Block 1 - Assignment 1

Tejashree R Mastamardi

Assignment 1: Spam Classification with nearest neighbors

```r
library(readxl)
spambase <- read_excel("spambase.xlsx")
View(spambase)
```

Question 1.1 Import the data into R and divide it into training and test sets (50%/50%)

```r
n=dim(spambase)[1]
set.seed(12345)
id=sample(1:n, floor(n*0.5))
train=spambase[id,]
test=spambase[-id,]
```

Question 1.2 Use logistic regression (functions glm(), predict()) to classify the training and test data by the classification principle Y_hat = 1 if p(Y=1|X) > 0.5, otherwise Y_hat = 0 and report the confusion matrices (use table()) and the misclassification rates for training and test data. Analyse the obtained results.

```r
GLM <- function(p){
  glm_model <- glm(Spam~., family = binomial(link="logit"), data = train)
  glm_prob <- predict(glm_model, type = "response")
  glm_pred <- ifelse(glm_prob > p, "Spam", "Not Spam")
  tab <- table(train$Spam, glm_pred)
  MSE <- (1 - (sum(diag(tab))/sum(tab)))*100
  tab1 <- table(test$Spam, glm_pred)
  MSE1 <- (1 - (sum(diag(tab1))/sum(tab1)))*100
  return(list("Confmat-train" = tab, "MSEtrain" = MSE,
              "Confmat-test" = tab1, "MSEtest" = MSE1))
}
GLM(0.5)
```

```
## $`Confmat-train`
##    glm_pred
##     Not Spam Spam
##   0      804  127
##   1       93  346
##
## $MSEtrain
## [1] 16.05839
##
## $`Confmat-test`
##    glm_pred
##     Not Spam Spam
##   0      616  335
##   1      281  138
##
## $MSEtest
## [1] 44.9635
```

Question 1.3 Use logistic regression (functions glm(), predict()) to classify the training and test data by the classification principle Y_hat = 1 if p(Y=1|X) > 0.9, otherwise Y_hat = 0 and report the confusion matrices (use table()) and the misclassification rates for training and test data. Analyse the obtained results.

```
GLM(0.9)
```

```
## $`Confmat-train`
##    glm_pred
##     Not Spam Spam
##   0      928    3
##   1      378   61
##
## $MSEtrain
## [1] 27.81022
##
## $`Confmat-test`
##    glm_pred
##     Not Spam Spam
##   0      910   41
##   1      396   23
##
## $MSEtest
## [1] 31.89781
```

Question 1.4 Use standard classifier kknn() with K=30 from package kknn, report the misclassification rates for the training and test data and compare the results with step 2.

```
#library(kknn)
kknn_model <- function(a, b,X){
  model1 <- kknn(Spam~., a, b, k=X)
  fitted_model <- predict(model1)
  kknn_train <- ifelse(fitted_model > 0.5, "Spam", "Not Spam")
  tab1 <- table(train$Spam, kknn_train)
  MSE1 <- (1 - (sum(diag(tab1))/sum(tab1)))*100
  tab2 = table(test$Spam, kknn_train)
  MSE2 = (1 - (sum(diag(tab2))/sum(tab2)))*100
  return(list("confmat_train"=tab1, "MSEtrain"=MSE1,
              "confmat_test"=tab2,"MSEtest"=MSE2))
}

kknn_model(train, train, X=30)
```

```
## $confmat_train
##    kknn_train
##     Not Spam Spam
##   0      779  152
##   1       77  362
##
## $MSEtrain
## [1] 16.71533
##
## $confmat_test
##    kknn_train
##     Not Spam Spam
##   0      580  371
##   1      276  143
##
## $MSEtest
## [1] 47.22628
```

```
kknn_model(train, test, X=30)
```

```
## $confmat_train
##    kknn_train
##     Not Spam Spam
##   0      589  342
##   1      293  146
##
## $MSEtrain
## [1] 46.35036
##
## $confmat_test
##    kknn_train
##     Not Spam Spam
##   0      702  249
##   1      180  239
##
## $MSEtest
## [1] 31.31387
```

