# Predicting Diagnosis of Liver Disease

```r
# Load libraries
library(tidyverse)
```

```
## -- Attaching packages ------------------------------------ tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.3     v purrr   0.3.4
## v tibble  3.0.6     v dplyr   1.0.4
## v tidyr   1.1.2     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.1
```

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

```r
library(dplyr)
library(ISLR)
library(janitor)
```

```
##
## Attaching package: 'janitor'
```

```
## The following objects are masked from 'package:stats':
##
##     chisq.test, fisher.test
```

```r
library(AppliedPredictiveModeling)
library(caret)
```

```
## Loading required package: lattice
```

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

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

```r
library(corrplot)
```

```
## corrplot 0.84 loaded
```

```
library(pROC)
```

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

##
## Attaching package: 'pROC'

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

```
library(MASS)
```

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

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

```
library(readxl)
library(glmnet)
```

```
## Loading required package: Matrix

##
## Attaching package: 'Matrix'

## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack

## Loaded glmnet 4.1
```

```
library(mlbench)
library(pdp)
```

```
##
## Attaching package: 'pdp'

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

```
library(vip)
```

```
##
## Attaching package: 'vip'

## The following object is masked from 'package:utils':
##
##     vi
```

```
library(klaR)
library(rpart)
library(rpart.plot)
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:dplyr':
##
##     combine
```

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

```
library(ranger)
```

```
##
## Attaching package: 'ranger'
```

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

```
library(ISLR)
library(caret)
library(e1071)
library(kernlab)
```

```
##
## Attaching package: 'kernlab'
```

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

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

```
library(DALEX)
```

```
## Registered S3 method overwritten by 'DALEX':
##   method            from
##   print.description questionr
```

```
## Welcome to DALEX (version: 2.2.0).
## Find examples and detailed introduction at: http://ema.drwhy.ai/


##
## Attaching package: 'DALEX'

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

```
library(gbm)
```

```
## Loaded gbm 2.1.8
```

```
library(ROCR)
```

# Import data

```
liver_df = read_excel("./data/liver.xlsx") %>%
  mutate(outcome = ifelse(is_patient == 1, "yes", "no"), outcome = as.factor(outcome)) %>%
  dplyr::select(-is_patient) %>%
  clean_names %>%
  rename(
    aspartate_aminotransferase = sgpt,
    alamine_aminotransferase = sgot,
    albumin_globulin_ratio = ag_ratio,
    alkaline_phosphate = alkphos) %>%
  drop_na

liver_df$gender=factor(x=liver_df$gender,levels = c('Female','Male'),labels=c(0, 1))
liver_df$gender = as.double(liver_df$gender)
# female = '1', male = '2'
```

# Exploratory Data Analysis

```
# Feature plots
theme1 <- transparentTheme(trans = .4)
trellis.par.set(theme1)
featurePlot(x = liver_df[, 1:10],
            y = liver_df$outcome,
            scales = list(x = list(relation = "free"),
                          y = list(relation = "free")),
            plot = "density", pch = "|",
            auto.key = list(columns = 2))
```
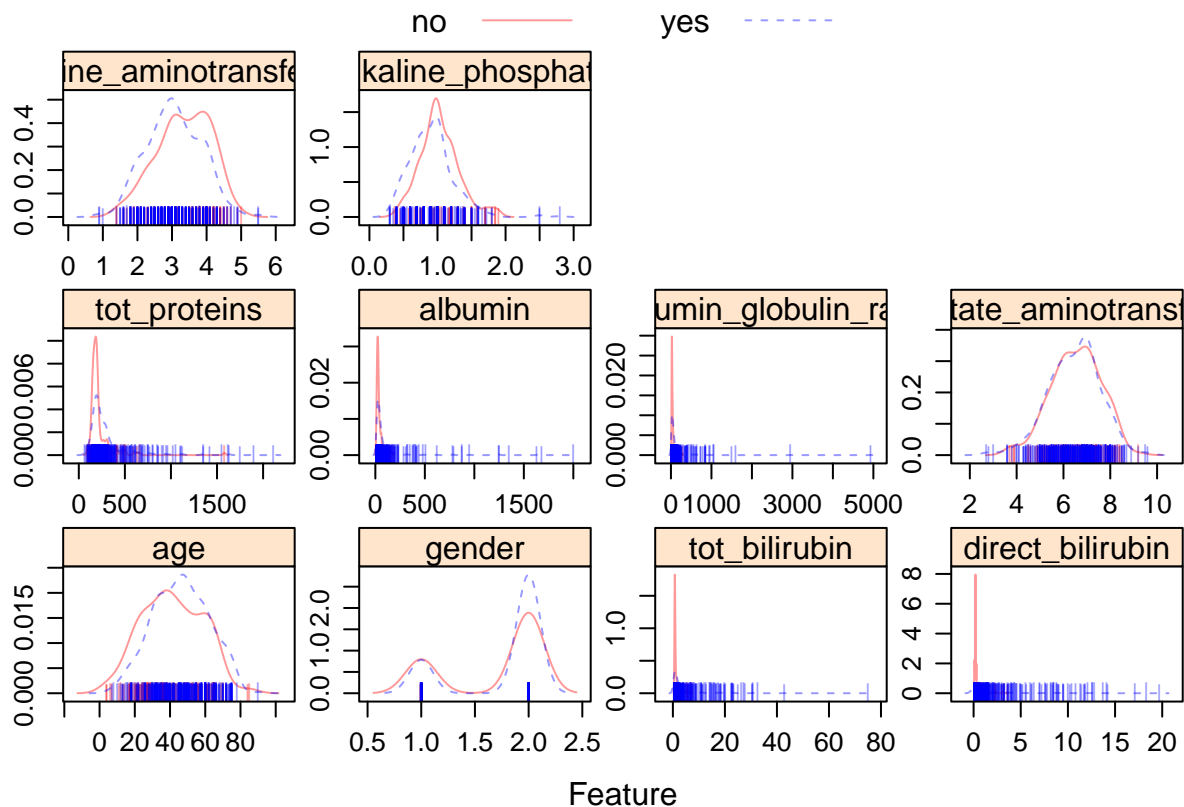
```r
# dataset with all the log-transformed predictor variables
liver_df1 =
  liver_df %>%
  mutate(logtot_bilirubin = log(tot_bilirubin) +1,
         logdirect_bilirubin = log(direct_bilirubin) +1,
         logtot_proteins = log(tot_proteins) +1,
         logalbumin = log(albumin) +1,
         loggender = log(gender) +1,
         logalbumin_globulin_ratio = log(albumin_globulin_ratio) +1,
         logage = log(age) +1,
         logaspartate_aminotransferase = log(aspartate_aminotransferase) +1,
         logalamine_transferase = log(alamine_aminotransferase ) +1,
         logalkaline_phosphate = log(alkaline_phosphate) +1) %>%
         dplyr::select(logage, loggender, logtot_bilirubin, logdirect_bilirubin, logtot_proteins,
                       logalbumin, logalbumin_globulin_ratio, logaspartate_aminotransferase,
                       logalamine_transferase, logalkaline_phosphate, outcome)


theme1 <- transparentTheme(trans = .4)
trellis.par.set(theme1)
featurePlot(x = liver_df1[, 1:10],
            y = liver_df1$outcome,
            scales = list(x = list(relation = "free"),
                          y = list(relation = "free")),
            plot = "density", pch = "|",
            auto.key = list(columns = 2))
```
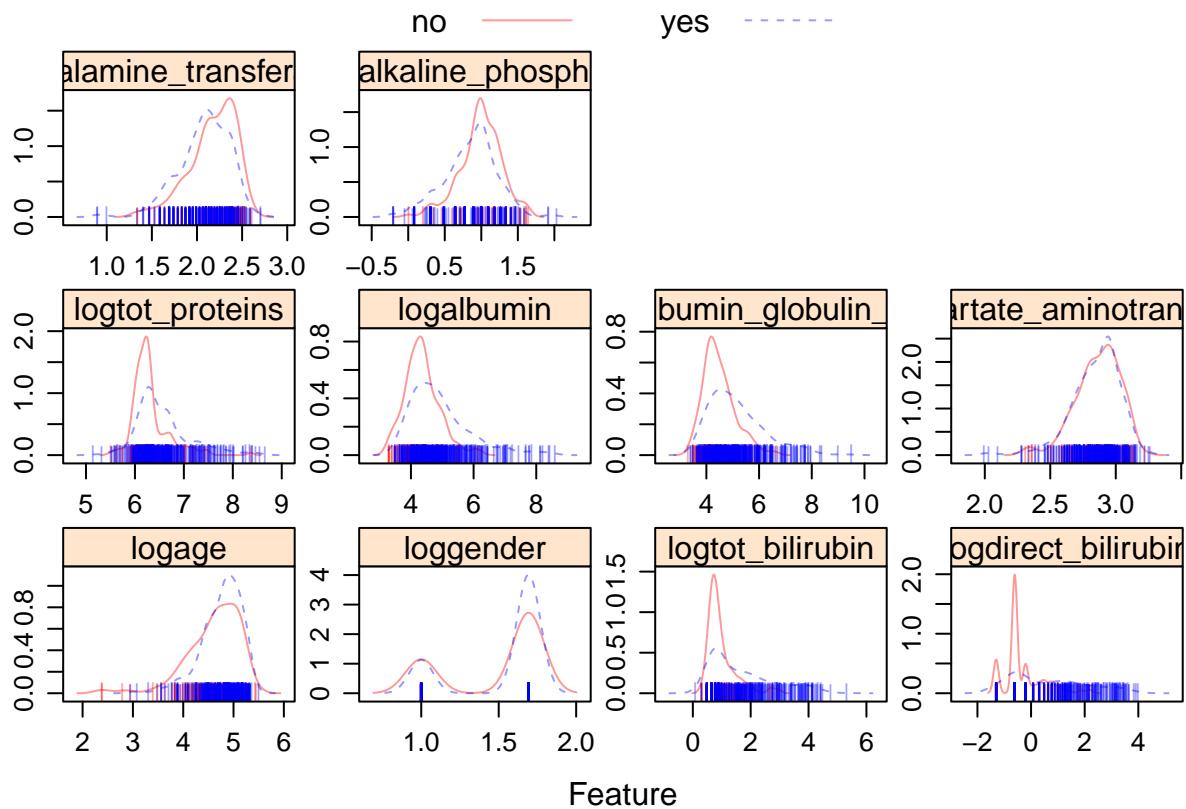
```
# Correlation plot
corrplot(cor(liver_df[,-11]), tl.srt = 45, order = 'hclust', type = 'upper')
```
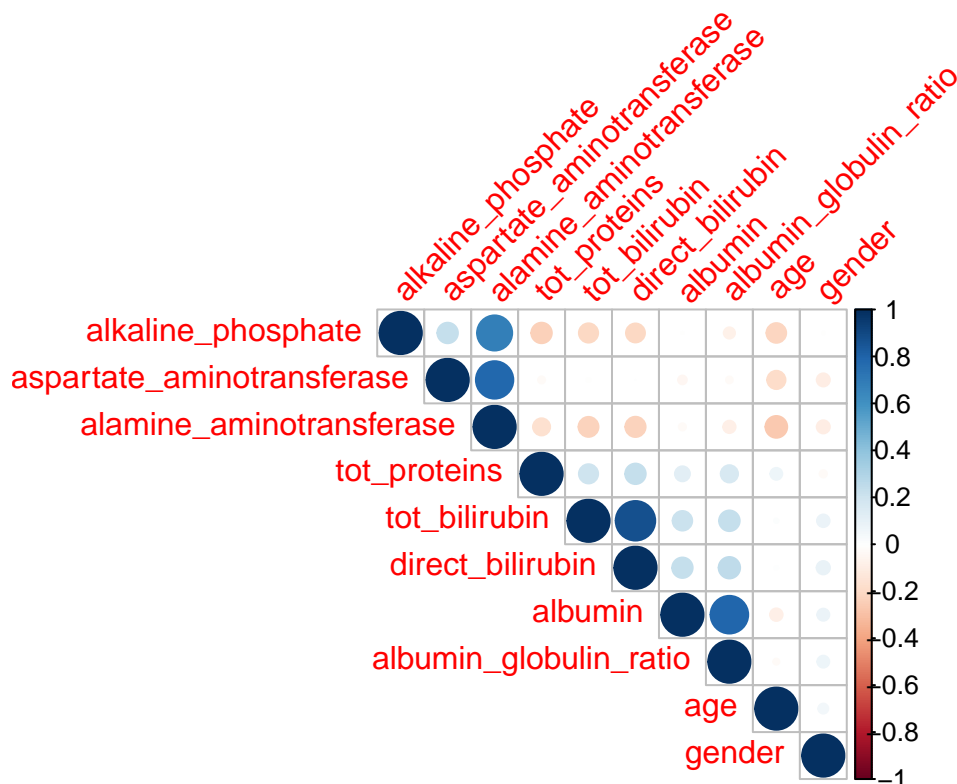
```
table(liver_df$outcome)
```

```
##
##  no yes
## 165 414
```

