Data Science 2 Final

Group 6

Contents

Set up

Load libraries and data

```
library(caret)
library(mgcv)
library(earth)
library(tidyverse)
library(summarytools)
library(corrplot)
library(ggpubr)
library(rpart)
library(rpart.plot)
library(randomForest)
library(ranger)
library(gbm)
library(pdp)
library(vip)

# setwd("D:/CUMC/Y2S2/DS2/Final/ds2_final")

load("./recovery.RData")
```

Subset 2 df and keep unique observations

```
set.seed(2543)

dat1 <- dat[sample(1:10000, 2000),]

set.seed(4017)

dat2 <- dat[sample(1:10000, 2000),]

dat_bind <- unique(rbind(dat1, dat2))
```

Exploratory analysis and data visualization

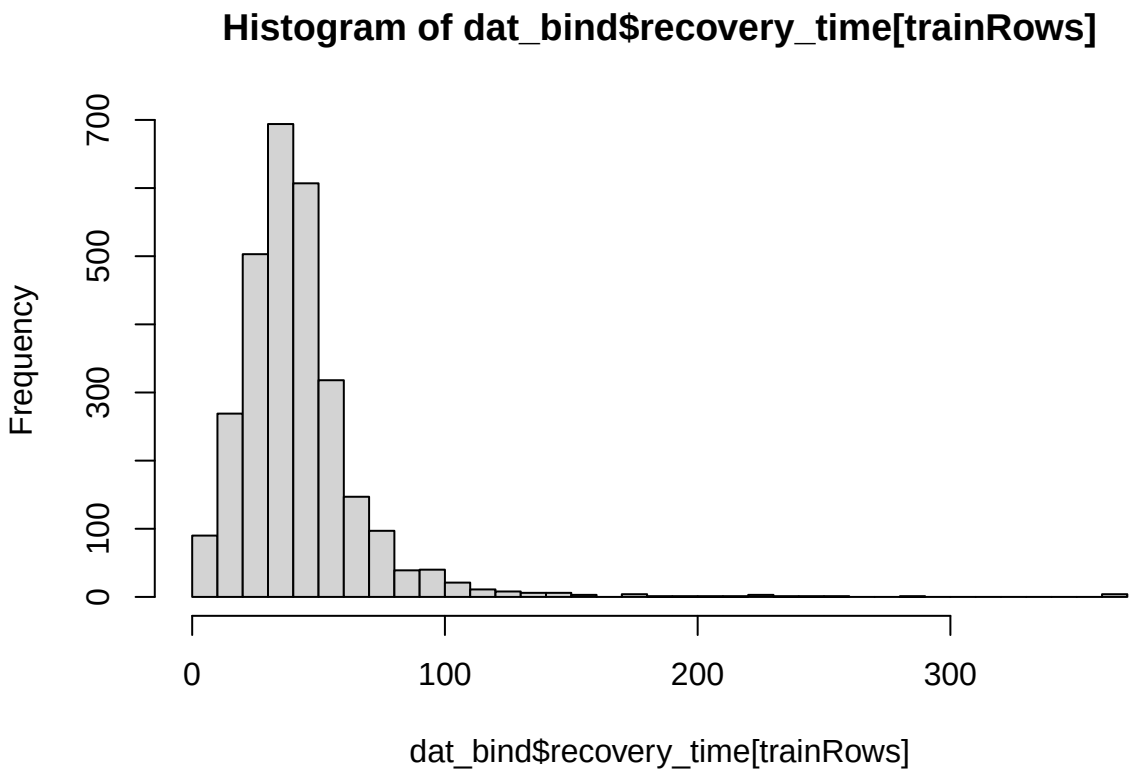
Data Partition

Here, we mainly want to investigate the EDA of the training dataset. Therefore, we will start with the data partition.

```
set.seed(2460)

trainRows <- createDataPartition(y = dat_bind$recovery_time,
                                 p = 0.8, list = FALSE)
```

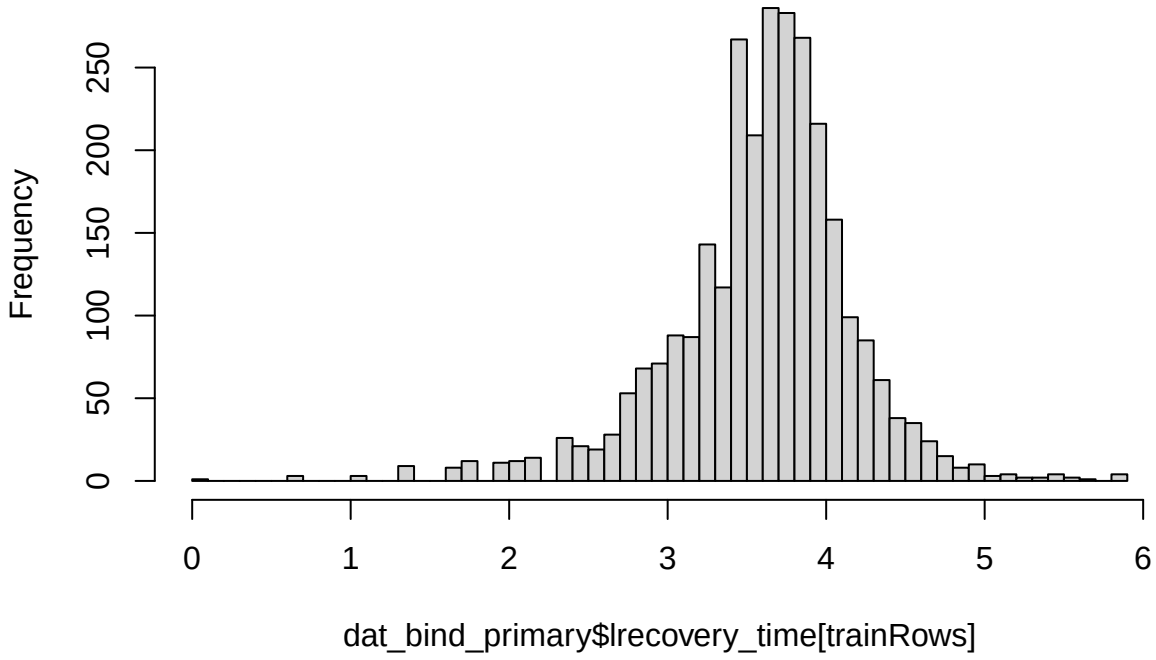
Understanding the outcome variable `recovery_time`

```
# check the outcome variable
hist(dat_bind$recovery_time[trainRows], breaks = 50)
```



The distribution of the outcome variable `recovery_time` is heavily right-skewed. To account for this, we will take the log-transformation of the outcome and use that variable for following analyses.

```
dat_bind_primary = dat_bind %>%
  na.omit(dat_bind) %>%
  mutate(lrecovery_time = log(recovery_time)) %>%
  dplyr::select(-recovery_time, -id)

# log-transformation helped with making it more normal
hist(dat_bind_primary$lrecovery_time[trainRows], breaks = 50)
```



Summary of the dataset

```
st_options(plain.ascii = F,
           style = "rmarkdown",
           dfSummary.silent = T,
           footnote = NA,
           subtitle.emphasis = F)

dfSummary(dat_bind_primary[trainRows, -1])
```

