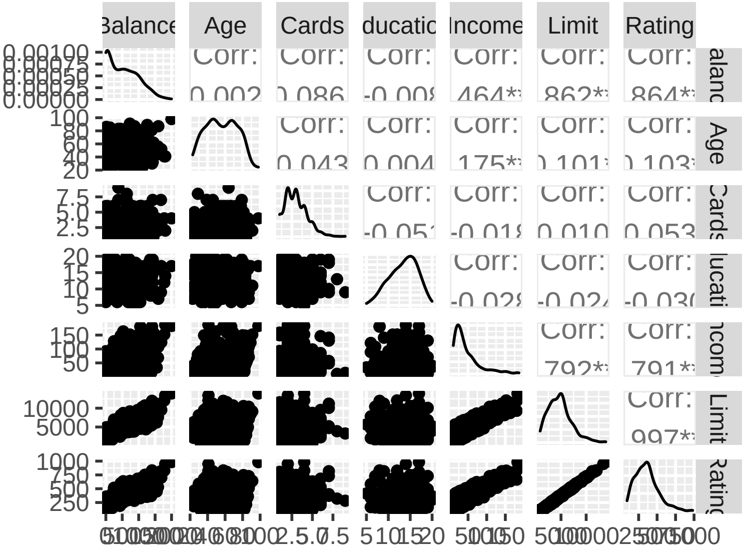
Oving5

2022-04-04

Task 2

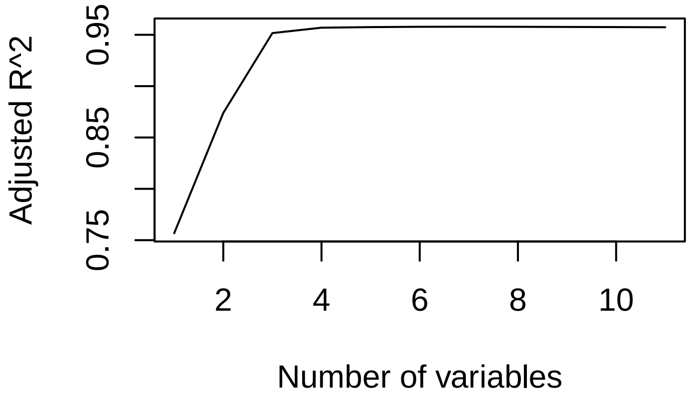
```
library(ISLR)


set.seed(1)

data <-Credit

w_d <- c("Balance", "Age", "Cards", "Education", "Income", "Limit", "Rating")

scatter_data <- Credit[,w_d]

library(GGally)

ggpairs(data=scatter_data)
```



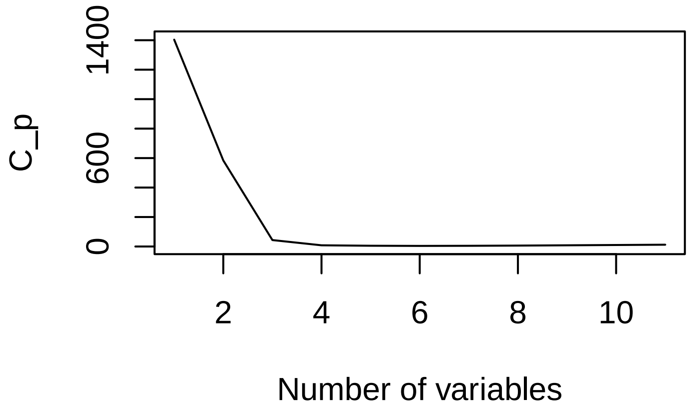
Task 3a

```
#We first want to get rid of the id column

credit_data = subset(Credit, select=-c(ID))

library(leaps)
```

