analysis_II

2023-05-07

```
library(janitor)
library(tidyverse)
library(AppliedPredictiveModeling)
library(lattice)
library(caret)
library(corrplot)
library(GGally)
library(miscset)
library(ggpubr)
library(knitr)
library(rpart)
library(rpart.plot)
library(ranger)
library(kernlab)

library(rpart)
library(rpart.plot)
library(party)
library(partykit)
library(pROC)

library(randomForest)
library(ranger)
library(gbm)
library(pdp)

library(doParallel)
library(gtsummary)
```

1. Load Data

```
load("final_data.RData")
```

2. Train/test split

```
set.seed(2)
final_data <- final_data %>%
  mutate(binary_recovery_time = factor(binary_recovery_time))
levels(final_data$binary_recovery_time) = c("low", "high")
training_rows <- createDataPartition(final_data$binary_recovery_time,
                                     p = 0.8,
                                     list = F)
```

```
train_x <- model.matrix(binary_recovery_time~., final_data %>% select(-id, -recovery_time))[training_rou
train_y <- final_data$binary_recovery_time[training_rows]
test_x <- model.matrix(binary_recovery_time~., final_data %>% select(-id, -recovery_time))[-training_rou
test_y <- final_data$binary_recovery_time[-training_rows]
```

```
training_set <- final_data[training_rows,]
```

3.EDA

basic summary statistics

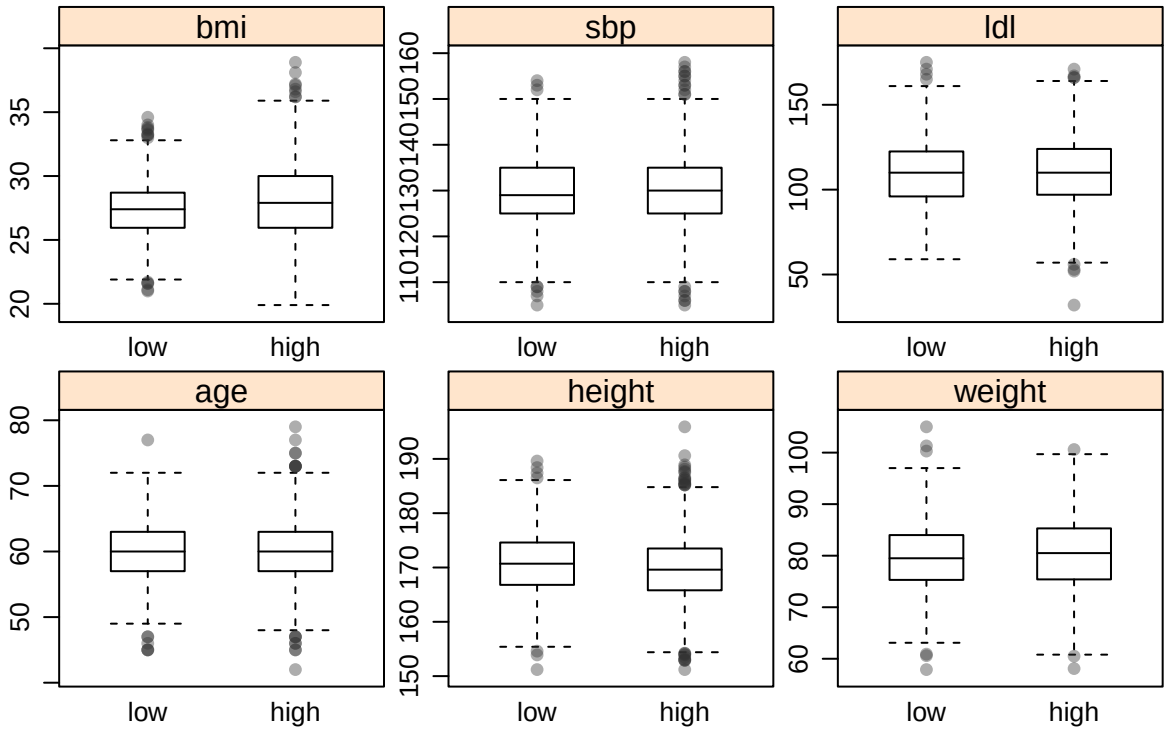
```
summary(training_set)
```

```
##        id             age        gender   race     smoking      height
##  Min.   :    5   Min.   :42.00   0:1475   1:1840   0:1784   Min.   :151.2
##  1st Qu.: 2510   1st Qu.:57.00   1:1413   2: 151   1: 832   1st Qu.:166.1
##  Median : 4909   Median :60.00            3: 599   2: 272   Median :170.1
##  Mean   : 4962   Mean   :60.07            4: 298            Mean   :169.9
##  3rd Qu.: 7469   3rd Qu.:63.00                              3rd Qu.:173.9
##  Max.   :10000   Max.   :79.00                              Max.   :195.9
##      weight           bmi        hypertension diabetes      sbp
##  Min.   : 57.90   Min.   :19.90   0:1525       0:2445   Min.   :105
##  1st Qu.: 75.40   1st Qu.:25.98   1:1363       1: 443   1st Qu.:125
##  Median : 80.10   Median :27.70                         Median :130
##  Mean   : 80.08   Mean   :27.80                         Mean   :130
##  3rd Qu.: 84.90   3rd Qu.:29.50                         3rd Qu.:135
##  Max.   :105.00   Max.   :38.90                         Max.   :158
##       ldl        vaccine  severity study    recovery_time
##  Min.   : 32.0   0:1177   0:2617   A: 582   Min.   :  2.00
##  1st Qu.: 97.0   1:1711   1: 271   B:1734   1st Qu.: 28.00
##  Median :110.0                     C: 572   Median : 39.00
##  Mean   :110.2                              Mean   : 42.96
##  3rd Qu.:123.0                              3rd Qu.: 50.00
##  Max.   :175.0                              Max.   :365.00
##  binary_recovery_time
##  low : 896
##  high:1992
##
##
##
##
```

