
Introducing pmtables

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Date: 2021-05-12

pmtables: v0.3.3.9000

Introduction: This is a simple introduction to the pmtables package for R. I hope this will be useful for those who are new to the package and those who just need a reminder on the syntax.

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1 A simple table: stable

1.1 Syntax

Pass your `data.frame` into `stable()`

```
stable(data)
```

Other formal arguments include:

- **align** to set column alignment
- **panel** to create groups of rows under a “panel” header
- **span** to group columns under a “spanner” header
- **notes** to create table notes
- **sumrows** to insert summary rows
- **units** that get placed below the corresponding column name
- **drop** to omit certain columns from the table
- **sizes** to set different table size attributes
- **escape_fun** a function to sanitize table items

You can also pass a bunch of other arguments through `...` to further format the table (see `?stable` for details)

1.2 Basics

`stable()` is the name of the workhorse function that is used to turn `data.frames` into TeX tables. This chapter will introduce the `stable()` function and how to use it to create basic tables.

To illustrate usage and features of `stable()`, we will use the `stdata` data set that comes with `pmtables`

```
data <- stdata()
```

```
head(data)
```

```
. # A tibble: 6 x 9
.   STUDY      DOSE  FORM    N    WT   CRCL  AGE  ALB  SCR
.   <chr>      <chr> <chr>  <chr> <chr> <chr> <chr> <chr> <chr>
. 1 12-DEMO-001 100 mg tablet 80   71.4  104   33.7  4.20  1.06
. 2 12-DEMO-001 150 mg capsule 16   89.4  122   24.4  4.63  1.12
. 3 12-DEMO-001 150 mg tablet 48   81.7  104   34.4  3.83  0.910
. 4 12-DEMO-001 150 mg troche 16   94.0  93.2   27.4  4.94  1.25
. 5 12-DEMO-001 200 mg tablet 64   67.9  100   27.5  4.25  1.10
. 6 12-DEMO-001 200 mg troche 16   76.6  99.2   22.8  4.54  1.15
```

We can turn this data frame into a TeX table by passing it into `stable()`.

```
out <- stable(data)
```

```
head(out, n = 10)
```

```
. [1] "\\setlength{\\tabcolsep}{5pt} "
. [2] "\\begin{threeparttable}"
. [3] "\\renewcommand{\\arraystretch}{1.3}"
. [4] "\\begin{tabular}[h]{l}{llllllllll}"
. [5] "\\hline"
. [6] "STUDY & DOSE & FORM & N & WT & CRCL & AGE & ALB & SCR \\\\"
. [7] "\\hline"
. [8] "12-DEMO-001 & 100 mg & tablet & 80 & 71.4 & 104 & 33.7 & 4.20 & 1.06 \\\\"
. [9] "12-DEMO-001 & 150 mg & capsule & 16 & 89.4 & 122 & 24.4 & 4.63 & 1.12 \\\\"
. [10] "12-DEMO-001 & 150 mg & tablet & 48 & 81.7 & 104 & 34.4 & 3.83 & 0.910 \\\\"
```

Note that we have shown the raw latex code that is generated by `stable()`. That is to say: the output from `stable()` is a character vector of latex code for the table. Note also that this character vector has a special class associated with it: `stable`. That means we can write functions that recognize this character vector as output from `stable()` and we can have those functions process the character vector in special ways.

We can render that table in TeX **in the current Rmarkdown document** by passing the text to `st_asis()`.

```
out %>% st_asis()
```

| STUDY | DOSE | FORM | N | WT | CRCL | AGE | ALB | SCR |
|-------------|--------|---------|-----|------|------|------|------|-------|
| 12-DEMO-001 | 100 mg | tablet | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| 12-DEMO-001 | 150 mg | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| 12-DEMO-001 | 150 mg | tablet | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |
| 12-DEMO-001 | 150 mg | troche | 16 | 94.0 | 93.2 | 27.4 | 4.94 | 1.25 |
| 12-DEMO-001 | 200 mg | tablet | 64 | 67.9 | 100 | 27.5 | 4.25 | 1.10 |
| 12-DEMO-001 | 200 mg | troche | 16 | 76.6 | 99.2 | 22.8 | 4.54 | 1.15 |
| 12-DEMO-002 | 100 mg | capsule | 36 | 61.3 | 113 | 38.3 | 4.04 | 1.28 |
| 12-DEMO-002 | 100 mg | tablet | 324 | 77.6 | 106 | 29.9 | 4.31 | 0.981 |
| 12-DEMO-002 | 50 mg | capsule | 36 | 74.1 | 112 | 37.1 | 4.44 | 0.900 |
| 12-DEMO-002 | 50 mg | tablet | 324 | 71.2 | 106 | 34.1 | 4.63 | 0.868 |
| 12-DEMO-002 | 75 mg | capsule | 36 | 72.4 | 105 | 38.2 | 3.89 | 0.900 |
| 12-DEMO-002 | 75 mg | tablet | 288 | 71.6 | 98.9 | 34.2 | 4.49 | 0.991 |
| 12-DEMO-002 | 75 mg | troche | 36 | 73.6 | 103 | 49.2 | 4.52 | 0.930 |

Remember to only call `st_asis()` when you are rendering tables inline in an Rmd document. If you are sending table code to a TeX report, then you will save them to a file and then include them into your report.

The remaining sections of this chapter will show you how to modify and enhance this output in the more basic ways. We will implement separate chapters for more complicated table manipulations.

1.3 Annotate with file names

`pmtables` can track and annotate your table with the filenames of the R code that generated the table (`r_file`) as well as the output file where you write the the table `.tex` code (`output_file`).

To have `pmtables` annotate your table with these file names, pass them in with the `r_file` and `output_file` arguments

```
out <- stable(data, r_file = "tables.R", output_file = "tables.tex")
```

When we look at the rendered table, these names will show up as annotations at the bottom of the table

```
out %>% st_asis()
```

| STUDY | DOSE | FORM | N | WT | CRCL | AGE | ALB | SCR |
|-------------|--------|---------|-----|------|------|------|------|-------|
| 12-DEMO-001 | 100 mg | tablet | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| 12-DEMO-001 | 150 mg | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| 12-DEMO-001 | 150 mg | tablet | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |
| 12-DEMO-001 | 150 mg | troche | 16 | 94.0 | 93.2 | 27.4 | 4.94 | 1.25 |
| 12-DEMO-001 | 200 mg | tablet | 64 | 67.9 | 100 | 27.5 | 4.25 | 1.10 |
| 12-DEMO-001 | 200 mg | troche | 16 | 76.6 | 99.2 | 22.8 | 4.54 | 1.15 |
| 12-DEMO-002 | 100 mg | capsule | 36 | 61.3 | 113 | 38.3 | 4.04 | 1.28 |
| 12-DEMO-002 | 100 mg | tablet | 324 | 77.6 | 106 | 29.9 | 4.31 | 0.981 |
| 12-DEMO-002 | 50 mg | capsule | 36 | 74.1 | 112 | 37.1 | 4.44 | 0.900 |
| 12-DEMO-002 | 50 mg | tablet | 324 | 71.2 | 106 | 34.1 | 4.63 | 0.868 |
| 12-DEMO-002 | 75 mg | capsule | 36 | 72.4 | 105 | 38.2 | 3.89 | 0.900 |
| 12-DEMO-002 | 75 mg | tablet | 288 | 71.6 | 98.9 | 34.2 | 4.49 | 0.991 |
| 12-DEMO-002 | 75 mg | troche | 36 | 73.6 | 103 | 49.2 | 4.52 | 0.930 |

Source code: tables.R

Source file: tables.tex

1.4 Saving your stable

Saving your stable **can** be as easy as sending it into `writeLines()`

```
writeLines(out, con = tempfile(tmpdir = '.', fileext = ".tex"))
```

But remember that we passed in the `output_file` argument to `stable()` and we can use that data to save the table code to the file we named in that argument.

Note that our `stable` object has another attribute now called `stable_file`

```
attributes(out)
```

```
. $class
. [1] "stable"
.
. $stable_file
. [1] "tables.tex"
```

This has the value that we passed in as `output_file`. To save our table to `stable_file`, we call `stable_save()`

```
stable_save(out)
```

There is a `dir` argument to `stable_save()` that we can use to select the directory where the file will be saved

```
stable_save(out, dir = tempdir())
```

And if you look at the default value for `dir` in `?stable_save`, you'll see that this is associated with an option called `pmtables.dir`; you can set that option to your default output directory and your tables will be saved there until you change that

```
options(pmtables.dir = tempdir())
stable_save(out)
```

1.5 Align columns

Use the `align` argument to align column data to the left, center or right. Use a `cols_*` function to specify the default alignment for all columns

```
tmp <- tibble(AB = 1, CDEFGHIJ = 2, KL = 3)
stable(tmp, align = cols_center()) %>% st_asis()
```

| AB | CDEFGHIJ | KL |
|----|----------|----|
| 1 | 2 | 3 |

You can pass in exceptions to the default

```
stable(tmp, align = cols_center(CDEFGHIJ = "r")) %>% st_asis()
```

| AB | CDEFGHIJ | KL |
|----|----------|----|
| 1 | 2 | 3 |

Or you can pass an alignment directive and the columns that are bound by that directive

```
stable(tmp, align = cols_center(.1 = "AB,KL")) %>% st_asis()
```

| AB | CDEFGHIJ | KL |
|----|----------|----|
| 1 | 2 | 3 |

A special directive called `.outer` lets you specify the alignment of the first and last column in the table. For example, this code puts the first column to the left and the last column to the right.


```
stable(tmp, align = cols_center(.outer = "lr")) %>% st_asis()
```

| AB | CDEFGHIJ | KL |
|----|----------|----|
| 1 | 2 | 3 |

1.5.1 Fixed column widths

Use `col_ragged(size)` to force a column to be a fixed size.

```
stable(tmp, align = cols_center(AB = col_ragged(2))) %>% st_asis()
```

| AB | CDEFGHIJ | KL |
|----|----------|----|
| 1 | 2 | 3 |

By default, the unit is cm so that the first column (AB) has a width of 2 cm regardless of the contents.

