Machine learning models for cancer predictive analysis

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```r
data <- read.csv("C://Users//Natalia//Desktop//ITMO//R//R project//cancer data//breast cancer coimbra//
View(data)
```

Analyse the dataset and tidy it up.

```r
# Analyse the data - checking for values, NAs, data type.
summary(data)
```

```
##       Age             BMI           Glucose          Insulin      
##  Min.   :24.0   Min.   :18.37   Min.   : 60.00   Min.   : 2.432  
##  1st Qu.:45.0   1st Qu.:22.97   1st Qu.: 85.75   1st Qu.: 4.359  
##  Median :56.0   Median :27.66   Median : 92.00   Median : 5.925  
##  Mean   :57.3   Mean   :27.58   Mean   : 97.79   Mean   :10.012  
##  3rd Qu.:71.0   3rd Qu.:31.24   3rd Qu.:102.00   3rd Qu.:11.189  
##  Max.   :89.0   Max.   :38.58   Max.   :201.00   Max.   :58.460  
##       HOMA              Leptin        Adiponectin        Resistin     
##  Min.   : 0.4674   Min.   : 4.311   Min.   : 1.656   Min.   : 3.210  
##  1st Qu.: 0.9180   1st Qu.:12.314   1st Qu.: 5.474   1st Qu.: 6.882  
##  Median : 1.3809   Median :20.271   Median : 8.353   Median :10.828  
##  Mean   : 2.6950   Mean   :26.615   Mean   :10.181   Mean   :14.726  
##  3rd Qu.: 2.8578   3rd Qu.:37.378   3rd Qu.:11.816   3rd Qu.:17.755  
##  Max.   :25.0503   Max.   :90.280   Max.   :38.040   Max.   :82.100  
##      MCP.1         Classification 
##  Min.   :  45.84   Min.   :1.000  
##  1st Qu.: 269.98   1st Qu.:1.000  
##  Median : 471.32   Median :2.000  
##  Mean   : 534.65   Mean   :1.552  
##  3rd Qu.: 700.09   3rd Qu.:2.000  
##  Max.   :1698.44   Max.   :2.000
```

```r
str(data)
```

```
## 'data.frame':    116 obs. of  10 variables:
##  $ Age           : int  48 83 82 68 86 49 89 76 73 75 ...
##  $ BMI           : num  23.5 20.7 23.1 21.4 21.1 ...
##  $ Glucose       : int  70 92 91 77 92 92 77 118 97 83 ...
##  $ Insulin       : num  2.71 3.12 4.5 3.23 3.55 ...
##  $ HOMA          : num  0.467 0.707 1.01 0.613 0.805 ...
##  $ Leptin        : num  8.81 8.84 17.94 9.88 6.7 ...
##  $ Adiponectin   : num  9.7 5.43 22.43 7.17 4.82 ...
##  $ Resistin      : num  8 4.06 9.28 12.77 10.58 ...
##  $ MCP.1         : num  417 469 555 928 774 ...
##  $ Classification: int  1 1 1 1 1 1 1 1 1 1 ...
```

```r
head(data)
```

```
##   Age      BMI Glucose Insulin      HOMA  Leptin Adiponectin Resistin
## 1  48 23.50000      70   2.707 0.4674087  8.8071    9.702400  7.99585
## 2  83 20.69049      92   3.115 0.7068973  8.8438    5.429285  4.06405
## 3  82 23.12467      91   4.498 1.0096511 17.9393   22.432040  9.27715
## 4  68 21.36752      77   3.226 0.6127249  9.8827    7.169560 12.76600
## 5  86 21.11111      92   3.549 0.8053864  6.6994    4.819240 10.57635
## 6  49 22.85446      92   3.226 0.7320869  6.8317   13.679750 10.31760
##     MCP.1 Classification
## 1 417.114              1
## 2 468.786              1
## 3 554.697              1
## 4 928.220              1
## 5 773.920              1
## 6 530.410              1
```

```
dim(data)
```

```
## [1] 116  10
```

```
library(tidyverse)
```

```
## -- Attaching packages ---------------------------------------------------------------- tidyverse 1.2

## v ggplot2 3.1.1       v purrr   0.3.2
## v tibble  2.1.1       v dplyr   0.8.0.1
## v tidyr   0.8.3       v stringr 1.4.0
## v readr   1.3.1       v forcats 0.4.0

## -- Conflicts ------------------------------------------------------------------- tidyverse_conflicts
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
map_int(data, function(.x) sum(is.na(.x)))
```

```
##            Age            BMI        Glucose        Insulin           HOMA
##              0              0              0              0              0
##         Leptin    Adiponectin       Resistin          MCP.1 Classification
##              0              0              0              0              0
```

```
library(plyr)
```

```
## ------------------------------------------------------------------------------

## You have loaded plyr after dplyr - this is likely to cause problems.
## If you need functions from both plyr and dplyr, please load plyr first, then dplyr:
## library(plyr); library(dplyr)

## ------------------------------------------------------------------------------

##
## Attaching package: 'plyr'

## The following objects are masked from 'package:dplyr':
##
##     arrange, count, desc, failwith, id, mutate, rename, summarise,
##     summarize

## The following object is masked from 'package:purrr':
##
##     compact
```

```
#change value names in "Classifications" for "healthy" and "cancer":
```

```r
data$Classification <- factor(as.character(data$Classification))
data$Classification <- revalue(data$Classification, c("1"="healthy"))
data$Classification <- revalue(data$Classification, c("2"="cancer"))
head(data)
```

```
##   Age      BMI Glucose Insulin      HOMA  Leptin Adiponectin Resistin
## 1  48 23.50000      70   2.707 0.4674087  8.8071    9.702400  7.99585
## 2  83 20.69049      92   3.115 0.7068973  8.8438    5.429285  4.06405
## 3  82 23.12467      91   4.498 1.0096511 17.9393   22.432040  9.27715
## 4  68 21.36752      77   3.226 0.6127249  9.8827    7.169560 12.76600
## 5  86 21.11111      92   3.549 0.8053864  6.6994    4.819240 10.57635
## 6  49 22.85446      92   3.226 0.7320869  6.8317   13.679750 10.31760
##     MCP.1 Classification
## 1 417.114        healthy
## 2 468.786        healthy
## 3 554.697        healthy
## 4 928.220        healthy
## 5 773.920        healthy
## 6 530.410        healthy
```

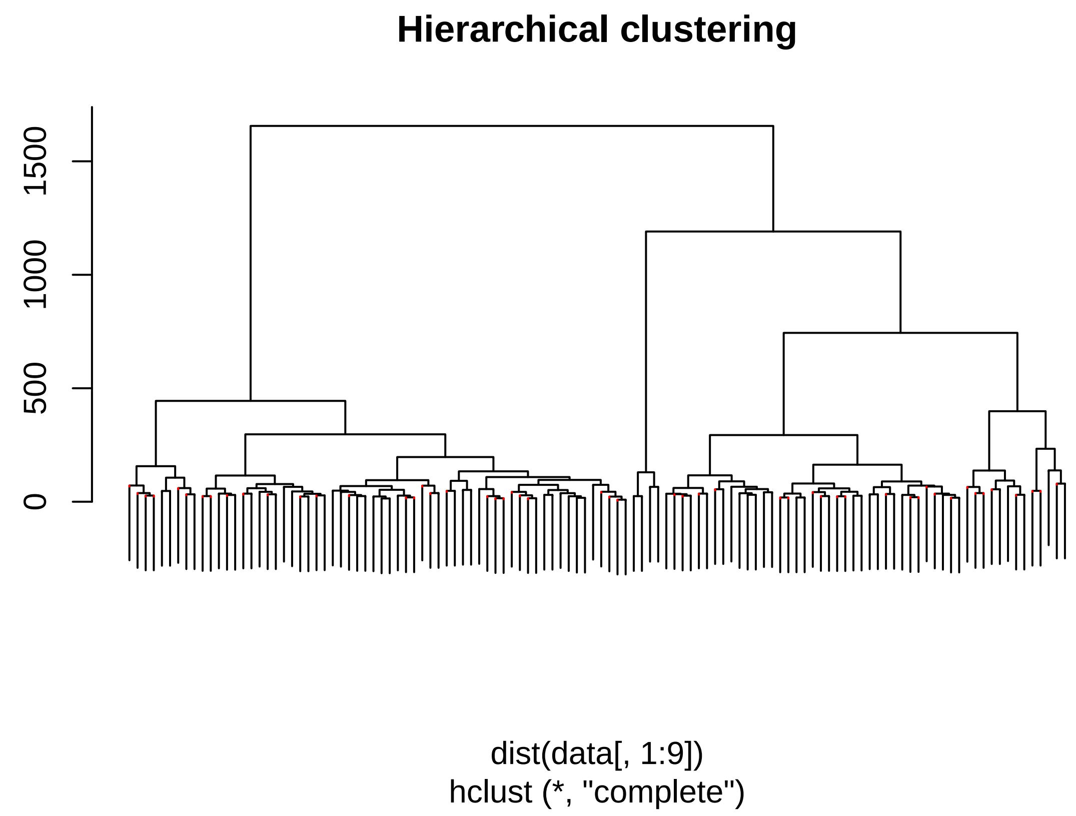
```r
data <- as.data.frame(data, stringsAsFactors=T)
data$Classification <- factor(as.character(data$Classification))
sapply(data,mode)
```

```
##            Age            BMI        Glucose        Insulin           HOMA
##      "numeric"      "numeric"      "numeric"      "numeric"      "numeric"
##         Leptin    Adiponectin      Resistin          MCP.1 Classification
##      "numeric"      "numeric"      "numeric"      "numeric"      "numeric"
```

DATA EXPLORATION

Hierarchical clustering

```r
library(sparcl)
hc <- hclust(dist(data[,1:9]), method = "complete")
ColorDendrogram(hc,y=factor(data$Classification), main = "Hierarchical clustering", branchlength=5)
```



Most of the benign (black) and malignant (red) samples cluster together.

K-means clustering

