# Changes to categorical data summaries

## Contents

	cat_wide	2
1.1	with by and panel	2
1.2	with panel	3
	with by	
1.4	ungrouped	5
1.5	Drop the N	5
	cont_long	6
2.1	With spanning data item (formulation)	6
2.2	Without spanning data item	9

### 1 pt\_cat\_wide

#### 1.1 with by and panel

• the N column is new

```
pt_cat_wide(
  pmt_first,
  cols = vars(Sex = SEXf, `Renal function` = RFf),
  by = vars(Study = STUDYf),
  panel = c(`Formulation: ` = "FORMf")
) %>% as_stable() %>% pt_wrap(stdout())
```

		Se	ex		Renal f	unction	
Study	N	male	female	normal	mild	moderate	severe
Formulation: ta	ablet						
12-DEMO-001	25	7 (28.0)	18 (72.0)	25 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
12-DEMO-002	42	16 (38.1)	26 (61.9)	42 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
11-DEMO-005	30	20 (66.7)	10 (33.3)	9 (30.0)	7 (23.3)	6 (20.0)	8 (26.7)
13-DEMO-001	33	19 (57.6)	14 (42.4)	33 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
Formulation: c	apsul	e					
12-DEMO-001	3	1 (33.3)	2 (66.7)	3 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
12-DEMO-002	6	2 (33.3)	4 (66.7)	6 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
11-DEMO-005	3	3 (100.0)	0 (0.0)	0 (0.0)	2 (66.7)	0 (0.0)	1 (33.3)
13-DEMO-001	3	1 (33.3)	2 (66.7)	3 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
Formulation: t	roche						
12-DEMO-001	2	2 (100.0)	0 (0.0)	2 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
12-DEMO-002	2	0 (0.0)	2 (100.0)	2 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
11-DEMO-005	7	6 (85.7)	1 (14.3)	1 (14.3)	1 (14.3)	4 (57.1)	1 (14.3)
13-DEMO-001	4	3 (75.0)	1 (25.0)	4 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)
All data	160	80 (50.0)	80 (50.0)	130 (81.2)	10 (6.2)	10 (6.2)	10 (6.2)

Summary is count (percent) N: subject count for the row

#### 1.2 with panel

- the N column is new
- I don't like the way this looks; would prefer using by here; but I think this output is what you would expect given the data and option

```
pt_cat_wide(
  pmt_first,
  cols = vars(Sex = SEXf, `Renal function` = RFf),
  panel = c(`Formulation: ` = "FORMf"),
  all_name = "All formulations"
) %>% as_stable() %>% pt_wrap(stdout())
```

	Sex		Renal function			
N	male	female	normal	mild	moderate	severe
Forn	nulation: t	ablet				
130	62 (47.7)	68 (52.3)	109 (83.8)	7 (5.4)	6 (4.6)	8 (6.2)
Forn	nulation: c	apsule				
15	7 (46.7)	8 (53.3)	12 (80.0)	2 (13.3)	0 (0.0)	1 (6.7)
Forn	nulation: t	roche				
15	11 (73.3)	4 (26.7)	9 (60.0)	1 (6.7)	4 (26.7)	1 (6.7)
All fo	ormulation	ıs				
160	80 (50.0)	80 (50.0)	130 (81.2)	10 (6.2)	10 (6.2)	10 (6.2)

Summary is count (percent) N: subject count for the row

#### 1.3 with by

• the N column is new

```
pt_cat_wide(
  pmt_first,
  cols = vars(Sex = SEXf, `Renal function` = RFf),
  by = c(Formulation = "FORMf")
) %>% as_stable() %>% pt_wrap(stdout())
```

		Se	Sex		Renal function		
Formulation	N	male	female	normal	mild	moderate	severe
tablet	130	62 (47.7)	68 (52.3)	109 (83.8)	7 (5.4)	6 (4.6)	8 (6.2)
capsule	15	7 (46.7)	8 (53.3)	12 (80.0)	2 (13.3)	0 (0.0)	1 (6.7)
troche	15	11 (73.3)	4 (26.7)	9 (60.0)	1 (6.7)	4 (26.7)	1 (6.7)
All data	160	80 (50.0)	80 (50.0)	130 (81.2)	10 (6.2)	10 (6.2)	10 (6.2)

Summary is count (percent) N: subject count for the row

#### 1.4 ungrouped

• the N column is new

```
pt_cat_wide(
  pmt_first,
  cols = vars(Sex = SEXf, `Renal function` = RFf)
) %>% as_stable() %>% pt_wrap(stdout())
```

	Se	ex	Renal function			
N	male	female	normal	mild	moderate	severe
160	80 (50.0)	80 (50.0)	130 (81.2)	10 (6.2)	10 (6.2)	10 (6.2)

Summary is count (percent) N: subject count for the row

#### 1.5 Drop the N

```
out <- pt_cat_wide(
  pmt_first,
  cols = vars(Sex = SEXf, `Renal function` = RFf),
  drop = "N"
)
out %>% as_stable() %>% pt_wrap(stdout())
```

Sex			Renal f	unction	
male	female	normal	mild	moderate	severe
80 (50.0)	80 (50.0)	130 (81.2)	10 (6.2)	10 (6.2)	10 (6.2)

#### 2 pt\_cont\_long

We now add a summary row to the bottom of the table.

