Library Imports

```
library(glue)
library(rpart)
library(RColorBrewer)
library(randomForest)
library(caret)

options(repr.plot.width=10, repr.plot.height=5)

set.seed(20)
options(warn=-1)
```

```
Loading required package: lattice
Loading required package: ggplot2

Attaching package: 'ggplot2'

The following object is masked from 'package:randomForest':

margin
```

Question 9.1

Using the same crime data set uscrime.txt as in Question 8.2, apply Principal Component Analysis and then create a regression model using the first few principal components. Specify your new model in terms of the original variables (not the principal components), and compare its quality to that of your solution to Question 8.2. You can use the R function prcomp for PCA. (Note that to first scale the data, you can include scale. = TRUE to scale as part of the PCA function. Don't forget that, to make a prediction for the new city, you'll need to unscale the coefficients (i.e., do the scaling calculation in reverse)!)

A few helper functions I need in order to evaluate the regression models are defined first.

The root mean squared error (RMSE) and the mean absolute error (MAE) functions are defined below. These functions will be used to understand the performance of the models. The lower the error the better the model.

```
# RMSE function
rmse <- function(resids) {
    sqrt(mean(resids^2))
}
# MAE function
mae <- function(resids) {
    mean(abs(resids))
}</pre>
```

The data is read in and defined as a data frame.

```
crime_data <- read.table('../data/9.luscrimeSummer2018.txt', sep='', header=TRUE)</pre>
```

The sample data that the final model is going to be used to predict on is:

```
M <- 14.0

So <- 0

Ed <- 10.0

Po1 <- 12.0

Po2 <- 15.5

LF <- 0.640

M.F <- 94.0

Pop <- 150

NW <- 1.1

U1 <- 0.120

U2 <- 3.6

Wealth <- 3200

Ineq <- 20.1

Prob <- 0.04

Time <- 39.0

sample_data <- data.frame(M,So,Ed,Po1,Po2,LF,M.F,Pop,NW,U1,U2,Wealth,Ineq,Prob,Time)
```

From homework 3 question 8.2, the best performing model I found had the following formula:

```
Crime ~ M + Ed + Po1 + U2 + Ineq + Prob + Time
```

The model from question 8.2 is defined and evaluated below.

```
model_8 <- lm(formula=Crime ~ M + Ed + Po1 + U2 + Ineq + Prob + Time,
data=crime_data)

sample_prediction <- round(predict(model_8, sample_data), 3)

print(glue("Prediction for the crime rate for the sample data is
{sample_prediction}"))
print("Model from Question 8.2")
print(summary(model_8))</pre>
```

```
(Intercept) -4911.094 960.729 -5.112 8.79e-06 ***

M 106.659 33.877 3.148 0.003144 **

Ed 189.408 48.288 3.922 0.000345 ***

Po1 115.704 13.993 8.269 4.16e-10 ***

U2 88.720 41.364 2.145 0.038249 *

Ineq 67.728 14.083 4.809 2.28e-05 ***

Prob -4249.756 1880.672 -2.260 0.029502 *

Time -2.310 5.538 -0.417 0.678810
---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 202.8 on 39 degrees of freedom

Multiple R-squared: 0.7669, Adjusted R-squared: 0.7251

F-statistic: 18.33 on 7 and 39 DF, p-value: 1.553e-10
```

The model from 8.2 had an adjusted R-squared of 0.7251 and a residual standard error of 202.8. Also, the predicted crime rate for the fictional city was 1285.283. This will be the baseline to compare the PCA models too.

Perform scaling and PCA on the crime data.

```
pca_crime <- prcomp(crime_data[,-16], scale=TRUE)

# Grab just the transformed data
pca_data <- pca_crime$x
pca_data <- cbind(pca_data, Crime=crime_data$Crime)</pre>
```

How many components to use will be determined by testing a few different values. I'll use values between 3 and 6 components and evaluate each model with a 5 fold cross validation.