## Data Partition

```
#Create Training and Test Datasets
set.seed(10)
dim(liver_df1)
```

```
## [1] 579  11
```

```
rowTrain <- createDataPartition(y = liver_df1$outcome,
                                p = 0.8,
                                list = FALSE)

liver.train = liver_df1[rowTrain, ]
liver.test = liver_df1[-rowTrain, ]
```

## Logistic Regression

```
#Fit Logistic Regression Model with all predictors
glm.fit <- glm(outcome ~ ., data = liver_df1,
              subset = rowTrain,
              family = binomial(link = "logit"))
summary(glm.fit)
```

```
##
## Call:
## glm(formula = outcome ~ ., family = binomial(link = "logit"),
##     data = liver_df1, subset = rowTrain)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.8567  -1.0195   0.4202   0.8414   1.6584
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -15.11618    4.47123  -3.381 0.000723 ***
## logage                  0.74111    0.26049   2.845 0.004440 **
## loggender               0.24539    0.37642   0.652 0.514469
## logtot_bilirubin        0.54443    0.53800   1.012 0.311554
## logdirect_bilirubin    -0.04189    0.35933  -0.117 0.907183
## logtot_proteins         0.31927    0.30501   1.047 0.295219
```

```
## logalbumin                      0.75082    0.28262   2.657 0.007893 **
## logalbumin_globulin_ratio       0.13377    0.25062   0.534 0.593500
## logaspartate_aminotransferase   5.03133    2.53732   1.983 0.047375 *
## logalamine_transferase         -4.88216    2.53278  -1.928 0.053906 .
## logalkaline_phosphate           1.55808    1.26055   1.236 0.216445
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 554.14  on 463  degrees of freedom
## Residual deviance: 456.81  on 453  degrees of freedom
## AIC: 478.81
##
## Number of Fisher Scoring iterations: 5
```

```r
# Confusion Matrix
test.pred.prob <- predict(glm.fit, newdata = liver_df1[-rowTrain,], type = "response")
test.pred <- rep("no", length(test.pred.prob))
test.pred[test.pred.prob > 0.5] <- "yes"
confusionMatrix(data = as.factor(test.pred), reference = liver_df1$outcome[-rowTrain],
                positive = "yes")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction no yes
##        no   7   5
##        yes 26  77
##
##                Accuracy : 0.7304
##                  95% CI : (0.6397, 0.8089)
##     No Information Rate : 0.713
##     P-Value [Acc > NIR] : 0.383747
##
##                   Kappa : 0.1866
##
##  Mcnemar's Test P-Value : 0.000328
##
##             Sensitivity : 0.9390
##             Specificity : 0.2121
##          Pos Pred Value : 0.7476
##          Neg Pred Value : 0.5833
##              Prevalence : 0.7130
##          Detection Rate : 0.6696
##    Detection Prevalence : 0.8957
##       Balanced Accuracy : 0.5756
##
##        'Positive' Class : yes
##
```

```r
# ROC Curve
roc.glm <- roc(liver_df1$outcome[-rowTrain], test.pred.prob)
```

```
## Setting levels: control = no, case = yes

## Setting direction: controls < cases
```

```
plot(roc.glm, legacy.axes = TRUE, print.auc = TRUE)
plot(smooth(roc.glm), col = 4, add = TRUE)
```
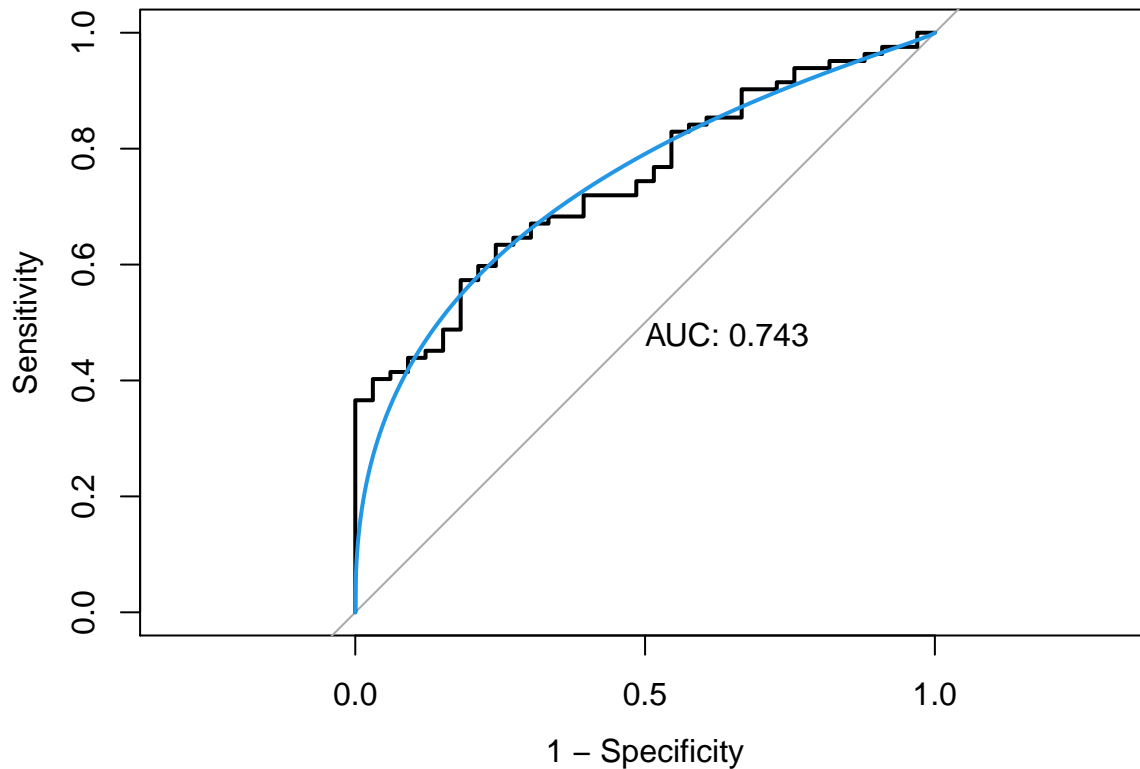


```
# Fit a logistic regression with CARET
set.seed(10)
ctrl1 <- trainControl(method = "cv",
                      summaryFunction = twoClassSummary,
                      classProbs = TRUE)
model.glm <- train(x = liver_df1[rowTrain,1:10],
                   y = liver_df1$outcome[rowTrain],
                   method = "glm",
                   preProcess = c("center", "scale"),
                   metric = "ROC",
                   trControl = ctrl1)
```

