210501867 Script

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Download all the datasets here

https://drive.google.com/drive/folders/1m5xdYpjSILphWonXFQVWelIzWCfUn34N?usp=sharing

Setting working directory

```
setwd("C:/Users/Admin/Desktop/datasets")
```

Loading library

```
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 4.1.3

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(tidyr)
```

```
## Warning: package 'tidyr' was built under R version 4.1.3
```

```
library(MASS)
```

```
## Warning: package 'MASS' was built under R version 4.1.3

##
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':
##
##     select
```

```r
library(ISLR2)
```

```
## Warning: package 'ISLR2' was built under R version 4.1.3
```

```
##
## Attaching package: 'ISLR2'
```

```
## The following object is masked from 'package:MASS':
##
##     Boston
```

```r
library(caTools)
```

```
## Warning: package 'caTools' was built under R version 4.1.3
```

```r
library(Metrics)
```

```
## Warning: package 'Metrics' was built under R version 4.1.3
```

```r
library(magrittr)
```

```
##
## Attaching package: 'magrittr'
```

```
## The following object is masked from 'package:tidyr':
##
##     extract
```

```r
library(fastDummies)
```

```
## Thank you for using fastDummies!
```

```
## To acknowledge our work, please cite the package:
```

```
## Kaplan, J. & Schlegel, B. (2023). fastDummies: Fast Creation of Dummy (Binary) Columns and Rows from
```

```r
library(randomForest)
```

```
## Warning: package 'randomForest' was built under R version 4.1.3
```

```
## randomForest 4.7-1.1
```

```
## Type rfNews() to see new features/changes/bug fixes.
```

```
##
## Attaching package: 'randomForest'

## The following object is masked from 'package:dplyr':
##
##     combine
```

```r
library(xgboost)
```

```
## Warning: package 'xgboost' was built under R version 4.1.3

##
## Attaching package: 'xgboost'

## The following object is masked from 'package:dplyr':
##
##     slice
```

```r
library(cluster)
library("ggrepel")
```

```
## Warning: package 'ggrepel' was built under R version 4.1.3

## Loading required package: ggplot2

##
## Attaching package: 'ggplot2'

## The following object is masked from 'package:randomForest':
##
##     margin
```

```r
library("factoextra")
```

```
## Warning: package 'factoextra' was built under R version 4.1.3

## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
```

```r
library(e1071)
```

```
## Warning: package 'e1071' was built under R version 4.1.3
```

```r
library(caret)
```

```
## Warning: package 'caret' was built under R version 4.1.3

## Loading required package: lattice
```

```
##
## Attaching package: 'caret'

## The following objects are masked from 'package:Metrics':
##
##     precision, recall
```

```r
library(pROC)
```

```
## Warning: package 'pROC' was built under R version 4.1.3

## Type 'citation("pROC")' for a citation.

##
## Attaching package: 'pROC'

## The following object is masked from 'package:Metrics':
##
##     auc

## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```r
library(magrittr)
library(scales)
```

```
## Warning: package 'scales' was built under R version 4.1.3
```

```r
library(igraph)
```

```
## Warning: package 'igraph' was built under R version 4.1.3

##
## Attaching package: 'igraph'

## The following object is masked from 'package:tidyr':
##
##     crossing

## The following objects are masked from 'package:dplyr':
##
##     as_data_frame, groups, union

## The following objects are masked from 'package:stats':
##
##     decompose, spectrum

## The following object is masked from 'package:base':
##
##     union
```

```
library(ggplot2)
library("ggpubr")
```

```
## Warning: package 'ggpubr' was built under R version 4.1.2
```

```
library(corrplot)
```

```
## Warning: package 'corrplot' was built under R version 4.1.3
```

```
## corrplot 0.92 loaded
```

```
library(RColorBrewer)
```

Regression Analysis

Loading and cleaning of dataset

```
movies <- read.csv("movies.csv")
summary.default(movies)
```

```
##         Length Class  Mode
## name    7658   -none- character
## genre   7658   -none- character
## year    7658   -none- numeric
## score   7658   -none- numeric
## votes   7658   -none- numeric
## budget  7658   -none- numeric
## gross   7658   -none- numeric
## runtime 7658   -none- numeric
## company 7658   -none- character
```

```
sum(is.na(movies))
```

```
## [1] 2366
```

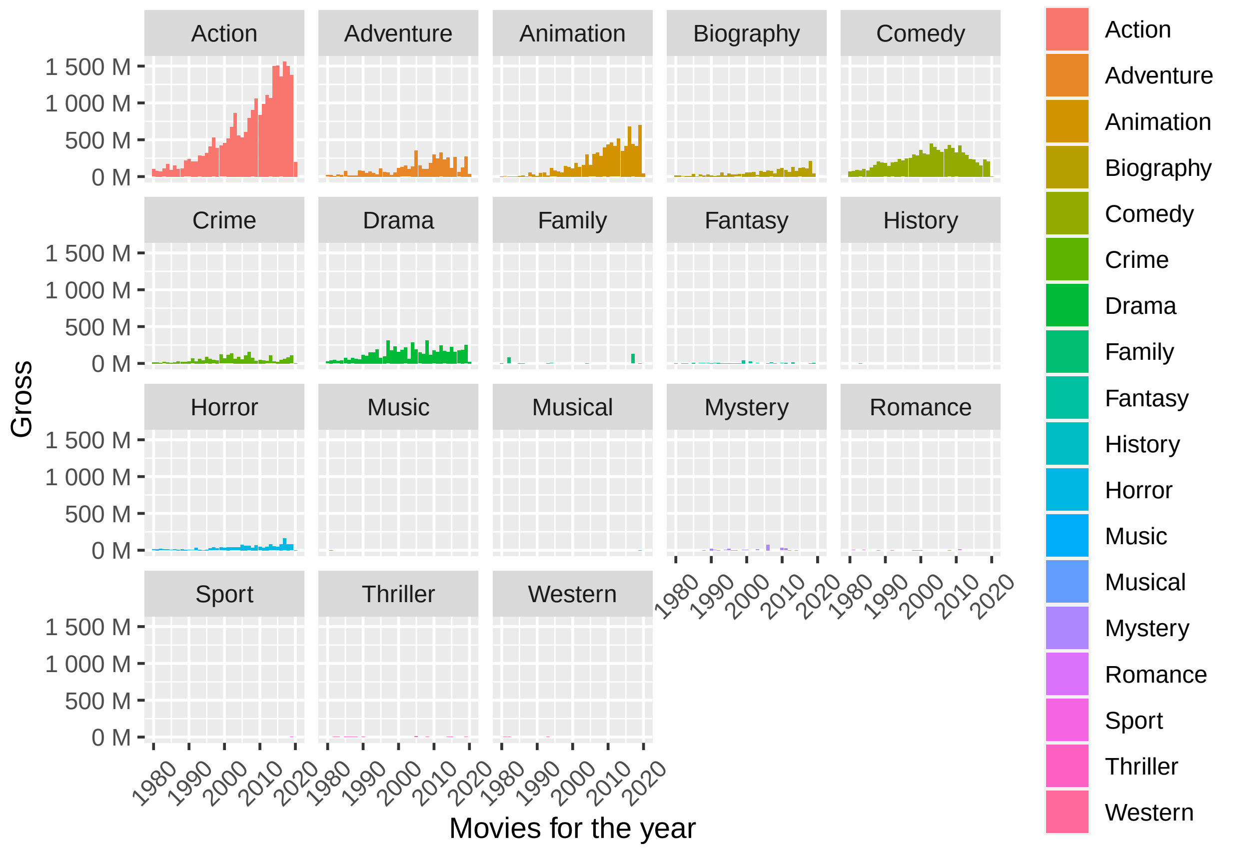
```
sum(duplicated(movies))
```

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

```
movies[is.na(movies)] <- 0
```

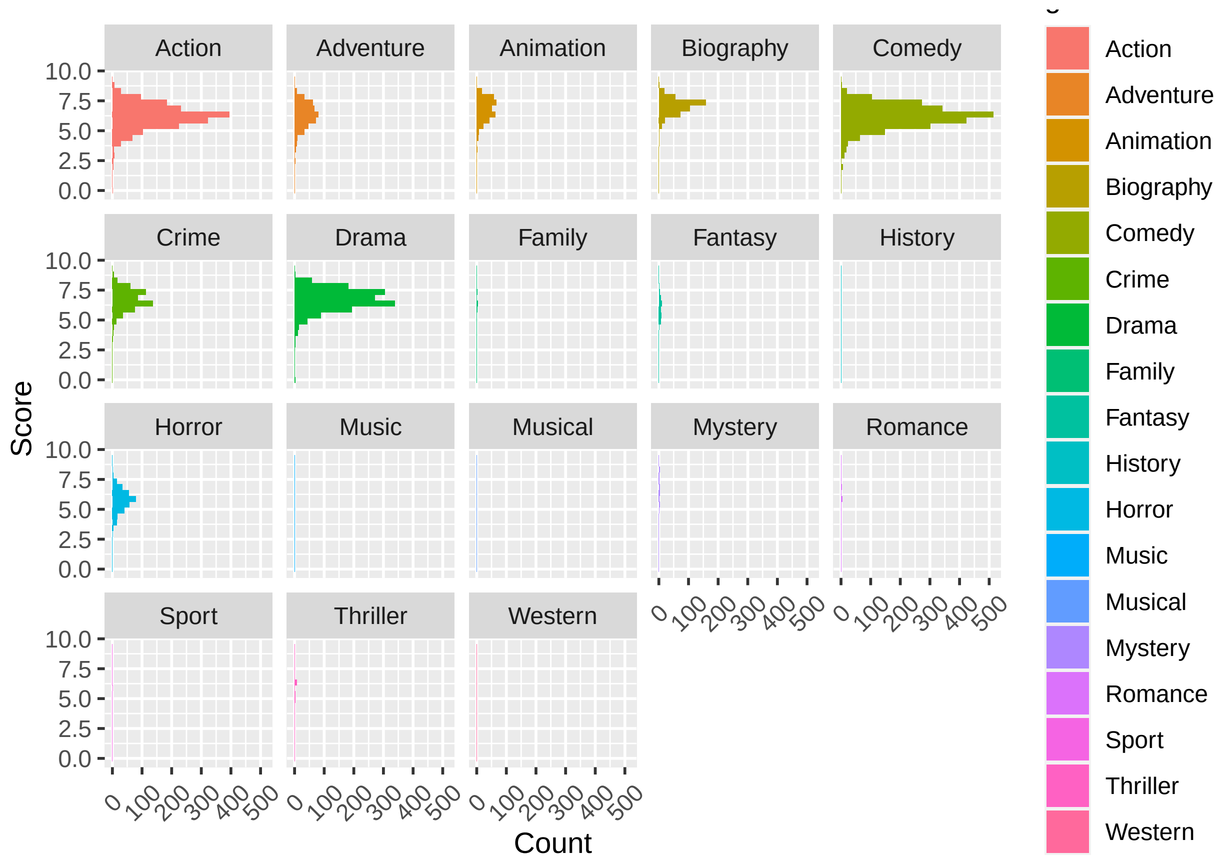
Exploring data

```
ggplot(data = movies, aes(x = year, y = gross, fill = genre)) +
  geom_col() +
  xlab("Movies for the year") +
  ylab("Gross") +
  scale_y_continuous(labels = unit_format(unit = "M", scale = 1e-7)) +
  facet_wrap("genre") +
  theme(axis.text.x = element_text(angle = 45, vjust = 0.5, hjust=0.5))
```



Gross by Genre from 1980 to 2020. Action genre made the most revenue while Western made the least.

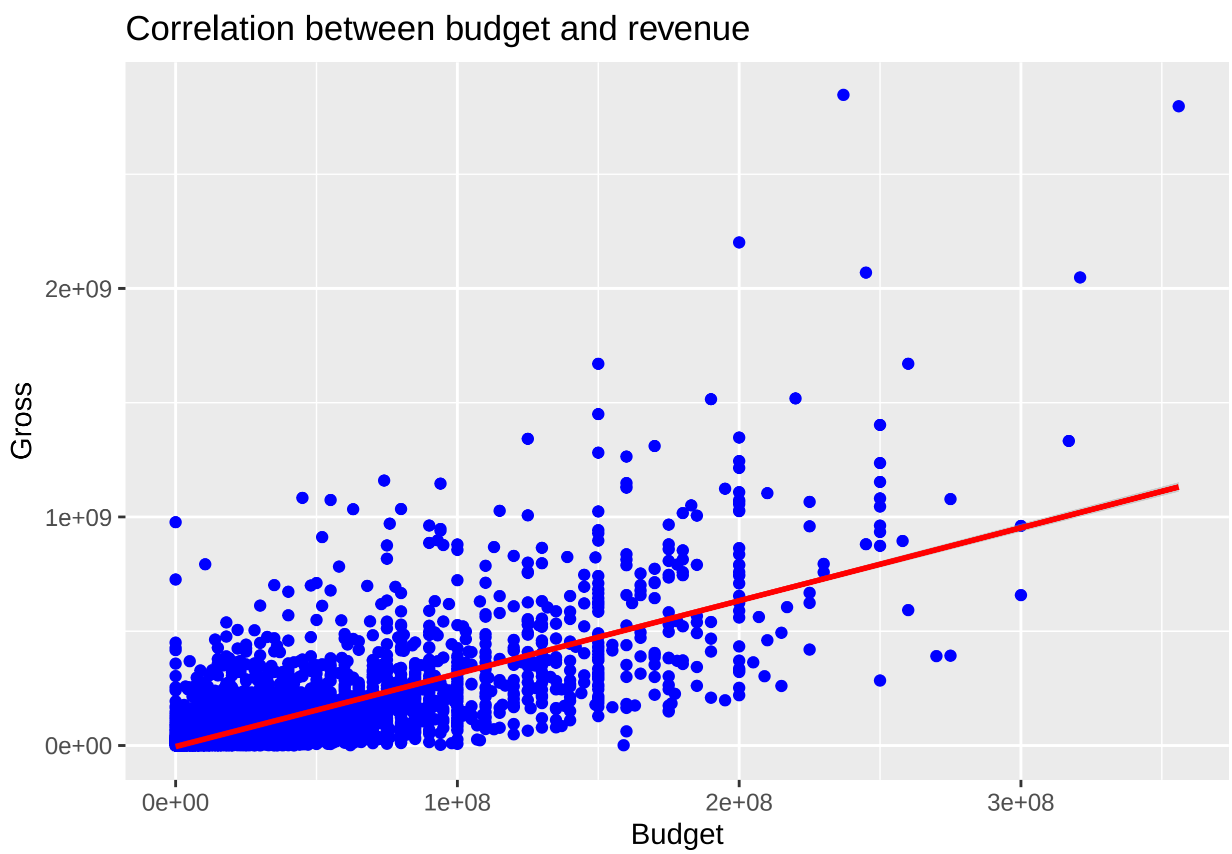
```
ggplot(data = movies, aes(y = score, fill = genre)) +
  geom_histogram(bins = 20) +
  xlab("Count") +
  ylab("Score") +
  facet_wrap("genre") +
  theme(axis.text.x = element_text(angle = 45, vjust = 0.5, hjust=0.5))
```



Score by Genre from 1980 to 2020. Comedy genre had the highest score followed by Action genre.

```
ggplot(data = movies, aes(x = budget, y = gross)) +
  geom_point(color = "blue") +
  geom_smooth(method = "lm", color = "red") +
  xlab("Budget") +
  ylab("Gross") +
  labs(title = "Correlation between budget and revenue")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



Correlation between budget and gross. This showed that there was a positive correlation between the two variables as seen with the regression line.

Setting dataset into test and train sets Removing name, year and company from this model as there will not be any significance for these categorical variables. Only exception would be genre.

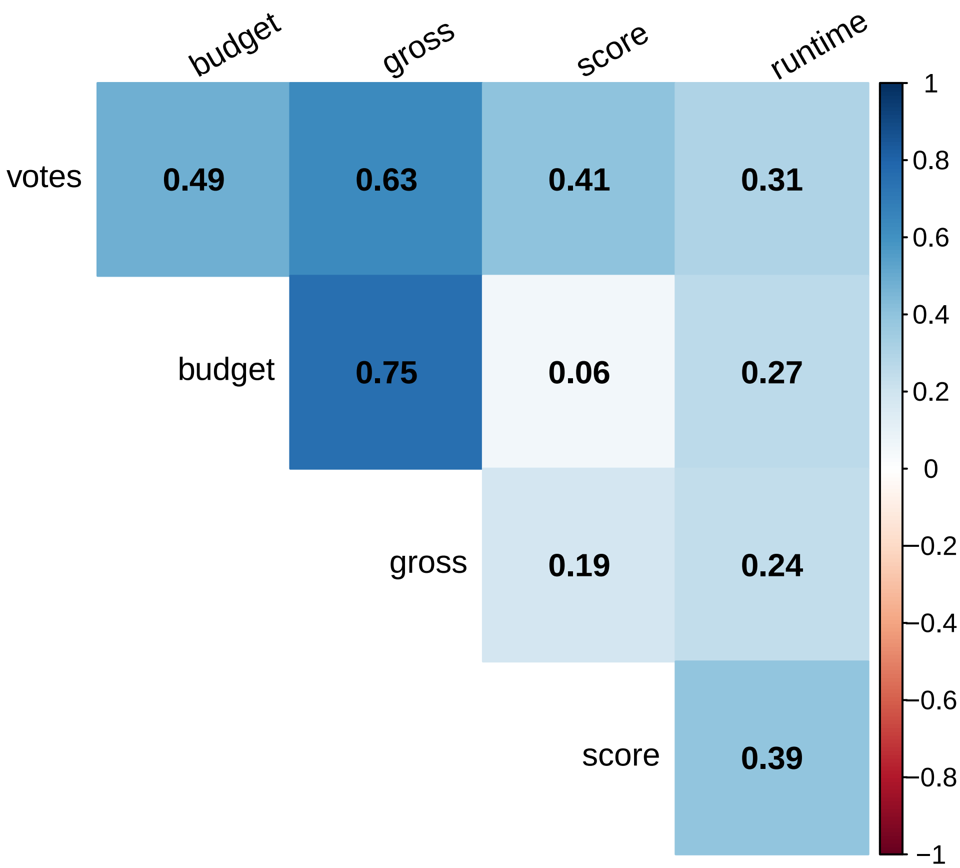
```
set.seed(5)
movies2 <- subset(movies, select= -c(name, year, company)) # removal of insignificant categorical varia
moviesf <- dummy_cols(movies2, select_columns = c("genre"), remove_selected_columns = TRUE, remove_firs
movies_set <- sample.split(moviesf, 0.8)
movies_train <- subset(moviesf, movies_set == TRUE)
movies_test <- subset(moviesf, movies_set == FALSE)
```

Correlation Matrix

```
movies3 <- subset(movies, select= -c(name, year, company, genre)) # removal of all categorical variable
rcorr_matrix <- cor(movies3)
round(rcorr_matrix, 4)
```

```
##          score  votes budget  gross runtime
## score   1.0000 0.4068 0.0568 0.1858  0.3945
## votes   0.4068 1.0000 0.4873 0.6330  0.3071
## budget  0.0568 0.4873 1.0000 0.7503  0.2683
## gross   0.1858 0.6330 0.7503 1.0000  0.2442
## runtime 0.3945 0.3071 0.2683 0.2442  1.0000
```

```r
corrplot(rcorr_matrix, type = "upper", order = "hclust",
         method = "color",
         tl.col = "black", tl.srt = 30,
         addCoef.col = "black",
         sig.level = 0.01,
         diag=FALSE)
```



We see from this correlation matrix that there is strong correlation between gross and budget.

Linear regression

We will make a dummy variable for genre.

