Project - STAT 151A

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```
load(url("http://www.stat.berkeley.edu/users/nolan/data/baseball2012.rda"))
baseball = as_tibble(baseball)
```

Data Exploration and Feature Creation

1)

The first step is to clean the `baseball` data by removing unecessary explanatory variables and entries missing a `salary (observed Yi)` value.

```
baseball = baseball %>% dplyr::select(-c("ID", "yearID", "teamID", "lgID", "nameFirst",
                                          "nameLast", "G_batting")) # remove unecessary variables
baseball = baseball %>% drop_na(salary) # remove units with no salary values
```

Next, I followed the author's process in creating new features as decribed in the textbook.

```
baseball = baseball %>% mutate(AVG = CH/CAB,
                               OBP = 100*(CH + CBB)/(CAB + CBB),
                               CAB.avg  = CAB/years,
                               CH.avg   = CH/years,
                               CHR.avg  = CHR/years,
                               CR.avg   = CR/years,
                               CRBI.avg = CRBI/years)
```

Finally, I cleaned the `Position` and `Years` explanatory variables through reimpementing them as dummy variables.

According to Fox's description of his analysis, he mentions **middle infielders** as players who consistently played second base or shortstop so I classified all individuals with either position as such.

```
new.pos = c()
MI = c("12", "1S", "23", "2B", "2S", "3S", "O2", "SS")
C  = c("C", "C1", "OC")
CF = c("CF")

# Assign new factor assignment for MI (middle infielders), C (catcher),
#  CF (center field), and O (other)
for (i in baseball$POS){
  if      (i %in% MI) { new.pos = c(new.pos, "MI") }
  else if (i %in% C)  { new.pos = c(new.pos, "C")  }
  else if (i %in% CF) { new.pos = c(new.pos, "CF") }
  else                { new.pos = c(new.pos, "O")  }
}

baseball$POS = relevel(factor(new.pos), "O")
```

```r
new.years = c()
neg.cont  = 6
neg.sal   = 3

for (i in baseball$years){
  if      (i >= neg.cont) { new.years = c(new.years, ".cont") }
  else if (i >= neg.sal)  { new.years = c(new.years, ".sal")   }
  else                    { new.years = c(new.years, "other")        }
}

baseball$neg = relevel(factor(new.years), "other")
```

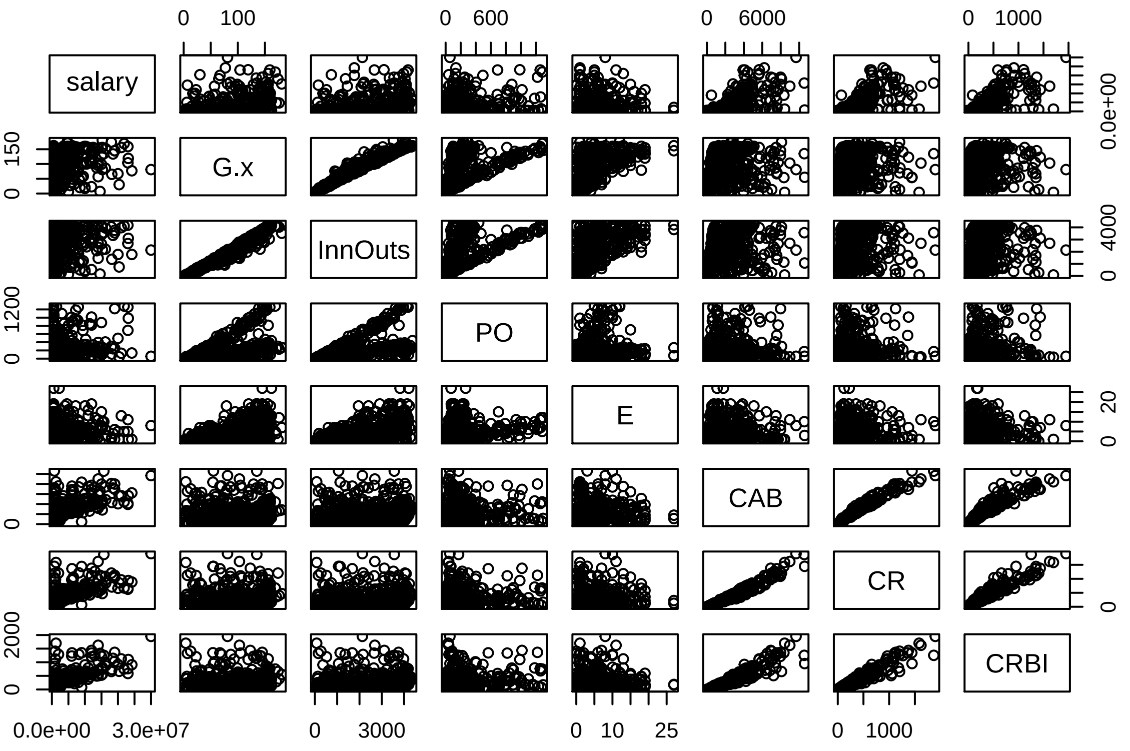
```r
lm.fit = lm(salary ~ ., data = baseball)
new.baseball = as_tibble(model.matrix(lm.fit)[,-1])
new.baseball$salary = baseball$salary
```

Now that we have completed the feature creation process, the next step is to analyze the data itself.

Firstly, I'll look at the the structure of the data itself and how the different variables are associated with each other. Since there are a lot of explanatory variables within the data, I will select a few key variables I believe to be the most influential in the model and investigate the structure.

Note: - `G.x` = Position played at specified position - `InnOut` = Time played in the field expressed as outs - `PO` = Putouts - `E` = Errors - `CAB` = Career at bats - `CR` = Career runs - `CRBI` = Career runs batted in

