Predicting Diagnosis of Liver Disease

```
# 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()
```

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

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

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

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

```
## Loading required package: lattice

##
## Attaching package: 'caret'

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

```
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)
```

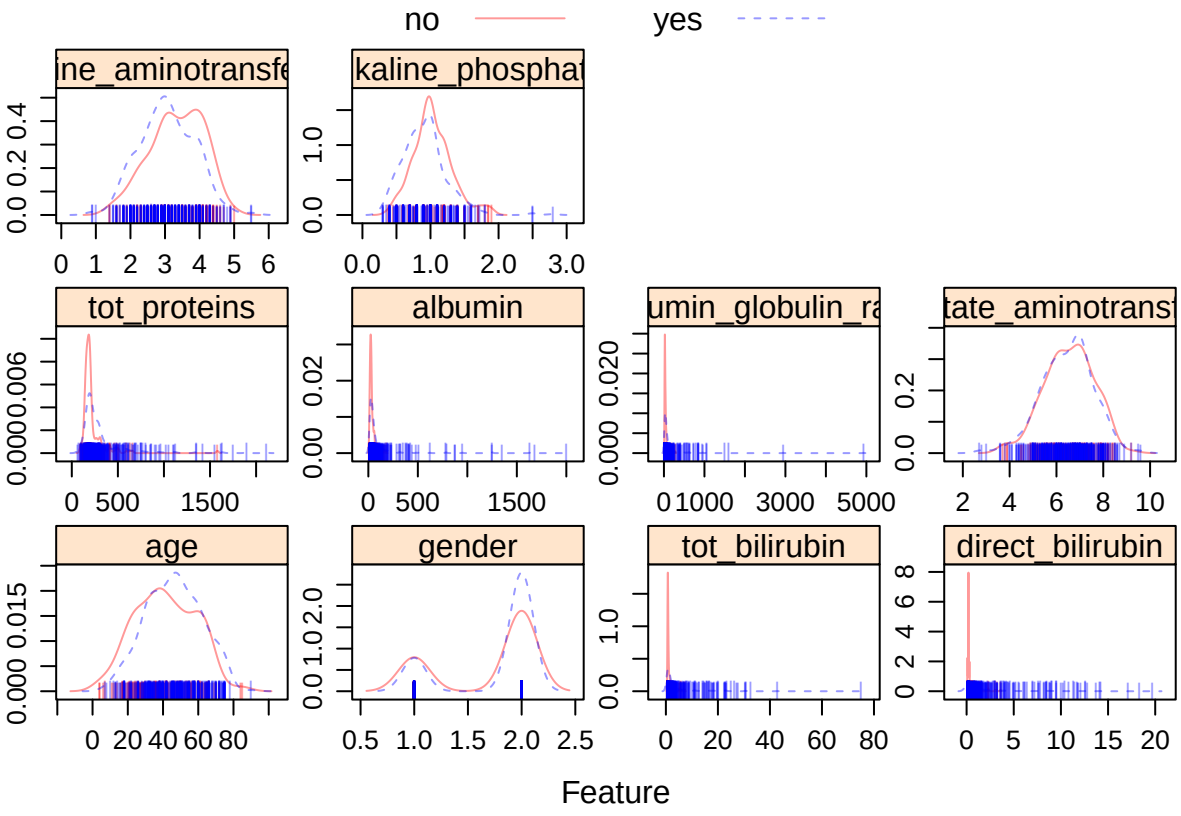
Import data