Question 1.5 Repeat step 4 for K=1 and compare the results with step 4. What effect does the decrease of K lead to and why?

```
kknn_model(train, train, X=1)
```

```
## $confmat_train
##    kknn_train
##     Not Spam Spam
##   0      931    0
##   1        0  439
##
## $MSEtrain
## [1] 0
##
## $confmat_test
##    kknn_train
##     Not Spam Spam
##   0      633  318
##   1      298  121
```

```
##
## $MSEtest
## [1] 44.9635
```

```
kknn_model(train, test, X=1)
```

```
## $confmat_train
##    kknn_train
##     Not Spam Spam
##   0      560  371
##   1      269  170
##
## $MSEtrain
## [1] 46.71533
##
## $confmat_test
##    kknn_train
##     Not Spam Spam
##   0      644  307
##   1      185  234
##
## $MSEtest
## [1] 35.91241
```

Assignment 3: Feature selection by cross validation in a linear model

```
library(MASS)
library(ggplot2)

my_data <- swiss
b <- as.vector(my_data[,1])
a <- as.matrix(my_data[,c(2:6)])
Nf <- 5

#function for calculating weights
function_weight <- function(X,Y)
{
  Z <- ginv(t(X)%*%X)%*%t(X)%*%Y
}
n <- dim(my_data)[1]
set.seed(12345)
sampleofn <- sample(1:n)
id <- list()
cvscore <- c()

#function for calculating cv score
cvfunction <- function(X,Y,Nf)
{
  start <- 1
  for(i in 1:Nf)
    {
      if(i<Nf)
      {
```

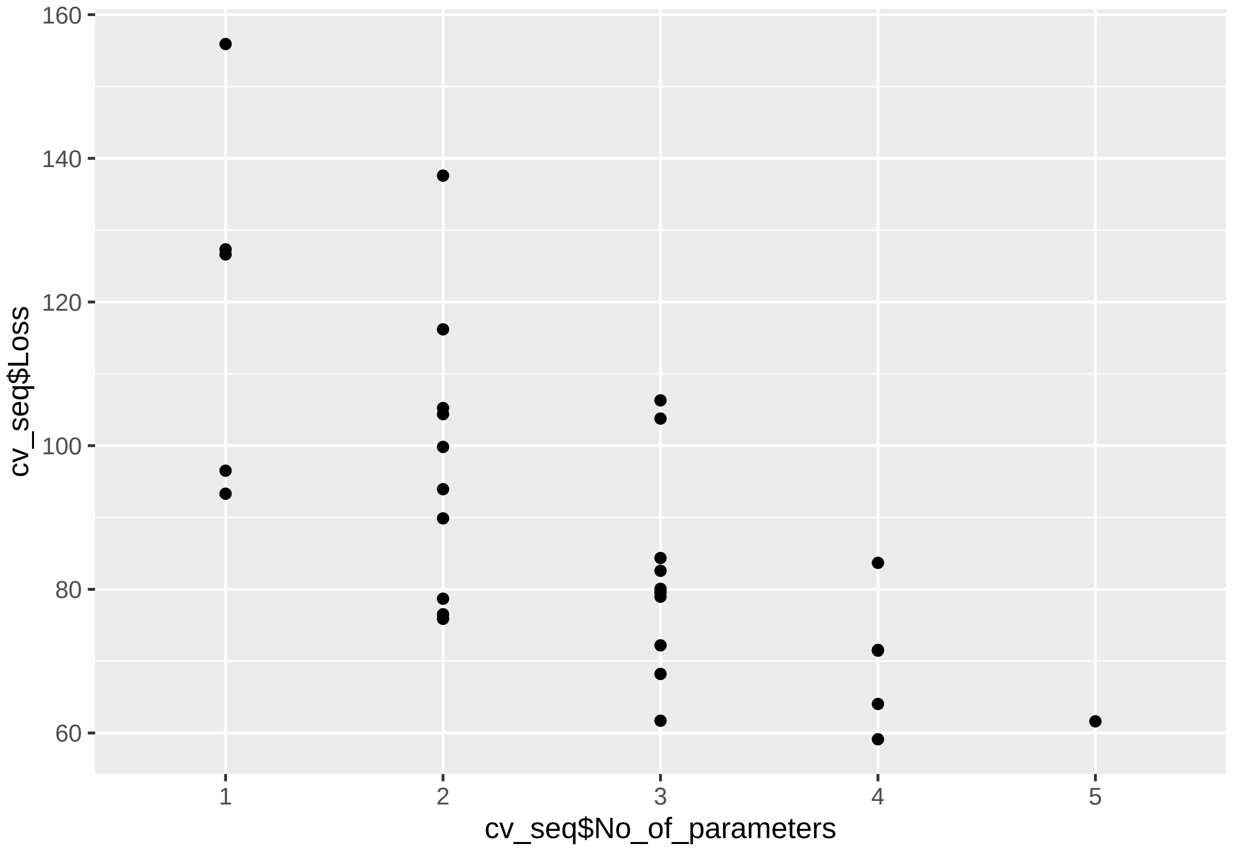
```r
        end <- start+(as.integer(n/Nf)-1)
        id[[i]] <- sampleofn[start:end]
        start <- end+1
      }
      else if(i==Nf)
      {
        end <- n
        id[[i]] <- sampleofn[start:end]
      }
      testX <- X[as.vector(id[[i]]),]
      trainX <- X[-as.vector(id[[i]]),]
      testY <- Y[as.vector(id[[i]])]
      trainY <- Y[-as.vector(id[[i]])]

      Weight <- as.matrix(function_weight(X=trainX,Y=trainY))
      b1 <- testX%*%Weight
      loss <- b1-testY
      cv <- sum(loss*loss)/length(testY)
      cvscore[i] <- cv
  }
  average_of_cv <- sum(cvscore)/Nf
}

cv_seq <- matrix(0, nrow = 0, ncol = 3)
for(k in 1:ncol(a))
{
  combinations <- combn(1:ncol(a),k)
  for(j in 1:ncol(combinations))
  {
    a1 <- as.matrix(a[,combinations[,j]])
    a1 <- cbind(a1, 1)
    seq <- paste(combinations[,j], collapse = ",")
    avg_score <- cvfunction(X = a1,Y = b,Nf)
    cv_seq <- rbind(cv_seq, c(seq,avg_score, k))
  }
}

cv_seq = as.data.frame(cv_seq)
colnames(cv_seq) = c("Sequence", "Loss","No_of_parameters")
cv_seq$Loss = as.numeric(as.character(cv_seq$Loss))
cv_seq$Sequence = as.character(cv_seq$Seq)

cvfunction(X= a,Y= b,Nf)

cat("Optimal Subset of Features: ",cv_seq$Seq[which.min(cv_seq$Loss)])
```

```
## Optimal Subset of Features:  1,3,4,5
```

```r
cat("Cross validation Score: ",min(cv_seq$Loss))
```

```
## Cross validation Score:  59.12837
```

```r
p <- ggplot(cv_seq,aes(x= cv_seq$No_of_parameters,y= cv_seq$Loss))+geom_point()
p
```