```r
pairs(salary ~ G.x + InnOuts + PO + E + CAB + CR + CRBI, data = new.baseball)
```



From observing the paired structures of data it is evident that some features are uncorrelated whereas others are strongly correlated. However, this is mostly expected as certain features relate to one another. For example, a player's career at bats would be associated with his career runs or career runs batted in since all tie into a players capability of scoring bases.

This indicates a possible issue in inference of coefficients through linear modeling since the standard error calculation will be grossly inflated.

In addition, I noticed some of the variables have a stronger correlation with the salary than that of other variables. For example, `G.x` and `InnOuts` do not seem to have a strong association with the other variables whereas `CAB`, `CR`, and `CRBI` have comparitively stronger correlations with each other. This indicates some sort of variable selection and model pruning may be of benefit.

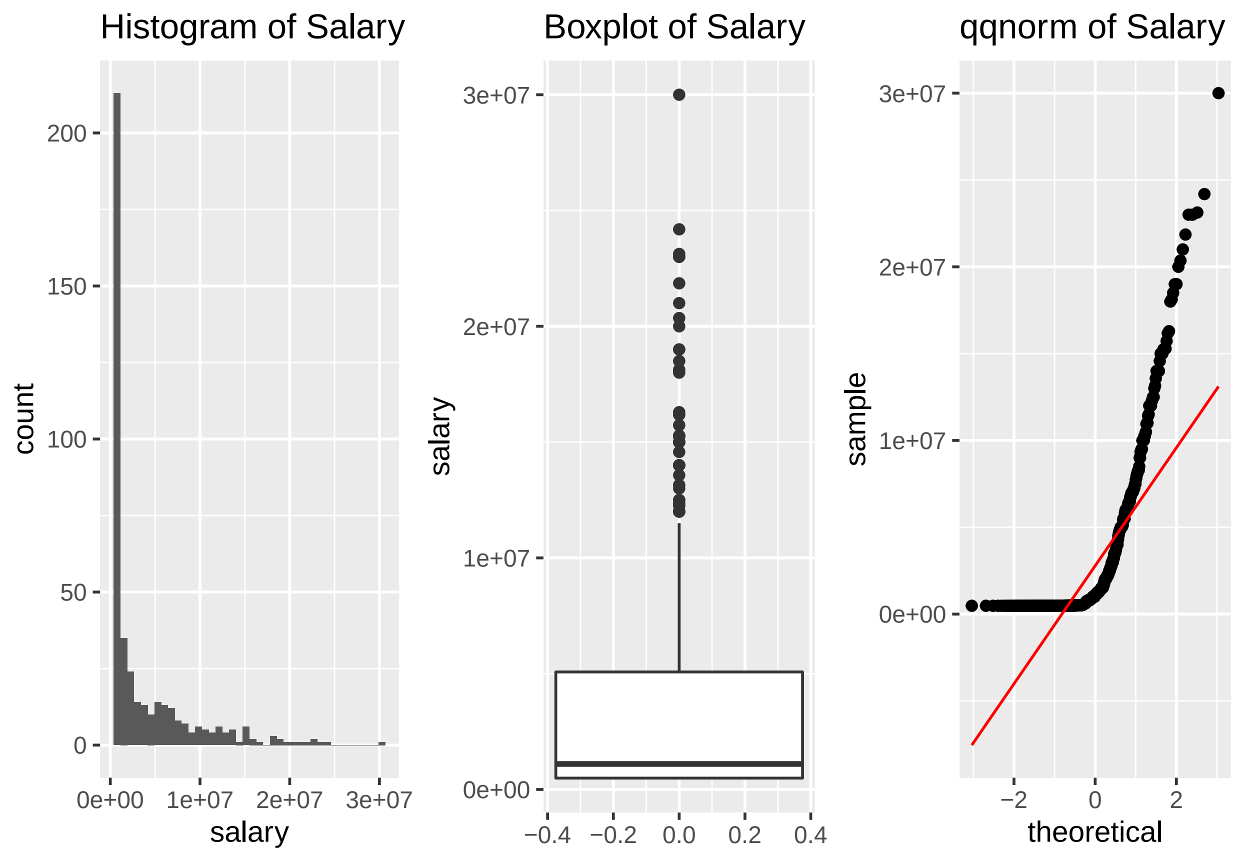
Next, I'd like to look into whether the data is distributed normally as per an assumption of guassian distributed errors in linear modelling.

```r
sal1 = ggplot(data = new.baseball, aes(x = salary)) +
  geom_histogram(bins = 40) +
  ggtitle("Histogram of Salary")

sal2 = ggplot(data = new.baseball, aes(y = salary)) +
  geom_boxplot() +
  ggtitle("Boxplot of Salary")

sal3 = ggplot(data = new.baseball, aes(sample=salary)) +
  geom_qq() +
  geom_qq_line(color = "red") +
  ggtitle("qqnorm of Salary")

grid.arrange(sal1, sal2, sal3, nrow = 1)
```



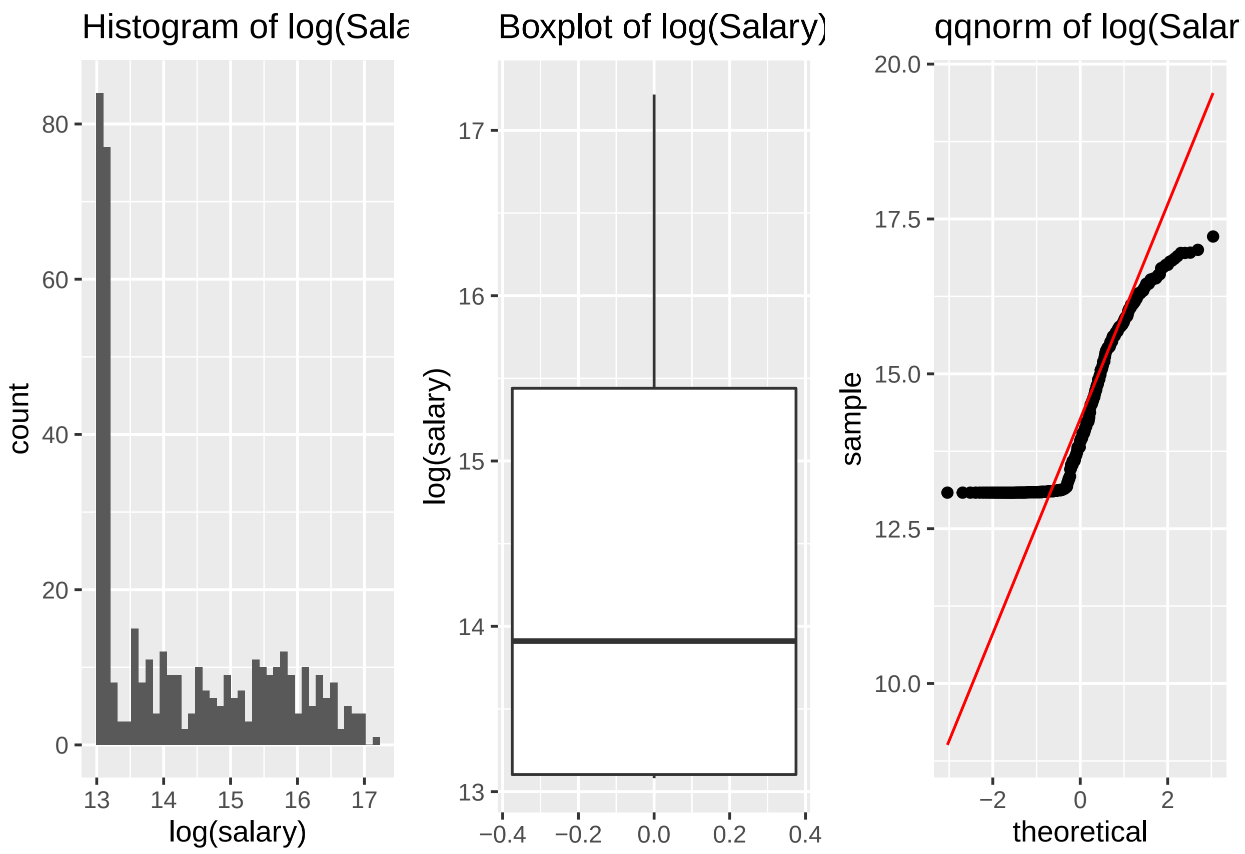
The plots above show that the observed outcome values are not distributed normally. Hence, some sort of transformation of the data is necessary in order to use linear modelling for proper inference.

