coloncancer

```
2024-10-20
 #only need to do this once, unhashtag these lines to run
 #install.packages("biostat3")
 #install.packages("gtsummary")
 #bring in the data, you would bring in your own data here
 library(biostat3)
## Loading required package: survival
## Loading required package: MASS
 ## Attaching package: 'biostat3'
## The following object is masked from 'package:survival':
 ##
      colon
 data(colon)
 head(colon)
                 stage mmdx yydx surv_mm surv_yy
       sex age
                                                 status
 ## 1 Female 77 Distant
                       3 1977
                               16.5
                                        1.5 Dead: cancer
 ## 2 Female 78 Localised
                       7 1978 82.5
                                        6.5 Dead: other
 ## 3 Male 78 Distant 10 1978
                                1.5
                                        0.5 Dead: cancer
      Male 76 Distant 10 1976
                                1.5
                                        0.5 Dead: cancer
 ## 5 Male 80 Localised 12 1980
                                8.5
                                        0.5 Dead: cancer
 ## 6 Female 75 Localised 11 1975 23.5
                                        1.5 Dead: cancer
                             year8594 agegrp
                                                  dx
                 subsite
                                                         exit id
              Transverse Diagnosed 75-84 75+ 1977-03-04 1978-07-20 1
 ## 1
## 2 Coecum and ascending Diagnosed 75-84 75+ 1978-07-26 1985-06-11 2
 ## 3 Descending and sigmoid Diagnosed 75-84 75+ 1978-10-10 1978-11-25 3
 ## 6 Coecum and ascending Diagnosed 75-84 75+ 1975-11-16 1977-11-01 6
         ydx yexit
 ## 1 1977.170 1978.548
 ## 2 1978.564 1985.441
 ## 3 1978.772 1978.898
## 4 1976.824 1976.950
 ## 5 1980.969 1981.676
 ## 6 1975.873 1977.832
 library(gtsummary)
## Attaching package: 'gtsummary'
```

```
## The following object is masked from 'package:MASS':
      select
```

colon |> tbl_summary(include = c(sex,age, stage,subsite))

Characteristic	N = 15,564 ¹
sex	
Male	6,340 (41%)
Female	9,224 (59%)
age	71 (62, 78)
stage	
Unknown	2,356 (15%)
Localised	6,274 (40%)
Regional	1,787 (11%)
Distant	5,147 (33%)
subsite	
Coecum and ascending	5,576 (36%)
Transverse	2,734 (18%)
Descending and sigmoid	6,270 (40%)
Other and NOS	984 (6.3%)
¹ n (%); Median (Q1, Q3)	

colon |> tbl_cross(row= stage, col= subsite) |> add_p()

	subsite					
	Coecum and ascending	Transverse	Descending and sigmoid	Other and NOS	Total	p-value ¹
stage						<0.001
Unknown	756	369	879	352	2,356	
Localised	2,235	1,025	2,761	253	6,274	
Regional	798	291	621	77	1,787	
Distant	1,787	1,049	2,009	302	5,147	
Гotal	5,576	2,734	6,270	984	15,564	

colon |> tbl_summary(include = c(age,stage,subsite), by = sex) |> add_p()

Characteristic	Male N = 6,340 ¹	Female N = 9,224 ⁷	p-value ²
age	69 (60, 76)	73 (64, 79)	<0.001
stage			0.004
Unknown	885 (14%)	1,471 (16%)	
Localised	2,620 (41%)	3,654 (40%)	
Regional	715 (11%)	1,072 (12%)	
Distant	2,120 (33%)	3,027 (33%)	
subsite			<0.001
Coecum and ascending	2,132 (34%)	3,444 (37%)	
Transverse	1,139 (18%)	1,595 (17%)	
Descending and sigmoid	2,671 (42%)	3,599 (39%)	
Other and NOS	398 (6.3%)	586 (6.4%)	
¹ Median (Q1, Q3); n (%) ² Wilcoxon rank sum test; Pear	rson's Chi-squa	red test	