# 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()

pmdata <- readRDS("datasets/pmdata.RDS")
head(pmdata)
```

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

```r
data <- select(pmdata, STUDY = STUDYf, DOSE = DOSEf, WT, AGE, CRCL, ALB, SCR)
```

# 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

- Columns are in bold by default (can be turned off)

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

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

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

```
stable(
  data,
  r_file = "foo.R",
  output_file = "foo.tex",
  note_config = noteconf(type = "minipage", width = 0.65),
  notes = c("Data were analyzed in quadruplicate.", "The results are very clear."),
) %>% pt_wrap(stdout())
```

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

Data were analyzed in quadruplicate.
The results are very clear.
Source code: foo.R
Source file: foo.tex

# 6 Align

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

# 7 Units

- Automatically put units under the column name

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

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

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

# 8 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 |

# 9 hline from column

- Use the column to determine where the hline should go

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

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

# 10 hline anywhere

- Give row numbers for hline

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

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

# 11    Remove duplicate values

- Discard repeating values in a column

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

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

## 12   Panel

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

```
stable(
  data,
  align = cols_center(DOSE = "l", SCR = "r"),
  panel = vars("Study number:" = STUDY)
) %>% pt_wrap(stdout())
```

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

# 13   Colspan

- Group columns

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

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

# 14 Colspan - multiple

- Multiple groupings
- Multiple levels

```
stable(
  data,
  panel  = list(Study = "STUDY"),
  align = cols_left(.c = "WT,AGE,CRCL"),
  units = ys_get_unit(spec, parens = TRUE),
  r_file = "foo.R", output_file = "foo.tex",
  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 | |
| **Meh** | | **Hrm** | | **Huh** | |
| DOSE | WT (kg) | AGE (years) | CRCL (ml/min) | ALB (g/dL) | SCR (mg/dL) |
|---|---|---|---|---|---|
| **12-DEMO-001** | | | | | |
| 100 mg | 71.4 | 33.7 | 104 | 4.20 | 1.06 |
| 150 mg | 89.4 | 24.4 | 122 | 4.63 | 1.12 |
| 150 mg | 81.7 | 34.4 | 104 | 3.83 | 0.910 |
| 150 mg | 94.0 | 27.4 | 93.2 | 4.94 | 1.25 |
| 200 mg | 67.9 | 27.5 | 100 | 4.25 | 1.10 |
| 200 mg | 76.6 | 22.8 | 99.2 | 4.54 | 1.15 |
| **12-DEMO-002** | | | | | |
| 100 mg | 61.3 | 38.3 | 113 | 4.04 | 1.28 |
| 100 mg | 77.6 | 29.9 | 106 | 4.31 | 0.981 |
| 50 mg | 74.1 | 37.1 | 112 | 4.44 | 0.900 |
| 50 mg | 71.2 | 34.1 | 106 | 4.63 | 0.868 |
| 75 mg | 72.4 | 38.2 | 105 | 3.89 | 0.900 |
| 75 mg | 71.6 | 34.2 | 98.9 | 4.49 | 0.991 |
| 75 mg | 73.6 | 49.2 | 103 | 4.52 | 0.930 |

Source code: foo.R
Source file: foo.tex

# 15 Colspan - from cols

- we have some columns of the form `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,
  panel  = c(Study = "STUDY"),
  span_split = colsplit(sep = '.'),
  align = cols_left(.c = "WT,AGE,CRCL"),
  r_file = "foo.R", output_file = "foo.tex"
) %>% pt_wrap(stdout())
```

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

Source code: foo.R
Source file: foo.tex

# 16 Handle wide columns

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

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

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

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

## 16.2 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 |

# 17   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
```

```
## # 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,
  units = ys_get_unit(spec, parens = TRUE),
  align = cols_center(STUDY = 'l'),
  r_file  = "foo.R", output_file = "output.tex",
  col_rename = c("Protocol no."  = "STUDY"),
  notes = "WT: weight; CRCL: creatinine clearance",
  sumrows = sumrow(
    df.total$STUDY == "all",
    label = "All Studies",
    bold = TRUE
  )
) %>% pt_wrap(stdout())
```

| Protocol no. | WT (kg) | AGE (years) | CRCL (ml/min) | ALB (g/dL) | SCR (mg/dL) |
|--------------|---------|-------------|---------------|------------|-------------|
| 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 |

WT: weight; CRCL: creatinine clearance
Source code: foo.R
Source file: output.tex

# 18    Save the table to file

- There is a output file attribute on the text that is returned

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

```
##  'stable' chr [1:26] "{\\def\\arraystretch{1.4}\\tabcolsep=5pt" ...
##  - attr(*, "stable_file")= chr "foo.tex"
```

This can be used to save

```
stable_save(tab)

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

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

Oops …

```
try(stable_save(as.character(tab)))
```

```
## Error : bad input - there is no stable_file attribute; maybe this object was corrupted or it wasn't
```

# 19 Pipeable interface

```
data %>%
  st_new() %>%
  st_files(r = "foo.R", output = "foo.tex") %>%
  st_panel("STUDY", prefix = "Study: ") %>%
  st_rename(Dose = DOSE) %>%
  st_notes("The analysis was done in triplicate") %>%
  st_args(units = ys_get_unit(spec, parens = TRUE)) %>%
  st_clear_reps(DOSE) %>%
  st_span("Included", AGE:CRCL) %>%
  st_span("All covariates", WT:SCR, level=2) %>%
  st_align("c", .outer = "lr") %>%
  st_make() %>%
  pt_wrap(stdout())
```

| | | **All covariates** | | | |
| | | **Included** | | | |
| Dose | WT (kg) | AGE (years) | CRCL (ml/min) | ALB (g/dL) | SCR (mg/dL) |
|---|---|---|---|---|---|
| **Study: 12-DEMO-001** | | | | | |
| 100 mg | 71.4 | 33.7 | 104 | 4.20 | 1.06 |
| 150 mg | 89.4 | 24.4 | 122 | 4.63 | 1.12 |
| | 81.7 | 34.4 | 104 | 3.83 | 0.910 |
| | 94.0 | 27.4 | 93.2 | 4.94 | 1.25 |
| 200 mg | 67.9 | 27.5 | 100 | 4.25 | 1.10 |
| | 76.6 | 22.8 | 99.2 | 4.54 | 1.15 |
| **Study: 12-DEMO-002** | | | | | |
| 100 mg | 61.3 | 38.3 | 113 | 4.04 | 1.28 |
| | 77.6 | 29.9 | 106 | 4.31 | 0.981 |
| 50 mg | 74.1 | 37.1 | 112 | 4.44 | 0.900 |
| | 71.2 | 34.1 | 106 | 4.63 | 0.868 |
| 75 mg | 72.4 | 38.2 | 105 | 3.89 | 0.900 |
| | 71.6 | 34.2 | 98.9 | 4.49 | 0.991 |
| | 73.6 | 49.2 | 103 | 4.52 | 0.930 |

The analysis was done in triplicate
Source code: foo.R
Source file: foo.tex

# 20 Fontsize

- Where's my glasses?

```
data %>% stable(fontsize = "tiny") %>% pt_wrap(stdout())
```

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

## 21 Row space

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

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

```
data %>% slice(1:3) %>% stable(row_space = 0.9) %>% pt_wrap(stdout())
```

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

```
data %>% slice(1:3) %>% stable(row_space = 2) %>% pt_wrap(stdout())
```

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

## 22 Col space

```
data %>% stable(col_space = 20) %>% pt_wrap(stdout())
```

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