```
fit <- kmeans(data[,c(1:9)], 2)
names(fit)
```

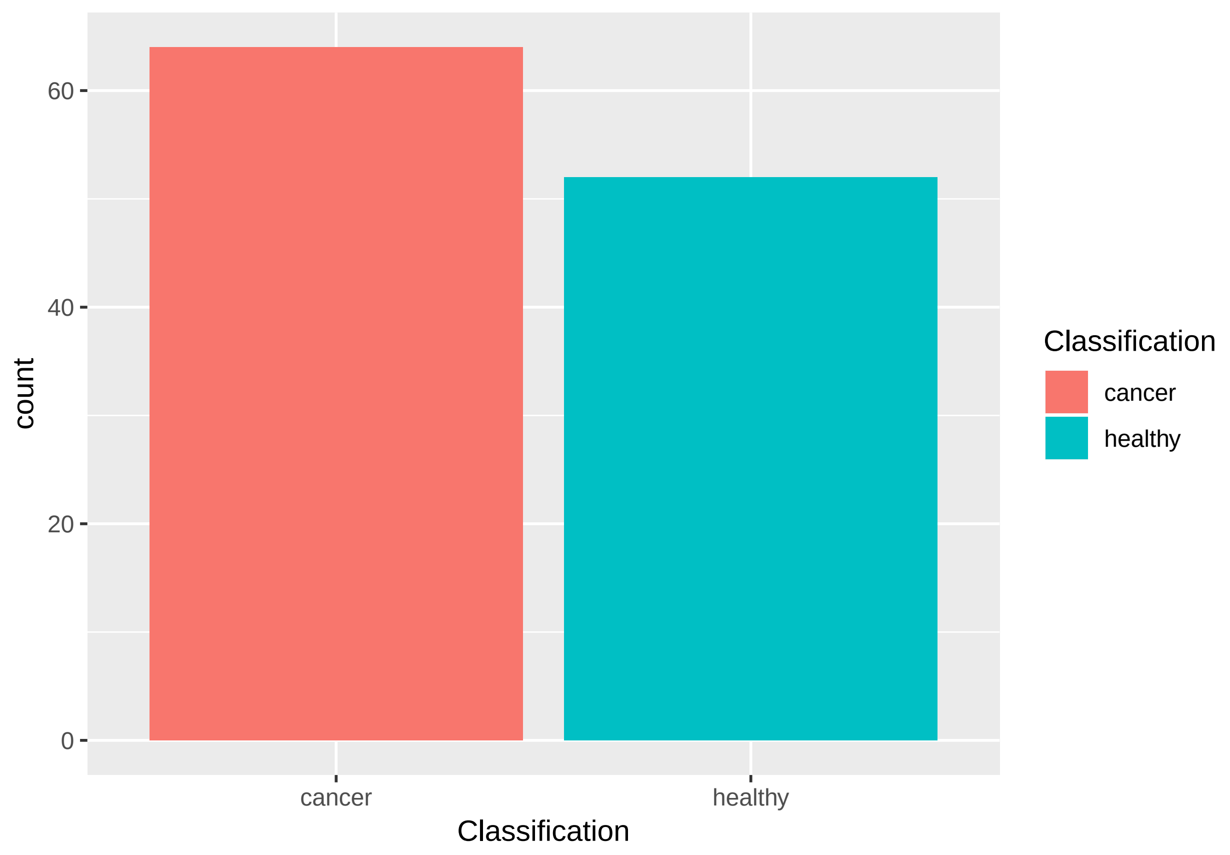
```
## [1] "cluster"      "centers"      "totss"        "withinss"
## [5] "tot.withinss" "betweenss"    "size"         "iter"
## [9] "ifault"
```

```
#k-means did a fairly good job
table(data.frame(fit$cluster,data[,10]))
```

```
##             data...10.
## fit.cluster cancer healthy
##           1     19      12
##           2     45      40
```

Response variable for classification

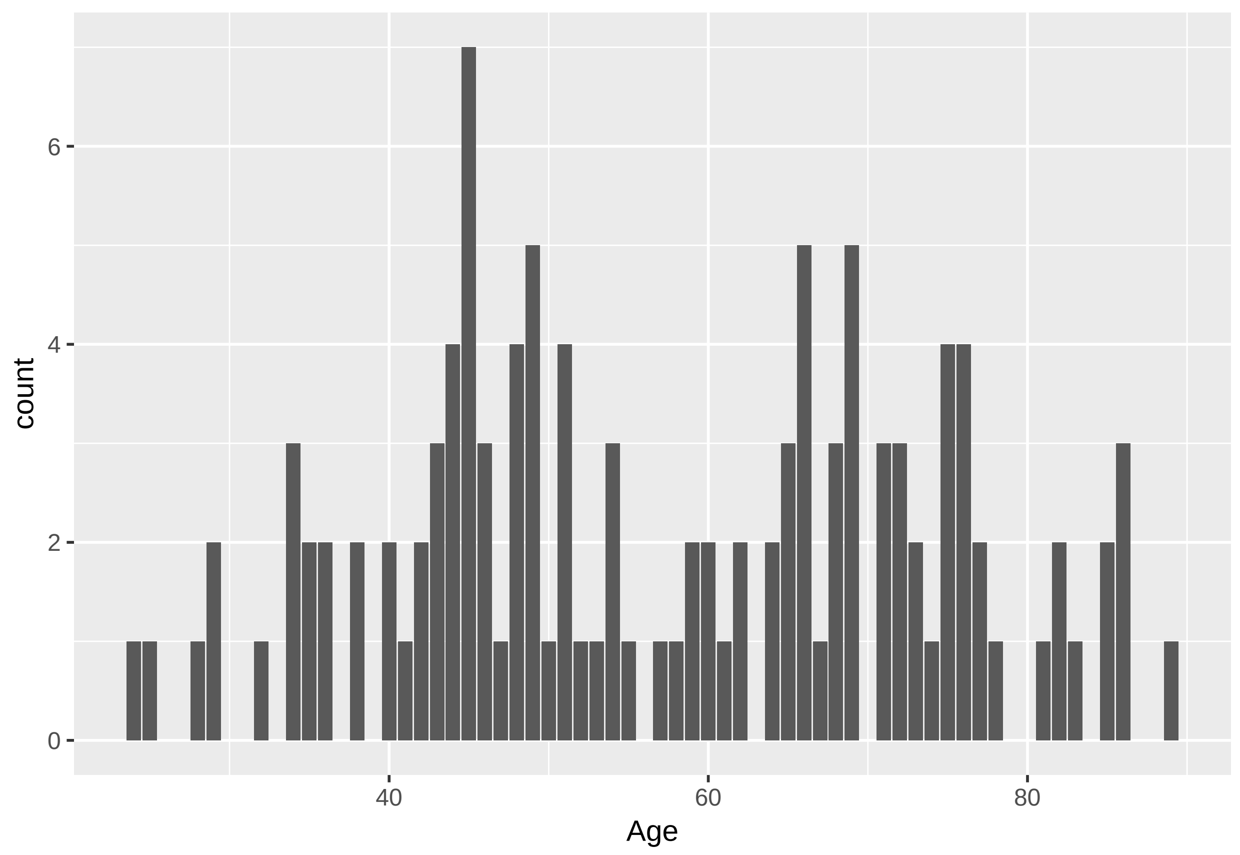
```
library(ggplot2)

ggplot(data, aes(x = Classification, fill = Classification)) +
  geom_bar()
```



Response variable for regression

```
ggplot(data, aes(x = Age)) +
  geom_histogram(stat = "count")
```

```
## Warning: Ignoring unknown parameters: binwidth, bins, pad
```



Principal Component Analysis

```r
library(pcaGoPromoter)
```

```
## Loading required package: ellipse

##
## Attaching package: 'ellipse'

## The following object is masked from 'package:graphics':
##
##     pairs

## Loading required package: Biostrings

## Loading required package: BiocGenerics

## Loading required package: parallel

##
## Attaching package: 'BiocGenerics'

## The following objects are masked from 'package:parallel':
##
##     clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##     clusterExport, clusterMap, parApply, parCapply, parLapply,
##     parLapplyLB, parRapply, parSapply, parSapplyLB

## The following objects are masked from 'package:dplyr':
```

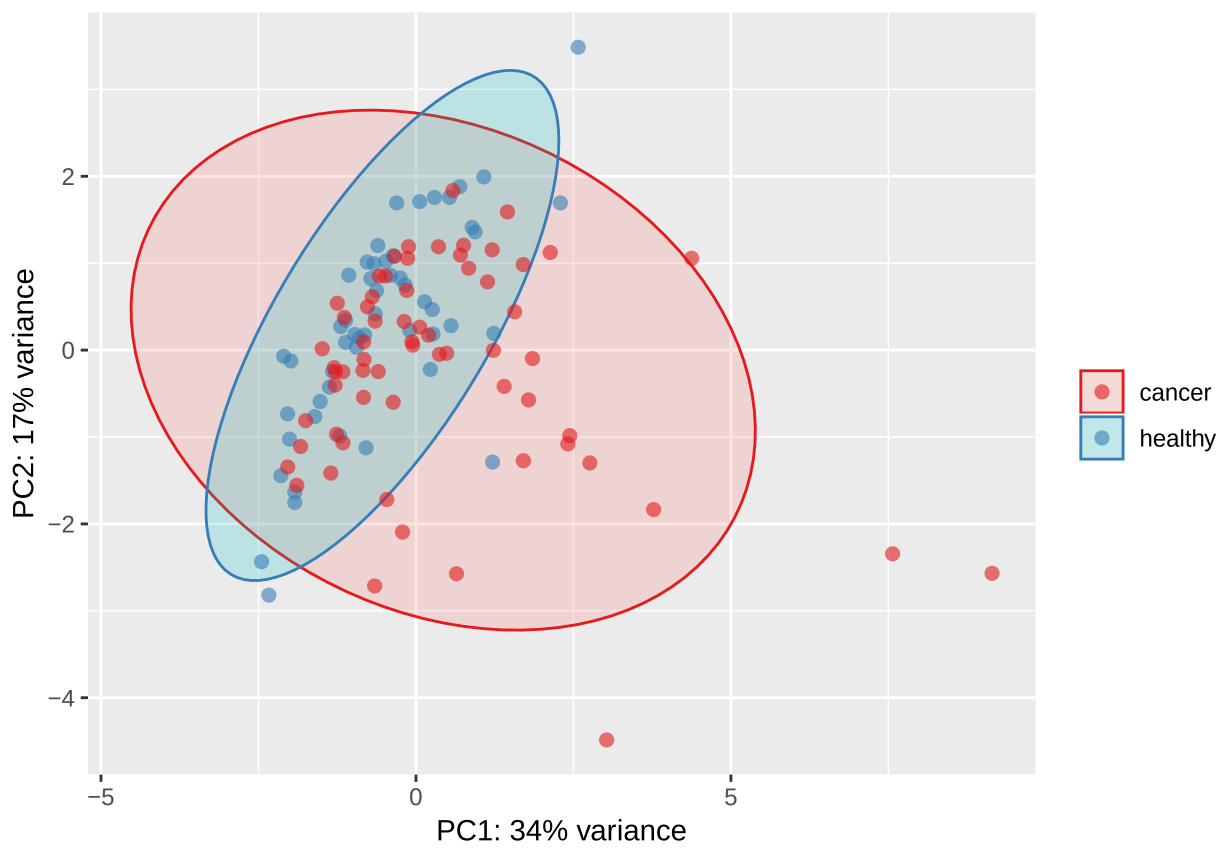
```
##
##     combine, intersect, setdiff, union

## The following objects are masked from 'package:stats':
##
##     IQR, mad, sd, var, xtabs

## The following objects are masked from 'package:base':
##
##     anyDuplicated, append, as.data.frame, basename, cbind,
##     colMeans, colnames, colSums, dirname, do.call, duplicated,
##     eval, evalq, Filter, Find, get, grep, grepl, intersect,
##     is.unsorted, lapply, lengths, Map, mapply, match, mget, order,
##     paste, pmax, pmax.int, pmin, pmin.int, Position, rank, rbind,
##     Reduce, rowMeans, rownames, rowSums, sapply, setdiff, sort,
##     table, tapply, union, unique, unsplit, which, which.max,
##     which.min