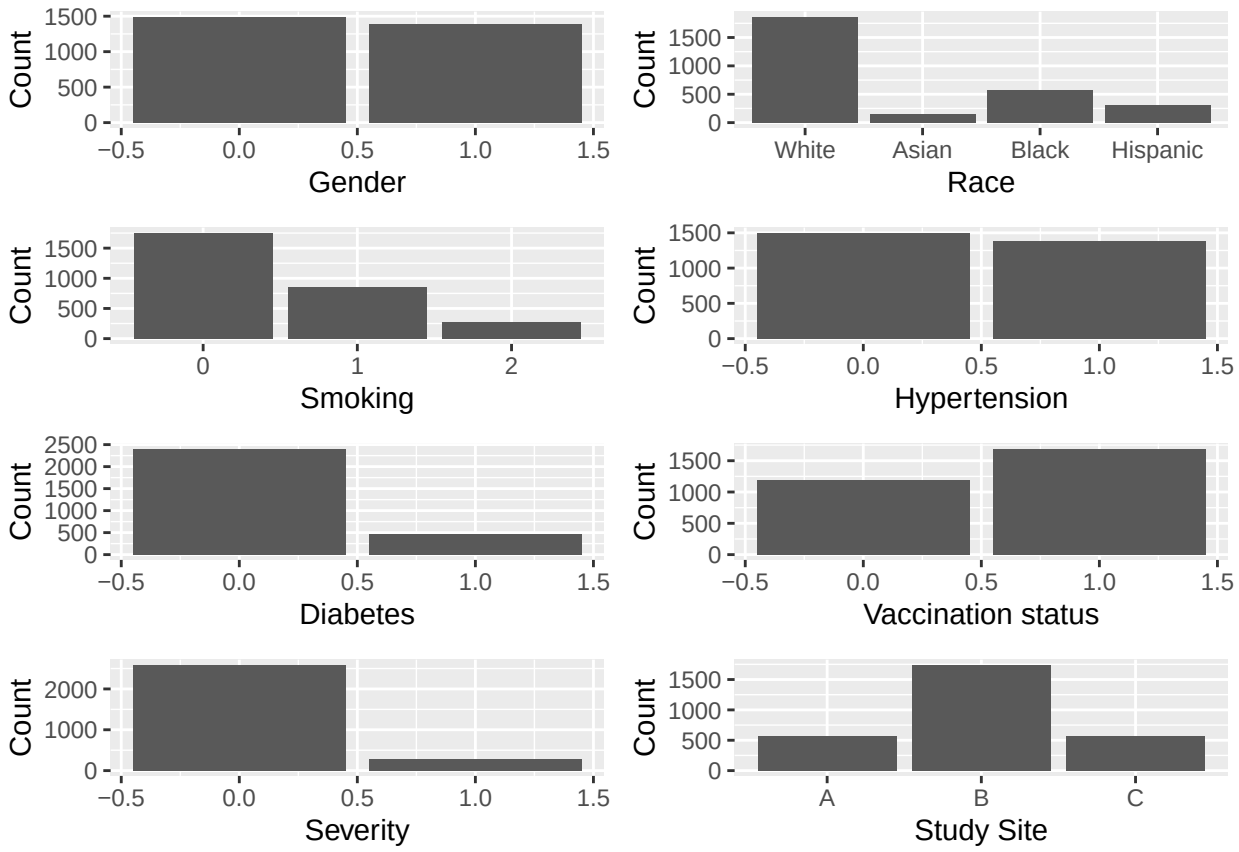
```
## ### Data Frame Summary
## **dat_bind_primary**
## **Dimensions:** 2878 x 14
## **Duplicates:** 0
##
## ----------------------------------------------------------------------------------------------------
## No   Variable          Stats / Values              Freqs (% of Valid)    Graph
## ---- ----------------- --------------------------- --------------------- ----------------------------
## 1    gender\           Min  : 0\                   0 : 1490 (51.8%)\     IIIIIIIIII \
##      [integer]         Mean : 0.5\                 1 : 1388 (48.2%)      IIIIIIIII
##                        Max  : 1
##
## 2    race\             1\. 1\                      1863 (64.7%)\         IIIIIIIIIII \
##      [factor]          2\. 2\                      145 ( 5.0%)\          I \
##                        3\. 3\                      569 (19.8%)\          III \
##                        4\. 4                       301 (10.5%)           II
##
## 3    smoking\          1\. 0\                      1753 (60.9%)\         IIIIIIIIIII \
##      [factor]          2\. 1\                      846 (29.4%)\          IIIII \
```

```
##                       3\. 2                      279 ( 9.7%)          I
##
## 4    height\          Mean (sd) : 170.1 (5.9)\   311 distinct values  \ \ \ \ \ \ . :\
##      [numeric]        min < med < max:\                               \ \ \ \ \ \ : :\
##                       150.7 < 170.4 < 190.6\                          \ \ \ \ . : : .\
##                       IQR (CV) : 7.9 (0)                              \ \ \ \ : : : :\
##                                                                       \ \ . : : : : : .
##
## 5    weight\          Mean (sd) : 79.9 (7)\      358 distinct values  \ \ \ \ \ \ \ \ :\
##      [numeric]        min < med < max:\                               \ \ \ \ \ \ : : .\
##                       55.9 < 80.1 < 111.6\                            \ \ \ \ \ \ : : :\
##                       IQR (CV) : 9.5 (0.1)                            \ \ \ \ : : : :\
##                                                                       \ \ . : : : : : :
##
## 6    bmi\             Mean (sd) : 27.7 (2.7)\    162 distinct values  \ \ \ \ \ \ . :\
##      [numeric]        min < med < max:\                               \ \ \ \ \ \ : :\
##                       19.7 < 27.5 < 38.1\                             \ \ \ \ . : : :\
##                       IQR (CV) : 3.6 (0.1)                            \ \ \ \ : : : : .\
##                                                                       \ \ : : : : : : : .
##
## 7    hypertension\    Min  : 0\                  0 : 1499 (52.1%)\    IIIIIIIIII \
##      [numeric]        Mean : 0.5\                1 : 1379 (47.9%)     IIIIIIIII
##                       Max  : 1
##
## 8    diabetes\        Min  : 0\                  0 : 2403 (83.5%)\    IIIIIIIIIIIIIII \
##      [integer]        Mean : 0.2\                1 :  475 (16.5%)     III
##                       Max  : 1
##
## 9    SBP\             Mean (sd) : 130.2 (8)\     51 distinct values   \ \ \ \ \ \ \ \ : .\
##      [numeric]        min < med < max:\                               \ \ \ \ \ \ . : :\
##                       106 < 130 < 157\                                \ \ \ \ \ \ : : : :\
##                       IQR (CV) : 11 (0.1)                             \ \ \ \ : : : : :\
##                                                                       \ \ : : : : : : : .
##
## 10   LDL\             Mean (sd) : 110.6 (19.9)\  121 distinct values  \ \ \ \ \ \ \ \ \ :\
##      [numeric]        min < med < max:\                               \ \ \ \ \ \ \ \ : : .\
##                       28 < 111 < 178\                                 \ \ \ \ \ \ \ \ : : :\
##                       IQR (CV) : 27 (0.2)                             \ \ \ \ \ \ . : : : :\
##                                                                       \ \ \ \ . : : : : : .
##
## 11   vaccine\         Min  : 0\                  0 : 1189 (41.3%)\    IIIIIIII \
##      [integer]        Mean : 0.6\                1 : 1689 (58.7%)     IIIIIIIIII
##                       Max  : 1
##
## 12   severity\        Min  : 0\                  0 : 2589 (90.0%)\    IIIIIIIIIIIIIIII \
##      [integer]        Mean : 0.1\                1 :  289 (10.0%)     II
##                       Max  : 1
##
## 13   study\           1\. A\                     571 (19.8%)\         III \
##      [character]      2\. B\                     1741 (60.5%)\        IIIIIIIIIII \
##                       3\. C                      566 (19.7%)          III
##
## 14   lrecovery_time\  Mean (sd) : 3.6 (0.6)\     147 distinct values  \ \ \ \ \ \ \ \ \ \ \ :\
##      [numeric]        min < med < max:\                               \ \ \ \ \ \ \ \ \ \ \ :\
```

```
##                         0 < 3.7 < 5.9\                                    \ \ \ \ \ \ \ \ \ \ : :\
##                         IQR (CV) : 0.6 (0.2)                              \ \ \ \ \ \ \ \ \ \ : :\
##                                                                           \ \ \ \ \ \ \ \ : : : :
## -------------------------------------------------------------------------------------------------
```

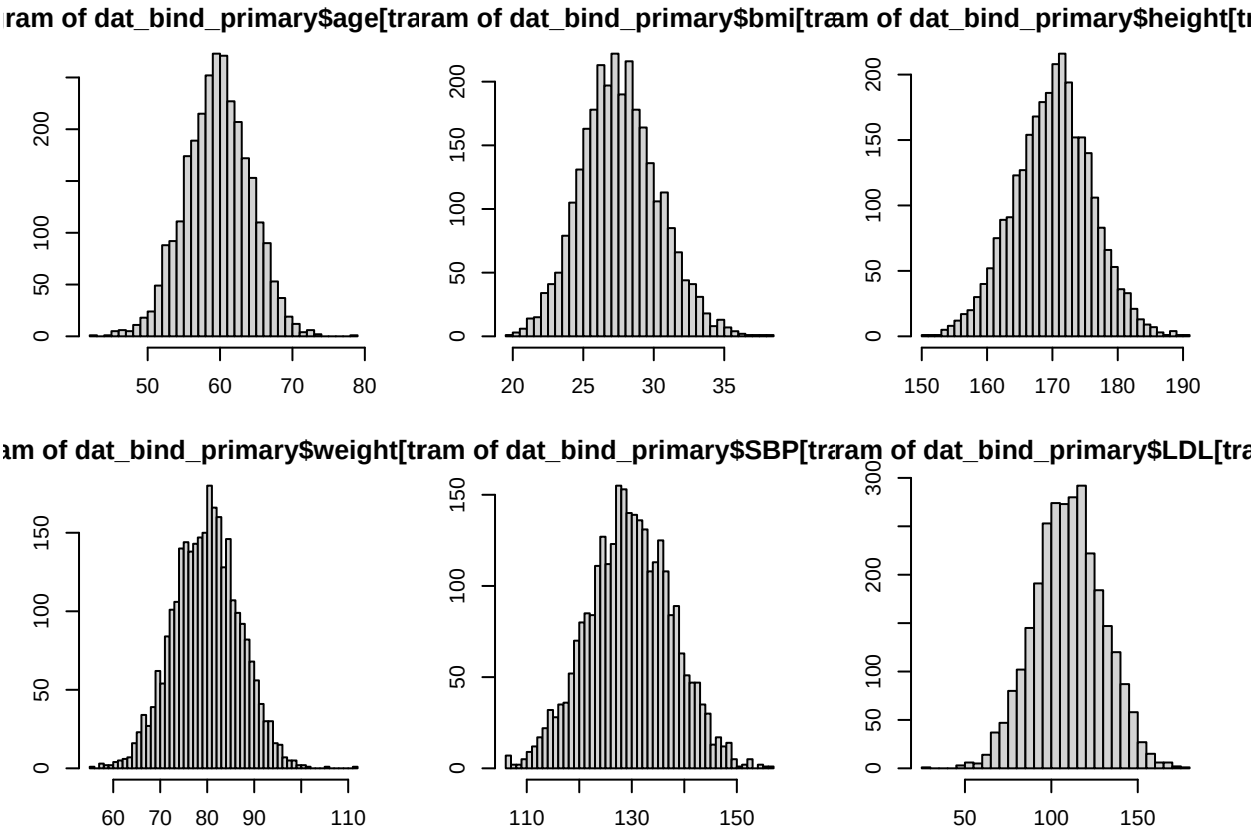
Understand categorical variables

```
gender = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = gender)) +  geom_bar() +  labs(x = "Gender", y = "Count")

race = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = race)) + geom_bar() + labs(x = "Race",y = "Count") +
  scale_x_discrete(labels = c("White", "Asian", "Black", "Hispanic"))

smoking = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = smoking)) + geom_bar() + labs(x = "Smoking", y = "Count")

hypertension = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = hypertension)) + geom_bar() + labs(x = "Hypertension",
                                                    y = "Count")
diabetes = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = diabetes)) + geom_bar() + labs(x = "Diabetes",y = "Count")

vaccine = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = vaccine)) + geom_bar() + labs(x = "Vaccination status",
                                               y = "Count")
severity = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = severity)) + geom_bar() + labs(x = "Severity", y = "Count")

study = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = study)) + geom_bar() + labs(x = "Study Site", y = "Count")

cat_combined_plot = ggarrange(gender, race, smoking, hypertension,
                              diabetes, vaccine,severity, study,
                          ncol = 2, nrow = 4)

cat_combined_plot
```



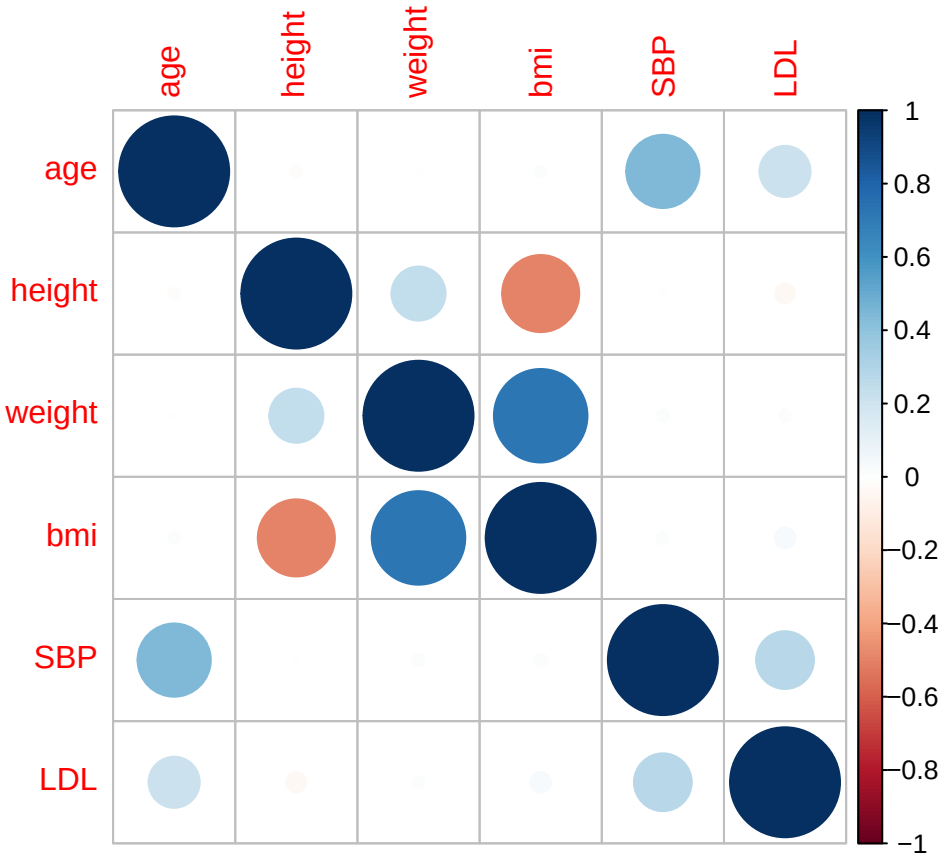
Understand continuous variables

```
par(mar = c(3, 3, 2, 2), mfrow = c(2, 3))

age = hist(dat_bind_primary$age[trainRows], breaks = 50)

bmi = hist(dat_bind_primary$bmi[trainRows], breaks = 50)

height = hist(dat_bind_primary$height[trainRows], breaks = 50)

weight = hist(dat_bind_primary$weight[trainRows], breaks = 50)

SBP = hist(dat_bind_primary$SBP[trainRows], breaks = 50)

LDL = hist(dat_bind_primary$LDL[trainRows], breaks = 50)
```



