Simple Tables Demo Doc

Contents

1 Basic table

```
out <- stable(data)

pt_wrap(out, con = 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

```
if(params$save) {
  stable_save(out, file = "basic-table.tex")
}
```

2 Bold cols

```
out <- stable(data, col_bold = TRUE)

pt_wrap(out, con = 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

```
if(params$save) {
  stable_save(out, file = "basic-table-bold.tex")
}
```

3   File names

```
out <- stable(data, r_file = "validate.Rmd", output_file = "file-names.tex")

pt_wrap(out, con = 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

Source code: validate.Rmd
Source file: file-names.tex

```
if(params$save) {
  stable_save(out)
}
file.exists("file-names.tex")
```

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

4 Notes tpt

```
out <- stable(data, notes = c("WT: weight", "ALB: albumin"))

pt_wrap(out, con = 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

WT: weight
ALB: albumin

```
if(params$save) {
  stable_save(out, file = "notes-tpt.tex")
}
```

5 Notes minipage

```
conf <- noteconf(type = 'minipage')

out <- stable(data, notes = c("WT: weight", "ALB: albumin"), note_config = conf)

pt_wrap(out, con = 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

WT: weight
ALB: albumin

```
if(params$save) {
  stable_save(out, file = "notes-mini.tex")
}
```

6 Panel basic

```
out <- stable(data, panel = "STUDY")

pt_wrap(out, con = 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

```
if(params$save) {
  stable_save(out, file = "panel-basic.tex")
}
```

7 Panel prefix

```
out <- stable(data, panel = as.panel("STUDY", prefix = "Study: "))

pt_wrap(out, con = stdout())
```

DOSE	WT	AGE	CRCL	ALB	SCR
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
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: 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

```
if(params$save) {
  stable_save(out, file = "panel-prefix.tex")
}
```

8 Clear reps

```
out <- stable(data, clear_reps = "STUDY")
```

```
pt_wrap(out, con = 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

```
if(params$save) {
  stable_save(out, file = "clear-reps.tex")
}
```

9 Clear grouped reps

```r
out <- stable(data, clear_grouped_reps = "STUDY,DOSE")

pt_wrap(out, con = 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
		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

```r
if(params$save) {
  stable_save(out, file = "clear-grouped-reps.tex")
}
```

10   hline at

```
out <- stable(data, hline_at = c(2,4,6))

pt_wrap(out, con = 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

```
if(params$save) {
  stable_save(out, file = "hline-at.tex")
}
```

11 hline from

```
out <- stable(data, hline_from = "STUDY")

pt_wrap(out, con = 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

```
if(params$save) {
  stable_save(out, file = "hline-from.tex")
}
```

12 hline from with clear

```
out <- stable(data, hline_from = "STUDY", clear_reps = "STUDY")

pt_wrap(out, con = 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

```
if(params$save) {
  stable_save(out, file = "hline-from-clear.tex")
}
```

13 Align

```
align <- cols_center(.outer = 'lr', DOSE = 'r')

out <- stable(data, align = align)

pt_wrap(out, con = 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

```
if(params$save) {
  stable_save(out, file = "align.tex")
}
```

14 rename

```
out <- stable(data, col_rename = c(Weight = "WT", Dose = "DOSE"))

pt_wrap(out, con = stdout())
```

STUDY	Dose	Weight	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

```
if(params$save) {
  stable_save(out, file = "cols-rename.tex")
}
```

15   blank

```
out <- stable(data, col_blank = "WT,ALB")

pt_wrap(out, con = stdout())
```

STUDY	DOSE		AGE	CRCL		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

```
if(params$save) {
  stable_save(out, file = "col-blank.tex")
}
```

16 multi-line

```
out <- stable(data, col_rename = c("Protocol...Number" = "STUDY", Weight = "WT"))

pt_wrap(out, con = stdout())
```

Protocol Number	DOSE	Weight	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

```
if(params$save) {
  stable_save(out, file = "col-multi-line.tex")
}
```

17 multi-line units

```
out <- stable(
  data,
  col_rename = c("Protocol...Number" = "STUDY", Weight = "WT"),
  units = units
)

pt_wrap(out, con = stdout())
```

Protocol Number	DOSE	Weight (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

```
if(params$save) {
  stable_save(out, file = "col-multi-line-units.tex")
}
```