```r
log.sal1 = ggplot(data = new.baseball, aes(x = log(salary))) +
  geom_histogram(bins=40) +
  ggtitle("Histogram of log(Salary)")

log.sal2 = ggplot(data = new.baseball, aes(y = log(salary))) +
  geom_boxplot() +
  ggtitle("Boxplot of log(Salary)")
```

```r
log.sal3 = ggplot(data = new.baseball, aes(sample=log(salary))) +
  geom_qq() +
  geom_qq_line(color = "red") +
  ggtitle("qqnorm of log(Salary)")

grid.arrange(log.sal1, log.sal2, log.sal3, nrow = 1)
```



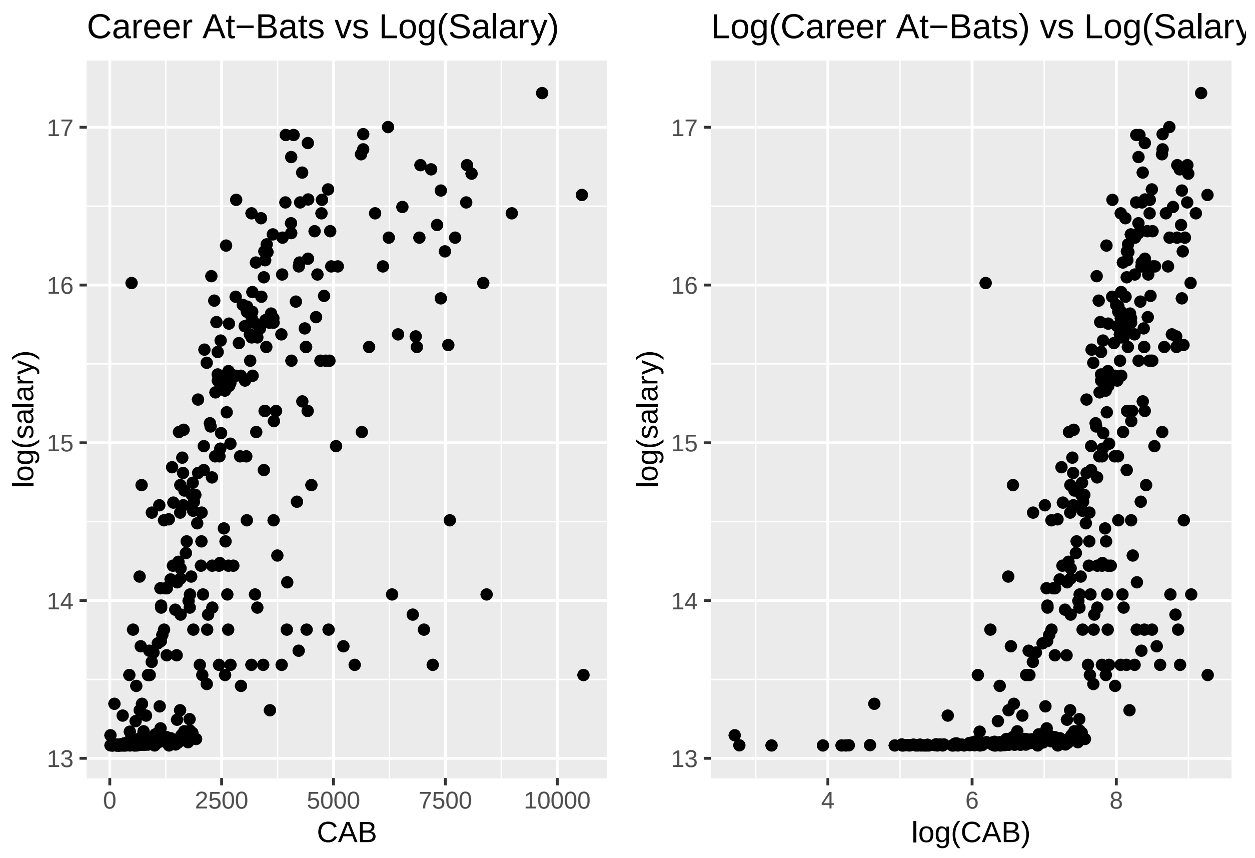
Fox mentions log transforming the `salary` data in his linear modelling analysis for this data and this is in line with the observed plots above. The histogram of the original salaries is right skewed whereas the histogram of the log transformed salaries is somewhat more stabilized. In addition, the boxplots and qqnorm plots shed more insight into how normality is improved through log transforming the data and so it would be better to use the log transormed salary values as the outcome instead.

Fox also suggests log transforming some feature variables (i.e. years in the majors, career at-bats) through preliminary examination, and so I will do the same to carry forward analysis in a similar manner. An argument for why this may be beneficial is that it might garner a stronger linear relationship between the seemingly most influential explanatory variables and the salary and thus improving the model's predictive capability overall which in turn helps in equalizing the variance.