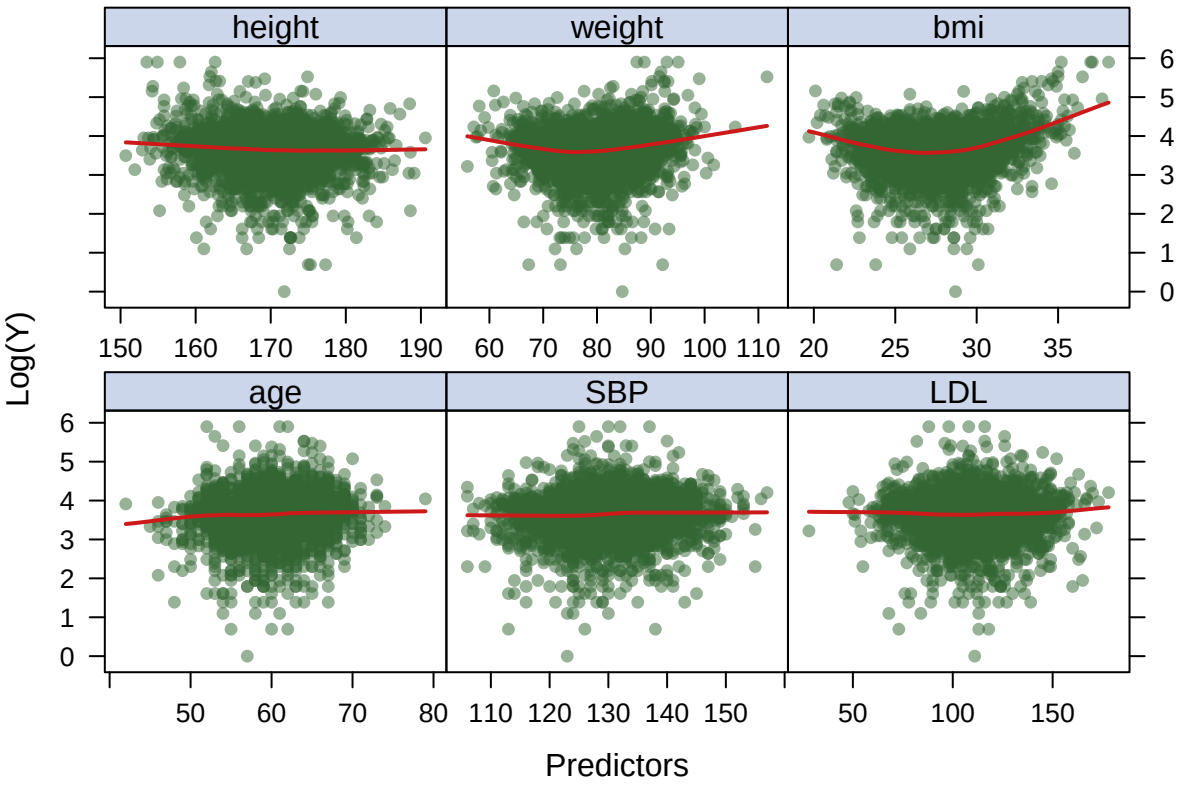
Understand the correlation between continuous predictors

```
correlation <- model.matrix(lrecovery_time ~ ., dat_bind_primary)[trainRows,-1]

corrplot(cor(dat_bind_primary[trainRows,c(1,5,6,7,10,11)]), method = "circle", type = "full")
```



Understand the relationship with continuous predictors and the outcome

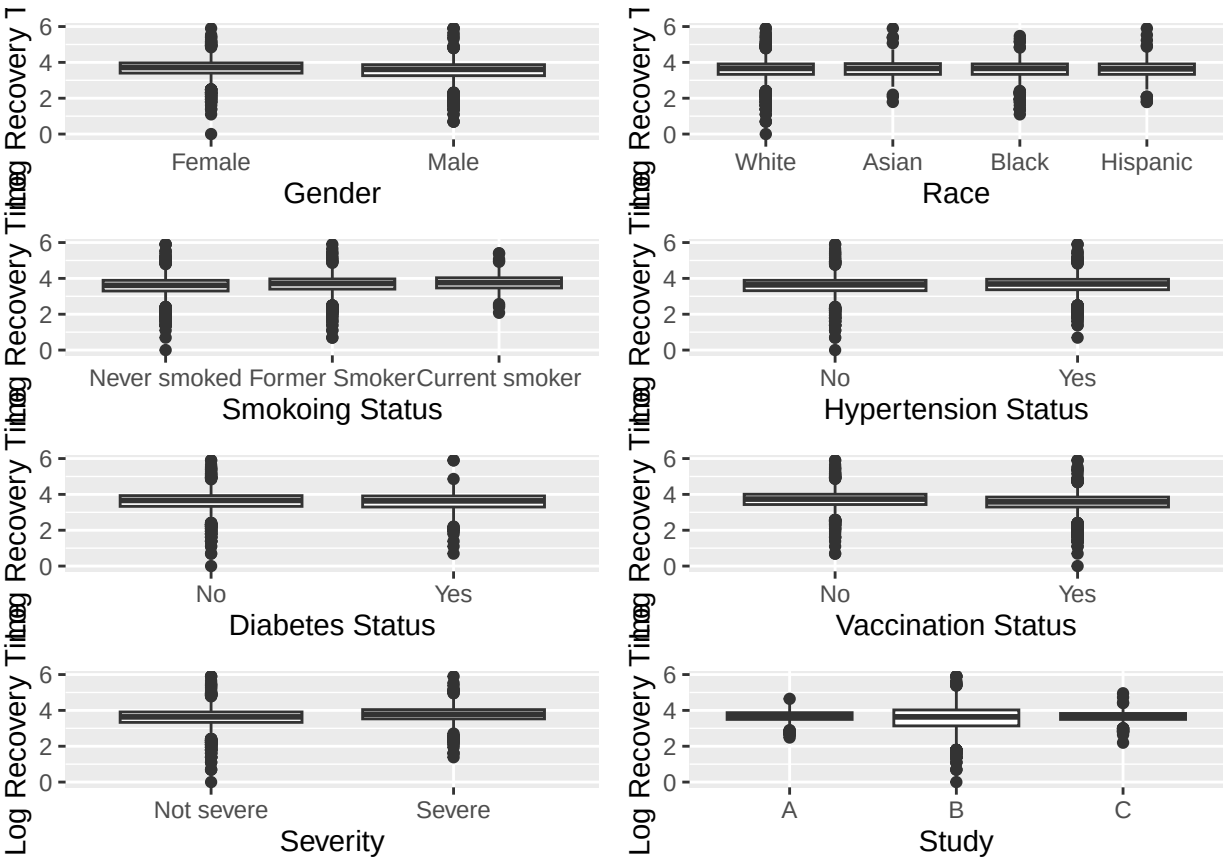
```
theme1 <- trellis.par.get()
theme1$plot.symbol$col <- rgb(.2, .4, .2, .5)
theme1$plot.symbol$pch <- 16
theme1$plot.line$col <- rgb(.8, .1, .1, 1)
theme1$plot.line$lwd <- 2
theme1$strip.background$col <- rgb(.0, .2, .6, .2)
trellis.par.set(theme1)

# plotting continuous predictors
featurePlot(x = model.matrix(lrecovery_time ~ ., dat_bind_primary)[trainRows,c("age", "SBP", "LDL", "he
            y = dat_bind_primary$lrecovery_time[trainRows],
            plot = "scatter",
            span = .5,
            labels = c("Predictors","Log(Y)"),
            type = c("p", "smooth"),
            layout = c(3,2))
```



Understand the relationship between categorical predictors and continuous outcome

```
gender3 = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = as.factor(gender), y = lrecovery_time)) + geom_boxplot() + labs(x = "Gender", y = "Log

race3 = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = as.factor(race), y = lrecovery_time)) + geom_boxplot() + labs(x = "Race", y = "Log Rec
  scale_x_discrete(labels = c("White", "Asian", "Black", "Hispanic"))

smoking3 = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = as.factor(smoking), y = lrecovery_time)) + geom_boxplot() + labs(x = "Smokoing Status"
  scale_x_discrete(labels = c("Never smoked", "Former Smoker", "Current smoker"))

hypertension3 = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = as.factor(hypertension), y = lrecovery_time)) + geom_boxplot() + labs(x = "Hypertensio
  scale_x_discrete(labels = c("No", "Yes"))

diabetes3 = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = as.factor(diabetes), y = lrecovery_time)) + geom_boxplot() + labs(x = "Diabetes Status
  scale_x_discrete(labels = c("No", "Yes"))

vaccine3 = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = as.factor(vaccine), y = lrecovery_time)) + geom_boxplot() + labs(x = "Vaccination Statu
  scale_x_discrete(labels = c("No", "Yes"))

severity3 = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = as.factor(severity), y = lrecovery_time)) + geom_boxplot() + labs(x = "Severity", y =
```

```
  scale_x_discrete(labels = c("Not severe", "Severe"))

study3 = (dat_bind_primary[trainRows, -1]) %>%
  ggplot(aes(x = as.factor(study), y = lrecovery_time)) + geom_boxplot() + labs(x = "Study", y = "Log Re

cat_combined_plot3 = ggarrange(gender3, race3, smoking3, hypertension3,
                               diabetes3, vaccine3, severity3, study3,
                          ncol = 2, nrow = 4)

cat_combined_plot3
```



Considering variables based on the EDA

From the correlation plot, we can observe that `bmi` is highly correlated with `weight` and `height`, which makes sense because BMI is calculated by weight divided by the square of height. This demonstrates collinearity between the variables.

We believe that the `study` variable is more of a geographical indicator to distinguish different study sites, and it will not be critical in predicting recovery time. Therefore, we will remove the `study` variable.

