# Risk Stratification

Risk stratification of diabetic patients for readmission

Logistic Regression

```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 3.5.2
```

```
library(ggplot2)
library(dplyr)
library(stringr)
library(caTools)
library(rpart)
library(caret)
library(car)
library(MASS)
```

Load the cleaned data

```
data <- read.csv("data/data_cleaned.csv", header=TRUE,
                 na.strings = c("NA","na","","  ","?"), stringsAsFactors = FALSE)
```

```
# save the ID of patients
ID <- data$ID
# Remove the ID before analysis
data <- data[2:42]
```

```
# change readmitted to numeric column
table(data$readmitted)
```

```
##
##    NO   YES
## 53316 46176
```

```
data$readmitted <- as.factor(data$readmitted)


# splitting the data between train and test
set.seed(100)

indices = sample.split(data$readmitted, SplitRatio = 0.7)

train = data[indices,]

test = data[!(indices),]
```

# Logistic Regression

```
model_1 <- glm(readmitted ~ ., data = train, family = "binomial")


#Initial model summary
summary(model_1)
```

```
##
## Call:
## glm(formula = readmitted ~ ., family = "binomial", data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.8776  -1.0473  -0.7875   1.1854   2.0948
##
## Coefficients:
##                            Estimate Std. Error z value Pr(>|z|)
## (Intercept)              -1.308e+00  2.682e-01  -4.875 1.09e-06 ***
## gender                    4.945e-02  1.623e-02   3.046 0.002320 **
## time_in_hospital          3.449e-02  9.697e-03   3.557 0.000375 ***
## num_lab_procedures        4.288e-02  9.271e-03   4.625 3.74e-06 ***
## num_procedures           -5.379e-02  9.056e-03  -5.939 2.86e-09 ***
## num_medications           2.023e-02  1.069e-02   1.892 0.058479 .
## number_outpatient         9.453e-02  9.447e-03  10.006  < 2e-16 ***
## number_emergency          2.046e-01  1.417e-02  14.433  < 2e-16 ***
## number_inpatient          4.904e-01  1.099e-02  44.628  < 2e-16 ***
## number_diagnoses          1.827e-01  9.511e-03  19.213  < 2e-16 ***
## change                   -4.819e-02  2.216e-02  -2.175 0.029657 *
## diabetesMed               2.687e-01  2.489e-02  10.794  < 2e-16 ***
## raceAsian                -2.980e-01  1.024e-01  -2.910 0.003618 **
## raceCaucasian             1.904e-02  2.114e-02   0.901 0.367777
## raceHispanic             -1.161e-01  5.904e-02  -1.967 0.049189 *
```

```
## raceOther                 -2.517e-01  6.865e-02  -3.667 0.000246 ***
## age2                       8.271e-01  2.766e-01   2.990 0.002787 **
## age3                       7.099e-01  2.627e-01   2.703 0.006882 **
## age4                       7.671e-01  2.612e-01   2.936 0.003321 **
## age5                       8.787e-01  2.616e-01   3.359 0.000782 ***
## age6                       9.247e-01  2.616e-01   3.535 0.000408 ***
## age7                       8.675e-01  2.619e-01   3.313 0.000923 ***
## admission_type_id3        -1.638e-01  2.688e-02  -6.094 1.10e-09 ***
## admission_type_id4        -1.960e-01  7.507e-01  -0.261 0.793991
## admission_type_id5         3.102e-01  3.648e-02   8.504  < 2e-16 ***
## admission_type_id7        -1.448e+01  3.604e+02  -0.040 0.967954
## discharge_disposition_id2  5.169e-05  1.903e-02   0.003 0.997833
## discharge_disposition_id3 -1.395e-01  3.699e-02  -3.770 0.000163 ***
## discharge_disposition_id4 -1.601e+01  4.130e+01  -0.388 0.698371
## admission_source_id2       2.283e-02  2.274e-02   1.004 0.315522
## admission_source_id3      -2.518e-01  4.433e-02  -5.679 1.35e-08 ***
## admission_source_id4      -1.511e+01  8.272e+02  -0.018 0.985428
## A1Cresult.8                8.320e-02  4.988e-02   1.668 0.095283 .
## A1CresultNone              1.293e-01  4.190e-02   3.084 0.002039 **
## A1CresultNorm             -5.748e-02  5.416e-02  -1.061 0.288489
## insulinNo                 -1.049e-01  3.200e-02  -3.279 0.001042 **
## insulinSteady             -1.989e-01  2.968e-02  -6.701 2.06e-11 ***
## insulinUp                 -5.624e-02  3.344e-02  -1.682 0.092582 .
## comorbidity1               2.130e-01  2.652e-02   8.031 9.70e-16 ***
## comorbidity2               1.819e-01  2.139e-02   8.501  < 2e-16 ***
## comorbidity3               2.889e-01  2.668e-02  10.828  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 96188  on 69643  degrees of freedom
## Residual deviance: 88997  on 69603  degrees of freedom
## AIC: 89079
##
## Number of Fisher Scoring iterations: 14
```