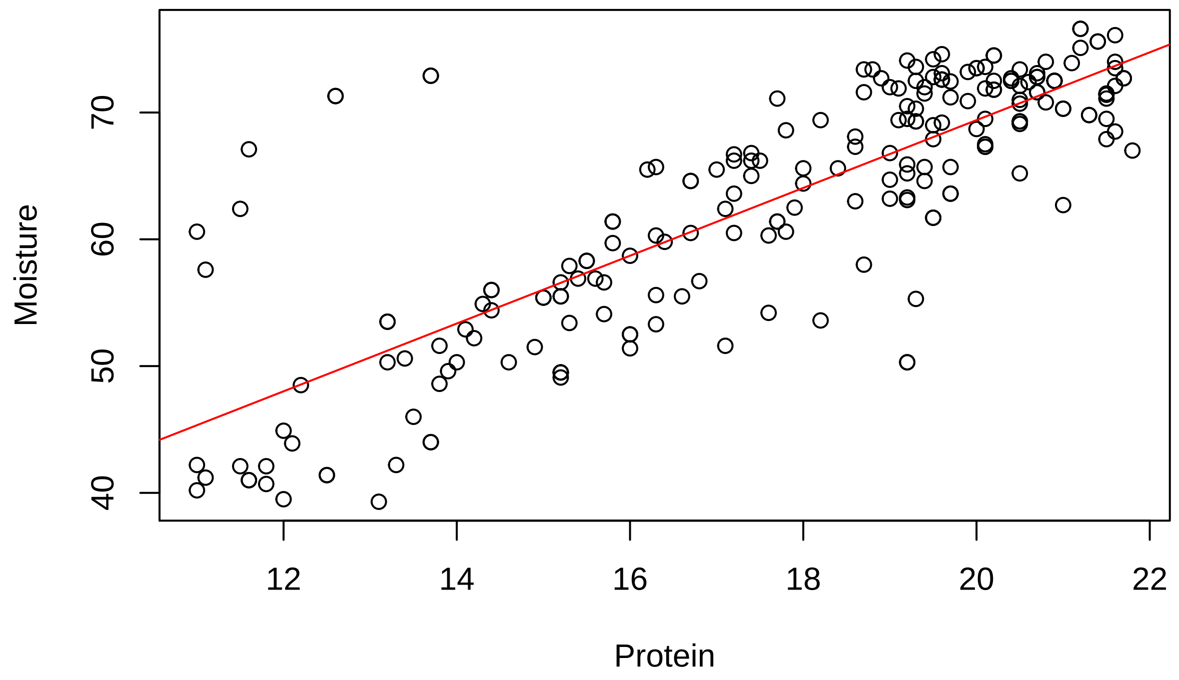


Assignment 4: Linear Regression and Regularization

```r
library(readxl)
tecator <- read_excel("tecator.xlsx")
#View(tecator)
```

