# Simple Tables Demo Doc

## Contents

# 1 Data

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

```r
library(pmtables)
library(yspec)
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
```

# 2 wrap

There is a wrap function in this document. Don't worry about that; it just puts the output into a table environment and sends the output to get rendered in markdown.

# 3 Simple table

- A data frame is wrapped in tabular environment
- The table is created with threeparttable

```
data %>% stable(cols_bold=TRUE) %>% pt_wrap(stdout())
```

| **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 |

# 4 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, provided as a character vector; item in the vector is placed on its own line

```
stable(
  data,
  r_file = "foo.R",
  output_file = "foo.tex",
  notes = c("Data were analyzed in quadruplicate.", "The results are very clear."),
) %>% pt_wrap(stdout())
```

| 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 |
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| 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

# 5 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
- The width of the minipage needs to be set by the user

```
stable(
  data,
  note_config = noteconf(type = "minipage", width = 0.85),
  notes = c("Data were analyzed in quadruplicate.", "The results are very clear."),
) %>% pt_wrap(stdout())
```

| 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 |
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| 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.

# 6 Align

- Columns can be aligned center, left or right

- Columns can be aligned with a fixed with and aligned left, center or right

- Helper functions are provided as `cols_center()`, `cols_left()`, `cols_right()`

- The syntax is to state the default / base alignment for all columns and then pass exceptions to that default setting

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

```
data %>%
  stable(align = cols_center(STUDY = 'l', .r = "DOSE,SCR")) %>%
  pt_wrap(stdout())
```

| 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 |
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| 12-DEMO-002 | 75 mg | troche | 36 | 73.6 | 103 | 49.2 | 4.52 | 0.930 |

# 7 Units

- Automatically put units under the column name
- Units are supplied as a named list, where names correspond with the column name prior to renaming
- The list can contain a subset of columns and can also contain names that are not in the table (there is no warning or error for the latter)

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

stable(
  data,
  units = units,
) %>% pt_wrap(stdout())
```

| 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 |
| 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 |

# 8  Expand header rows

- Multi-line table header
- Unlimited number
- Use `...` to break; pass `cols_break` to alter the break sequence
- Units go on the bottom row when they are supplied
- Items are always pushed to the bottom

```
stable(
  data,
  cols_rename = vars("Study...Number" = STUDY, "Serum...Albumin" = ALB),
  units = units
) %>% pt_wrap(stdout())
```

| 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 |

# 9 Extra column information

- Pass in a data frame any number of rows but same column layout (number and order) as the input data to add information to the header row
- I'm adding units in this example, but think of this as having general application

```
tmp <- slice(ptdata(), 1:5)

xtra0 <- slice(tmp,1) %>% mutate(across(everything(), ~""))
xtra0
```

```
## # A tibble: 1 x 9
##    STUDY DOSE  FORM  N     WT    CRCL  AGE   ALB   SCR
##    <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr>
## 1 ""    ""    ""    ""    ""    ""    ""    ""    ""
```

```
xtra1 <- mutate(xtra0, DOSE = "(mg)", N = "(number)", WT = "(kg)")

xtra2 <- mutate(xtra0, WT = "[baseline]")

xtra <- bind_rows(xtra2,xtra1)

xtra
```

```
## # A tibble: 2 x 9
##    STUDY DOSE   FORM  N          WT         CRCL  AGE   ALB   SCR
##    <chr> <chr>  <chr> <chr>      <chr>      <chr> <chr> <chr> <chr>
## 1 ""    ""     ""    ""         [baseline] ""    ""    ""    ""
## 2 ""    "(mg)" ""    "(number)" (kg)       ""    ""    ""    ""
```

```
stable(tmp, cols_extra = xtra) %>% st_wrap()
```

| STUDY | DOSE (mg) | FORM | N (number) | WT [baseline] (kg) | 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 |

# 10 Math

- Columns with at least two $ are "math" and will not be sanitized
- Otherwise the 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
```

```
## # A tibble: 4 x 6
##    .type            Parameter          Symbol   Math            Estimate    SE
##    <chr>            <chr>              <chr>    <chr>              <dbl> <dbl>
## 1 Fixed-effects     Clearance          CL (L/h~ "$\\exp(\\thet~    1.22  0.4
## 2 Fixed-effects     Volume of distribu~ V2 (L)   "$\\exp(\\thet~    5.87  0.89
## 3 Fixed-effects     Absorption rate co~ KA (1/h~ "$\\theta_3$"     1.23  0.1
## 4 Unexplained varia~ Additive_error     RUV      "$\\sigma_1$"     0.02  0.01
```

```
stable(
  ptab,
  align = cols_center(Parameter =  col_ragged(3), .l = "Symbol"),
  panel = ".type"
) %>% pt_wrap(stdout())
```

