

pmt

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1 Introduction

You can label chapter and section titles using {#label} after them, e.g., we can reference Chapter @ref(intro). If you do not manually label them, there will be automatic labels anyway, e.g., Chapter @ref(methods).

```
library(tidyverse)
library(pmtables)

stdata() %>% stable() %>% 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

```
stdata() %>% 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
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

2 A simple table: stable

2.1 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)

2.2 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.

2.3 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

2.4 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)
```


3 Group table rows with panel

3.1 Syntax

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

To set a prefix for the panel header:

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

3.2 Basics

Paneling your table is a way to group sets of rows together into a “panel” with a panel header in bold. 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 carb
. 1   Datsun 710 22.8   4 108.0  93 3.85  2.320 18.61 1  1   4   1
. 2  Hornet 4 Drive 21.4   6 258.0 110 3.08  3.215 19.44 1  0   3   1
. 3    Valiant 18.1   6 225.0 105 2.76  3.460 20.22 1  0   3   1
. 4    Fiat 128 32.4   4  78.7  66 4.08  2.200 19.47 1  1   4   1
. 5 Toyota Corolla 33.9   4  71.1  65 4.22  1.835 19.90 1  1   4   1
. 6 Toyota Corona 21.5   4 120.1  97 3.70  2.465 20.01 1  0   3   1
. 7    Fiat X1-9 27.3   4  79.0  66 4.08  1.935 18.90 1  1   4   1
. 8    Merc 240D 24.4   4 146.7  62 3.69  3.190 20.00 1  0   4   2
. 9    Merc 230 22.8   4 140.8  95 3.92  3.150 22.90 1  0   4   2
. 10   Honda Civic 30.4   4  75.7  52 4.93  1.615 18.52 1  1   4   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

“““

3.3 panel: important points

1. Most of the time, the data frame should be sorted by the `panel` column
- 2.

4 Group table columns with spanners

4.1 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))
```

4.2 Introduction

5 Tables that span multiple pages: longtable

5.1 Syntax

To create a long table

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

5.2 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.

5.3 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}
```

You should not wrap your longtable input code in `\begin{table}/\end{table}` as you would with a regular tabular table.

6 The pipe interface

6.1 Data

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

```
library(pmtables)
library(yspec)
library(dplyr)
spec <- ys_help$spec()

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
```

6.2 Simple table

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

6.3 Annotate

- Arguments to identify the name of the generating R script and the output file name
- The output file name is retained as an attribute to be used later when saving the table data
- Arbitrary notes are also allowed (encouraged)

```
data %>%
  st_data() %>%
  st_files(r = "foo.R", output = "foo.tex") %>%
  st_notes(
    "Data were analyzed in quadruplicate.",
    "The results are very clear."
  ) %>% stable() %>% 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

Data were analyzed in quadruplicate.

The results are very clear.

Source code: foo.R

Source file: foo.tex

6.4 Notes in minipage

- By default, notes are put in the 3rd part of threeparttable
- Alternatively, we can put them in a minipage just below the table

```
data %>%
  st_new() %>%
  st_files("foo.R", "foo.tex") %>%
  st_noteconf(type = "minipage", width = 0.85) %>%
  st_notes(
    "Data were analyzed in quadruplicate.",
    "The results are very clear."
  ) %>% stable() %>% 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

Data were analyzed in quadruplicate.

The results are very clear.

Source code: foo.R

Source file: foo.tex

6.5 Align

- Center everything except for
- STUDY (left)
- DOSE and SCR (right)

```
data %>%
  st_new() %>%
  st_align("c", STUDY = 'l', .r = "DOSE,SCR") %>%
  stable() %>% 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

6.6 Units

- Automatically put units under the column name

```
data %>%
  st_new() %>%
  st_center(STUDY = '1', .r = "DOSE,SCR") %>%
  st_units(WT = "kg", SCR = "mg/dL", DOSE = "mg") %>%
  stable() %>% st_asis()
```