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```

# Regularized logistic regression

```r
ctrl2 <- trainControl(method = "cv",
                      summaryFunction = twoClassSummary,
                      classProbs = TRUE)

set.seed(10)
glmnGrid <- expand.grid(.alpha = seq(0,1,length =6),
                        .lambda = exp(seq(-6,0,length =20)))
model.glmn <- train(x=liver_df1[rowTrain,1:10],
                    y=liver_df1$outcome[rowTrain],
                    method ="glmnet",
                    #preProcess = c("center", "scale"),
                    tuneGrid =glmnGrid,
                    metric ="ROC",
                    trControl =ctrl2)
```

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```

```r
ggplot(model.glmn,xTrans = function(x)log(x), highlight = TRUE)
```

```
max(model.glmn$result$ROC)
```

```
## [1] 0.7565993
```

```
model.glmn$bestTune # alpha of 0 indicates a ridge regression.
```

```
##    alpha      lambda
## 11     0 0.05830279
```

```
coef(model.glmn$finalModel, s = model.glmn$bestTune$lambda)
```

```
## 11 x 1 sparse Matrix of class "dgCMatrix"
##                                          1
## (Intercept)                     -6.8753424
## logage                           0.5276037
## loggender                        0.2611549
## logtot_bilirubin                 0.2293340
## logdirect_bilirubin              0.1501621
## logtot_proteins                  0.2906986
## logalbumin                       0.3735016
## logalbumin_globulin_ratio        0.2415046
## logaspartate_aminotransferase    0.3935637
## logalamine_transferase          -0.4353867
## logalkaline_phosphate           -0.3668267
```

# MARS

```r
set.seed(10)
model.mars <- train(x = liver_df1[rowTrain,1:10],
                    y = liver_df1$outcome[rowTrain],
                    method = "earth",
                    tuneGrid = expand.grid(degree = 1:3, nprune = 2:20),
                    metric = "ROC",
                    trControl = ctrl2)
```

```
## Warning: Setting row names on a tibble is deprecated.

## Loading required package: earth

## Loading required package: Formula

## Loading required package: plotmo

## Loading required package: plotrix

## Loading required package: TeachingDemos

##
## Attaching package: 'TeachingDemos'

## The following object is masked from 'package:klaR':
##
##      triplot

## Warning: Setting row names on a tibble is deprecated.

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## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

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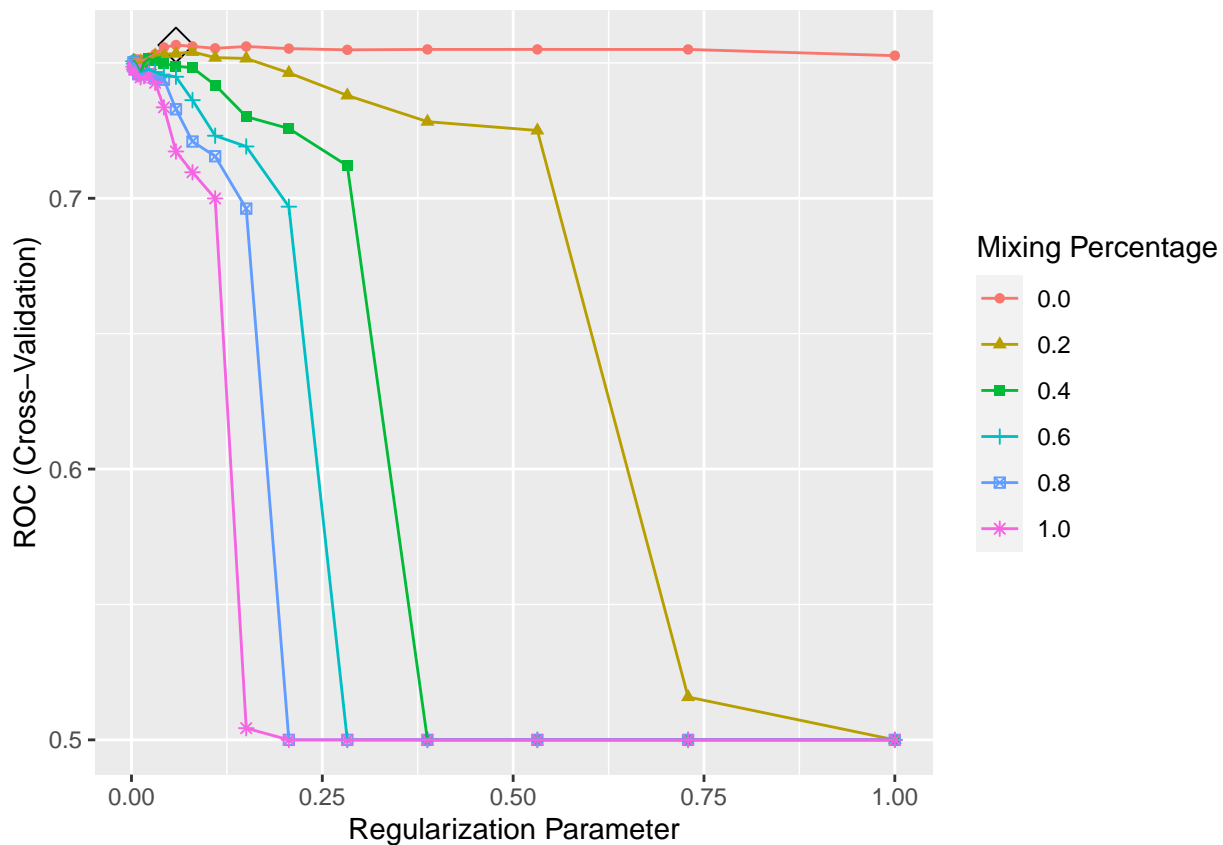
```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

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```

```
plot(model.mars)
```
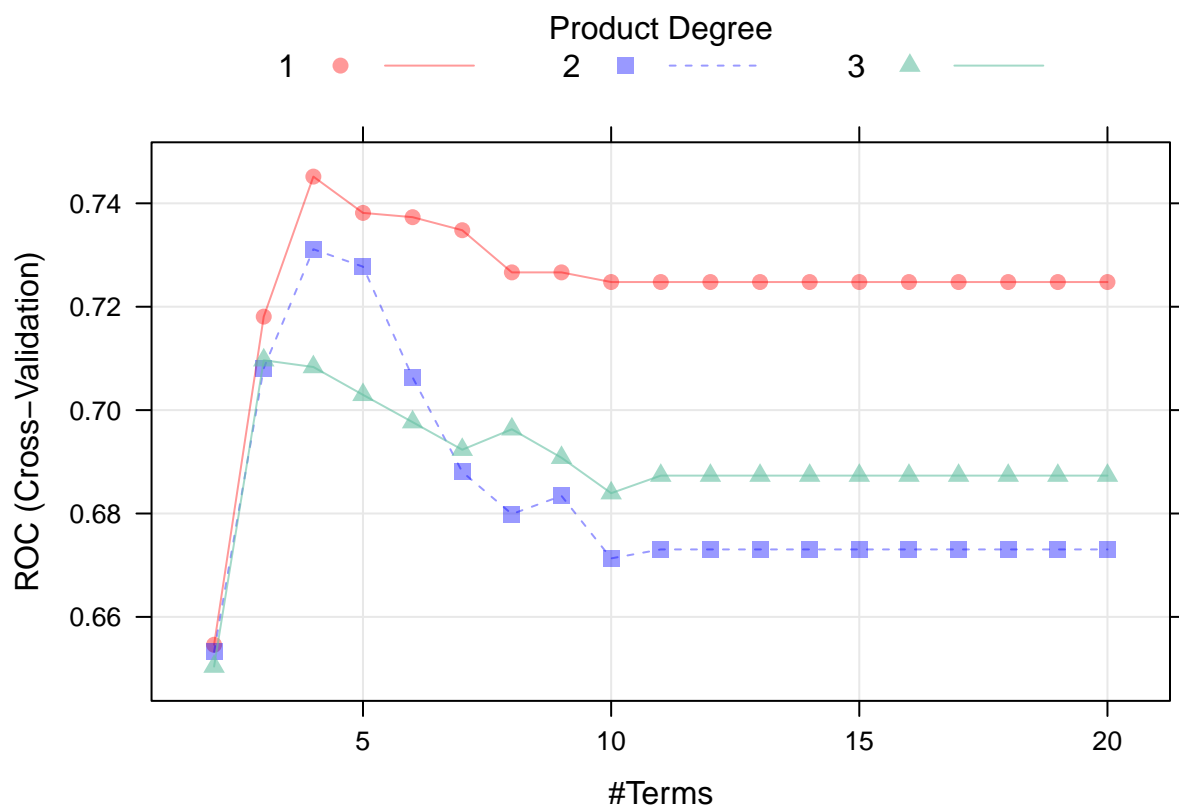
```
coef(model.mars$finalModel)
```

```
##                     (Intercept) h(logdirect_bilirubin- -0.609438)
##                       1.9750727                         0.5984348
##         h(5.70048-logalbumin)               h(5.31749-logage)
##                      -0.8982652                        -0.7549458
```

```
vip(model.mars$finalModel)
```