18 span

```
out <- stable(
  data,
  span = colgroup("Final model", AGE:CRCL)
)

pt_wrap(out, con = stdout())
```

| STUDY | DOSE | WT | Final model | | ALB | SCR |
			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

```
if(params$save) {
  stable_save(out, file = "span.tex")
}
```

19 span levels

```
out <- stable(
  data,
  span = list(
    colgroup("All covariates", WT:SCR, level = 2),
    colgroup("Final model", AGE:CRCL)
  )
)

pt_wrap(out, con = stdout())
```

			All covariates			
			Final model			
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

```
if(params$save) {
  stable_save(out, file = "span-levels.tex")
}
```

20   Continuous long panel

```
out <- pt_cont_long(pmdata, cols = "WT,CRCL,ALB", panel = "STUDYf",
                    units = units) %>%
  as_stable()

pt_wrap(out, con = stdout())
```

Variable	n	Mean	Median	SD	Min / Max
12-DEMO-001					
WT (kg)	29	72.2	70.0	14.3	50.9 / 97.2
CRCL (ml/min)	29	106	104	9.46	93.2 / 126
ALB (g/dL)	29	4.28	4.08	0.474	3.56 / 5.15
12-DEMO-002					
WT (kg)	49	72.4	72.1	11.5	51.5 / 96.6
CRCL (ml/min)	49	103	103	8.35	90.6 / 121
ALB (g/dL)	50	4.47	4.43	0.468	3.65 / 5.39
11-DEMO-005					
WT (kg)	39	68.9	65.4	14.5	43.6 / 92.8
CRCL (ml/min)	39	58.8	56.2	29.7	15.4 / 103
ALB (g/dL)	39	4.41	4.44	0.537	3.51 / 5.39
13-DEMO-001					
WT (kg)	40	69.4	68.1	11.6	50.7 / 96.6
CRCL (ml/min)	37	102	102	8.19	90.7 / 119
ALB (g/dL)	38	3.58	3.65	1.15	1.28 / 5.38
All data					
WT (kg)	157	70.7	70.0	12.8	43.6 / 97.2
CRCL (ml/min)	154	92.1	98.8	25.5	15.4 / 126
ALB (g/dL)	156	4.20	4.32	0.793	1.28 / 5.39

```
if(params$save) {
  stable_save(out, file = "continuous-long-panel.tex")
}
```

21 Continuous wide by

```
out <- pt_cont_wide(
  pmdata, cols = "WT,CRCL,ALB", by = "STUDYf",
  units = units
) %>% as_stable()

pt_wrap(out, con = stdout())
```

STUDYf	WT (kg)	CRCL (ml/min)	ALB (g/dL)
12-DEMO-001	72.2 (14.3) [29]	106 (9.46) [29]	4.28 (0.474) [29]
12-DEMO-002	72.4 (11.5) [49]	103 (8.35) [49]	4.47 (0.468) [50]
11-DEMO-005	68.9 (14.5) [39]	58.8 (29.7) [39]	4.41 (0.537) [39]
13-DEMO-001	69.4 (11.6) [40]	102 (8.19) [37]	3.58 (1.15) [38]
All data	70.7 (12.8) [157]	92.1 (25.5) [154]	4.20 (0.793) [156]

Summary is mean (sd) [count]

```
if(params$save) {
  stable_save(out, file = "continuous-wide-by.tex")
}
```

22 Categorical long by

```
out <- pt_cat_long(
  pmdata,
  cols = "SEXf,RFf,FORMf",
  by = "STUDYf"
) %>% as_stable()

pt_wrap(out, con = stdout())
```

	STUDYf				
	12-DEMO-001	12-DEMO-002	11-DEMO-005	13-DEMO-001	**All Groups**
.blank SEXf					
male	10 (33.3)	18 (36.0)	29 (72.5)	23 (57.5)	80 (50.0)
female	20 (66.7)	32 (64.0)	11 (27.5)	17 (42.5)	80 (50.0)
.blank RFf					
normal	30 (100.0)	50 (100.0)	10 (25.0)	40 (100.0)	130 (81.2)
mild	0 (0.0)	0 (0.0)	10 (25.0)	0 (0.0)	10 (6.2)
moderate	0 (0.0)	0 (0.0)	10 (25.0)	0 (0.0)	10 (6.2)
severe	0 (0.0)	0 (0.0)	10 (25.0)	0 (0.0)	10 (6.2)
.blank FORMf					
tablet	25 (83.3)	42 (84.0)	30 (75.0)	33 (82.5)	130 (81.2)
capsule	3 (10.0)	6 (12.0)	3 (7.5)	3 (7.5)	15 (9.4)
troche	2 (6.7)	2 (4.0)	7 (17.5)	4 (10.0)	15 (9.4)