```
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'
```

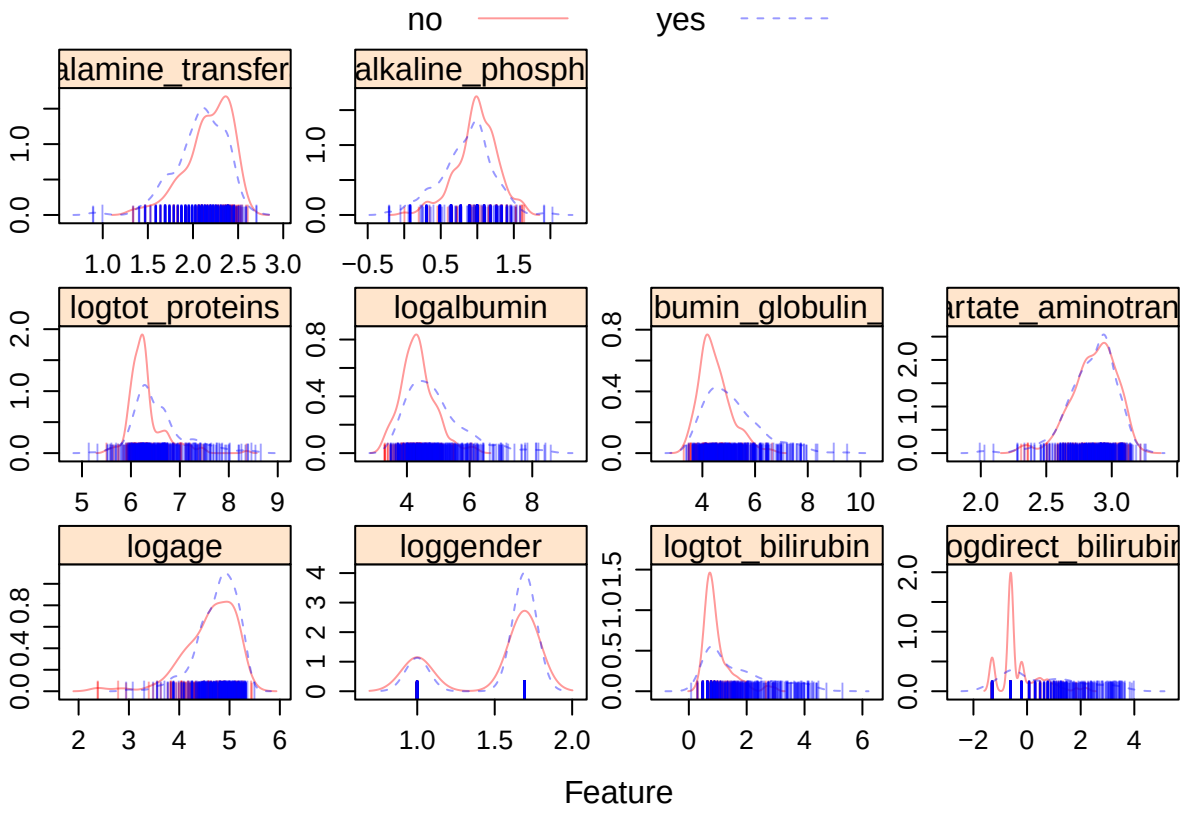
Exploratory Data Analysis

```
# 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))
```

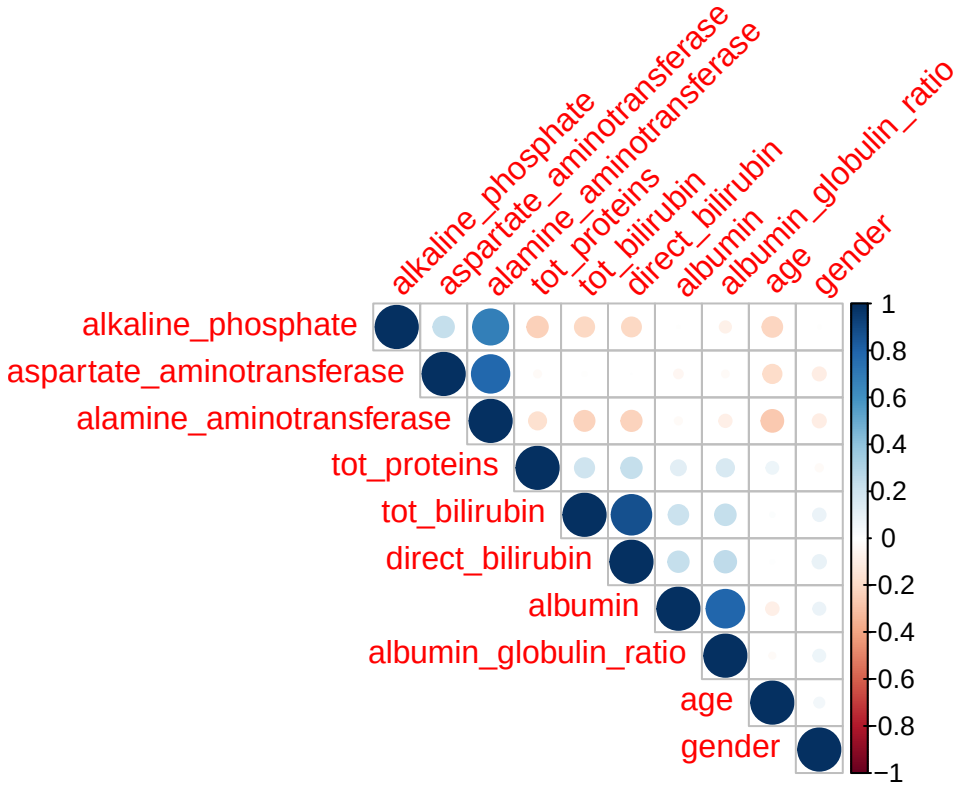