Question 4.1 Import data to R and create a plot of Moisture versus Protein. Do you think that these data are described well by a linear model?

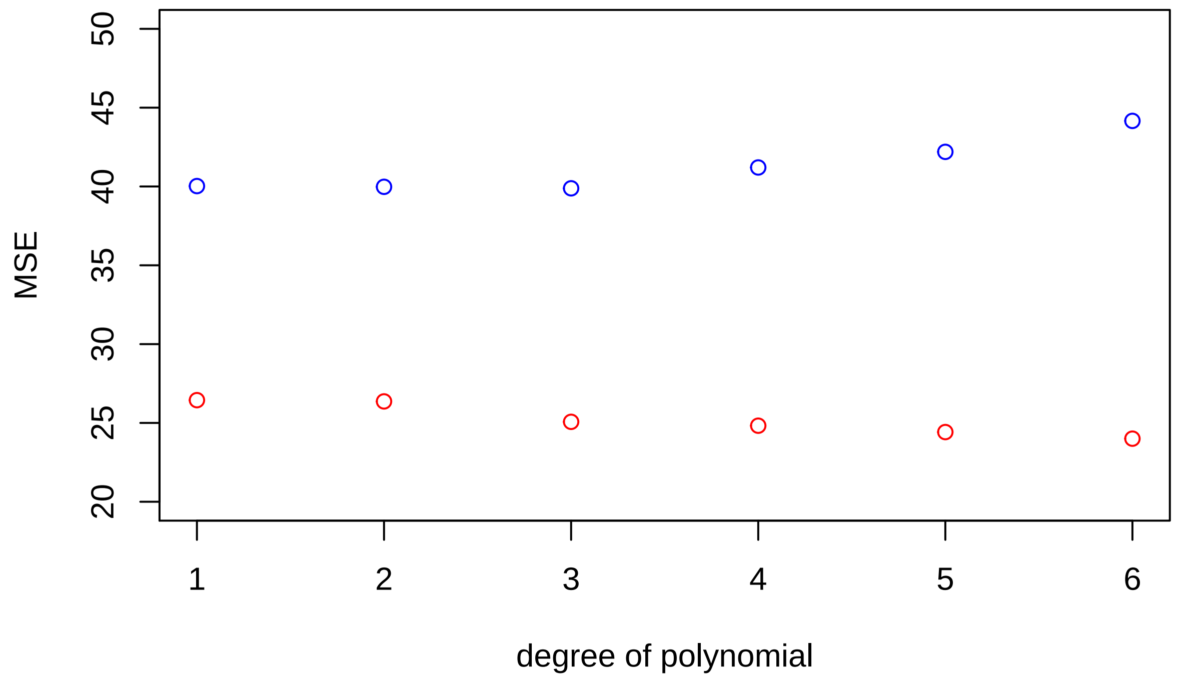
```r
#Plot of Moisture vs protein
plot(Moisture~Protein, data = tecator)

#do you think that these data are described well by a linear model
Model <- lm(Moisture~Protein, data = tecator)

plot(Moisture~Protein, data = tecator)
abline(Model, col = "red")
```



Yes, the data is well described by a linear model

Question 4.3 Divide the data into training and validation sets(50%/50%) and fit models Mi,i=1…6. For each model, record the training and the validation MSE and present a plot showing how training and validation MSE depend on i (write some R code to make this plot). Which model is best according to the plot? How do the MSE values change and why? Interpret this picture in terms of bias-variance tradeoff.

```r
n=dim(tecator)[1]
set.seed(12345)
id=sample(1:n, floor(n*0.5))
train=tecator[id,]
valid=tecator[-id,]

ModelPlot <- function(){
 training_MSE <- rep(0,6)
 validation_MSE <- rep(0,6)
 for (i in 1:6) {
  model <- lm(Moisture~poly(Protein,i), data = train)
  fitted_train <- predict(model, train)
  fitted_valid <- predict(model, valid)
  training_MSE[i] <- mean((train$Moisture - fitted_train)^2) #mean((Y-Y_hat)^2)
  validation_MSE[i] <- mean((valid$Moisture - fitted_valid)^2)
 }
 plot(seq(1:6), training_MSE, col = "red", ylim = c(20,50), ylab = "MSE", xlab = "degree of polynomial"
 points(seq(1:6), validation_MSE, col = "blue")
}
ModelPlot()
```