In order to limit the amount of results shown, I will calculate the RMSE and MAE for each model and only for the best model will I show the summary of the model.

```
for (n in 3:6) {
    # Shuffle data
    shuffled_df <- pca_data[sample(nrow(pca_data)), c(1:n, 16)]

# 5 fold split
    folds <- cut(seq(1, nrow(pca_data)), breaks=5, labels=FALSE)

# For each fold, train and test on Linear Regression algorithm
    resids <- c(1:nrow(pca_data))
    preds <- c(1:nrow(pca_data))
    for (i in 1:5) {
        test_indices <- which(folds=i, arr.ind=TRUE)
        test_data <- as.data.frame(shuffled_df[test_indices, ])
        train_data <- as.data.frame(shuffled_df[-test_indices, ])

        temp_fit <- lm(formula=Crime ~., data=train_data)

# Perform prediction step on test data since model was fit using the</pre>
```

```
3-Component PCA
RMSE: 352.926
MAE: 281.825
4-Component PCA
RMSE: 350.955
MAE: 278.844
5-Component PCA
RMSE: 275.227
MAE: 222.131
6-Component PCA
RMSE: 273.053
MAE: 220.4
```

Based on the RMSE and MAE above, a 6-component PCA model is the best performing given a 5-fold CV. Using the full dataset, a final model with 6 components will be trained.

```
model_6_comp <- lm(formula=Crime ~ ., data=as.data.frame(pca_data[, c(1:6, 16)]))
# Transform the sample data into the same PCA vector space by first scaling the data
# around the center and the same scale range used when transforming the original dataset.
# Then multiply by the rotation.
sample_data_transformed <- scale(sample_data, pca_crime$center, pca_crime$scale)
%*% pca_crime$rotation

sample_prediction_pca <- round(predict(model_6_comp,
as.data.frame(t(sample_data_transformed[, 1:6]), 3)))

print(glue("Prediction for the crime rate for the sample data is
{sample_prediction_pca}"))
print("6-Component PCA Model")
print(summary(model_6_comp))</pre>
```

```
Prediction for the crime rate for the sample data is 1248
[1] "6-Component PCA Model"

Call:
lm(formula = Crime ~ ., data = as.data.frame(pca_data[, c(1:6,
```

```
16)]))
Residuals:
  Min 1Q Median 3Q
-377.15 -172.23 25.81 132.10 480.38
Coefficients:
          Estimate Std. Error t value Pr(>|t|)
PC1
PC2
PC3
                       25.23 0.998 0.32409
                      33.14 2.095 0.04252 *
36.50 -6.275 1.94e-07 ***
PC4
PC5
PC6
                       48.04 -1.253 0.21734
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
Residual standard error: 242.3 on 40 degrees of freedom
Multiple R-squared: 0.6586, Adjusted R-squared: 0.6074
F-statistic: 12.86 on 6 and 40 DF, p-value: 4.869e-08
```

The adjusted R-squared was 0.6074 and the residual standard error was 242.3 which are both worse than the values for the model generated in question 8.2. Interestingly, the predicted crime rate was 1248 which was very similar to the 1285.283 value predicted by the model in question 8.2.

This shows that the componenets generated by PCA are not the best predictors when predicting crime rate. Using the original predictors give better results.

Question 10.1

Using the same crime data set uscrime.txt as in Questions 8.2 and 9.1, find the best model you can using 1. a regression tree model, and 2. a random forest model.

In R, you can use the tree package or the rpart package, and the randomForest package. For each model, describe one or two qualitative takeaways you get from analyzing the results (i.e., don't just stop when you have a good model, but interpret it too).

Regression Tree Model

For the regression tree model, I decided to use the rpart library to build the model. The original dataset without any feature selection was used. Also, the complexity parameter (CP) is used to prune the tree. The printcp() function shows the CP at each split in the tree.

