MSCR 509: Homework Assignment 1

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Assignment Description

The treatment regimen for patients who have been diagnosed as having cancer of the prostate is crucially dependent upon whether or not the cancer has spread to the surrounding lymph nodes. Indeed, a laparotomy (a surgical incision into the abdominal cavity) may be performed to ascertain the extent of this nodal involvement. However, there are a number of variables that are indicative of nodal involvement that can be measured noninvasively, and the aim of a study reported by Brown (1980) was to determine whether a combination of variables could be used to forecast whether or not the cancer has spread to the lymph nodes. The response variable (Y) is the presence or absence of nodal involvement (Y: 1 = present, 0 = absent).

The prognostic variables considered are:

- AGE age of patient at diagnosis (in years)
- ACID level of serum acid phosphatase (in King-Armstrong units)
- XRAY the result of an X-ray examination (0 = negative, 1 = positive)
- SIZE the size of the tumor as determined by a rectal examination (0 = small, 1 = large)
- GRADE a summary of the pathological grade of the tumor determined from a biopsy (0 = less serious, 1 = more serious)
- SES income (high, middle, low)

Data intake

The data frame to be loaded can be seen as below, in its raw form.

```
# Show first few lines
head(prostate)
```

```
## # A tibble: 6 x 11
       age acid xray size grade
##
                                                 id income
                                                            qual enzyme ses
                                           V
                                                     <dbl> <dbl>
##
     <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <
                                                                    <dbl> <chr>
## 1
        66
             0.48
                       0
                              0
                                           0
                                                  1
                                                          1 0.122
                                                                     2.40 high
## 2
        68
            0.56
                       0
                              0
                                    0
                                           0
                                                  2
                                                          1 0.387
                                                                     3.12 high
            0.5
                                    0
                                                  3
        66
                       0
                                                          1 0.970
                                                                     2.55 high
            0.52
                              0
                                    0
                                           0
                                                  4
## 4
        56
                       0
                                                          1 0.353
                                                                     2.50 high
        58
             0.5
                              0
                                    0
                                           0
                                                  5
## 5
                       0
                                                         1 0.119
                                                                     3.21 high
                              0
                                    0
                                           0
                                                          1 0.648
            0.49
                                                  6
                                                                     3.23 high
```

This will need to be modified to be *publication ready* by adding in the appropriate labels.

Table presentation

```
# Data set
df <- prostate</pre>
```

```
## Relabel the variables for prettier data
# Outcome variable
df\$y \leftarrow factor(df\$y, levels = c(0,1),
               labels = c("No Spread", "Lymph Node Involvment"))
attr(df$y, "label") <- "Nodal Spread"</pre>
# Age
attr(df$age, "label") <- "Age (years)"</pre>
# Acid phosphatase
attr(df$acid, "label") <- "Acid Phosphatase (King-Armstrong units)"</pre>
# Xray
df$xray <- factor(df$xray, levels = c(0,1),</pre>
                   labels = c("Normal x-Ray", "Abnormal X-Ray"))
attr(df$xray, "label") <- "X-Ray Findings"</pre>
# Size
df$size <- factor(df$size, levels = c(0,1),</pre>
                   labels = c("Small", "Larger"))
attr(df$size, "label") <- "Tumor Size"</pre>
# Grade
df$grade <- factor(df$grade, levels = c(0,1),</pre>
                    labels = c("Less Serious Pathology", "Serious Pathology"))
attr(df$grade, "label") <- "Pathological Grade Finding"</pre>
# SES
df$ses <- ordered(df$ses, levels = c("low", "middle", "high"),</pre>
                   labels = c("Low SES", "Middle SES", "High SES"))
attr(df$ses, "label") <- "Socioeconomic Class (SES)"</pre>
# Correct shape of table
compareGroups(y ~ age + acid + xray + size + grade + ses, data = df) %>%
    createTable(., show.p.overall = TRUE) %>%
    export2md(., size = 8,
                 caption = "Difference in Characteristics Between Prostate Cancer with and Without Noda
```

Table 1: Difference in Characteristics Between Prostate Cancer with and Without Nodal Involvement

	No Spread N=56	Lymph Node Involvment N=36	p.overall
Age (years)	60.0 (5.54)	58.2 (6.80)	0.201
Acid Phosphatase (King-Armstrong units)	0.66 (0.29)	0.77 (0.22)	0.046
X-Ray Findings:	()	(- ,	< 0.001
Normal x-Ray	51 (91.1%)	17(47.2%)	
Abnormal X-Ray	5 (8.93%)	19 (52.8%)	
Tumor Size:		,	0.005
Small	32 (57.1%)	9 (25.0%)	
Larger	24 (42.9%)	27 (75.0%)	
Pathological Grade Finding:	,	, ,	0.045
Less Serious Pathology	38 (67.9%)	16 (44.4%)	
Serious Pathology	18 (32.1%)	20 (55.6%)	
Socioeconomic Class (SES):	,	` ,	0.005
Low SES	23 (41.1%)	19 (52.8%)	
Middle SES	8 (14.3%)	12 (33.3%)	
High SES	25 (44.6%)	5 (13.9%)	