Lastly, we will remove variables `race` and `smoking` since we have created dummy variables for them and we will use the dummy variables in further analyses.

```
primary = dat_bind_primary %>%
  mutate(
  # create dummy variables for categorical variables
    # set up 3 dummy variables for `race`, reference = White:
```

```
        race_2 = ifelse(race == 2, 1, 0),
        race_3 = ifelse(race == 3, 1, 0),
        race_4 = ifelse(race == 4, 1, 0),
    # set up 2 dummy variables for `smoking`, reference = Never smoked:
        smoking_1 = ifelse(smoking == 1, 1, 0),
        smoking_2 = ifelse(smoking == 2, 1, 0))

# remove variables that will not be used
primary = primary %>%
  select(-study, -race, -smoking)

# partition again based on the new outcome variable
x <- model.matrix(lrecovery_time ~ ., primary)[trainRows,-1]

y <- primary$lrecovery_time[trainRows]

x2 <- model.matrix(lrecovery_time ~ ., primary)[-trainRows,-1]

y2 <- primary$lrecovery_time[-trainRows]

ctrl1 <- trainControl(method = "cv")
```

Primary analysis: continuous time to recovery

Model 1: Linear model

```
set.seed(2460)

lm.fit <- train(x, y,
                method = "glm",
                preProcess = c("center", "scale"),
                trControl = ctrl1)

summary(lm.fit)
```

```
##
## Call:
## NULL
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.4481  -0.2424   0.0685   0.3126   2.0007
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.601182   0.010003 360.010  < 2e-16 ***
## age           0.036999   0.011244   3.291  0.00101 **
## gender       -0.061087   0.010035  -6.088 1.30e-09 ***
## height        1.002011   0.103072   9.722  < 2e-16 ***
## weight       -1.279007   0.129968  -9.841  < 2e-16 ***
## bmi           1.509986   0.144853  10.424  < 2e-16 ***
## hypertension  0.036686   0.016726   2.193  0.02836 *
## diabetes     -0.008605   0.010030  -0.858  0.39098
```

```
## SBP          -0.001969   0.017667  -0.111  0.91125
## LDL          -0.009753   0.010504  -0.929  0.35320
## vaccine      -0.089295   0.010018  -8.914  < 2e-16 ***
## severity      0.049651   0.010029   4.951 7.83e-07 ***
## race_2        0.009397   0.010144   0.926  0.35432
## race_3       -0.006895   0.010253  -0.672  0.50134
## race_4        0.001614   0.010243   0.158  0.87481
## smoking_1     0.046423   0.010264   4.523 6.35e-06 ***
## smoking_2     0.053878   0.010270   5.246 1.67e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.287973)
##
##     Null deviance: 937.87  on 2877  degrees of freedom
## Residual deviance: 823.89  on 2861  degrees of freedom
## AIC: 4603.6
##
## Number of Fisher Scoring iterations: 2
```

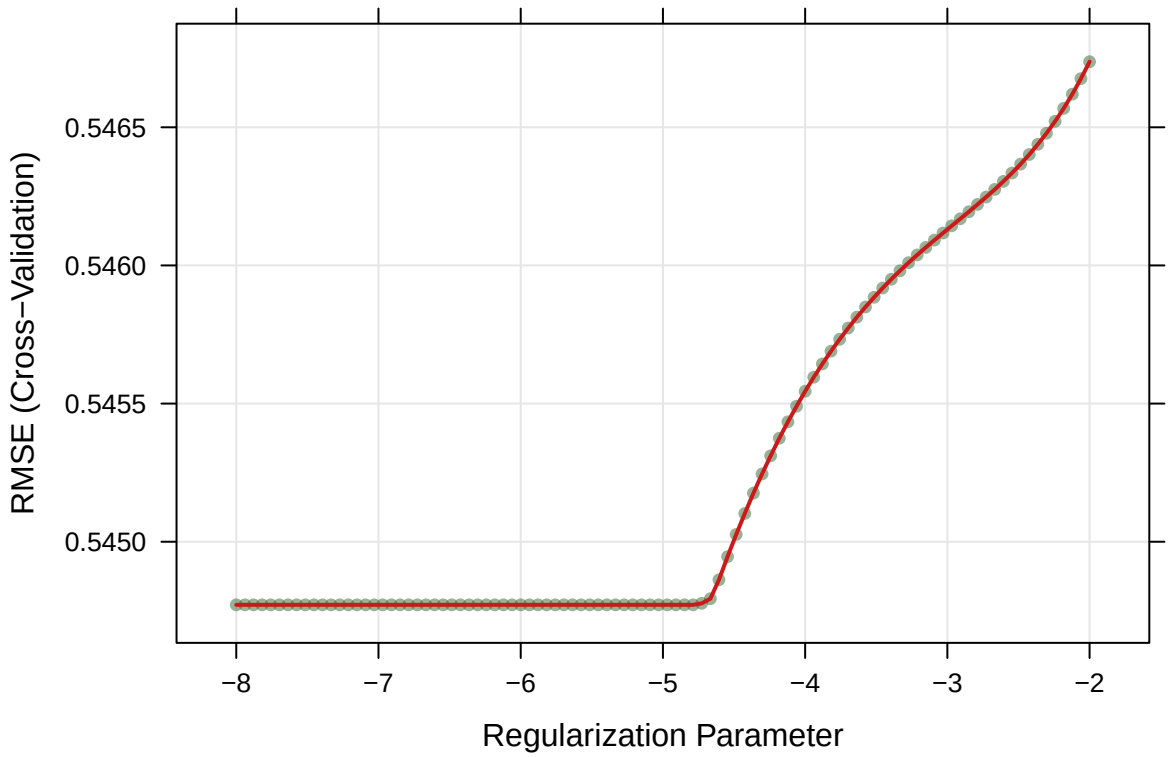
```
coef(lm.fit$finalModel) %>% round(2) %>%
  as.matrix() %>% as.data.frame() %>% View()
```

Model 2: Ridge

```
set.seed(2460)

ridge.fit <- train(x, y,
                   method = "glmnet",
                   tuneGrid = expand.grid(alpha = 0,
                                          lambda = exp(seq(-2, -8, length = 100))),
                   preProc = c("center", "scale"),
                   trControl = ctrl1)

ridge.fit$bestTune
```

```
##    alpha      lambda
## 54     0 0.008330109
```

```
plot(ridge.fit, xTrans = log)
```



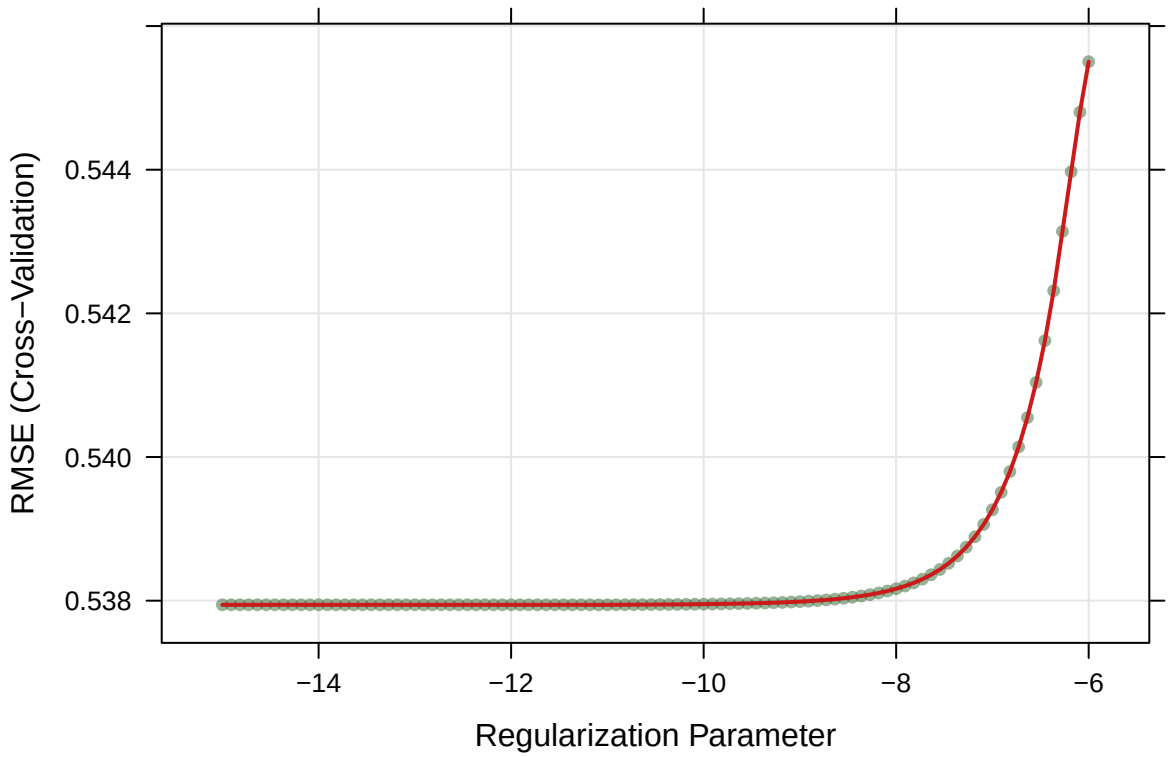

```
coef(ridge.fit$finalModel, s = ridge.fit$bestTune$lambda) %>%
  round(2) %>%
  as.matrix() %>% as.data.frame() %>% View()
```

Model 3: Lasso

```
set.seed(2460)

lasso.fit <- train(x, y,
                   method = "glmnet",
                   tuneGrid = expand.grid(alpha = 1,
                                          lambda = exp(seq(-15, -6, length = 100))),
                   preProcess = c("center", "scale"),
                   trControl = ctrl1)

lasso.fit$bestTune
```

```
##    alpha       lambda
## 44     1 1.525033e-05
```

```
plot(lasso.fit, xTrans = log)
```