Stepwise selection is used for modeling: stepAIC(model_1, direction="both")

# Redundant and correlated variables are removed with the help of p-value and vif values to reach significant variables and low vif values. This is the final model

```
model_16 <- glm(formula = readmitted ~ gender + time_in_hospital + num_lab_procedures
                  num_procedures + number_outpatient + number_emergency + number_inpa
                  number_diagnoses + diabetesMed +
                  raceOther + age5 + age6 + admission_type_id3 +
                  admission_type_id5 +
                  admission_source_id3 +
                  A1CresultNone + insulinSteady +
```

```
                  comorbidity1 + comorbidity2 + comorbidity3, family = "binomial",
                data = train)
```

```
summary(model_16)
```

```
##
## Call:
## glm(formula = readmitted ~ gender + time_in_hospital + num_lab_procedures +
##     num_procedures + number_outpatient + number_emergency + number_inpatient +
##     number_diagnoses + diabetesMed + raceOther + age5 + age6 +
##     admission_type_id3 + admission_type_id5 + admission_source_id3 +
##     A1CresultNone + insulinSteady + comorbidity1 + comorbidity2 +
##     comorbidity3, family = "binomial", data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.8241  -1.0439  -0.8247   1.2029   1.8422
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -0.644830   0.032374 -19.918  < 2e-16 ***
## gender                0.058613   0.015914   3.683 0.000230 ***
## time_in_hospital      0.048142   0.008657   5.561 2.68e-08 ***
## num_lab_procedures    0.033138   0.008892   3.727 0.000194 ***
## num_procedures       -0.065594   0.008402  -7.807 5.84e-15 ***
## number_outpatient     0.094861   0.009209  10.301  < 2e-16 ***
## number_emergency      0.199424   0.013815  14.435  < 2e-16 ***
## number_inpatient      0.467029   0.010596  44.075  < 2e-16 ***
## number_diagnoses      0.189992   0.009067  20.954  < 2e-16 ***
## diabetesMed           0.309105   0.020414  15.142  < 2e-16 ***
## raceOther            -0.256197   0.066088  -3.877 0.000106 ***
## age5                  0.082087   0.020287   4.046 5.20e-05 ***
## age6                  0.110401   0.019193   5.752 8.81e-09 ***
## admission_type_id3   -0.150461   0.021900  -6.870 6.40e-12 ***
## admission_type_id5    0.304362   0.035108   8.669  < 2e-16 ***
## admission_source_id3 -0.261607   0.042304  -6.184 6.25e-10 ***
## A1CresultNone         0.097085   0.022228   4.368 1.26e-05 ***
## insulinSteady        -0.130970   0.018455  -7.097 1.28e-12 ***
## comorbidity1          0.228236   0.025895   8.814  < 2e-16 ***
## comorbidity2          0.198403   0.020909   9.489  < 2e-16 ***
## comorbidity3          0.316445   0.026276  12.043  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 96188  on 69643  degrees of freedom
```

```
## Residual deviance: 90724  on 69623  degrees of freedom
## AIC: 90766
##
## Number of Fisher Scoring iterations: 4
```

```
sort(vif(model_16))
```

```
##            raceOther               gender    number_outpatient
##             1.001881             1.009186             1.031500
##     number_emergency     number_inpatient        A1CresultNone
##             1.053574             1.056132             1.104054
##       num_procedures                 age5                 age6
##             1.131038             1.136119             1.143113
##   admission_type_id3        insulinSteady          diabetesMed
##             1.147387             1.155037             1.164921
##     time_in_hospital   num_lab_procedures     number_diagnoses
##             1.208802             1.271439             1.278833
##         comorbidity3         comorbidity1         comorbidity2
##             1.629075             1.654840             1.687841
##   admission_type_id5 admission_source_id3
##             1.853042             1.860836
```

```
# Final Model With only significant variables in the model
final_model <- model_16
```