```r
cab.plot1 = ggplot(data = new.baseball, aes(x = CAB, y = log(salary))) +
  geom_point() +
  ggtitle(label = "Career At-Bats vs Log(Salary)")

cab.plot2 = ggplot(data = new.baseball, aes(x = log(CAB), y = log(salary))) +
  geom_point() +
  ggtitle(label = "Log(Career At-Bats) vs Log(Salary)")
```

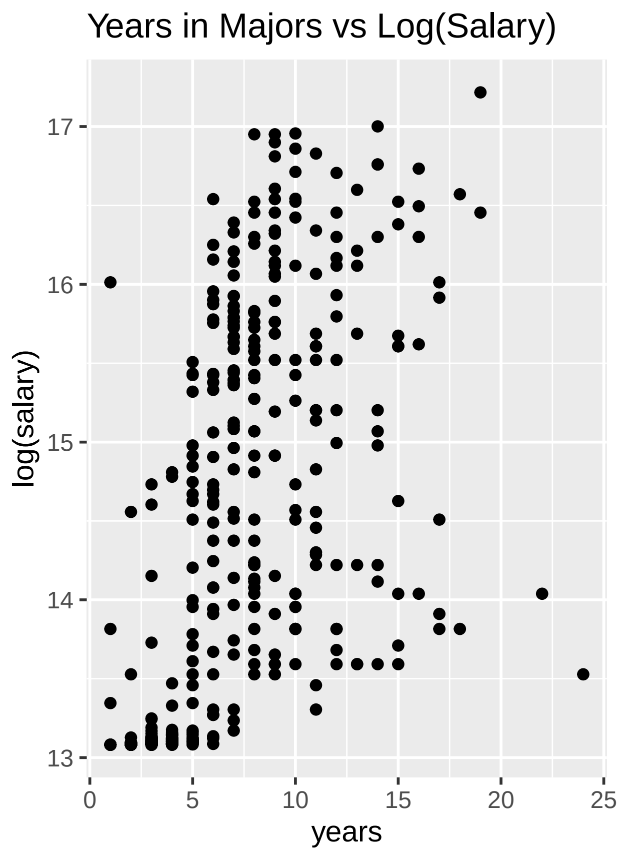
```r
grid.arrange(cab.plot1, cab.plot2, nrow = 1)
```

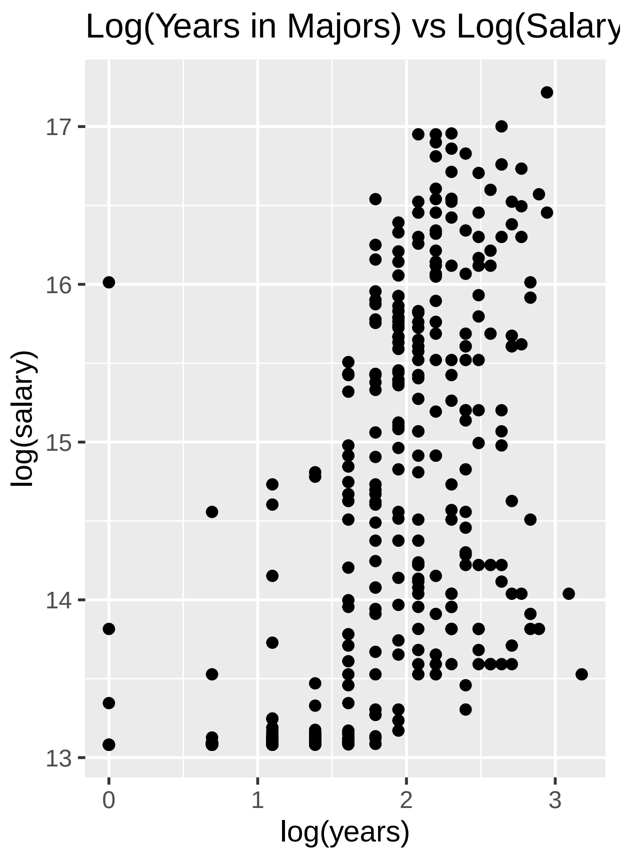


```r
yrs.plot1 = ggplot(data = new.baseball, aes(x = years, y = log(salary))) +
  geom_point() +
  ggtitle(label = "Years in Majors vs Log(Salary)")

yrs.plot2 = ggplot(data = new.baseball, aes(x = log(years), y = log(salary))) +
  geom_point() +
  ggtitle(label = "Log(Years in Majors) vs Log(Salary)")

grid.arrange(yrs.plot1, yrs.plot2, nrow = 1)
```





```
new.baseball$log.CAB    = log(new.baseball$CAB)
new.baseball$log.years  = log(new.baseball$years)
new.baseball$log.salary = log(new.baseball$salary)
new.baseball = new.baseball %>% dplyr::select(-c(CAB, years, salary))
```

Data Analysis

1)

For the first of the project, I will be fitting a simple model that predicts `log(salary)` from the **dummy variables** for `years in majors` and `log(career runs)`, allowing for an interactio between the feature variables.

```
dat1 = new.baseball %>% dplyr::select(log.salary, CR, neg.sal, neg.cont)
simple.model = lm(log.salary ~ log(1+CR)*(neg.cont + neg.sal), data = dat1)
simple.model
```

```

Call:
lm(formula = log.salary ~ log(1 + CR) * (neg.cont + neg.sal),
    data = dat1)

Coefficients:
         (Intercept)           log(1 + CR)              neg.cont
            12.88064               0.08743              -3.96431
             neg.sal  log(1 + CR):neg.cont   log(1 + CR):neg.sal
            -1.06871               0.94036               0.24940
```

2)

Although I have fitted the simple model above, I want to check for any outliers, high leverage points, and influential observations for further evaulation of the simple model. All criterions in determining such observations will be in line with what Fox suggests using.

```
hat.vals = hatvalues(simple.model)
stud.res = studres(simple.model)
cook.dis = cooks.distance(simple.model)

measures = tibble(Hat.Values = hat.vals,
                  Studentized.Residuals = stud.res,
                  Cooks.Distance = cook.dis)
```

First, I'd like to take a look at the **high leverage** points, which are observations with explanatory variables markedly different from that of the average. In terms of numerical cutoffs for diagnostic statistics, *hat values exceeding* ***twice*** *the average hat value* `(k+1)/n` *are noteworthy.*

```
h.3 = 3*length(simple.model$coefficients)/nrow(new.baseball)
high.leverage = measures[hat.vals > h.3,]
high.leverage %>% head(n = 5)
```

```
# A tibble: 5 x 3
  Hat.Values Studentized.Residuals Cooks.Distance
       <dbl>                 <dbl>          <dbl>
1     0.0477                 1.87       0.0289
2     0.0486                 0.525      0.00235
3     0.0565                 0.0299     0.00000898
4     0.0428                -0.305      0.000695
5     0.0733                 0.0664     0.0000582
```

There appears to be ***17*** data points which have a relatively high leverage.

In addition to high leverage points, I'll analyze discrepant observations to detect outliers within the data through utilizing **studentized residuals** with a numerical cutoff of `|t-test statistic| > 2`

```
outliers = measures[abs(stud.res) > 2,]
outliers %>% head(n = 5)
```

```
# A tibble: 5 x 3
  Hat.Values Studentized.Residuals Cooks.Distance
       <dbl>                 <dbl>          <dbl>
1    0.0258                   2.41        0.0254
2    0.00468                 -2.18        0.00370
3    0.0274                   4.12        0.0768
4    0.00804                 -3.01        0.0120
5    0.00476                 -2.54        0.00510
```

There are ***26*** observations which are determined to be outliers.

Although I have determined observations that have high leverage or are outliers, what I am most conerned about are the subset of these points which have an influence on the determined coefficients of the model. Such points greatly alter the predictive capability of the simple model and thus cannot be overlooked.

Through recommendation by Fox, the criterion I will be using to determine highly influential points is `D_i > 4/(n-k-1)`