STUDY	DOSE (mg)	FORM	N	WT (kg)	CRCL	AGE	ALB	SCR (mg/dL)
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

Alternatively

```
units <- ys_get_unit(spec, parens = TRUE)

data[1:3,] %>%
  st_new() %>%
  st_center(STUDY = '1', .r = "DOSE,SCR") %>%
  st_units(units) %>%
  stable() %>% st_asis()
```

STUDY	DOSE	FORM	N	WT (kg)	CRCL (ml/min)	AGE (years)	ALB (g/dL)	SCR (mg/dL)
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

6.7 Expand header rows

- Multiline table header
- Unlimited number
- Use ... to break

```
data %>%
  st_new() %>%
  st_rename("Study...Number" = STUDY, "Serum...Albumin" = ALB) %>%
  st_units(units) %>%
  stable() %>% st_asis()
```

Study Number	DOSE	FORM	N	WT (kg)	CRCL (ml/min)	AGE (years)	Serum Albumin (g/dL)	SCR (mg/dL)
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

6.8 Math

- Columns with at least two \$ are “math” and will not be sanitized
- Otherwise they are functions to “prime” the data frame
- The default is to convert every column to character
- Then walk the columns, look for non-math columns and sanitize them

```
ptab <- readRDS("datasets/ptab.RDS")  
ptab
```

```
ptab %>%  
  st_data() %>%  
  st_center(Parameter = col_ragged(3), .l = "Symbol") %>%  
  st_panel(".type") %>%  
  stable() %>% st_asis()
```

6.9 hline from column

- Use the column to determine where the hline should go

```
st_new(data) %>%
  st_hline(from = "STUDY") %>%
  stable() %>% 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

6.10 hline anywhere

- Give row numbers for hline

```
st_new(data) %>%
  st_hline(at = c(3,nrow(data))-1) %>%
  stable() %>% 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

6.11 hline pattern

```
tmp <- readRDS("datasets/with-total.RDS")

st_new(tmp) %>%
  st_hline(pattern = "all", cols = "STUDY", n = 2) %>%
  stable() %>% st_asis()
```

6.12 hline multiple

```
tmp <- readRDS("datasets/with-total.RDS")

st_new(tmp) %>%
  st_hline(at = 3, n = 2) %>%
  stable() %>% st_asis()
```

6.13 Mark a summary row (cf sumrows)

```
tmp <- readRDS("datasets/with-total.RDS")

st_new(tmp) %>%
  st_hline(at = 3, n = 2) %>%
  st_bold(cols = "STUDY", pattern = "all") %>%
  st_edit(pattern = "all", replacement = "All studies") %>%
  stable() %>% st_asis()
```


6.14 Remove duplicate values

- Discard repeating values in a column

```
data %>%
  st_new() %>%
  st_hline(from = "STUDY") %>%
  st_clear_reps("STUDY") %>%
  stable() %>% 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

6.15 Add styling to data frame

- `tex_bold` will make table cells bold when they match pattern
- `tex_it` will make table cells italics when they match pattern
- styling is only added when there is at least one character
- input must be string
- combine this with `clear_rep` and `hline_from` to partition the table

```
tmp <- ptdata()
tmp <- mutate(tmp, STUDY = tex_bold(as.character(STUDY)))
```

```
tmp %>%
  st_new() %>%
  st_clear_reps(STUDY) %>%
  st_hline(from = "STUDY") %>%
  stable() %>% 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

6.16 Add styling in the pipeline

```
tmp <- ptdata()
```

```
tmp %>%
  st_new() %>%
  st_clear_reps(STUDY, .now = TRUE) %>%
  st_hline(pattern = "\\S+", cols = "STUDY") %>%
  st_bold(cols = "STUDY") %>%
  st_it("DOSE") %>%
  st_edit("\\bmale", "dude") %>%
  st_edit("female", "gal") %>%
  stable() %>% st_asis()
```