# Logistic regression - Model Evaluation

final_model taken was model_16 Predicted probabilities of readmitted for test data

```
test_pred = predict(final_model, type = "response",
                    newdata = test)
```

```
summary(test_pred)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.1850  0.3718  0.4381  0.4637  0.5245  1.0000
```

Using the probability cutoff of 50% evaluate the predicted and true values

```
test_pred_readmitted <- factor(ifelse(test_pred >= 0.50, "YES", "NO"))
test_actual_readmitted <- factor(test$readmitted)
test_conf <- confusionMatrix(test_pred_readmitted, test_actual_readmitted, positive =
test_conf
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction    NO   YES
##        NO  12708  8101
##        YES  3287  5752
##
##                Accuracy : 0.6185
##                  95% CI : (0.6129, 0.624)
##     No Information Rate : 0.5359
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.2147
##  Mcnemar's Test P-Value : < 2.2e-16
##
##             Sensitivity : 0.4152
##             Specificity : 0.7945
##          Pos Pred Value : 0.6364
##          Neg Pred Value : 0.6107
##              Prevalence : 0.4641
##          Detection Rate : 0.1927
##    Detection Prevalence : 0.3028
##       Balanced Accuracy : 0.6049
##
##        'Positive' Class : YES
##
```

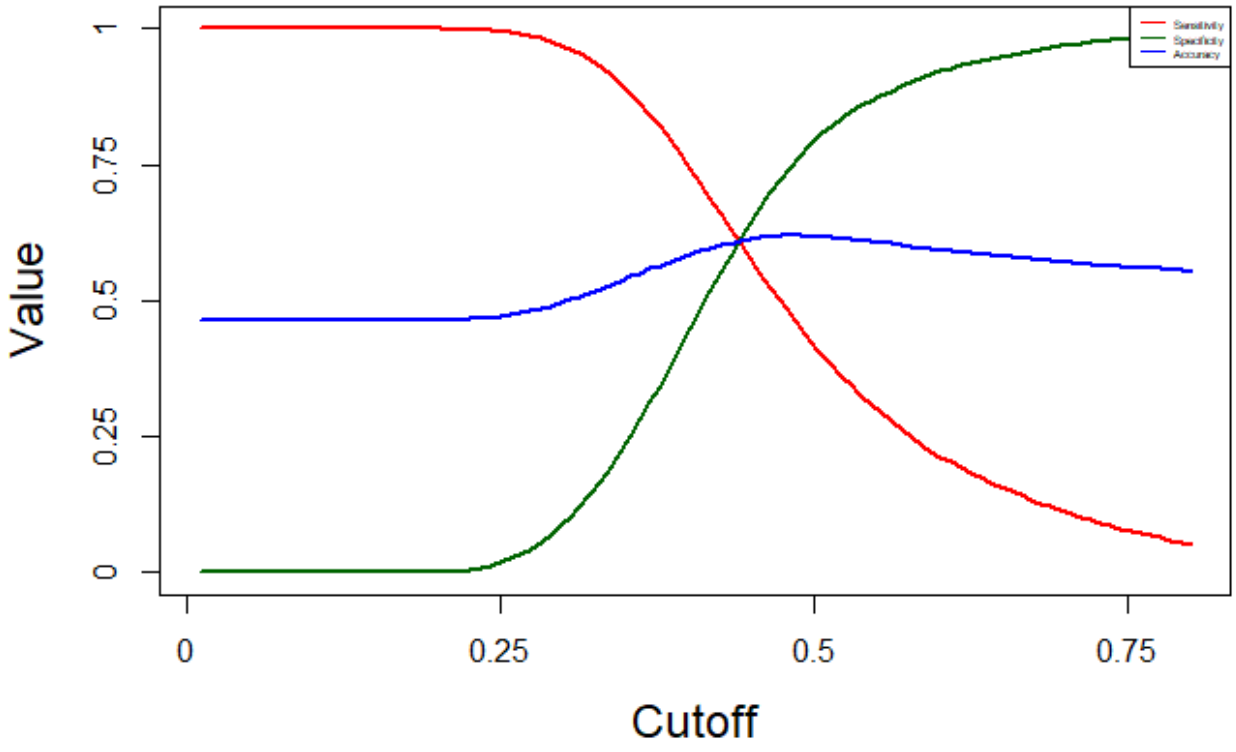
Sensitivity is very low. So let's choose a different cutoff value

