

Demo Doc - pipe interface

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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 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 = '1', .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 = '1', .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 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
```

```
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

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

```
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)
```

| 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 |

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 | 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 |

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)
```

| 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 |

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

```
s1 <- data %>% slice(1:3)
s1 %>% 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 |

```
s1 %>% 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 |

```
s1 %>% 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 |