## Loading required package: S4Vectors

## Loading required package: stats4

##
## Attaching package: 'S4Vectors'

## The following object is masked from 'package:plyr':
##
##     rename

## The following objects are masked from 'package:dplyr':
##
##     first, rename

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

## The following object is masked from 'package:base':
##
##     expand.grid

## Loading required package: IRanges

##
## Attaching package: 'IRanges'

## The following object is masked from 'package:plyr':
##
##     desc

## The following objects are masked from 'package:dplyr':
##
##     collapse, desc, slice

## The following object is masked from 'package:purrr':
##
##     reduce

## The following object is masked from 'package:grDevices':
##
##     windows
## Loading required package: XVector

##
## Attaching package: 'XVector'

## The following object is masked from 'package:plyr':
##
##     compact

## The following object is masked from 'package:purrr':
##
##     compact

##
## Attaching package: 'Biostrings'

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

```
library(ellipse)
```

```
data <-na.omit(data)
```

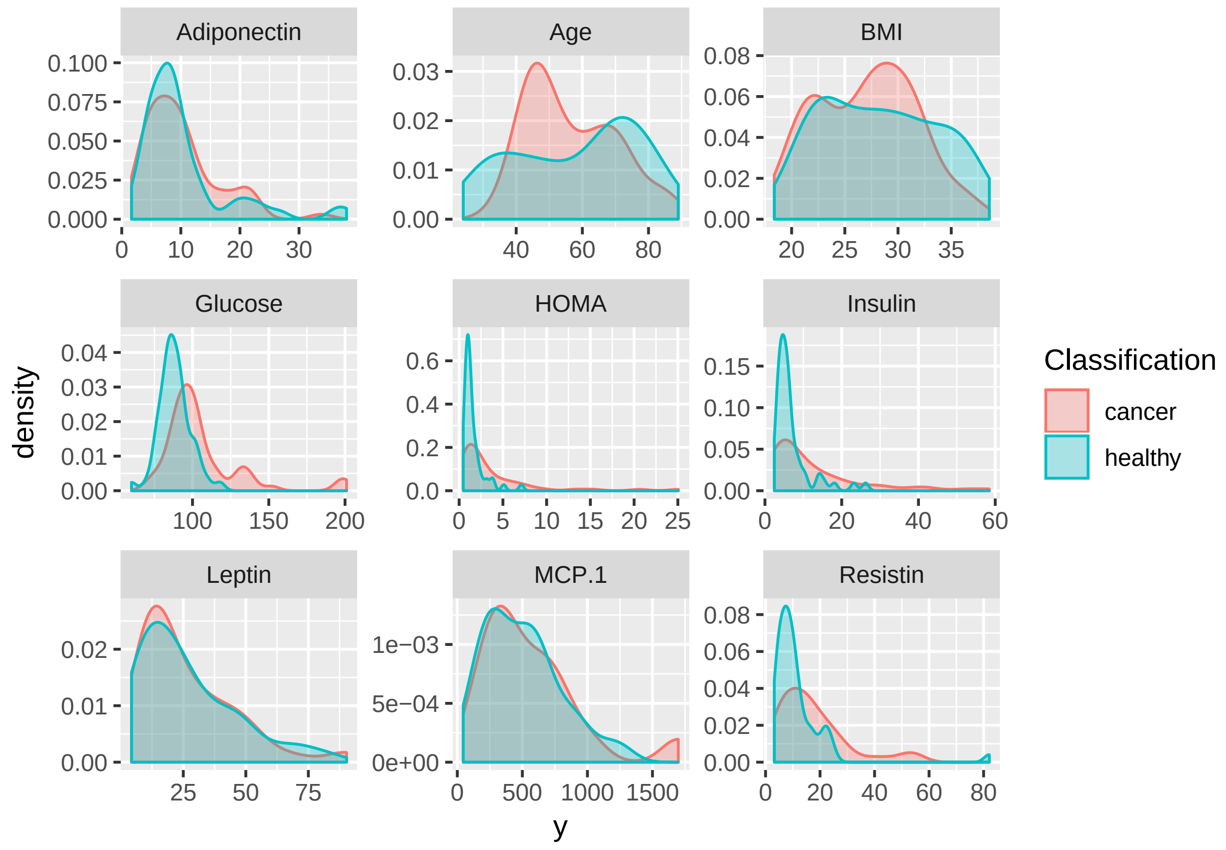
```
# perform pca and extract scores
pcaOutput <- pca(t(data[, 1:9]), printDropped = FALSE, scale = TRUE, center = TRUE)
pcaOutput2 <- as.data.frame(pcaOutput$scores)
```

```
# define groups for plotting:

pcaOutput2$groups <- data$Classification

centroids <- aggregate(cbind(PC1, PC2) ~ groups, pcaOutput2, mean)

conf.rgn  <- do.call(rbind, lapply(unique(pcaOutput2$groups), function(t)
  data.frame(groups = as.character(t),
             ellipse(cov(pcaOutput2[pcaOutput2$groups == t, 1:2]),
                   centre = as.matrix(centroids[centroids$groups == t, 2:3]),
                   level = 0.95),
             stringsAsFactors = FALSE)))


#Plot PCA with variance %:

ggplot(data = pcaOutput2, aes(x = PC1, y = PC2, group = groups, color = groups)) +
    geom_polygon(data = conf.rgn, aes(fill = groups), alpha = 0.2) +
    geom_point(size = 2, alpha = 0.6) +
    scale_color_brewer(palette = "Set1") +
    labs(color = "",
         fill = "",
         x = paste0("PC1: ", round(pcaOutput$pov[1], digits = 2) * 100, "% variance"),
         y = paste0("PC2: ", round(pcaOutput$pov[2], digits = 2) * 100, "% variance"))
```



Features

```r
library(tidyr)

gather(data, x, y, Age:MCP.1) %>%
  ggplot(aes(x = y, color = Classification, fill = Classification)) +
    geom_density(alpha = 0.3) +
    facet_wrap( ~ x, scales = "free")
```



MACHINE LEARNING PACKAGES FOR R

caret

```r
# configure multicore
library(doParallel)
```

```
## Loading required package: foreach

##
## Attaching package: 'foreach'

## The following objects are masked from 'package:purrr':
##
##     accumulate, when

## Loading required package: iterators
```

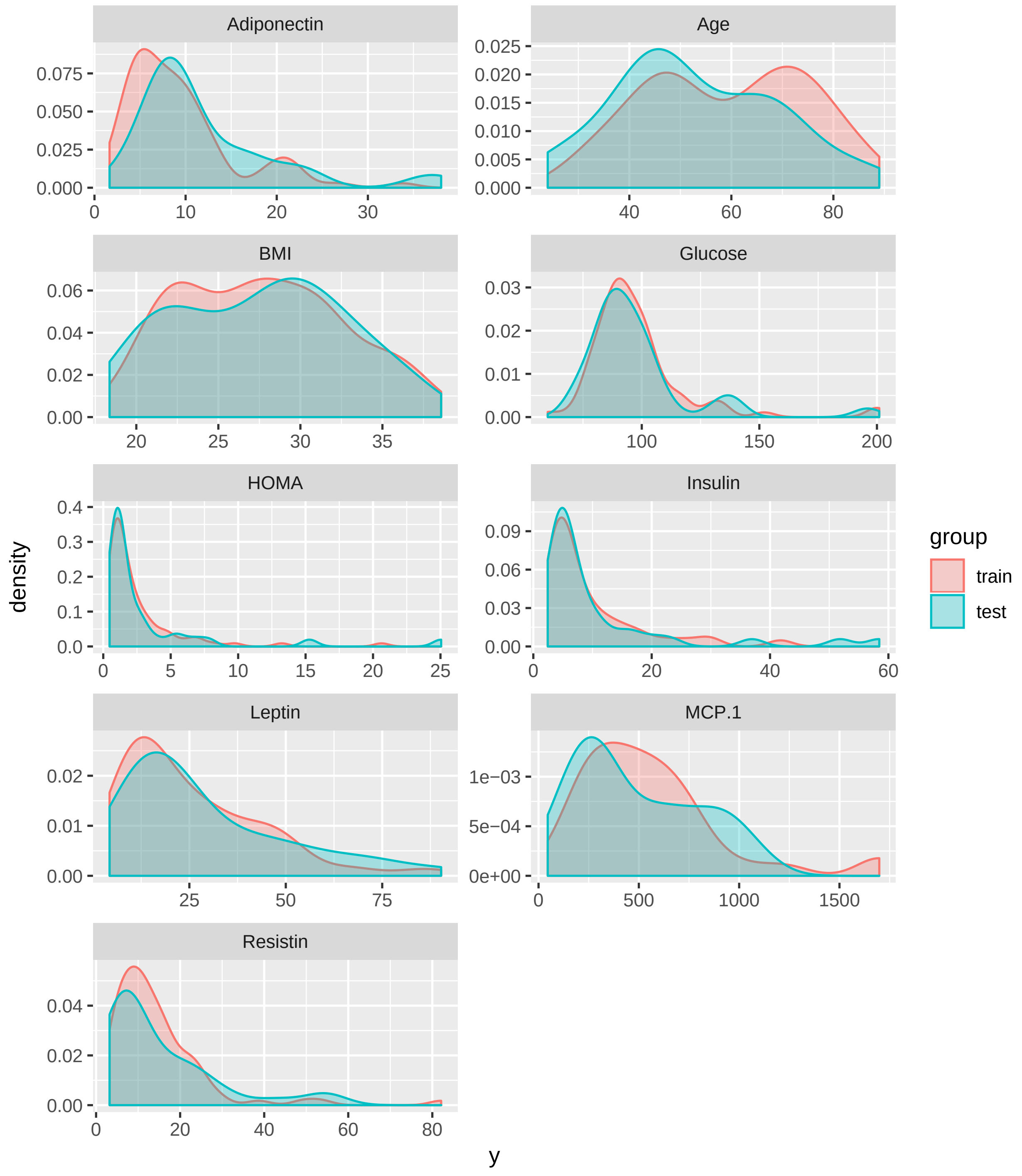
```r
cl <- makeCluster(detectCores())
registerDoParallel(cl)

library(caret)
```

```
## Loading required package: lattice

##
## Attaching package: 'caret'
## The following object is masked from 'package:purrr':
##
##     lift
```

Training, validation and test data

```r
set.seed(42)
index <- createDataPartition(data$Classification, p = 0.7, list = FALSE)
train_data <- data[index, ]
test_data  <- data[-index, ]
```

```r
library(dplyr)

rbind(data.frame(group = "train", train_data),
      data.frame(group = "test", test_data)) %>%
  gather(x, y,Age:MCP.1) %>%
  ggplot(aes(x = y, color = group, fill = group)) +
    geom_density(alpha = 0.3) +
    facet_wrap( ~ x, scales = "free", ncol = 2)
```