See `cols_align()` help topic for more information and argument descriptions.

1.6 Manipulating columns and names

1.6.1 Rename columns

You can change the name that appears in the rendered table with `cols_rename`

```
data %>%
  slice(1:3) %>%
  stable(cols_rename = c(Age = "AGE", Weight = "WT")) %>%
  st_asis()
```

| STUDY | DOSE | FORM | N | Weight | CRCL | Age | ALB | SCR |
|-------------|--------|---------|----|--------|------|------|------|-------|
| 12-DEMO-001 | 100 mg | tablet | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| 12-DEMO-001 | 150 mg | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| 12-DEMO-001 | 150 mg | tablet | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |

Note that the rename syntax follows the tidyselect convention of putting the new name on the left and the old name on the right.

1.6.2 Hide a column name

You can also “erase” the name of a column in the output

```
data %>%
  slice(1:3) %>%
  stable(cols_blank = "WT,ALB,SCR") %>%
  st_asis()
```

| STUDY | DOSE | FORM | N | WT | CRCL | AGE | ALB | SCR |
|-------------|--------|---------|----|------|------|------|------|-------|
| 12-DEMO-001 | 100 mg | tablet | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| 12-DEMO-001 | 150 mg | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| 12-DEMO-001 | 150 mg | tablet | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |

1.6.3 Unmask column names

In tibbles, you can't have duplicate column names. The `cols_split` argument lets you unmask the names when duplicate names are prefixed with a tag and a delimiter

```
tmp <- tibble(a.A = 1, b.A = 2, c.A = 3)
```

```
tmp %>% stable(cols_split = '.') %>% st_asis()
```

| A | A | A |
|---|---|---|
| 1 | 2 | 3 |

1.6.4 Make column names bold

```
data %>% slice(1:2) %>% stable(cols_bold = TRUE) %>% st_asis()
```

| STUDY | DOSE | FORM | N | WT | CRCL | AGE | ALB | SCR |
|--------------|-------------|-------------|----------|-----------|-------------|------------|------------|------------|
| 12-DEMO-001 | 100 mg | tablet | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| 12-DEMO-001 | 150 mg | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |

1.6.5 Drop a column from the table

If we want to prevent a column from appearing in the output table (e.g. FORM)

```
head(data)
```

```
. # A tibble: 6 x 9
.   STUDY      DOSE  FORM    N    WT  CRCL  AGE  ALB  SCR
.   <chr>      <chr> <chr>  <chr> <chr> <chr> <chr> <chr> <chr>
. 1 12-DEMO-001 100 mg tablet  80   71.4  104   33.7  4.20  1.06
. 2 12-DEMO-001 150 mg capsule 16   89.4  122   24.4  4.63  1.12
. 3 12-DEMO-001 150 mg tablet  48   81.7  104   34.4  3.83  0.910
. 4 12-DEMO-001 150 mg troche 16   94.0  93.2  27.4  4.94  1.25
. 5 12-DEMO-001 200 mg tablet  64   67.9  100   27.5  4.25  1.10
. 6 12-DEMO-001 200 mg troche 16   76.6  99.2  22.8  4.54  1.15
```

list the column name as drop

```
stable(data, drop = "FORM") %>% st_asis()
```

| STUDY | DOSE | N | WT | CRCL | AGE | ALB | SCR |
|-------------|--------|-----|------|------|------|------|-------|
| 12-DEMO-001 | 100 mg | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| 12-DEMO-001 | 150 mg | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| 12-DEMO-001 | 150 mg | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |
| 12-DEMO-001 | 150 mg | 16 | 94.0 | 93.2 | 27.4 | 4.94 | 1.25 |
| 12-DEMO-001 | 200 mg | 64 | 67.9 | 100 | 27.5 | 4.25 | 1.10 |
| 12-DEMO-001 | 200 mg | 16 | 76.6 | 99.2 | 22.8 | 4.54 | 1.15 |
| 12-DEMO-002 | 100 mg | 36 | 61.3 | 113 | 38.3 | 4.04 | 1.28 |
| 12-DEMO-002 | 100 mg | 324 | 77.6 | 106 | 29.9 | 4.31 | 0.981 |
| 12-DEMO-002 | 50 mg | 36 | 74.1 | 112 | 37.1 | 4.44 | 0.900 |
| 12-DEMO-002 | 50 mg | 324 | 71.2 | 106 | 34.1 | 4.63 | 0.868 |
| 12-DEMO-002 | 75 mg | 36 | 72.4 | 105 | 38.2 | 3.89 | 0.900 |
| 12-DEMO-002 | 75 mg | 288 | 71.6 | 98.9 | 34.2 | 4.49 | 0.991 |
| 12-DEMO-002 | 75 mg | 36 | 73.6 | 103 | 49.2 | 4.52 | 0.930 |

Of course some tidyverse could accomplish the same thing

```
data %>% select(-FORM) %>% stable()
```

1.7 Other customizations

1.7.1 Notes

Arbitrary notes can get added to any table using the `notes` argument.

```
data %>%
  slice(1:3) %>%
  stable(notes = "Showing just the first three rows") %>%
  st_asis()
```

| STUDY | DOSE | FORM | N | WT | CRCL | AGE | ALB | SCR |
|-------------|--------|---------|----|------|------|------|------|-------|
| 12-DEMO-001 | 100 mg | tablet | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| 12-DEMO-001 | 150 mg | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| 12-DEMO-001 | 150 mg | tablet | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |

Showing just the first three rows

The appearance of the notes can be controlled by calling `noteconf()` and passing the result as `note_config`. See `?tab_notes()` for more details.

1.7.2 Units

pmtables can automatically place units underneath the appropriate column. To do this, generate a list with names that match the column names you want to label with units.

```
u <- list(
  WT = "kg", CRCL = "ml/min", AGE = "year", ALB = "g/dL",
  SCR = "mg\\%"
) %>% map(~paste0("(", .x, ")"))
```

Then pass that list as units to `stable()`

```
stable(data, units = u) %>% st_asis()
```

| STUDY | DOSE | FORM | N | WT (kg) | CRCL (ml/min) | AGE (year) | ALB (g/dL) | SCR (mg%) |
|-------------|--------|---------|-----|------------|------------------|---------------|---------------|--------------|
| 12-DEMO-001 | 100 mg | tablet | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| 12-DEMO-001 | 150 mg | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| 12-DEMO-001 | 150 mg | tablet | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |
| 12-DEMO-001 | 150 mg | troche | 16 | 94.0 | 93.2 | 27.4 | 4.94 | 1.25 |
| 12-DEMO-001 | 200 mg | tablet | 64 | 67.9 | 100 | 27.5 | 4.25 | 1.10 |
| 12-DEMO-001 | 200 mg | troche | 16 | 76.6 | 99.2 | 22.8 | 4.54 | 1.15 |
| 12-DEMO-002 | 100 mg | capsule | 36 | 61.3 | 113 | 38.3 | 4.04 | 1.28 |
| 12-DEMO-002 | 100 mg | tablet | 324 | 77.6 | 106 | 29.9 | 4.31 | 0.981 |
| 12-DEMO-002 | 50 mg | capsule | 36 | 74.1 | 112 | 37.1 | 4.44 | 0.900 |
| 12-DEMO-002 | 50 mg | tablet | 324 | 71.2 | 106 | 34.1 | 4.63 | 0.868 |
| 12-DEMO-002 | 75 mg | capsule | 36 | 72.4 | 105 | 38.2 | 3.89 | 0.900 |
| 12-DEMO-002 | 75 mg | tablet | 288 | 71.6 | 98.9 | 34.2 | 4.49 | 0.991 |
| 12-DEMO-002 | 75 mg | troche | 36 | 73.6 | 103 | 49.2 | 4.52 | 0.930 |

1.7.3 Multi-line column headers

If the column header is long, you can break it across multiple lines. By default, use `...` in the column name

```
tibble(`First line ... Second line` = 123456789) %>%
  stable() %>% st_asis()
```

| |
|-------------|
| First line |
| Second line |
| 123456789 |

The break can be introduced through the rename mechanism

```
tibble(a = 1) %>%
  stable(cols_rename = c(`First ... Second` = "a")) %>%
  st_asis()
```

| First Second |
|-----------------|
| 1 |

Look at the `?tab_cols` help topic for the `cols_break` argument; this lets you change the character sequence used for the break.