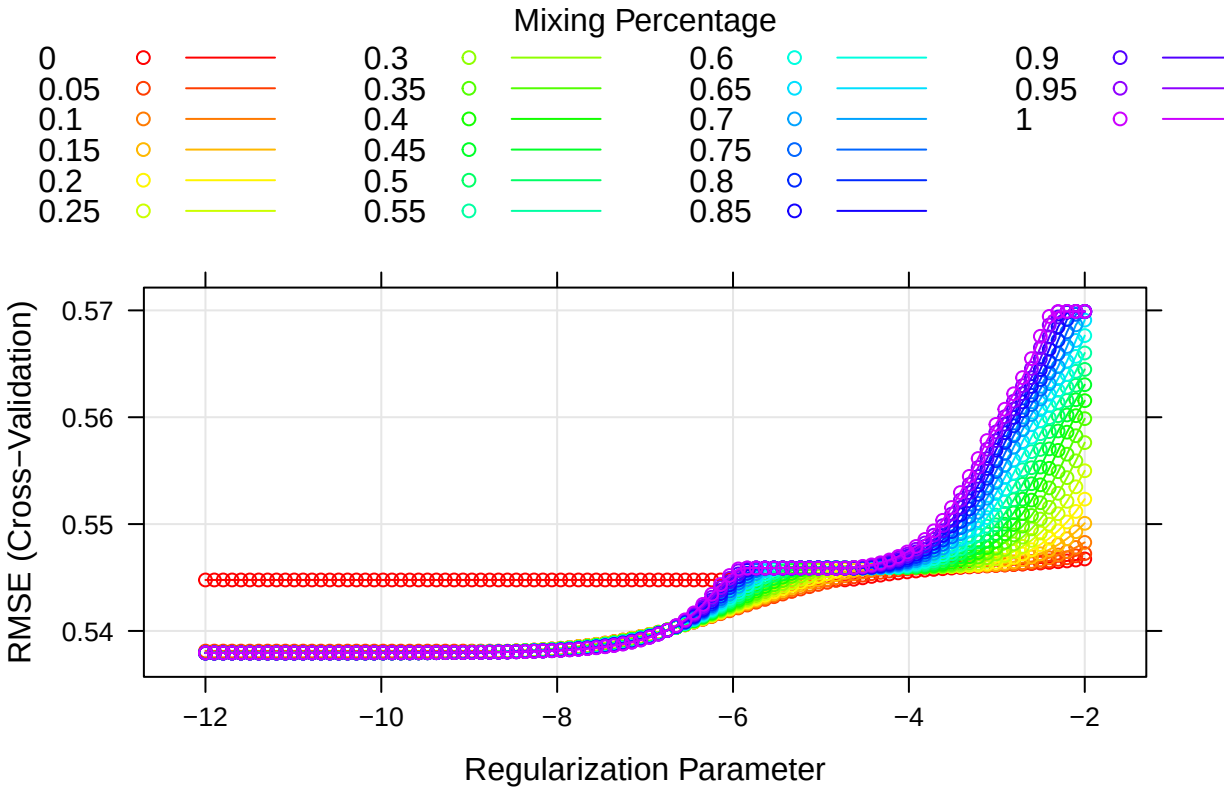

```
coef(lasso.fit$finalModel, s = lasso.fit$bestTune$lambda) %>%
  round(2) %>%
  as.matrix() %>% as.data.frame() %>% View()
```

Model 4: Elastic net

```
set.seed(2460)

enet.fit <- train(x, y,
                  method = "glmnet",
                  tuneGrid = expand.grid(alpha = seq(0, 1, length = 21),
                                         lambda = exp(seq(-12, -2,
                                                          length = 100))),
                  preProcess = c("center", "scale"),
                  trControl = ctrl1)

enet.fit$bestTune
```

```
##      alpha       lambda
## 1808   0.9 1.246072e-05
```

```
myCol <- rainbow(25)

myPar <- list(superpose.symbol = list(col = myCol),
              superpose.line = list(col = myCol))

plot(enet.fit, par.settings = myPar, xTrans = log)
```



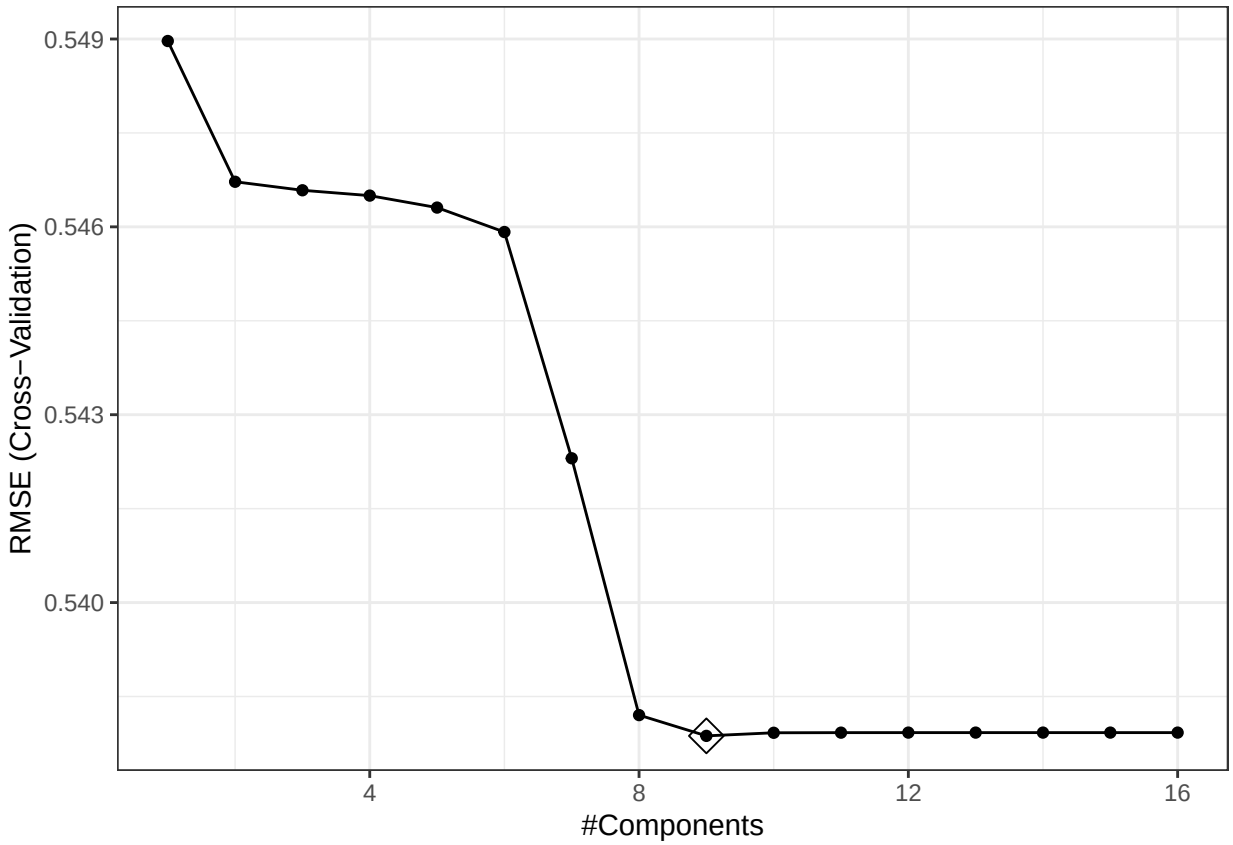

```
coef(enet.fit$finalModel, s = enet.fit$bestTune$lambda) %>%
  round(2) %>%
  as.matrix() %>% as.data.frame() %>% View()
```

Model 5: Partial least square

```
set.seed(2460)

pls.fit <- train(x, y,
                 method = "pls",
                 tuneGrid = data.frame(ncomp = 1:16),
                 trControl = ctrl1,
                 preProcess = c("center", "scale"))

pls.fit$bestTune
```

```
##   ncomp
## 9     9
```

```
ggplot(pls.fit, highlight = TRUE) + theme_bw()
```




```
summary(pls.fit)
```

```
## Data:    X dimension: 2878 16
##  Y dimension: 2878 1
## Fit method: oscorespls
## Number of components considered: 9
## TRAINING: % variance explained
##           1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps
## X           9.942   19.262   30.232   35.946   39.500   45.093    49.15
## .outcome    7.980    8.969    9.033    9.078    9.185    9.273    10.31
##           8 comps  9 comps
## X           51.69    57.20
## .outcome    12.06    12.15
```

```
coef(pls.fit$finalModel) %>% round(2) %>%
  as.matrix() %>% as.data.frame() %>% View()
```

Model 6: GAM

```
set.seed(2460)

gam.fit <- train(x, y,
                 method = "gam",
                 tuneGrid = data.frame(method = "GCV.Cp", select = c(TRUE,FALSE)),
                 preProcess = c("center", "scale"),
                 trControl = ctrl1)
```

```
gam.fit$bestTune
```

```
##   select method
## 1  FALSE GCV.Cp
```

```
gam.fit$finalModel
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ gender + hypertension + diabetes + vaccine + severity +
##     race_2 + race_3 + race_4 + smoking_1 + smoking_2 + s(age) +
##     s(SBP) + s(LDL) + s(bmi) + s(height) + s(weight)
##
## Estimated degrees of freedom:
## 1.00 1.00 1.89 6.33 1.00 1.00  total = 23.22
##
## GCV score: 0.2698475
```

```
summary(gam.fit)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ gender + hypertension + diabetes + vaccine + severity +
##     race_2 + race_3 + race_4 + smoking_1 + smoking_2 + s(age) +
##     s(SBP) + s(LDL) + s(bmi) + s(height) + s(weight)
##
## Parametric coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.6011822  0.0096439 373.414  < 2e-16 ***
## gender       -0.0596870  0.0096791  -6.167 7.96e-10 ***
## hypertension  0.0452988  0.0161533   2.804  0.00508 **
## diabetes     -0.0040637  0.0096880  -0.419  0.67491
## vaccine      -0.0894786  0.0096702  -9.253  < 2e-16 ***
## severity      0.0452155  0.0096825   4.670 3.15e-06 ***
## race_2        0.0028659  0.0098071   0.292  0.77014
## race_3       -0.0052124  0.0098904  -0.527  0.59822
## race_4        0.0002138  0.0098871   0.022  0.98275
## smoking_1     0.0496972  0.0099135   5.013 5.68e-07 ***
## smoking_2     0.0572652  0.0099145   5.776 8.48e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##             edf Ref.df      F p-value
## s(age)    1.000  1.000 10.180 0.00143 **
## s(SBP)    1.000  1.000  0.118 0.73090
## s(LDL)    1.890  2.414  1.318 0.24710
## s(bmi)    6.332  7.422 44.640 < 2e-16 ***
## s(height) 1.000  1.000  1.631 0.20171
```