```r
cook.cutoff = 4/(nrow(new.baseball)-length(simple.model$coefficients))
influential.points = measures[cook.dis > cook.cutoff,]
influential.points %>% arrange(desc(Cooks.Distance))
```

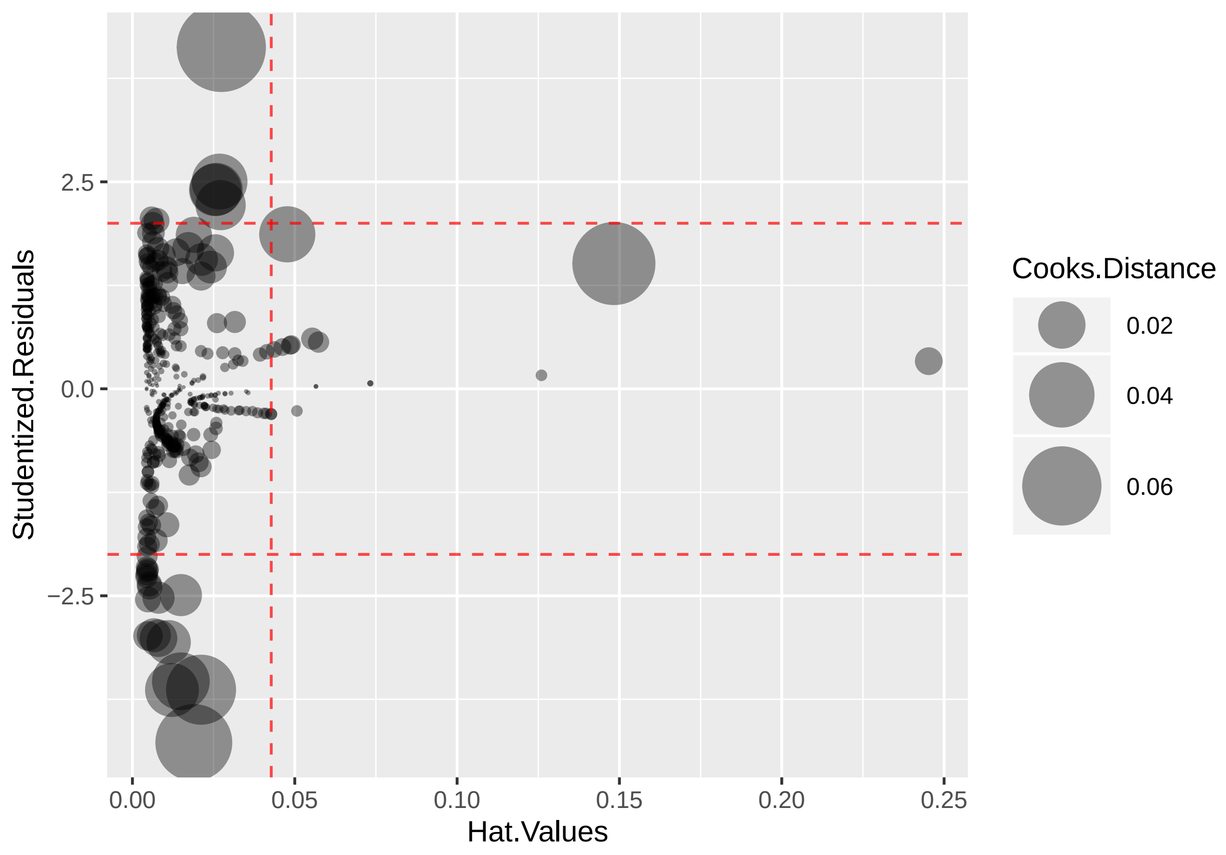
```
# A tibble: 16 x 3
   Hat.Values Studentized.Residuals Cooks.Distance
        <dbl>                 <dbl>          <dbl>
 1    0.0274                   4.12         0.0768
 2    0.148                    1.51         0.0663
 3    0.0189                  -4.27         0.0563
 4    0.0211                  -3.63         0.0462
 5    0.0149                  -3.53         0.0306
 6    0.0477                   1.87         0.0289
 7    0.0268                   2.50         0.0285
 8    0.0122                  -3.64         0.0264
 9    0.0258                   2.41         0.0254
10    0.0255                   2.40         0.0249
11    0.0272                   2.22         0.0227
12    0.0112                  -3.06         0.0173
13    0.0149                  -2.49         0.0155
14    0.00804                 -3.01         0.0120
15    0.0256                   1.64         0.0118
16    0.0189                   1.86         0.0111
```

It appears there are ***16*** influential points within the dataset. I'm not very surprised as players' baseball data is incredibly varied and prone to uniquely performing individuals, thus causing there to be influential observations.

To better grasp the idea behind the information produced above, the following is a plot of the `hat` values representing the leverage with relation to the `studentized residuals`. Each circle represents an obervation with it's area proportional to it's calculated `Cook's Distance`.

Note: The horizontal line represents `3 times the average hat value` and the 2 vertical lines mark `t-test statistics of -2 and 2`.

```r
ggplot(aes(x = Hat.Values, y = Studentized.Residuals, size = Cooks.Distance), data = measures) +
  geom_point(alpha=0.4) + scale_size(range = c(0, 15)) +
  geom_vline(xintercept = 3*6/421, color = 'red', alpha = .7, linetype = "dashed") +
  geom_hline(yintercept = -2, color='red', alpha = .7, linetype = "dashed") +
  geom_hline(yintercept = 2, color='red', alpha = .7, linetype = "dashed")
```



Lastly, I'd like to take a look at these influential points and observe the feature values.