```r
lr <- lm(gross ~ . , data = movies_train)
summary(lr)
```

```
##
## Call:
## lm(formula = gross ~ ., data = movies_train)
##
## Residuals:
##        Min         1Q     Median         3Q        Max
## -726820373  -30062077    5149112   22539302 1888561673
##
## Coefficients: (1 not defined because of singularities)
```

```
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -4.497e+07  1.114e+07  -4.039 5.45e-05 ***
## score            1.392e+06  1.632e+06   0.853   0.3939
## votes            3.617e+02  9.993e+00  36.194  < 2e-16 ***
## budget           2.460e+00  4.308e-02  57.094  < 2e-16 ***
## runtime          7.395e+04  8.197e+04   0.902   0.3670
## genre_Adventure  1.020e+07  5.960e+06   1.711   0.0871 .
## genre_Animation  7.386e+07  6.988e+06  10.570  < 2e-16 ***
## genre_Biography -1.839e+06  6.235e+06  -0.295   0.7681
## genre_Comedy     1.507e+07  3.767e+06   4.000 6.42e-05 ***
## genre_Crime     -6.701e+06  5.547e+06  -1.208   0.2271
## genre_Drama      8.283e+06  4.214e+06   1.965   0.0494 *
## genre_Family     1.799e+08  3.258e+07   5.520 3.54e-08 ***
## genre_Fantasy    7.793e+06  1.747e+07   0.446   0.6556
## genre_History           NA         NA      NA       NA
## genre_Horror     2.438e+07  7.000e+06   3.483   0.0005 ***
## genre_Music      2.207e+07  9.743e+07   0.227   0.8208
## genre_Musical    2.547e+07  6.904e+07   0.369   0.7122
## genre_Mystery   -1.952e+07  2.382e+07  -0.819   0.4126
## genre_Romance    2.961e+06  3.692e+07   0.080   0.9361
## genre_Sport      3.063e+07  9.741e+07   0.314   0.7532
## genre_Thriller   2.256e+07  3.693e+07   0.611   0.5413
## genre_Western    2.260e+07  5.630e+07   0.401   0.6881
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 97360000 on 5897 degrees of freedom
## Multiple R-squared:  0.6627, Adjusted R-squared:  0.6616
## F-statistic: 579.4 on 20 and 5897 DF,  p-value: < 2.2e-16
```

```r
radj <- summary(lr)$adj.r.squared # 0.661584
lr_pred <- predict(lr, movies_test, type = "response")
```

```
## Warning in predict.lm(lr, movies_test, type = "response"): prediction from a
## rank-deficient fit may be misleading
```

```r
lr_rmse <- rmse(lr_pred, movies_test$gross) # 87368985
lr_result <- c("Adjusted R Square" = radj, "RMSE" = lr_rmse)
```

Our objective here is to find out how is gross (dependent variable) affected by the other independent variables available. As the dummy variables were created, we can now see which genre has significant impact on gross and for the numerical variables as well. The adjusted R-squared is 0.6736.

> Linear regression without runtime, score, and certain genres that was not significant (Better r-squared)

```r
lr2 <- lm(gross ~ . -runtime -score -genre_Adventure -genre_Biography -genre_Crime -genre_Fantasy -genre
summary(lr2)
```

```
##
## Call:
## lm(formula = gross ~ . - runtime - score - genre_Adventure -
```

```
##     genre_Biography - genre_Crime - genre_Fantasy - genre_History -
##     genre_Music - genre_Musical - genre_Mystery - genre_Romance -
##     genre_Sport - genre_Thriller - genre_Western, data = movies_train)
##
## Residuals:
##        Min         1Q     Median         3Q        Max
## -730679821  -30363390    4977005   22413458 1887786626
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -2.864e+07  2.352e+06 -12.179  < 2e-16 ***
## votes            3.663e+02  8.865e+00  41.316  < 2e-16 ***
## budget           2.469e+00  3.983e-02  61.990  < 2e-16 ***
## genre_Animation  7.257e+07  6.421e+06  11.302  < 2e-16 ***
## genre_Comedy     1.448e+07  3.127e+06   4.631 3.72e-06 ***
## genre_Drama      9.082e+06  3.543e+06   2.563 0.010390 *
## genre_Family     1.794e+08  3.250e+07   5.518 3.57e-08 ***
## genre_Horror     2.267e+07  6.624e+06   3.423 0.000624 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 97330000 on 5910 degrees of freedom
## Multiple R-squared:  0.6622, Adjusted R-squared:  0.6618
## F-statistic:  1655 on 7 and 5910 DF,  p-value: < 2.2e-16
```

```r
radj2 <- summary(lr2)$adj.r.squared # 0.661801
lr2_pred <- predict(lr, movies_test, type = "response")
```

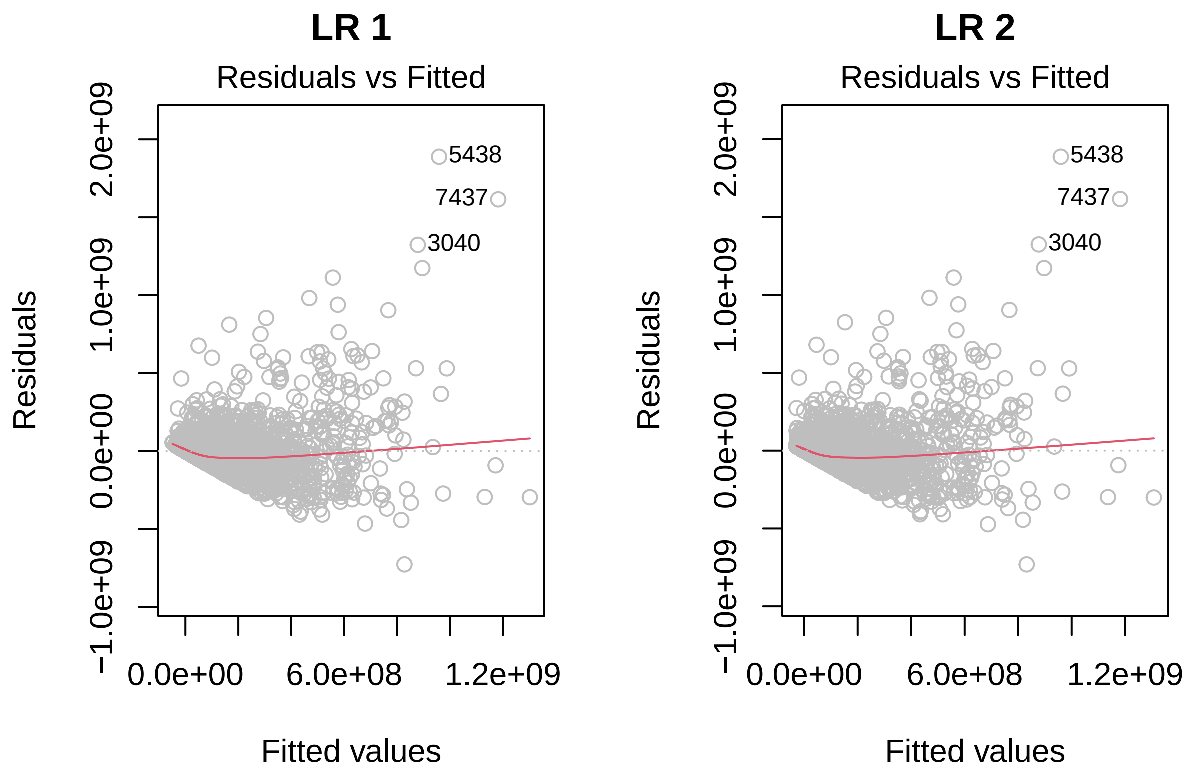
```
## Warning in predict.lm(lr, movies_test, type = "response"): prediction from a
## rank-deficient fit may be misleading
```

```r
lr2_rmse <- rmse(lr_pred, movies_test$gross) # 87368985
lr2_result <- cbind("Adjusted R Square" = radj2, "RMSE" = lr2_rmse)
```

After removing the insignificant variables, the adjusted r-squared improved by 0.0002 at 0.6738 from previous model.

Plots

```r
par(mfrow=c(1,2))
plot(lr, c(1), main = "LR 1", col = "grey")
plot(lr2, c(1), main = "LR 2",col = "grey")
```



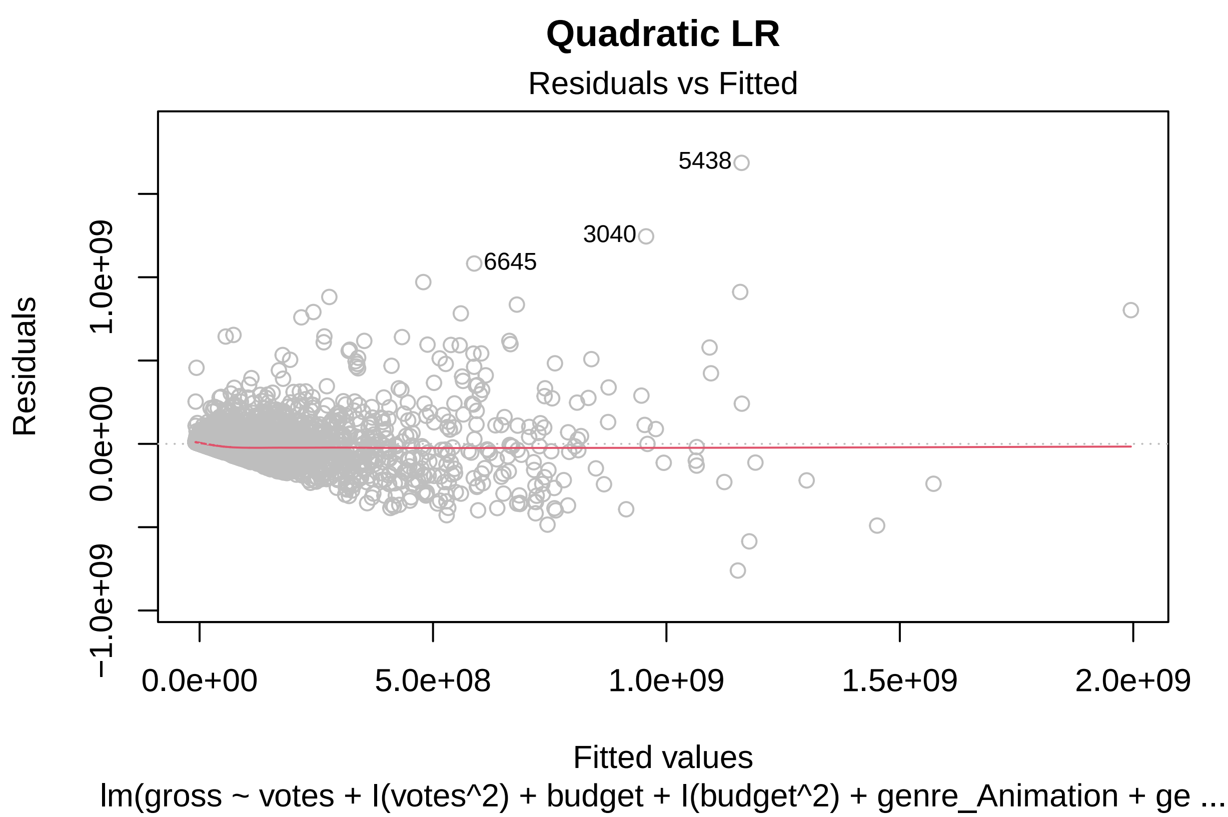
Non-linear transformation of predictors

```
qlr <- lm(gross ~ votes + I(votes^2) + budget + I(budget^2) + genre_Animation + genre_Comedy + genre_Dra
summary(qlr)
```

```
##
## Call:
## lm(formula = gross ~ votes + I(votes^2) + budget + I(budget^2) +
##     genre_Animation + genre_Comedy + genre_Drama + genre_Family +
##     genre_Horror, data = movies_train)
##
## Residuals:
##        Min         1Q     Median         3Q        Max
## -760150418  -19153775    -920646   11835068 1686257373
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -8.958e+06  2.399e+06  -3.734 0.000190 ***
## votes            5.347e+02  1.573e+01  33.998  < 2e-16 ***
## I(votes^2)      -1.539e-04  1.248e-05 -12.338  < 2e-16 ***
## budget           4.832e-01  7.620e-02   6.341 2.45e-10 ***
## I(budget^2)      1.164e-08  4.036e-10  28.827  < 2e-16 ***
## genre_Animation  7.811e+07  5.982e+06  13.057  < 2e-16 ***
## genre_Comedy     1.023e+07  2.918e+06   3.505 0.000461 ***
## genre_Drama      1.512e+06  3.313e+06   0.456 0.648187
```

```
## genre_Family     1.608e+08  3.028e+07   5.310 1.14e-07 ***
## genre_Horror     1.133e+07  6.180e+06   1.833 0.066844 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 90630000 on 5908 degrees of freedom
## Multiple R-squared:  0.7072, Adjusted R-squared:  0.7067
## F-statistic:  1585 on 9 and 5908 DF,  p-value: < 2.2e-16
```

```r
radj3 <- summary(qlr)$adj.r.squared # 0.7067
qlr_pred <- predict(qlr, movies_test, type = "response")
qlr_rmse <- rmse(qlr_pred, movies_test$gross) # 84423164
qlr_result <- cbind("Adjusted R Square" = radj2, "RMSE" = qlr_rmse)
plot(qlr, c(1), main = "Quadratic LR", col = "grey")
```



The non-zero p-value associated with the newly implemented quadratic term resulted in an improved model seen in the increased adjust R-squared.

Random Forest

```r
set.seed(15)
rrf <- randomForest(gross ~ . , data = movies_train, type = "regression")
rrf # r-squared = 73.03%
```