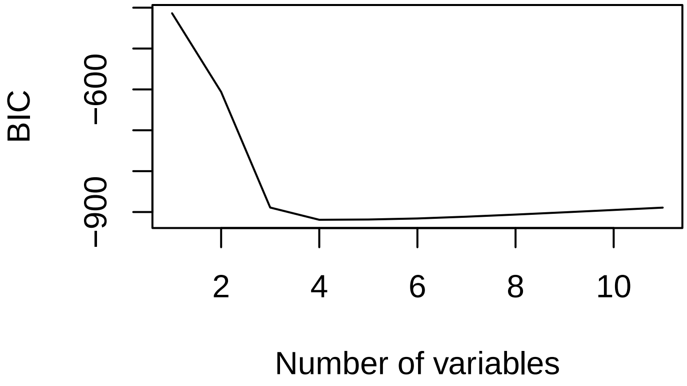
```
variables = dim(credit_data)[2]

index = sample(1:nrow(credit_data), nrow(credit_data)*0.75)

training_data <- credit_data[index,]
testing_data <- credit_data[-index,]

model = regsubsets(Balance~., data = training_data, nvmax = variables)

model_summary = summary(model)


plot(model_summary$adjr2, xlab = "Number of variables", ylab = "Adjusted R^2", type = "l")
```



```
plot(model_summary$cp, xlab = "Number of variables", ylab = "C_p", type = "l")
```



```
plot(model_summary$bic, xlab = "Number of variables", ylab = "BIC", type = "l")
```

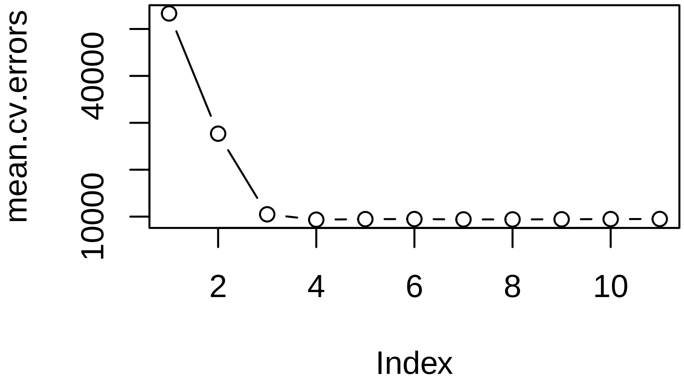


We observe from the plots that the BIC has a minimum in 4 variables, Cp has a minimum of around 4 variables, and adjusted R^2 has a maximum around 3 variables.

We choose the simplest model with the lowest Cp and BIC, and highest adjusted R^2, therefore 4 variable model is optimal.

Task 3b

```
K = 10    #We want k = 10 folds

set.seed(1)

#Creating K folds from 300 rows of data

folds = sample(1:K, nrow(training_data), replace=TRUE)

#Making a predict function for the regsubsets

predict.regsubsets=function(object,data, id){
  form = as.formula(object$call[[2]])   #?
  mat = model.matrix(form,data)         #Creates a design matrix
  coefi = coef(object,id=id)            #extracts the coefficients og the models
  xvars = names(coefi)
  mat[,xvars]%*%coefi                   #Multiplies the matrix by the coefficients
}

cv.errors = matrix(NA, K, variables, dimnames = list(NULL, paste(1:variables)))

# For each fold
for(j in 1:K){
  # Fit the model with each subset of predictors on the training part of the fold
  best.fit=regsubsets(Balance~.,data=training_data[folds!=j,], nvmax=variables)
  # For each subset
  for(i in 1:variables){
    # Predict on the hold out part of the fold for that subset
    pred=predict(best.fit, training_data[folds==j,],id=i)
    # Get the mean squared error for the model trained on the fold with the subset
    cv.errors[j,i]=mean((training_data$Balance[folds==j]-pred)^2)
  }
}
mean.cv.errors = apply(cv.errors,2,mean)

plot(mean.cv.errors,type= "b")
```



We observe that the CV error also reaches a minimum for 4 variables, comparing to the other methods of calculating errors, this seesm quite reasonable.