REGRESSION

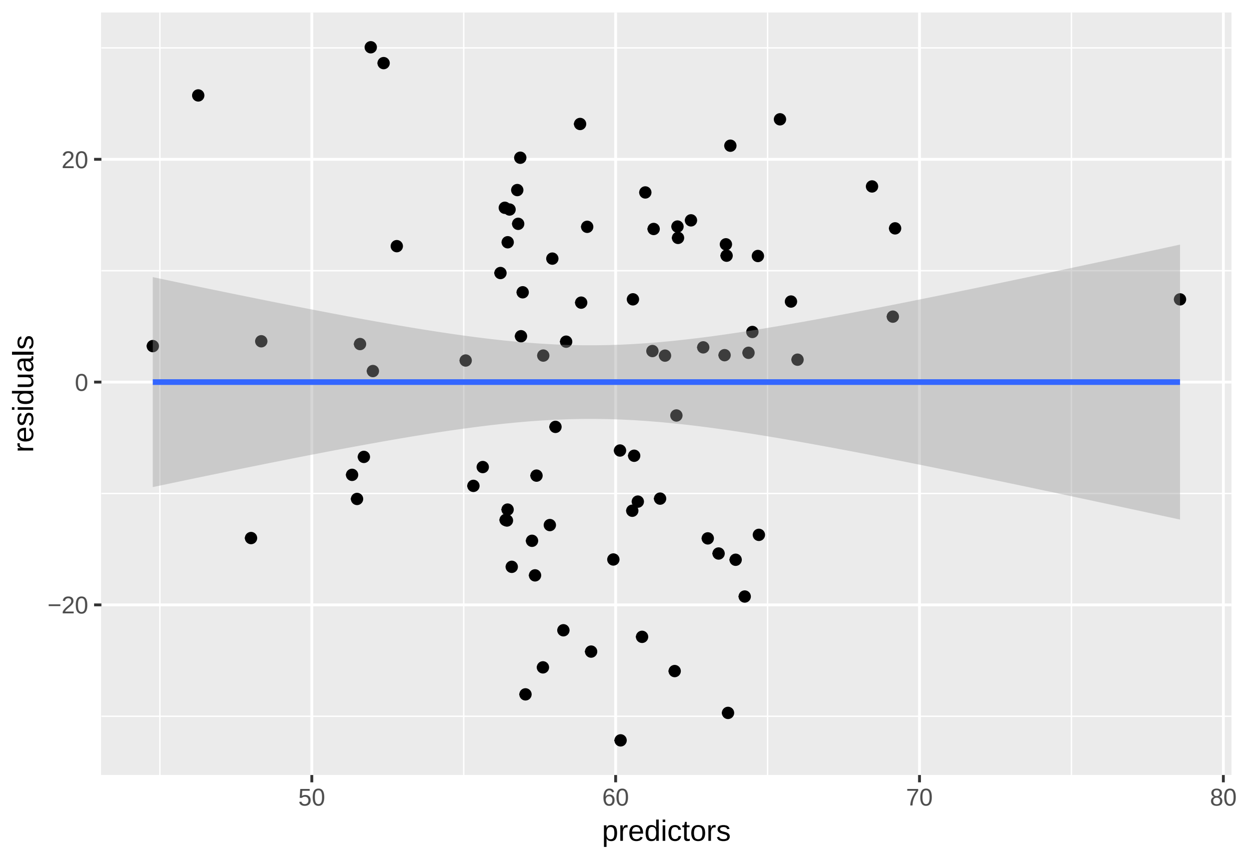
```r
set.seed(42)
model_glm <- caret::train(Age ~ .,
                          data = train_data,
                          method = "glm",
                          preProcess = c("scale", "center"),
                          trControl = trainControl(method = "repeatedcv",
                                                  number = 10,
                                                  repeats = 10,
                                                  savePredictions = TRUE,
                                                  verboseIter = FALSE))
```

```
model_glm
```

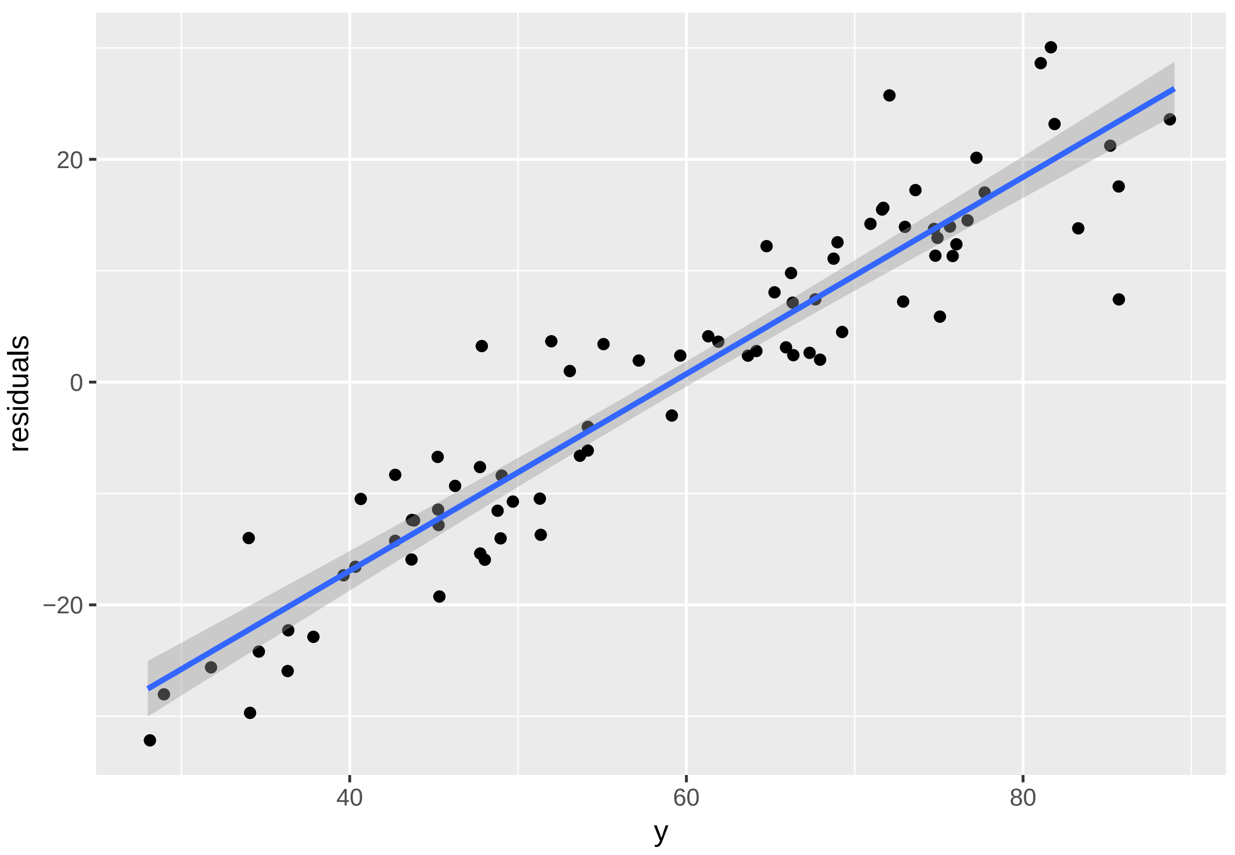
```
## Generalized Linear Model
##
## 82 samples
##  9 predictor
##
## Pre-processing: scaled (9), centered (9)
## Resampling: Cross-Validated (10 fold, repeated 10 times)
## Summary of sample sizes: 74, 74, 74, 72, 74, 74, ...
## Resampling results:
##
##   RMSE      Rsquared   MAE
##   17.63297  0.1196448  14.88396
```

```
predictions <- predict(model_glm, test_data)
```

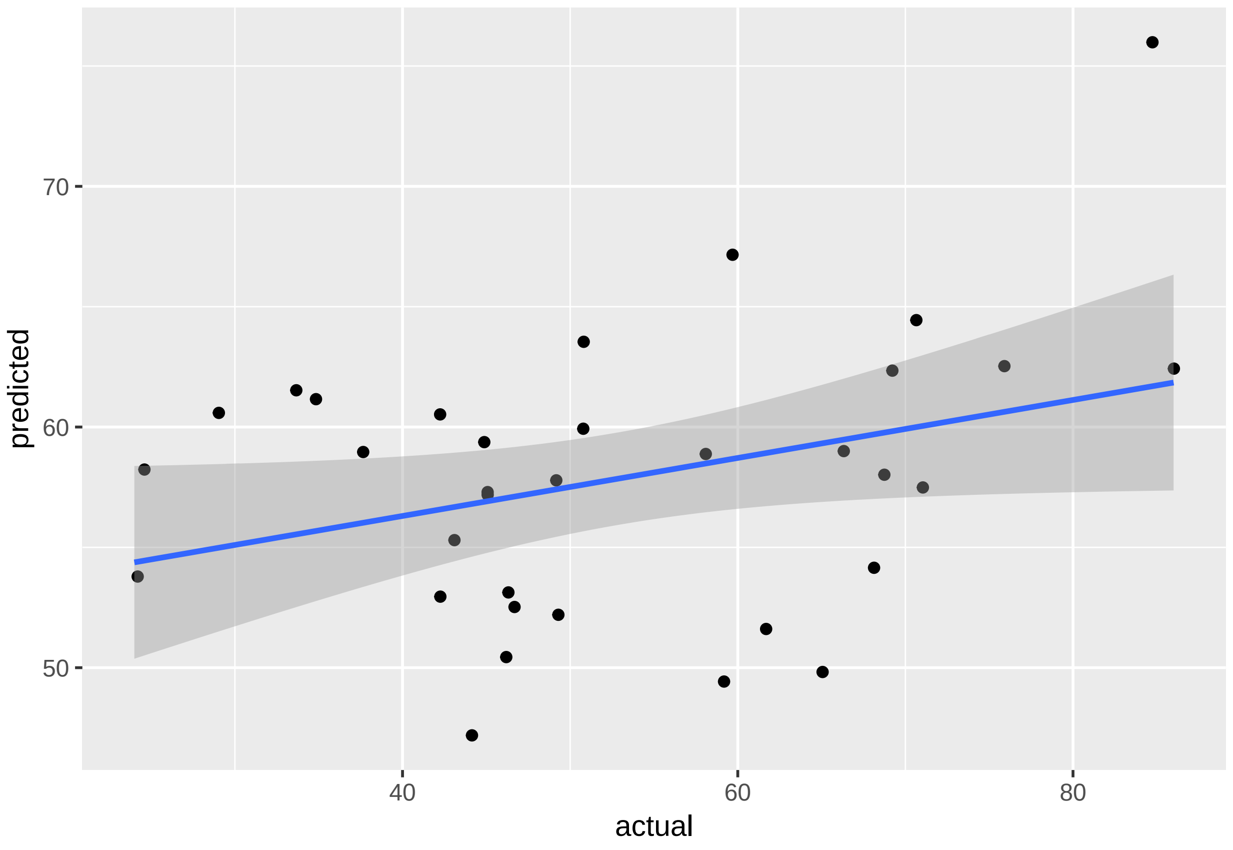
```
# model_glm$finalModel$linear.predictors == model_glm$finalModel$fitted.values
data.frame(residuals = resid(model_glm),
           predictors = model_glm$finalModel$linear.predictors) %>%
  ggplot(aes(x = predictors, y = residuals)) +
    geom_jitter() +
    geom_smooth(method = "lm")
```



```r
# y == train_data$Age
data.frame(residuals = resid(model_glm),
           y = model_glm$finalModel$y) %>%
  ggplot(aes(x = y, y = residuals)) +
    geom_jitter() +
    geom_smooth(method = "lm")
```