KNN

```r
set.seed(10)

model.knn <- train(x = liver_df1[rowTrain,1:10],
                   y = liver_df1$outcome[rowTrain],
                   method = "knn",
                   preProcess = c("center", "scale"),
                   tuneGrid = data.frame(k = seq(1, 200, by = 5)),
                   trControl = ctrl1)
```

```
## Warning in train.default(x = liver_df1[rowTrain, 1:10], y =
## liver_df1$outcome[rowTrain], : The metric "Accuracy" was not in the result set.
## ROC will be used instead.

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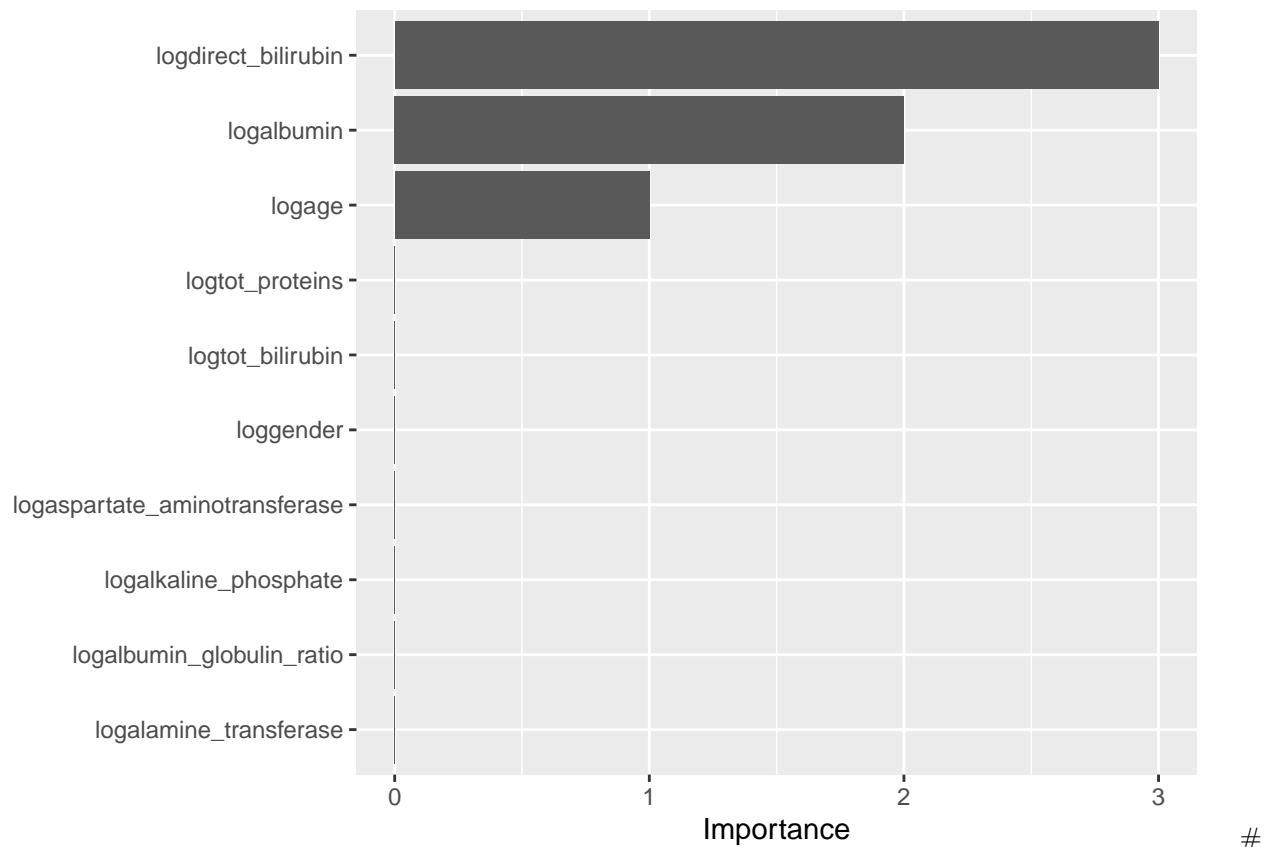
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```
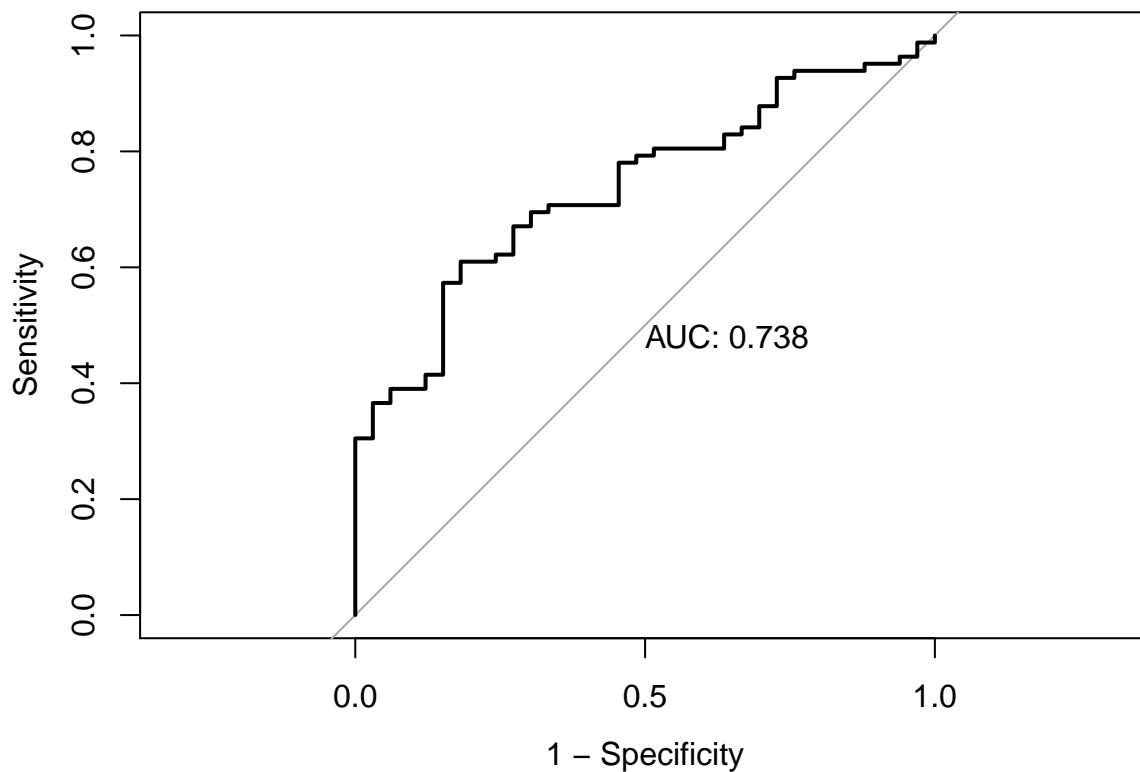
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```
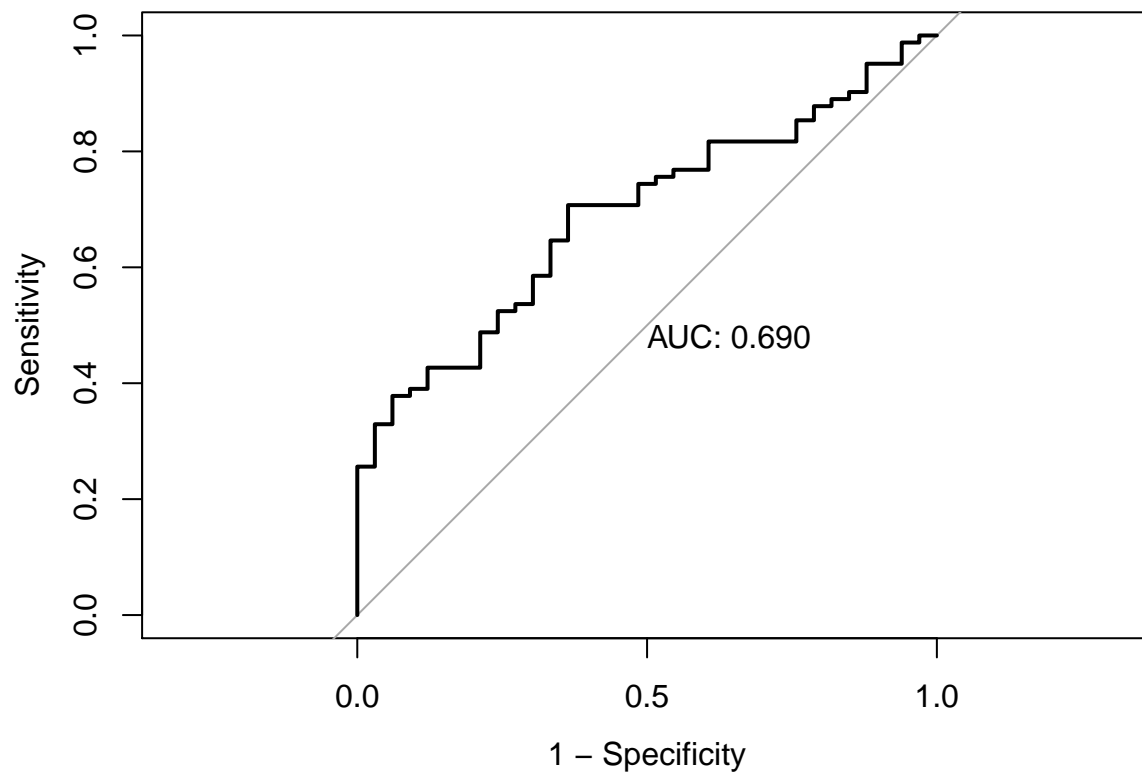
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```

```
liver_df1$outcome[-rowTrain]
```

```
##   [1] yes yes no  no  yes yes yes yes yes yes yes no  yes no  yes yes no  yes
##  [19] yes yes yes yes yes no  no  yes yes yes yes no  yes no  yes yes yes yes
##  [37] yes yes yes no  no  yes yes yes yes no  no  yes no  yes no  yes yes yes
##  [55] yes yes yes no  yes yes no  no  no  yes yes yes yes yes yes no  no  no
##  [73] yes yes no  yes yes yes yes yes no  yes yes yes yes yes yes no  yes no
##  [91] no  yes yes yes no  yes yes yes yes no  yes no  no  no  yes yes yes yes
## [109] yes yes yes yes yes yes no
## Levels: no yes
```