quantatative variables

```
theme <- transparentTheme(trans = 0.4)
theme$plot.symbol$col = rgb(.2, .2, .2, .4)
theme$plot.symbol$pch = 16
theme$plot.line$col = rgb(1, 0, 0, .7)
theme$plot.line$lwd <- 2
trellis.par.set(theme)
featurePlot(x = training_set %>% dplyr::select(-recovery_time, -binary_recovery_time, -id, -gender, -ra
            y = training_set$binary_recovery_time,
            plot = "box",
            pch = "|",
            scales = list(x = list(relation = "free"),
```

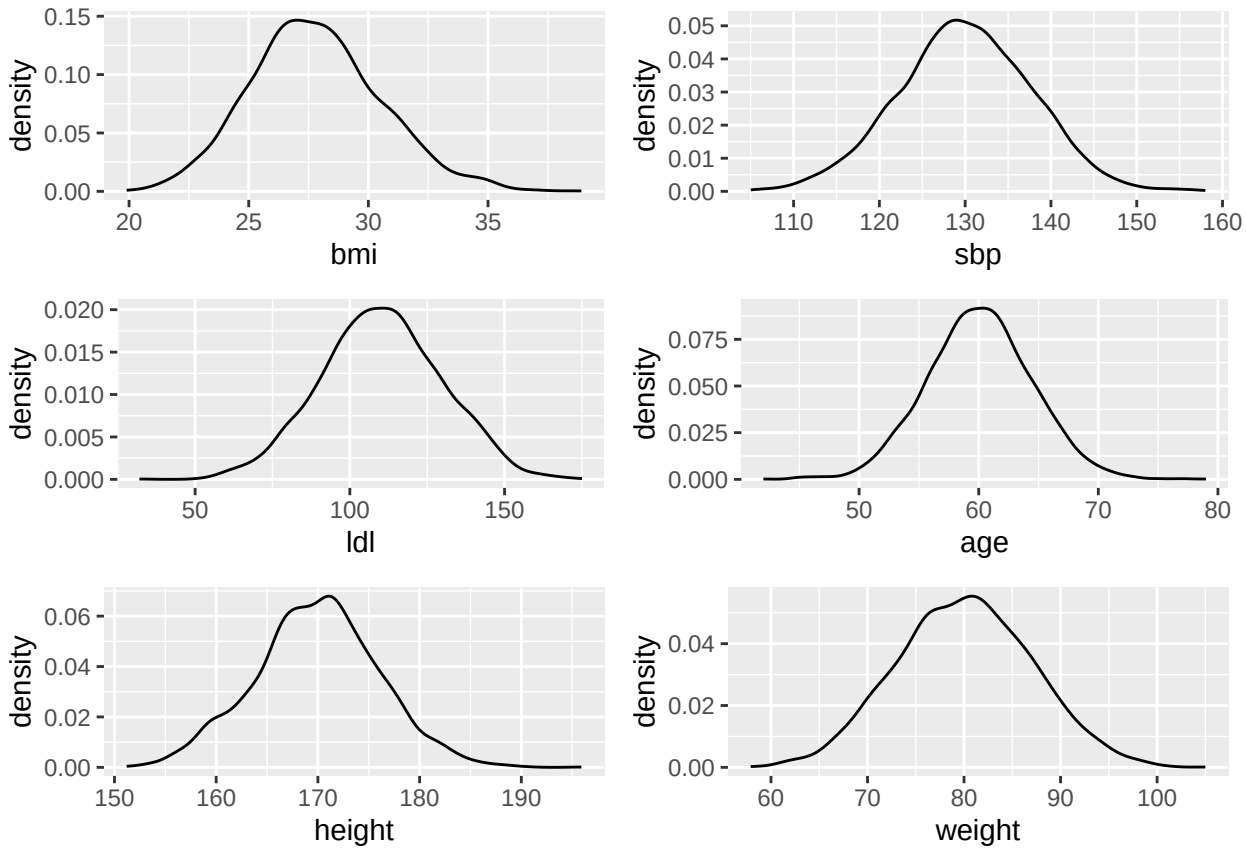
```
                        y = list(relation = "free")),
            auto.key = list(columns = 2),
            labels = c("Binary Recovery Time", ""))
```