```
new.baseball[cook.dis > cook.cutoff,]
```

```
# A tibble: 16 x 44
    POSC POSCF POSMI   G.x    GS InnOuts    PO     A     E    DP   G.y    AB
   <dbl> <dbl> <dbl> <dbl> <dbl>   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
 1     0     0     1   153   147    3953   289   398     8    96   153   607
 2     0     0     0   154   149    4030   297     8     6     1   155   560
 3     0     0     0   104   102    2702   221     9     3     0   129   487
 4     0     0     0    74    56    1523    85    91     6     7   113   278
 5     0     0     0    13    12     269    86     3     0     7    60    89
 6     0     0     0   131   131    3383   207     7     4     0   135   518
 7     0     0     0    93    76    1953   131     2     0     0   130   384
 8     0     0     0    70    55    1358    81     3     1     2    94   233
 9     0     0     0    50    49    1239    37    81     8     7    74   273
10     0     0     0   107    98    2399   156     1     1     0   130   394
11     0     0     1   158   157    4176   227   434    12    93   158   593
12     0     0     0   105   103    2562    73   208    13    14   108   396
13     0     1     0   125   122    3220   339     6     4     3   128   516
14     0     0     0     4     4      81    35     2     1     4    58   163
15     0     0     1    55    37    1063    58   103     3    19    60   153
16     0     0     0     1     0       0     0     0     0     0    78     2
# ... with 32 more variables: R <dbl>, H <dbl>, X2B <dbl>, X3B <dbl>, HR <dbl>,
#   RBI <dbl>, SB <dbl>, CS <dbl>, BB <dbl>, SO <dbl>, IBB <dbl>, HBP <dbl>,
#   SH <dbl>, SF <dbl>, GIDP <dbl>, CH <dbl>, CHR <dbl>, CR <dbl>, CRBI <dbl>,
#   CBB <dbl>, AVG <dbl>, OBP <dbl>, CAB.avg <dbl>, CH.avg <dbl>,
#   CHR.avg <dbl>, CR.avg <dbl>, CRBI.avg <dbl>, neg.cont <dbl>, neg.sal <dbl>,
#   log.CAB <dbl>, log.years <dbl>, log.salary <dbl>
```

Through manual obervation of the feature vaues of these influential points it appears that these observation have much higher or lower values for certain features such as `G.x`, `InnOuts`, `PO` compared to those of non-influential points. The table of encompassing Cook's Distance with Leverage Hat Value and Studentized Residuals do a much better job providing insight into why a point is influential, however.

3)

```r
all.fit = lm(log.salary ~ ., data = new.baseball)
summary(all.fit)
```

```

Call:
lm(formula = log.salary ~ ., data = new.baseball)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.63762 -0.31246  0.06423  0.31947  1.51943 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept) 14.2702482  0.5240182  27.232  < 2e-16 ***
POSC        -0.0426637  0.1518434  -0.281 0.778886    
POSCF       -0.0268705  0.1494435  -0.180 0.857403    
POSMI        0.0780726  0.1027617   0.760 0.447882    
G.x          0.0039647  0.0046887   0.846 0.398321    
GS          -0.0062069  0.0109901  -0.565 0.572567    
InnOuts      0.0001452  0.0004900   0.296 0.767175    
PO           0.0002185  0.0003197   0.683 0.494768    
A            0.0003503  0.0008990   0.390 0.697023    
E            0.0026430  0.0104617   0.253 0.800687    
DP          -0.0042697  0.0029331  -1.456 0.146306    
G.y         -0.0118007  0.0033350  -3.538 0.000453 ***
AB           0.0065267  0.0016068   4.062 5.92e-05 ***
R           -0.0093742  0.0063621  -1.473 0.141465    
H           -0.0065391  0.0048988  -1.335 0.182729    
X2B         -0.0063059  0.0070018  -0.901 0.368367    
X3B          0.0006723  0.0184037   0.037 0.970877    
HR          -0.0102874  0.0121474  -0.847 0.397599    
RBI          0.0039993  0.0057956   0.690 0.490580    
SB          -0.0013153  0.0058889  -0.223 0.823382    
CS          -0.0276728  0.0185481  -1.492 0.136549    
BB           0.0056713  0.0039142   1.449 0.148192    
SO          -0.0012819  0.0019363  -0.662 0.508337    
IBB          0.0093704  0.0136217   0.688 0.491937    
HBP          0.0036525  0.0110282   0.331 0.740680    
SH           0.0093553  0.0161609   0.579 0.563012    
SF           0.0014463  0.0204969   0.071 0.943783    
GIDP        -0.0086423  0.0093884  -0.921 0.357889    
CH           0.0021802  0.0010424   2.091 0.037157 *  
CHR          0.0076434  0.0038205   2.001 0.046147 *  
CR          -0.0022325  0.0016753  -1.333 0.183480    
CRBI        -0.0026771  0.0018308  -1.462 0.144502    
CBB         -0.0011839  0.0005733  -2.065 0.039609 *  
AVG          0.5156185  3.3598388   0.153 0.878113    
OBP         -0.0025942  0.0291738  -0.089 0.929190    
CAB.avg     -0.0042031  0.0030973  -1.357 0.175589    
CH.avg      -0.0133749  0.0133111  -1.005 0.315641    
CHR.avg     -0.0709547  0.0361205  -1.964 0.050219 .  
CR.avg       0.0534385  0.0151076   3.537 0.000455 ***
```

```
CRBI.avg     0.0469204  0.0166307   2.821 0.005036 **
neg.cont     1.2416258  0.2315305   5.363 1.43e-07 ***
neg.sal      0.0541843  0.1522766   0.356 0.722168
log.CAB     -0.3434284  0.1713702  -2.004 0.045783 *
log.years    0.2802810  0.2404271   1.166 0.244447
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5807 on 377 degrees of freedom
Multiple R-squared:  0.8082,    Adjusted R-squared:  0.7863
F-statistic: 36.95 on 43 and 377 DF,  p-value: < 2.2e-16
```

From former analysis I am aware of collinearity within the explanatory variables and hence inflated standard errors. However, it appears several of the coefficients are statistically significant and that the omnibus F-statistic is also statistically significant. In addition, the adjusted R-squared value is a bit lower than the R-squared of the model. This all leans toward the argument of the model requiring the explanatory variables but with possible variable selection that may improve the model's regression capability.

4)

Next, I'll be finding the best **10** models for each model size using **forward selection**. I won't output the results of the summary as they are a bit extensive and in anyways I will select 5 specific models from all of these models in the next part.