1.7.4 Insert horizontal lines

Pass `hlines_at` to insert horizontal lines above specific rows. This can be either logical vector with the same length as the number of rows in the table or a vector of integers.

```
stable(stdata(), hline_at = c(3,5)) %>% st_asis()
```

| STUDY | DOSE | FORM | N | WT | CRCL | AGE | ALB | SCR |
|-------------|--------|---------|-----|------|------|------|------|-------|
| 12-DEMO-001 | 100 mg | tablet | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| 12-DEMO-001 | 150 mg | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| 12-DEMO-001 | 150 mg | tablet | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |
| 12-DEMO-001 | 150 mg | troche | 16 | 94.0 | 93.2 | 27.4 | 4.94 | 1.25 |
| 12-DEMO-001 | 200 mg | tablet | 64 | 67.9 | 100 | 27.5 | 4.25 | 1.10 |
| 12-DEMO-001 | 200 mg | troche | 16 | 76.6 | 99.2 | 22.8 | 4.54 | 1.15 |
| 12-DEMO-002 | 100 mg | capsule | 36 | 61.3 | 113 | 38.3 | 4.04 | 1.28 |
| 12-DEMO-002 | 100 mg | tablet | 324 | 77.6 | 106 | 29.9 | 4.31 | 0.981 |
| 12-DEMO-002 | 50 mg | capsule | 36 | 74.1 | 112 | 37.1 | 4.44 | 0.900 |
| 12-DEMO-002 | 50 mg | tablet | 324 | 71.2 | 106 | 34.1 | 4.63 | 0.868 |
| 12-DEMO-002 | 75 mg | capsule | 36 | 72.4 | 105 | 38.2 | 3.89 | 0.900 |
| 12-DEMO-002 | 75 mg | tablet | 288 | 71.6 | 98.9 | 34.2 | 4.49 | 0.991 |
| 12-DEMO-002 | 75 mg | troche | 36 | 73.6 | 103 | 49.2 | 4.52 | 0.930 |

or

```
stable(stdata(), hline_at = data$FORM == "tablet") %>% st_asis()
```

| STUDY | DOSE | FORM | N | WT | CRCL | AGE | ALB | SCR |
|-------------|--------|---------|-----|------|------|------|------|-------|
| 12-DEMO-001 | 100 mg | tablet | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| 12-DEMO-001 | 150 mg | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| 12-DEMO-001 | 150 mg | tablet | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |
| 12-DEMO-001 | 150 mg | troche | 16 | 94.0 | 93.2 | 27.4 | 4.94 | 1.25 |
| 12-DEMO-001 | 200 mg | tablet | 64 | 67.9 | 100 | 27.5 | 4.25 | 1.10 |
| 12-DEMO-001 | 200 mg | troche | 16 | 76.6 | 99.2 | 22.8 | 4.54 | 1.15 |
| 12-DEMO-002 | 100 mg | capsule | 36 | 61.3 | 113 | 38.3 | 4.04 | 1.28 |
| 12-DEMO-002 | 100 mg | tablet | 324 | 77.6 | 106 | 29.9 | 4.31 | 0.981 |
| 12-DEMO-002 | 50 mg | capsule | 36 | 74.1 | 112 | 37.1 | 4.44 | 0.900 |
| 12-DEMO-002 | 50 mg | tablet | 324 | 71.2 | 106 | 34.1 | 4.63 | 0.868 |
| 12-DEMO-002 | 75 mg | capsule | 36 | 72.4 | 105 | 38.2 | 3.89 | 0.900 |
| 12-DEMO-002 | 75 mg | tablet | 288 | 71.6 | 98.9 | 34.2 | 4.49 | 0.991 |
| 12-DEMO-002 | 75 mg | troche | 36 | 73.6 | 103 | 49.2 | 4.52 | 0.930 |

Pass `hlines_from` to derive `hline` locations based on non-repeating values in a table column. Notice how this behaves.

```
stable(stdata(), hline_from = "DOSE") %>% st_asis()
```

| STUDY | DOSE | FORM | N | WT | CRCL | AGE | ALB | SCR |
|-------------|--------|---------|-----|------|------|------|------|-------|
| 12-DEMO-001 | 100 mg | tablet | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| 12-DEMO-001 | 150 mg | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| 12-DEMO-001 | 150 mg | tablet | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |
| 12-DEMO-001 | 150 mg | troche | 16 | 94.0 | 93.2 | 27.4 | 4.94 | 1.25 |
| 12-DEMO-001 | 200 mg | tablet | 64 | 67.9 | 100 | 27.5 | 4.25 | 1.10 |
| 12-DEMO-001 | 200 mg | troche | 16 | 76.6 | 99.2 | 22.8 | 4.54 | 1.15 |
| 12-DEMO-002 | 100 mg | capsule | 36 | 61.3 | 113 | 38.3 | 4.04 | 1.28 |
| 12-DEMO-002 | 100 mg | tablet | 324 | 77.6 | 106 | 29.9 | 4.31 | 0.981 |
| 12-DEMO-002 | 50 mg | capsule | 36 | 74.1 | 112 | 37.1 | 4.44 | 0.900 |
| 12-DEMO-002 | 50 mg | tablet | 324 | 71.2 | 106 | 34.1 | 4.63 | 0.868 |
| 12-DEMO-002 | 75 mg | capsule | 36 | 72.4 | 105 | 38.2 | 3.89 | 0.900 |
| 12-DEMO-002 | 75 mg | tablet | 288 | 71.6 | 98.9 | 34.2 | 4.49 | 0.991 |
| 12-DEMO-002 | 75 mg | troche | 36 | 73.6 | 103 | 49.2 | 4.52 | 0.930 |

See the `?tab_hlines` help topic for more info. See also `st_hline()` for the pipe equivalent with additional feature.

1.7.5 Clear replicate values

You can create groups in a table by “clearing” replicate values

```
stable(stdata(), clear_reps = "STUDY") %>% st_asis()
```

| STUDY | DOSE | FORM | N | WT | CRCL | AGE | ALB | SCR |
|-------------|--------|---------|-----|------|------|------|------|-------|
| 12-DEMO-001 | 100 mg | tablet | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| | 150 mg | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| | 150 mg | tablet | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |
| | 150 mg | troche | 16 | 94.0 | 93.2 | 27.4 | 4.94 | 1.25 |
| | 200 mg | tablet | 64 | 67.9 | 100 | 27.5 | 4.25 | 1.10 |
| | 200 mg | troche | 16 | 76.6 | 99.2 | 22.8 | 4.54 | 1.15 |
| 12-DEMO-002 | 100 mg | capsule | 36 | 61.3 | 113 | 38.3 | 4.04 | 1.28 |
| | 100 mg | tablet | 324 | 77.6 | 106 | 29.9 | 4.31 | 0.981 |
| | 50 mg | capsule | 36 | 74.1 | 112 | 37.1 | 4.44 | 0.900 |
| | 50 mg | tablet | 324 | 71.2 | 106 | 34.1 | 4.63 | 0.868 |
| | 75 mg | capsule | 36 | 72.4 | 105 | 38.2 | 3.89 | 0.900 |
| | 75 mg | tablet | 288 | 71.6 | 98.9 | 34.2 | 4.49 | 0.991 |
| | 75 mg | troche | 36 | 73.6 | 103 | 49.2 | 4.52 | 0.930 |

This can be combined with an hline

```
stable(stdata(), clear_reps = "STUDY", hline_from = "STUDY") %>%
  st_asis()
```

| STUDY | DOSE | FORM | N | WT | CRCL | AGE | ALB | SCR |
|-------------|--------|---------|-----|------|------|------|------|-------|
| 12-DEMO-001 | 100 mg | tablet | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| | 150 mg | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| | 150 mg | tablet | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |
| | 150 mg | troche | 16 | 94.0 | 93.2 | 27.4 | 4.94 | 1.25 |
| | 200 mg | tablet | 64 | 67.9 | 100 | 27.5 | 4.25 | 1.10 |
| | 200 mg | troche | 16 | 76.6 | 99.2 | 22.8 | 4.54 | 1.15 |
| 12-DEMO-002 | 100 mg | capsule | 36 | 61.3 | 113 | 38.3 | 4.04 | 1.28 |
| | 100 mg | tablet | 324 | 77.6 | 106 | 29.9 | 4.31 | 0.981 |
| | 50 mg | capsule | 36 | 74.1 | 112 | 37.1 | 4.44 | 0.900 |
| | 50 mg | tablet | 324 | 71.2 | 106 | 34.1 | 4.63 | 0.868 |
| | 75 mg | capsule | 36 | 72.4 | 105 | 38.2 | 3.89 | 0.900 |
| | 75 mg | tablet | 288 | 71.6 | 98.9 | 34.2 | 4.49 | 0.991 |
| | 75 mg | troche | 36 | 73.6 | 103 | 49.2 | 4.52 | 0.930 |

See `?tab_clear_reps` for other options, including an option for clearing based on several grouping variables.

2 Group table rows with panel

2.1 Syntax

To panel a table by STUDY

```
stable(stdata(), panel = "STUDY")
```

To set a prefix for the panel header:

```
stable(stdata(), panel = as.panel("STUDY", prefix = "Study: "))
```

2.2 Basics

Paneling your table is a way to group sets of rows together into a “panel” with a panel header rendered in bold font. For example, we can panel a table of mtcars by carb. We will be working with an abbreviated version of mtcars:

```
smcars
```

```
.
.           name mpg cyl  disp  hp drat   wt  qsec vs am gear
. Datsun 710      Datsun 710 22.8   4 108.0  93 3.85 2.320 18.61  1  1    4
. Hornet 4 Drive Hornet 4 Drive 21.4   6 258.0 110 3.08 3.215 19.44  1  0    3
. Valiant          Valiant 18.1   6 225.0 105 2.76 3.460 20.22  1  0    3
. Fiat 128          Fiat 128 32.4   4  78.7  66 4.08 2.200 19.47  1  1    4
. Toyota Corolla Toyota Corolla 33.9   4  71.1  65 4.22 1.835 19.90  1  1    4
. Toyota Corona    Toyota Corona 21.5   4 120.1  97 3.70 2.465 20.01  1  0    3
. Fiat X1-9         Fiat X1-9 27.3   4  79.0  66 4.08 1.935 18.90  1  1    4
. Merc 240D         Merc 240D 24.4   4 146.7  62 3.69 3.190 20.00  1  0    4
. Merc 230          Merc 230 22.8   4 140.8  95 3.92 3.150 22.90  1  0    4
. Honda Civic       Honda Civic 30.4   4  75.7  52 4.93 1.615 18.52  1  1    4
.
.           carb
. Datsun 710      1
. Hornet 4 Drive  1
. Valiant          1
. Fiat 128         1
. Toyota Corolla  1
. Toyota Corona   1
. Fiat X1-9        1
. Merc 240D        2
. Merc 230         2
. Honda Civic     2
```