```
##
```

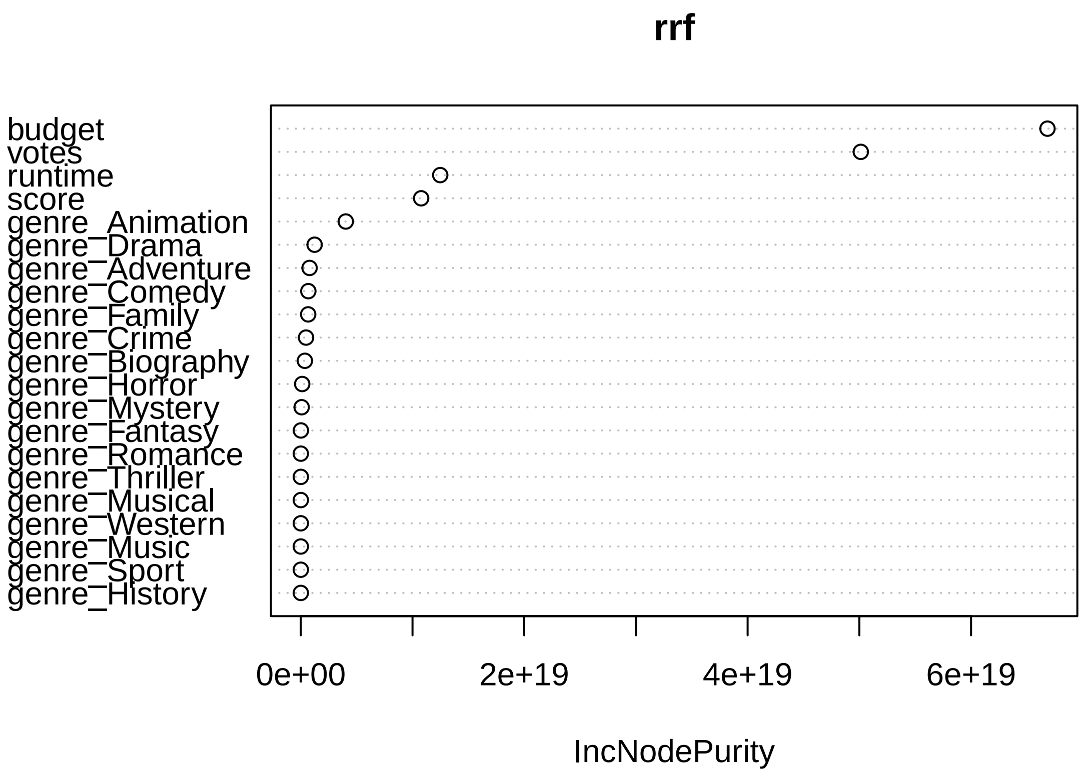
```
## Call:
##  randomForest(formula = gross ~ ., data = movies_train, type = "regression")
##                Type of random forest: regression
##                      Number of trees: 500
## No. of variables tried at each split: 7
##
##           Mean of squared residuals: 7.553173e+15
##                     % Var explained: 73.03
```

```
rrf_pred <- predict(rrf, movies_test)
rrf_rmse <- rmse(rrf_pred, movies_test$gross) # 77096427

#Variables we should take note of
impt_rrf <- varImp(rrf, scale = T)
impt_rrf
```

```
##                      Overall
## score           1.077311e+19
## votes           5.013082e+19
## budget          6.684200e+19
## runtime         1.248073e+19
## genre_Adventure 7.829328e+17
## genre_Animation 4.026380e+18
## genre_Biography 3.626013e+17
## genre_Comedy    6.734470e+17
## genre_Crime     4.690549e+17
## genre_Drama     1.235803e+18
## genre_Family    6.596846e+17
## genre_Fantasy   7.967383e+15
## genre_History   0.000000e+00
## genre_Horror    1.254980e+17
## genre_Music     1.091526e+14
## genre_Musical   7.625776e+14
## genre_Mystery   7.366227e+16
## genre_Romance   1.552712e+15
## genre_Sport     1.593942e+13
## genre_Thriller  8.591671e+14
## genre_Western   1.406925e+14
```

```
varImpPlot(rrf)
```



The two most important variables are budget and votes that would have significant impact on gross can be observed from the Random Forest plot.

Support Vector Machine (worse than rf)

```
rsvm <- svm(gross ~ . , data = movies_train, cost = 10, scale = FALSE)
rsvm_pred <- predict(rsvm, movies_test) # predict target label
rsvm_rmse <- rmse(rsvm_pred, movies_test$gross) # 162413205
```

XGBoost

```
set.seed(10)
rxgb <- caret::train(gross ~ .,
              data = movies_train,
              method = "xgbTree",
              trControl = trainControl("cv", verboseIter = FALSE, number = 10, allowParallel = TRUE),
              verbose = TRUE)
```

```
## [10:48:47] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterat
## [10:48:47] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterat
## [10:48:47] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterat
## [10:48:47] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterat
## [10:48:47] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterat
## [10:48:47] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterat
## [10:48:47] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterat
```

```
## [10:48:47] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
## [10:48:47] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
## [10:48:47] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
## [10:48:47] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
## [10:48:47] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
## [10:48:48] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
## [10:48:48] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
## [10:48:48] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
## [10:48:48] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
## [10:48:48] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
## [10:48:48] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
## [10:48:48] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
## [10:48:48] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
## [10:48:49] WARNING: amalgamation/../src/c_api/c_api.cc:785: `ntree_limit` is deprecated, use `iterati
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```
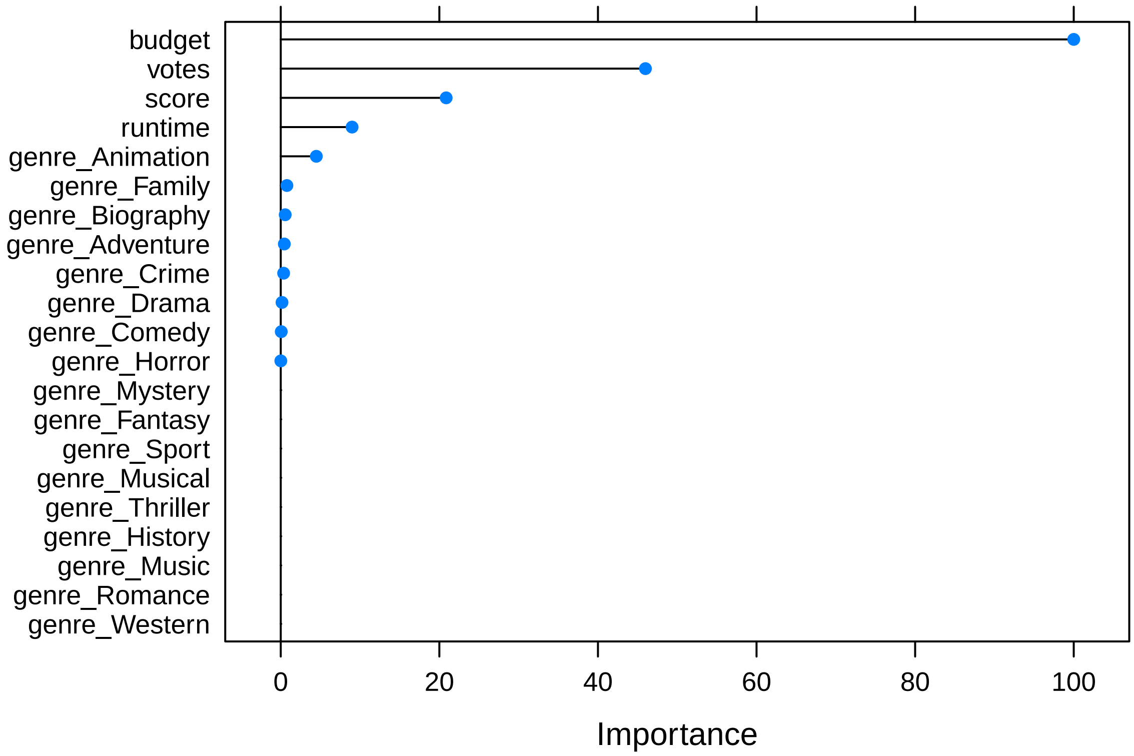

```r
rxgb_pred <- predict(rxgb, movies_test)
rxgb_rmse <- rmse(rxgb_pred, movies_test$gross) # 81609432

#Variables we should take note of
impt_rxgb <- varImp(rxgb, scale = T)
impt_rxgb
```

```
## xgbTree variable importance
##
##   only 20 most important variables shown (out of 21)
##
##                   Overall
## budget          100.00000
## votes            45.99125
## score            20.86238
## runtime           8.99660
## genre_Animation   4.48795
## genre_Family      0.77761
## genre_Biography   0.56420
## genre_Adventure   0.45136
## genre_Crime       0.36302
## genre_Drama       0.15790
## genre_Comedy      0.06691
## genre_Horror      0.01081
## genre_Fantasy     0.00000
## genre_History     0.00000
## genre_Thriller    0.00000
## genre_Musical     0.00000
## genre_Romance     0.00000
## genre_Mystery     0.00000
## genre_Music       0.00000
## genre_Sport       0.00000
```

```r
plot(impt_rxgb)
```

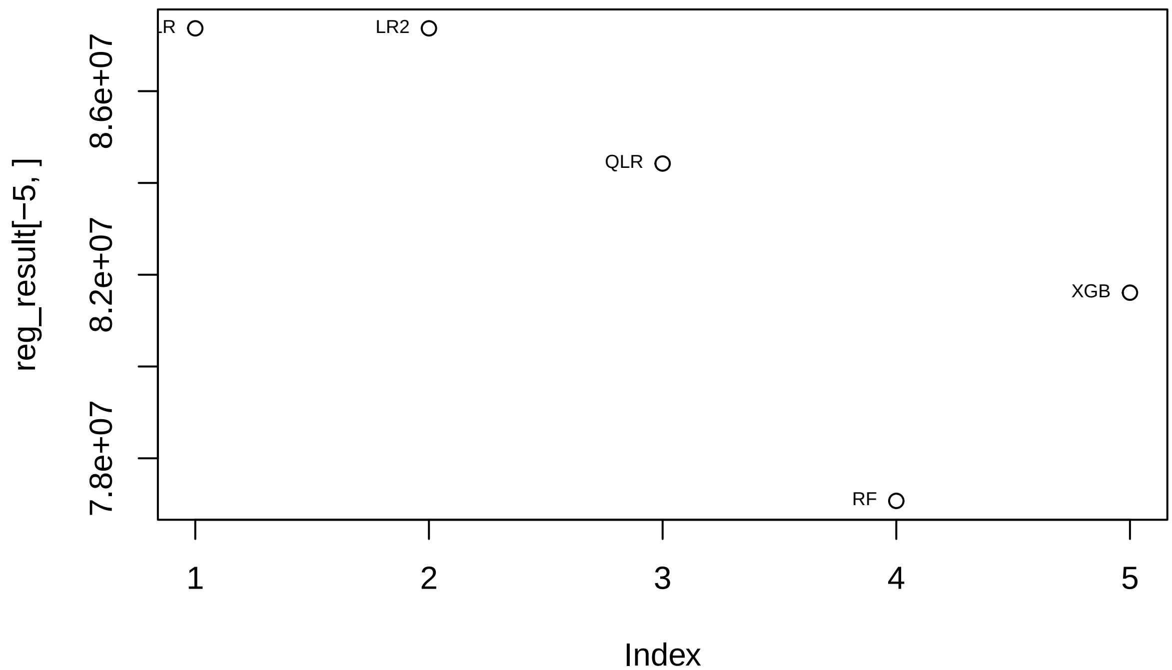


Final result of all model

```
RMSE <- c(lr_rmse, lr2_rmse, qlr_rmse, rrf_rmse, rsvm_rmse, rxgb_rmse)
reg_result <- data.frame(RMSE,
                         row.names = c("Linear Regression", "Linear Regression 2", "Quadratic LR", "Ranc
reg_result
```

```
##                               RMSE
## Linear Regression         87368985
## Linear Regression 2       87368985
## Quadratic LR              84423164
## Random Forest             77072280
## Support Vector Machine 162413205
## XGBoost                   81609432
```

```
outlier <- reg_result > 90000000
plot(reg_result[-5, ])
text(reg_result[-5, ], labels = c("LR", "LR2", "QLR", "RF","XGB"), pos = 2, cex = 0.6)
```



From the plot, we can observe that XGBoost has the best model in predicting gross as it has the best AUC of 0.9804 and second lowest RMSE of 81609432.

Classification Analysis

Loading and cleaning of dataset

```
heart_m <- read.csv("heart.csv")
summary(heart_m)
```

```
##       age             sex               cp            trestbps
##  Min.   :29.00   Min.   :0.0000   Min.   :0.0000   Min.   : 94.0
##  1st Qu.:48.00   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:120.0
##  Median :56.00   Median :1.0000   Median :1.0000   Median :130.0
##  Mean   :54.43   Mean   :0.6956   Mean   :0.9424   Mean   :131.6
##  3rd Qu.:61.00   3rd Qu.:1.0000   3rd Qu.:2.0000   3rd Qu.:140.0
##  Max.   :77.00   Max.   :1.0000   Max.   :3.0000   Max.   :200.0
##       chol          fbs             restecg          thalach
##  Min.   :126   Min.   :0.0000   Min.   :0.0000   Min.   : 71.0
##  1st Qu.:211   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:132.0
##  Median :240   Median :0.0000   Median :1.0000   Median :152.0
##  Mean   :246   Mean   :0.1493   Mean   :0.5298   Mean   :149.1
##  3rd Qu.:275   3rd Qu.:0.0000   3rd Qu.:1.0000   3rd Qu.:166.0
##  Max.   :564   Max.   :1.0000   Max.   :2.0000   Max.   :202.0
##      exang              ca              thal            target
```

```
##  Min.   :0.0000   Min.   :0.0000   Min.   :0.000   Min.   :0.0000
##  1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:2.000   1st Qu.:0.0000
##  Median :0.0000   Median :0.0000   Median :2.000   Median :1.0000
##  Mean   :0.3366   Mean   :0.7541   Mean   :2.324   Mean   :0.5132
##  3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:3.000   3rd Qu.:1.0000
##  Max.   :1.0000   Max.   :4.0000   Max.   :3.000   Max.   :1.0000
```

```
sum(is.na(heart_m))
```

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

```
sum(duplicated(heart_m))
```

```
## [1] 723
```

No NAs to omit. Clean data.

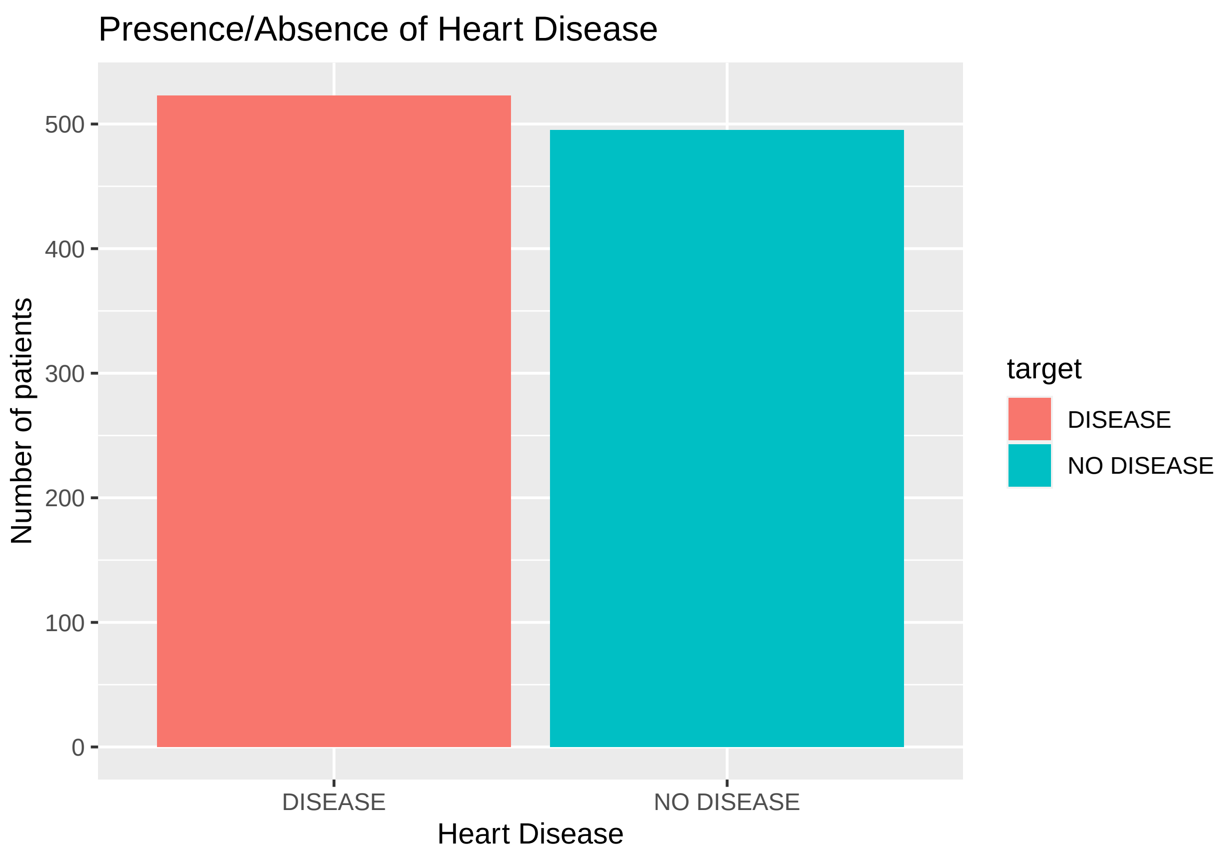
Exploring data

```
heart_m["thal"][heart_m["thal"] == 0] <- NA
heart_dropna <- heart_m %>% drop_na(thal)
heart <- heart_dropna %>%
  mutate(sex = if_else(sex == 1, "MALE", "FEMALE"),
         fbs = if_else(fbs == 1, ">120", "<=120"),
         exang = if_else(exang == 1, "YES" ,"NO"),
         thal = if_else(thal == 1, "NORMAL", if_else(thal == 2, "FIXED", "REVERSABLE")),
         target = if_else(target == 1, "DISEASE", "NO DISEASE")
         ) %>%
  mutate_if(is.character, as.factor) # changing to factor
summary(heart)
```

```
##       age            sex            cp           trestbps         chol
##  Min.   :29.00   FEMALE:309   Min.   :0.000   Min.   : 94.0   Min.   :126.0
##  1st Qu.:48.00   MALE  :709   1st Qu.:0.000   1st Qu.:120.0   1st Qu.:211.0
##  Median :56.00                Median :1.000   Median :130.0   Median :240.0
##  Mean   :54.45                Mean   :0.943   Mean   :131.6   Mean   :246.3
##  3rd Qu.:61.00                3rd Qu.:2.000   3rd Qu.:140.0   3rd Qu.:275.8
##  Max.   :77.00                Max.   :3.000   Max.   :200.0   Max.   :564.0
##     fbs          restecg          thalach        exang          ca
##  <=120:869   Min.   :0.0000   Min.   : 71.0   NO :677   Min.   :0.0000
##  >120 :149   1st Qu.:0.0000   1st Qu.:132.0   YES:341   1st Qu.:0.0000
##              Median :1.0000   Median :152.0             Median :0.0000
##              Mean   :0.5295   Mean   :149.2             Mean   :0.7593
##              3rd Qu.:1.0000   3rd Qu.:166.0             3rd Qu.:1.0000
##              Max.   :2.0000   Max.   :202.0             Max.   :4.0000
##          thal              target
##  FIXED     :544   DISEASE   :523
##  NORMAL    : 64   NO DISEASE:495
##  REVERSABLE:410
##
##
##
```

