

Simple Tables Demo Doc

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1 Data

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

```
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
```

```
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

```
data %>% stable(col_bold=TRUE) %>% 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,  
  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.

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,  
  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 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
```

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

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

STUDY	Expert opinion					
	Meh		Hrm		Huh	
	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

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

STUDY	Normal			ESRD		
	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

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,
  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

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
```

19 Long table

```
long <- ptdata()
long <- map_dfr(1:5, ~ long) %>% arrange(STUDYf,SEXf)
```

```
long %>%
  stable_long(
    panel = "STUDYf", col_bold = TRUE,
    units = ys_get_unit(spec, parens = TRUE),
    notes = "The results look great!",
    col_rename = c("Sex" = "SEXf", "Study" = "STUDYf"),
    r_file = "foo.R", output_file = "../deliv/table/output.tex",
    note_config = noteconf(type = "minipage", width = 0.5, table_skip = 0.2)
  ) %>% as.character() %>% writeLines
```

```
{
```

Sex	WT (kg)	SCR (mg/dL)	ALB (g/dL)	N
12-DEMO-001				
male	76.3	1.09	4.33	10
male	76.3	1.09	4.33	10
male	76.3	1.09	4.33	10
male	76.3	1.09	4.33	10
male	76.3	1.09	4.33	10
female	70.0	1.01	4.25	20
female	70.0	1.01	4.25	20
female	70.0	1.01	4.25	20
female	70.0	1.01	4.25	20
female	70.0	1.01	4.25	20
12-DEMO-002				
male	71.9	1.01	4.57	18
male	71.9	1.01	4.57	18
male	71.9	1.01	4.57	18
male	71.9	1.01	4.57	18
male	71.9	1.01	4.57	18
female	72.6	0.949	4.42	32
female	72.6	0.949	4.42	32
female	72.6	0.949	4.42	32
female	72.6	0.949	4.42	32
female	72.6	0.949	4.42	32
11-DEMO-005				
male	69.2	2.51	4.46	29
male	69.2	2.51	4.46	29
male	69.2	2.51	4.46	29
male	69.2	2.51	4.46	29

continued ...

Sex	WT (kg)	SCR (mg/dL)	ALB (g/dL)	N
male	69.2	2.51	4.46	29
female	67.9	2.53	4.26	11
female	67.9	2.53	4.26	11
female	67.9	2.53	4.26	11
female	67.9	2.53	4.26	11
female	67.9	2.53	4.26	11
13-DEMO-001				
male	71.1	0.922	3.68	23
male	71.1	0.922	3.68	23
male	71.1	0.922	3.68	23
male	71.1	0.922	3.68	23
male	71.1	0.922	3.68	23
female	67.0	0.988	3.45	17
female	67.0	0.988	3.45	17
female	67.0	0.988	3.45	17
female	67.0	0.988	3.45	17
female	67.0	0.988	3.45	17

The results look great!
Source code: foo.R
Source file: output.tex

}

20 Fontsize

- Where's my glasses?

```
data %>% stable(sizes = tab_size(font = "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(sizes = tab_size(row = 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(sizes = tab_size(row = 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(sizes = tab_size(col = 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