| Parameter | Symbol | Math | Estimate | SE |
|---|---|---|---|---|
| **Fixed-effects** | | | | |
| Clearance | CL (L/hr) | $\exp(\theta_1)$ | 1.22 | 0.4 |
| Volume of distribution | V2 (L) | $\exp(\theta_2)$ | 5.87 | 0.89 |
| Absorption rate constant | KA (1/hr) | $\theta_3$ | 1.23 | 0.1 |
| **Unexplained variability** | | | | |
| Additive_error | RUV | $\sigma_1$ | 0.02 | 0.01 |

# 11 hline from column

- Use the column to determine where the hline should go

```
stable(
  data,
  hline_from = "STUDY",
) %>% pt_wrap(stdout())
```

| 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 |

# 12 hline anywhere

- Give row numbers for hline as logical or integer vector

```
stable(
  data,
  hline_at = c(3,nrow(data))-1,
) %>% pt_wrap(stdout())
```

| 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 |
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| 12-DEMO-002 | 100 mg | tablet | 324 | 77.6 | 106 | 29.9 | 4.31 | 0.981 |
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| 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 |

# 13 Remove duplicate values

- Discard repeating values in a column
- Also `clear_grouped_reps` which recursively groups by the column names supplied and clears the most distant column name in the groups

```
stable(
  data,
  clear_reps = "STUDY",
) %>% pt_wrap(stdout())
```

| 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 |

# 14 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)))

stable(
  tmp,
  clear_reps = "STUDY",
  hline_from = "STUDY",
) %>% pt_wrap(stdout())
```

| 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 |

# 15 Panel

- Divide the table using column contents
- The panel column data is split in non-repeating chunks
- An error is generated if there are multiple panels with the same name; this can be overridden
- A prefix can be supplied that gets pasted on the front of the column title; the prefix can also come from the name of the supplied panel panel ID (e.g. `c(prefix_text = panel_name)`)

```
stable(
  data,
  panel = as.panel("STUDY", prefix = "Study number: "),
) %>% pt_wrap(stdout())
```

| 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 |

# 16 Drop column

- name columns that can be dropped from the table

```
stable(data[1:3,], drop = "STUDY,FORM,DOSE") %>% pt_wrap(stdout())
```

| N  | WT   | CRCL | AGE  | ALB  | SCR   |
|----|------|------|------|------|-------|
| 80 | 71.4 | 104  | 33.7 | 4.20 | 1.06  |
| 16 | 89.4 | 122  | 24.4 | 4.63 | 1.12  |
| 48 | 81.7 | 104  | 34.4 | 3.83 | 0.910 |

- this works when there is a panel

```
stable(data[1:3,], drop = "SCR,FORM,DOSE", panel = "STUDY") %>% pt_wrap(stdout())
```

| N  | WT   | CRCL | AGE  | ALB  |
|----|------|------|------|------|
| **12-DEMO-001** | | | | |
| 80 | 71.4 | 104  | 33.7 | 4.20 |
| 16 | 89.4 | 122  | 24.4 | 4.63 |
| 48 | 81.7 | 104  | 34.4 | 3.83 |

# 17 Colspan

## 17.1 Basic

- Group columns with a spaning line and a title
- The span goes above the highest row in the column header box

```
stable(
  data,
  span = colgroup("In final model", WT:CRCL),
) %>% pt_wrap(stdout())
```

| | | | | In final model | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 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 |

## 17.2 Multiple

- Multiple groupings
- Multiple levels

```
stable(
  data,
  span = list(
    colgroup("Meh", DOSE:WT),
    colgroup("Hrm", AGE:CRCL),
    colgroup("Huh", ALB:SCR),
    colgroup("Expert opinion", CRCL:SCR, level = 2)
  )
) %>% pt_wrap(stdout())
```

| | | | | | Expert opinion | | | |
| | | | | | Hrm | | Huh | |
| | Meh | | | | | | | |
| 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 |

## 17.3    Split from columns

- We have some columns of the form `tag.name`
- These are split on the `sep` argument; the `tag` (common across columns in the group) forms the spanner title
- The column names are formed by splitting `tag.` off of `tag.name`

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

```
## # A tibble: 2 x 7
##    STUDY       Normal.WT Normal.CRCL Normal.ALB ESRD.WT ESRD.CRCL ESRD.ALB
##    <chr>       <chr>     <chr>       <chr>       <chr>   <chr>     <chr>
## 1 12-DEMO-001 71.4      104         4.20        78.5    26.0      2.10
## 2 12-DEMO-001 81.7      104         3.83        89.9    26.1      1.92
```