Question 4.4 Perform variable selection of a linear model in which Fat is response and Channel1-Channel100 are predictors by using stepAIC. Comment on how many variables were selected.

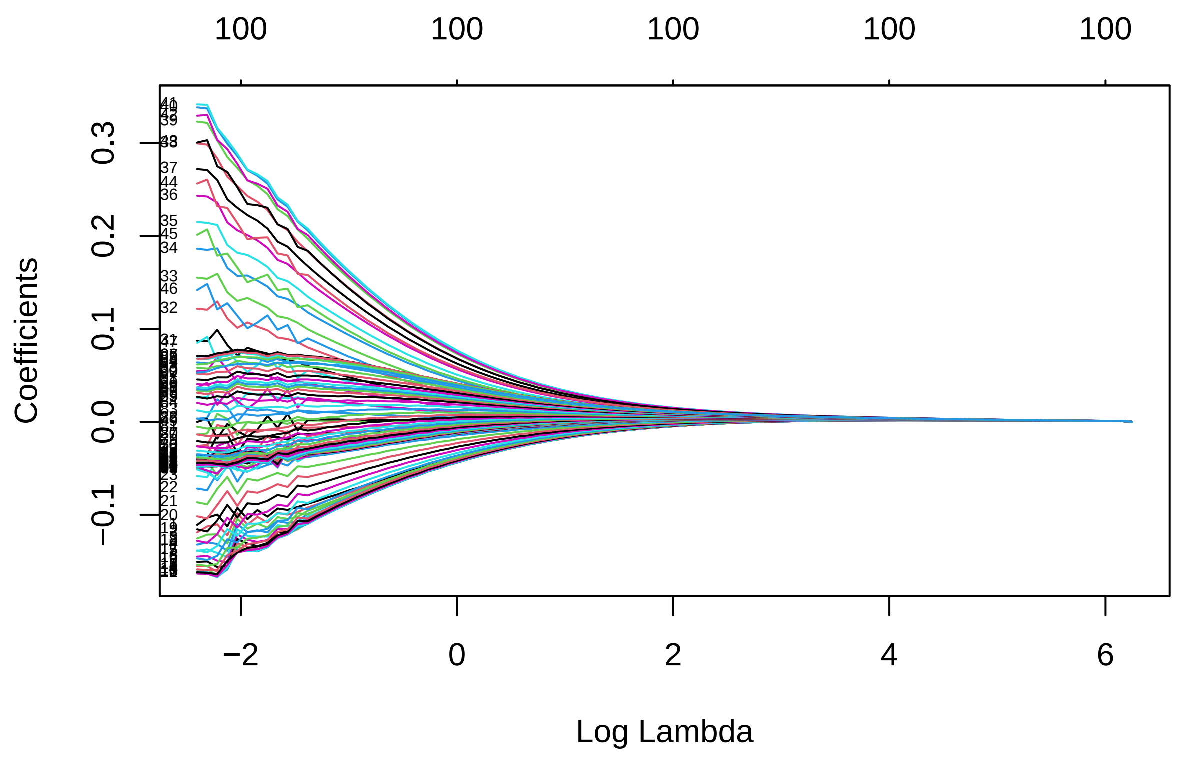
```
library(mltools)
library(MASS)
new_data <- as.data.frame(as.matrix(tecator[,2:102]))

#Perform variable selection of a linear model in which Fat is response and Channel1-Channel100 are pred
myAIC <- lm(Fat ~., new_data)
step <- stepAIC(myAIC, direction = "both", trace = FALSE)

#Comment on how many variables were selected
selected_variables <- length(step$coefficients) - 1 #removing the intercept term
selected_variables
```

```
## [1] 63
```

Question 4.5 Fit a Ridge regression model with the same predictor and response variables. Present a plot showing how model coefficients depend on the log of the penalty factor lambda and report how the coefficients change with lambda.

```
library(readxl)
library(glmnet)

covariates <- scale(new_data[,1:100])
```