Summary of the data after data transformation

```
ggplot(heart, aes(x = target, fill = target)) +
  geom_bar() +
  xlab("Heart Disease") +
  ylab("Number of patients") +
  ggtitle("Presence/Absence of Heart Disease")
```




```
table(heart$target)
```

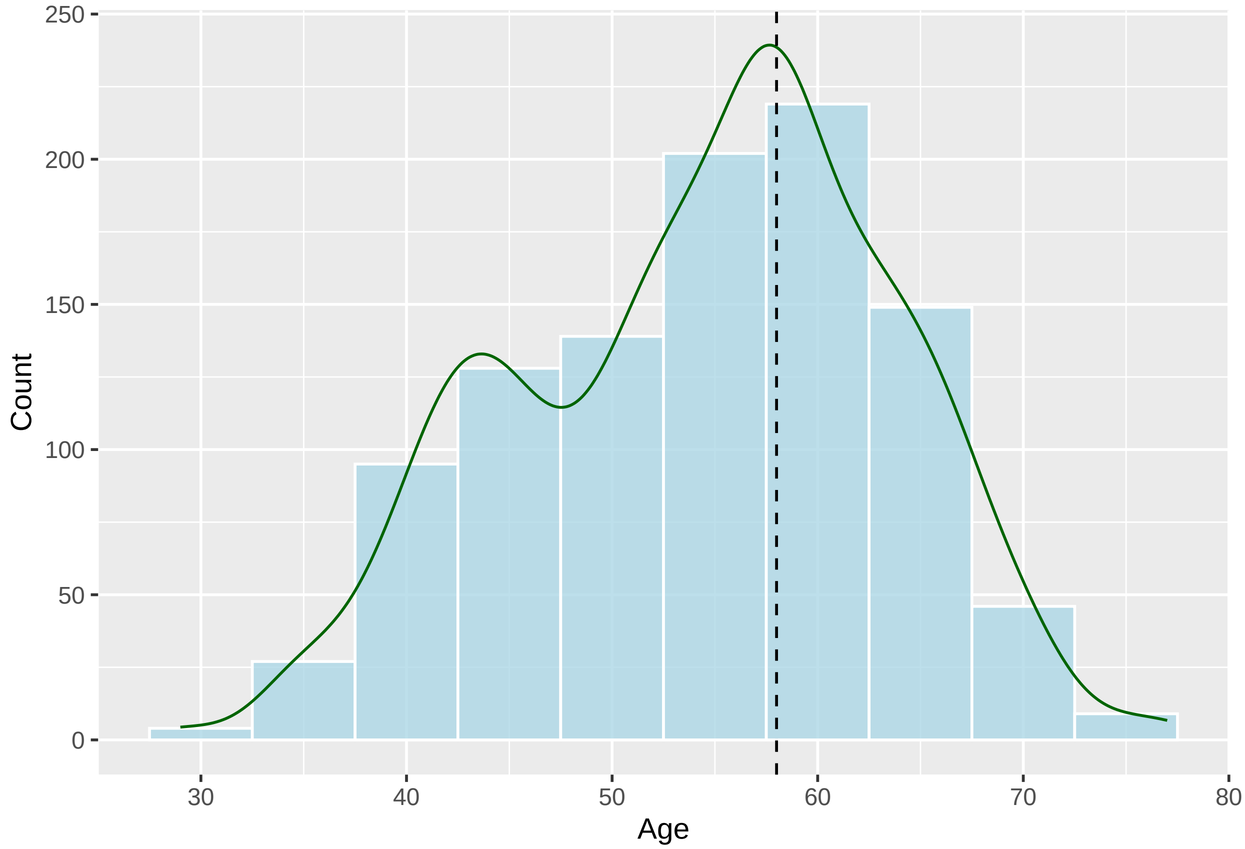
```
##
##    DISEASE NO DISEASE
##        523        495
```

Visualization of target showing no imbalance issue.

```
ggplot(heart, aes(x = age)) +
  geom_histogram(binwidth = 5, colour = "white", fill = "lightblue", alpha = 0.8) +
  geom_density(eval(bquote(aes(y=..count..*5))),colour="darkgreen", alpha=0.3) +
  geom_vline(xintercept = 58, linetype="dashed") +
  xlab("Age") +
  ylab("Count")
```

```
## Warning: The dot-dot notation (`..count..`) was deprecated in ggplot2 3.4.0.
```

```
## i Please use `after_stat(count)` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



Showing a normal distribution of age.

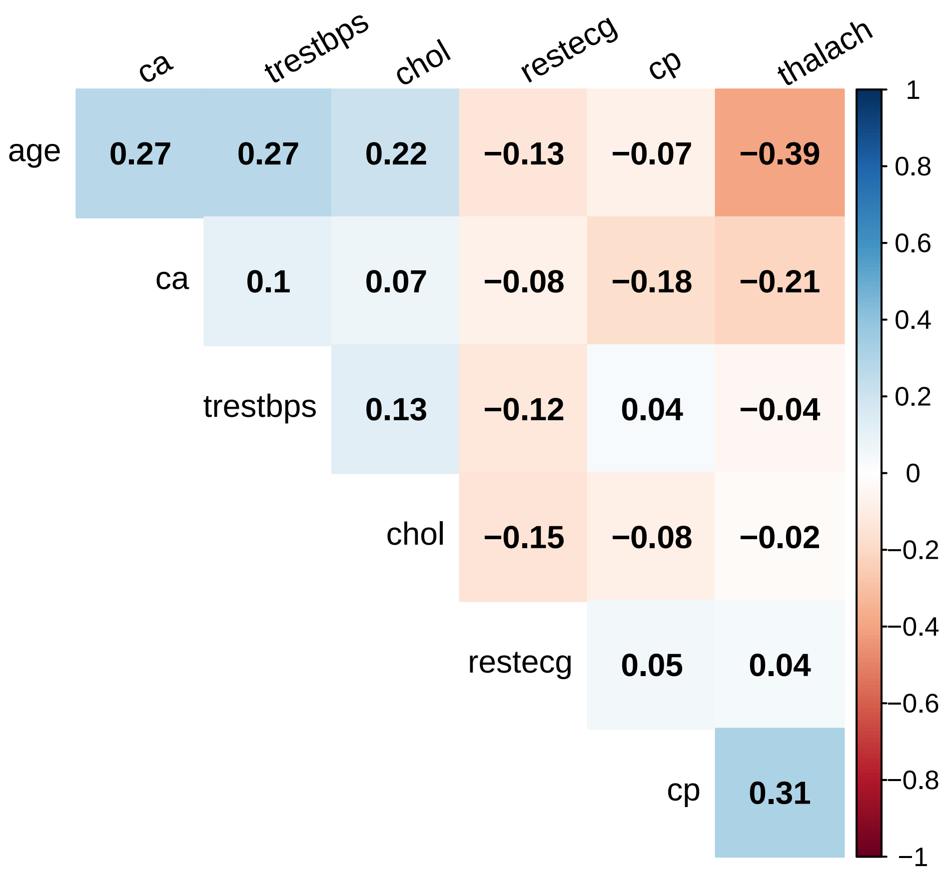
Continuous Variables

```
num.cols <- sapply(heart, is.numeric)
ccorr_matrix <- cor(heart[,num.cols])
round(ccorr_matrix, 4)
```

```
##              age      cp trestbps    chol restecg thalach      ca
## age       1.0000 -0.0727   0.2709  0.2191 -0.1327 -0.3920  0.2710
## cp       -0.0727  1.0000   0.0382 -0.0832  0.0501  0.3144 -0.1775
## trestbps  0.2709  0.0382   1.0000  0.1272 -0.1241 -0.0401  0.1037
## chol      0.2191 -0.0832   0.1272  1.0000 -0.1470 -0.0235  0.0709
## restecg  -0.1327  0.0501  -0.1241 -0.1470  1.0000  0.0433 -0.0781
## thalach  -0.3920  0.3144  -0.0401 -0.0235  0.0433  1.0000 -0.2113
## ca        0.2710 -0.1775   0.1037  0.0709 -0.0781 -0.2113  1.0000
```

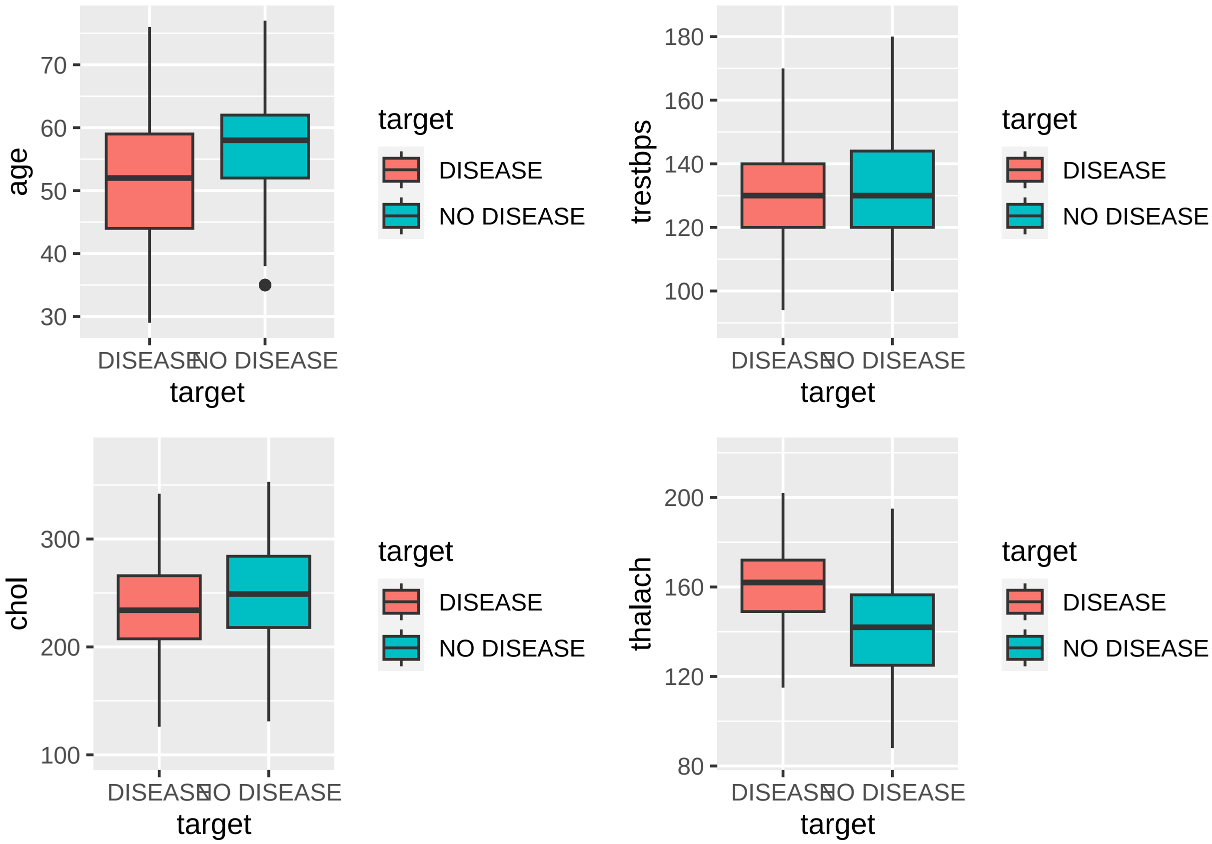
```
corrplot(ccorr_matrix, type = "upper", order = "hclust",
         method = "color",
         tl.col = "black", tl.srt = 30,
```

```
        addCoef.col = "black",
        sig.level = 0.01,
        diag=FALSE)
```



Correlation plot. Barely shown any correlation between the numeric variables, meaning it may require the categorical variables for further analysis.

```
tar_age <- ggplot(heart, aes(target, age, fill = target)) +
  geom_boxplot()

tar_trest <- ggplot(heart, aes(target, trestbps, fill = target)) +
  geom_boxplot(outlier.shape = NA) +
  coord_cartesian(ylim = c(90,185))

tar_chol <- ggplot(heart, aes(target, chol, fill = target)) +
  geom_boxplot(outlier.shape = NA) +
  coord_cartesian(ylim = c(100,380))

tar_thalach <- ggplot(heart, aes(target, thalach, fill = target)) +
  geom_boxplot(outlier.shape = NA) +
  coord_cartesian(ylim = c(85,220))

tar_conplots <- ggarrange(tar_age, tar_trest, tar_chol, tar_thalach,
                          ncol = 2, nrow = 2)
tar_conplots
```

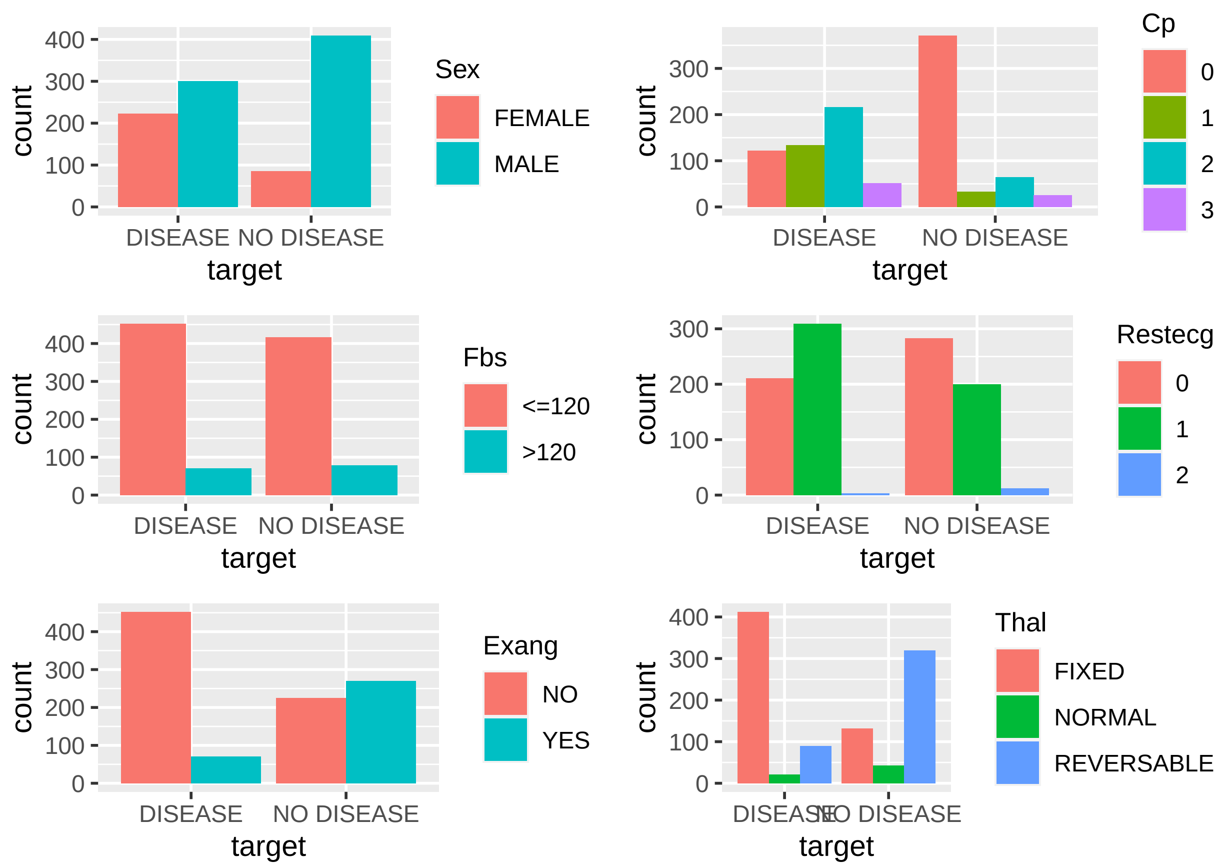


Categorical variables

All target related EDA