My understanding of what this function is doing is that the tree is built out completely and then the tree is then pruned by removing the splits in data one by one. As each split is being removed, the CP is calculated. The CP has a minimum threshold of 0.01 and if the next split does not improve the R^2 value by 0.01 then the model is finished.

The model below ended up with 3 splits before hitting the 0.01 threshold value. At each split the

cross-validated error (xerror) is calculated and the tree at which the minimum xerror is found is the optimal model to use.

```
tree <- rpart(formula=Crime ~., method="anova", data=crime_data)

printcp(tree)
```

Interestingly, only the NW, Pol and Pop features were used in creating the tree model. The optimal model, surprisingly, is when there is no split in the data.. Excluding this case leaves the tree with one split to have the lowest xerror value.

```
plotcp(tree)
```



The plotcp() function above plots the cross-validated error against the CP values from the tree model as its being pruned.

```
# prune the tree
pfit<- prune(tree, cp=tree$cptable[which.min(tree$cptable[,"xerror"]),"CP"])</pre>
```

```
printcp(pfit)
```

```
Regression tree:

rpart(formula = Crime ~ ., data = crime_data, method = "anova")

Variables actually used in tree construction:

character(0)

Root node error: 6880928/47 = 146403
```

Pruning the tree model so that the minimum xerror is used yields a single node with no split which is not very helpful.

The takeaways from this exercise is that a single decision tree is not very good at predicting something complicated like crime rate. Even with more splits in the data, the cross-validated error did not decrease which means the variation in the data is not properly accounted for in the model.

Random Forest Model

The random forest algorithm was used with every predictor.

```
# Shuffle data
shuffled df <- crime data[sample(nrow(crime data)),]</pre>
# 5 fold split
folds <- cut(seq(1, nrow(crime data)), breaks=5, labels=FALSE)</pre>
# For each fold, train and test on RF algorithm
resids <- c(1:nrow(crime data))</pre>
preds <- c(1:nrow(crime data))</pre>
for (i in 1:5) {
    test indices <- which(folds==i, arr.ind=TRUE)</pre>
    test data <- as.data.frame(shuffled df[test indices, ])</pre>
    temp fit <- randomForest(formula=Crime ~., data=train data)</pre>
    # Perform prediction step on test data since model was fit using the training
data
    preds[test indices] <- predict(temp fit, test data)</pre>
    resids[test indices] <- test data$Crime - preds[test indices]</pre>
    print(glue("Fold Number: {i}"))
    print(importance(temp fit))
overall rmse <- round(rmse(resids), 3)</pre>
overall mae <- round(mae(resids), 3)</pre>
print(glue("RMSE: {overall rmse}"))
print(glue("MAE: {overall_mae}"))
```

```
556680.976
Po1
         513041.557
Po2
LF
         125229.082
          67854.648
M.F
         432049.094
Pop
         253423.385
          90634.725
          96753.300
         408001.602
Wealth
         101494.754
Ineq
         710772.143
Prob
Time
         283103.346
Fold Number: 2
      IncNodePurity
           20368.92
          193300.66
         1084819.76
Po1
          967155.71
          344948.39
M.F
          264777.86
          320945.27
Pop
NW
           700732.17
          109479.21
          134470.84
Wealth
          530953.04
Ineq
Prob
          669296.24
Time
           178030.68
Fold Number: 3
      IncNodePurity
          186292.21
           19158.05
          145769.43
          905368.34
Po1
Po2
          873145.60
LF
          141066.78
          313657.72
M.F
          215304.27
Pop
         268758.21
          83337.07
           91243.93
Wealth
         238473.49
         142973.55
Ineq
Prob
          475601.06
           94612.52
Time
Fold Number: 4
       IncNodePurity
           156631.6
            25960.6
           165800.3
Po1
           1167463.3
Po2
          1114705.9
           166693.8
LF
M.F
            196358.4
           173793.3
Pop
NW
           345801.2
```

```
113838.9
          126682.8
Wealth
Ineq
Prob
Time 159722.7
Fold Number: 5
     IncNodePurity
         151906.26
          15248.45
         218176.11
Po1
        1062797.14
Po2
         246356.17
LF
M.F
         214079.08
Pop
         439809.10
         396089.21
NW
         121920.63
U2 338742.99
Wealth 591686.08
         207998.16
Ineq
         594151.59
Prob
         175687.24
Time
RMSE: 314.025
MAE: 226.957
```

The RMSE and the MAE are comparable to the model generated in question 9 using PCA and linear regression.