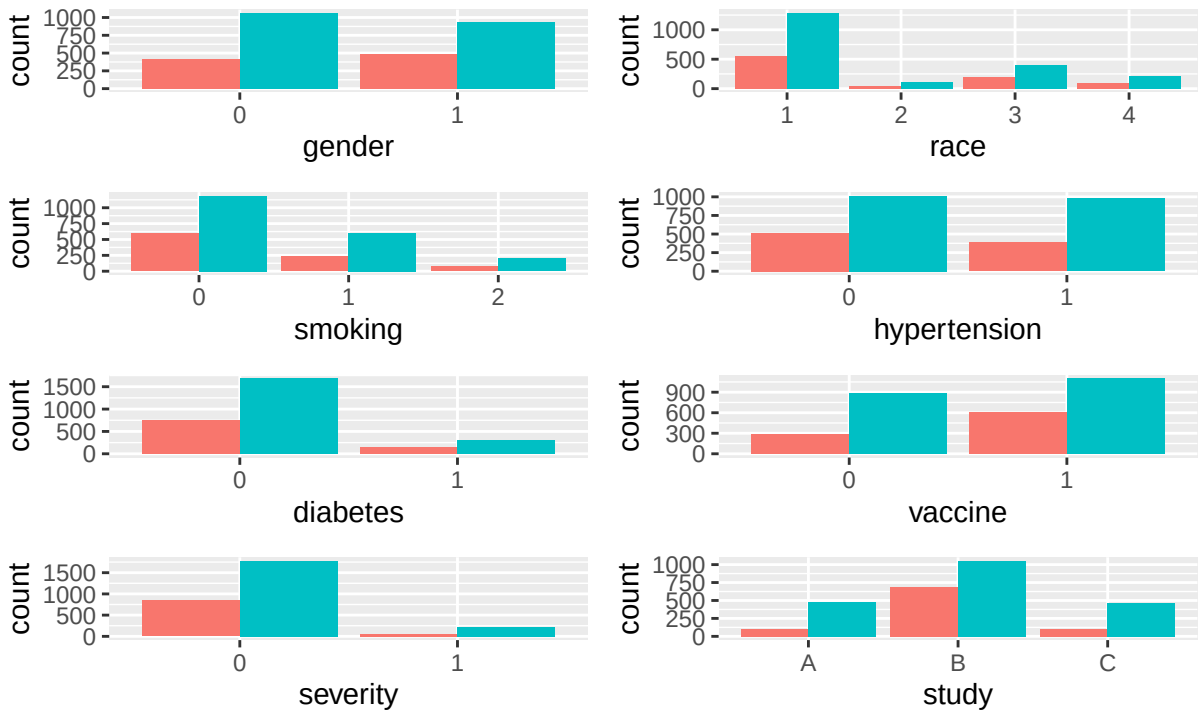

```
ggplotGrid(ncol = 2,
  lapply(c("bmi", "sbp", "ldl","age", "height", "weight"),
    function(col) {
        ggplot(training_set, aes_string(col)) + geom_density(aes(y = ..density..))
    }))
```

```
## Warning: `aes_string()` was deprecated in ggplot2 3.0.0.
## i Please use tidy evaluation idioms with `aes()`.
## i See also `vignette("ggplot2-in-packages")` for more information.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## Warning: The dot-dot notation (`..density..`) was deprecated in ggplot2 3.4.0.
## i Please use `after_stat(density)` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```




```
l <-
  lapply(c("gender", "race", "smoking","hypertension", "diabetes", "vaccine", "severity", "study"),
    function(col) {
        ggplot(training_set, aes_string(col)) + geom_bar(aes(fill = binary_recovery_time),stat="count",
    })
patchwork::wrap_plots(l, ncol = 2, guides = "collect") & theme(legend.position = "bottom")
```




```
sum(train_y == "low")
```

```
## [1] 896
```

```
sum(train_y == "high")
```

```
## [1] 1992
```

```
sum(test_y == "low")
```

```
## [1] 223
```

```
sum(test_y == "high")
```

```
## [1] 498
```

```
sum(final_data$binary_recovery_time == "low")
```

```
## [1] 1119
```

```
sum(final_data$binary_recovery_time == "high")
```

```
## [1] 2490
```

4. set up control

```
ctrl2 = trainControl(method = "cv", number = 10)
```

5. Model training

a. Logistic regression

```
set.seed(2)
#fit a logistic regression using caret
model.glm = train(train_x, train_y, method = "glm", metric = "Accuracy",
                  trControl = ctrl2)
summary(model.glm)
```

```
##
## Call:
## NULL
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.4670  -1.1407   0.6120   0.8681   1.6411
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -7.460e+01  1.388e+01  -5.374 7.70e-08 ***
## age            1.720e-02  1.092e-02   1.575 0.115307
## gender1       -3.090e-01  8.555e-02  -3.611 0.000304 ***
## race2         -3.677e-02  1.961e-01  -0.188 0.851260
## race3         -1.764e-01  1.070e-01  -1.648 0.099291 .
## race4          1.095e-03  1.439e-01   0.008 0.993928
## smoking1       2.959e-01  9.780e-02   3.026 0.002480 **
## smoking2       4.111e-01  1.549e-01   2.654 0.007949 **
## height         4.321e-01  8.133e-02   5.313 1.08e-07 ***
## weight        -4.735e-01  8.678e-02  -5.457 4.84e-08 ***
## bmi            1.437e+00  2.506e-01   5.737 9.66e-09 ***
## hypertension1  2.714e-01  1.415e-01   1.918 0.055148 .
## diabetes1     -3.350e-02  1.193e-01  -0.281 0.778852
## sbp           -1.345e-04  9.589e-03  -0.014 0.988810
## ldl           -5.396e-04  2.260e-03  -0.239 0.811341
## vaccine1      -5.989e-01  8.919e-02  -6.715 1.88e-11 ***
## severity1      6.580e-01  1.656e-01   3.974 7.07e-05 ***
## studyB        -1.103e+00  1.211e-01  -9.111  < 2e-16 ***
## studyC         3.074e-02  1.557e-01   0.197 0.843475
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3577.1  on 2887  degrees of freedom
## Residual deviance: 3253.9  on 2869  degrees of freedom
## AIC: 3291.9
##
## Number of Fisher Scoring iterations: 4
```