```
# dataset with all the log-transformed predictor variables
liver_df1 =
  liver_df %>%
  mutate(logtot_bilirubin = log(tot_bilirubin) +1,
         logdirect_bilirubin = log(direct_bilirubin) +1,
         logtot_proteins = log(tot_proteins) +1,
         logalbumin = log(albumin) +1,
         loggender = 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, logall
                       logalbumin_globulin_ratio, logaspartate_aminotransferase, logalamine_transfe
                       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')
```



```r
table(liver_df$outcome)
```

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

Data Partition

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

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

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

Logistic Regression

```r
#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
```

```
# 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")
```

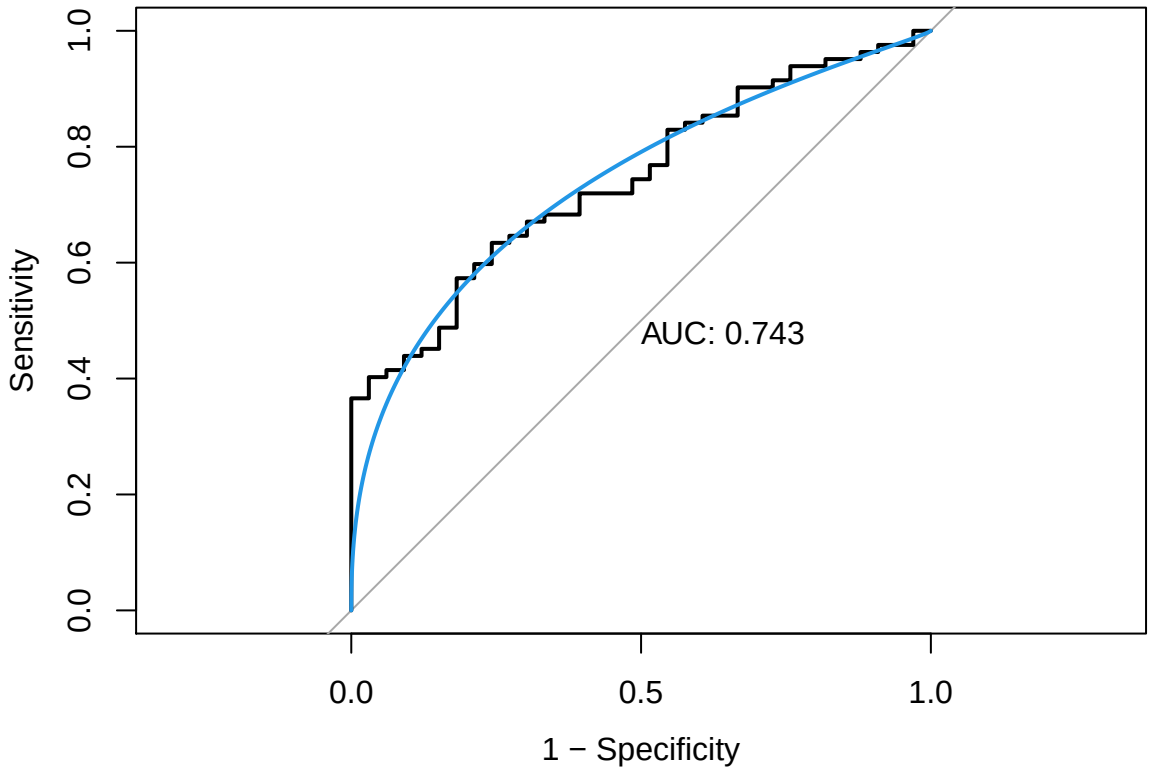
```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction no yes
##        no   7   5
##        yes 26  77
##
##                Accuracy : 0.7304
##                  95% CI : (0.6397, 0.8089)
##     No Information Rate : 0.713
##     P-Value [Acc > NIR] : 0.383747
##
##                   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
##
```

```
# 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)
ctrl <- trainControl(method = "repeatedcv", repeats = 10,
                     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 = ctrl)
```

```
## Warning: The ‘i‘ argument of ‘‘[‘()‘ can’t be a matrix as of tibble 3.0.0.
## Convert to a vector.
## This warning is displayed once every 8 hours.
## Call ‘lifecycle::last_warnings()‘ to see where this warning was generated.