Looking at the importance of each predictor for each k-fold step, the predictors that show up most frequently are police protection investment (Po1 and Po2), probability of being imprisoned (prob), and median wealth (Wealth). These make sense since economic stability affects police funding, which in turn probably affects the number of people being imprisoned.

One thing I wish that random forest could show is the positive or negative correlation a predictor has with the response variable.

Question 10.2

Describe a situation or problem from your job, everyday life, current events, etc., for which a logistic regression model would be appropriate. List some (up to 5) predictors that you might use.

ANSWER:

A situation where logistic regression might be useful in my everyday life is predicting the probability that I snooze my alarm in the morning before work. The 5 predictors that I might use to model this situation are:

- 1. How many hours did I sleep last night?
- 2. Is it the weekend or a weekday?

- 3. Do I have a meeting I cannot be late for?
- 4. Did I go out drinking last night?
- 5. Was yesterday an especially tiring day?

Question 10.3

1. Using the GermanCredit data set germancredit.txt from

http://archive.ics.uci.edu/ml/machine-learning-databases/statlog/german / (description at http://archive.ics.uci.edu/ml/datasets/Statlog+%28German+Credit+Data%29), use logistic regression to find a good predictive model for whether credit applicants are good credit risks or not. Show your model (factors used and their coefficients), the software output, and the quality of fit. You can use the glm function in R. To get a logistic regression (logit) model on data where the response is either zero or one, use family=binomial(link="logit") in your glm function call.

```
german_data <- read.table('../data//10.3germancreditSummer2018_numeric.txt', sep='', header=FALSE)
german_data$V25 <- german_data$V25 - 1
```

Using a 5-fold cross-validation, the logistic regression algorithm was implemented with every predictor. The summary of the model at each fold in the cross-validation step is shown.

```
# Shuffle data
shuffled df <- german data[sample(nrow(german data)),]</pre>
# 5 fold split
folds <- cut(seq(1, nrow(german data)), breaks=5, labels=FALSE)</pre>
# For each fold, train and test on Linear Regression algorithm
resids <- c(1:nrow(german data))</pre>
preds <- c(1:nrow(german data))</pre>
    test indices <- which(folds==i, arr.ind=TRUE)</pre>
    test data <- as.data.frame(shuffled df[test indices, ])</pre>
    train data <- as.data.frame(shuffled df[-test indices, ])</pre>
    temp fit <- glm(V25 ~., family=binomial(link='logit'), data=train data)</pre>
    # Perform prediction step on test data since model was fit using the training
data
   preds[test_indices] <- predict(temp_fit, newdata=test_data, type='response')</pre>
    print(glue("Fold number {i}"))
    print(summary(temp fit))
binary preds <- ifelse(preds > 0.5,1,0)
```

```
Fold number 1
Call:
glm(formula = V25 ~ ., family = binomial(link = "logit"), data = train_data)
```

```
1Q Median
                      3Q
-2.1716 -0.7298 -0.4182 0.8177 2.5710
Coefficients:
         Estimate Std. Error z value Pr(>|z|)
(Intercept) 3.570281 1.343636 2.657 0.007880 **
        V4
         0.003639 0.004372 0.832 0.405160
         -0.168531 0.086785 -1.942 0.052145 .
V6
        V8
        -0.009899 0.091469 -0.108 0.913817
         0.148272 0.109908
V9
                         1.349 0.177321
V10
        -0.018791 0.009674 -1.942 0.052083 .
V11
        0.172163 0.193264 0.891 0.373027
V12
         0.039297 0.268766 0.146 0.883754
V14
        -0.221315 0.211779 -1.045 0.296009
         -1.366569 0.722074 -1.893 0.058416 .
V15
V16
V17
        -0.955346   0.377364   -2.532   0.011353 *
         1.090891 0.464125 2.350 0.018752 *
V18
V19
         -0.174579 0.367848 -0.475 0.635075
V21
V22
         -0.091596 0.358584 -0.255 0.798385
V23
        -0.113003 0.291557 -0.388 0.698323
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 984.07 on 799 degrees of freedom
Residual deviance: 762.13 on 775 degrees of freedom
AIC: 812.13
Number of Fisher Scoring iterations: 5
Fold number 2
glm(formula = V25 ~ ., family = binomial(link = "logit"), data = train data)
Deviance Residuals:
       1Q Median
                     3Q
                             Max
-2.1186 -0.6809 -0.3879 0.7471 2.6178
Coefficients:
         Estimate Std. Error z value Pr(>|z|)
(Intercept) 2.824790 1.324471 2.133 0.032944 *
         0.038095 0.009772 3.898 9.68e-05 ***
         V3
```