```
coef(model.glm$finalModel) %>%
  as.matrix() %>%
  as.data.frame() %>%
  rename(value = V1) %>%
  kable(caption = "Logistic Regression Parameter Coefficients")
```

Table 1: Logistic Regression Parameter Coefficients

	value
(Intercept)	-74.5985809
age	0.0171971
gender1	-0.3089547
race2	-0.0367652
race3	-0.1764199
race4	0.0010954
smoking1	0.2959354
smoking2	0.4110928
height	0.4320885
weight	-0.4735363
bmi	1.4373521
hypertension1	0.2714113
diabetes1	-0.0334999
sbp	-0.0001345
ldl	-0.0005396
vaccine1	-0.5989130
severity1	0.6579947
studyB	-1.1031862
studyC	0.0307435

```
contrasts(final_data$binary_recovery_time)
```

```
##      high
## low     0
## high    1
```

```
#We first consider the simple classifier with a cut-off of 0.5 and evaluate its performance on the test

test.pred.prob = predict(model.glm$finalModel, newdata = as.data.frame(test_x), type = "response")
test.pred = rep("low", length(test.pred.prob))
test.pred[test.pred.prob > 0.5] = "high"

confusionMatrix = confusionMatrix(data = as.factor(test.pred),
                reference = test_y,
                positive = "high")
```

```
## Warning in confusionMatrix.default(data = as.factor(test.pred), reference =
## test_y, : Levels are not in the same order for reference and data. Refactoring
## data to match.
```

```
confusionMatrix
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction low high
##       low   54   42
##       high 169  456
##
##                Accuracy : 0.7074
##                  95% CI : (0.6726, 0.7403)
##     No Information Rate : 0.6907
```

```
##     P-Value [Acc > NIR] : 0.1772
##
##                   Kappa : 0.1873
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.9157
##             Specificity : 0.2422
##          Pos Pred Value : 0.7296
##          Neg Pred Value : 0.5625
##              Prevalence : 0.6907
##          Detection Rate : 0.6325
##    Detection Prevalence : 0.8669
##       Balanced Accuracy : 0.5789
##
##        'Positive' Class : high
##
```

```
#Testing error rate is 0.2926491
1 - confusionMatrix$overall["Accuracy"]
```

```
##  Accuracy
## 0.2926491
```

```
#Training error rate is 0.2939751
train.pred.prob = predict(model.glm$finalModel, newdata = as.data.frame(train_x), type = "response")
train.pred.prob[train.pred.prob > 0.5] = "high"
train.pred.prob[train.pred.prob < 0.5] = "low"
table(train_y, train.pred.prob)
```

```
##        train.pred.prob
## train_y high  low
##    low   682  214
##    high 1825  167
```

```
mean(train.pred.prob != train_y)
```

```
## [1] 0.2939751
```

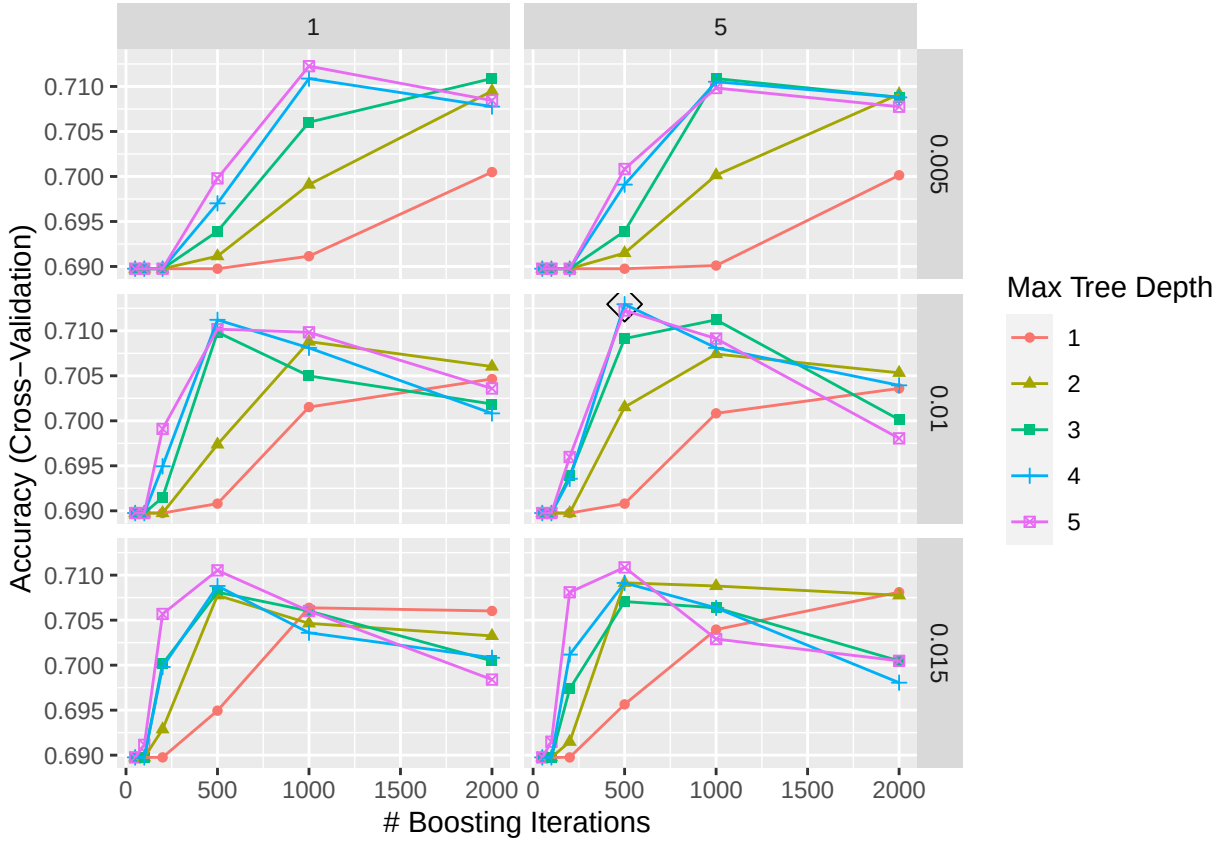
b. Random Forest