Summary is count (percent)

```
if(params$save) {
  stable_save(out, file = "cat-long-by.tex")
}
```

23 Categorical wide by panel

```
out <- pt_cat_wide(
  pmdata,
  cols = "SEXf,RFf",
  by = "FORMf",
  panel = "STUDYf"
) %>% as_stable()

pt_wrap(out, con = stdout())
```

	SEXf		RFf			
FORMf	male	female	normal	mild	moderate	severe
12-DEMO-001						
tablet	7 (28.0)	18 (72.0)	25 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
capsule	1 (33.3)	2 (66.7)	3 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
troche	2 (100.0)	0 (0.0)	2 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
12-DEMO-002						
tablet	16 (38.1)	26 (61.9)	42 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
capsule	2 (33.3)	4 (66.7)	6 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
troche	0 (0.0)	2 (100.0)	2 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
11-DEMO-005						
tablet	20 (66.7)	10 (33.3)	9 (30.0)	7 (23.3)	6 (20.0)	8 (26.7)
capsule	3 (100.0)	0 (0.0)	0 (0.0)	2 (66.7)	0 (0.0)	1 (33.3)
troche	6 (85.7)	1 (14.3)	1 (14.3)	1 (14.3)	4 (57.1)	1 (14.3)
13-DEMO-001						
tablet	19 (57.6)	14 (42.4)	33 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
capsule	1 (33.3)	2 (66.7)	3 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
troche	3 (75.0)	1 (25.0)	4 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
All data	80 (50.0)	80 (50.0)	130 (81.2)	10 (6.2)	10 (6.2)	10 (6.2)

Summary is count (percent)

```
if(params$save) {
  stable_save(out, file = "cat-wide-by-panel.tex")
}
```

24 Inventory basic

```r
out <- pt_data_inventory(
  pk,
  by = "STUDYf"
) %>% as_stable()

pt_wrap(out, con = stdout())
```

STUDYf	Number				Percent	
	SUBJ	MISS	OBS	BQL	OBS	BQL
12-DEMO-001	30	8	427	15	13.9	0.5
12-DEMO-002	50	10	1152	38	37.4	1.2
11-DEMO-005	40	10	920	30	29.9	1.0
13-DEMO-001	40	7	582	11	18.9	0.4
All data	160	35	3081	94	100.0	3.1

SUBJ: subjects
BQL: below quantitation limit
MISS: missing observations (not BQL)
OBS: observations

```r
if(params$save) {
  stable_save(out, file = "inventory-basic.tex")
}
```

25 Inventory stacked

```
out <- pt_data_inventory(
  obs,
  by = "STUDYf",
  panel = "SEQf",
  stacked = TRUE
) %>% as_stable()

pt_wrap(out, con = stdout())
```

STUDYf	Number				Percent	
	SUBJ	MISS	OBS	BQL	OBS	BQL
DEMO PK						
12-DEMO-001	30	8	427	15	13.9	0.5
12-DEMO-002	50	10	1152	38	37.4	1.2
11-DEMO-005	40	10	920	30	29.9	1.0
13-DEMO-001	40	7	582	11	18.9	0.4
Group Total	160	35	3081	94	100.0	3.1
ESTRDIOL						
11-DEMO-005	40	0	40	0	50.6	0.0
13-DEMO-001	40	1	39	0	49.4	0.0
Group Total	80	1	79	0	100.0	0.0
BMD						
11-DEMO-005	40	9	111	0	49.1	0.0
13-DEMO-001	40	5	115	0	50.9	0.0
Group Total	80	14	226	0	100.0	0.0

SUBJ: subjects
BQL: below quantitation limit
MISS: missing observations (not BQL)
OBS: observations

```
if(params$save) {
  stable_save(out, file = "inventory-basic.tex")
}
```