```
tar_sex <- ggplot(heart, aes(target)) +
  geom_bar(aes(fill = factor(sex)), position = "dodge") +
  labs(fill = "Sex") +
  theme(legend.title = element_text(size = 10))

tar_cp <- ggplot(heart, aes(target)) +
  geom_bar(aes(fill = factor(cp)), position = "dodge") +
  labs(fill = "Cp") +
  theme(legend.title = element_text(size = 10))

tar_fbs <- ggplot(heart, aes(target)) +
  geom_bar(aes(fill = factor(fbs)), position = "dodge") +
  labs(fill = "Fbs") +
  theme(legend.title = element_text(size = 10)) # though not that accurate as research says that if its

tar_restecg <- ggplot(heart, aes(target)) +
  geom_bar(aes(fill = factor(restecg)), position = "dodge") +
  labs(fill = "Restecg") +
  theme(legend.title = element_text(size = 10))

tar_exang <- ggplot(heart, aes(target)) +
```

```r
  geom_bar(aes(fill = factor(exang)), position = "dodge") +
  labs(fill = "Exang") +
  theme(legend.title = element_text(size = 10))

tar_thal <- ggplot(heart, aes(target)) +
  geom_bar(aes(fill = factor(thal)), position = "dodge") +
  labs(fill = "Thal") +
  theme(legend.title = element_text(size = 10))

tar_catplots <- ggarrange(tar_sex, tar_cp, tar_fbs, tar_restecg, tar_exang, tar_thal,
                          ncol = 2, nrow = 3)
print(tar_catplots)
```



Setting dataset into training and testing sets

```r
set.seed(10)
heart_set <- sample.split(heart_dropna, 0.8)
heart_train <- subset(heart_dropna, heart_set == TRUE)
heart_test <- subset(heart_dropna, heart_set == FALSE)
```

Logistic Regression

Training Log model

```r
library(car)
```

```
## Warning: package 'car' was built under R version 4.1.3

## Loading required package: carData

## Warning: package 'carData' was built under R version 4.1.2

##
## Attaching package: 'car'

## The following object is masked from 'package:dplyr':
##
##     recode
```

```r
lgm <- glm(target ~ . , data = heart_train, family = "binomial")
summary(lgm) # AIC = 610.61
```

```
##
## Call:
## glm(formula = target ~ ., family = "binomial", data = heart_train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.2525  -0.4998   0.1115   0.5927   2.7783
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.413207   1.533294   2.226  0.02601 *
## age          0.001366   0.014220   0.096  0.92349
## sex         -1.597452   0.272327  -5.866 4.47e-09 ***
## cp           0.722906   0.105650   6.842 7.78e-12 ***
## trestbps    -0.023991   0.006070  -3.953 7.73e-05 ***
## chol        -0.006054   0.002203  -2.748  0.00599 **
## fbs          0.183344   0.310814   0.590  0.55527
## restecg      0.506864   0.201258   2.518  0.01179 *
## thalach      0.029793   0.005887   5.061 4.18e-07 ***
## exang       -1.137073   0.244701  -4.647 3.37e-06 ***
## ca          -0.809376   0.110747  -7.308 2.70e-13 ***
## thal        -0.922307   0.176899  -5.214 1.85e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1059.00  on 763  degrees of freedom
## Residual deviance:  586.61  on 752  degrees of freedom
## AIC: 610.61
##
## Number of Fisher Scoring iterations: 5
```

```r
vif(lgm)
```

```
##      age      sex       cp trestbps     chol      fbs  restecg  thalach
## 1.414884 1.308671 1.146207 1.141986 1.261657 1.092062 1.083157 1.278136
##    exang       ca     thal
## 1.137667 1.101462 1.042433
```

AIC is at 610.10 (smaller the AIC the better). Since all VIF are less than three, there is no multicollinearity between the variables, only insignificant variables for this model.

```r
lgm2 <- glm(target ~ . -fbs - age, data = heart_train, family = "binomial")
summary(lgm2)
```

```
##
## Call:
## glm(formula = target ~ . - fbs - age, family = "binomial", data = heart_train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.2586  -0.4846   0.1100   0.5835   2.7740
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.506511   1.295967   2.706  0.00682 **
## sex         -1.608548   0.270981  -5.936 2.92e-09 ***
## cp           0.731408   0.104966   6.968 3.21e-12 ***
## trestbps    -0.023509   0.005854  -4.016 5.92e-05 ***
## chol        -0.006037   0.002156  -2.800  0.00512 **
## restecg      0.491305   0.197758   2.484  0.01298 *
## thalach      0.029496   0.005450   5.412 6.22e-08 ***
## exang       -1.127526   0.244309  -4.615 3.93e-06 ***
## ca          -0.797647   0.107294  -7.434 1.05e-13 ***
## thal        -0.930064   0.175857  -5.289 1.23e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1059.00  on 763  degrees of freedom
## Residual deviance:  586.98  on 754  degrees of freedom
## AIC: 606.98
##
## Number of Fisher Scoring iterations: 5
```

```r
vif(lgm2)
```

```
##      sex       cp trestbps     chol  restecg  thalach    exang       ca
## 1.291700 1.130583 1.062990 1.215954 1.048399 1.100107 1.132012 1.037208
##     thal
## 1.033195
```

We removed fbs and age as they were insignificant from the previous model and the AIC improved at 606.98. This would be our final model as there are nothing else to be removed.

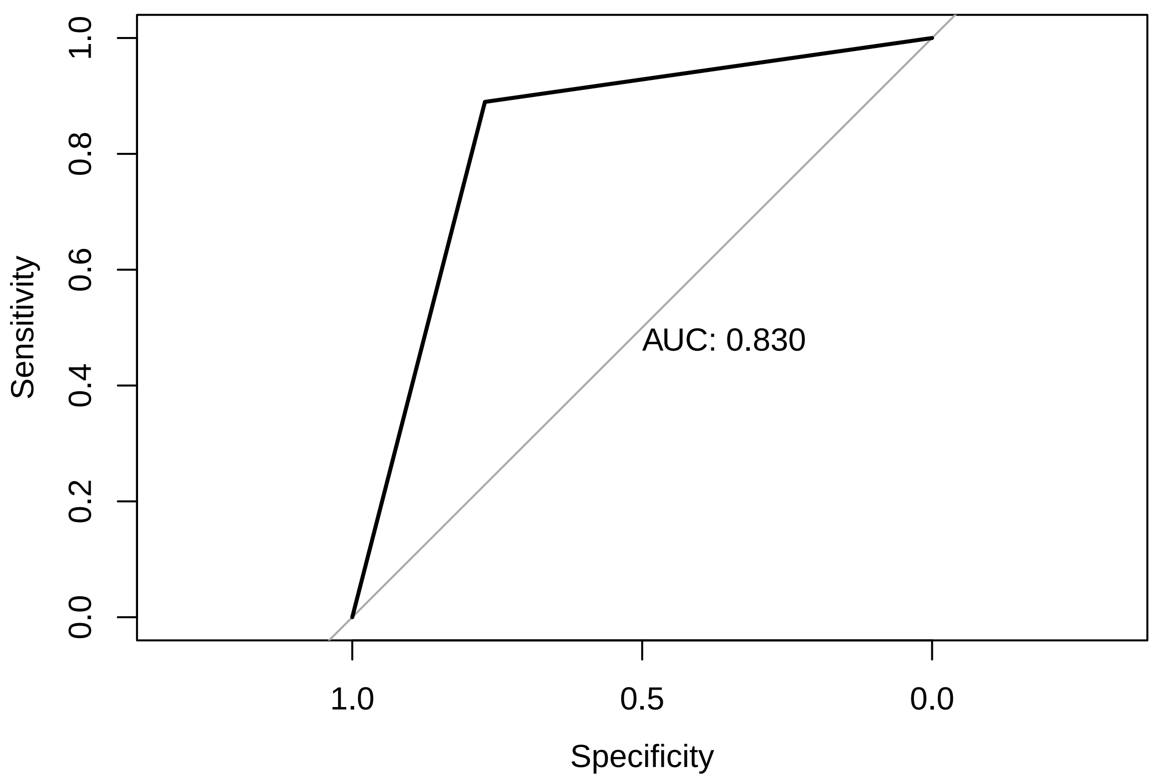
Making predictions

```
clgm_pred <- predict(lgm2, heart_test, type = "response")
clgm_pred <- ifelse(clgm_pred >= 0.5, 1, 0)

# Confusion Matrix
clgm_cm <- confusionMatrix(factor(heart_test$target), factor(clgm_pred))

# ROC-AUC & Accuracy
clgm_roc <- roc(heart_test$target, clgm_pred)
```

```
## Setting levels: control = 0, case = 1
```

```
## Setting direction: controls < cases
```

```
plot(clgm_roc, plot = TRUE, print.auc = TRUE)
```




```
clgm_acc <- clgm_cm$overall[1]
clgm_auc <- clgm_roc$auc
clgm_result <- cbind("Accuracy" = clgm_acc, "AUC" = clgm_auc) # acc = 0.8346 / auc = 0.8304
```

Random Forest

Training RF model

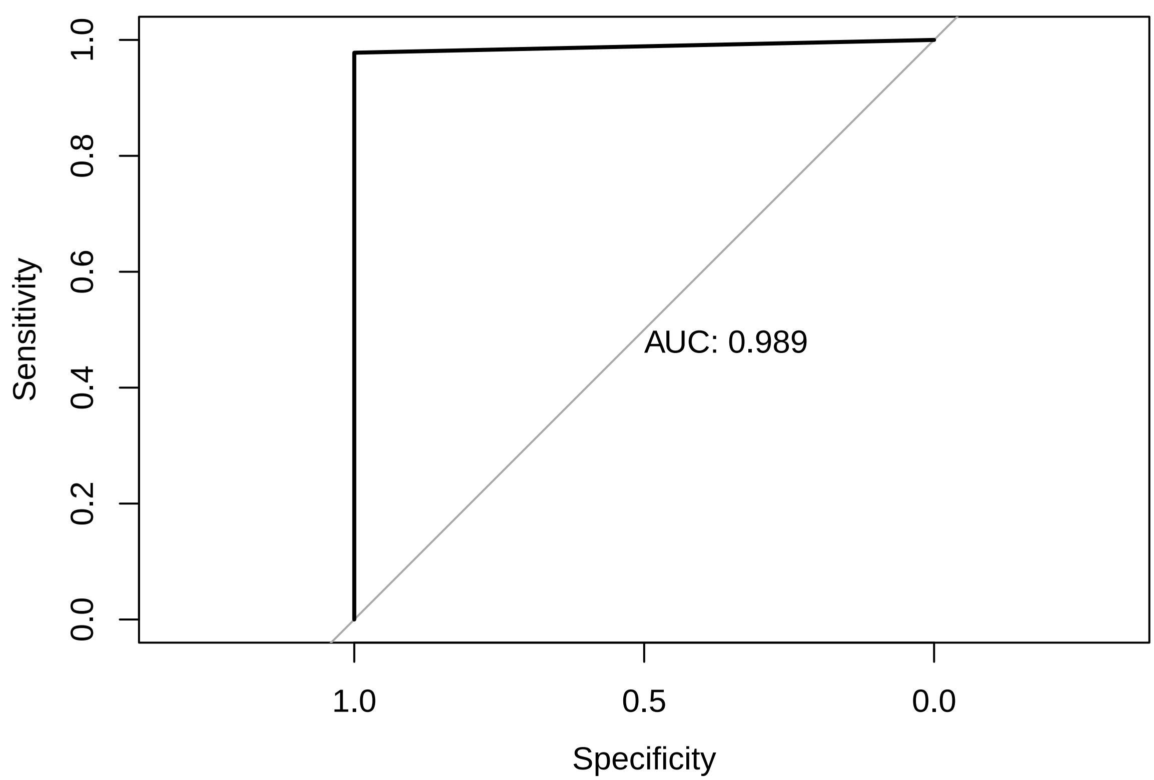
```
set.seed(20)
crf <- randomForest(factor(target) ~ . , data = heart_train)
```

Making predictions

```
crf_pred <- predict(crf, heart_test, type = "class")

# Confusion Matrix
crf_cm <- confusionMatrix(factor(heart_test$target), factor(crf_pred))

# ROC-AUC & Accuracy
crf_roc <- roc(heart_test$target, as.numeric(crf_pred))
```

```
## Setting levels: control = 0, case = 1

## Setting direction: controls < cases
```

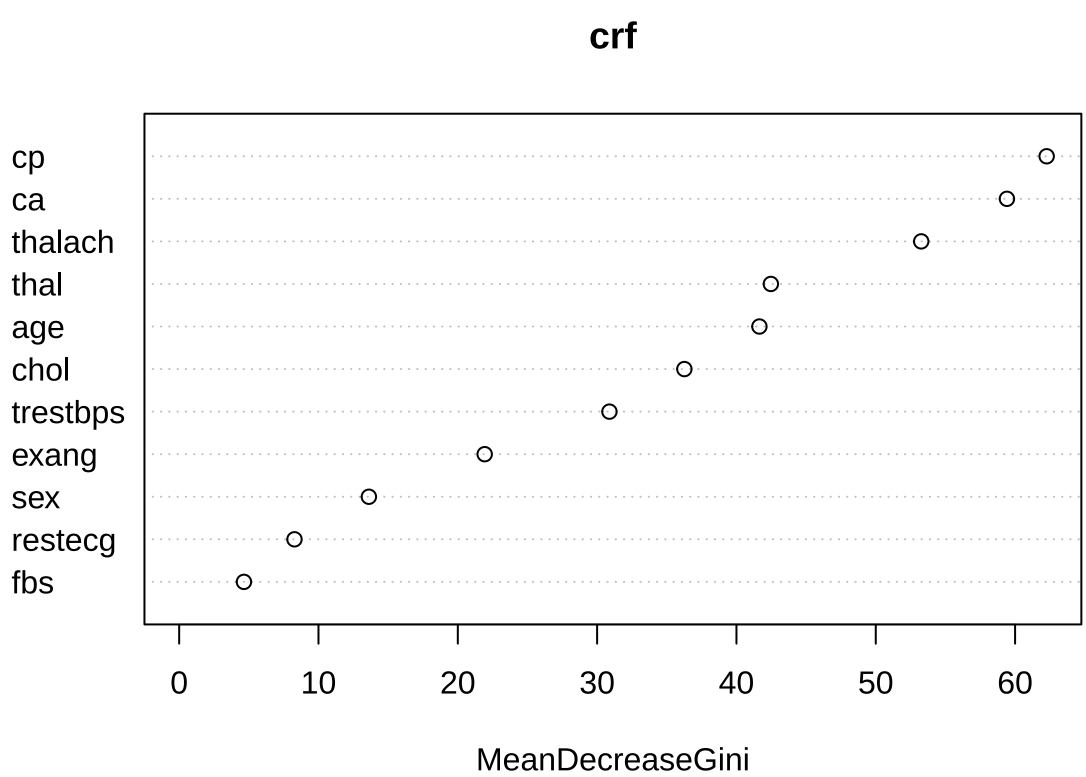
```
plot(crf_roc, plot = TRUE, print.auc = TRUE)
```



```r
crf_acc <- crf_cm$overall[1]
crf_auc <- crf_roc$auc
crf_result <- cbind("Accuracy" = crf_acc, "AUC" = crf_auc) # acc = 0.9882 / auc = 0.98

# Variables we should take note of
impt_crf <- varImp(crf, scale = T)
impt_crf
```

```
##             Overall
## age       41.649579
## sex       13.617770
## cp        62.266709
## trestbps  30.883876
## chol      36.263029
## fbs        4.649603
## restecg    8.277402
## thalach   53.262774
## exang     21.930416
## ca        59.415013
## thal      42.469137
```

```r
varImpPlot(crf)
```



Important variables to take note of are chest pain and ca

Decision Tree

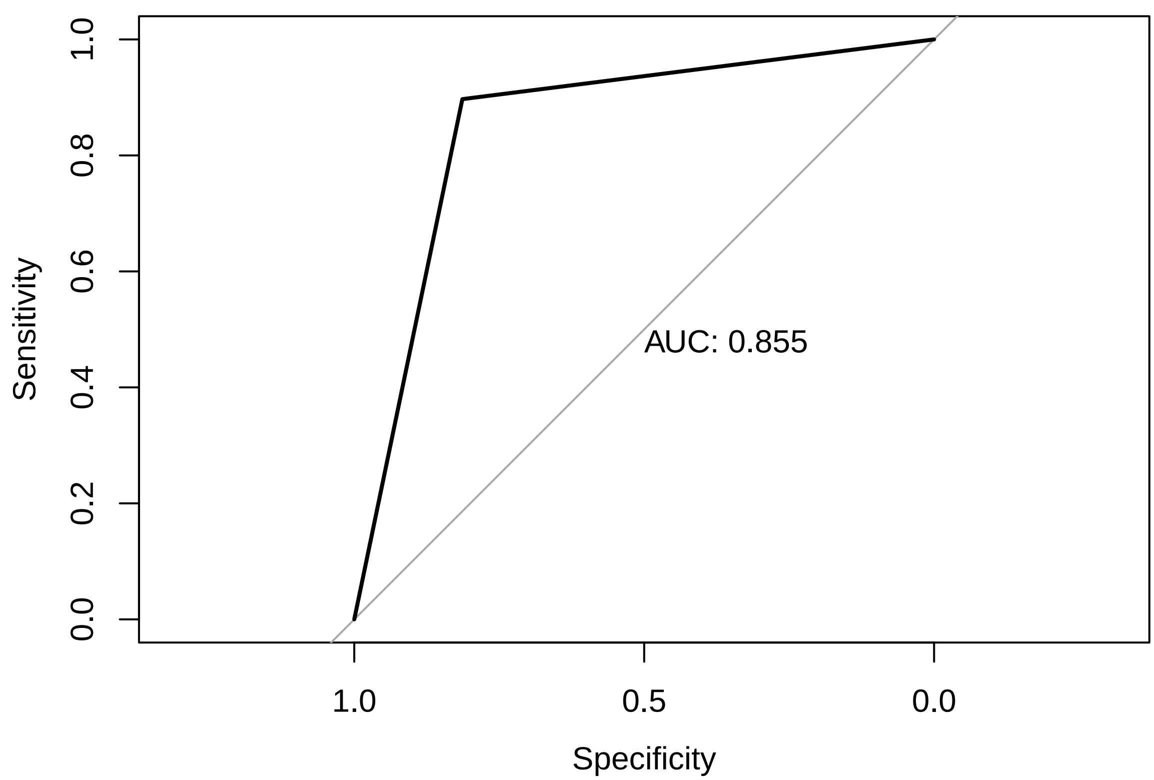
```r
library(rpart)
cdt <- rpart(factor(target) ~ . , data = heart_train, method = "class")
```

Making predictions