```
set.seed(2)
gbm_grid <- expand.grid(
  # upper bound for number of trees
  n.trees = c(50, 100, 200, 500, 1000, 2000),
  # similar to number of splits in the tree
  # number of layers in the tree
  interaction.depth = 1:5,
  shrinkage = c(0.005,0.01,0.015),
  # min obs allowed in a node
  n.minobsinnode = c(1,5))
```

```
Mycluster = makeCluster(detectCores() - 2)
registerDoParallel(Mycluster)

boost_fit <- train(train_x,
```

```
                    train_y,
                    method = "gbm",
                    tuneGrid = gbm_grid,
                    trControl = ctrl2,
                    distribution = "adaboost",
                    verbose = FALSE)

stopCluster(Mycluster)
registerDoSEQ()
```

```
ggplot(boost_fit, highlight = TRUE)
```

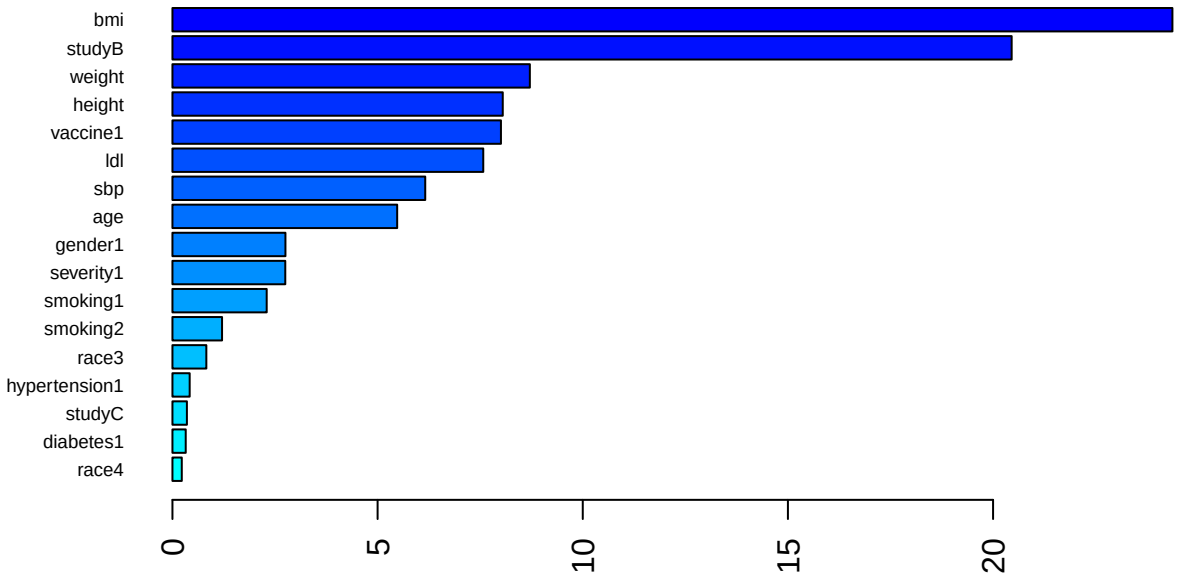



```
boost_fit$bestTune
```

```
##     n.trees interaction.depth shrinkage n.minobsinnode
## 106     500                 4      0.01              5
```

variable importance