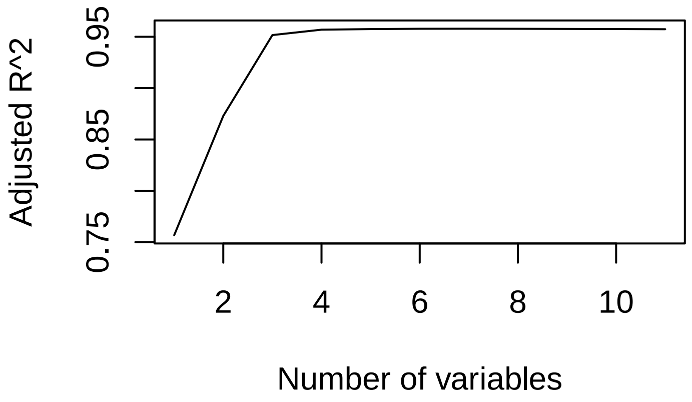
```
#Implementing the optimal model

predictors = 4   #We found this to be the optimal amounts of predictors

variables_chosen = names(coef(best.fit$call[[2]], predictors))  #?
variables_chosen = variables[!variables %in% "(intercept"]      #?

mformula = as.formula(best.fit$call[[2]])
m_design_matrix = model.matrix(mformula, training_data)[,variables]

m_data_train = data.frame(Balance = training_data$Balance, m_design_matrix)

#Fitting the best model using only the selected predictors on the training data
best_model = lm(formula = mformula, m_data_train)

#Make predictions on test set
m_design_matrix_test = model.matrix(mformula, testing_data)[,variables_chosen]
predictions = predict(object = best_model, data = as.data.frame(m_design_matrix_test))

m_squared_errors = (testing_data$Balance - predictions)^2
```

```
mean(m_squared_errors)
```

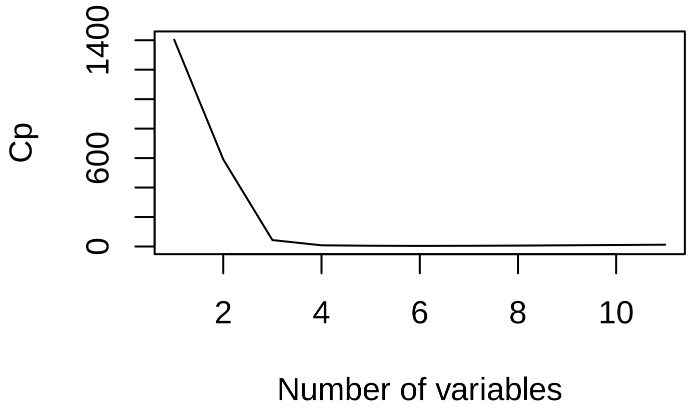
```
## [1] 202704.7
```

Task 4

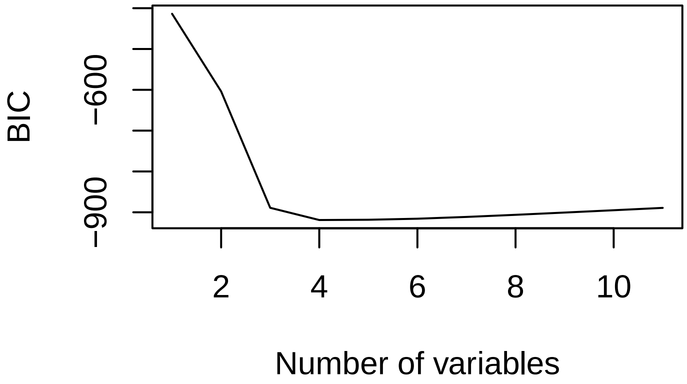
```
#Defining the backward stepwise selection
backward_model <- regsubsets(Balance~.,data=training_data, nvmax = variables, method = "backward")

#Storing the summary
summary_backward_model = summary(backward_model)

plot(summary_backward_model$adjr2, xlab = "Number of variables", ylab = "Adjusted R^2", type= "l")
```



```
plot(summary_backward_model$cp, xlab = "Number of variables", ylab = "Cp", type= "l")
```



```
plot(summary_backward_model$bic, xlab = "Number of variables", ylab = "BIC", type= "l")
```