```r
best10 = regsubsets(log.salary ~ .,
                    data   = new.baseball,
                    nvmax  = 43,
                    nbest  = 10,
                    method = "forward")
# summary(best10)
```

5)

```r
lowest5.bic  = sort(summary(best10)$bic)[1:5]
top5.bic.loc = order(summary(best10)$bic)[1:5]
top5.models  = summary(best10)$which[top5.bic.loc,]
models = c()

for(i in 1:nrow(top5.models)){
  cat(sprintf("Model %d:", i))
  cat(sprintf("\nBIC: %f", lowest5.bic[i]))

  models = c(models, list(names(which(top5.models[i,]))[-1]))
  cat(sprintf("\nFeatures: %s", paste(models[[i]], collapse = ", ")))
  cat("\n\n")
}
```

```
Model 1:
BIC: -586.225215
Features: GS, G.y, AB, R, BB, CH, CBB, CAB.avg, CR.avg, CRBI.avg, neg.cont, log.CAB, log.years

Model 2:
BIC: -583.405937
Features: GS, R, CH, CBB, CAB.avg, CR.avg, CRBI.avg, neg.cont, log.CAB, log.years

Model 3:
BIC: -582.502074
Features: G.x, GS, G.y, AB, R, BB, CH, CBB, CAB.avg, CR.avg, CRBI.avg, neg.cont, log.CAB, log.years

Model 4:
BIC: -582.402615
Features: GS, G.y, AB, R, X2B, BB, CH, CBB, CAB.avg, CR.avg, CRBI.avg, neg.cont, log.CAB, log.years

Model 5:
BIC: -582.248168
Features: GS, G.y, AB, R, H, BB, CH, CBB, CAB.avg, CR.avg, CRBI.avg, neg.cont, log.CAB, log.years
```

6)

Using BIC as a criterion may not be sufficient and hence I will use 10-fold cross validation to re-rank the 5 models determined above. Rather than hard-code the k-fold procedure, I will be using built-in functions available in the caret package.

The output will show the features of each model for clarity as well as the previously determined BIC value and the newly determined mean-MSE (through 10-fold CV).

```r
# 10-fold cross validation setup
train.control = trainControl(method = "cv", number = 10)
mean.mse = c()

for (i in 1:5){
  model.to.train.test  = as.formula(paste("log.salary ~",
                                    paste(models[[i]], collapse=" + ")))
  model.trained.tested = train(model.to.train.test,
                               data = new.baseball,
                               method = "lm",
                               trControl = train.control)
  mean.mse =  c(mean.mse, model.trained.tested$results[[2]]**2)

  cat(sprintf("Model %d:\nBIC: %f\nFeature: %s\n--> MSE: %f\n\n",
            i,
            lowest5.bic[i],
            paste(models[[i]], collapse = ", "),
            mean.mse[i]))
}
```

```
Model 1:
BIC: -586.225215
Feature: GS, G.y, AB, R, BB, CH, CBB, CAB.avg, CR.avg, CRBI.avg, neg.cont, log.CAB, log.years
--> MSE: 0.344688

Model 2:
BIC: -583.405937
Feature: GS, R, CH, CBB, CAB.avg, CR.avg, CRBI.avg, neg.cont, log.CAB, log.years
--> MSE: 0.356297

Model 3:
BIC: -582.502074
Feature: G.x, GS, G.y, AB, R, BB, CH, CBB, CAB.avg, CR.avg, CRBI.avg, neg.cont, log.CAB, log.years
--> MSE: 0.341484

Model 4:
BIC: -582.402615
Feature: GS, G.y, AB, R, X2B, BB, CH, CBB, CAB.avg, CR.avg, CRBI.avg, neg.cont, log.CAB, log.years
--> MSE: 0.343067

Model 5:
BIC: -582.248168
Feature: GS, G.y, AB, R, H, BB, CH, CBB, CAB.avg, CR.avg, CRBI.avg, neg.cont, log.CAB, log.years
--> MSE: 0.349388
```

From the values above, it is evident the following is the model with the lowest mean-MSE:

```r
i = which.min(mean.mse)
cat(sprintf("Model %d:\nBIC: %f\nFeature: %s\n--> MSE: %f",
            i,
            lowest5.bic[i],
            paste(models[[i]], collapse = ", "),
            mean.mse[i]))
```

```
Model 3:
BIC: -582.502074
Feature: G.x, GS, G.y, AB, R, BB, CH, CBB, CAB.avg, CR.avg, CRBI.avg, neg.cont, log.CAB, log.years
--> MSE: 0.341484
```

Through many repetitions it appears that the choice of model changes (stemming from the variabibity in how data is partitioned in 10-fold CV). It appears that it isn't always the case the model with lowest BIC has the lowest mean-MSE.

7)

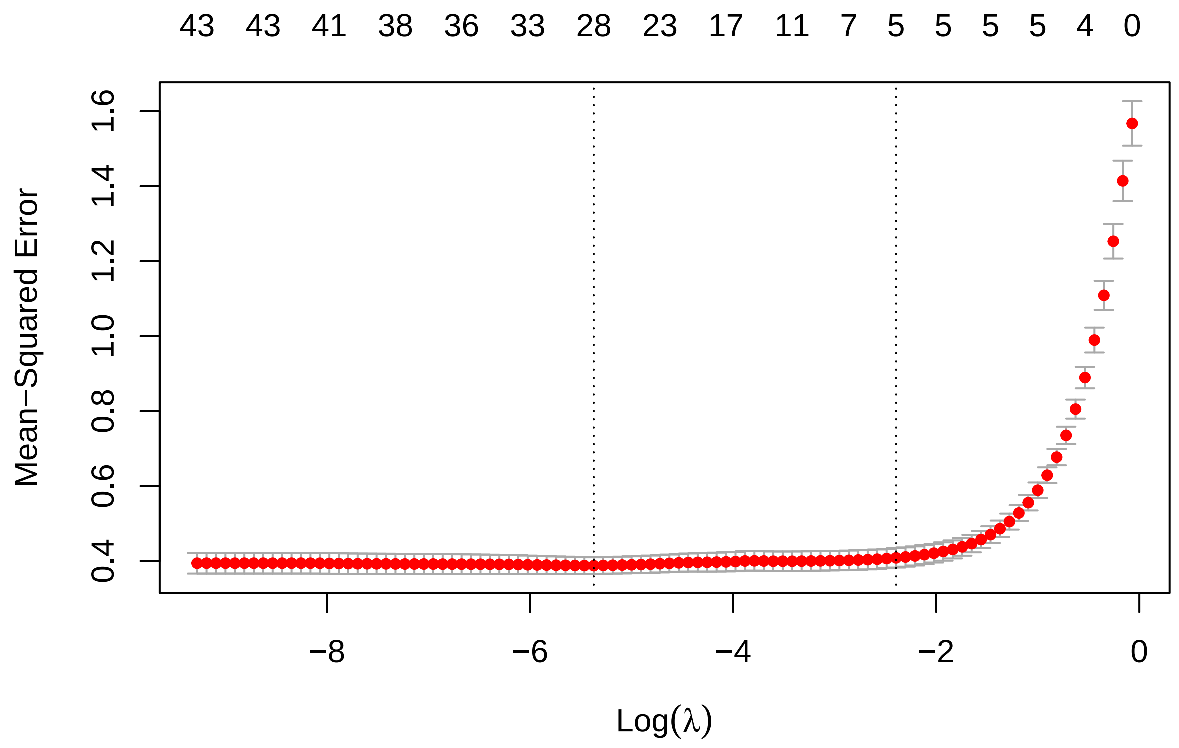
In determining the value of the hyperparameter `lambda` to use for the LASSO model (original feature variables), I will be using 10-fold cross validation with an average MSE for the criterion.