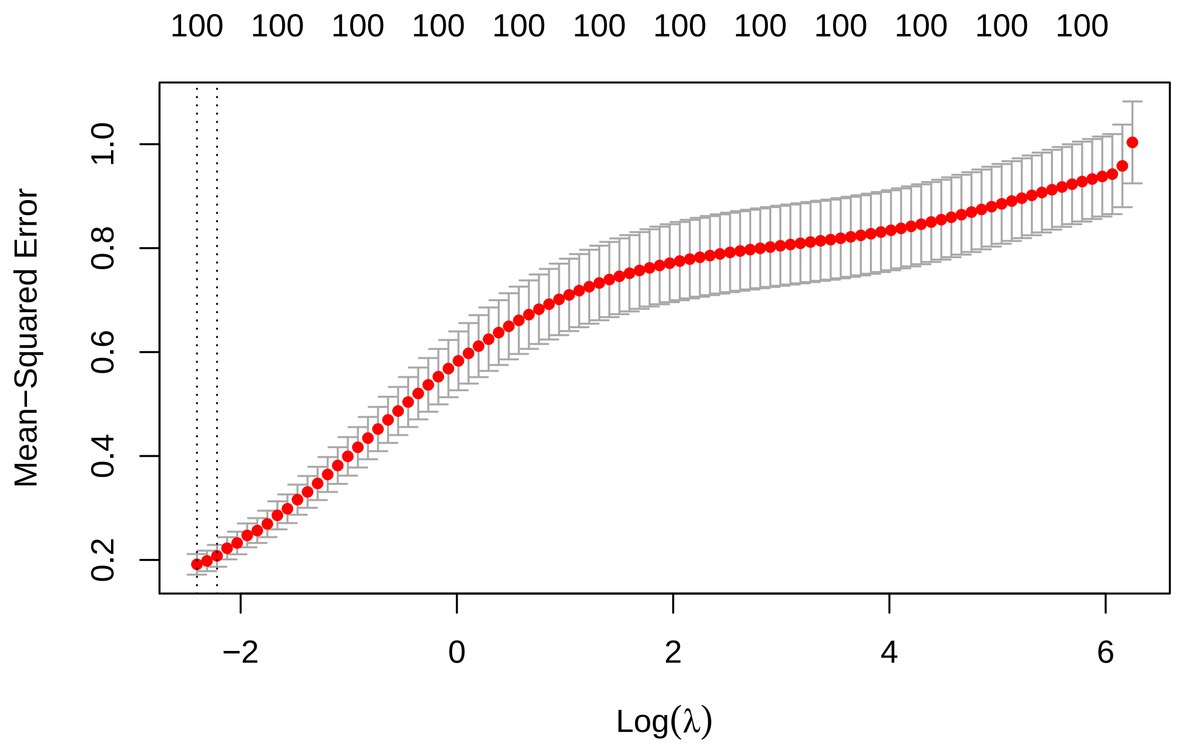
```
response <- scale(new_data[,101])

model <- glmnet(as.matrix(covariates), response, alpha=0, family = "gaussian")
plot(model, xvar = "lambda", label = TRUE)
```



```
model=cv.glmnet(as.matrix(covariates),response, alpha=0,family="gaussian")#Lambda value is selected usi
model$lambda.min
```

