

# Package ‘tibbleOne’

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**Type** Package

**Title** Table One for 'Latex', 'Word', and 'Html' 'R Markdown'  
Documents

**Version** 0.1.0

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**Description** Table one is a tabular description of characteristics, e.g., demographics of patients in a clinical trial, presented overall and also stratified by a categorical variable, e.g. treatment group. There are many excellent packages available to create table one. This package focuses on providing table one objects that seamlessly fit into 'R Markdown' analyses.

**License** GPL-3

**Depends** R (>= 3.5.0)

**Imports** tibble (>= 2.1.3),  
knitr (>= 1.23),  
officer,  
flextable,  
kableExtra,  
forcats,  
labelled,  
tidyr (>= 1.0.0),  
tidyselect,  
stringr,  
rlang,  
vctrs,  
purrr,  
glue,  
stats,  
magrittr,  
dplyr,  
lifecycle

**Suggests** rmarkdown,  
survival,  
tidyverse,  
testthat (>= 2.1.0),  
covr

**VignetteBuilder** knitr

```
RdMacros lifecycle
Encoding UTF-8
LazyData true
Roxygen list(markdown = TRUE, roclets = c("`rd", ``namespace",
  ``collate"))
RoxygenNote 6.1.1
```

**R topics documented:**

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tibbleOne-package	<i>tibbleOne: tidy characteristics tables</i>
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**Description**

In many academic papers, table 1 shows participant characteristics, often stratified by a categorical variable such as treatment group. There are many excellent packages available to compute the numbers in table 1. This package focuses on getting those numbers into a nice format that works with R Markdown. Additionally, there is a fair amount of diversity in researchers' preferred writing mediums. Some may prefer LaTeX, while others want to work in Microsoft Word. Recently, html documents have grown more common for research papers. tibbleOne is meant to be applicable for each of these settings, and should meet the needs of most studies.

To learn more about tibbleOne, start with the vignettes: `browseVignettes(package = "tibbleOne")`

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adapt_round	<i>Adaptive rounding for tables</i>
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**Description**

Adaptive rounding for tables

**Usage**

```
adapt_round(x)
```

**Arguments**

x                      a numeric vector

**Value**

a character vector comprising rounded values.

**Examples**

```
adapt_round(c(0.12, 10.12, 100.12))
```

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build_meta	<i>Meta data builder</i>
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**Description**

creates a dataset that describes the characteristics of another dataset

**Usage**

```
build_meta(data, expand_binary_catgs = FALSE, add_perc_to_cats = TRUE,
           max_catgs = 10)
```

**Arguments**

data                      a data frame with any combination of the following attributes: label, unit, group, abbrs, and notes. Columns in the meta data are based on these attributes.

expand\_binary\_catgs      T/F, should all categories be included for binary categorical variables? (This only applies to binary variables.)

add\_perc\_to\_cats          T/F, should categorical variables in Table 1 have a the user specifies include\_freq = TRUE in [tibble\\_one](#), then the when include\_freq = FALSE, setting this to TRUE should clarify the table.

max\_catgs                largest number of categories accepted in a factor variable. A warning message is printed if a factor variable has more categories than max\_catg.

**Value**

A list containing components of data, group\_levels, and var\_levels. The data component comprises 8 columns:

- variable: variable name - this is the column name of the variable.
- label: variable labels - this is presented in tables
- type: type of variable (numeric or factor)
- unit: units for continuous variables
- group: a group identifier for each variable
- abbr: abbreviations associated with the label of a variable
- note: strings that will be place in tables as a footnote
- labels: labels of variables, including categories of factors.

data is also a [tibble](#).

The group\_levels component shows the order that groups will appear in the table, and var\_levels shows the order that variables will appear in the table and within groups.

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pbc\_tbl1

*Mayo Clinic Primary Biliary Cirrhosis*

---

**Description**

These data contain a subset of the columns found in the pbc data in the survival package. Also, the description below is taken from the description provided by the survival package.

cirrhosis (PBC) of the liver conducted between 1974 and 1984. A total of 424 PBC patients, referred to Mayo Clinic during that ten-year interval, met eligibility criteria for the randomized placebo controlled trial of the drug D-penicillamine. The first 312 cases in the data set participated in the randomized trial and contain largely complete data. The additional 112 cases did not participate in the clinical trial, but consented to have basic measurements recorded and to be followed for survival. Six of those cases were lost to follow-up shortly after diagnosis, so the data here are on an additional 106 cases as well as the 312 randomized participants.