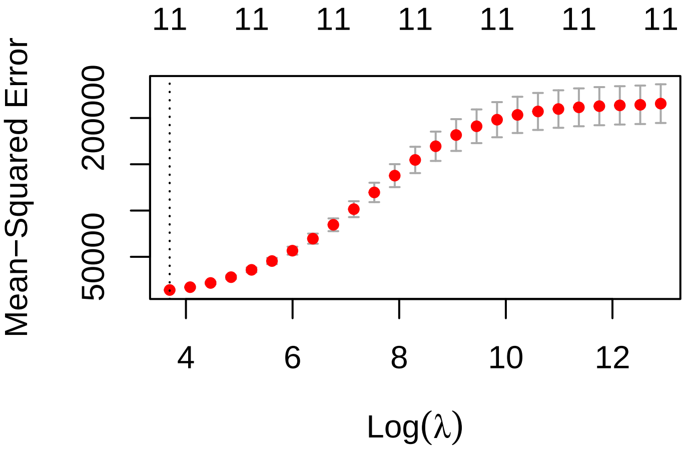
We see the same results here.

Task 5

Ridge regression is an extension of linear regression where the loss function is modified to minimize the complexity of the model.

alpha = 0 for ridge regression, family = gaussian

```
library(glmnet)

x_train = model.matrix(Balance ~., training_data)[,-1]
y_train = training_data$Balance

x_test =model.matrix(Balance ~., testing_data)[,-1]
y_test = testing_data$Balance

lambdas = 10^seq(2,-3, by = -.1)

ridge_regression = glmnet(x_train,y_train, nlambda = 25, alpha = 0, family = "gaussian")

set.seed(1)

cv = cv.glmnet(x_train,y_train, nlambda = 25, alpha = 0, family = "gaussian")

plot(cv)
```



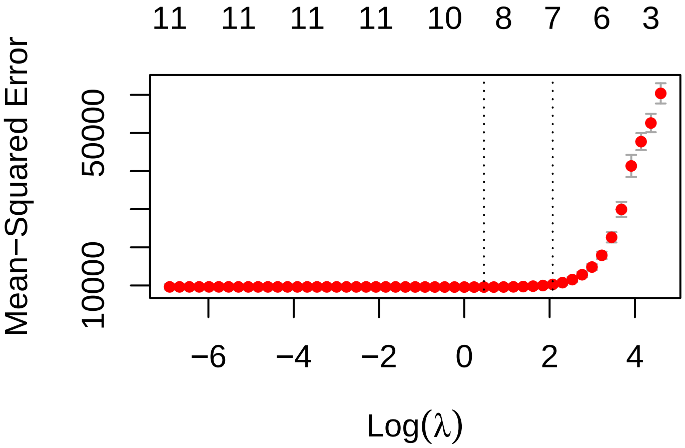
```
best_lambda = cv$lambda.min

ridge_prediction = predict(ridge_regression, s=best_lambda, newx = x_test)

ridge_squared_errors = (y_test - ridge_prediction)^2
mean(ridge_squared_errors)
```

```
## [1] 15741.72
```

Task 6

alpha = 1 for lasso regression

```
lasso_regression = cv.glmnet(x_train, y_train, alpha = 1, lambda = lambdas,standardize = TRUE, nfolds =
plot(lasso_regression)
```

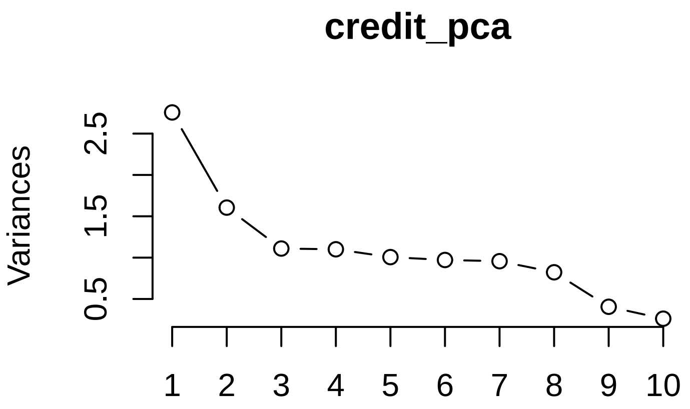


```
lambda_best = lasso_regression$lambda.min

lasso_model = glmnet(x_train, y_train, alpha = 1, lambda = lambda_best, standardize = TRUE)

predictions = predict(lasso_model, s = lambda_best, newx = x_test)

squared_errors = (predictions-y_test)^2
mean(squared_errors)
```

```
## [1] 12333.23
```