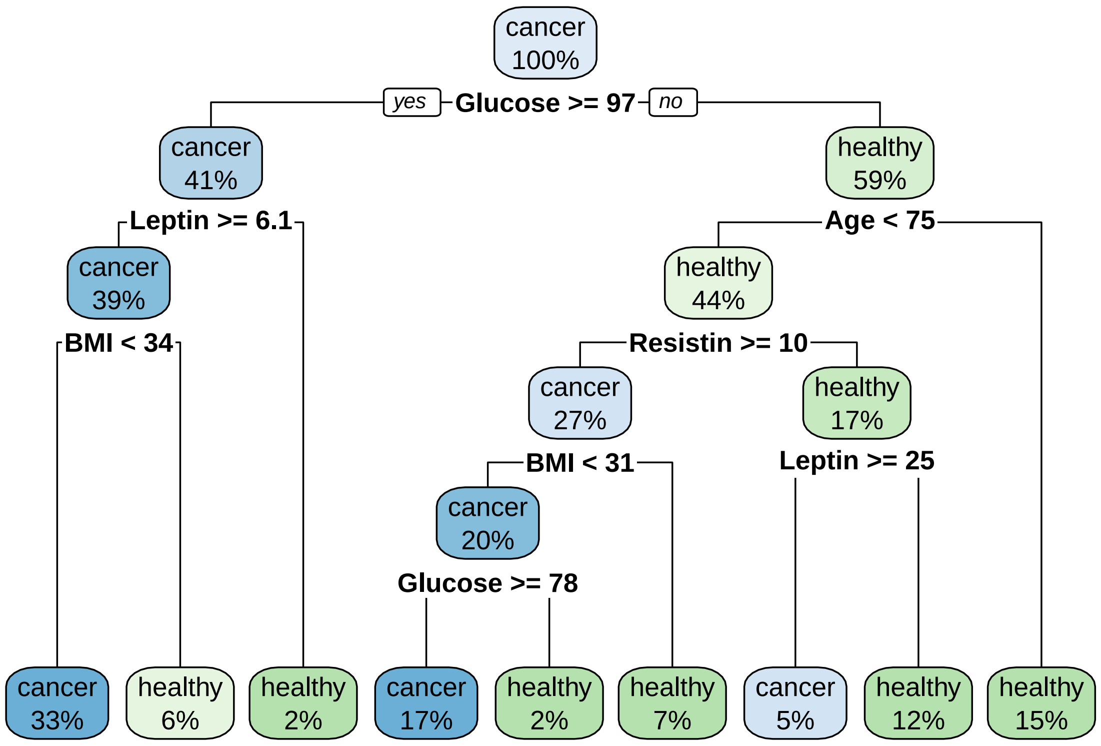
```
data.frame(actual = test_data$Age,
           predicted = predictions) %>%
  ggplot(aes(x = actual, y = predicted)) +
    geom_jitter() +
    geom_smooth(method = "lm")
```



CLASSIFICATION

Decision trees

```
library(rpart)
library(rpart.plot)

set.seed(42)
fit <- rpart(Classification ~ .,
             data = train_data,
             method = "class",
             control = rpart.control(xval = 10,
                                     minbucket = 2,
                                     cp = 0),
              parms = list(split = "information"))

rpart.plot(fit, extra = 100)
```



Random Forests

```
#Random Forests predictions are based on the generation of
#multiple classification trees.
#They can be used for both, classification and regression tasks.
#Here, it is classification task.
```

```
set.seed(42)
library(randomForest)
```

```
## randomForest 4.6-14

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

##
## Attaching package: 'randomForest'

## The following object is masked from 'package:BiocGenerics':
##
##     combine

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

## The following object is masked from 'package:ggplot2':
##
##     margin
```

```
model_rf <- caret::train(Classification ~ .,
                         data = train_data,
                         method = "rf",
                         preProcess = c("scale", "center"),
                         trControl = trainControl(method = "repeatedcv",
                                                  number = 10,
                                                  repeats = 10,
                                                  savePredictions = TRUE,
                                                  verboseIter = FALSE))
```

```
#When savePredictions = TRUE is specified,
#can access the cross-validation resuls with model_rf$pred.

model_rf$finalModel$confusion
```

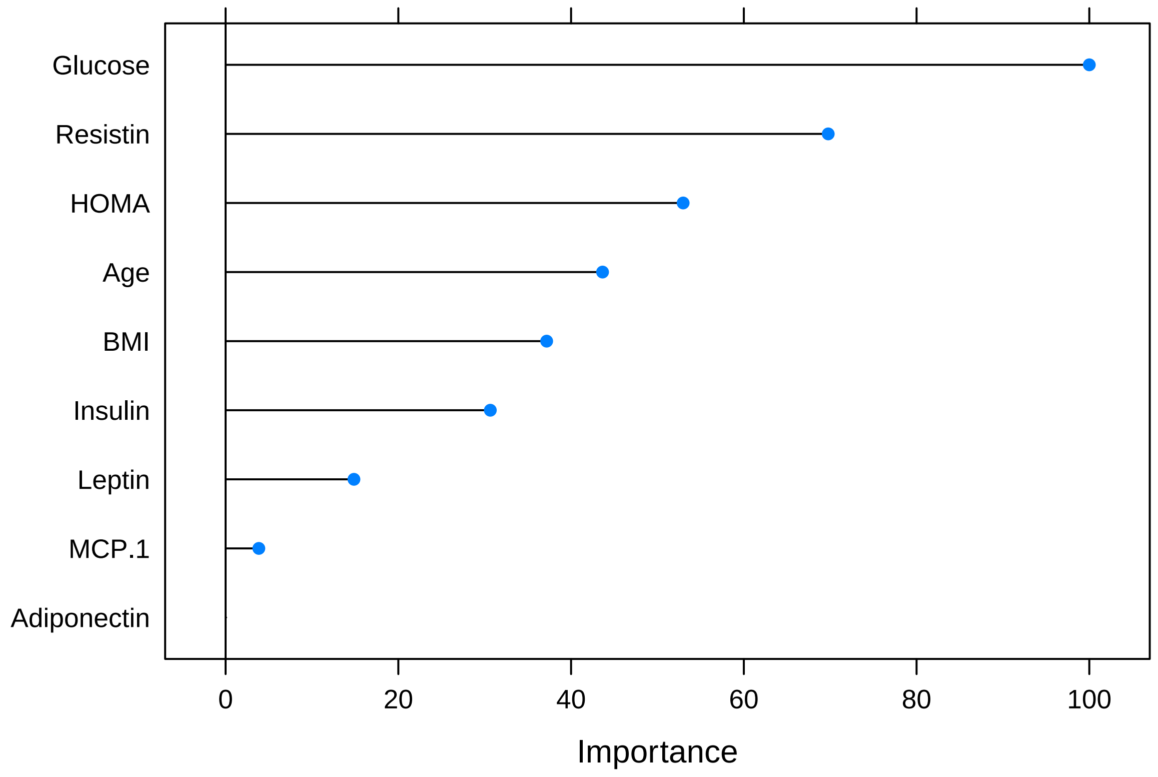
```
##         cancer healthy class.error
## cancer      35      10   0.2222222
## healthy     10      27   0.2702703
```

Feature Importance

```
imp <- model_rf$finalModel$importance
imp[order(imp, decreasing = TRUE), ]
```

```
##     Glucose    Resistin        HOMA         Age         BMI     Insulin
##    7.011906    5.740823    5.034404    4.642025    4.369878    4.095543
##      Leptin       MCP.1 Adiponectin
##    3.431462    2.968458    2.806573
```

```
# estimate variable importance
importance <- varImp(model_rf, scale = TRUE)
plot(importance)
```