```
stable(
  dotdata,
  span_split = colsplit(sep = '.'),
) %>% pt_wrap(stdout())
```

| | Normal | | | ESRD | | |
|---|---|---|---|---|---|---|
| STUDY | WT | CRCL | ALB | WT | CRCL | ALB |
| 12-DEMO-001 | 71.4 | 104 | 4.20 | 78.5 | 26.0 | 2.10 |
| 12-DEMO-001 | 81.7 | 104 | 3.83 | 89.9 | 26.1 | 1.92 |
| 12-DEMO-001 | 89.4 | 122 | 4.63 | 98.4 | 30.6 | 2.32 |
| 12-DEMO-001 | 94.0 | 93.2 | 4.94 | 103 | 23.3 | 2.47 |
| 12-DEMO-001 | 67.9 | 100 | 4.25 | 74.7 | 25.1 | 2.13 |
| 12-DEMO-001 | 76.6 | 99.2 | 4.54 | 84.2 | 24.8 | 2.27 |
| 12-DEMO-002 | 77.6 | 106 | 4.31 | 85.4 | 26.4 | 2.16 |
| 12-DEMO-002 | 61.3 | 113 | 4.04 | 67.4 | 28.2 | 2.02 |
| 12-DEMO-002 | 71.2 | 106 | 4.63 | 78.3 | 26.4 | 2.32 |
| 12-DEMO-002 | 74.1 | 112 | 4.44 | 81.5 | 28.0 | 2.22 |
| 12-DEMO-002 | 71.6 | 98.9 | 4.49 | 78.8 | 24.7 | 2.25 |
| 12-DEMO-002 | 72.4 | 105 | 3.89 | 79.6 | 26.3 | 1.94 |
| 12-DEMO-002 | 73.6 | 103 | 4.52 | 81.0 | 25.8 | 2.26 |

## 17.4   With titles breaking across lines

You can include . . .  in the title it will break in to multiple lines.  You can alter the split sequence with the `span_title_break` argument (default is . . .) . See `?tab_spanners`.

This feature is in addition to the functionality allowing you to break column names (control the split seqence with `cols_break`, where default is also . . .).

```
out <- stable(
  stdata(),
  span = colgroup("Final model ... Covariates", WT:SCR),
  cols_rename = c("Study Protocol ... Number" = "STUDY")
) %>% st_wrap(stdout())
```

| Study Protocol Number | DOSE | FORM | N | Final model Covariates | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| | | | | 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 |

## 18   Handle wide columns

- This shows using `col_ragged()` alignment to fix the width of a column that has a lot of text in it

### 18.1   `descr is` **taking over the table**

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

stable(ptable) %>% pt_wrap(stdout())
```

| symbol | descr | estimate | standard.error |
|--------|-------|----------|----------------|
| CL (L) | Metabolic clearance in adults who graduated high school before 1973 and live in Muncie. | 100 | 200 |

### 18.2   **Limit** `descr` **to 5 cm**

```
stable(
  ptable,
  align = cols_center(descr = col_ragged(5))
) %>% pt_wrap(stdout())
```

| symbol | descr | estimate | standard.error | rse |
|--------|-------|----------|----------------|-----|
| CL (L) | Metabolic clearance in adults who graduated high school before 1973 and live in Muncie. | 100 | 200 | 2 |

# 19  Identify a summary row

- We can point to one or more rows and style it up as a "summary row"
- The summary row can be styled
    - with a horizontal line above
    - with bold text in a designated column
    - with alternate text in a designated column
- Multiple summary rows can be specified in a list

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

```
## # A tibble: 3 x 6
##   STUDY       WT    AGE   CRCL  ALB   SCR
##   <chr>       <chr> <chr> <chr> <chr> <chr>
## 1 12-DEMO-001 80.2  28.4  104   4.40  1.10
## 2 12-DEMO-002 71.7  37.3  106   4.33  0.979
## 3 all         75.9  32.8  105   4.37  1.04
```

```
stable(
  df.total,
  sumrows = sumrow(
    df.total$STUDY == "all",
    label = "All Studies",
    bold = TRUE
  )
) %>% pt_wrap(stdout())
```

| STUDY | WT | AGE | CRCL | ALB | SCR |
|---|---|---|---|---|---|
| 12-DEMO-001 | 80.2 | 28.4 | 104 | 4.40 | 1.10 |
| 12-DEMO-002 | 71.7 | 37.3 | 106 | 4.33 | 0.979 |
| **All Studies** | 75.9 | 32.8 | 105 | 4.37 | 1.04 |