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

6.17 Panel

- Divide the table using column contents
- there's a bug somewhere there

```
data %>%  
  st_new() %>%  
  st_center(DOSE = 'l', SCR = 'r') %>%  
  st_panel("STUDY", prefix = "Study number: ") %>%  
  stable() %>% st_asis()
```

DOSE	FORM	N	WT	CRCL	AGE	ALB	SCR
Study number: 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
Study number: 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

6.18 Colspan

- Group columns

```
data %>%
  st_new() %>%
  st_left(.c = "WT,AGE,CRCL") %>%
  st_span("In final model", WT:CRCL) %>%
  stable() %>% st_asis()
```

STUDY	DOSE	FORM	N	In final model		AGE	ALB	SCR
				WT	CRCL			
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

6.19 Colspan - multiple

- Multiple groupings
- Multiple levels

```
data %>%
  st_new() %>%
  st_span("Meh", DOSE:WT) %>%
  st_span("Hrm", AGE:CRCL) %>%
  st_span("Huh", ALB:SCR) %>%
  st_span("Expert opinion", CRCL:SCR, level = 2) %>%
  stable() %>% st_asis()
```

STUDY	Expert opinion							
	DOSE	Meh			Hrm		Huh	
		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

6.20 Colspan - from cols

- we have some columns of the form tag.name

```
dotdata <- readRDS("datasets/with-dots.RDS")  
head(dotdata, n=2)
```

```
dotdata %>%  
  st_new() %>%  
  st_span_split(sep = '.') %>%  
  stable() %>% st_asis()
```

6.21 Handle wide columns

6.21.1 descr is taking over the table

```
ptable <- readRDS("datasets/ptable.RDS")  
ptable %>% st_new() %>% stable() %>% st_asis()
```

6.21.2 Limit descr to 5 cm

```
ptable %>%  
  st_new() %>%  
  st_align(descr = col_ragged(5)) %>%  
  stable() %>% st_asis()
```


6.22 Identify a summary row

We can point to one or more rows and style it up as a “summary row”

```
df.total <- readRDS(file = "datasets/with-total.RDS")
df.total
```

```
st_new(df.total) %>%
  st_sumrow(pattern = "all", label = "All studies", bold = TRUE) %>%
  stable() %>% st_asis()
```

6.23 Fontsize

- Where's my glasses?

```
data %>% st_new() %>% st_sizes(font = "tiny") %>% stable() %>% 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

6.24 Row space

```
sl <- data %>% slice(1:3)
sl %>% st_new() %>% stable() %>% 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

```
sl %>% st_new() %>% st_sizes(row = 0.9) %>% stable() %>% 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

```
sl %>% st_new() %>% st_sizes(row = 2 ) %>% stable() %>% 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

6.25 Col space

```
data %>% st_new() %>% st_sizes(col = 20) %>% stable() %>% st_asis()
```

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

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_new
```

```
. [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}"
```

```

.
. $cols
. [1] "STUDY" "DOSE" "FORM" "N" "WT" "CRCL" "AGE" "ALB" "SCR"
.
. $span
. $span$`1`
. # A tibble: 9 x 7
.   coln col newcol title level flg align
.   <int> <chr> <chr> <chr> <dbl> <dbl> <chr>
. 1     1 STUDY STUDY "" 1 1 c
. 2     2 DOSE DOSE "" 1 1 c
. 3     3 FORM FORM "" 1 1 c
. 4     4 N N "" 1 1 c
. 5     5 WT WT "foo_this" 1 2 c
. 6     6 CRCL CRCL "foo_this" 1 2 c
. 7     7 AGE AGE "foo_this" 1 2 c
. 8     8 ALB ALB "foo_this" 1 2 c
. 9     9 SCR SCR "foo_this" 1 2 c

```

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 \\% % \\\\"

```