To find the optimal probalility cutoff, create a function to find the accuracy, sensitivity and specificity for a given cutoff

```
perform_fn <- function(cutoff)
 {
   predicted_readmitted <- factor(ifelse(test_pred >= cutoff, "YES", "NO"))
   conf <- confusionMatrix(predicted_readmitted, test_actual_readmitted, positive = "
   acc <- conf$overall[1]
   sens <- conf$byClass[1]
   spec <- conf$byClass[2]
   out <- t(as.matrix(c(sens, spec, acc)))
```

```
   colnames(out) <- c("sensitivity", "specificity", "accuracy")
   return(out)
 }
# Creating cutoff values from 0.01 to 0.80 for plotting and initiallizing a matrix of
s = seq(.01,.80,length=100)
OUT = matrix(0,100,3)
for(i in 1:100)
 {
   OUT[i,] = perform_fn(s[i])
 }

plot(s, OUT[,1],xlab="Cutoff",ylab="Value",cex.lab=1.5,cex.axis=1.5,ylim=c(0,1),type=
axis(1,seq(0,1,length=5),seq(0,1,length=5),cex.lab=1.5)
axis(2,seq(0,1,length=5),seq(0,1,length=5),cex.lab=1.5)
lines(s,OUT[,2],col="darkgreen",lwd=2)
lines(s,OUT[,3],col=4,lwd=2)
box()
legend("topright",col=c(2,"darkgreen",4,"darkred"),
        lwd=c(1,1,1,1),c("Sensitivity","Specificity","Accuracy"), cex=0.4)
```




```
cutoff <- s[which(abs(OUT[,1]-OUT[,2])<0.01)]
cutoff
```

```
## [1] 0.4409091
```

```
# Let's choose a cutoff value of 0.42 for final model
```

```
 test_cutoff_readmitted <- factor(ifelse(test_pred >= cutoff, "YES", "NO"))
```

```
 conf_final <- confusionMatrix(test_cutoff_readmitted, test_actual_readmitted, positi
```

```
 acc <- conf_final$overall[1]
```

```
 sens <- conf_final$byClass[1]
```

```
 spec <- conf_final$byClass[2]
```

```
 acc
```

```
##  Accuracy
## 0.6094881
```

```
 sens
```

```
## Sensitivity
##   0.6059337
```

```
 spec
```

```
## Specificity
##   0.6125664
```

```
test_cutoff_readmitted <- ifelse(test_cutoff_readmitted=="YES",1,0)
test_actual_readmitted <- ifelse(test_actual_readmitted=="YES",1,0)
```

## Exporting Data for Excel Analysis (KS, Gain, Lift etc)

```
myeval <- matrix(nrow = length(test_pred),ncol = 2)
myeval[,1] <- test_pred
```

```
myeval[,2] <- test_actual_readmitted
colnames(myeval) <- c("Predicted_Prob","Actual_Labels")
```

## KS -statistic - Test Data

```
# on testing  data
pred_object_test<- prediction(test_cutoff_readmitted, test_actual_readmitted)
performance_measures_test<- performance(pred_object_test, "tpr", "fpr")
ks_table_test <- attr(performance_measures_test, "y.values")[[1]] -
   (attr(performance_measures_test, "x.values")[[1]])
max(ks_table_test)
```

```
## [1] 0.2185002
```

## Lift & Gain Chart

```
readmitted_decile = lift(test_actual_readmitted, test_pred, groups = 10)
readmitted_decile
```

```
## # A tibble: 10 x 6
##    bucket total totalresp Cumresp  Gain Cumlift
##     <int> <int>     <dbl>   <dbl> <dbl>   <dbl>
##  1      1  2985      2180    2180  15.7    1.57
##  2      2  2985      1852    4032  29.1    1.46
##  3      3  2985      1671    5703  41.2    1.37
##  4      4  2985      1480    7183  51.9    1.30
##  5      5  2984      1354    8537  61.6    1.23
##  6      6  2985      1267    9804  70.8    1.18
##  7      7  2985      1186   10990  79.3    1.13
##  8      8  2985      1120   12110  87.4    1.09
##  9      9  2985       982   13092  94.5    1.05
## 10     10  2984       761   13853 100      1
```