# 20 Save the table to file

- There is a output file attribute on the text that is returned
- When the `stable` output is passed to `stable_save()`, the attribute is used as the output file name

```
tab <- stable(data, output_file = "foo.tex")
str(tab)
```

```
##  'stable' chr [1:26] "\\setlength{\\tabcolsep}{5pt} " ...
##  - attr(*, "stable_file")= chr "foo.tex"
```

This can be used to save

```
stable_save(tab)

file.exists("foo.tex")
```

```
## [1] TRUE
```

# 21   Long table

- Long table is based on a call to `stable`
- The table header, tabular environemnt and table notes are reused

```
long <- ptdata()
long <- map_dfr(1:2, ~ long) %>% arrange(STUDY,DOSE,FORM)
```

```
long %>%
  stable_long(
    panel = "STUDY", cols_bold = TRUE,
    units = ys_get_unit(spec, parens = TRUE),
    notes = "The results look great!",
    clear_reps = "DOSE",
    cols_rename = c(Formulation  = "FORM"),
    r_file = "foo.R", output_file = "../deliv/table/output.tex",
    note_config = noteconf(type = "minipage", width = 0.8,table_skip = 0.2)
  ) %>% st_wrap(table = FALSE)
```

| DOSE | Formulation | 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 |
| | tablet | 80 | 71.4 | 104 | 33.7 | 4.20 | 1.06 |
| 150 mg | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| | capsule | 16 | 89.4 | 122 | 24.4 | 4.63 | 1.12 |
| | tablet | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |
| | tablet | 48 | 81.7 | 104 | 34.4 | 3.83 | 0.910 |
| | troche | 16 | 94.0 | 93.2 | 27.4 | 4.94 | 1.25 |
| | 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 |
| | tablet | 64 | 67.9 | 100 | 27.5 | 4.25 | 1.10 |
| | troche | 16 | 76.6 | 99.2 | 22.8 | 4.54 | 1.15 |
| | 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 |
| | capsule | 36 | 61.3 | 113 | 38.3 | 4.04 | 1.28 |
| | tablet | 324 | 77.6 | 106 | 29.9 | 4.31 | 0.981 |
| | tablet | 324 | 77.6 | 106 | 29.9 | 4.31 | 0.981 |
| 50 mg | capsule | 36 | 74.1 | 112 | 37.1 | 4.44 | 0.900 |
| | capsule | 36 | 74.1 | 112 | 37.1 | 4.44 | 0.900 |
| | tablet | 324 | 71.2 | 106 | 34.1 | 4.63 | 0.868 |
| | tablet | 324 | 71.2 | 106 | 34.1 | 4.63 | 0.868 |
| 75 mg | capsule | 36 | 72.4 | 105 | 38.2 | 3.89 | 0.900 |
| | capsule | 36 | 72.4 | 105 | 38.2 | 3.89 | 0.900 |
| | tablet | 288 | 71.6 | 98.9 | 34.2 | 4.49 | 0.991 |

| DOSE | Formulation | N | WT (kg) | CRCL (ml/min) | AGE (years) | ALB (g/dL) | SCR (mg/dL) |
|---|---|---|---|---|---|---|---|
| | tablet | 288 | 71.6 | 98.9 | 34.2 | 4.49 | 0.991 |
| | troche | 36 | 73.6 | 103 | 49.2 | 4.52 | 0.930 |
| | troche | 36 | 73.6 | 103 | 49.2 | 4.52 | 0.930 |

The results look great!

Source code: foo.R

Source file: output.tex

# 22  Fontsize

- Tables should be rendered with \\normalsize for the most part
- The font size can get bumped up or down in special circumstances

```
data %>% stable(sizes = tab_size(font = "tiny")) %>% pt_wrap(stdout())
```

| 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 |

## 23  Row space

- The default rowspacing is 1.4; this is a multiplication factor
- The user can bring this up or down so that row spacing of 1 is no extension or compression of row padding

```
data %>% slice(1:3) %>% stable() %>% pt_wrap(stdout())
```

| 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 |

```
data %>% slice(1:3) %>% stable(sizes = tab_size(row = 0.9)) %>% pt_wrap(stdout())
```

| 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 |

```
data %>% slice(1:3) %>% stable(sizes = tab_size(row = 2))   %>% pt_wrap(stdout())
```

| 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 |

## 24  Col space

- The default is 5

```
data %>% stable(sizes = tab_size(col = 20)) %>% pt_wrap(stdout())
```

| 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 |

# 25 Still ok

```
stable(data) %>% pt_wrap(stdout())
```

| 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 |