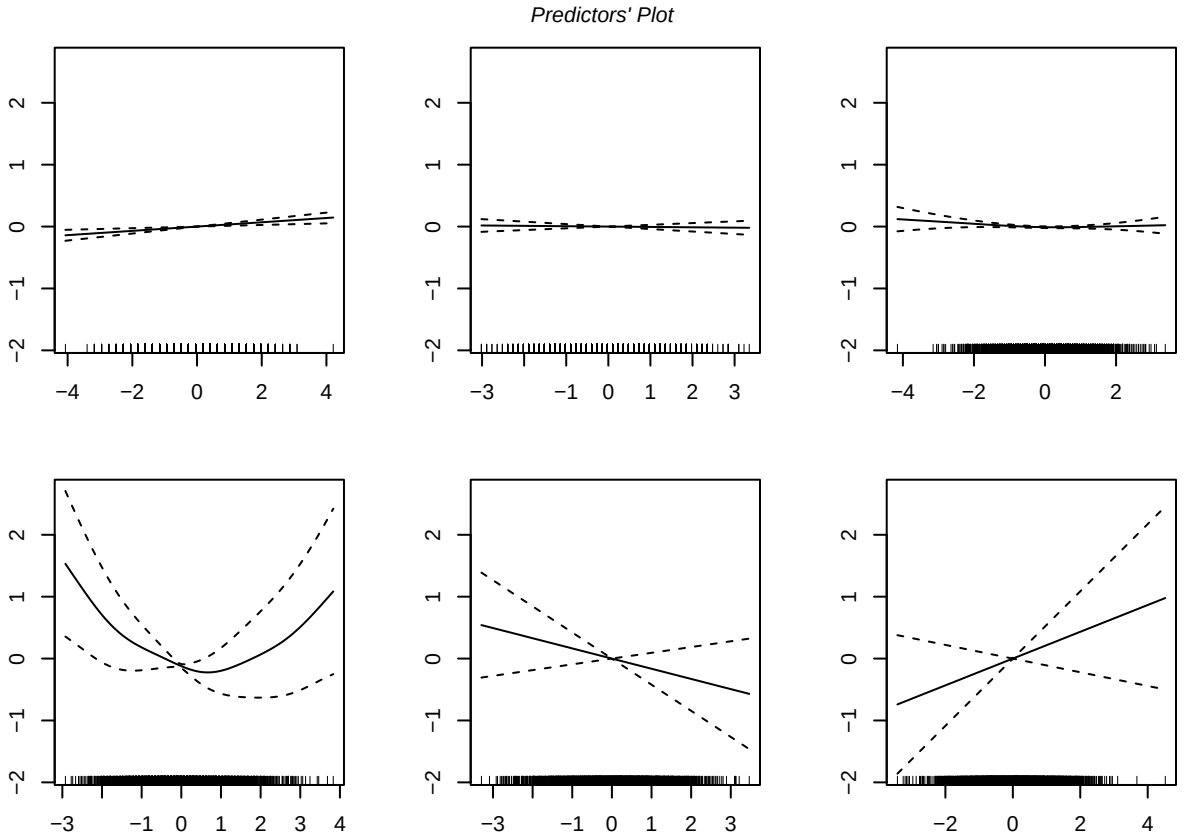
```
## s(weight) 1.000  1.000  1.752 0.18568
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.179   Deviance explained = 18.5%
## GCV = 0.26985  Scale est. = 0.26767   n = 2878
```

Plot continuous predictors in GAM

```
var.names <- c("age", "SBP", "LDL", "bmi", "height", "weight")

# make a matrix for easier comprehension of the plot with 16 predictors
matrix <- matrix(var.names, nrow = 2, ncol = 3, byrow = TRUE)

# use the matrix to correspond each plot with each predictor
print(matrix)
```

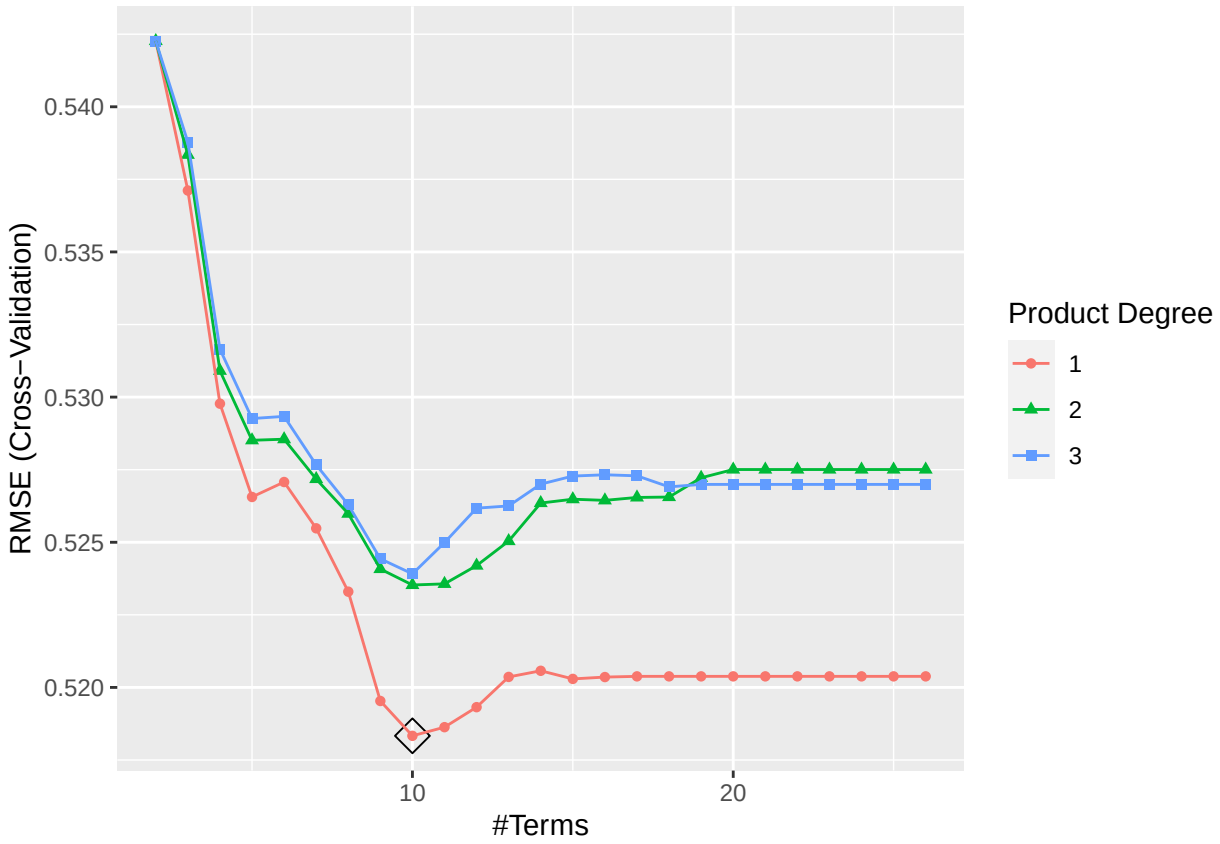
```
##      [,1]  [,2]     [,3]
## [1,] "age" "SBP"    "LDL"
## [2,] "bmi" "height" "weight"
```

```
gam.plot <- gam.fit$finalModel

# make 16 plots into one
par(mar = c(3, 3, 2, 2), mfrow = c(2, 3))

plot(gam.plot)

title(main = "Predictors' Plot", cex.main = 1, font.main = 3, outer = TRUE, line = -1)
```



Model 7: MARS

```
mars_grid <- expand.grid(degree = 1:3,
                         nprune = 2:26)

set.seed(2460)

mars.fit <- train(x, y,
                  method = "earth",
                  tuneGrid = mars_grid,
                  preProcess = c("center", "scale"),
                  trControl = ctrl1)

ggplot(mars.fit, highlight = TRUE)
```




```
mars.fit$bestTune
```

```
##   nprune degree
## 9     10      1
```

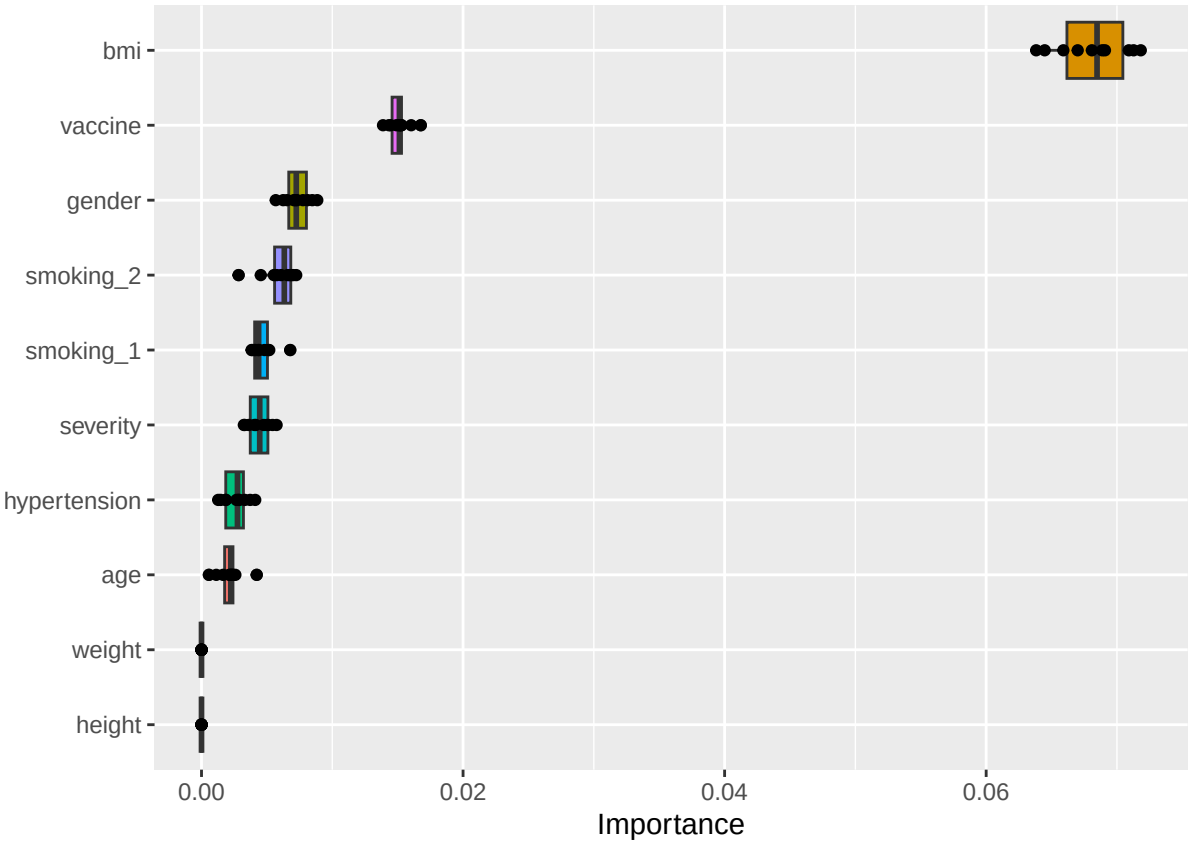
```
summary(mars.fit)
```

```
## Call: earth(x=matrix[2878,16], y=c(3.584,3.761,3...), keepxy=TRUE, degree=1,
##             nprune=10)
##
##                   coefficients
## (Intercept)         2.32744078
## gender             -0.06033598
## hypertension        0.03804629
## vaccine            -0.08929877
## severity            0.04637756
## smoking_1           0.04943934
## smoking_2           0.05566747
## h(age- -2.7261)     0.03261911
## h(bmi- -1.4908)     0.49599535
## h(0.638255-bmi)     0.53847499
##
## Selected 10 of 19 terms, and 8 of 16 predictors (nprune=10)
## Termination condition: RSq changed by less than 0.001 at 19 terms
## Importance: bmi, vaccine, gender, hypertension, smoking_2, smoking_1, ...
## Number of terms at each degree of interaction: 1 9 (additive model)
## GCV 0.2705204    RSS 768.3118    GRSq 0.170441    RSq 0.1807888
```

```
coef(mars.fit$finalModel) %>% round(2) %>%
  as.matrix() %>% as.data.frame() %>% View()
```