```
model.knn$bestTune
```

```
##    k
## 6 26
```

```
pred_knn = predict(model.knn, newdata = liver.test, type = 'prob')
roc_knn <- roc(liver_df1$outcome[-rowTrain], pred_knn[,2])
```

```
## Setting levels: control = no, case = yes
```

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

```
plot.roc(roc_knn, legacy.axes = TRUE, print.auc = TRUE)
```
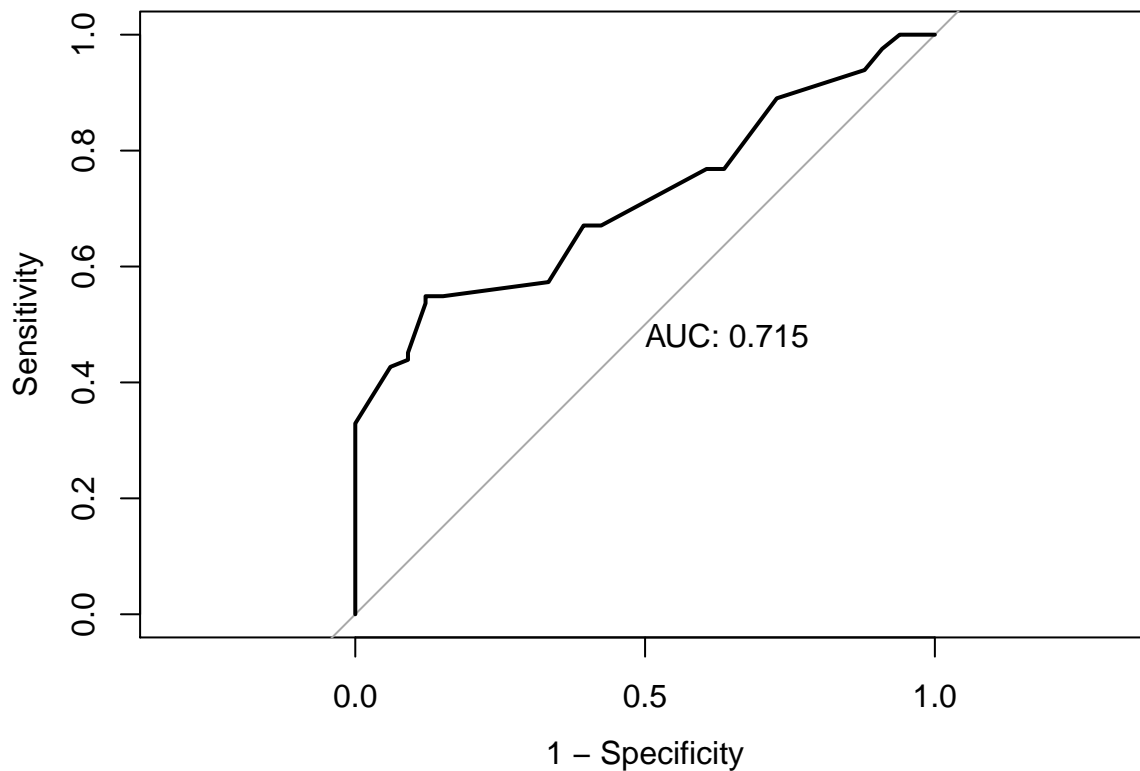


## LDA

```
set.seed(10)
lda.fit <- lda(outcome~.,
               data = liver.train)

set.seed(10)
model.lda <- train(x = liver_df1[rowTrain,1:10],
                   y = liver_df1$outcome[rowTrain],
                   method = "lda",
                   metric = "ROC",
                   trControl = ctrl1)
```

```
## Warning: Setting row names on a tibble is deprecated.
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```

```r
lda.pred <- predict(lda.fit, newdata = liver.test)
roc.lda <- roc(liver_df1[-rowTrain,]$outcome, lda.pred$posterior[,2])
```

```
## Setting levels: control = no, case = yes

## Setting direction: controls < cases
```

```r
plot(roc.lda, legacy.axes = TRUE, print.auc = TRUE)
```

# QDA

```
set.seed(10)
qda.fit <- qda(outcome~.,
               data = liver.train)

set.seed(10)
model.qda <- train(x = liver_df1[rowTrain,1:10],
                   y = liver_df1$outcome[rowTrain],
                   method = "qda",
                   metric = "ROC",
                   trControl = ctrl1)
```

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```

```
qda.pred <- predict(qda.fit, newdata = liver.test)
roc.qda <- roc(liver_df1[-rowTrain,]$outcome, qda.pred$posterior[,2])
```

```
## Setting levels: control = no, case = yes

## Setting direction: controls < cases
```

```
plot(roc.qda, legacy.axes = TRUE, print.auc = TRUE)
```

AUC: 0.690

```
auc <- c(roc.lda$auc[1], roc.qda$auc[1])
```

## Naive Bayes

```
nbGrid <- expand.grid(usekernel = c(FALSE,TRUE),
                      fL = 1,
                      adjust = seq(.2, 3, by = .2))
model.nb <- train(x = liver_df1[rowTrain,1:10],
                  y = liver_df1$outcome[rowTrain],
                  method = "nb",
                  tuneGrid = nbGrid,
                  metric = "ROC",
                  trControl = ctrl1)
```

```
## Warning: Setting row names on a tibble is deprecated.
```

```
## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 34
```

```
## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 34
```

```
## Warning: Setting row names on a tibble is deprecated.
```

```
## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
```

```
## observation 19

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 19

## Warning: Setting row names on a tibble is deprecated.

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 34

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 34

## Warning: Setting row names on a tibble is deprecated.

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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 34

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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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```

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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 34

## Warning: Setting row names on a tibble is deprecated.

## Warning: Setting row names on a tibble is deprecated.

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 12

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 12

## Warning: Setting row names on a tibble is deprecated.

## Warning: Setting row names on a tibble is deprecated.
```

```
## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 12

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 12

## Warning: Setting row names on a tibble is deprecated.

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 12

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 12

## Warning: Setting row names on a tibble is deprecated.

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 12

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 12

## Warning: Setting row names on a tibble is deprecated.

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 12

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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 33

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 33
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## Warning: Setting row names on a tibble is deprecated.

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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 33

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## Warning: Setting row names on a tibble is deprecated.

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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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## Warning: Setting row names on a tibble is deprecated.

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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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## Warning: Setting row names on a tibble is deprecated.

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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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## Warning: Setting row names on a tibble is deprecated.

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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 12

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 14
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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## observation 12

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## observation 14
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## observation 12

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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
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## observation 14

## Warning: Setting row names on a tibble is deprecated.

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42

## Warning: Setting row names on a tibble is deprecated.

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42

## Warning: Setting row names on a tibble is deprecated.

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42

## Warning: Setting row names on a tibble is deprecated.

## Warning: Setting row names on a tibble is deprecated.

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42

## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42

## Warning: Setting row names on a tibble is deprecated.

## Warning: Setting row names on a tibble is deprecated.
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42
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## Warning: Setting row names on a tibble is deprecated.
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## Warning: Setting row names on a tibble is deprecated.
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42
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## Warning: Setting row names on a tibble is deprecated.
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## Warning: Setting row names on a tibble is deprecated.
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42
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## Warning: Setting row names on a tibble is deprecated.
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## Warning: Setting row names on a tibble is deprecated.
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42
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## Warning: Setting row names on a tibble is deprecated.
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42
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## Warning: Setting row names on a tibble is deprecated.
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## Warning: Setting row names on a tibble is deprecated.
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## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 42
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```

```
plot(model.nb)
```



## CLASSIFICATION TREE

```
set.seed(1)
tree1 = rpart(formula = outcome ~ ., data = liver_df1, subset = rowTrain,
              control = rpart.control(cp = 0))
rpart.plot(tree1)
```
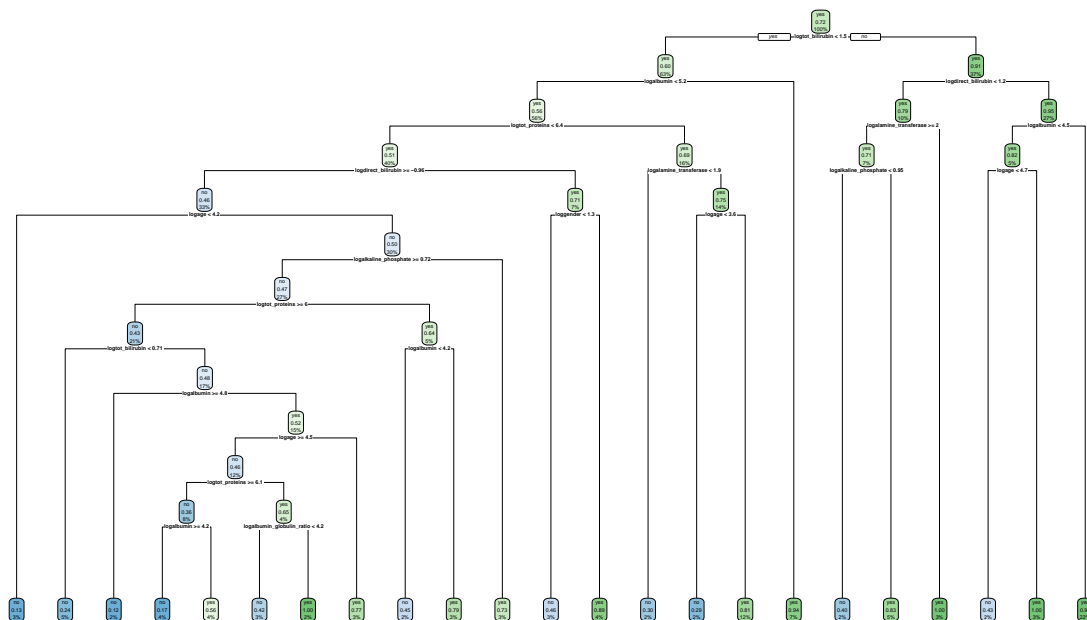
```
#summary(tree1)
```

# RANDOM FORESTS