```r
cdt_pred <- predict(cdt, heart_test, type = "class")

# Confusion Matrix
cdt_cm <- confusionMatrix(factor(heart_test$target), factor(cdt_pred))

# ROC-AUC & Accuracy
cdt_roc <- roc(heart_test$target, as.numeric(cdt_pred))
```

```
## Setting levels: control = 0, case = 1

## Setting direction: controls < cases
```

```r
plot(cdt_roc, plot = TRUE, print.auc = TRUE)
```



```r
cdt_acc <- cdt_cm$overall[1]
cdt_auc <- cdt_roc$auc
cdt_result <- cbind("Accuracy" = cdt_acc, "AUC" = cdt_auc) # acc = 0.8582677 / auc = 0.8553091
```

Accuracy and AUC is lower than RF

Support Vector Machine

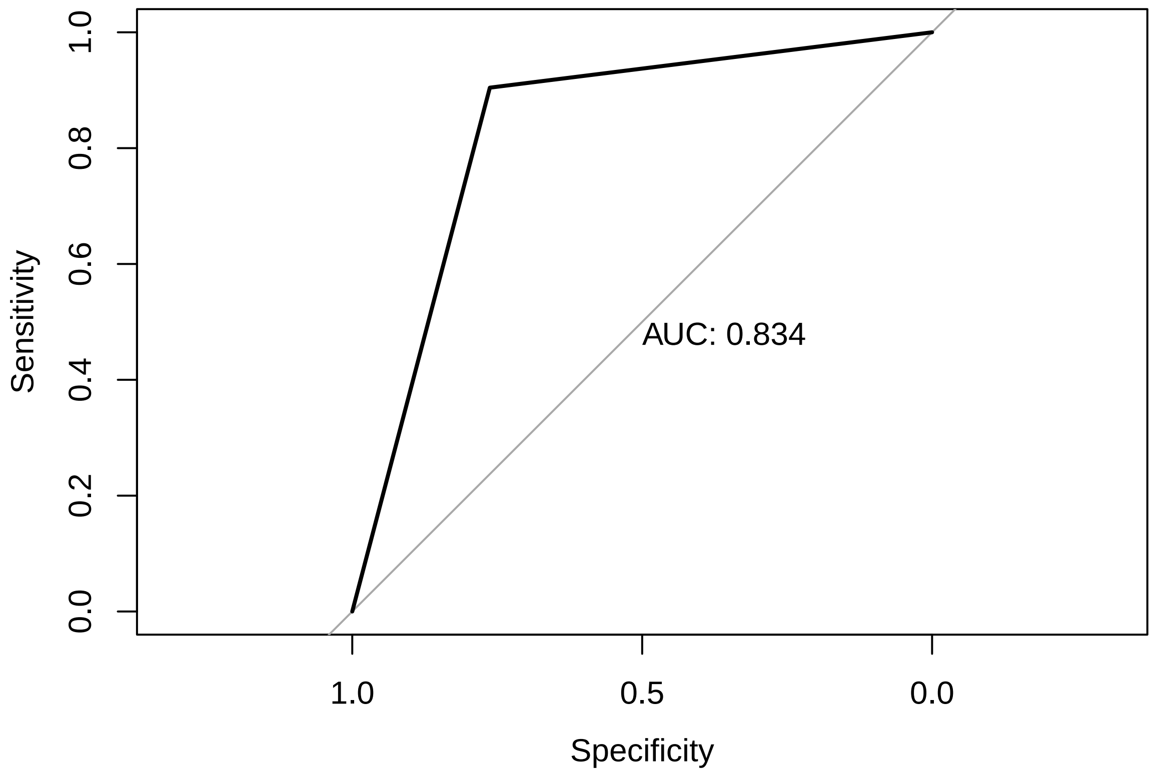
```r
csvm <- svm(target ~ . ,
            data = heart_train,
            kernel = "linear",
            type = "C-classification",
            cost = 10,
            scale = FALSE)
```

Making predictions

```r
csvm_pred <- predict(csvm, heart_test)

# Confusion Matrix
csvm_cm <- confusionMatrix(as.factor(heart_test$target), csvm_pred)

# ROC-AUC & Accuracy
csvm_roc <- roc(heart_test$target, as.numeric(csvm_pred))
```

```
## Setting levels: control = 0, case = 1

## Setting direction: controls < cases
```

```r
plot(csvm_roc, plot = TRUE, print.auc = TRUE)
```



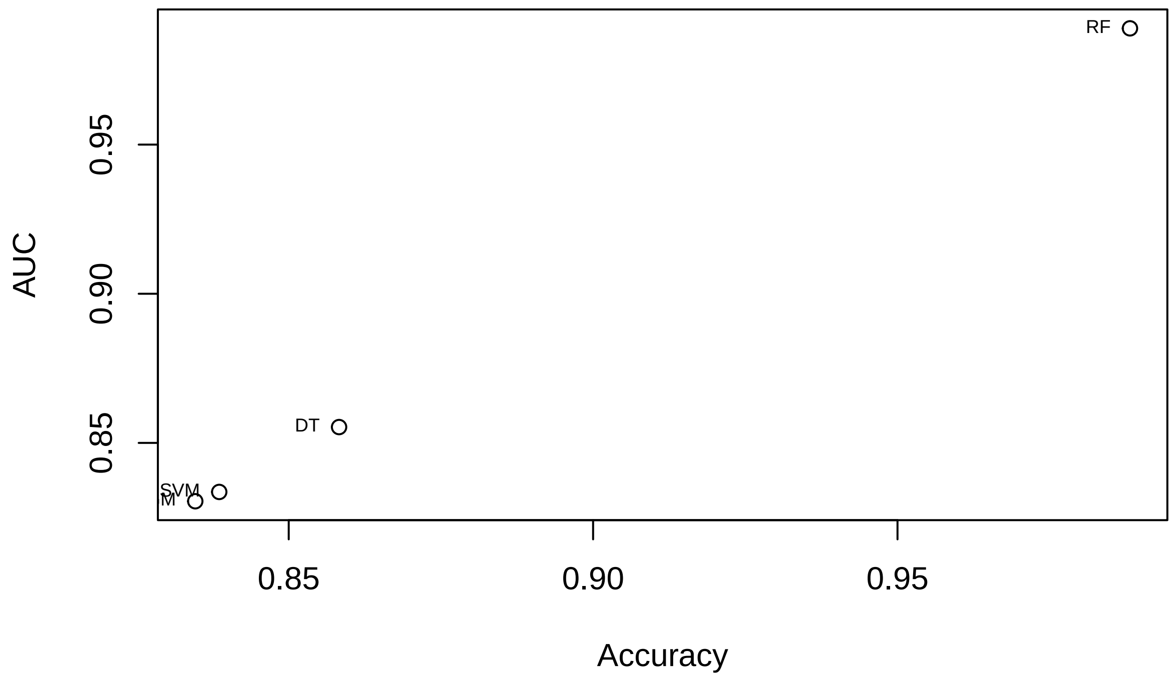

```r
csvm_acc <- csvm_cm$overall[1]
csvm_auc <- csvm_roc$auc
csvm_result <- cbind("Accuracy" = csvm_acc, "AUC" = csvm_auc) # acc = 0.8385827 / auc = 0.8335618
```

Final result of all model

```r
cres <- rbind(clgm_result, crf_result, cdt_result, csvm_result)
cat_result <- data.frame(cres,
                         row.names = c("Log Regression", "Random Forest", "Decision Tree", "Support Vec
cat_result
```

```
##                         Accuracy       AUC
## Log Regression         0.8346457 0.8304462
## Random Forest          0.9881890 0.9889706
## Decision Tree          0.8582677 0.8553091
## Support Vector Machine 0.8385827 0.8335618
```

```r
plot(cat_result)
text(cat_result, labels = c("LGM", "RF", "DT", "SVM"), pos = 2, cex = 0.6)
```



From the plot, we can observe that Random Forest has the best model in targeting patients with heart disease as it has the best Accuracy of 0.9882 and AUC of 0.9890.

Unsupervised Learning

Loading and cleaning dataset

```
customer <- read.csv("Mall_Customers.csv")
summary(customer)
```

```
##    CustomerID        Gender               Age        Annual.Income..k..
##  Min.   :  1.00   Length:200         Min.   :18.00   Min.   : 15.00
##  1st Qu.: 50.75   Class :character   1st Qu.:28.75   1st Qu.: 41.50
##  Median :100.50   Mode  :character   Median :36.00   Median : 61.50
##  Mean   :100.50                      Mean   :38.85   Mean   : 60.56
##  3rd Qu.:150.25                      3rd Qu.:49.00   3rd Qu.: 78.00
##  Max.   :200.00                      Max.   :70.00   Max.   :137.00
##  Spending.Score..1.100.
##  Min.   : 1.00
##  1st Qu.:34.75
##  Median :50.00
##  Mean   :50.20
##  3rd Qu.:73.00
##  Max.   :99.00
```

```r
sum(is.na(customer))
```

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

```r
sum(duplicated(customer))
```

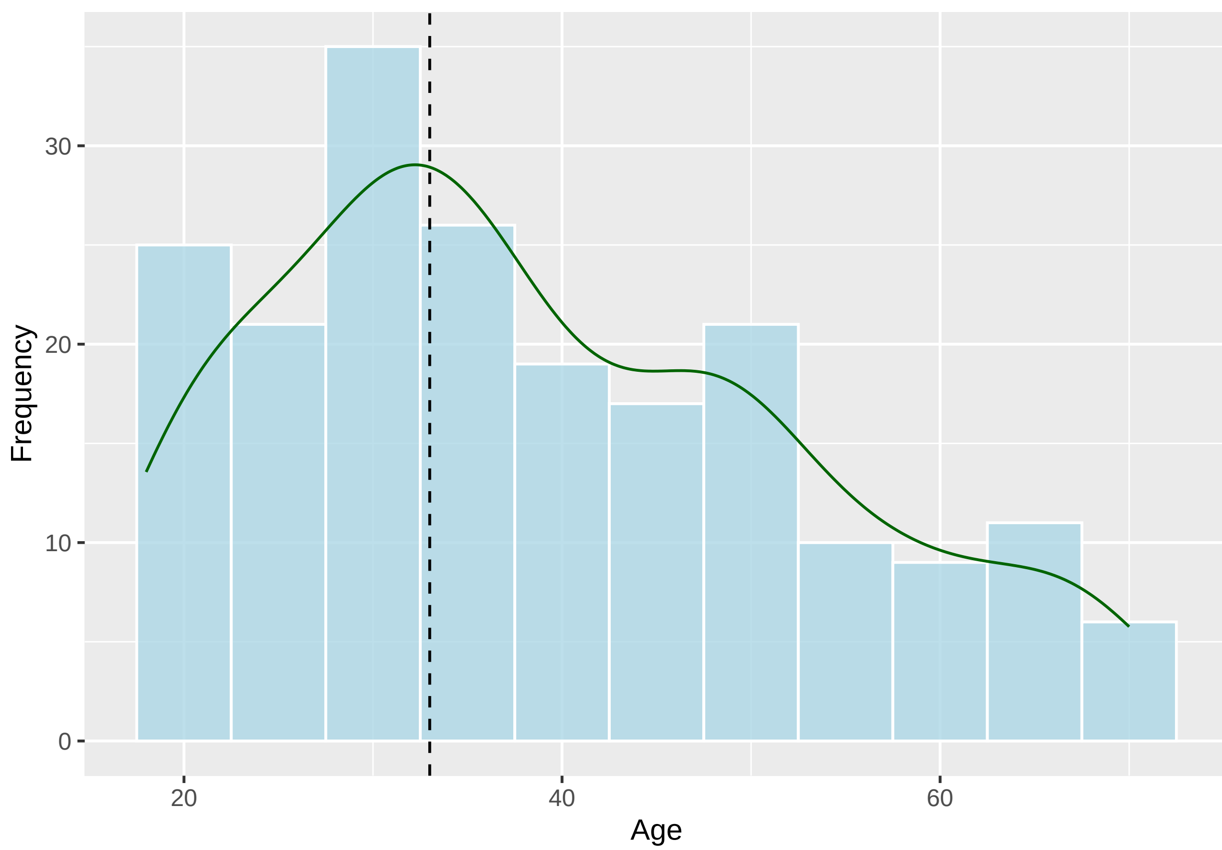
```
## [1] 0
```

No NAs or duplicates found.

Exploring data

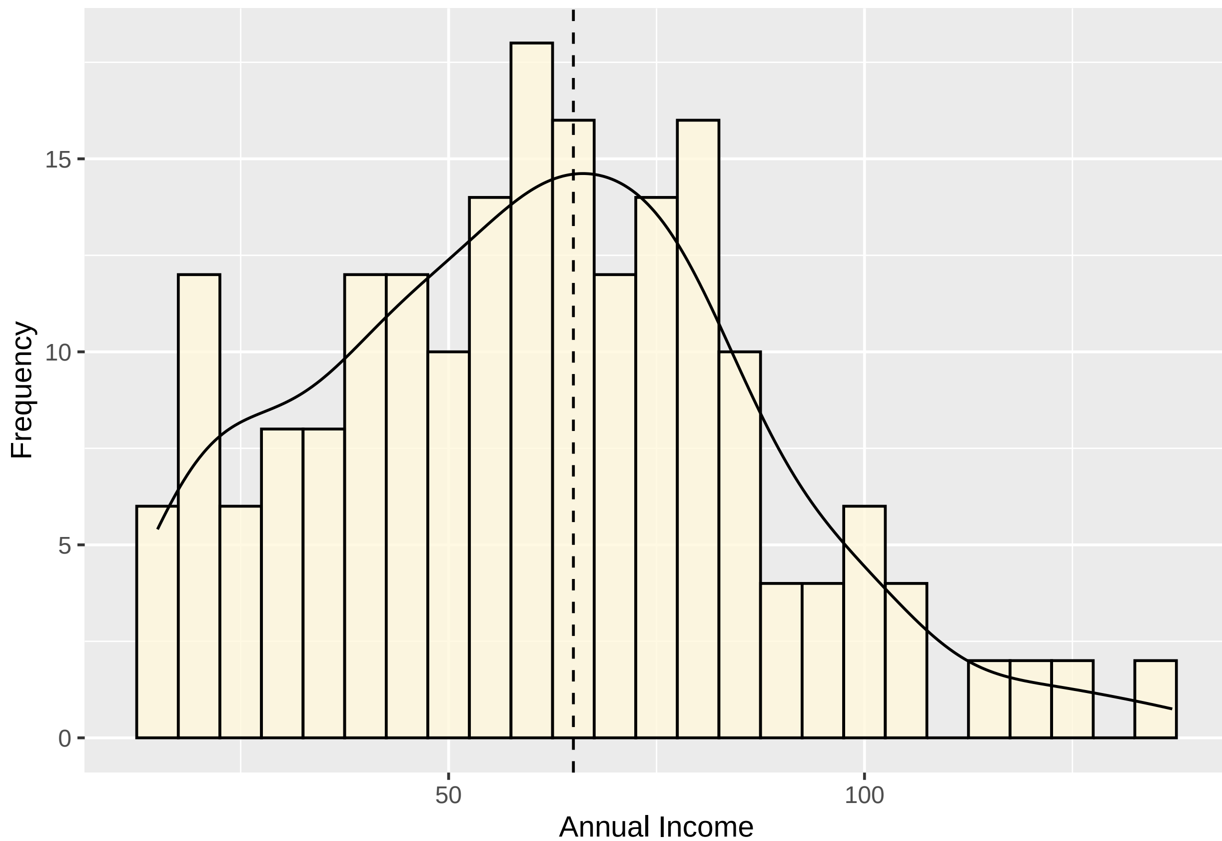
```r
avg_age <- summary(customer$Age) # 38.85
avg_income <- summary(customer$Annual.Income..k..) # 60.56
avg_spendingscore <- summary(customer$Spending.Score..1.100.) #50.20
```

```r
ggplot(customer, aes(Age)) +
  geom_histogram(binwidth = 5, colour = "white", fill = "lightblue", alpha = 0.8) +
  geom_density(eval(bquote(aes(y=..count..*5))),colour="darkgreen", alpha=0.3) +
  geom_vline(xintercept = 33, linetype="dashed") +
  xlab("Age") +
  ylab("Frequency")
```



The highest count of customer's age were between 30 to 35.

