td_boosting

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```
library(tidyverse)
library(dplyr)
library(ggplot2)

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

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

1. Load Data

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

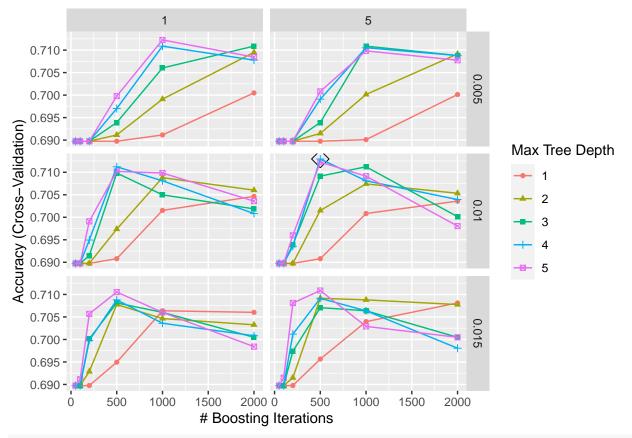
2. Train/test split

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

```
training_set <- final_data[training_rows,]</pre>
```

Classification: Random Forest with boosting

```
ctrl.c <- trainControl(method = "cv", number = 10)</pre>
set.seed(2)
gbm_grid <- expand.grid(</pre>
  # 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)
library(doParallel)
## Loading required package: foreach
## Attaching package: 'foreach'
## The following objects are masked from 'package:purrr':
##
##
       accumulate, when
## Loading required package: iterators
## Loading required package: parallel
Mycluster = makeCluster(detectCores() - 2)
registerDoParallel(Mycluster)
boost_fit <- train(train_x,</pre>
                   train_y,
                   method = "gbm",
                   tuneGrid = gbm_grid,
                    trControl = ctrl.c,
                   distribution = "adaboost",
                    #metric = "ROC",
                   verbose = FALSE)
stopCluster(Mycluster)
registerDoSEQ()
ggplot(boost_fit, highlight = TRUE)
```

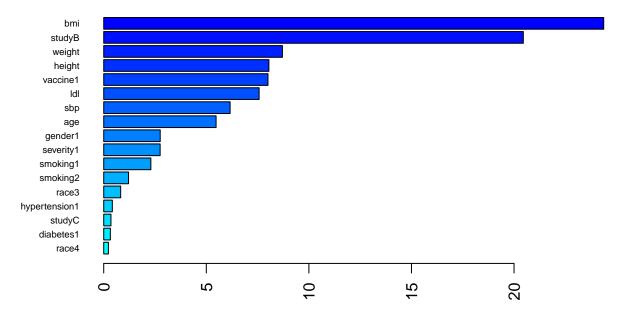


boost_fit\$bestTune

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)



Relative influence

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

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</pre>
```

[1] 0.2690443

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

```
## 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</pre>
```

[1] 0.2884882