```
#rf.grid = expand.grid(mtry = 1:10, splitrule = "gini",
                       #min.node.size = seq(from = 2, to = 10, by = 2))

#set.seed(1)
#model.rf = train(outcome ~ ., liver_df1, subset = rowTrain, method = "ranger",
             #tuneGrid = rf.grid, metric = "ROC", trControl = ctrl1)

#RF.pred = predict(model.rf, newdata = liver_df1[-rowTrain, ], type = "prob")
#roc.rf = roc(liver_df1$outcome[-rowTrain], RF.pred) #error appears for this line
#auc.rf = c(roc.rf$auc[1])
#auc.rf
```

# SVM

```
#linear
ctrl4 <-trainControl(method = "cv")
set.seed(10)
svm.linear.model <- train(
  outcome ~., data = liver.train, method = "svmLinear",
  trControl = ctrl4,
  #preProcess = c("center", "scale"),
  tuneGrid =data.frame(C =exp(seq(-10,1,len=20))),
  )
```

```
plot(svm.linear.model, highlight = TRUE, xTrans = log)
```
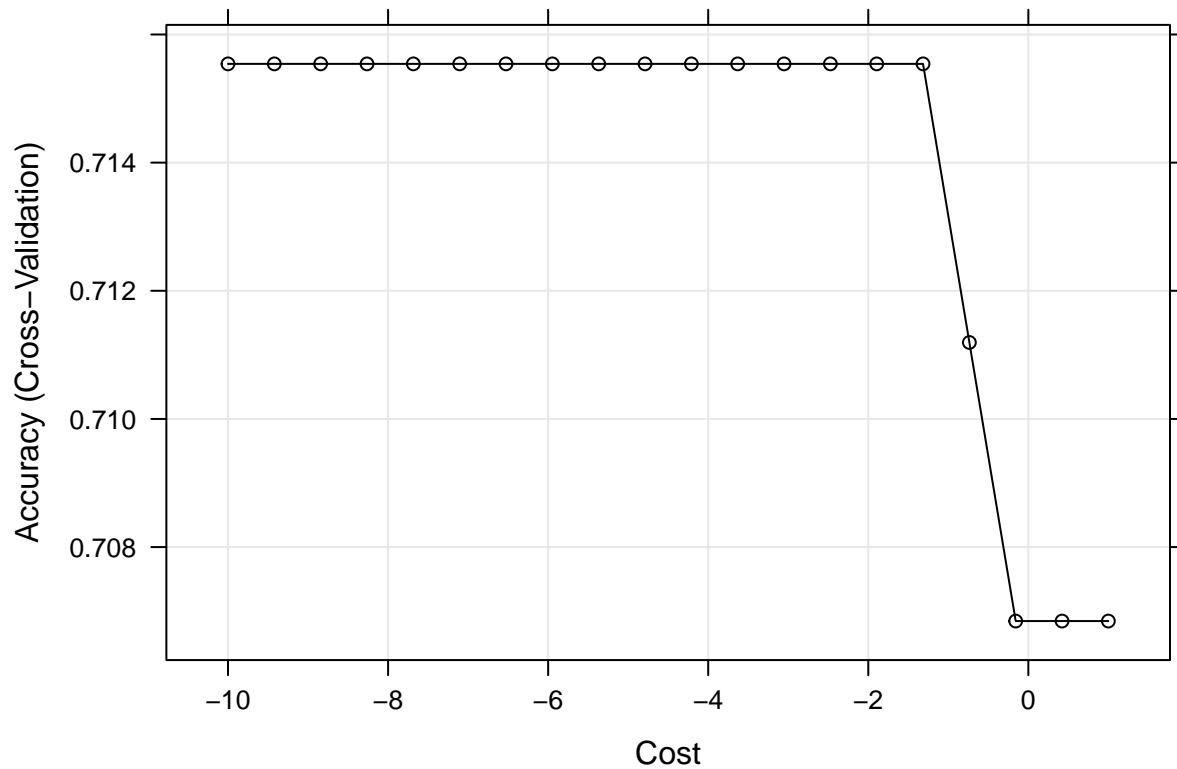


```
svm.linear.model$bestTune
```

```
##              C
## 1 4.539993e-05
```

```
svm.linear.model$finalModel
```

```
## Support Vector Machine object of class "ksvm"
##
## SV type: C-svc  (classification)
##  parameter : cost C = 4.53999297624849e-05
##
## Linear (vanilla) kernel function.
##
## Number of Support Vectors : 265
##
## Objective Function Value : -0.012
## Training error : 0.284483
```

```
ctrl4 <-trainControl(method = "cv")
set.seed(10)
svm.linear2.model <- train(
  outcome ~.,
  data = liver.train,
```

```
  method = "svmLinear2",
  trControl = ctrl4,
  #preProcess = c("center", "scale"),
  tuneGrid =data.frame(cost =exp(seq(-10,1,len=20))),
  )

plot(svm.linear2.model, highlight = TRUE, xTrans = log)
```
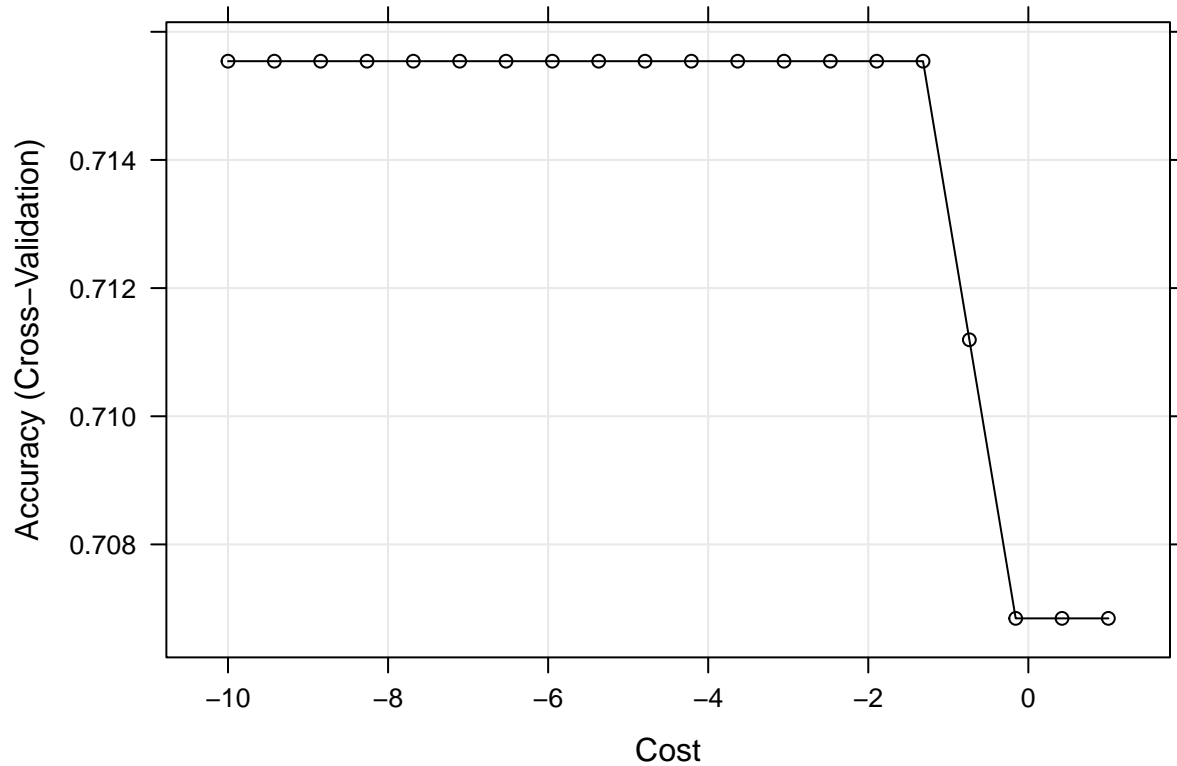


```
svm.linear2.model$bestTune
```

```
##           cost
## 1 4.539993e-05
```

```
svm.linear2.model$finalModel
```

```
##
## Call:
## svm.default(x = as.matrix(x), y = y, kernel = "linear", cost = param$cost,
##     probability = classProbs)
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  linear
##        cost:  4.539993e-05
##
## Number of Support Vectors:  265
```

```
svmr.grid <- expand.grid(C = exp(seq(-1, 4,len = 10)), sigma = exp(seq(-10,0,len = 10)))