Task 7

```
x <- model.matrix(Balance~., credit_data)[,-1]
credit_pca = prcomp(x, center=TRUE, scale. = TRUE)
plot(credit_pca, type = "l")
```



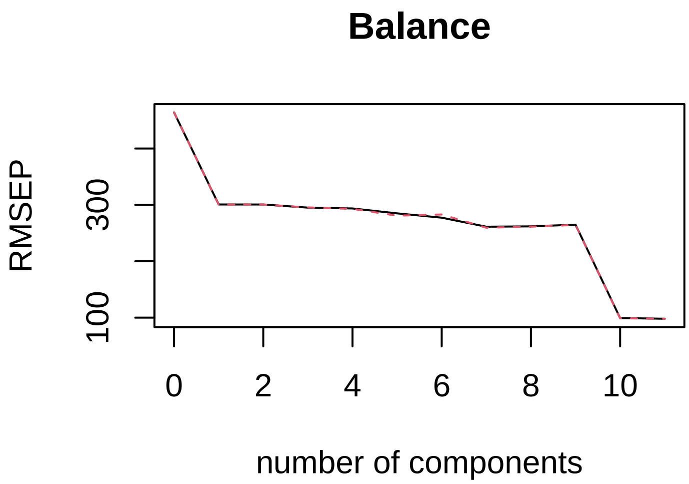
```
summary(credit_pca)
```

```
## Importance of components:
##                           PC1    PC2    PC3    PC4    PC5     PC6     PC7
## Standard deviation     1.6601 1.2669 1.0536 1.0493 1.0032 0.98577 0.97831
## Proportion of Variance 0.2505 0.1459 0.1009 0.1001 0.0915 0.08834 0.08701
## Cumulative Proportion  0.2505 0.3964 0.4973 0.5974 0.6889 0.77727 0.86427
##                            PC8     PC9    PC10    PC11
## Standard deviation     0.90715 0.63723 0.51174 0.04618
## Proportion of Variance 0.07481 0.03691 0.02381 0.00019
## Cumulative Proportion  0.93908 0.97600 0.99981 1.00000
```

We see that the first PC explain 25% of the variability in the data, the second one about 14,6% and the third one about 11%. It is not until the 9th one that we see a huge decline in proportion of variance (3,691 %), therefore I would use the first 8 principal components.

Task 8

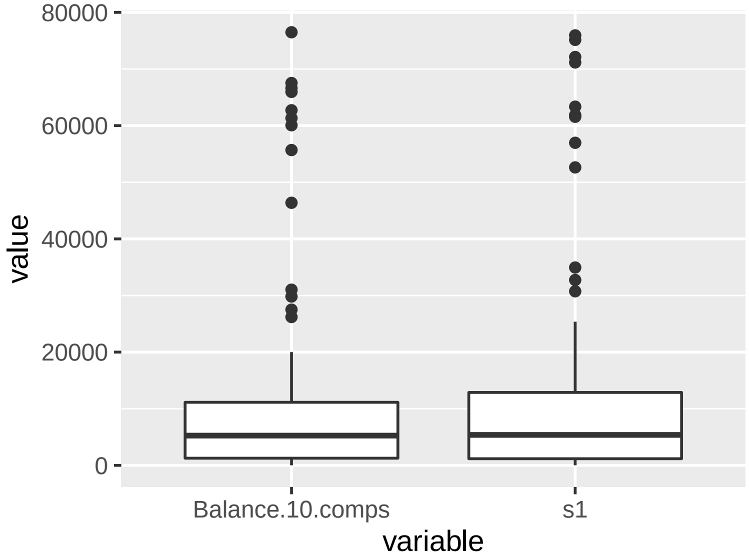
```
library(pls)

pcr_model <- pcr(Balance ~., data = training_data, scale = TRUE, validation = "CV")

validationplot(pcr_model)
```



```
predictions = predict(pcr_model, testing_data, ncomp = 10)
pcr_squared_errors = (predictions - testing_data$Balance)^2
squared_errors <- data.frame(pcr_squared_errors = pcr_squared_errors, squared_errors)

mean(pcr_squared_errors)
```