Then we pass into `stable()` and name the paneling column:

```
smcars %>% stable(panel = "carb") %>% st_asis()
```


| name | mpg | cyl | disp | hp | drat | wt | qsec | vs | am | gear |
|----------------|------|-----|-------|-----|------|-------|-------|----|----|------|
| 1 | | | | | | | | | | |
| Datsun 710 | 22.8 | 4 | 108 | 93 | 3.85 | 2.32 | 18.61 | 1 | 1 | 4 |
| Hornet 4 Drive | 21.4 | 6 | 258 | 110 | 3.08 | 3.215 | 19.44 | 1 | 0 | 3 |
| Valiant | 18.1 | 6 | 225 | 105 | 2.76 | 3.46 | 20.22 | 1 | 0 | 3 |
| Fiat 128 | 32.4 | 4 | 78.7 | 66 | 4.08 | 2.2 | 19.47 | 1 | 1 | 4 |
| Toyota Corolla | 33.9 | 4 | 71.1 | 65 | 4.22 | 1.835 | 19.9 | 1 | 1 | 4 |
| Toyota Corona | 21.5 | 4 | 120.1 | 97 | 3.7 | 2.465 | 20.01 | 1 | 0 | 3 |
| Fiat X1-9 | 27.3 | 4 | 79 | 66 | 4.08 | 1.935 | 18.9 | 1 | 1 | 4 |
| 2 | | | | | | | | | | |
| Merc 240D | 24.4 | 4 | 146.7 | 62 | 3.69 | 3.19 | 20 | 1 | 0 | 4 |
| Merc 230 | 22.8 | 4 | 140.8 | 95 | 3.92 | 3.15 | 22.9 | 1 | 0 | 4 |
| Honda Civic | 30.4 | 4 | 75.7 | 52 | 4.93 | 1.615 | 18.52 | 1 | 1 | 4 |

Now, all of the `carb==1` rows are grouped with the heading 1 and similarly the `carb==2` rows are grouped with the heading 2 in bold.

This is ok, but a more informative heading would be helpful. To do this, we'll call `as.panel()` to both name the panel column and set some options:

```
smcars %>% stable(panel = as.panel("carb", prefix = "carb: ")) %>% st_asis()
```

| name | mpg | cyl | disp | hp | drat | wt | qsec | vs | am | gear |
|----------------|------|-----|-------|-----|------|-------|-------|----|----|------|
| carb: 1 | | | | | | | | | | |
| Datsun 710 | 22.8 | 4 | 108 | 93 | 3.85 | 2.32 | 18.61 | 1 | 1 | 4 |
| Hornet 4 Drive | 21.4 | 6 | 258 | 110 | 3.08 | 3.215 | 19.44 | 1 | 0 | 3 |
| Valiant | 18.1 | 6 | 225 | 105 | 2.76 | 3.46 | 20.22 | 1 | 0 | 3 |
| Fiat 128 | 32.4 | 4 | 78.7 | 66 | 4.08 | 2.2 | 19.47 | 1 | 1 | 4 |
| Toyota Corolla | 33.9 | 4 | 71.1 | 65 | 4.22 | 1.835 | 19.9 | 1 | 1 | 4 |
| Toyota Corona | 21.5 | 4 | 120.1 | 97 | 3.7 | 2.465 | 20.01 | 1 | 0 | 3 |
| Fiat X1-9 | 27.3 | 4 | 79 | 66 | 4.08 | 1.935 | 18.9 | 1 | 1 | 4 |
| carb: 2 | | | | | | | | | | |
| Merc 240D | 24.4 | 4 | 146.7 | 62 | 3.69 | 3.19 | 20 | 1 | 0 | 4 |
| Merc 230 | 22.8 | 4 | 140.8 | 95 | 3.92 | 3.15 | 22.9 | 1 | 0 | 4 |
| Honda Civic | 30.4 | 4 | 75.7 | 52 | 4.93 | 1.615 | 18.52 | 1 | 1 | 4 |

Note that the prefix is completely specified by the user (including any spaces or a colon).

2.3 panel: important points

1. Most of the time, the data frame should be sorted by the `panel` column
2. `pmtables` creates panels by non-repeating values in the `panel` column; there will be an error if duplicate panel names are found and this can be overridden by passing `duplicates_ok` to `as.panel()`.

3 Group table columns with spanners

3.1 Syntax

Set the `span` argument to the output of `as.span()`. The key arguments for `as.span()` are the `spanner title` and the names of the columns over which you want the `spanner` to run

```
stable(stdata(), span = as.span("Covariates", WT:SCR))
```

The equivalent pipe syntax is

```
st_new(stdata()) %>% st_span("Covariates", WT:SCR)
```

3.2 Basics

A column `spanner` puts a horizontal line over a sequence of column names and places a title above that line forming a column group.

As a trivial example:

```
data <-
  tibble(
    Tariffville = "06081", Connecticut = "CT",
    Minnesota = "MN", Minneapolis = "55455"
  )

data %>% stable(span = as.span("States", Connecticut:Minnesota)) %>% st_asis()
```

| | States | | |
|-------------|-------------|-----------|-------------|
| Tariffville | Connecticut | Minnesota | Minneapolis |
| 06081 | CT | MN | 55455 |

3.3 Multiple spanners

Multiple `spanners` can be added to a table by specifying the `level` for any `spanner` that you want to be placed above the lowest level `spanner`. For example,

```
sp <- list(
  as.span("States", Connecticut:Minnesota),
  as.span("Important Locations", Tariffville:Minneapolis, level = 2)
)

data %>% stable(span = sp) %>% st_asis()
```

| | Important Locations | | |
|-------------|---------------------|-----------|-------------|
| | States | | |
| Tariffville | Connecticut | Minnesota | Minneapolis |
| 06081 | CT | MN | 55455 |

Note that to specify multiple spanners, we pass a list of span objects. I've simplified the code a bit here by creating that list as a standalone object and then passing the whole list as `span`.

3.3.1 Using pipe syntax

For problems like this, it might be preferable to use the pipe syntax

```
data %>%
  st_new() %>%
  st_span("States", Connecticut:Minnesota) %>%
  st_span("Important Locations", Tariffville:Minneapolis, level = 2) %>%
  stable() %>%
  st_asis()
```

| Important Locations | | | |
|---------------------|-------------|-----------|-------------|
| States | | | |
| Tariffville | Connecticut | Minnesota | Minneapolis |
| 06081 | CT | MN | 55455 |

3.4 Breaking span title

We can make the title of the span break across multiple lines by using `...`

```
stable(data, span = as.span("Important ... States", Connecticut:Minnesota)) %>%
  st_asis()
```

| Important States | | | |
|---------------------|-------------|-----------|-------------|
| Tariffville | Connecticut | Minnesota | Minneapolis |
| 06081 | CT | MN | 55455 |

4 Tables that span multiple pages: longtable

4.1 Syntax

To create a long table from a data frame

```
stable_long(stdata())
```

To create a long table from pipeline

```
st_new(data) %>% stable_long()
```

To create a long table from pmtable

```
pt_cont_long(data, cols = "WT,EGFR") %>% stable_long()
```

4.2 Basics

You can create longtables that span multiple pages of your pdf document. Tables using the `longtable` environment are very different than the basic table from `stable()` which are built using `tabular` environment.

4.3 Inserting longtable into your latex document

Once you have written your long table out to a file, you can source it into your latex document with a simple input command

```
\input{my-table.tex}
```

IMPORTANT

- Do not wrap the input in `\begin{table} / \end{table}`; the table will not show up properly that way
- Do not include any `\caption{...}` statement; the caption must be provided in a special way (see below)

4.4 Writing a caption

Longtable is different than regular tabular table in that the caption (and label) need to be included in the longtable environment. This means that you have to enter this information **when you create the table**.

4.4.1 Method 1: in the R script

`stable_long()` has an argument called `lt_cap_text` that will allow you to provide the text for the caption. This text must be passed to the `stable_long()` call (or `st_make()`)

```
out <- stable_long(data, lt_cap_text = "A long table (example 3)")
```

You will see in the TeX code that a caption is included in the longtable environemt.

4.4.2 Method 2: as a TeX macro

Rather than passing the text for the caption, you can name a macro that should (will) be defined at the time the table is rendered in the TeX document.

Use the `lt_cap_macro` argument:

```
out <- stable_long(data, lt_cap_macro = "ltexfourcap")
```

Now, there is a call to that macro in the table and you **must** define that macro prior to sourcing in your tex document.

```
\newcommand{\ltexfourcap}{  
  Another long table - example 4  
}  
  
\input{example4.tex}
```

4.5 Add a label

To add a label, pass in a caption (either as text or as a macro) and then use the `lt_cap_label` argument:

```
data %>%  
  stable_long(lt_cap_label = "tab:example", lt_cap_macro = "example")
```

4.6 Include a longtable in an Rmd document

If you want to dump a table into an R markdown document, pass it to `st_asis()`. There is a method for `stable_long()` and it will wrap the table properly.

```
out <- stable_long(data) %>% st_asis()
```

5 The pipe interface

5.1 Basics

Mostly working with this data; but some others come in later to illustrate certain features.

```
data <- pmt_summarized
head(data)
```

```
. # A tibble: 6 x 9
.   STUDY      DOSE  FORM    N    WT   CRCL  AGE  ALB  SCR
.   <chr>      <chr> <chr>  <chr> <chr> <chr> <chr> <chr> <chr>
. 1 12-DEMO-001 100 mg tablet  80   71.4  104   33.7  4.20  1.06
. 2 12-DEMO-001 150 mg capsule 16   89.4  122   24.4  4.63  1.12
. 3 12-DEMO-001 150 mg tablet  48   81.7  104   34.4  3.83  0.910
. 4 12-DEMO-001 150 mg troche 16   94.0  93.2  27.4  4.94  1.25
. 5 12-DEMO-001 200 mg tablet  64   67.9  100   27.5  4.25  1.10
. 6 12-DEMO-001 200 mg troche 16   76.6  99.2  22.8  4.54  1.15
```

You start out a pipeline by passing your data frame into `st_new()`

```
data %>% st_new() %>% class
```

```
. [1] "stobject"      "environment"
```

This creates an object that gets revised by subsequent steps in the pipeline, adding features and styling as you go.