```r
X = new.baseball %>% dplyr::select(-c(log.salary)) %>% as.matrix()
y = new.baseball$log.salary

lasso.model    = glmnet(x = X, y = y, alpha = 1)
cv.lasso.model = cv.glmnet(x = X, y = y, alpha = 1, nfolds = 10)
```

The following is the plot of the `log of the hyperparameter lambda` with respect to the resulting `average MSE`.

```r
plot(cv.lasso.model)
```



The left-most dashed vertical line in the plot represents the lambda corresponding to the minimum MSE whereas the right-most dashed vertical line represents the lambda 1 standard error away from the min lambda.

I believe the data intrinsically contains a lot of collinear explanatory variables and would like to reduce the number of features used in model prediction. I believe the lambda corresponding to the minimum MSE would be suitable as it not only performs variable selection through utilizing just 28 feature variables for regression rather than all 43, it also has the lowest MSE out of all other possible lambda hyperparameter values and thus seems to be the best choice in prediction.

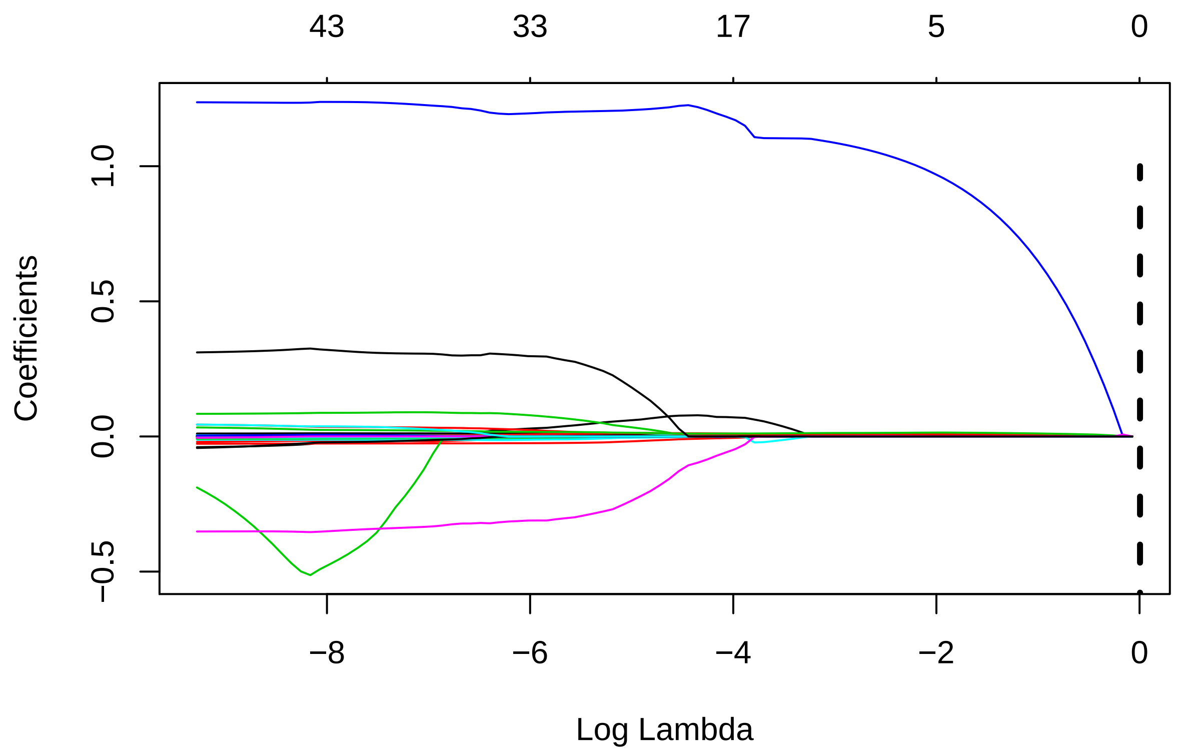
The value of `lambda` I will use for the LASSO model is the following:

```
best.lasso.lambda = cv.lasso.model$lambda.min
best.lasso.lambda
```

```
[1] 0.00464043
```

The following is a visualization of how different values of lambda influence the coefficient values of the regression model:

```
plot(lasso.model, xvar = "lambda", )
lines(c(best.lasso.lambda, best.lasso.lambda), c(-1, 1), lty = "dashed", lwd = 3)
```



Lastly, using the hyperparameter value of lambda specified above, I'd like to analyze which coefficients are retained through implicit variable selection of LASSO.

```
best.lasso.coefs = predict(lasso.model, type = 'coefficients', s = best.lasso.lambda)
best.lasso.coefs
```

```
44 x 1 sparse Matrix of class "dgCMatrix"
                         1
(Intercept)  1.392036e+01
POSC         4.819060e-02
POSCF        .
POSMI        5.389061e-02
G.x          7.148762e-04
```

```
GS             .
InnOuts        8.253821e-05
PO             2.248210e-05
A              .
E              .
DP            -1.477442e-03
G.y           -6.109311e-03
AB             1.353649e-03
R              .
H              .
X2B           -2.861447e-03
X3B            .
HR            -8.452375e-03
RBI            1.503657e-03
SB            -2.788658e-04
CS            -2.260273e-02
BB             4.007321e-03
SO             .
IBB            8.545359e-03
HBP            1.690402e-03
SH             7.327374e-03
SF             1.045290e-02
GIDP           .
CH             1.384542e-05
CHR            9.327663e-04
CR             8.514916e-04
CRBI           .
CBB           -1.026886e-03
AVG            .
OBP            .
CAB.avg       -3.898353e-04
CH.avg         .
CHR.avg        .
CR.avg         1.469175e-02
CRBI.avg       1.560951e-02
neg.cont       1.203511e+00
neg.sal        .
log.CAB       -2.850154e-01
log.years      2.542452e-01
```

From analyzing the output summary of the LASSO model coefficients, it appears 28 explanatory variables have non-zero coeffients.

I chose the `lambda` value corresponding to the minimum MSE value for the LASSO model, which is the following value:

```
best.lasso.lambda
```

```
[1] 0.00464043
```

In the previous part, I found the top 5 models with the lowest BIC and then used 10-fold cross validation with a mean-MSE criterion to find the best model with the lowest MSE. I'd like compare the that result with the model I determined using LASSO.

```r
min(cv.lasso.model$cvm) <= mean.mse
```

```
[1] FALSE FALSE FALSE FALSE FALSE
```

The expression above compared the MSE of the LASSO model to the other 5 models but it turns out LASSO produces a regression model with a higher MSE compared to all.