# tunes over both cost and sigma
set.seed(10)

svm.radial.model <- train(outcome ~ . , liver_df1,
                    subset = rowTrain,
                    method = "svmRadialSigma",
                    preProcess = c("center", "scale"),
                    trControl = ctrl4)

plot(svm.radial.model, highlight = TRUE)
```
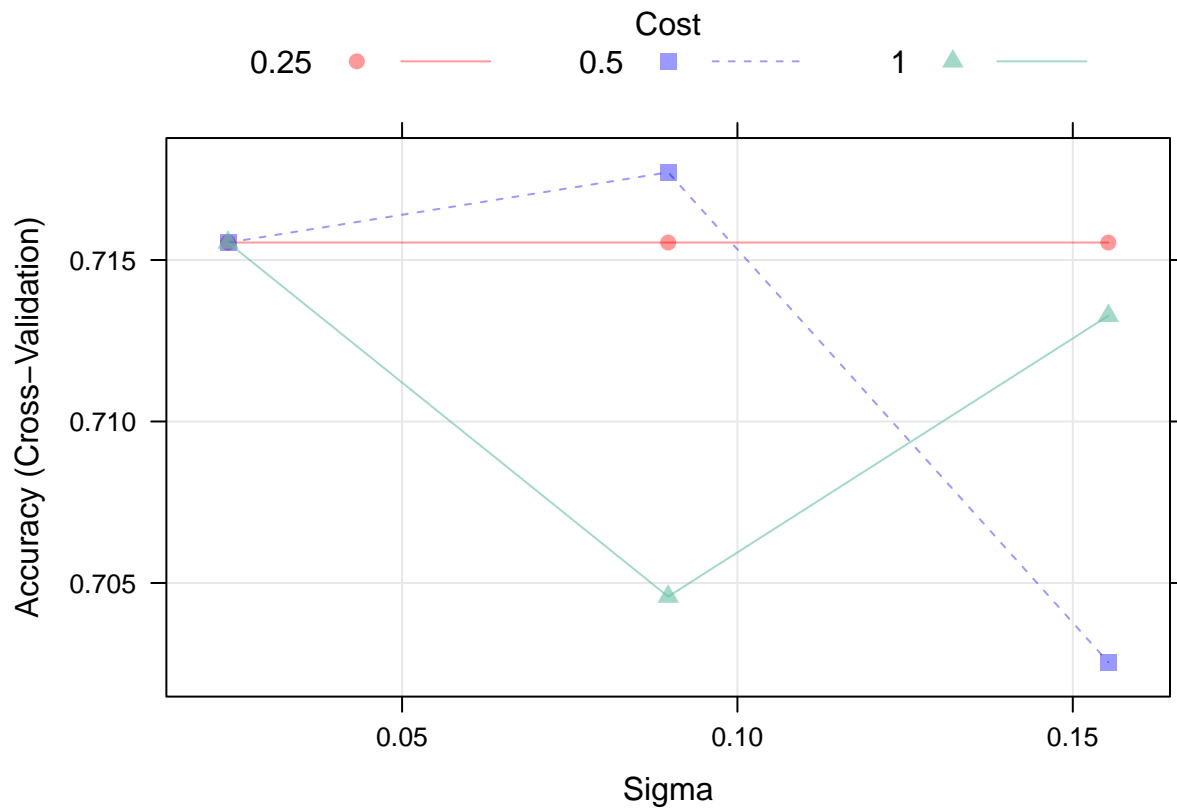


```
svm.radial.model$bestTune
```

```
##         sigma   C
## 5 0.08967636 0.5
```

```
svm.radial.model$finalModel
```

```
## Support Vector Machine object of class "ksvm"
##
## SV type: C-svc  (classification)
##  parameter : cost C = 0.5
##
## Gaussian Radial Basis kernel function.
```

```
##  Hyperparameter : sigma =  0.0896763614303736
##
## Number of Support Vectors : 304
##
## Objective Function Value : -128.1327
## Training error : 0.280172
```

```r
x_train <- as.matrix(liver.train[,1:10])

explainer_svm <- explain(svm.radial.model,
                         label = "svmr",
                         data = x_train,
                         y = as.numeric(liver_df1$outcome[rowTrain] == "yes"),
                         verbose = FALSE)
```

```
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```r
vi_svm <- model_parts(explainer_svm)
```

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```

```
plot(vi_svm)
```
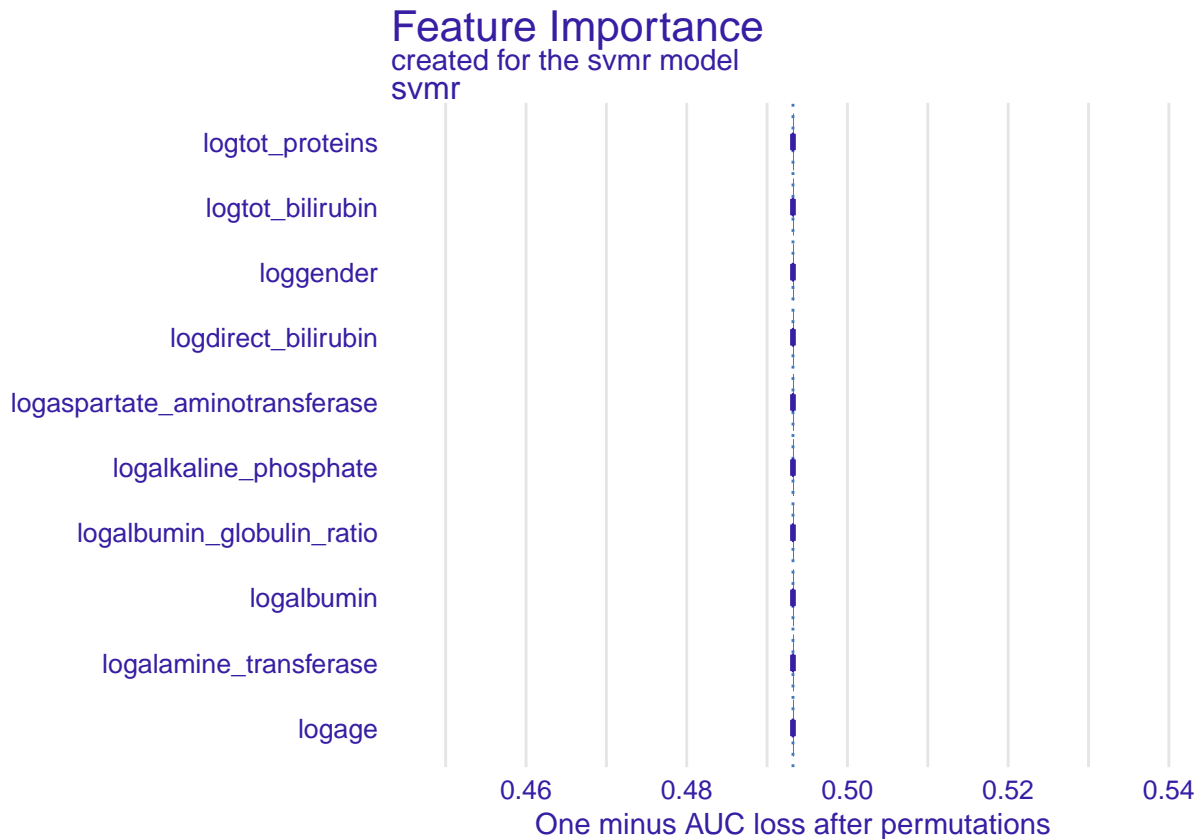


## Boosting

```
gbmA.grid <- expand.grid(n.trees = c(2000,3000,4000),
                         interaction.depth = 1:6,
                         shrinkage = c(0.001,0.003,0.005),
                         n.minobsinnode = 1)

ctrl.boost <- trainControl(method = "cv",
                    classProbs = TRUE,
                    summaryFunction = twoClassSummary)
set.seed(10)
gbmA.model <- train(outcome ~ . ,
```

```
                data = liver.train,
                tuneGrid = gbmA.grid,
                trControl = ctrl.boost,
                method = "gbm",
                distribution = "adaboost",
                metric = "ROC",
                verbose = FALSE)

ggplot(gbmA.model, highlight = TRUE)
```
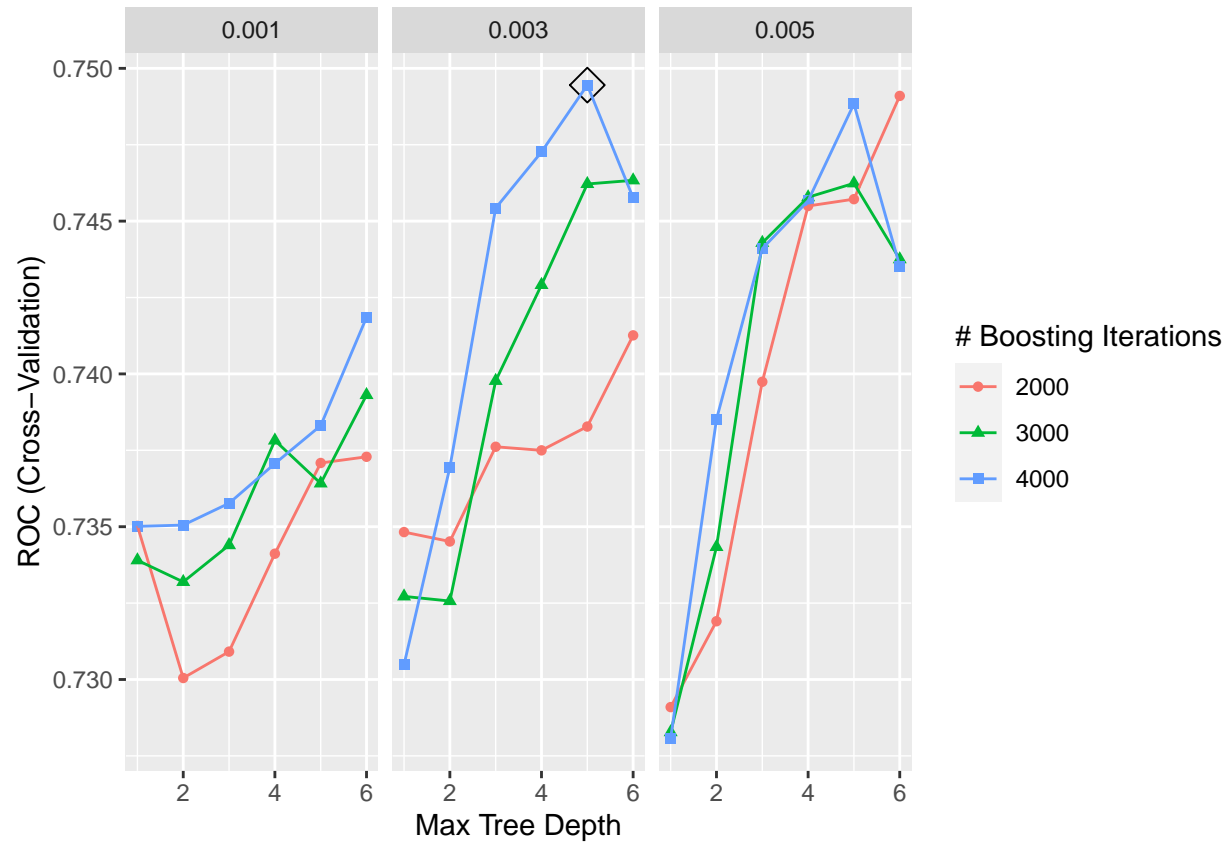