```
summary(boost_fit$finalModel,las = 2, cBars = 17, cex.names = 0.6)
```




```
##                          var     rel.inf
## bmi                      bmi 24.37052777
## studyB                studyB 20.45243388
## weight                weight  8.71029731
## height                height  8.04982577
## vaccine1            vaccine1  8.00572107
## ldl                      ldl  7.57484863
## sbp                      sbp  6.16092664
## age                      age  5.47703636
## gender1              gender1  2.75357894
## severity1          severity1  2.74995110
## smoking1            smoking1  2.29700139
## smoking2            smoking2  1.20859525
## race3                  race3  0.82622068
## hypertension1 hypertension1  0.41987580
## studyC                studyC  0.35222659
## diabetes1          diabetes1  0.32341450
## race4                  race4  0.22773196
## race2                  race2  0.03978636
```

partial dependence plots

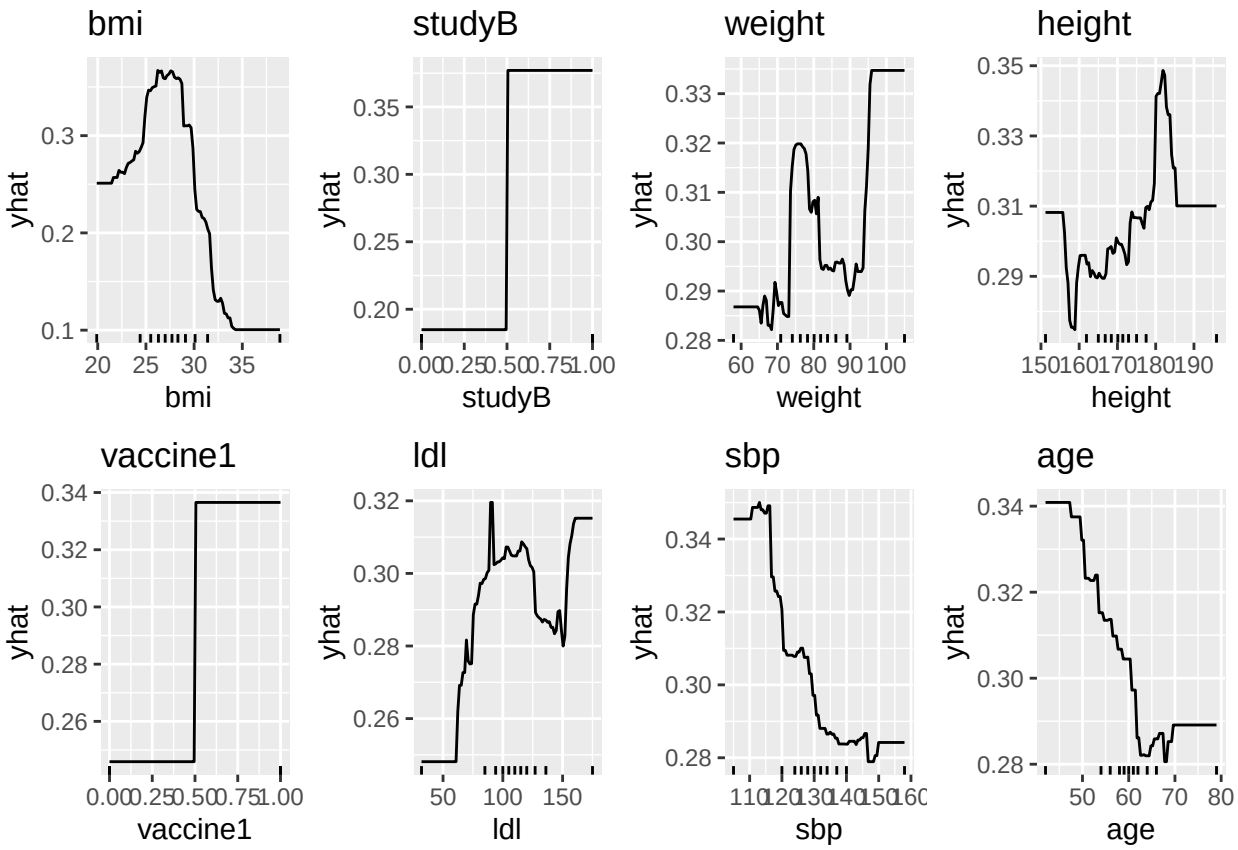
```
pdp.1 <- boost_fit %>%
  partial(pred.var = "bmi",
          grid.resolution = 100,
          prob = TRUE) %>%
  autoplot(rug = TRUE, train = train_x) +
  ggtitle("bmi")

pdp.2 <- boost_fit %>%
  partial(pred.var = "studyB",
          grid.resolution = 100,
          prob = TRUE) %>%
  autoplot(rug = TRUE, train = train_x) +
```

```
  ggtitle("studyB")

pdp.3 <- boost_fit %>%
  partial(pred.var = "weight",
          grid.resolution = 100,
          prob = TRUE) %>%
  autoplot(rug = TRUE, train = train_x) +
  ggtitle("weight")

pdp.4 <- boost_fit %>%
  partial(pred.var = "height",
          grid.resolution = 100,
          prob = TRUE) %>%
  autoplot(rug = TRUE, train = train_x) +
  ggtitle("height")

pdp.5 <- boost_fit %>%
  partial(pred.var = "vaccine1",
          grid.resolution = 100,
          prob = TRUE) %>%
  autoplot(rug = TRUE, train = train_x) +
  ggtitle("vaccine1")

pdp.6 <- boost_fit %>%
  partial(pred.var = "ldl",
          grid.resolution = 100,
          prob = TRUE) %>%
  autoplot(rug = TRUE, train = train_x) +
  ggtitle("ldl")

pdp.7 <- boost_fit %>%
  partial(pred.var = "sbp",
          grid.resolution = 100,
          prob = TRUE) %>%
  autoplot(rug = TRUE, train = train_x) +
  ggtitle("sbp")

pdp.8 <- boost_fit %>%
  partial(pred.var = "age",
          grid.resolution = 100,
          prob = TRUE) %>%
  autoplot(rug = TRUE, train = train_x) +
  ggtitle("age")

library(gridExtra)
```

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

```
##     combine
```

```
grid.arrange(pdp.1, pdp.2, pdp.3, pdp.4, pdp.5, pdp.6, pdp.7, pdp.8,
             nrow = 2, ncol = 4)
```




```
trboost_prediction <- predict(boost_fit$finalModel, newdata = train_x, type = "response")
```