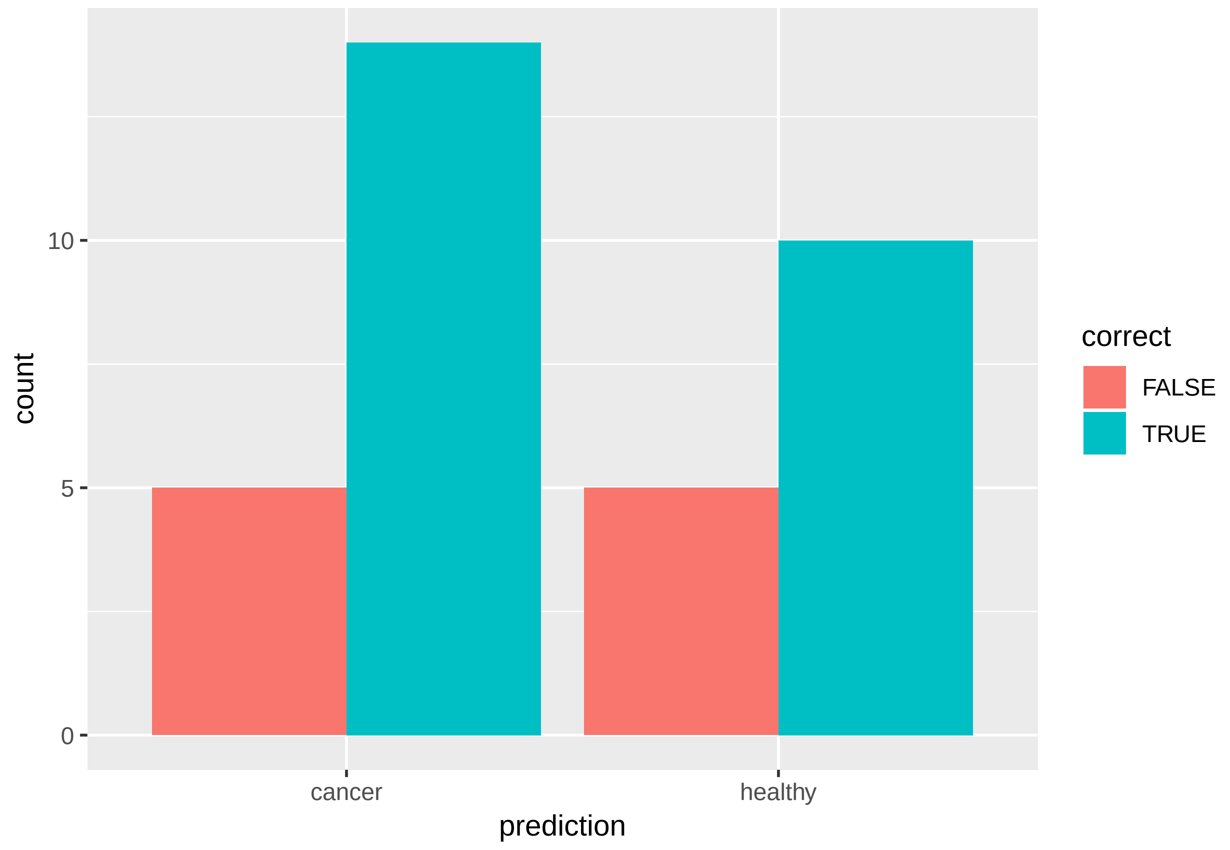


Predicting test data

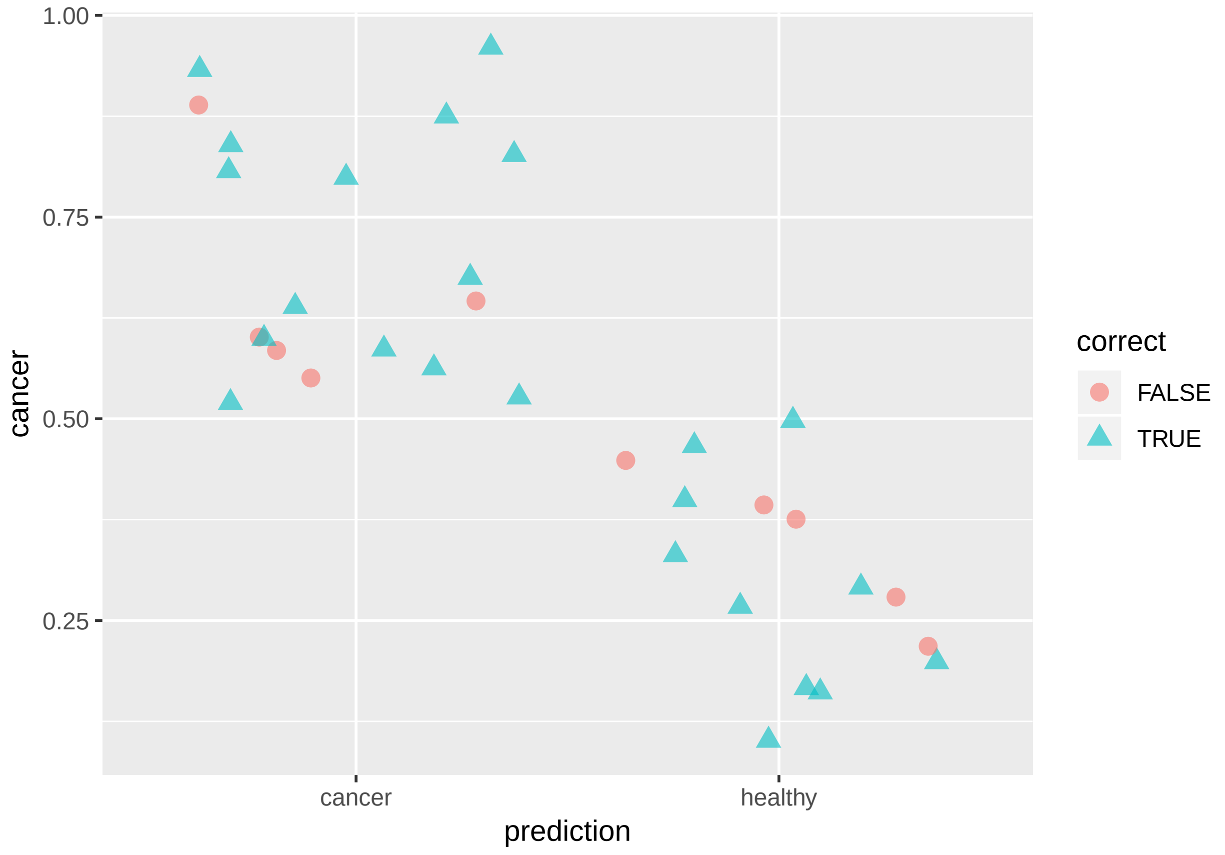
```r
confusionMatrix(predict(model_rf, test_data), test_data$Classification)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction cancer healthy
##    cancer      14       5
##    healthy      5      10
##
##                Accuracy : 0.7059
##                  95% CI : (0.5252, 0.849)
##     No Information Rate : 0.5588
##     P-Value [Acc > NIR] : 0.0582
##
##                   Kappa : 0.4035
##
##  Mcnemar's Test P-Value : 1.0000
##
##             Sensitivity : 0.7368
##             Specificity : 0.6667
##          Pos Pred Value : 0.7368
##          Neg Pred Value : 0.6667
##              Prevalence : 0.5588
##          Detection Rate : 0.4118
##    Detection Prevalence : 0.5588
##       Balanced Accuracy : 0.7018
##
##        'Positive' Class : cancer
##
```

```
results <- data.frame(actual = test_data$Classification,
                      predict(model_rf, test_data, type = "prob"))

results$prediction <- ifelse(results$healthy > 0.5, "healthy",
                             ifelse(results$cancer > 0.5, "cancer", NA))

results$correct <- ifelse(results$actual == results$prediction, TRUE, FALSE)

ggplot(results, aes(x = prediction, fill = correct)) +
  geom_bar(position = "dodge")
```



```
ggplot(results, aes(x = prediction, y = cancer, color = correct, shape = correct)) +
  geom_jitter(size = 3, alpha = 0.6)
```



EXTREME GRADIENT BOOSTING.

Extreme gradient boosting (XGBoost) is a faster and improved implementation of gradient boosting for supervised learning.

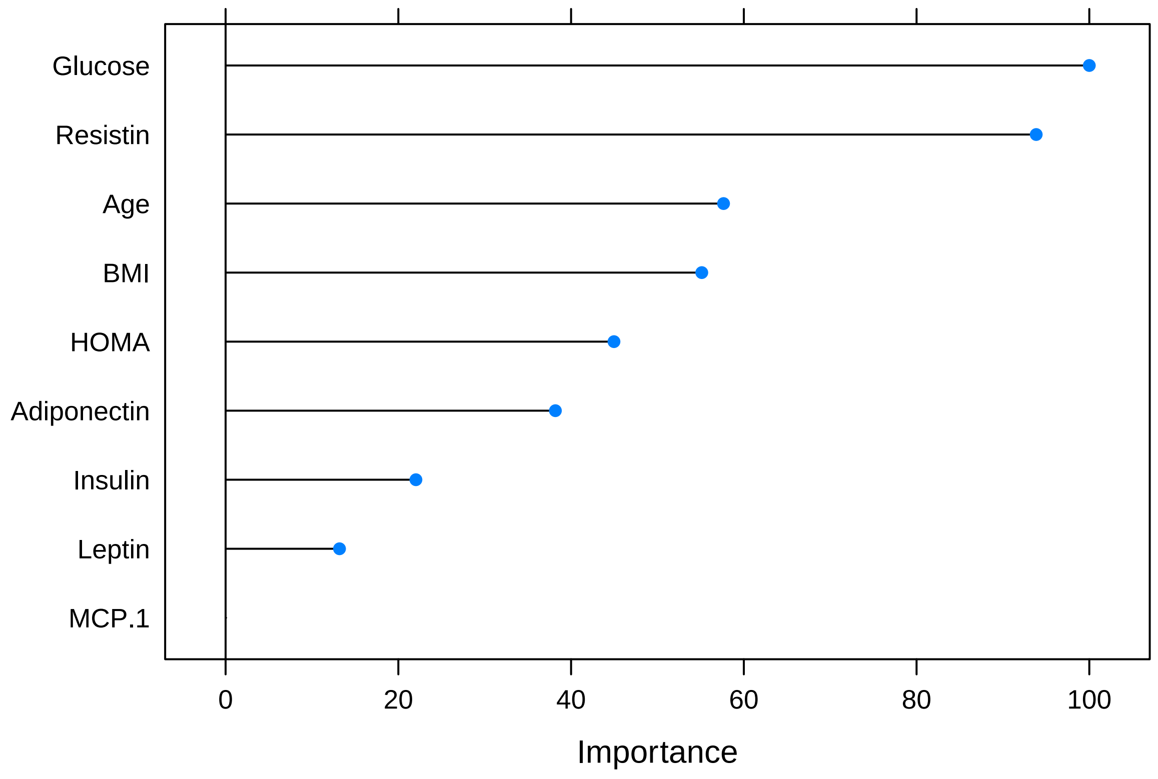
```
set.seed(42)
library(xgboost)
```

```
##
## Attaching package: 'xgboost'

## The following object is masked from 'package:XVector':
##
##     slice

## The following object is masked from 'package:IRanges':
##
##     slice

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

```
model_xgb <- caret::train(Classification ~ .,
                          data = train_data,
                          method = "xgbTree",
                          preProcess = c("scale", "center"),
                          trControl = trainControl(method = "repeatedcv",
                                                  number = 10,
                                                  repeats = 10,
                                                  savePredictions = TRUE,
                                                  verboseIter = FALSE))
```

Feature Importance

```r
importance <- varImp(model_xgb, scale = TRUE)
plot(importance)
```



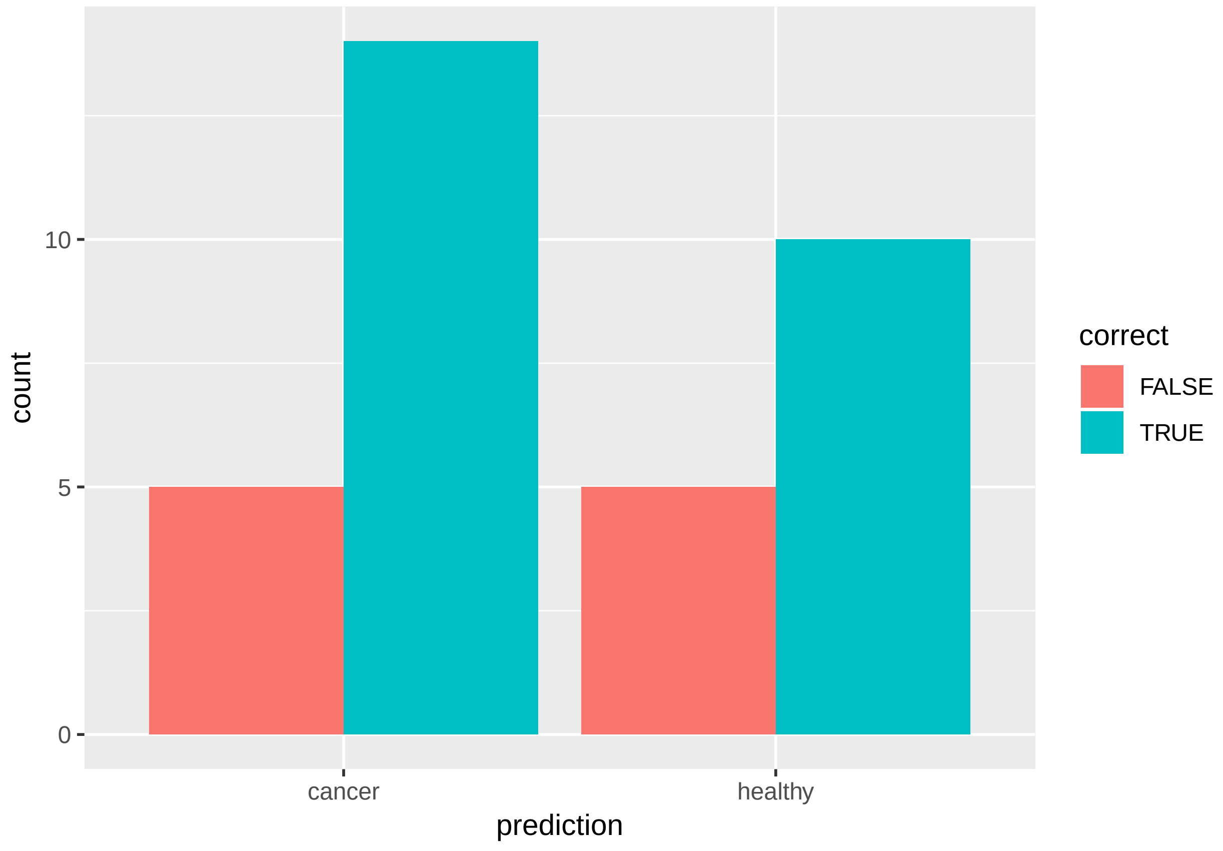
#Predicting test data