```
gbmImp <- varImp(gbmA.model, scale = FALSE)
plot(gbmImp)
```
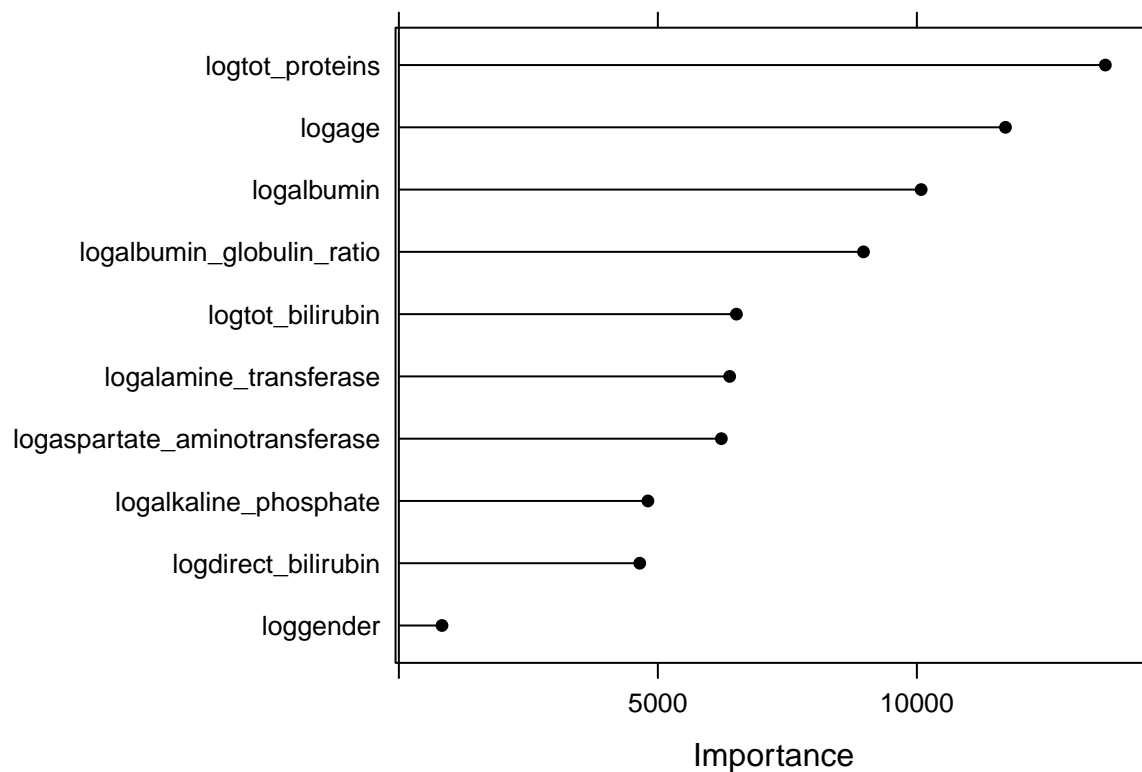
```r
#res <- resamples(list(MARS = model.mars, RF = model.rf, SVM = svm.radial.model, GBM = gbmA.model, LDA
#summary(res)
# bwplot(res, metric = "ROC")  #This line doesn't run
```

## Let's look at the test set performance: comparing ROC MODELS

```r
mars.pred = predict(model.mars, newdata = liver_df1[-rowTrain, ], type = "prob")[,1]
#RF.pred = predict(model.rf, newdata = liver_df1[-rowTrain, ], type = "prob")[,1]
LDA.pred = predict(model.lda, newdata = liver_df1[-rowTrain, ], type = "prob")[,1]
QDA.pred = predict(model.qda, newdata = liver_df1[-rowTrain, ], type = "prob")[,1]
NB.pred = predict(model.nb, newdata = liver_df1[-rowTrain, ], type = "prob")[,1]
```

```
## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 21
```

```
## Warning in FUN(X[[i]], ...): Numerical 0 probability for all classes with
## observation 49
```

```
SVM.pred = predict(svm.radial.model, newdata = liver_df1[-rowTrain, ])
GBM.pred = predict(gbmA.model, newdata = liver_df1[-rowTrain, ], type = "prob")[,1]
GLM.pred = predict(model.glm, newdata = liver_df1[-rowTrain, ], type = "prob")[,1]
GLMN.pred = predict(model.glmn, newdata = liver_df1[-rowTrain, ], type = "prob")[,1]
KNN.pred = predict(model.knn, newdata = liver_df1[-rowTrain, ], type = "prob")[,1]

pred1 = prediction(as.numeric(mars.pred), liver_df1$outcome[-rowTrain])
perf1 = performance(pred1, "tpr", "fpr")

#pred2 = prediction(as.numeric(RF.pred), liver_df1$outcome[-rowTrain])
#perf2 = performance(pred2, "tpr", "fpr")

pred3 = prediction(as.numeric(LDA.pred), liver_df1$outcome[-rowTrain])
perf3 = performance(pred3, "tpr", "fpr")

pred4 = prediction(as.numeric(QDA.pred), liver_df1$outcome[-rowTrain])
perf4 = performance(pred4, "tpr", "fpr")

pred5 = prediction(as.numeric(NB.pred), liver_df1$outcome[-rowTrain])
perf5 = performance(pred5, "tpr", "fpr")

pred6 = prediction(as.numeric(SVM.pred), liver_df1$outcome[-rowTrain])
perf6 = performance(pred6, "tpr", "fpr")

pred7 = prediction(as.numeric(GBM.pred), liver_df1$outcome[-rowTrain])
perf7 = performance(pred7, "tpr", "fpr")

pred8 = prediction(as.numeric(GLM.pred), liver_df1$outcome[-rowTrain])
perf8 = performance(pred8, "tpr", "fpr")

pred9 = prediction(as.numeric(GLMN.pred), liver_df1$outcome[-rowTrain])
perf9 = performance(pred9, "tpr", "fpr")

pred10 = prediction(as.numeric(KNN.pred), liver_df1$outcome[-rowTrain])
perf10 = performance(pred10, "tpr", "fpr")


plot(perf1, col = "red"); par(new = T)
#plot(perf2, col = "blue"); par(new = T)
plot(perf3, col = "green"); par(new = T)
plot(perf4, col = "orange"); par(new = T)
plot(perf5, col = "yellow"); par(new = T)
plot(perf6, col = "purple"); par(new = T)
plot(perf7, col = "pink"); par(new = T)
plot(perf8, col = "brown"); par(new = T)
plot(perf9, col = "turquoise"); par(new = T)
plot(perf10, col = "navy")
```
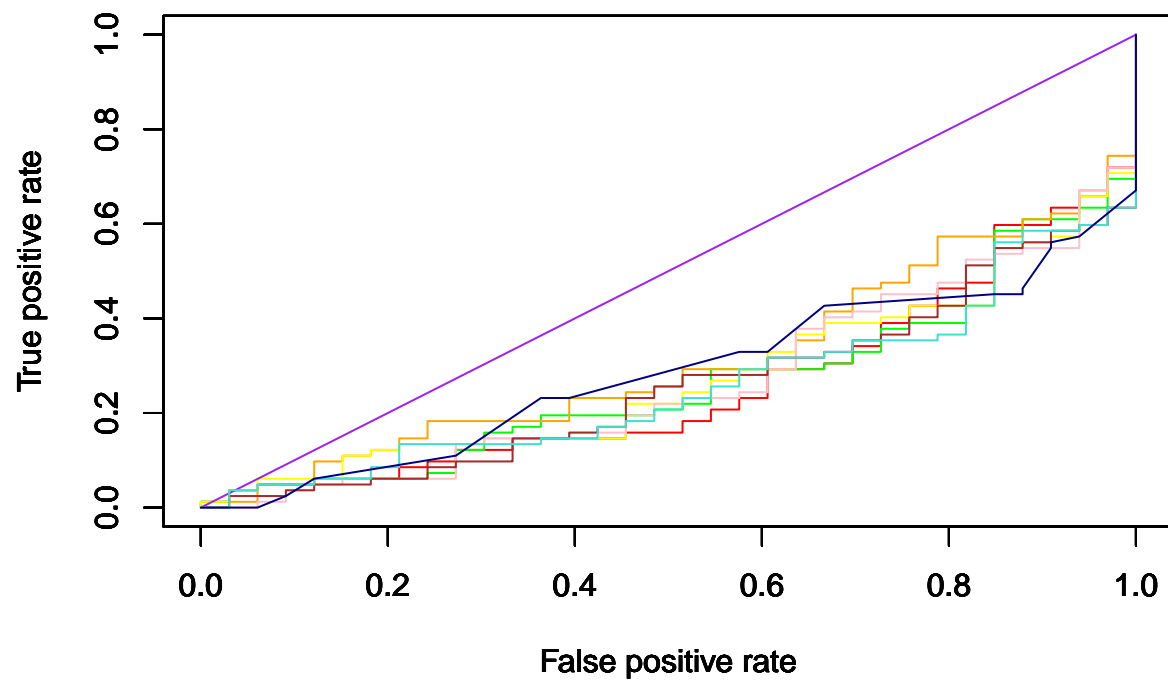
```
#legend("topleft", c("Mars","RF SVM", "LDA", "QDA", "NB", "SVM", "GBM", "GLM", "GLMN", "KNN"),
       #lty = c(1,1), lwd = c(2.5,2.5),
       #col = c("red", "blue", "green", "orange", "yellow", "purple", "pink", "black", "brown",
              #"turquoise", "navy"), bty = "n")
```