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)	θ_3	1.23	0.1
Unexplained variability				
Additive_error	RUV	σ_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())
```

```
## Warning in data[[dd$col]][dd$dup] <- rep("", dd$n): number of items to replace
## is not a multiple of replacement length
```

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.error
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(vars(Study = 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_make() %>%
  pt_wrap(stdout())
```

			All covariates			
			Included			
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
	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
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

```r
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