#### 2.1 With spanning data item (formulation)

```
pt_cat_long(
  pmt_first,
  cols = vars(Sex = SEXf, `Renal function` = RFf, `Child-Pugh` = CPf),
  span = vars(Study = STUDYf)
) %>% as_stable() %>% pt_wrap(stdout())
```

		Stu	ıdy	
	12-DEMO-001	12-DEMO-002	11-DEMO-005	13-DEMO-001
Sex				
male	10 (33.3)	18 (36.0)	29 (72.5)	23 (57.5)
female	20 (66.7)	32 (64.0)	11 (27.5)	17 (42.5)
Renal fund	ction			
normal	30 (100.0)	50 (100.0)	10 (25.0)	40 (100.0)
mild	0 (0.0)	0 (0.0)	10 (25.0)	0 (0.0)
moderate	0 (0.0)	0 (0.0)	10 (25.0)	0 (0.0)
severe	0 (0.0)	0 (0.0)	10 (25.0)	0 (0.0)
Child-Pug	h			
Score=0	30 (100.0)	50 (100.0)	40 (100.0)	10 (25.0)
Score=1	0 (0.0)	0 (0.0)	0 (0.0)	10 (25.0)
Score=2	0 (0.0)	0 (0.0)	0 (0.0)	10 (25.0)
Score=3	0 (0.0)	0 (0.0)	0 (0.0)	10 (25.0)
All Data	30 (18.8)	50 (31.2)	40 (25.0)	40 (25.0)

```
pt_cat_long(
  pmt_first,
  cols = vars(Sex = SEXf, `Renal function` = RFf, `Child-Pugh` = CPf),
  span = vars(Formulation = FORMf),
  all_name_span = "All ... Formulations",
  summarize = "both"
) %>% as_stable() %>% pt_wrap(stdout())
```

	F	ormulation	1	
	tablet	capsule	troche	All Formulations
Sex				
male	62 (47.7)	7 (46.7)	11 (73.3)	80 (50.0)
female	68 (52.3)	8 (53.3)	4 (26.7)	80 (50.0)
Renal fund	ction			
normal	109 (83.8)	12 (80.0)	9 (60.0)	130 (81.2)
mild	7 (5.4)	2 (13.3)	1 (6.7)	10 (6.2)
moderate	6 (4.6)	0 (0.0)	4 (26.7)	10 (6.2)
severe	8 (6.2)	1 (6.7)	1 (6.7)	10 (6.2)
Child-Pug	h			
Score=0	106 (81.5)	12 (80.0)	12 (80.0)	130 (81.2)
Score=1	7 (5.4)	1 (6.7)	2 (13.3)	10 (6.2)
Score=2	8 (6.2)	1 (6.7)	1 (6.7)	10 (6.2)
Score=3	9 (6.9)	1 (6.7)	0 (0.0)	10 (6.2)
All Data	130 (81.2)	15 (9.4)	15 (9.4)	160 (100.0)

```
pt_cat_long(
  pmt_first,
  cols = vars(Sex = SEXf, `Renal function` = RFf, `Child-Pugh` = CPf),
  span = vars(Study = STUDYf),
  summarize = "none"
) %>% as_stable() %>% pt_wrap(stdout())
```

		Stu	ıdy	
	12-DEMO-001	12-DEMO-002	11-DEMO-005	13-DEMO-001
Sex				
male	10 (33.3)	18 (36.0)	29 (72.5)	23 (57.5)
female	20 (66.7)	32 (64.0)	11 (27.5)	17 (42.5)
Renal fund	tion			
normal	30 (100.0)	50 (100.0)	10 (25.0)	40 (100.0)
mild	0 (0.0)	0 (0.0)	10 (25.0)	0 (0.0)
moderate	0 (0.0)	0 (0.0)	10 (25.0)	0 (0.0)
severe	0 (0.0)	0 (0.0)	10 (25.0)	0 (0.0)
Child-Pug	h			
Score=0	30 (100.0)	50 (100.0)	40 (100.0)	10 (25.0)
Score=1	0 (0.0)	0 (0.0)	0 (0.0)	10 (25.0)
Score=2	0 (0.0)	0 (0.0)	0 (0.0)	10 (25.0)
Score=3	0 (0.0)	0 (0.0)	0 (0.0)	10 (25.0)

#### 2.2 Without spanning data item

```
mini <- noteconf(type = "minipage", width = 0.3)
pt_cat_long(
   pmt_first,
   cols = vars(Sex = SEXf, `Renal function` = RFf, `Child-Pugh` = CPf)
) %>% as_stable(note_config = mini) %>% pt_wrap(stdout())
```

	Summary			
Sex				
male	80 (50.0)			
female	80 (50.0)			
Renal function				
normal	130 (81.2)			
mild	10 (6.2)			
moderate	10 (6.2)			
severe	10 (6.2)			
Child-Pug	h			
Score=0	130 (81.2)			
Score=1	10 (6.2)			
Score=2	10 (6.2)			
Score=3	10 (6.2)			
All Data	160 (100.0)			