```r
ggplot(customer, aes(Annual.Income..k..)) +
  geom_histogram(binwidth = 5, colour = "black", fill = "cornsilk", alpha = 0.8) +
  geom_density(eval(bquote(aes(y=..count..*5))),colour="black", alpha=0.3) +
  geom_vline(xintercept = 65, linetype="dashed") +
  xlab("Annual Income") +
  ylab("Frequency")
```



Customer's annual income is around 55k to 75k.

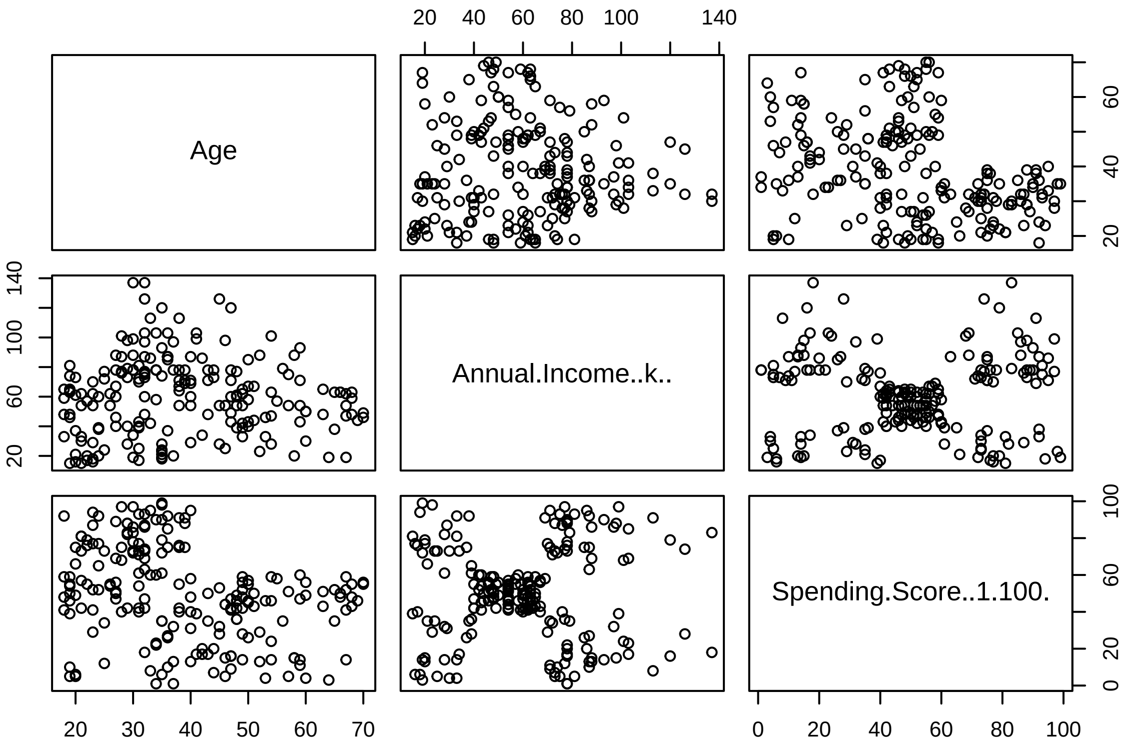
```r
ggplot(customer, aes(Spending.Score..1.100.)) +
  geom_histogram(binwidth = 5, colour = "white", fill = "darkseagreen", alpha = 0.8) +
  geom_density(eval(bquote(aes(y=..count..*5))),colour="black", alpha=0.3) +
  geom_vline(xintercept = 50, linetype="dashed") +
  xlab("Spending Score") +
  ylab("Frequency")
```

Most of the customer's spending score are around 40 to 60 out of 100

K-means clustering

Correlation plot & matrix

```
# Removing CustomerID from dataframe
customer <- subset(customer, select = -c(CustomerID))

# converting Gender to binary variables
customer <- customer %>%
  mutate(Gender = if_else(Gender == "Male", 0, 1))
plot(customer[, 2:4])
```



Principal Component Analysis

```r
pca <- prcomp(customer, scale = F)
summary(pca)
```

```
## Importance of components:
##                           PC1     PC2     PC3     PC4
## Standard deviation     26.4625 26.1597 12.9317 0.49548
## Proportion of Variance  0.4512  0.4409  0.1077 0.00016
## Cumulative Proportion   0.4512  0.8921  0.9998 1.00000
```

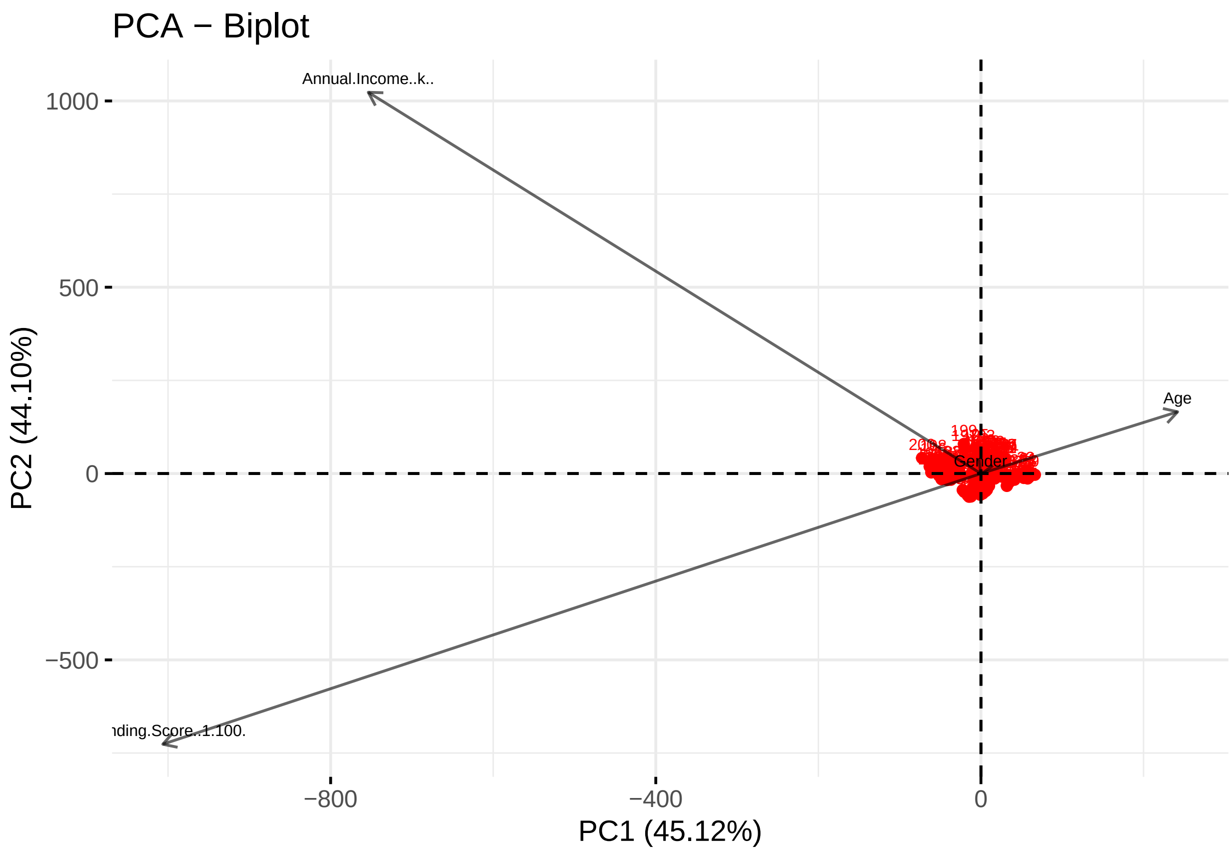
```r
pca$rotation
```

```
##                                PC1          PC2          PC3           PC4
## Gender                 -0.0003327282 -0.001578712  0.001462466  0.9999976291
## Age                     0.1889772912  0.130961404 -0.973208009  0.0016929157
## Annual.Income..k..     -0.5886227558  0.808388308 -0.005514570  0.0010884284
## Spending.Score..1.100. -0.7860093664 -0.573894557 -0.229855656 -0.0008313877
```

We are only using PC1 and PC2 because PC3 variance is close to 0.1 suggesting that it does not have much interpretive value.

Biplot of PCA

```r
biplot <- fviz_pca_biplot(pca,
                          col.var = "black",
                          col.ind = "red",
                          alpha.var = 0.6,
                          labelsize = 2) +
  labs(x = "PC1 (45.12%)",
       y = "PC2 (44.10%)")
biplot
```



Elbow Method

```r
# Taking out Gender to proceed with formula as they cannot calculate binary values
customer_f <- customer[, 2:4]
kmeans(customer_f,3) #Initial cluster sum of squares by cluster = 49.2%
```

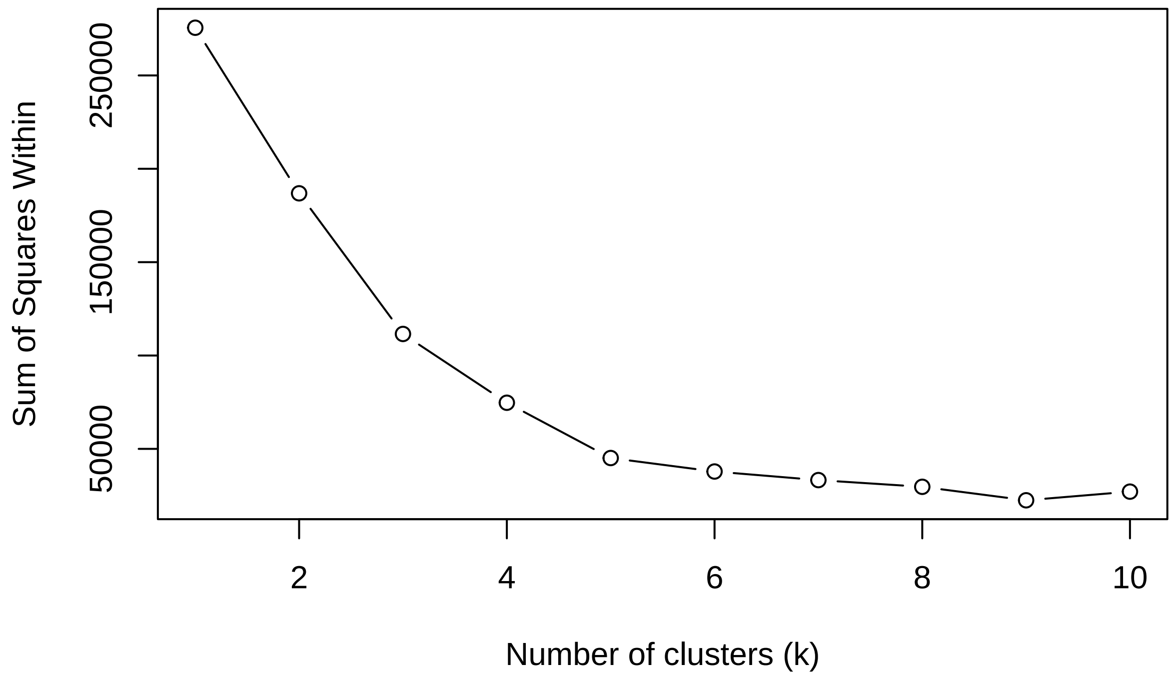
```
## K-means clustering with 3 clusters of sizes 76, 86, 38
##
## Cluster means:
##        Age Annual.Income..k.. Spending.Score..1.100.
## 1 28.75000           65.36842               75.06579
## 2 47.09302           44.62791               42.17442
## 3 40.39474           87.00000               18.63158
##
## Clustering vector:
```

```
##   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20
##   2   1   2   1   2   1   2   1   2   2   2   1   2   1   2   1   2   2   2   1
##  21  22  23  24  25  26  27  28  29  30  31  32  33  34  35  36  37  38  39  40
##   2   1   2   2   2   1   2   2   2   1   2   1   2   1   2   1   2   1   2   1
##  41  42  43  44  45  46  47  48  49  50  51  52  53  54  55  56  57  58  59  60
##   2   1   2   2   2   1   2   2   2   2   2   2   2   2   2   2   2   2   2   2
##  61  62  63  64  65  66  67  68  69  70  71  72  73  74  75  76  77  78  79  80
##   2   1   2   2   2   1   2   2   1   2   2   2   2   2   2   1   2   2   1   2
##  81  82  83  84  85  86  87  88  89  90  91  92  93  94  95  96  97  98  99 100
##   2   2   2   2   1   2   2   1   1   2   2   2   2   2   2   1   2   1   2   1
## 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
##   2   2   2   1   2   2   2   2   2   2   2   1   2   1   1   1   2   1   2   2
## 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140
##   1   2   1   1   3   1   3   1   3   1   3   1   3   1   3   1   3   1   3   1
## 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160
##   3   1   3   1   3   1   3   1   3   1   3   1   3   1   3   1   3   1   3   1
## 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
##   3   1   3   1   3   1   3   1   3   1   3   1   3   1   3   1   3   1   3   1
## 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200
##   3   1   3   1   3   1   3   1   3   1   3   1   3   1   3   1   3   1   3   1
##
## Within cluster sum of squares by cluster:
## [1] 77572.61 58007.73 18993.92
##  (between_SS / total_SS =  49.9 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"
```

```r
pca_score <- data.frame(pca$x[, 1:2])

set.seed(25)
ssw <- vector()

for(i in 1:10){
  x <- sum(kmeans(pca_score, i)$withinss)
  ssw[i] = x
  print(x)
}
```

```
## [1] 275534.7
## [1] 186865.9
## [1] 111540.7
## [1] 74701.15
## [1] 45092.05
## [1] 37876.15
## [1] 33277.53
## [1] 29685.22
## [1] 22467.23
## [1] 27096.42
```

```r
plot(x = 1:10, ssw,
     type = "b",
     xlab = "Number of clusters (k)",
     ylab = "Sum of Squares Within")
```



From the plot, we conclude that 5 is the optimal number of clusters as its observed that the bent starts from in this elbow plot.

Taking $k = 5$ as our optimal cluster into the model

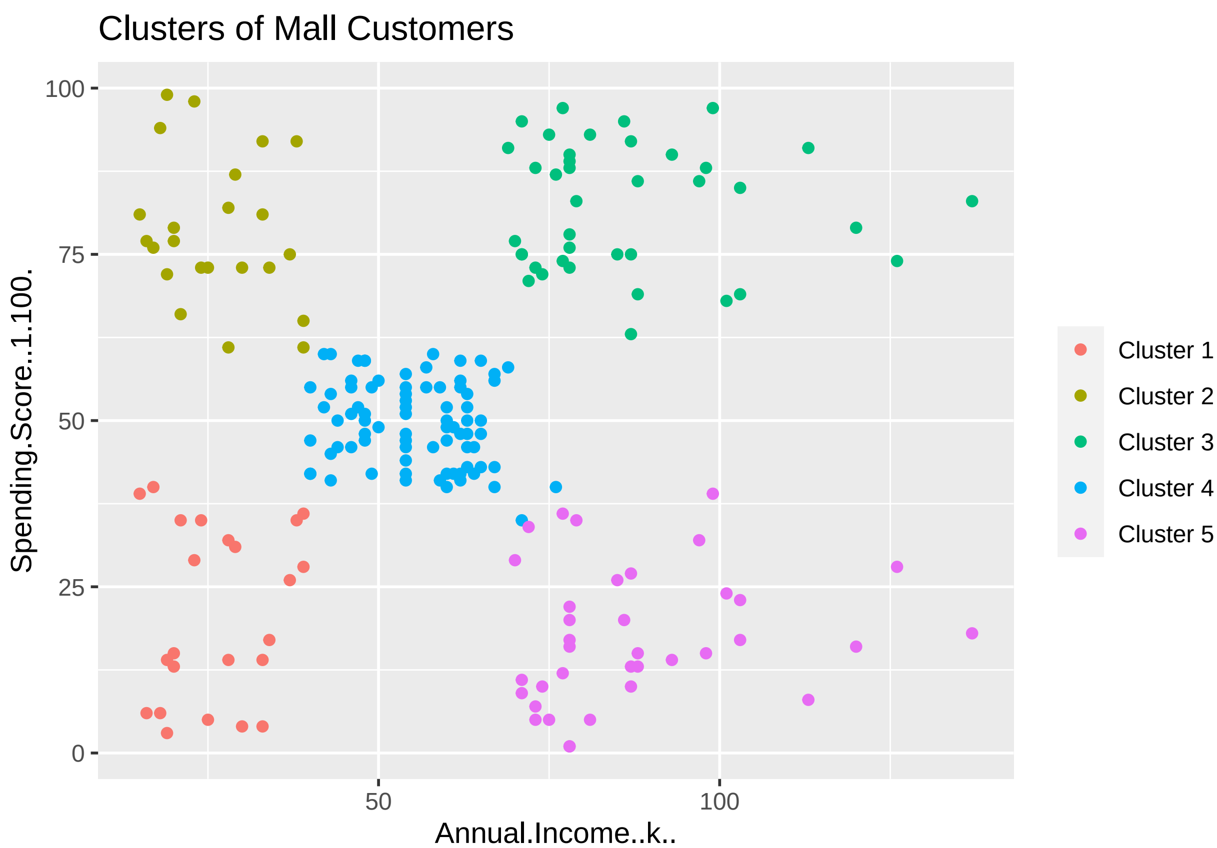
```r
kmeans_model <- kmeans(customer_f, 5) # css went to 75.6%
kmeans_model
```

