Demo Doc - pipe interface

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 Simple table

```
data %>% st_new() %>% st_make(col_bold = TRUE, .cat = TRUE)
```

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

3 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)

```
data %>%
  st_data() %>%
  st_files(r = "foo.R", output = "foo.tex") %>%
  st_notes(
    "Data were analyzed in quadruplicate.",
    "The results are very clear."
  ) %>%
  st_make(.cat =TRUE)
```

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

4 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

```
data %>%
  st_new() %>%
  st_files("foo.R", "foo.tex") %>%
  st_noteconf(type = "minipage", width = 0.65) %>%
  st_notes(
    "Data were analyzed in quadruplicate.",
    "The results are very clear."
  ) %>%
  st_make(.cat = TRUE)
```

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 Align

- Center everything except for
- STUDY (left)
- DOSE and SCR (right)

```
data %>%
  st_new() %>%
  st_align("c", STUDY = 'l', .r = "DOSE,SCR") %>%
  st_make(.cat = TRUE)
```

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

6 Units

- Automatically put units under the column name

```
data %>%
  st_new() %>%
  st_center(STUDY = 'l', .r = "DOSE,SCR") %>%
  st_units(WT = "kg", SCR = "mg/dL", DOSE = "mg") %>%
  st_make(.cat = TRUE)
```

STUDY	DOSE (mg)	WT (kg)	AGE	CRCL	ALB	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

Alternatively

```
units <- ys_get_unit(spec, parens = TRUE)

data[1:3,] %>%
  st_new() %>%
  st_center(STUDY = 'l', .r = "DOSE,SCR") %>%
  st_units(units) %>%
  st_make(.cat = TRUE)
```

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

7   Expand header rows

- Multiline table header
- Unlimited number
- Use . . . to break

```
data %>%
  st_new() %>%
  st_rename("Study...Number" = STUDY, "Serum...Albumin" = ALB) %>%
  st_units(units) %>%
  st_make(.cat = TRUE)
```

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

8 Math

- Columns with at least two $ are "math" and will not be sanitized
- Otherwise the 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
```

```
ptab %>%
  st_data() %>%
  st_center(Parameter = col_ragged(3), .l = "Symbol") %>%
  st_panel(".type") %>%
  st_make(.cat = TRUE)
```

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

```
st_new(data) %>%
  st_hline(from = "STUDY") %>%
  st_make(.cat = TRUE)
```

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

```
st_new(data) %>%
  st_hline(at = c(3,nrow(data))-1) %>%
  st_make(.cat = TRUE)
```

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

```
data %>%
  st_new() %>%
  st_hline(from = "STUDY") %>%
  st_clear_reps("STUDY") %>%
  st_make(.cat = TRUE)
```

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 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

```r
tmp <- ptdata() %>% rename(STUDY = STUDYf, SEX = SEXf)
tmp <- mutate(tmp, STUDY = tex_bold(as.character(STUDY)))
```

```r
tmp %>%
  st_new() %>%
  st_clear_reps(STUDY) %>%
  st_hline(from = "STUDY") %>%
  st_make(.cat = TRUE)
```

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

13 Panel

- Divide the table using column contents
- there's a bug somewhere there

```
data %>%
  st_new() %>%
  st_center(DOSE = 'l', SCR = 'r') %>%
  st_panel("STUDY", prefix = "Study number: ") %>%
  st_make(.cat = TRUE)
```

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

14 Colspan

- Group columns

```
data %>%
  st_new() %>%
  st_left(.c = "WT,AGE,CRCL") %>%
  st_span("In final model", WT:CRCL) %>%
  st_make(.cat = TRUE)
```

		In 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

15 Colspan - multiple

- Multiple groupings
- Multiple levels

```
data %>%
  st_new() %>%
  st_span("Meh", DOSE:WT) %>%
  st_span("Hrm", AGE:CRCL) %>%
  st_span("Huh", ALB:SCR) %>%
  st_span("Expert opinion", CRCL:SCR, level = 2) %>%
  st_make(.cat = TRUE)
```

STUDY	Meh		Hrm		Expert opinion 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

16   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
```

```
dotdata %>%
  st_new() %>%
  st_span_split(sep = '.') %>%
  st_make(.cat = TRUE)
```

	Normal			**ESRD**		
STUDY	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

17   Handle wide columns

17.1   `descr` is **taking over the table**

```
ptable <- readRDS("datasets/ptable.RDS")

ptable %>% st_new() %>% st_make(.cat = TRUE)
```

symbol	descr	estimate	standard.error
CL (L)	Metabolic clearance in adults who graduated high school before 1973 and live in Muncie.	100	200

17.2   **Limit** `descr` **to 5 cm**

```
ptable %>%
  st_new() %>%
  st_align(descr = col_ragged(5)) %>%
  st_make(.cat = TRUE)
```

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

18 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
```

```
st_new(df.total) %>%
  st_sumrow(.$data$STUDY=="all", label = "All studies", bold = TRUE) %>%
  st_make(.cat = TRUE)
```

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

19 Fontsize

- Where's my glasses?

```
data %>% st_new() %>% st_sizes(font = "tiny") %>% st_make(.cat = TRUE)
```

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

20 Row space

```
sl <- data %>% slice(1:3)
sl %>% st_new() %>%                      st_make(.cat = TRUE)
```

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

```
sl %>% st_new() %>% st_sizes(row = 0.9) %>% st_make(.cat = TRUE)
```

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

```
sl %>% st_new() %>% st_sizes(row = 2  ) %>% st_make(.cat = TRUE)
```

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

21 Col space

```
data %>% st_new() %>% st_sizes(col = 20) %>% st_make(.cat = TRUE)
```

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