**Usage**

pbc\_tbl1

**Format**

a data frame with 418 rows and 9 variables.

- age: in years
- sex: male or female
- status death, censor, or transplant.
- trt D-penicillmain, placebo, and not randomized (NA).
- stage: histologic stage of disease (needs biopsy)
- ascites: presence of ascites
- bili: serum bilirunbin (mg/dl)
- edema: no edema, untreated or successfully treated edema, or edema despite diuretic therapy
- albumin: serum albumin (g/dl)

**Source**

T Therneau and P Grambsch (2000), Modeling Survival Data: Extending the Cox Model, Springer-Verlag, New York. ISBN: 0-387-98784-3.

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select_labelled	<i>Select and label variables</i>
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**Description**

Select and label variables

**Usage**

```
select_labelled(data, ...)
```

**Arguments**

data	a data frame
...	name-value pairs of variable labels

**Value**

a data frame containing the columns indicated by ..., adorned with attributes based on a user's specified labels.

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set_variable_labels	<i>Set variable attributes</i>
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**Description**

These functions allow you to embed attributes in data so that you only need to think about them once. Some functions may overwrite or delete attributes in data, so it is recommended that you create a meta data object with the [build\\_meta](#) function after you have set variable labels, groups, notes, abbreviations, and units.

**Usage**

```
set_variable_labels(data, ...)
```

```
set_variable_groups(data, ...)
```

```
set_variable_abbrs(data, ...)
```

```
set_variable_notes(data, ...)
```

```
set_variable_units(data, ...)
```

## Arguments

`data` a data frame.  
`...` name-value pairs of variable groups and names (see examples)

## Details

- `tibble_one` will handle attributes of data automatically, e.g., replacing variable names with variable labels, and placing variable acronyms (i.e., abbreviations) at the bottom of the table in a footnote.
- Use `set_variable_labels()` to set the values that will represent variables in table one.
- Use `set_variable_groups()` to change the variables that are listed in the variable categories of table one.
- Use `set_variable_notes` to add descriptions of variables that will be placed at the bottom of table one as a footnote.
- Use `set_variable_abbrs` to indicate what acronyms in variable labels mean (see examples).
- Use `set_variable_units` to indicate the unit of measurement for continuous variables.

For `set_variable_labels`, names are variables and values are labels. For example, writing `gfr_variable = "estimated GFR"` as an input to `set_variable_labels` will set the label for `gfr_variable` as the indicated string. Since GFR is an acronym, we would also want to use `set_variable_abbrs()` and say `gfr_variable = c("GFR" = "glomerular filtration rate")` (see examples).

## Value

a `tibble`, adorned with additional attributes based on user input.

## Note

The `set_variable_labels` function in `tibbleOne` is a wrapper of the `labelled` function, developed by Joseph Larmarange.

## Examples

```
df <- data.frame(
  gfr = c(1,2,3),
  sbp = c(3,2,1)
)

df <- set_variable_labels(df,
  gfr = 'Estimated GFR',
  sbp = 'Systolic BP'
)

df <- set_variable_units(df,
  gfr = 'mL/min/1.73 m2',
  sbp = 'mm Hg'
)

df <- set_variable_abbrs(df,
  gfr = c("GFR" = "glomerular filtration rate", "min" = 'minute'),
  sbp = c("BP" = "blood pressure")
)
```

```
df <- set_variable_notes(df,
  sbp = "blood pressure was measured by trained personnel"
)

build_meta(df)
```

---

tibble\_one

*Tidy characteristics data*


---

## Description

### Stable

Table one is a tabular description of characteristics, e.g., demographics of patients in a clinical trial, presented overall and also stratified by a categorical variable, e.g. treatment group.

## Usage

```
tibble_one(data, formula = NULL, meta_data = NULL, row_vars = NULL,
  strat = NULL, by = NULL, specs_table_vals = NULL,
  specs_table_tests = NULL, include_pval = FALSE,
  expand_binary_catgs = FALSE, include_freq = FALSE,
  add_perc_to_cats = TRUE)
```

## Arguments

data	a data frame
formula	an optional formula object. The left hand side of the formula should be blank. The right hand side of the formula should contain row variables for the table. The 'I' symbol can be used to include stratifying variables. If this option is used, no more than two stratifying variables should be used, and they must be separated by a * symbol. If formula is used, the strat, by, and row_vars inputs are ignored.
meta_data	a meta data frame. If unspecified, a meta data frame will be created using data.
row_vars	a character vector indicating column names of row variables in the table. If unspecified, all columns are used.
strat	a character value indicating the column name in data that will be used to stratify the table
by	a character value indicating the column name in data that will be used to split the table into groups, prior to stratification.
specs_table_vals	named vector of character values. Names should be variables, while values should be specs. Valid specs are 'mean' and 'median' (see examples).
specs_table_tests	named vector of character values. Names should be variables, while values should be specs. Valid specs are 'params' or 'noparm' (see examples).