For the final step in the pipeline, we'll send the object to `stable()` to create the table

```
data %>% st_new() %>% stable() %>% head(n=9)
```

```
. [1] "\\setlength{\\tabcolsep}{5pt} "
. [2] "\\begin{threeparttable}"
. [3] "\\renewcommand{\\arraystretch}{1.3}"
. [4] "\\begin{tabular}[h]{l|lllllllll}"
. [5] "\\hline"
. [6] "STUDY & DOSE & FORM & N & WT & CRCL & AGE & ALB & SCR \\\\"
. [7] "\\hline"
. [8] "12-DEMO-001 & 100 mg & tablet & 80 & 71.4 & 104 & 33.7 & 4.20 & 1.06 \\\\"
. [9] "12-DEMO-001 & 150 mg & capsule & 16 & 89.4 & 122 & 24.4 & 4.63 & 1.12 \\\\"
```

5.2 Simple table

You can terminate the pipeline and create a tabular table by sending to `stable()`

```
data %>% st_new() %>% stable()
```

Equivalent call

```
data %>% stable()
```

5.3 Long table

You can also pipe to `stable_long()` to make a long table

```
data %>% st_new() %>% stable_long()
```

5.4 Annotate with file names

```
st_new(data) %>% st_files(r = "foo.R", output = "foo.tex")
```

Equivalent call

```
stable(data, r_file = "foo.R", output_file = "foo.tex")
```

Note that in the pipe version, we already have `file` in the function name so that gets dropped from the argument name.

5.5 Save a table

First convert with `stable()` or `stable_long()` then save with `stable_save()`

```
st_new(data) %>%  
  st_files(output = "foo.tex") %>%  
  stable() %>%  
  stable_save()
```

5.6 Align columns

- `st_center(...)`
- `st_left(...)`
- `st_right(...)`
- `st_align(...)`

```
st_new(data) %>%  
  st_center() %>%  
  stable()
```

Equivalent call

```
stable(data, align = cols_center())
```

5.7 Rename columns

```
st_new(data) %>%  
  st_rename(Weight = "WT") %>%  
  stable()
```

Equivalent call

```
stable(data, cols_rename = c(Weight = "WT"))
```

5.8 Blank columns

```
st_new(data) %>% st_blank(WT, ALB, DOSE) %>% stable()
```

Equivalent call

```
stable(data, cols_blank = "WT,ALB,DOSE")
```

5.9 Drop columns

```
st_new(data) %>% st_drop(WT, ALB, DOSE) %>% stable()
```

Equivalent call

```
stable(data, drop = "WT, ALB, DOSE")
```

5.10 Notes

- Multiple calls are allowed; notes will accumulate

```
st_new(data) %>%  
  st_notes("first note") %>%  
  st_notes("second note") %>%  
  stable()
```

Equivalent call


```
stable(  
  data,  
  notes = c("first note", "second note")  
)
```

5.11 Units

```
st_new(data) %>%  
  st_units(WT = "kg", AGE = "years") %>%  
  stable()
```

Note that `st_units()` will automatically add parens to your units; this can be suppressed with the `parens` argument.

Units can also be added as a list

```
u <- list(WT = "kg", AGE = "years")  
  
st_new(data) %>%  
  st_units(u) %>%  
  stable()
```

Equivalent call

```
stable(data, units = u)
```

5.12 panel

```
st_new(data) %>%  
  st_panel("STUDY") %>%  
  stable()
```

Equivalent call

```
stable(data, panel = "STUDY")
```

5.13 span

```
st_new(data) %>%  
  st_span("Covariates", c(WT, ALB, EGFR)) %>%  
  stable()
```

Equivalent call

```
stable(data, span = as.span("Covariates", c(WT, ALB, EGFR)))
```

5.14 hlines - at

To put horizontal lines at specific rows

```
st_new(data) %>% st_hline(at = c(2,4,6))
```

Equivalent call

```
stable(data, hline_at = c(2,4,6))
```

5.15 hlines - from

To calculate hlines based on data frame column values (for example, to break the table by changing values of STUDYf)

```
st_new(data) %>% st_hline(from = "STUDYf")
```

Equivalent call

```
stable(data, hline_from = "STUDYf")
```

5.16 hlines - pattern

To search the table for a pattern and add hlines above matches

```
st_new(data) %>% st_hline(pattern = "All", cols = "Summary")
```

The cols argument limits the search to the Summary column; omit this argument to search the whole table.

There is no equivalent call for this using straight stable().

5.17 Clear replicate values

To create groups by “clearing” replicate values in a column

```
st_new(data) %>% st_clear_reps(STUDY) %>% stable()
```

Equivalent call

```
stable(data, clear_reps = "STUDY")
```

6 Options for previewing the table

6.1 st2report

Take a table or a list of tables and render them in a report-like document with a table of contents and a (faux) caption for each table

```
data %>% stable() %>% st2report()
```

You might try passing `ntex` to force the document to build more than once (sometimes the layout settles down after the second build)

```
data %>% stable() %>% st2report(ntex = 2)
```

Pass in a list of tables and you will get one table on each page with a listing of tables in the table of contents

```
list(table1, table2, table3) %>% st2report()
```

6.2 st2viewer

This function relies on `texPreview()` to render your table and display it as a graphic in the viewer window

```
data %>% stable() %>% st2viewer()
```

This method is more convenient because the tables always go to the viewer. But the rendering will not be like what you will see in the report.

6.3 st2article

Like `st2report()` but less report-like. You should use `st2report()` instead.

```
data %>% stable() %>% st2article()
```

6.4 st2doc

The original. Rather than building a TeX article, it runs the table in a Rmd document via pandoc. Not recommended; it is much slower to get the preview because there has to be a call to pandoc

```
data %>% stable() %>% st2doc()
```

7 A word about sanitizing table contents

7.1 Notes

```
x <- ptdata() %>% st_new(notes = "EDA_summary = TRUE") %>%  
  st_make(inspect = TRUE) %>%  
  get_stable_data()  
  
x$notes
```

```
. [1] "EDA\\_summary = TRUE"
```

7.2 File names

```
x <- ptdata() %>% st_new() %>%  
  st_files(r = "my_script.R") %>%  
  st_make(inspect = TRUE) %>%  
  get_stable_data()  
  
x$notes
```

```
. [1] "Source code: my\\_script.R"
```

7.3 Column names

```
out <-  
  tibble(a_1 = 5) %>%  
  stable(inspect = TRUE) %>%  
  get_stable_data()  
  
out$cols_tex
```

```
. [1] "a\\_1 \\\\"
```

7.4 Main table contents

```
out <-  
  tibble(a = "5_2") %>%  
  stable(inspect = TRUE) %>%  
  get_stable_data()  
  
out$tab
```

```
. [1] "5\\_2 \\\\"
```

7.5 Span titles

```
out <-
  ptdata() %>%
  stable(inspect = TRUE, span = colgroup("foo_this", WT:SCR)) %>%
  get_stable_data()

out$span_data$tex

. [1] "\\multicolumn{4}{c}{ } & \\multicolumn{5}{c}{foo\\_this} \\\\"
. [2] "\\cmidrule(lr){5-9}"
```

7.6 Panel names

```
data <- tibble(a = c("a_1", "a_1", "a_1", "a_2", "a_2"),
              b = letters[1:5])

out <- stable(data, panel = "a")
out[grepl("multicolumn", out)]

. [1] "\\multicolumn{1}{l}{\\textbf{a\\_1}}\\\\"
. [2] "\\hline \\multicolumn{1}{l}{\\textbf{a\\_2}}\\\\"
```

7.7 cols_extra input

```
x <- letters[1:5]
data <- tibble(a = x, b = x, c = x)
xtra <- tibble(a = "foo%", b = "$\\mu$g", c = "1234 \\% %")
out <- stable(data, cols_extra = xtra)
out[grepl("%", out, fixed = TRUE)]

. [1] "foo\\% & $\\mu$g & 1234 \\% % \\\\"
```

8 pmtable

Some setup

```
units = yspec::ys_get_unit(yspec::ys_help$spec(), parens = TRUE)
```

```
data <- pmt_first
data_pk <- pmt_pk
data_all <- pmt_obs
```

8.1 Principles

These functions expect that the user passes in all data that is to be summarized and nothing more. We will not filter your data.