```
## Using 500 trees...
```

```
# As predictions are made for the positive class, we set a threshold 0.5 and assign anything above to b
trboost_prediction[trboost_prediction > 0.50] = "low"
trboost_prediction[trboost_prediction < 0.50] = "high"

boost_tr_mse <- mean(trboost_prediction != train_y)
boost_tr_mse
```

```
## [1] 0.2690443
```

```
boost_prediction <- predict(boost_fit$finalModel, newdata = test_x, type = "response")
```

```
## Using 500 trees...
```

```
# As predictions are made for the positive class, we set a threshold 0.5 and assign anything above to b
boost_prediction[boost_prediction > 0.50] = "low"
boost_prediction[boost_prediction < 0.50] = "high"

boost_ts_mse <- mean(boost_prediction != test_y)
boost_ts_mse
```

```
## [1] 0.2884882
```

roc

```
library(pROC)

boost_prediction_pl <- predict(boost_fit$finalModel, newdata = test_x, type = "response")
```

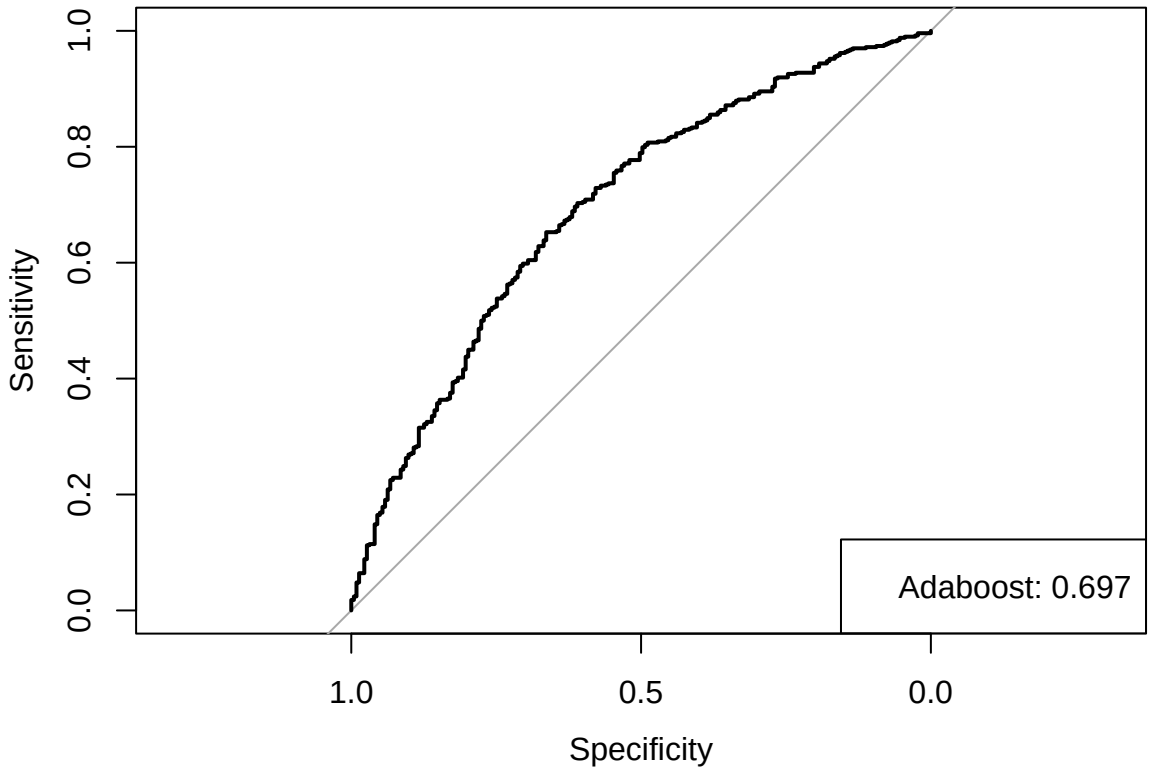
```
## Using 500 trees...
```

```
roc.gbm <- roc(test_y, boost_prediction_pl)
```

```
## Setting levels: control = low, case = high
```

```
## Setting direction: controls > cases
```

```
plot(roc.gbm, col = 1)

auc <- roc.gbm$auc[1]

modelNames <- c("Adaboost")

legend("bottomright", legend = paste0(modelNames, ": ", round(auc,3)))
```




```
test.pred.prob = predict(boost_fit$finalModel, newdata = as.data.frame(test_x), type = "response")
```

```
## Using 500 trees...
```

```
test.pred = rep("high", length(test.pred.prob))
test.pred[test.pred.prob > 0.5] = "low"