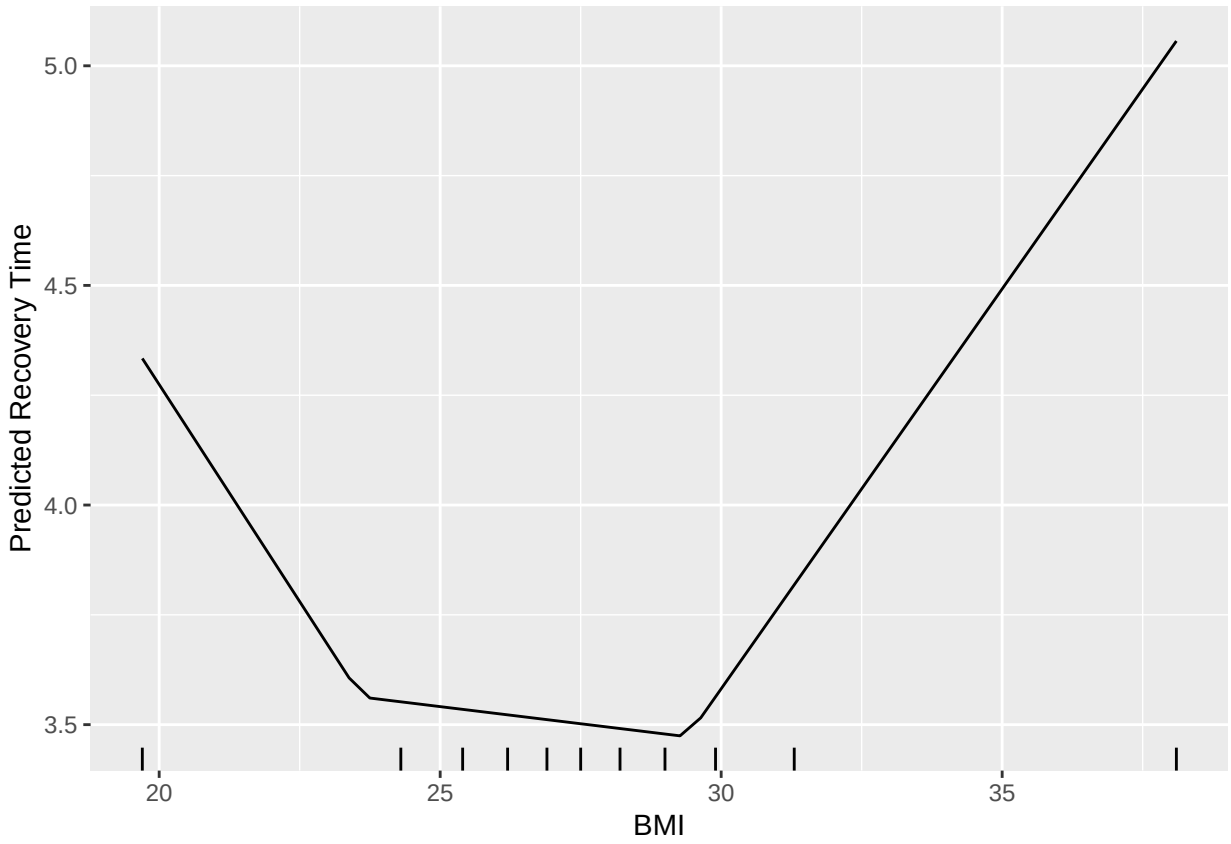
Variable importance

```
vip(mars.fit,
    method = "permute",
    train = primary[trainRows,],
    target = "lrecovery_time",
    metric = "RMSE",
    nsim = 10,
    pred_wrapper = predict,
    geom = "boxplot",
    all_permutations = TRUE,
    mapping = aes_string(fill = "Variable"))
```



Partial dependence

```
pdp1 <- mars.fit %>%
  partial(pred.var = c("bmi")) %>%
  autoplot(train = primary[trainRows,], rug = TRUE,
           xlab = "BMI", ylab = "Predicted Recovery Time")

pdp1
```

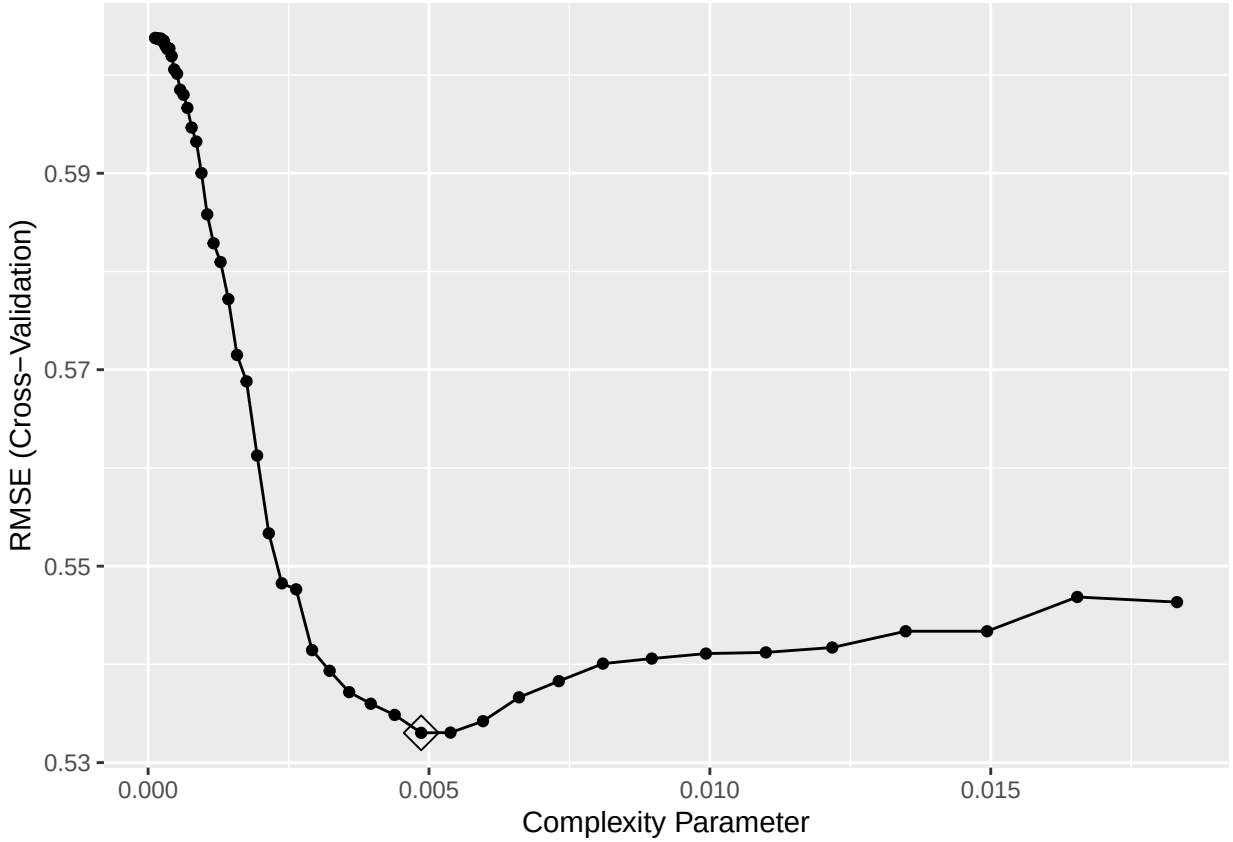


Model 8: Regression tree

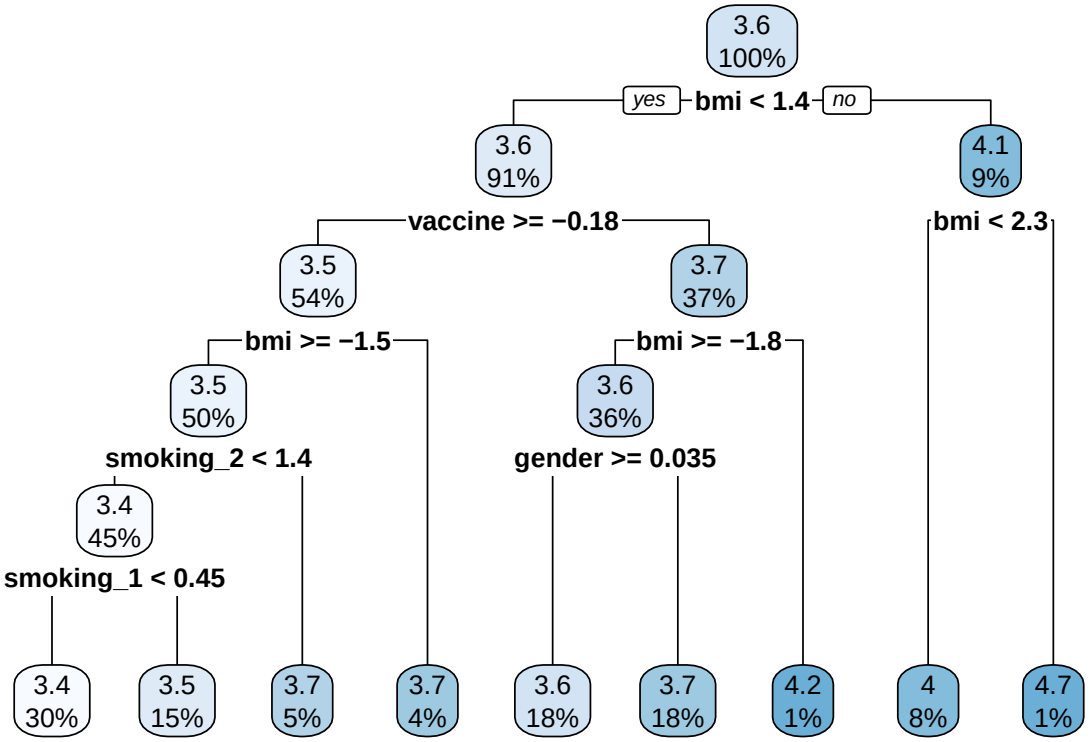
```
set.seed(2460)

rpart.fit <- train(lrecovery_time ~ . ,
                   primary[trainRows,],
                   method = "rpart",
                   tuneGrid = data.frame(cp = exp(seq(-9,-4, length = 50))),
                   trControl = ctrl1,
                   preProcess = c("center", "scale"))

rpart.fit$bestTune
```

```
##             cp
## 37 0.004860905
```

```
ggplot(rpart.fit, highlight = TRUE)
```




```
rpart.plot(rpart.fit$finalModel)
```