8.2 Rename cols

When you select columns to summarize, you can generally pass in alternate (nicer) names that you want to show up in the table. For example, if I have a column called WT in the data frame and I want it to show up as Weight this can be accomplished during the call

```
pt_cont_wide(data, cols = c(Weight = "WT")) %>%
  stable(notes = NULL) %>% st_asis()
```

| Weight |
|-------------------|
| 70.7 (12.8) [157] |

Alternatively, you can use the table argument to enter rename info. Note that table is a list that should have names that match up with columns in the data frame and values that are the new names

```
tab <- list(SEXf = "Sex", ASIANf = "Race group")

pt_cat_wide(data, cols = "SEXf,ASIANf", table = tab) %>%
  stable() %>% st_asis()
```

| | Sex | | Race group | |
|-----|-----------|-----------|------------|-----------|
| n | male | female | Asian | non-Asian |
| 160 | 80 (50.0) | 80 (50.0) | 66 (41.2) | 94 (58.8) |

Summary is count (percent)

n: number of records summarized

8.3 Data inventory tables

- Count number of
 - individuals

- observations
 - BQL observations
 - missing values
- Calculate the percent of observations or BQL in different sub groups

8.3.1 Stacked by endpoint

- The stacked plot creates multiple independent tables to summarize different endpoints; there is no single overall summary for the table because we are summarizing different endpoints

```
out <- pt_data_inventory(
  data_all,
  by = c(Study = "STUDYf"),
  panel = as.panel("SEQf", prefix = "Endpoint: "),
  stacked = TRUE
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_axis()
```

| Study | Number | | | | Percent | |
|---------------------------|--------|------|------|-----|---------|-----|
| | SUBJ | MISS | OBS | BQL | OBS | BQL |
| Endpoint: DEMO PK | | | | | | |
| 12-DEMO-001 | 30 | 8 | 427 | 15 | 13.4 | 0.5 |
| 12-DEMO-002 | 50 | 10 | 1152 | 38 | 36.3 | 1.2 |
| 11-DEMO-005 | 40 | 10 | 920 | 30 | 29.0 | 0.9 |
| 13-DEMO-001 | 40 | 7 | 582 | 11 | 18.3 | 0.3 |
| <i>Group Total</i> | 160 | 35 | 3081 | 94 | 97.0 | 3.0 |
| Endpoint: ESTRDIOL | | | | | | |
| 11-DEMO-005 | 40 | 0 | 40 | 0 | 50.6 | 0.0 |
| 13-DEMO-001 | 40 | 1 | 39 | 0 | 49.4 | 0.0 |
| <i>Group Total</i> | 80 | 1 | 79 | 0 | 100.0 | 0.0 |
| Endpoint: BMD | | | | | | |
| 11-DEMO-005 | 40 | 9 | 111 | 0 | 49.1 | 0.0 |
| 13-DEMO-001 | 40 | 5 | 115 | 0 | 50.9 | 0.0 |
| <i>Group Total</i> | 80 | 14 | 226 | 0 | 100.0 | 0.0 |

SUBJ: subjects

BQL: below quantitation limit

MISS: missing observations (not BQL)

OBS: observations

Source code: test.R

Source file: test.tex

8.3.2 Paneled

- Just summarize a single endpoint

```
out <- pt_data_inventory(
  data_pk,
  by = c(Study = "STUDYf"),
  panel = "ASIANf"
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()
```

| Study | Number | | | | Group percent | | Overall percent | |
|------------------|--------|------|------|-----|---------------|-----|-----------------|-----|
| | SUBJ | MISS | OBS | BQL | OBS | BQL | OBS | BQL |
| Asian | | | | | | | | |
| 12-DEMO-001 | 17 | 4 | 241 | 10 | 18.8 | 0.8 | 7.6 | 0.3 |
| 12-DEMO-002 | 18 | 4 | 414 | 14 | 32.3 | 1.1 | 13.0 | 0.4 |
| 11-DEMO-005 | 16 | 5 | 366 | 13 | 28.6 | 1.0 | 11.5 | 0.4 |
| 13-DEMO-001 | 15 | 3 | 218 | 4 | 17.0 | 0.3 | 6.9 | 0.1 |
| non-Asian | | | | | | | | |
| 12-DEMO-001 | 13 | 4 | 186 | 5 | 9.8 | 0.3 | 5.9 | 0.2 |
| 12-DEMO-002 | 32 | 6 | 738 | 24 | 38.9 | 1.3 | 23.2 | 0.8 |
| 11-DEMO-005 | 24 | 5 | 554 | 17 | 29.2 | 0.9 | 17.4 | 0.5 |
| 13-DEMO-001 | 25 | 4 | 364 | 7 | 19.2 | 0.4 | 11.5 | 0.2 |
| All data | 160 | 35 | 3081 | 94 | — | — | 97.0 | 3.0 |

SUBJ: subjects

BQL: below quantitation limit

MISS: missing observations (not BQL)

OBS: observations

Source code: test.R

Source file: test.tex

8.3.3 Grouped (by study)

```
out <- pt_data_inventory(
  data_pk,
  by = c(Study = "STUDYf")
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()
```

| Study | Number | | | | Percent | |
|-----------------|--------|------|------|-----|---------|-----|
| | SUBJ | MISS | OBS | BQL | OBS | BQL |
| 12-DEMO-001 | 30 | 8 | 427 | 15 | 13.4 | 0.5 |
| 12-DEMO-002 | 50 | 10 | 1152 | 38 | 36.3 | 1.2 |
| 11-DEMO-005 | 40 | 10 | 920 | 30 | 29.0 | 0.9 |
| 13-DEMO-001 | 40 | 7 | 582 | 11 | 18.3 | 0.3 |
| All data | 160 | 35 | 3081 | 94 | 97.0 | 3.0 |

SUBJ: subjects

BQL: below quantitation limit

MISS: missing observations (not BQL)

OBS: observations

Source code: test.R

Source file: test.tex

8.4 Wide categorical table

- Summary of categorical data in wide format
- The summary is number (percent within group)
- Wide refers to the fact that the covariates go across the table

8.4.0.1 Ungrouped

```
out <- pt_cat_wide(  
  data = data,  
  cols = vars(Formulation = FORMf, Sex = SEXf, "Race group" = ASIANf)  
)  
  
out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()
```

| n | Formulation | | | Sex | | Race group | |
|-----|-------------|----------|----------|-----------|-----------|------------|-----------|
| | tablet | capsule | troche | male | female | Asian | non-Asian |
| 160 | 130 (81.2) | 15 (9.4) | 15 (9.4) | 80 (50.0) | 80 (50.0) | 66 (41.2) | 94 (58.8) |

Summary is count (percent)

n: number of records summarized

Source code: test.R

Source file: test.tex

8.4.1 Paneled (limited utility, IMO)

- Provided here for completeness

```
out <- pt_cat_wide(
  data = data,
  cols = vars(Formulation = FORMf, Sex = SEXf, "Race group" = ASIANf),
  panel = as.panel("STUDYf", prefix = "Study: ")
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()
```

| n | Formulation | | | Sex | | Race group | |
|---------------------------|-------------|----------|----------|-----------|-----------|------------|-----------|
| | tablet | capsule | troche | male | female | Asian | non-Asian |
| Study: 12-DEMO-001 | | | | | | | |
| 30 | 25 (83.3) | 3 (10.0) | 2 (6.7) | 10 (33.3) | 20 (66.7) | 17 (56.7) | 13 (43.3) |
| Study: 12-DEMO-002 | | | | | | | |
| 50 | 42 (84.0) | 6 (12.0) | 2 (4.0) | 18 (36.0) | 32 (64.0) | 18 (36.0) | 32 (64.0) |
| Study: 11-DEMO-005 | | | | | | | |
| 40 | 30 (75.0) | 3 (7.5) | 7 (17.5) | 29 (72.5) | 11 (27.5) | 16 (40.0) | 24 (60.0) |
| Study: 13-DEMO-001 | | | | | | | |
| 40 | 33 (82.5) | 3 (7.5) | 4 (10.0) | 23 (57.5) | 17 (42.5) | 15 (37.5) | 25 (62.5) |
| All data | | | | | | | |
| 160 | 130 (81.2) | 15 (9.4) | 15 (9.4) | 80 (50.0) | 80 (50.0) | 66 (41.2) | 94 (58.8) |

Summary is count (percent)

n: number of records summarized

Source code: test.R

Source file: test.tex

8.4.2 Grouped (by male / female)

```
out <- pt_cat_wide(
  data = data,
  by = c(Sex = "SEXf"),
  cols = vars(Formulation = FORMf, "Race group" = ASIANf)
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()
```

| Sex | n | Formulation | | | Race group | |
|-----------------|-----|-------------|----------|-----------|------------|-----------|
| | | tablet | capsule | troche | Asian | non-Asian |
| male | 80 | 62 (77.5) | 7 (8.8) | 11 (13.8) | 28 (35.0) | 52 (65.0) |
| female | 80 | 68 (85.0) | 8 (10.0) | 4 (5.0) | 38 (47.5) | 42 (52.5) |
| All data | 160 | 130 (81.2) | 15 (9.4) | 15 (9.4) | 66 (41.2) | 94 (58.8) |

Summary is count (percent)

n: number of records summarized

Source code: test.R

Source file: test.tex

8.4.3 Paneled and grouped

```

out <- pt_cat_wide(
  data = data,
  cols = vars(Formulation = FORMf, Sex = SEXf, "Race group" = ASIANf),
  panel = as.panel("STUDYf", prefix = "Study: "),
  by = c("RF Group" = "RFf")
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()