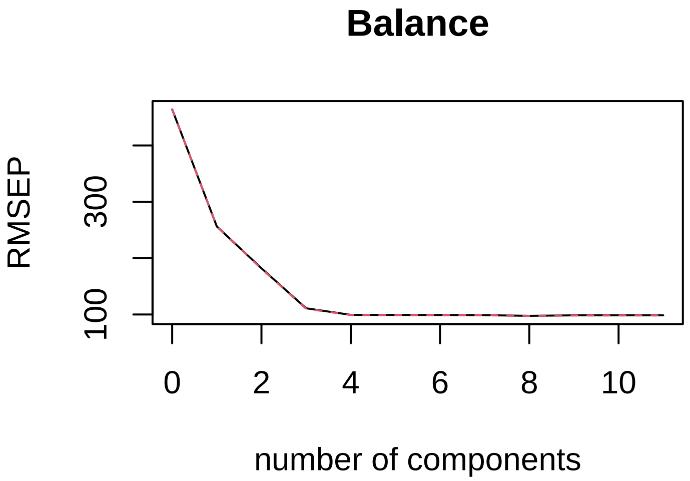
```
## [1] 11578.1
```

```
library(ggplot2)
library(reshape2)

ggplot(melt(squared_errors)) + geom_boxplot(aes(variable, value))
```



Task 9

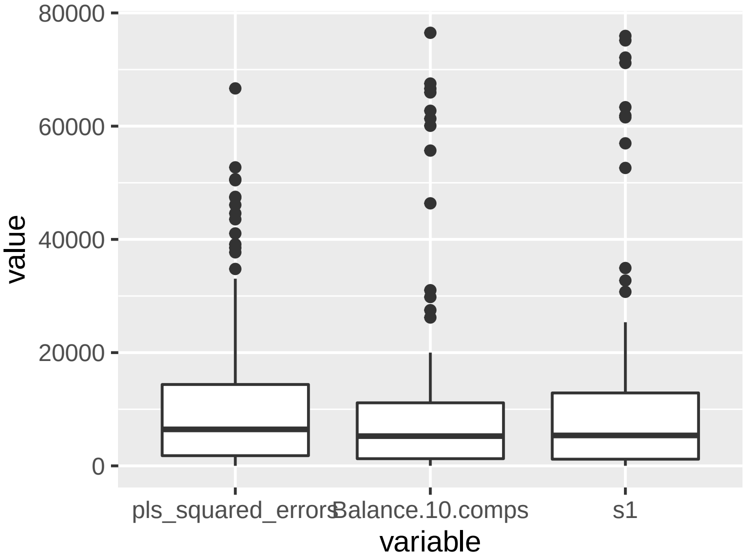
```
set.seed(1)

pls_model = plsr(Balance ~., data = training_data, scale = TRUE, validation = "CV")

validationplot(pls_model)
```



```
pls_predictions = predict(pls_model, testing_data, ncomp = 3)

pls_squared_errors = as.numeric((pls_predictions - testing_data$Balance)^2)
squared_errors <- data.frame(pls_squared_errors = pls_squared_errors, squared_errors)

mean(pls_squared_errors)
```

```
## [1] 12476.32
```

```
ggplot(melt(squared_errors)) + geom_boxplot(aes(variable, value))
```



```
colMeans(squared_errors)
```

```
## pls_squared_errors   Balance.10.comps                 s1
##           12476.32           11578.10           12333.23
```