list of quosures representing either text labels or variable names used in grouping. Variable names must exist within the target dataset. Text strings submitted do not need to exist in the target dataset.

`cols` A list of quosures used to determine the variables that are used to display in columns.

`where` A quosure of a call that contains the filter logic used to subset the target dataset. This filtering is in addition to any subsetting done based on where criteria specified in [tplyr\\_table](#)

`layers` A list with class `tplyr_layer_container`. Initialized as empty, but serves as the container for any sublayers of the current layer. Used internally.

Different layer types will have some different bindings specific to that layer's needs.

**See Also**

[tplyr\\_table](#)

**Examples**

```
tab <- tplyr_table(iris, Sepal.Width)

l <- group_count(tab, by=vars('Label Text', Species),
                 target_var=Species, where= Sepal.Width < 5.5,
                 cols = Species)
```

---

tplyr\_table

*Create a Tplyr table object*

---

**Description**

The `tplyr_table` object is the main container upon which a Tplyr table is constructed. Tplyr tables are made up of one or more layers. Each layer contains an instruction for a summary to be performed. The `tplyr_table` object contains those layers, and the general data, metadata, and logic necessary.

**Usage**

```
tplyr_table(target, treat_var, where = TRUE, cols = vars())
```

## Arguments

target	Dataset upon which summaries will be performed
treat_var	Variable containing treatment group assignments. Supply unquoted.
where	A general subset to be applied to all layers. Supply as programming logic (i.e. <code>x &lt; 5 &amp; y == 10</code> )
cols	A grouping variable to summarize data by column (in addition to <code>treat_var</code> ). Provide multiple column variables by using <a href="#">vars</a>

## Details

When a `tplyr_table` is created, it will contain the following bindings:

- `target` - The dataset upon which summaries will be performed
- `pop_data` - The data containing population information. This defaults to the target dataset
- `cols` - A categorical variable to present summaries grouped by column (in addition to `treat_var`)
- `table_where` - The `where` parameter provided, used to subset the target data
- `treat_var` - Variable used to distinguish treatment groups.
- `header_n` - Default header N values based on `treat_var`
- `pop_treat_var` - The treatment variable for `pop_data` (if different)
- `layers` - The container for individual layers of a `tplyr_table`
- `treat_grps` - Additional treatment groups to be added to the summary (i.e. Total)

`tplyr_table` allows you a basic interface to instantiate the object. Modifier functions are available to change individual parameters catered to your analysis. For example, to add a total group, you can use the [add\\_total\\_group](#).

In future releases, we will provide vignettes to fully demonstrate these capabilities.

## Value

A `tplyr_table` object

## Examples

```
tab <- tplyr_table(iris, Species, where = Sepal.Length < 5.8)
```

---

treat_var	<i>Return or set the treatment variable binding</i>
-----------	---

---

**Description**

Return or set the treatment variable binding

**Usage**

```
treat_var(table)
set_treat_var(table, treat_var)
```

**Arguments**

table	A tplyr_table object to set or return treatment variable the table is split by.
treat_var	Variable containing treatment group assignments. Supply unquoted.

**Value**

For tplyr\_treat\_var the treat\_var binding of the tplyr\_table object. For set\_tplyr\_treat\_var the modified object.

**Examples**

```
tab <- tplyr_table(mtcars, cyl)
set_treat_var(tab, gear)
```



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