```

| RF Group | n | Formulation | | | Sex | | Race group | |
|--------------------|-----|-------------|----------|----------|-----------|-----------|------------|-----------|
| | | tablet | capsule | troche | male | female | Asian | non-Asian |
| Study: 12-DEMO-001 | | | | | | | | |
| normal | 30 | 25 (83.3) | 3 (10.0) | 2 (6.7) | 10 (33.3) | 20 (66.7) | 17 (56.7) | 13 (43.3) |
| Study: 12-DEMO-002 | | | | | | | | |
| normal | 50 | 42 (84.0) | 6 (12.0) | 2 (4.0) | 18 (36.0) | 32 (64.0) | 18 (36.0) | 32 (64.0) |
| Study: 11-DEMO-005 | | | | | | | | |
| normal | 10 | 9 (90.0) | 0 (0.0) | 1 (10.0) | 7 (70.0) | 3 (30.0) | 3 (30.0) | 7 (70.0) |
| mild | 10 | 7 (70.0) | 2 (20.0) | 1 (10.0) | 7 (70.0) | 3 (30.0) | 5 (50.0) | 5 (50.0) |
| moderate | 10 | 6 (60.0) | 0 (0.0) | 4 (40.0) | 8 (80.0) | 2 (20.0) | 6 (60.0) | 4 (40.0) |
| severe | 10 | 8 (80.0) | 1 (10.0) | 1 (10.0) | 7 (70.0) | 3 (30.0) | 2 (20.0) | 8 (80.0) |
| Study: 13-DEMO-001 | | | | | | | | |
| normal | 40 | 33 (82.5) | 3 (7.5) | 4 (10.0) | 23 (57.5) | 17 (42.5) | 15 (37.5) | 25 (62.5) |
| All data | 160 | 130 (81.2) | 15 (9.4) | 15 (9.4) | 80 (50.0) | 80 (50.0) | 66 (41.2) | 94 (58.8) |

Summary is count (percent)

n: number of records summarized

Source code: test.R

Source file: test.tex

8.4.4 No summary

```

out <- pt_cat_wide(
  data = data,
  summarize = "none",
  cols = vars(Formulation = FORMf, Sex = SEXf, "Race group" = ASIANf),
  panel = as.panel("STUDYf", prefix = "Study: "),
  by = c("RF Group" = "RFf")
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()

```

| | | Formulation | | | Sex | | Race group | |
|--------------------|----|-------------|----------|----------|-----------|-----------|------------|-----------|
| RF Group | n | tablet | capsule | troche | male | female | Asian | non-Asian |
| Study: 12-DEMO-001 | | | | | | | | |
| normal | 30 | 25 (83.3) | 3 (10.0) | 2 (6.7) | 10 (33.3) | 20 (66.7) | 17 (56.7) | 13 (43.3) |
| Study: 12-DEMO-002 | | | | | | | | |
| normal | 50 | 42 (84.0) | 6 (12.0) | 2 (4.0) | 18 (36.0) | 32 (64.0) | 18 (36.0) | 32 (64.0) |
| Study: 11-DEMO-005 | | | | | | | | |
| normal | 10 | 9 (90.0) | 0 (0.0) | 1 (10.0) | 7 (70.0) | 3 (30.0) | 3 (30.0) | 7 (70.0) |
| mild | 10 | 7 (70.0) | 2 (20.0) | 1 (10.0) | 7 (70.0) | 3 (30.0) | 5 (50.0) | 5 (50.0) |
| moderate | 10 | 6 (60.0) | 0 (0.0) | 4 (40.0) | 8 (80.0) | 2 (20.0) | 6 (60.0) | 4 (40.0) |
| severe | 10 | 8 (80.0) | 1 (10.0) | 1 (10.0) | 7 (70.0) | 3 (30.0) | 2 (20.0) | 8 (80.0) |
| Study: 13-DEMO-001 | | | | | | | | |
| normal | 40 | 33 (82.5) | 3 (7.5) | 4 (10.0) | 23 (57.5) | 17 (42.5) | 15 (37.5) | 25 (62.5) |

Summary is count (percent)

n: number of records summarized

Source code: test.R

Source file: test.tex

8.5 Long categorical table

- Categorical table in long format
- Long indicates that the covariates go down the table

8.5.1 Ungrouped

```
out <- pt_cat_long(
  data = data,
  cols = vars(Study = STUDYf, Sex = SEXf, "Race group" = ASIANf, "Child-Pugh" = CPf)
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()
```

| | Summary n = 160 |
|-------------------|--------------------|
| Study | |
| 12-DEMO-001 | 30 (18.8) |
| 12-DEMO-002 | 50 (31.2) |
| 11-DEMO-005 | 40 (25.0) |
| 13-DEMO-001 | 40 (25.0) |
| Sex | |
| male | 80 (50.0) |
| female | 80 (50.0) |
| Race group | |
| Asian | 66 (41.2) |
| non-Asian | 94 (58.8) |
| Child-Pugh | |
| Score=0 | 130 (81.2) |
| Score=1 | 10 (6.2) |
| Score=2 | 10 (6.2) |
| Score=3 | 10 (6.2) |

Summary is count (percent)
n: number of records summarized

Source code: test.R

Source file: test.tex

8.5.2 Grouped (by formulation)

```

out <- pt_cat_long(
  data = data,
  cols = vars(Study = STUDYf, Sex = SEXf, "Race group" = ASIANf, "Child-Pugh" = CPf),
  span = c(Formulation = "FORMf")
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()

```

| | Formulation | | | Summary n = 160 |
|-------------|-------------------|-------------------|------------------|--------------------|
| | tablet n = 130 | capsule n = 15 | troche n = 15 | |
| Study | | | | |
| 12-DEMO-001 | 25 (19.2) | 3 (20.0) | 2 (13.3) | 30 (18.8) |
| 12-DEMO-002 | 42 (32.3) | 6 (40.0) | 2 (13.3) | 50 (31.2) |
| 11-DEMO-005 | 30 (23.1) | 3 (20.0) | 7 (46.7) | 40 (25.0) |
| 13-DEMO-001 | 33 (25.4) | 3 (20.0) | 4 (26.7) | 40 (25.0) |
| Sex | | | | |
| male | 62 (47.7) | 7 (46.7) | 11 (73.3) | 80 (50.0) |
| female | 68 (52.3) | 8 (53.3) | 4 (26.7) | 80 (50.0) |
| Race group | | | | |
| Asian | 53 (40.8) | 7 (46.7) | 6 (40.0) | 66 (41.2) |
| non-Asian | 77 (59.2) | 8 (53.3) | 9 (60.0) | 94 (58.8) |
| Child-Pugh | | | | |
| Score=0 | 106 (81.5) | 12 (80.0) | 12 (80.0) | 130 (81.2) |
| Score=1 | 7 (5.4) | 1 (6.7) | 2 (13.3) | 10 (6.2) |
| Score=2 | 8 (6.2) | 1 (6.7) | 1 (6.7) | 10 (6.2) |
| Score=3 | 9 (6.9) | 1 (6.7) | 0 (0.0) | 10 (6.2) |

Summary is count (percent)

n: number of records summarized

Source code: test.R

Source file: test.tex

8.5.3 Summary on bottom and right

```
out <- pt_cat_long(
  data = data,
  summarize = "both",
  cols = vars(Formulation = FORMf, Sex = SEXf, "Race group" = ASIANf),
  span = vars(Study = STUDYf)
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()
```

| | Study | | | | Summary n = 160 |
|--------------------|-----------------------|-----------------------|-----------------------|-----------------------|--------------------|
| | 12-DEMO-001 n = 30 | 12-DEMO-002 n = 50 | 11-DEMO-005 n = 40 | 13-DEMO-001 n = 40 | |
| Formulation | | | | | |
| tablet | 25 (83.3) | 42 (84.0) | 30 (75.0) | 33 (82.5) | 130 (81.2) |
| capsule | 3 (10.0) | 6 (12.0) | 3 (7.5) | 3 (7.5) | 15 (9.4) |
| troche | 2 (6.7) | 2 (4.0) | 7 (17.5) | 4 (10.0) | 15 (9.4) |
| Sex | | | | | |
| male | 10 (33.3) | 18 (36.0) | 29 (72.5) | 23 (57.5) | 80 (50.0) |
| female | 20 (66.7) | 32 (64.0) | 11 (27.5) | 17 (42.5) | 80 (50.0) |
| Race group | | | | | |
| Asian | 17 (56.7) | 18 (36.0) | 16 (40.0) | 15 (37.5) | 66 (41.2) |
| non-Asian | 13 (43.3) | 32 (64.0) | 24 (60.0) | 25 (62.5) | 94 (58.8) |

Summary is count (percent)

n: number of records summarized

Source code: test.R

Source file: test.tex

8.5.4 No summary

```

out <- pt_cat_long(
  data = data,
  summarize = "none",
  cols = vars(Formulation = FORMf, Sex = SEXf, "Race group" = ASIANf),
  span = vars(Study = STUDYf)
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()

```

| | Study | | | |
|--------------------|-------------|-------------|-------------|-------------|
| | 12-DEMO-001 | 12-DEMO-002 | 11-DEMO-005 | 13-DEMO-001 |
| Formulation | | | | |
| tablet | 25 (83.3) | 42 (84.0) | 30 (75.0) | 33 (82.5) |
| capsule | 3 (10.0) | 6 (12.0) | 3 (7.5) | 3 (7.5) |
| troche | 2 (6.7) | 2 (4.0) | 7 (17.5) | 4 (10.0) |
| Sex | | | | |
| male | 10 (33.3) | 18 (36.0) | 29 (72.5) | 23 (57.5) |
| female | 20 (66.7) | 32 (64.0) | 11 (27.5) | 17 (42.5) |
| Race group | | | | |
| Asian | 17 (56.7) | 18 (36.0) | 16 (40.0) | 15 (37.5) |
| non-Asian | 13 (43.3) | 32 (64.0) | 24 (60.0) | 25 (62.5) |

Summary is count (percent)

n: number of records summarized

Source code: test.R

Source file: test.tex

8.6 Wide continuous table

- Continuous table in wide format
- Wide means that the covariates go across the table

8.6.1 Ungrouped

```
out <- pt_cont_wide(  
  data = data,  
  cols = "WT,SCR,AGE,ALB,HT",  
  units = units  
)  
  
out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()
```

| WT (kg) | SCR (mg/dL) | AGE (years) | ALB (g/dL) | HT (cm) |
|-------------------|--------------------|-------------------|--------------------|------------------|
| 70.7 (12.8) [157] | 1.36 (0.986) [160] | 33.7 (8.83) [160] | 4.20 (0.793) [156] | 179 (17.7) [160] |

