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 Long table

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

```r
data %>%
  stable_long(
    panel = "STUDYf", col_bold = TRUE,
    units = ys_get_unit(spec, parens = TRUE),
    notes = "The results look great!",
    clear_reps = "SEXf",
    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
	76.3	1.09	4.33	10
	76.3	1.09	4.33	10
	76.3	1.09	4.33	10
	76.3	1.09	4.33	10
female	70.0	1.01	4.25	20
	70.0	1.01	4.25	20
	70.0	1.01	4.25	20
	70.0	1.01	4.25	20
	70.0	1.01	4.25	20
12-DEMO-002				
male	71.9	1.01	4.57	18
	71.9	1.01	4.57	18
	71.9	1.01	4.57	18
	71.9	1.01	4.57	18
	71.9	1.01	4.57	18
female	72.6	0.949	4.42	32
	72.6	0.949	4.42	32
	72.6	0.949	4.42	32
	72.6	0.949	4.42	32
	72.6	0.949	4.42	32
11-DEMO-005				
male	69.2	2.51	4.46	29
	69.2	2.51	4.46	29
	69.2	2.51	4.46	29

continued ...

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

The results look great!

Source code: foo.R

Source file: output.tex

}

5 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)

```r
stable(
  data[1:10,],
  r_file = "foo.R",
  output_file = "foo.tex",
  notes = c("Data were analyzed in quadruplicate.", "The results are very clear."),
) %>% pt_wrap(stdout())
```

STUDYf	SEXf	WT	SCR	ALB	N
12-DEMO-001	male	76.3	1.09	4.33	10
12-DEMO-001	male	76.3	1.09	4.33	10
12-DEMO-001	male	76.3	1.09	4.33	10
12-DEMO-001	male	76.3	1.09	4.33	10
12-DEMO-001	male	76.3	1.09	4.33	10
12-DEMO-001	female	70.0	1.01	4.25	20
12-DEMO-001	female	70.0	1.01	4.25	20
12-DEMO-001	female	70.0	1.01	4.25	20
12-DEMO-001	female	70.0	1.01	4.25	20
12-DEMO-001	female	70.0	1.01	4.25	20

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