```
## K-means clustering with 5 clusters of sizes 23, 23, 39, 79, 36
##
## Cluster means:
##        Age Annual.Income..k.. Spending.Score..1.100.
## 1 45.21739           26.30435               20.91304
## 2 25.52174           26.30435               78.56522
## 3 32.69231           86.53846               82.12821
## 4 43.08861           55.29114               49.56962
## 5 40.66667           87.75000               17.58333
##
## Clustering vector:
##   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20
##   1   2   1   2   1   2   1   2   1   2   1   2   1   2   1   2   1   2   1   2
```

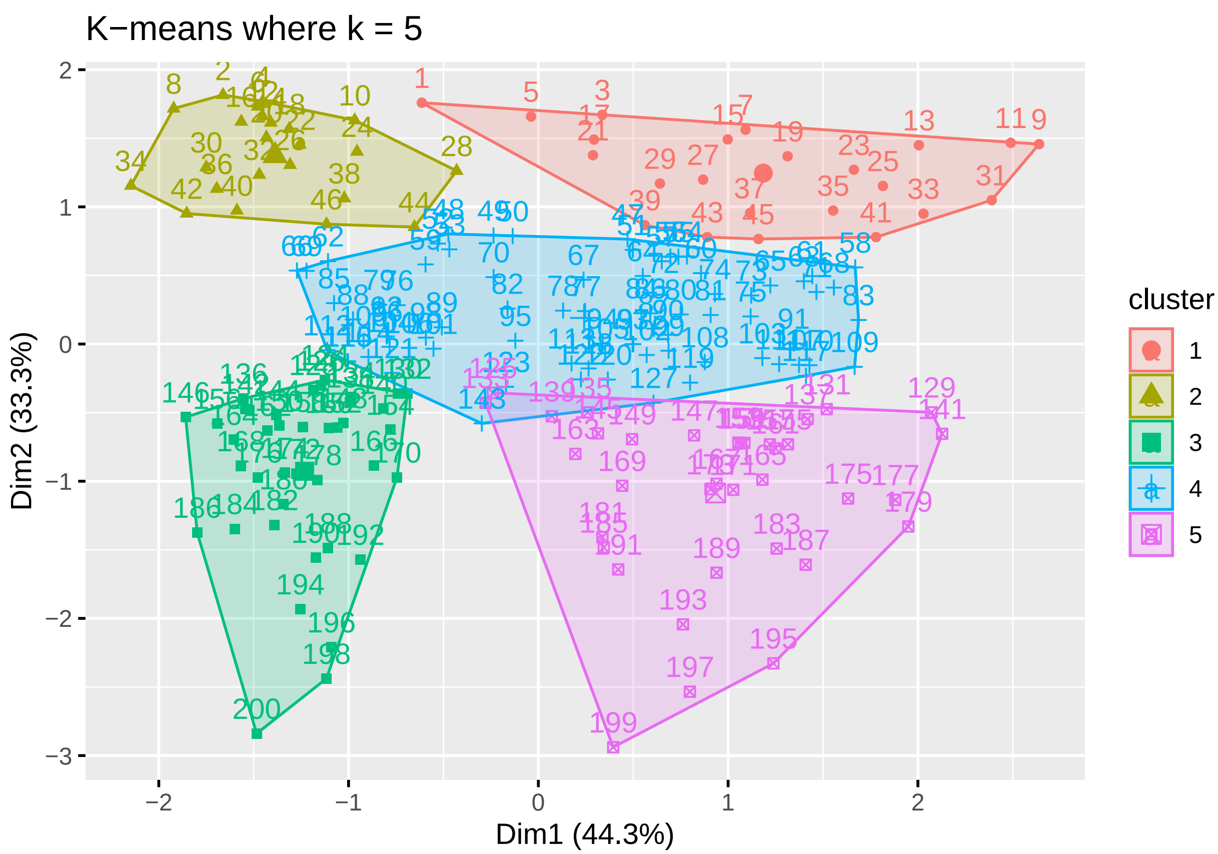
```
##  21  22  23  24  25  26  27  28  29  30  31  32  33  34  35  36  37  38  39  40
##   1   2   1   2   1   2   1   2   1   2   1   2   1   2   1   2   1   2   1   2
##  41  42  43  44  45  46  47  48  49  50  51  52  53  54  55  56  57  58  59  60
##   1   2   1   2   1   2   4   4   4   4   4   4   4   4   4   4   4   4   4   4
##  61  62  63  64  65  66  67  68  69  70  71  72  73  74  75  76  77  78  79  80
##   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4
##  81  82  83  84  85  86  87  88  89  90  91  92  93  94  95  96  97  98  99 100
##   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4
## 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
##   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4   4
## 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140
##   4   4   4   3   5   3   4   3   5   3   5   3   5   3   5   3   5   3   5   3
## 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160
##   5   3   4   3   5   3   5   3   5   3   5   3   5   3   5   3   5   3   5   3
## 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
##   5   3   5   3   5   3   5   3   5   3   5   3   5   3   5   3   5   3   5   3
## 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200
##   5   3   5   3   5   3   5   3   5   3   5   3   5   3   5   3   5   3   5   3
##
## Within cluster sum of squares by cluster:
## [1]  8948.609  4622.261 13972.359 30138.051 17669.500
##  (between_SS / total_SS =  75.6 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"
```

Visualizing the clusters

```
set.seed(30)
ggplot(customer_f, aes(x = Annual.Income..k.., y = Spending.Score..1.100.)) +
  geom_point(stat = "identity", aes(color = as.factor(kmeans_model$cluster))) +
  scale_color_discrete(name = " ",
                       breaks = c("1", "2", "3", "4", "5"),
                       labels = c("Cluster 1", "Cluster 2", "Cluster 3", "Cluster 4", "Cluster 5")) +
  ggtitle("Clusters of Mall Customers")
```




```
fviz_cluster(kmeans_model, data = customer_f) +
  ggtitle("K-means where k = 5")
```



Hierarchical Clustering (Agglomerative Method)

We will be using Euclidean distance metric

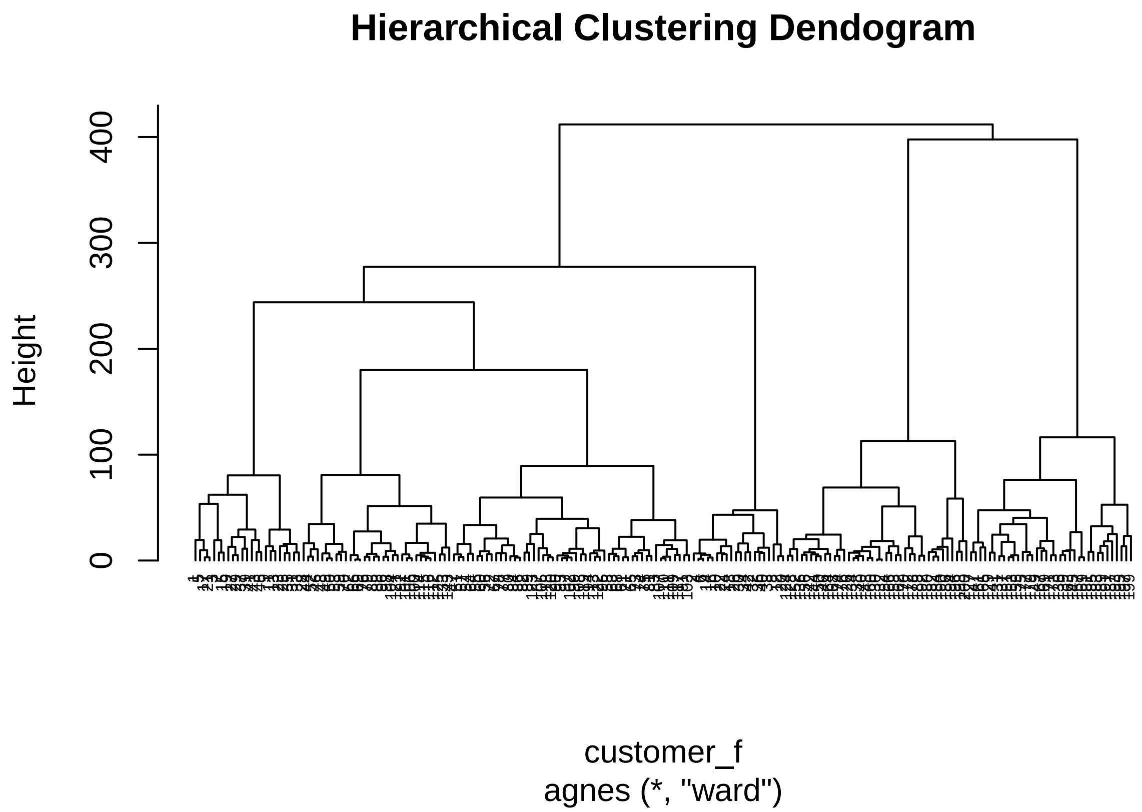
Best linkage method to use

```
x <- c("ward", "single", "complete", "average")
names(x) <- c("ward", "single", "complete", "average")

coeff <- function(x){
  agnes(customer_f, method = x)$ac
}

sapply(x, coeff) # 0.9835
```

```
##      ward    single  complete   average
## 0.9835084 0.7031423 0.9535158 0.8978845
```

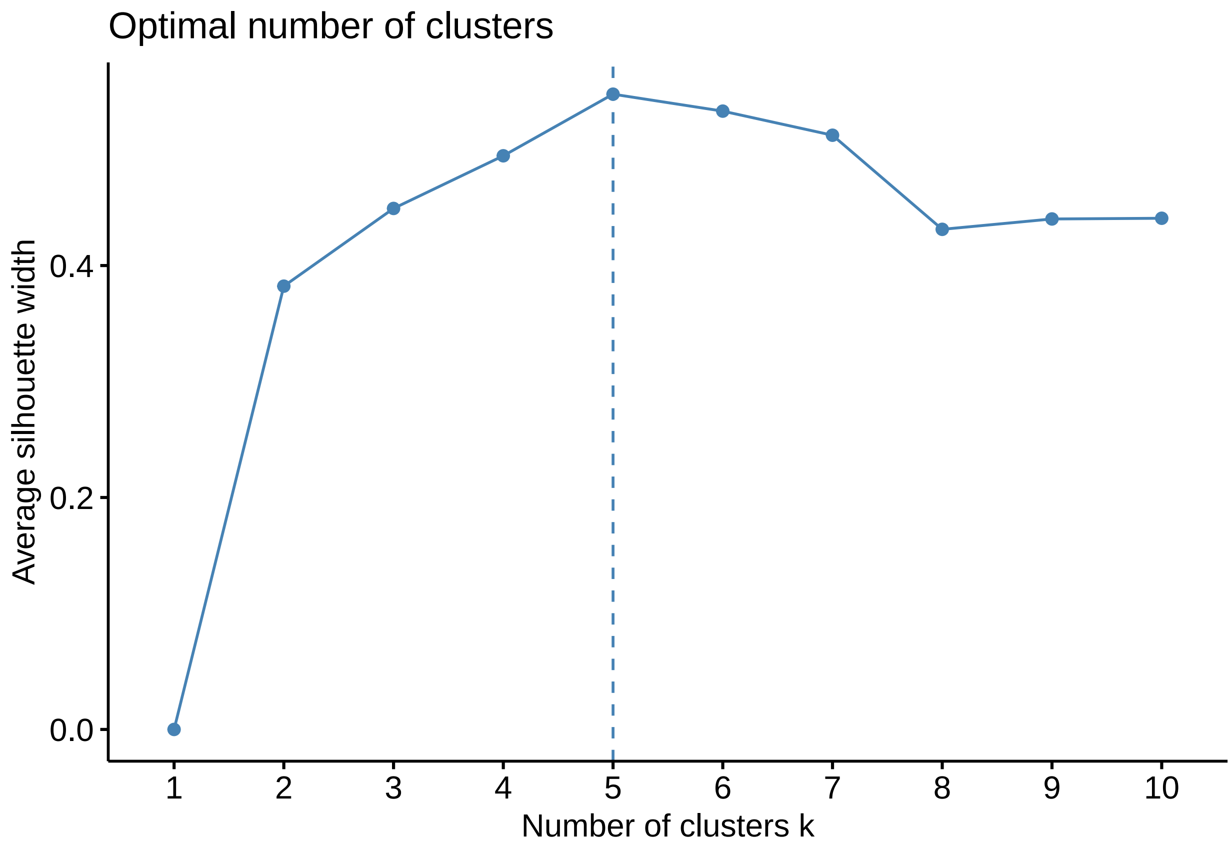
The best linkage method to use would be Ward's method so we will be using this for our clustering

```
hclust <- agnes(customer_f, method = "ward")

pltree(hclust, cex = 0.5, hang = -1, main = "Hierarchical Clustering Dendogram")
```



Optimal cluster

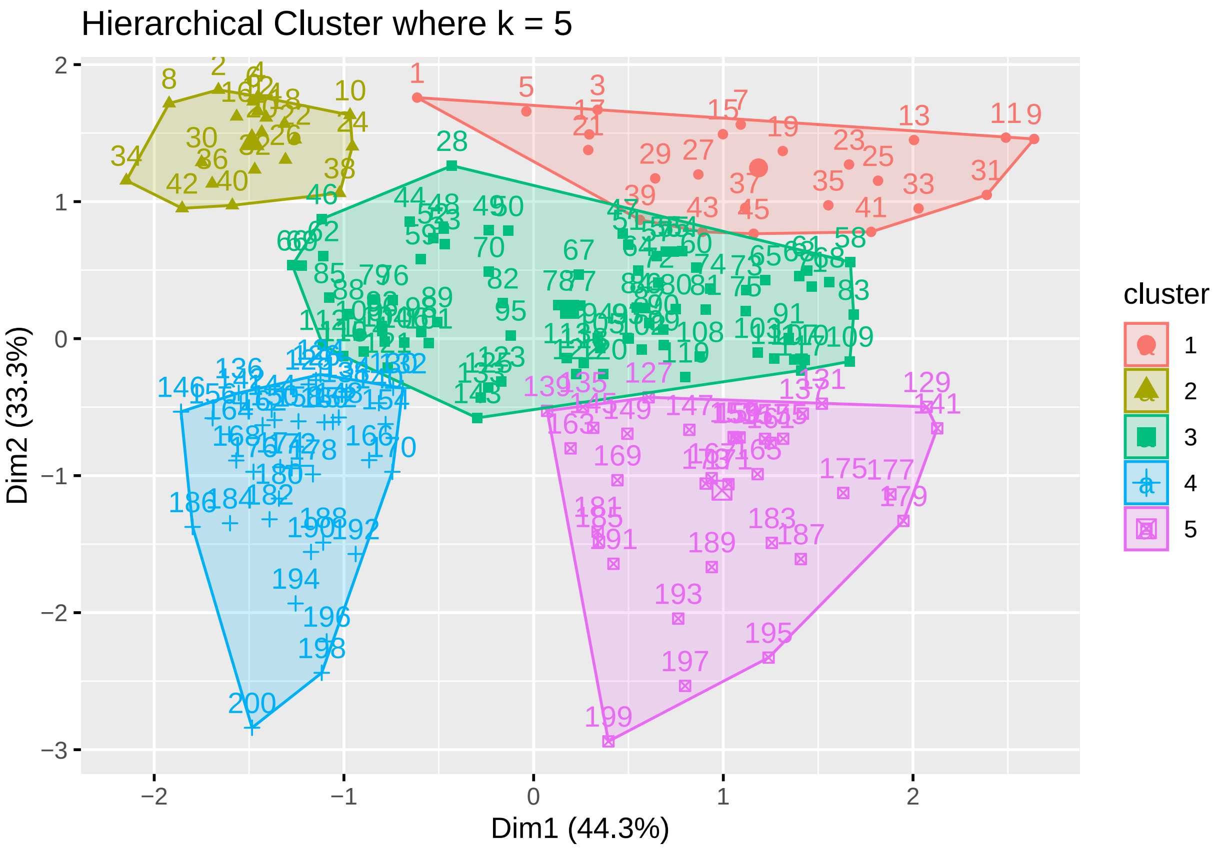
```
fviz_nbclust(pca_score, FUN = hcut, method = "silhouette")
```



We are using silhouette method here instead of elbow method, both of which shows to use k = 5.

Cutting the dendogram at k =5

```
final_hclust <- cutree(hclust, k = 5)

fviz_cluster(list(cluster = final_hclust, data = customer_f)) +
  ggtitle("Hierarchical Cluster where k = 5")
```


Hierarchical Cluster where k = 5
Dim1 (44.3%)
Dim2 (33.3%)
cluster
1
2
3
4
5