

# 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

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

```
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, 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	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
- The width of the minipage needs to be set by the user

```
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

- Columns can be aligned center, left or right
- Columns can be aligned with a fixed width 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	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 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	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 Expand header rows

- Multiline table header
- Unlimited number
- Use ... to break
- Units go on the bottom row when they are supplied
- Items are always pushed to the bottom

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

Study Number	DOSE	WT (kg)	AGE (years)	CRCL (ml/min)	Serum Albumin (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



## 9 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
<b>Fixed-effects</b>				
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
<b>Unexplained variability</b>				
Additive_error	RUV	$\sigma_1$	0.02	0.01

## 10 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

## 11 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	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

## 12 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	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 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() %>% rename(STUDY = STUDYf, SEX = SEXf)
```

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

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

STUDY	SEX	WT	SCR	ALB	N
<b>12-DEMO-001</b>	male	76.3	1.09	4.33	10
	female	70.0	1.01	4.25	20
<b>12-DEMO-002</b>	male	71.9	1.01	4.57	18
	female	72.6	0.949	4.42	32
<b>11-DEMO-005</b>	male	69.2	2.51	4.46	29
	female	67.9	2.53	4.26	11
<b>13-DEMO-001</b>	male	71.1	0.922	3.68	23
	female	67.0	0.988	3.45	17

## 14 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	WT	AGE	CRCL	ALB	SCR
<b>Study number: 12-DEMO-001</b>					
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
<b>Study number: 12-DEMO-002</b>					
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

## 15 Colspan

- Group columns with a spanning 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())
```

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

## 16 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



## 17 Colspan - from cols

- 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())
```

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

## 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
<b>All Studies</b>	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] "{\\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
```

## 21 Long table

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

```
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

{
```

Table 1:

Sex	WT (kg)	SCR (mg/dL)	ALB (g/dL)	N
<b>12-DEMO-001</b>				
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
<b>12-DEMO-002</b>				
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
<b>11-DEMO-005</b>				
male	69.2	2.51	4.46	29

continued on next page

<b>Sex</b>	<b>WT</b> (kg)	<b>SCR</b> (mg/dL)	<b>ALB</b> (g/dL)	<b>N</b>
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
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
<b>13-DEMO-001</b>				
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: ../deliv/table/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	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

## 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	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



## 24 Col space

- The default is 5

```
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