```r
confusionMatrix(predict(model_xgb, test_data), test_data$Class)
```

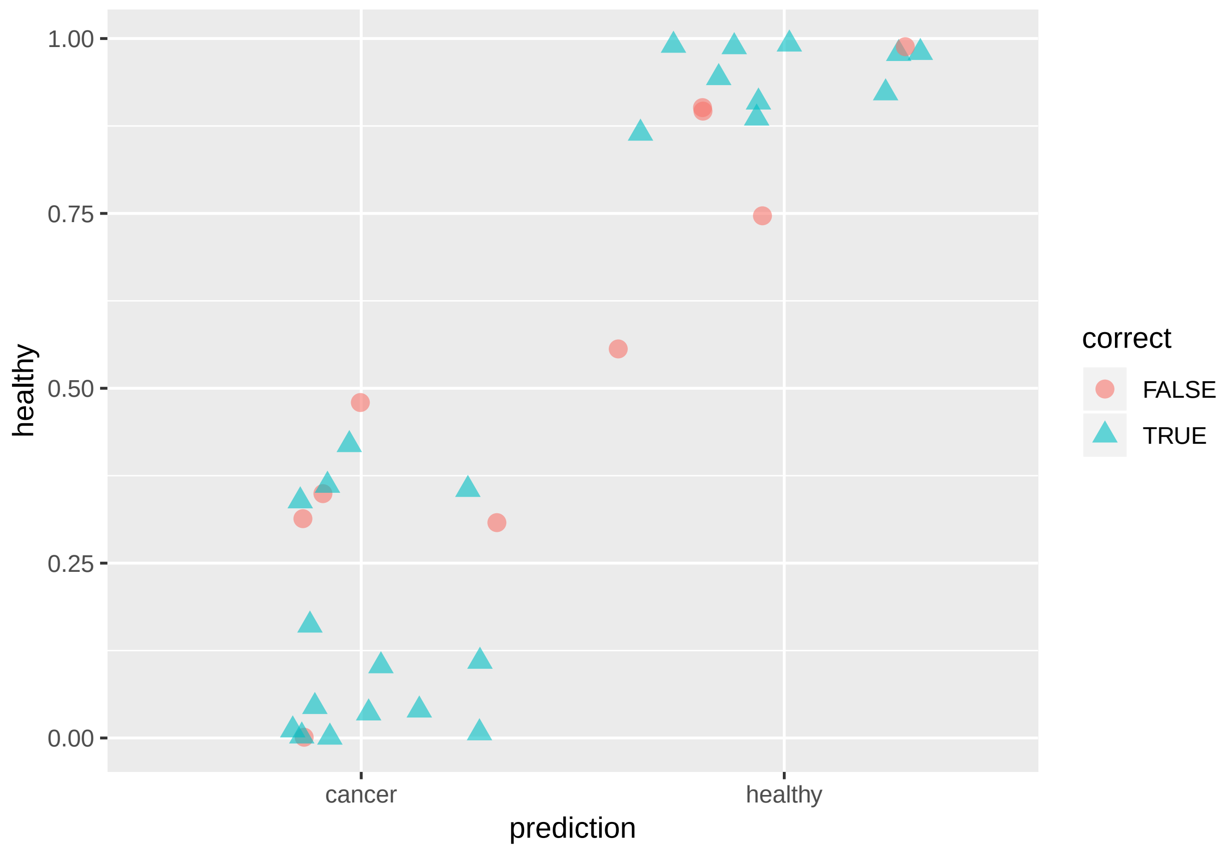
```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction cancer healthy
##    cancer      14       5
##    healthy      5      10
##
##                Accuracy : 0.7059
##                  95% CI : (0.5252, 0.849)
##     No Information Rate : 0.5588
##     P-Value [Acc > NIR] : 0.0582
##
```

```
##                   Kappa : 0.4035
##
##  Mcnemar's Test P-Value : 1.0000
##
##             Sensitivity : 0.7368
##             Specificity : 0.6667
##          Pos Pred Value : 0.7368
##          Neg Pred Value : 0.6667
##              Prevalence : 0.5588
##          Detection Rate : 0.4118
##    Detection Prevalence : 0.5588
##       Balanced Accuracy : 0.7018
##
##        'Positive' Class : cancer
##
```

```
results <- data.frame(actual = test_data$Classification,
                      predict(model_xgb, test_data, type = "prob"))

results$prediction <- ifelse(results$healthy > 0.5, "healthy",
                             ifelse(results$cancer > 0.5, "cancer", NA))

results$correct <- ifelse(results$actual == results$prediction, TRUE, FALSE)

ggplot(results, aes(x = prediction, fill = correct)) +
  geom_bar(position = "dodge")
```



```
ggplot(results, aes(x = prediction, y = healthy, color = correct, shape = correct)) +
  geom_jitter(size = 3, alpha = 0.6)
```



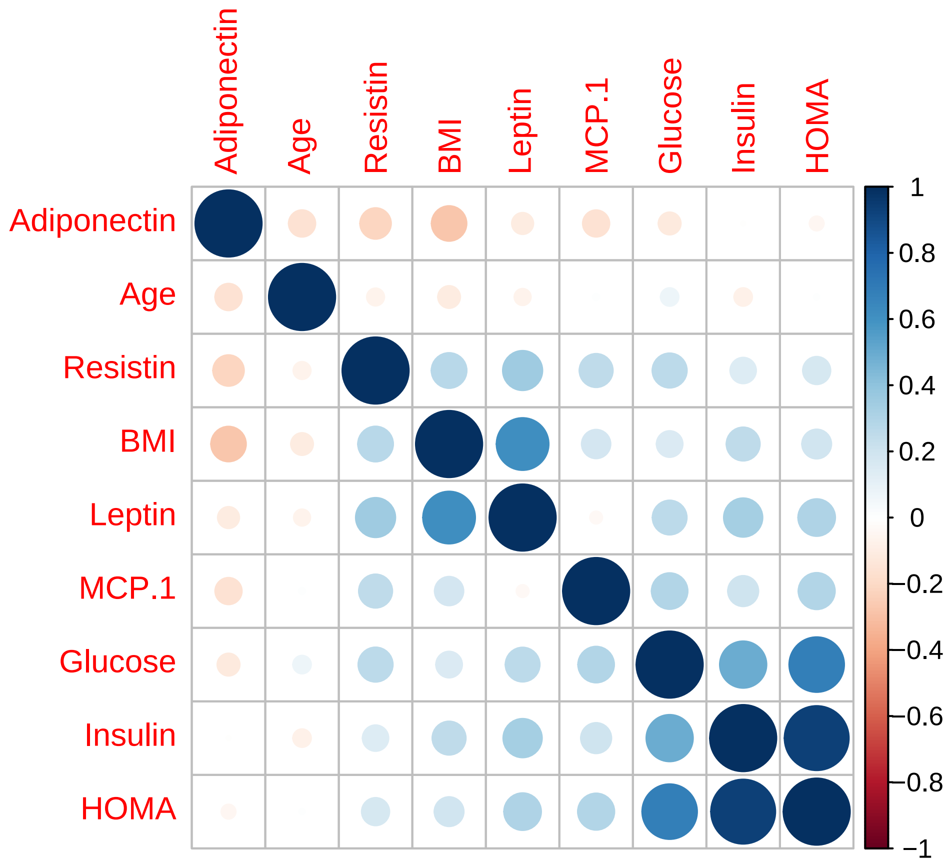
Feature Selection

Correlation

```
library(corrplot)
```

```
## corrplot 0.84 loaded
```

```
# calculate correlation matrix
corMatMy <- cor(train_data[, 1:9])
corrplot(corMatMy, order = "hclust")
```



```r
#Apply correlation filter at 0.70:
highlyCor <- colnames(train_data[, -1])[findCorrelation(corMatMy, cutoff = 0.7, verbose = TRUE)]
```

```
## Compare row 5  and column  4 with corr  0.935
##   Means:  0.33 vs 0.217 so flagging column 5
## All correlations <= 0.7
```

```r
# which variables are flagged for removal?
highlyCor
```

```
## [1] "Leptin"
```

```r
#then we remove these variables
train_data_cor <- train_data[, which(!colnames(train_data) %in% highlyCor)]
```

GRID SEARCH WITH CARET

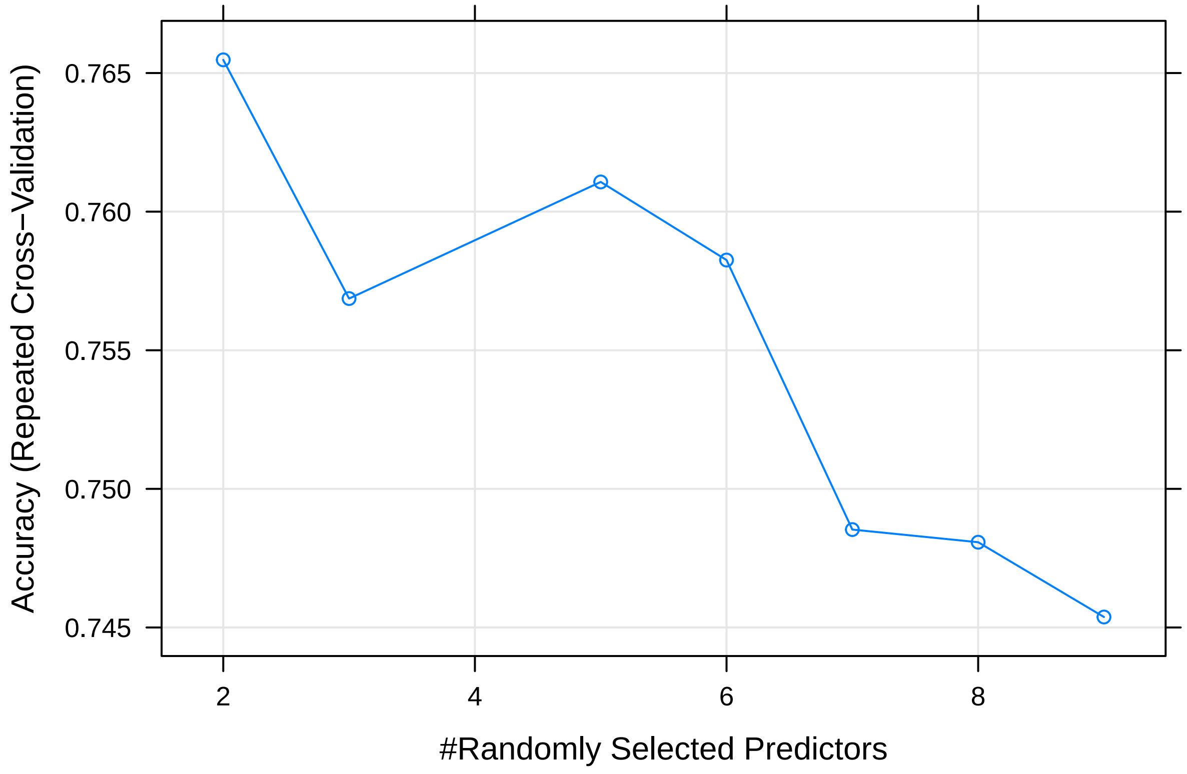
Automatic Grid