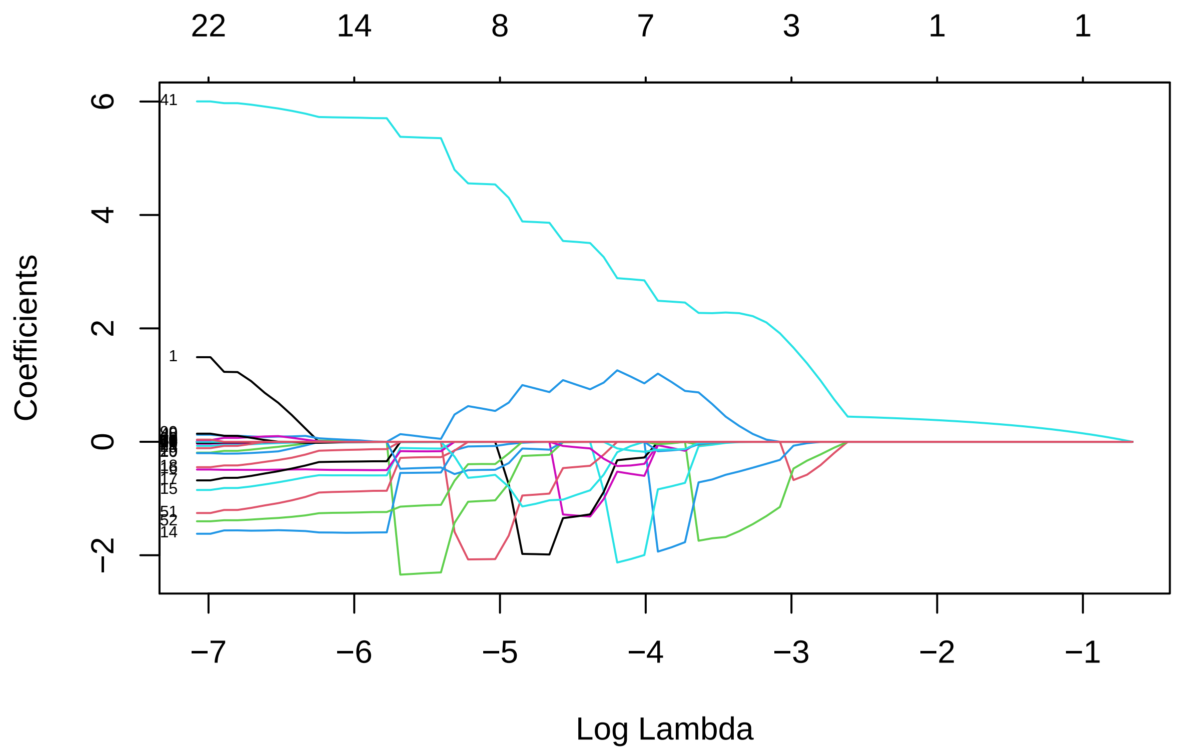
```
## [1] 0.09030492
```

```
plot(model)
```



Question 4.6 Fit a LASSO regression model with the same predictor and response variables. Present a plot showing how model coefficients depend on the log of the penalty factor lambda and report how the coefficients change with lambda.

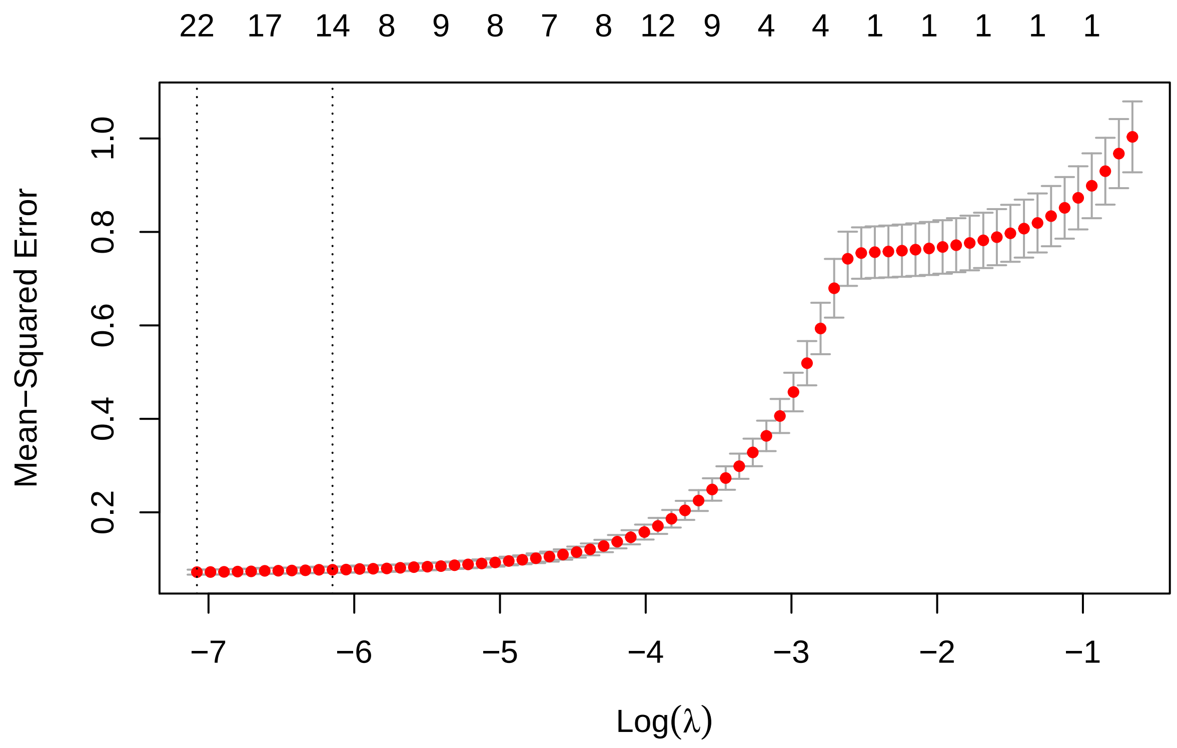
```
covariates <- scale(new_data[,1:100])
response <- scale(new_data[,101])

model <- glmnet(as.matrix(covariates), response, alpha=1, family = "gaussian")
plot(model, xvar = "lambda", label = TRUE)
```



```r
model=cv.glmnet(as.matrix(covariates),response, alpha=1,family="gaussian")
model$lambda.min
```