Summary is mean (sd) [count]

Source code: test.R

Source file: test.tex

8.6.2 Paneled

```
out <- pt_cont_wide(
  data = data,
  cols = "WT,SCR,AGE,ALB,HT",
  panel = c(Study = "STUDYf"),
  units = units
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()
```

| WT (kg) | SCR (mg/dL) | AGE (years) | ALB (g/dL) | HT (cm) |
|------------------------------|--------------------|-------------------|--------------------|------------------|
| Study 12-DEMO-001 | | | | |
| 72.2 (14.3) [29] | 1.03 (0.155) [30] | 32.0 (9.19) [30] | 4.28 (0.474) [29] | 180 (19.3) [30] |
| Study 12-DEMO-002 | | | | |
| 72.4 (11.5) [49] | 0.971 (0.161) [50] | 35.0 (8.20) [50] | 4.47 (0.468) [50] | 182 (15.4) [50] |
| Study 11-DEMO-005 | | | | |
| 68.9 (14.5) [39] | 2.52 (1.43) [40] | 32.8 (8.48) [40] | 4.41 (0.537) [39] | 175 (19.2) [40] |
| Study 13-DEMO-001 | | | | |
| 69.4 (11.6) [40] | 0.950 (0.165) [40] | 34.2 (9.67) [40] | 3.58 (1.15) [38] | 179 (17.2) [40] |
| All data | | | | |
| 70.7 (12.8) [157] | 1.36 (0.986) [160] | 33.7 (8.83) [160] | 4.20 (0.793) [156] | 179 (17.7) [160] |
| Summary is mean (sd) [count] | | | | |
| Source code: test.R | | | | |
| Source file: test.tex | | | | |

8.6.3 Grouped (by study)

```
out <- pt_cont_wide(
  data = data,
  cols = "WT,SCR,AGE,ALB,HT",
  by = c(Study = "STUDYf"),
  units = units
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()
```

| Study | WT (kg) | SCR (mg/dL) | AGE (years) | ALB (g/dL) | HT (cm) |
|-----------------|-------------------|--------------------|-------------------|--------------------|------------------|
| 12-DEMO-001 | 72.2 (14.3) [29] | 1.03 (0.155) [30] | 32.0 (9.19) [30] | 4.28 (0.474) [29] | 180 (19.3) [30] |
| 12-DEMO-002 | 72.4 (11.5) [49] | 0.971 (0.161) [50] | 35.0 (8.20) [50] | 4.47 (0.468) [50] | 182 (15.4) [50] |
| 11-DEMO-005 | 68.9 (14.5) [39] | 2.52 (1.43) [40] | 32.8 (8.48) [40] | 4.41 (0.537) [39] | 175 (19.2) [40] |
| 13-DEMO-001 | 69.4 (11.6) [40] | 0.950 (0.165) [40] | 34.2 (9.67) [40] | 3.58 (1.15) [38] | 179 (17.2) [40] |
| All data | 70.7 (12.8) [157] | 1.36 (0.986) [160] | 33.7 (8.83) [160] | 4.20 (0.793) [156] | 179 (17.7) [160] |

Summary is mean (sd) [count]

Source code: test.R

Source file: test.tex

8.6.4 Paneled and grouped

```

out <- pt_cont_wide(
  data = data,
  cols = "WT,SCR,AGE,ALB,HT",
  by = c(Study = "STUDYf"),
  panel = c(Formulation = "FORMf"),
  units = units
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()

```

| Study | WT (kg) | SCR (mg/dL) | AGE (years) | ALB (g/dL) | HT (cm) |
|----------------------------|-------------------|--------------------|-------------------|--------------------|------------------|
| Formulation tablet | | | | | |
| 12-DEMO-001 | 71.0 (14.2) [24] | 1.01 (0.157) [25] | 32.6 (9.23) [25] | 4.22 (0.459) [24] | 179 (19.7) [25] |
| 12-DEMO-002 | 72.2 (11.8) [41] | 0.966 (0.166) [42] | 34.0 (7.93) [42] | 4.49 (0.495) [42] | 182 (15.9) [42] |
| 11-DEMO-005 | 68.8 (15.2) [29] | 2.48 (1.47) [30] | 33.2 (8.73) [30] | 4.37 (0.568) [29] | 173 (19.7) [30] |
| 13-DEMO-001 | 69.4 (11.0) [33] | 0.967 (0.163) [33] | 33.7 (9.67) [33] | 3.53 (1.14) [31] | 178 (16.5) [33] |
| Formulation capsule | | | | | |
| 12-DEMO-001 | 72.9 (17.3) [3] | 1.12 (0.0700) [3] | 32.2 (12.0) [3] | 4.49 (0.593) [3] | 184 (23.0) [3] |
| 12-DEMO-002 | 70.9 (10.3) [6] | 1.03 (0.146) [6] | 37.7 (7.59) [6] | 4.38 (0.354) [6] | 181 (15.4) [6] |
| 11-DEMO-005 | 73.9 (11.1) [3] | 3.06 (2.19) [3] | 31.8 (4.99) [3] | 4.65 (0.240) [3] | 181 (16.4) [3] |
| 13-DEMO-001 | 58.4 (4.04) [3] | 0.973 (0.195) [3] | 36.5 (6.69) [3] | 3.09 (1.50) [3] | 167 (8.88) [3] |
| Formulation troche | | | | | |
| 12-DEMO-001 | 85.3 (12.4) [2] | 1.20 (0.0707) [2] | 25.1 (3.28) [2] | 4.74 (0.283) [2] | 194 (0.163) [2] |
| 12-DEMO-002 | 79.7 (8.61) [2] | 0.910 (0.0283) [2] | 48.0 (1.79) [2] | 4.49 (0.0354) [2] | 182 (10.9) [2] |
| 11-DEMO-005 | 66.8 (13.9) [7] | 2.45 (1.05) [7] | 31.4 (9.34) [7] | 4.49 (0.509) [7] | 177 (19.8) [7] |
| 13-DEMO-001 | 77.4 (15.9) [4] | 0.795 (0.0777) [4] | 37.3 (12.9) [4] | 4.32 (0.994) [4] | 193 (22.4) [4] |
| All data | 70.7 (12.8) [157] | 1.36 (0.986) [160] | 33.7 (8.83) [160] | 4.20 (0.793) [156] | 179 (17.7) [160] |

Summary is mean (sd) [count]

Source code: test.R

Source file: test.tex

8.7 Long continuous table

- Continuous summary table in long format
- Long indicates that covariates go down the table

8.7.1 Ungrouped

```
out <- pt_cont_long(  
  data = data,  
  cols = "WT,SCR,AGE",  
  units = units  
)  
  
out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()
```

| Variable | n | Mean | Median | SD | Min / Max |
|-------------|-----|------|--------|-------|--------------|
| WT (kg) | 157 | 70.7 | 70.0 | 12.8 | 43.6 / 97.2 |
| SCR (mg/dL) | 160 | 1.36 | 1.04 | 0.986 | 0.710 / 5.59 |
| AGE (years) | 160 | 33.7 | 33.4 | 8.83 | 18.9 / 49.5 |

n: number of records summarized

SD: standard deviation

Min: minimum; Max: maximum

Source code: test.R

Source file: test.tex

8.7.2 Paneled

```

out <- pt_cont_long(
  data = data,
  cols = "WT,SCR,AGE",
  panel = vars(Study = STUDYf),
  units = units
)

out %>% stable(r_file = "test.R", output_file = "test.tex") %>% st_asis()

```

| Variable | n | Mean | Median | SD | Min / Max |
|--------------------------|-----|-------|--------|-------|--------------|
| Study 12-DEMO-001 | | | | | |
| WT (kg) | 29 | 72.2 | 70.0 | 14.3 | 50.9 / 97.2 |
| SCR (mg/dL) | 30 | 1.03 | 1.04 | 0.155 | 0.740 / 1.30 |
| AGE (years) | 30 | 32.0 | 28.0 | 9.19 | 19.9 / 47.8 |
| Study 12-DEMO-002 | | | | | |
| WT (kg) | 49 | 72.4 | 72.1 | 11.5 | 51.5 / 96.6 |
| SCR (mg/dL) | 50 | 0.971 | 0.970 | 0.161 | 0.720 / 1.30 |
| AGE (years) | 50 | 35.0 | 36.0 | 8.20 | 20.3 / 49.2 |
| Study 11-DEMO-005 | | | | | |
| WT (kg) | 39 | 68.9 | 65.4 | 14.5 | 43.6 / 92.8 |
| SCR (mg/dL) | 40 | 2.52 | 2.33 | 1.43 | 0.720 / 5.59 |
| AGE (years) | 40 | 32.8 | 33.4 | 8.48 | 19.2 / 49.5 |
| Study 13-DEMO-001 | | | | | |
| WT (kg) | 40 | 69.4 | 68.1 | 11.6 | 50.7 / 96.6 |
| SCR (mg/dL) | 40 | 0.950 | 0.975 | 0.165 | 0.710 / 1.26 |
| AGE (years) | 40 | 34.2 | 35.2 | 9.67 | 18.9 / 49.5 |
| All data | | | | | |
| WT (kg) | 157 | 70.7 | 70.0 | 12.8 | 43.6 / 97.2 |
| SCR (mg/dL) | 160 | 1.36 | 1.04 | 0.986 | 0.710 / 5.59 |
| AGE (years) | 160 | 33.7 | 33.4 | 8.83 | 18.9 / 49.5 |

n: number of records summarized

SD: standard deviation

Min: minimum; Max: maximum

Source code: test.R

Source file: test.tex