```r
set.seed(42)
model_rf_tune_auto <- caret::train(Classification ~ .,
                         data = train_data,
                         method = "rf",
                         preProcess = c("scale", "center"),
                         trControl = trainControl(method = "repeatedcv",
                                                  number = 10,
                                                  repeats = 10,
                                                  savePredictions = TRUE,
                                                  verboseIter = FALSE,
                                                  search = "random"),
                         tuneLength = 15)
```

```
model_rf_tune_auto
```

```
## Random Forest
##
## 82 samples
##  9 predictor
##  2 classes: 'cancer', 'healthy'
##
## Pre-processing: scaled (9), centered (9)
## Resampling: Cross-Validated (10 fold, repeated 10 times)
## Summary of sample sizes: 74, 75, 73, 74, 74, 74, ...
## Resampling results across tuning parameters:
##
##   mtry  Accuracy   Kappa
##   2     0.7654762  0.5207469
##   3     0.7568651  0.5033515
##   5     0.7610714  0.5134804
##   6     0.7582540  0.5092464
##   7     0.7485317  0.4869195
##   8     0.7480754  0.4881144
##   9     0.7453770  0.4815800
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 2.
```

```
plot(model_rf_tune_auto)
```

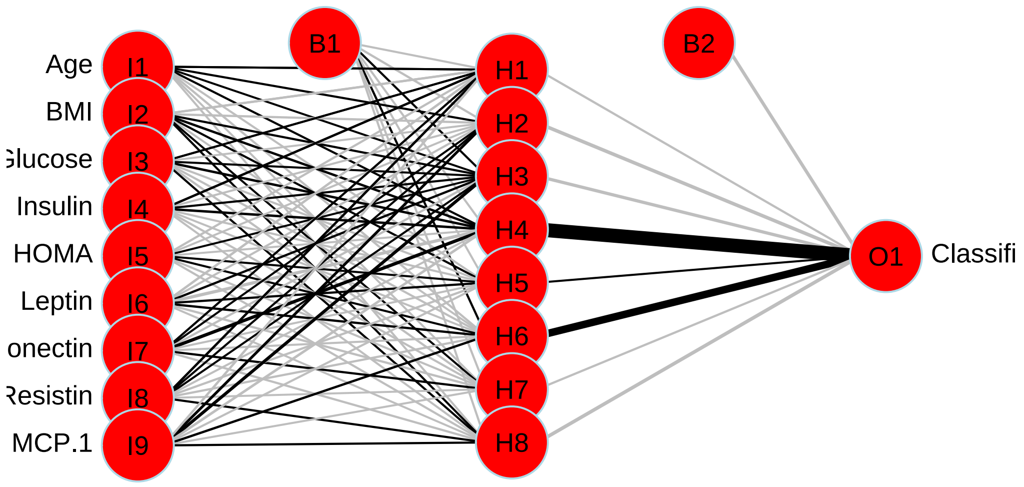


NEURAL NETWORK MODEL

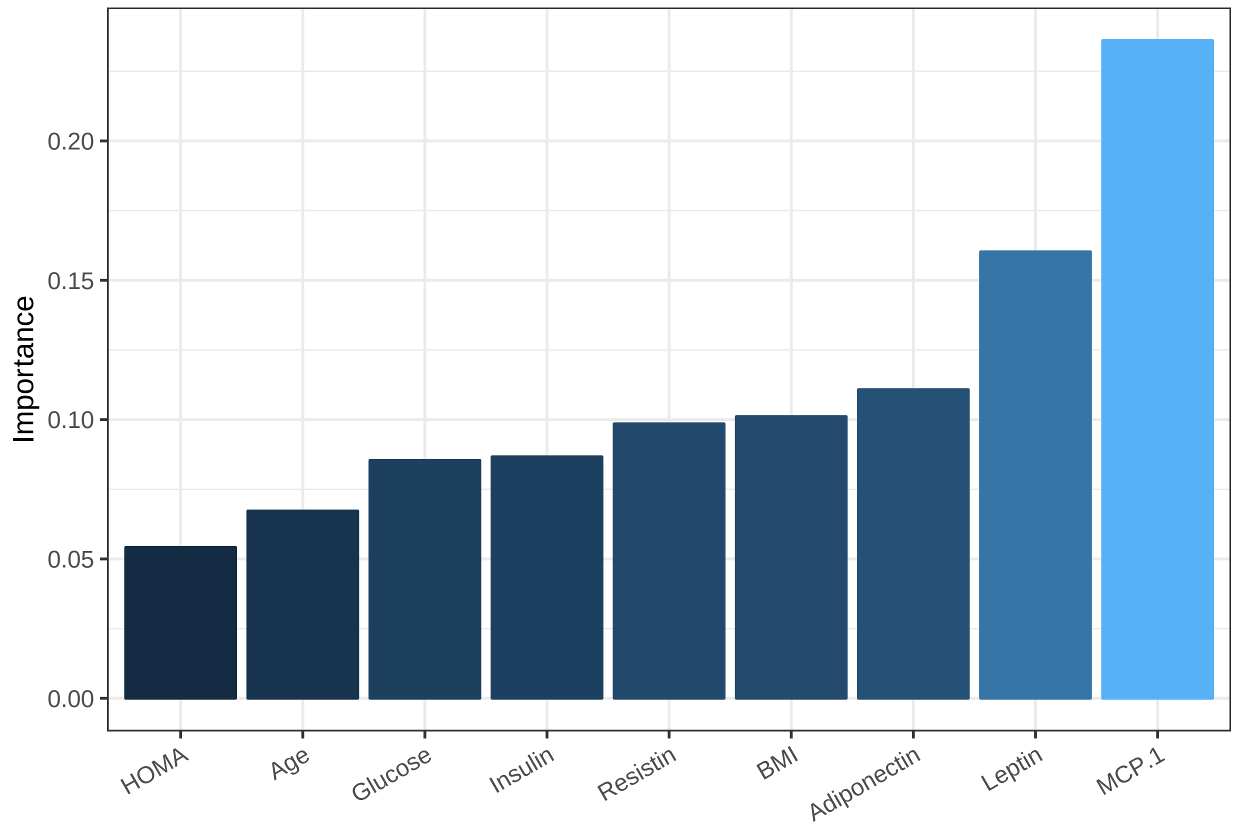
```
library(nnet)
model_nnet<-nnet(Classification ~. ,
                 data= train_data,
                 size=8
)
```

```
## # weights:  89
## initial  value 58.952401
## iter  10 value 54.963035
## iter  20 value 54.245492
## iter  30 value 54.244855
## iter  30 value 54.244855
## iter  30 value 54.244855
## final  value 54.244855
## converged
```

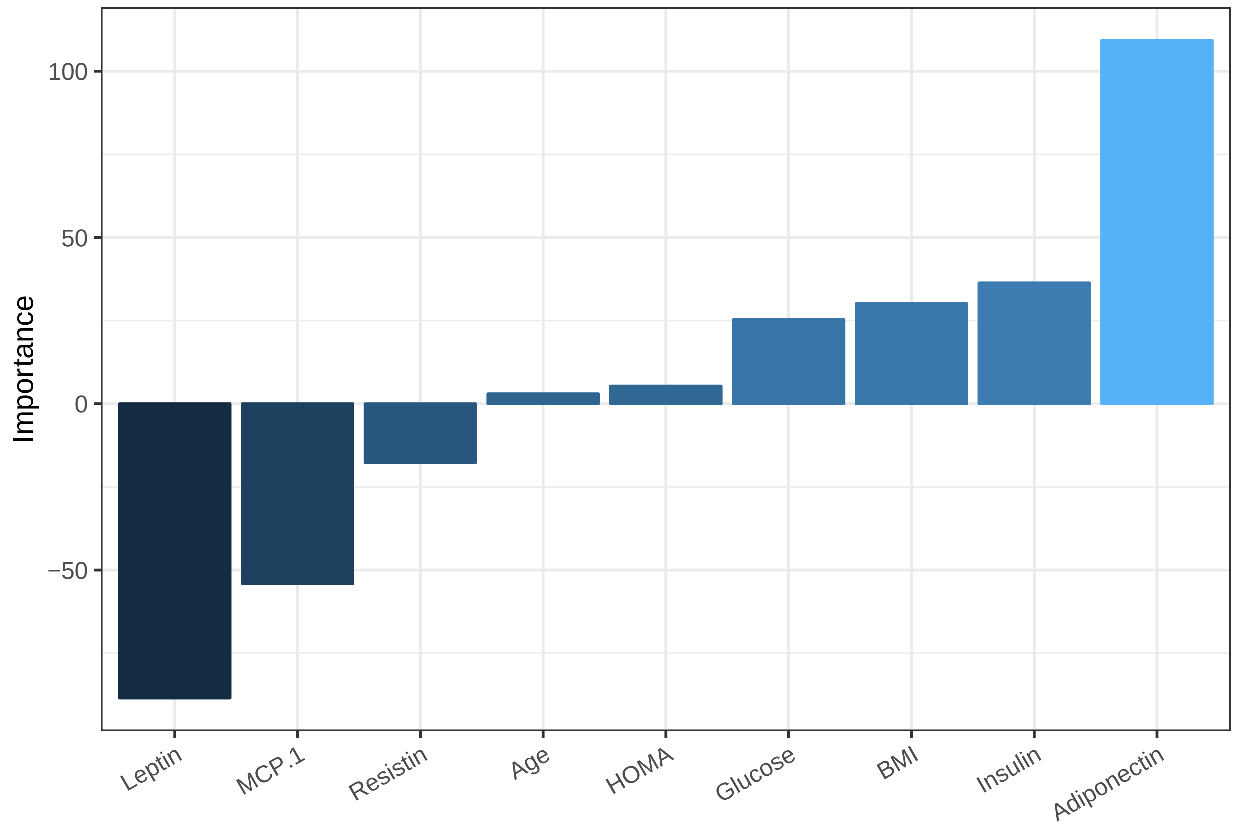
```
library(NeuralNetTools)
# Plot a neural interpretation diagram for a neural network object
plotnet(model_nnet, cex_val =.8,max_sp=T,circle_cex=5,circle_col = 'red')
```



```
#Relative importance of input variables in neural networks using Garson's algorithm:
garson(model_nnet) +
  theme(axis.text.x = element_text(angle = 30, hjust = 1))
```



```r
olden(model_nnet) +
   theme(axis.text.x = element_text(angle = 30, hjust = 1))
```



Here both the positve and negative value represents relative contibutions of each connection weight among the variables

```
#Predict
predict_nnet <- predict(model_nnet,test_data, type = "class")
```

```
#Draw the crosstable

library(gmodels)
CrossTable(test_data$Class,predict_nnet,prop.chisq = F,prop.r = F,prop.c = F,dnn =c("Actual Diagnosis",
```

```
##
##
##    Cell Contents
## |-------------------------|
## |                       N |
## |         N / Table Total |
## |-------------------------|
##
##
## Total Observations in Table:  34
##
##
##                 | predict_nnet
## test_data$Class |    cancer | Row Total |
## ----------------|-----------|-----------|
##          cancer |        19 |        19 |
##                 |     0.559 |           |
## ----------------|-----------|-----------|
##         healthy |        15 |        15 |
##                 |     0.441 |           |
## ----------------|-----------|-----------|
##    Column Total |        34 |        34 |
## ----------------|-----------|-----------|
##
##
```