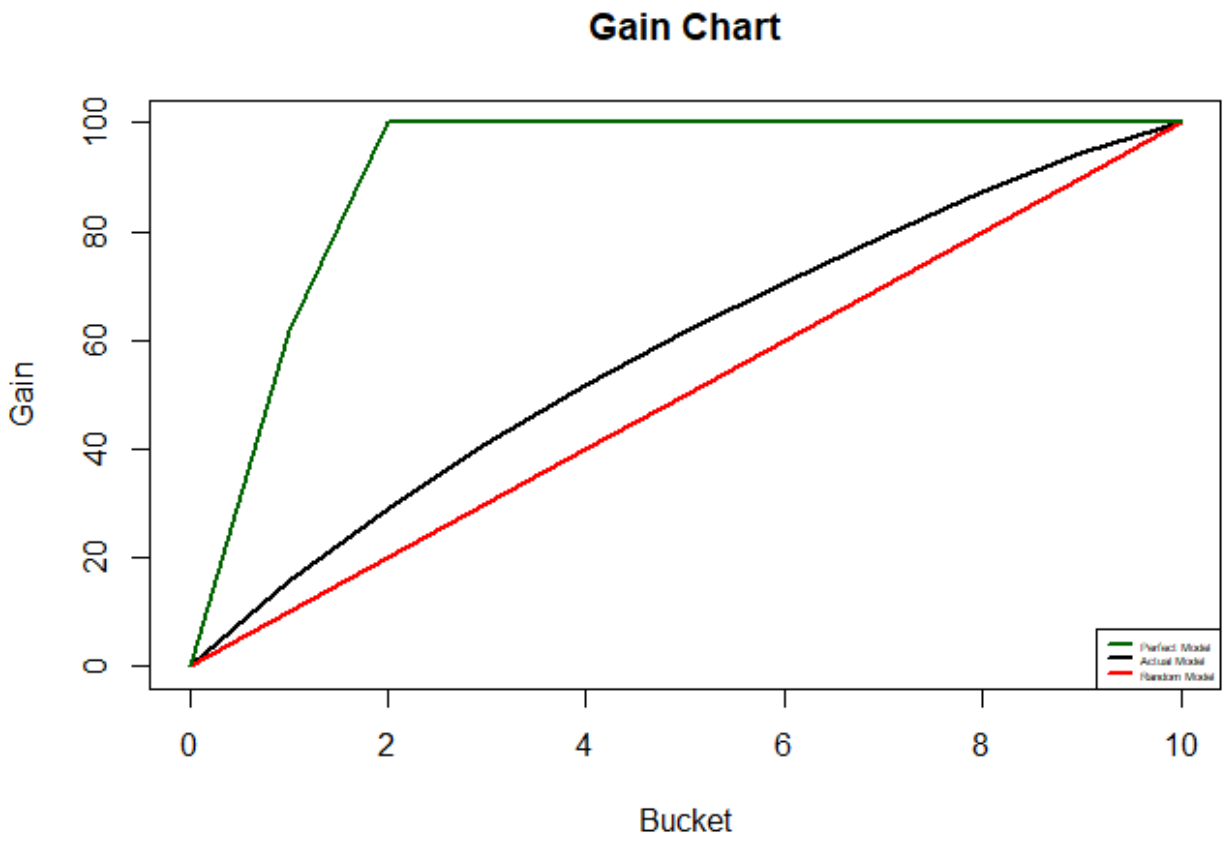
## Gain chart

```
Gain <- c(0,readmitted_decile$Gain)
Deciles <- c(0,readmitted_decile$bucket)
plot(y=Gain,x=Deciles,type ="l",lwd = 2,xlab="Bucket",ylab="Gain",main = "Gain Chart"

Random_Gain <- seq(from=0,to=100,by=10)
lines(y=Random_Gain,x=Deciles,type ="l",lwd = 2, col="red")

Perfect_Gain <- vector(mode = "numeric", length = 11)
```