Deviance Residuals:

```
0.002328 0.004445 0.524 0.600440
         V6
         -0.098075 0.084987 -1.154 0.248500
         0.027609 0.094224 0.293 0.769511
V8
         0.141688 0.112265 1.262 0.206916
V9
V10
         -0.001783 0.009852 -0.181 0.856353
V11
        0.131410 0.180447 0.728 0.466462
V13
        -0.349757 0.218278 -1.602 0.109079
V14
V15
        -1.181958 0.668007 -1.769 0.076830 .
V16
V17
         V18
         1.149912 0.455245 2.526 0.011540 *
         1.272696 0.645370 1.972 0.048605 *
V19
         0.472985 0.406256 1.164 0.244322
V21
         -0.316872 0.678792 -0.467 0.640630
V22
V23
V24
         0.005350 0.289491 0.018 0.985255
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 972.25 on 799 degrees of freedom
Residual deviance: 723.60 on 775 degrees of freedom
AIC: 773.6
Number of Fisher Scoring iterations: 5
Fold number 3
Call:
glm(formula = V25 \sim ., family = binomial(link = "logit"), data = train data)
Deviance Residuals:
                              Max
-2.2406 -0.6978 -0.4007 0.7375 2.6816
Coefficients:
         Estimate Std. Error z value Pr(>|z|)
(Intercept) 3.182748 1.288165 2.471 0.01348 *
         V1
V3
         1.099 0.27166
V4
         0.004779 0.004347
         V6
         -0.215977 0.133412 -1.619 0.10548
V8
         -0.005577 0.092102 -0.061 0.95171
V9
         0.106497 0.114224 0.932 0.35116
         -0.008031 0.009893 -0.812 0.41695
V10
V11
         V12
         0.265954 0.181115 1.468 0.14199
         0.105416 0.268319 0.393 0.69441
V13
```

```
V14
          V15
          -1.176222 0.633404 -1.857 0.06331 .
V16
V17
          -1.339983 0.422687 -3.170 0.00152 **
V18
          1.056840 0.460653 2.294 0.02178 *
          1.476987 0.627844 2.352 0.01865 *
V19
          -0.094189 0.422387 -0.223 0.82354
          -0.356566 0.369183 -0.966 0.33413
V21
V22
V23
          -0.148466 0.371885 -0.399 0.68973
          -0.177599 0.303494 -0.585 0.55843
V24
Signif. codes: 0 \*** 0.001 \** 0.01 \*' 0.05 \.' 0.1 \' 1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 972.25 on 799 degrees of freedom
Residual deviance: 733.26 on 775 degrees of freedom
AIC: 783.26
Number of Fisher Scoring iterations: 5
Fold number 4
Call:
glm(formula = V25 ~ ., family = binomial(link = "logit"), data = train data)
Deviance Residuals:
        1Q Median
                                 Max
-2.1284 -0.7160 -0.4293 0.7784 2.5806
Coefficients:
(Intercept) 3.007958 1.334627 2.254 0.024210 *
          -0.535891 0.080714 -6.639 3.15e-11 ***
V1
          -0.401864 0.097910 -4.104 4.05e-05 ***
          0.004642 0.004089 1.135 0.256218
V4
V6
          -0.158269 0.084010 -1.884 0.059575 .
V7
          -0.143882 0.130888 -1.099 0.271650
V8
          0.193243 0.111983 1.726 0.084412 .
V10
          -0.008548 0.009222 -0.927 0.353979
          V11
V12
          0.261923 0.176513 1.484 0.137842
V13
          0.013331 0.256113 0.052 0.958486
          -0.157867 0.211424 -0.747 0.455253
V14
V15
          -1.690419 0.691375 -2.445 0.014485 *
          V16
          -0.865764 0.379802 -2.280 0.022637 *
V17
V18
          0.670760 0.464135 1.445 0.148406
V19
          1.134520 0.621714 1.825 0.068027 .
          0.568704 0.393079 1.447 0.147955
          0.070850 0.348357 0.203 0.838835
          -0.302046 0.679323 -0.445 0.656588
V22
          V23
```

```
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 963.44 on 799 degrees of freedom
Residual deviance: 753.12 on 775 degrees of freedom
Number of Fisher Scoring iterations: 5
Fold number 5
Call:
glm(formula = V25 ~ ., family = binomial(link = "logit"), data = train data)
Deviance Residuals:
            Median 3Q
                             Max
-2.2420 -0.7161 -0.4024 0.7628 2.6580
Coefficients:
         Estimate Std. Error z value Pr(>|z|)
(Intercept) 3.635328 1.324215 2.745 0.006046 **
        V1
         V4
         0.005916 0.004179 1.416 0.156866
        V6
        V7
        -0.230813 0.129834 -1.778 0.075444 .
         0.016800 0.091208 0.184 0.853861
V8
V9
         V10
        -0.009812 0.009203 -1.066 0.286345
        V11
V12
V13
        0.189689 0.263675 0.719 0.471891
        -0.377618 0.216551 -1.744 0.081197 .
V14
V15
        -1.861453 0.694944 -2.679 0.007394 **
V16
         V17
V18
        1.365786 0.638255 2.140 0.032365 *
         0.379289 0.402723 0.942 0.346289
V21
V22
V23
        -0.130295 0.362669 -0.359 0.719396
        -0.013896 0.283952 -0.049 0.960970
V24
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 993.74 on 799 degrees of freedom
Residual deviance: 748.09 on 775 degrees of freedom
AIC: 798.09
```