- include\_pval     T/F, should the table include a column for p-values? If p-values are included, factor variables are handled using chi-square tests, continuous variables are handled using t-tests or ANOVA, depending on the number of categories in the table stratification.
- expand\_binary\_catgs     T/F, should all categories be included for binary categorical variables? (This only applies to binary variables.)
- include\_freq     T/F, should frequency values be included for categorical variables?
- add\_perc\_to\_cats     T/F, should categorical variable labels be appended with a percent sign?

**Value**

a [tibble](#) containing summary values that describe characteristics of observations in data , which can subsequently be sent to different modes of output (see [to\\_word](#) and [to\\_kable](#)).

**Examples**

```
data("pbc_tbl1")
# report median albumin instead of mean
# use kruskal wallis test for albumin
tibble_one(
  pbc_tbl1,
  formula = ~ . | trt,
  include_freq = FALSE,
  include_pval = TRUE,
  specs_table_vals = c(albumin = 'median'),
  specs_table_tests = c(albumin = 'nopars')
)
```

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to_kable	<i>Pass tibble_one to kable</i>
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**Description**

**Stable**

Tabular summaries of characteristics (i.e., table one) are generally presented in a table with columns that describe the overall sample and subsets of the sample designated by a grouping variable. In addition, it is expected that variable labels and units will be indicated, and footnotes will be placed at the bottom of the table with full descriptions of variables and abbreviations that appear in the table. This function automates these tasks.

**Usage**

```
to_kable(object, use_groups = TRUE, indent_groups = FALSE,
  footnote_notation = "symbol", include_1st_header = TRUE,
  include_2nd_header = TRUE, include_3rd_header = TRUE,
  bold_headers = TRUE, ...)
```

## Arguments

object	a <code>tibble_one</code> object
use_groups	T/F, should rows be grouped?
indent_groups	T/F, should entries within groups be indented? (this has no effect if <code>use_groups</code> is FALSE)
footnote_notation	character value indicating footnote symbols to use in tables. Eligible values are symbol, number, and alphabet.
include_1st_header	T/F, should bottom header be included?
include_2nd_header	T/F, should middle header be included?
include_3rd_header	T/F, should top header be included?
bold_headers	T/F, should header labels be printed in bold?
...	Arguments passed on to <code>knitr::kable</code>
<b>format</b>	A character string. Possible values are <code>latex</code> , <code>html</code> , <code>markdown</code> , <code>pandoc</code> , and <code>rst</code> ; this will be automatically determined if the function is called within <b>knitr</b> ; it can also be set in the global option <code>knitr.table.format</code> . If <code>format</code> is a function, it must return a character string.
<b>caption</b>	The table caption.
<b>label</b>	The table reference label. By default, the label is obtained from <code>knitr::opts_current\$get('</code>

## Value

A character vector of the table source code, i.e., code that can be presented in 'R Markdown' documents.

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to_word	<i>pass tibble_one to flextable</i>
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## Description

### Stable

Tabular summaries of characteristics (i.e., table one) are generally presented in a table with columns that describe the overall sample and subsets of the sample designated by a grouping variable. In addition, it is expected that variable labels and units will be indicated, and footnotes will be placed at the bottom of the table with full descriptions of variables and abbreviations that appear in the table. This function automates these tasks.

## Usage

```
to_word(object, font_size = 11, use_groups = TRUE,
  indent_groups = TRUE, footnote_notation = "symbol",
  include_1st_header = TRUE, include_2nd_header = TRUE,
  include_3rd_header = TRUE)
```

**Arguments**

object	a tibble_one object
font_size	the size of font in the table.
use_groups	T/F, should rows be grouped?
indent_groups	T/F, should entries within groups be indented? (this has no effect if use_groups is FALSE)
footnote_notation	character value indicating footnote symbols to use in tables. Eligible values are symbol, number, and alphabet.
include_1st_header	T/F, should bottom header be included?
include_2nd_header	T/F, should middle header be included?
include_3rd_header	T/F, should top header be included?

**Value**

a [flextable](#).

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