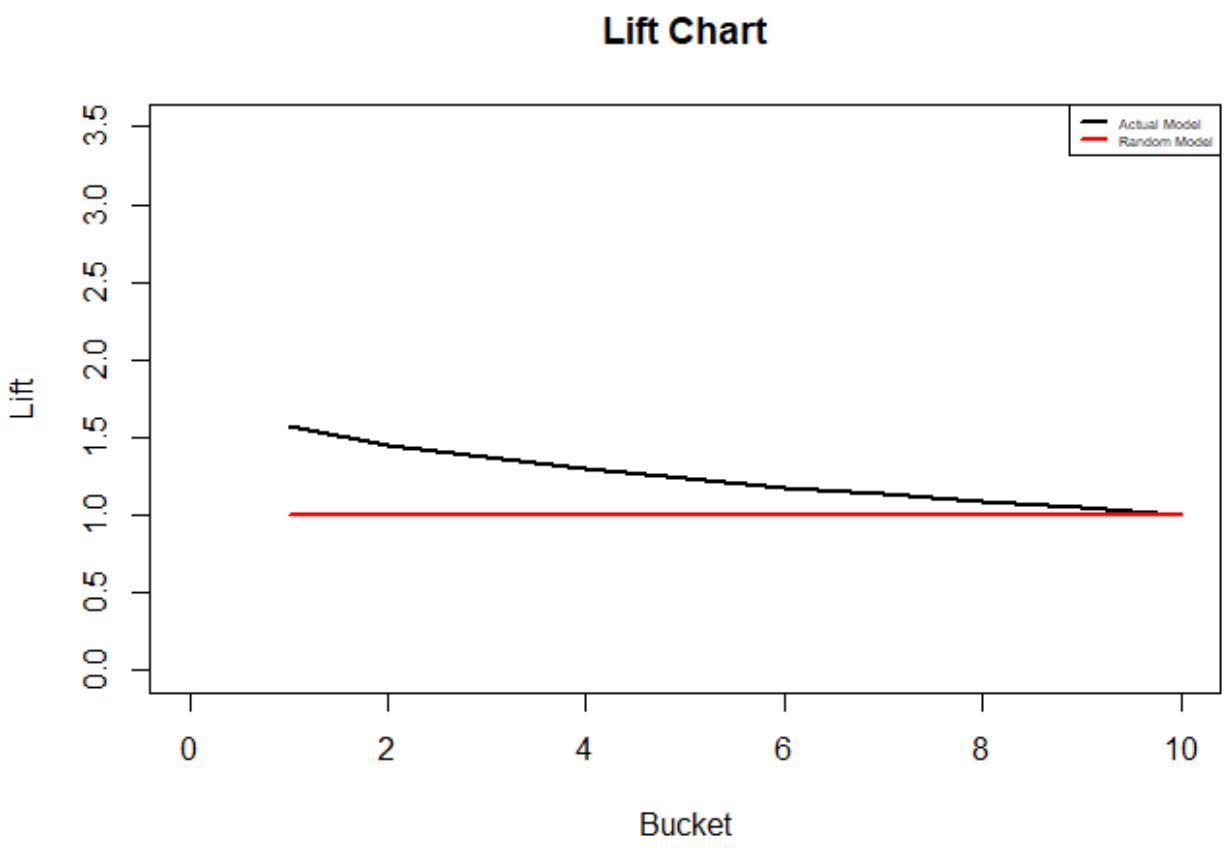
```
for (i in 2:11){Perfect_Gain[i] <- 100*min(1,129*(i-1)/209)}
lines(y=Perfect_Gain,x=Deciles,type ="l",lwd = 2, col="darkgreen")
legend("bottomright",col=c("darkgreen","black","red"),
       lwd =c(2,2,2,2),c("Perfect Model","Actual Model","Random Model"), cex = 0.4)
```




Lift chart

```
Lift <- Gain/Random_Gain
Random_Lift <- Random_Gain/Random_Gain

plot(y=Lift,x=Deciles,type ="l",ylim=c(0,3.5),lwd = 2,xlab="Bucket",ylab="Lift",main
lines(y=Random_Lift,x=Deciles,type ="l",lwd = 2, col="red")
legend("topright",col=c("black","red"),lwd =c(2,2,2),c("Actual Model","Random Model")
```


Lift Chart
Actual Model
Random Model
Lift
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
0
2
4
6
8
10
Bucket