0.031114 0.288309 0.108 0.914060

V24

```
Number of Fisher Scoring iterations: 5
```

After the training and validation step, the final model using all available data is built.

```
final model <- glm(V25 ~., family=binomial(link='logit'), data=german data)
# Perform prediction step on test data since model was fit using the training data
final preds <- predict(final model, newdata=german data, type='response')</pre>
print(summary(final model))
binary final preds <- ifelse(final preds > 0.5,1,0)
Call:
glm(formula = V25 ~ ., family = binomial(link = "logit"), data = german data)
Deviance Residuals:
   Min 1Q Median
                                   Max
-2.1675 -0.7082 -0.4129 0.7890 2.6220
Coefficients:
           Estimate Std. Error z value Pr(>|z|)
(Intercept) 3.231152 1.171518 2.758 0.005814 **
          -0.575461 0.071065 -8.098 5.60e-16 ***
V1
           0.034089 0.008587 3.970 7.20e-05 ***
          -0.373500 0.086952 -4.295 1.74e-05 ***
V4
          0.004294 0.003801 1.130 0.258535
          -0.145873 0.075689 -1.927 0.053945 .
V6
V7
          -0.211760 0.114816 -1.844 0.065132 .
           0.011961 0.081916 0.146 0.883906
V8
V9
           0.167814 0.099152 1.692 0.090552 .
          -0.009432 0.008478 -1.112 0.265925
          V11
V12
          0.208317 0.161724 1.288 0.197710
V13
          0.084091 0.234396 0.359 0.719778
          -0.271055 0.191837 -1.413 0.157674
V14
V15
V16
          V17
V18
V19
          1.337142 0.556082 2.405 0.016191 *
          0.318564 0.359882 0.885 0.376053
          -0.132711 0.317574 -0.418 0.676028
V21
V22
          -0.063827 0.319117 -0.200 0.841473
V23
          -0.050021 0.258695 -0.193 0.846678
V24
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 1221.73 on 999 degrees of freedom
Residual deviance: 935.33 on 975 degrees of freedom
AIC: 985.33
```

```
confusionMatrix(data = as.factor(binary final preds), as.factor(german data$V25))
```

```
Reference
Prediction 0 1
0 629 144
1 71 156

Accuracy: 0.785
95% CI: (0.7582, 0.8101)
No Information Rate: 0.7
P-Value [Acc > NIR]: 9.063e-10

Kappa: 0.4498
Mcnemar's Test P-Value: 9.091e-07

Sensitivity: 0.8986
Specificity: 0.5200
Pos Pred Value: 0.8137
Neg Pred Value: 0.6872
Prevalence: 0.7000
Detection Rate: 0.6290
Detection Prevalence: 0.7730
Balanced Accuracy: 0.7093

'Positive' Class: 0
```

The overall accuracy of the model is 78.5% and the most important predictors seem to be status of existing checking account, credit history, and credit amount.

2. Because the model gives a result between 0 and 1, it requires setting a threshold probability to separate between "good" and "bad" answers. In this data set, they estimate that incorrectly identifying a bad customer as good, is 5 times worse than incorrectly classifying a good customer as bad. Determine a good threshold probability based on your model.

Based on the confusion matrix above, there are 71 data points being misclassified as "bad" credit risks when they're actually "good" credit risks and 144 data points being misclassified as "good" credit risks when they're actually "bad" credit risks. So, the cost for this model becomes:

```
Cost = 71 \times 1 + 144 \times 5 = 791
```

I want to minimize this by removing as many false positives as possible without putting too many people into the false negative category. Its important to note that the positive class is 0 in this case. This means I need a lower threshold value in order for a person to be classified as a "good" credit risk. If the positive class was 1 then I would need a higher threshold value.

```
new_preds <- ifelse(final_preds > 0.2,1,0)
confusionMatrix(data = as.factor(new_preds), as.factor(german_data$V25))
```

```
Reference
Prediction 0 1
0 412 45
1 288 255

Accuracy: 0.667
95% CI: (0.6368, 0.6962)
No Information Rate: 0.7
P-Value [Acc > NIR]: 0.9891

Kappa: 0.3561
Mcnemar's Test P-Value: <2e-16

Sensitivity: 0.5886
Specificity: 0.8500
Pos Pred Value: 0.9015
Neg Pred Value: 0.4696
Prevalence: 0.7000
Detection Rate: 0.4120
Detection Prevalence: 0.4570
Balanced Accuracy: 0.7193

'Positive' Class: 0
```

With a threshold of 0.2, I got 45 false positives and 288 false negatives for a cost of 513, which is more than 35% lower than the cost at a 0.5 threshold. However, its important to note that the number of true positives goes down *significantly* from 629 to 412 users. This is critical because if I keep increasing the threshold lower and lower, then the cost may decrease but I may end up having no users that are correctly predicted to be a "good" credit risk.