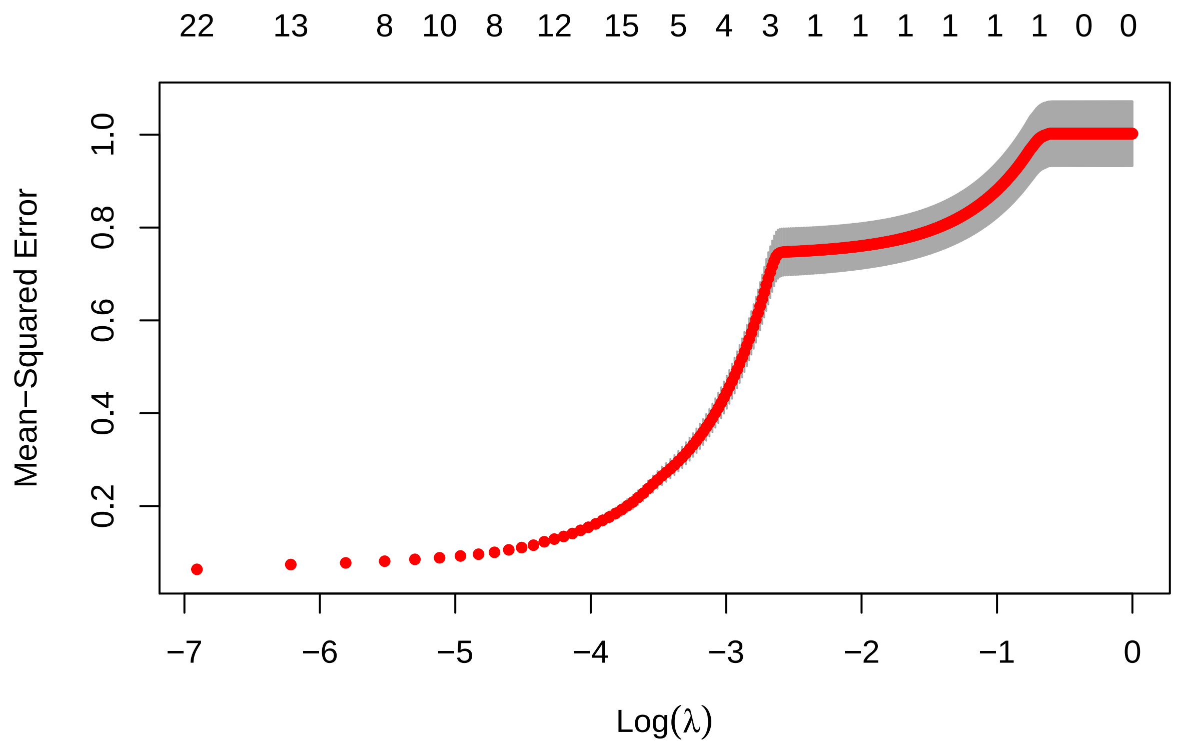
```
## [1] 0.0008421867
```

```r
plot(model)
```



Question 4.7 Use cross-validation to find the optimal LASSO model, report the optimal lambda and how many variables were chosen by the model and make conclusions.

```
scaled_data <- scale(tecator[,2:102])

covariates <- scaled_data[,1:100]
response <- scaled_data[,101]

model_cv <- cv.glmnet(as.matrix(covariates), response, alpha = 1, family = "gaussian", lambda = seq(0,1
plot(model_cv, xvar="lambda", label=TRUE)
```



```
#optimal Lambda
opt_lambda <- model_cv$lambda.min
opt_lambda
```

```
## [1] 0
```

```
cat(paste("number of variables chosen = ",length(coef(model_cv,s="lambda.min"))-1))
```

```
## number of variables chosen =  100
```