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

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Regularized logistic regression

```
ctrl <- trainControl(method = "repeatedcv",
                     repeats = 5,
                     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 =ctrl)
```

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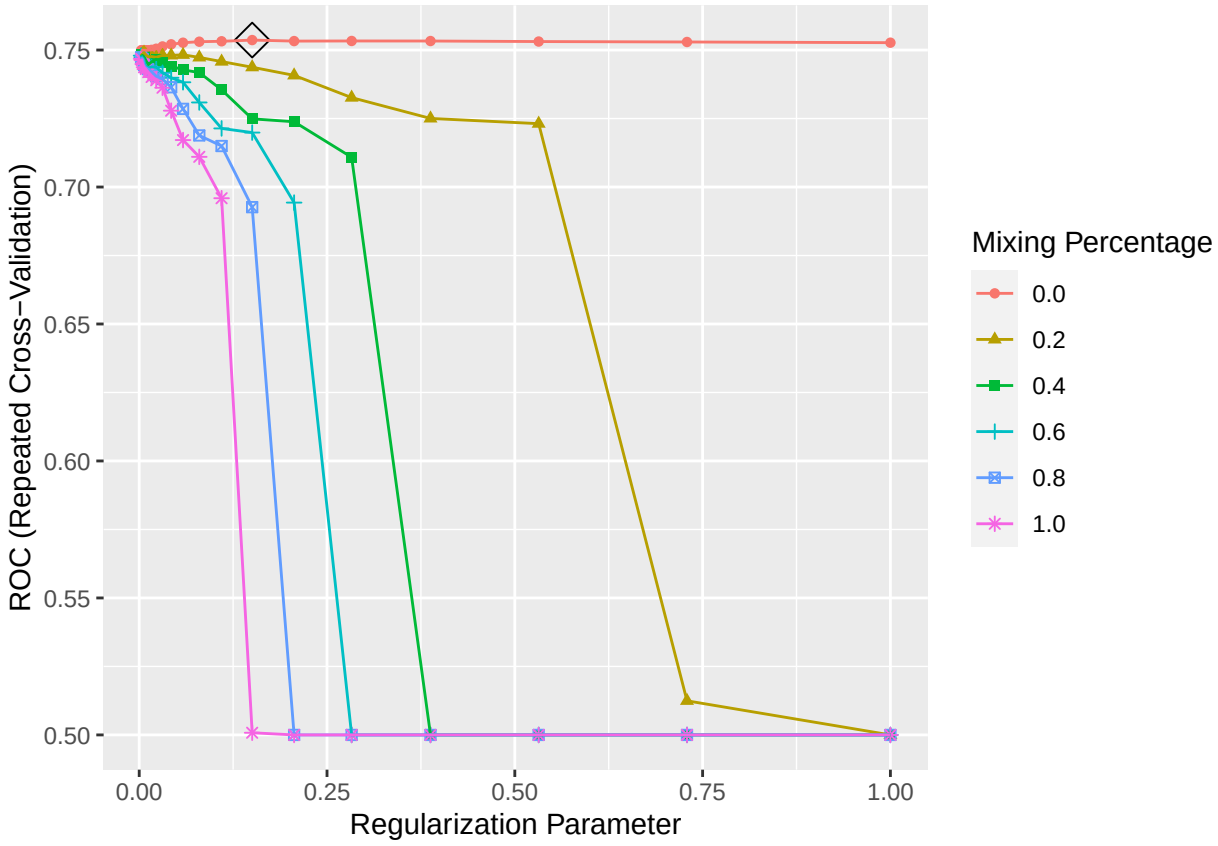
```
ggplot(model.glmn,xTrans = function(x)log(x), highlight = TRUE)
```




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

```
## [1] 0.7536379
```

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

```
##    alpha    lambda
## 14     0 0.1503579
```

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

```
## 11 x 1 sparse Matrix of class "dgCMatrix"
##                                       1
## (Intercept)                -4.8091934
```

```
## logage                          0.3880113
## loggender                       0.2410487
## logtot_bilirubin                0.1845745
## logdirect_bilirubin             0.1342574
## logtot_proteins                 0.2520828
## logalbumin                      0.2631151
## logalbumin_globulin_ratio       0.1996150
## logaspartate_aminotransferase   0.1483546
## logalamine_transferase         -0.3099717
## logalkaline_phosphate          -0.3247082
```