confusionMatrix.2 = confusionMatrix(data = as.factor(test.pred),
                                    reference = test_y,
                                    positive = "low")
```

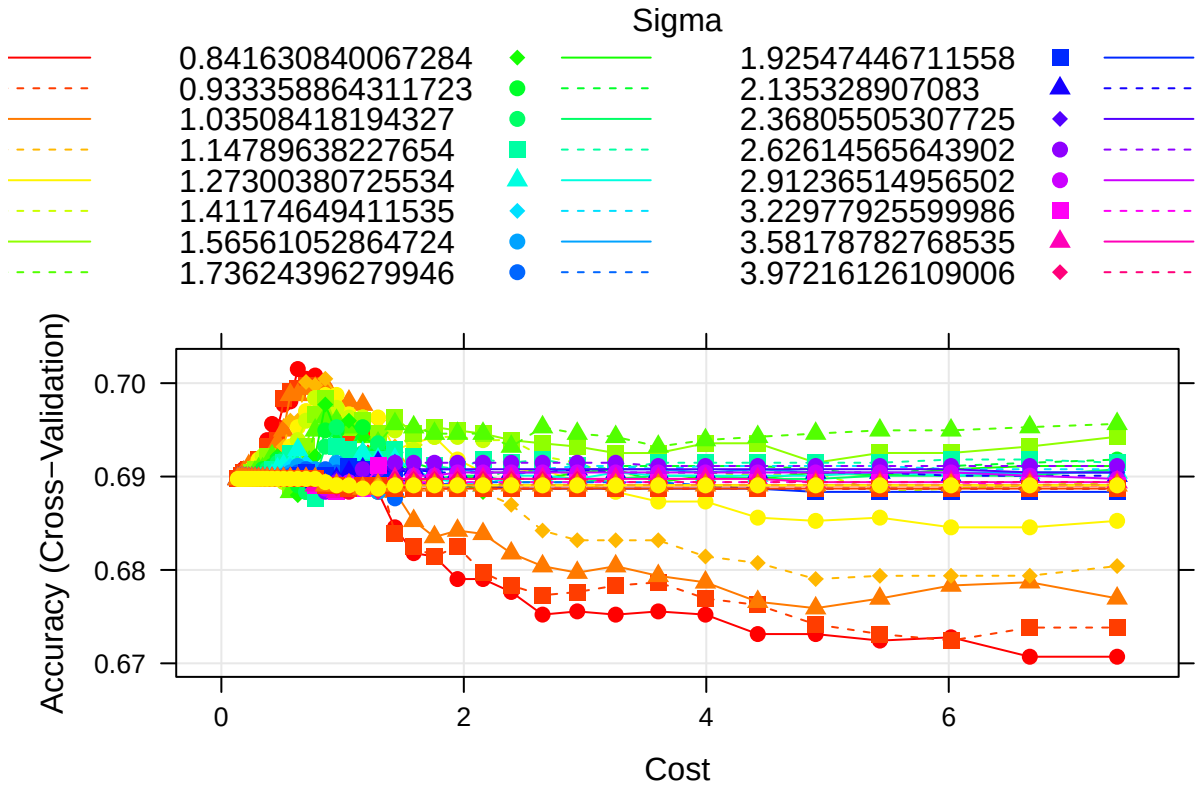
```
## Warning in confusionMatrix.default(data = as.factor(test.pred), reference =
## test_y, : Levels are not in the same order for reference and data. Refactoring
## data to match.
```

```
confusionMatrix.2
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction low high
##       low   55   40
##       high 168  458
##
##                Accuracy : 0.7115
##                  95% CI : (0.6769, 0.7444)
##     No Information Rate : 0.6907
##     P-Value [Acc > NIR] : 0.1209
##
##                   Kappa : 0.1976
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.24664
##             Specificity : 0.91968
##          Pos Pred Value : 0.57895
##          Neg Pred Value : 0.73163
##              Prevalence : 0.30929
##          Detection Rate : 0.07628
##    Detection Prevalence : 0.13176
##       Balanced Accuracy : 0.58316
##
##        'Positive' Class : low
##
```

c. SVM

```
svmr_grid <- expand.grid(C = exp(seq(-2,2,len=40)),
                         sigma = exp(seq(-1,2,len=30)))
set.seed(2)

Mycluster = makeCluster(detectCores()-2)
registerDoParallel(Mycluster)
svmr_fit <- train(binary_recovery_time ~.,
                  data = training_set %>% select(-id, -recovery_time),
                  method = "svmRadialSigma",
                  tuneGrid = svmr_grid,
                  trControl = ctrl2)
stopCluster(Mycluster)
registerDoSEQ()

myCol<- rainbow(25)
myPar <- list(superpose.symbol = list(col = myCol),
              superpose.line = list(col = myCol))
plot(svmr_fit, highlight = TRUE, par.settings = myPar)
```




```
svmr_fit$bestTune
```

```
##         sigma         C
## 451 0.3678794 0.6303132
```

```
svm_train_prediction <- predict(svmr_fit$finalModel, newdata = train_x)
mean(svm_train_prediction!=train_y)
```

```
## [1] 0.2171053
```

```
svm_test_prediction <- predict(svmr_fit$finalModel, newdata = test_x)
```

```
mean(svm_test_prediction!=test_y)
```

```
## [1] 0.2884882
```

6. Comparison

Resample

```
set.seed(2)
resamp <- resamples(list(
                         Logistic = model.glm,
                         Random_Forest = boost_fit,
                         SVM = svmr_fit))
summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
##
```

```
## Models: Logistic, Random_Forest, SVM
## Number of resamples: 10
##
## Accuracy
##                    Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## Logistic      0.6608997 0.6825260 0.7019115 0.6991054 0.7124282 0.7370242    0
## Random_Forest 0.6747405 0.7004367 0.7214533 0.7129559 0.7253053 0.7361111    0
## SVM           0.6805556 0.6963668 0.7019115 0.7015132 0.7077206 0.7206897    0
##
## Kappa
##                     Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## Logistic      0.07408134 0.1262342 0.1821818 0.1656036 0.1868010 0.2744450    0
## Random_Forest 0.12480860 0.1715600 0.2130027 0.1966640 0.2263556 0.2424081    0
## SVM           0.02563818 0.0783677 0.1054410 0.1001623 0.1309254 0.1535135    0
```

```
bwplot(resamp)
```