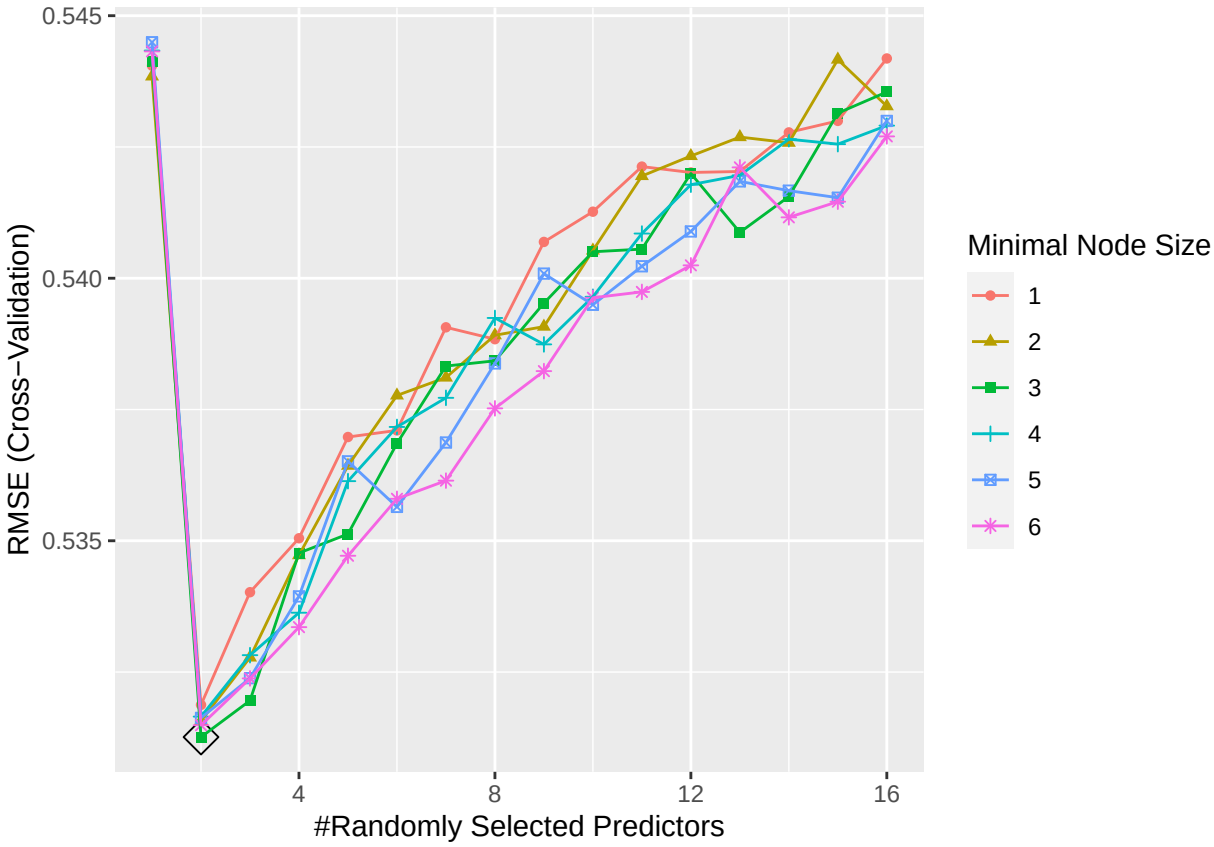


Model 9: Random forest

```
rf.grid <- expand.grid(mtry = 1:16, #16 predictors
                       splitrule = "variance",
                       min.node.size = 1:6)

set.seed(2460)

rf.fit <- train(lrecovery_time ~ . ,
                primary[trainRows,],
                method = "ranger",
                tuneGrid = rf.grid,
                trControl = ctrl1,
                preProcess = c("center", "scale"))

rf.fit$bestTune
```

```
##   mtry splitrule min.node.size
## 9    2  variance             3
```

```
ggplot(rf.fit, highlight = TRUE)
```



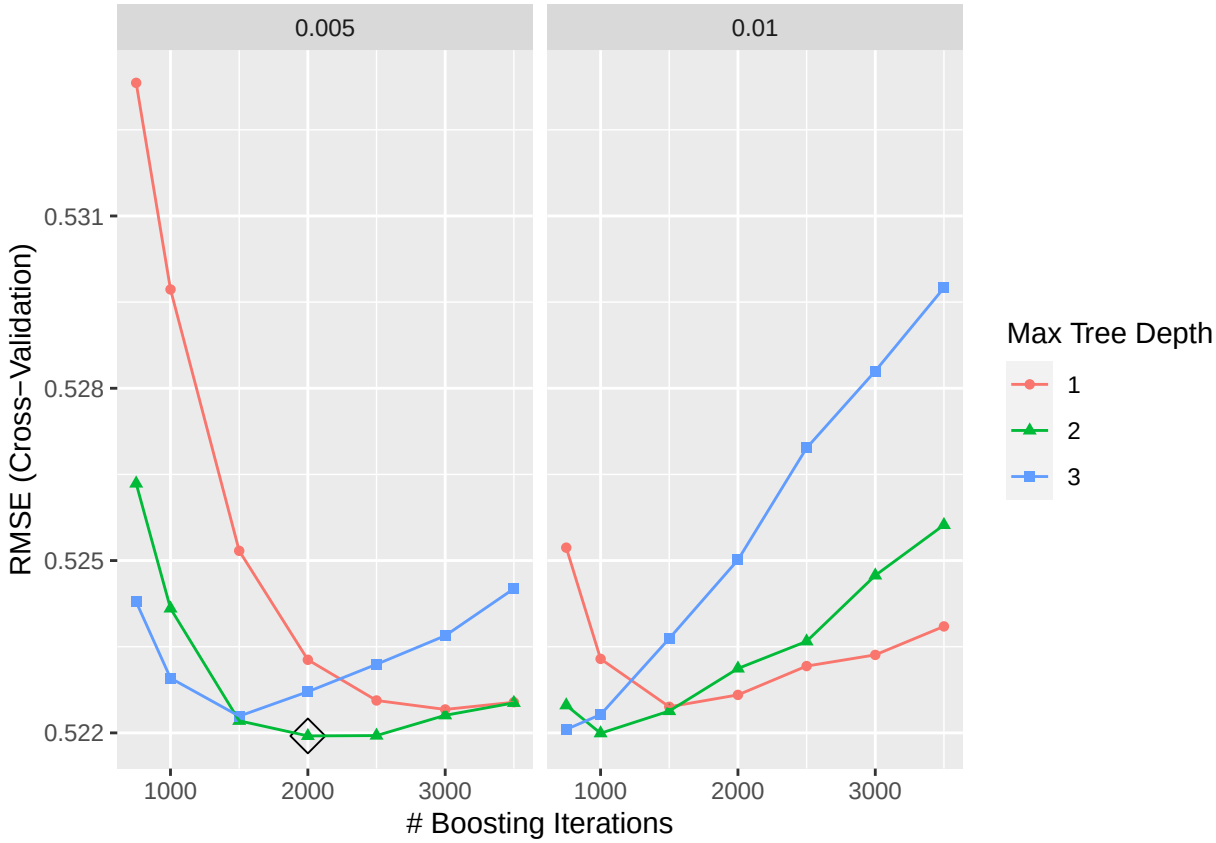
Model 10: Boosting

```
gbm.grid <- expand.grid(n.trees = c(750,1000,1500,2000,2500,3000,3500),
                        interaction.depth = 1:3,
                        shrinkage = c(0.005,0.01),
```

```
                        n.minobsinnode = c(1))

set.seed(2460)

gbm.fit <- train(lrecovery_time ~ . ,
                 primary[trainRows,],
                 method = "gbm",
                 tuneGrid = gbm.grid,
                 trControl = ctrl1,
                 preProcess = c("center", "scale"),
                 verbose = F)

gbm.fit$bestTune
```

```
##    n.trees interaction.depth shrinkage n.minobsinnode
## 11    2000                 2     0.005              1
```

```
ggplot(gbm.fit, highlight = T)
```



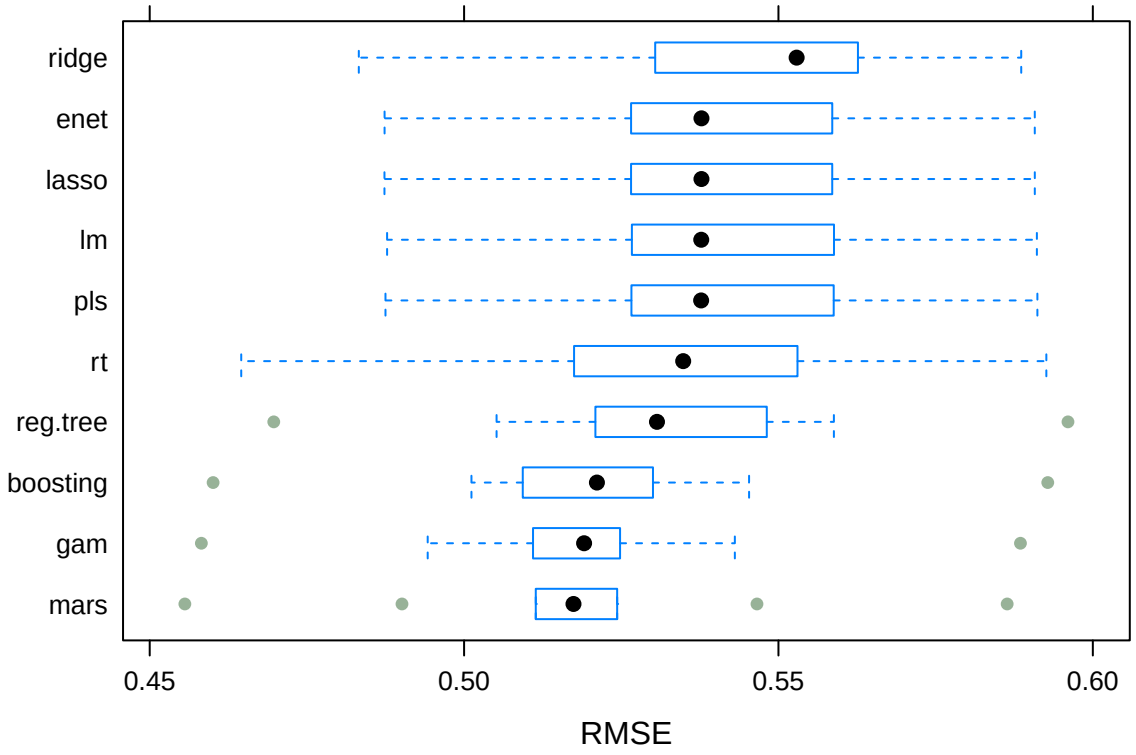
Model comparison

```
res_pri <- resamples(list(lm = lm.fit,
                          ridge = ridge.fit,
                          lasso = lasso.fit,
                          enet = enet.fit,
                          pls = pls.fit,
                          gam = gam.fit,
```

```
                          mars = mars.fit,
                          reg.tree = rpart.fit,
                          rt = rf.fit,
                          boosting = gbm.fit))

summary(res_pri)
```

```
##
## Call:
## summary.resamples(object = res_pri)
##
## Models: lm, ridge, lasso, enet, pls, gam, mars, reg.tree, rt, boosting
## Number of resamples: 10
##
## MAE
##                Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## lm       0.3715813 0.3801875 0.3891606 0.3905957 0.3974587 0.4168473    0
## ridge    0.3668470 0.3845314 0.3995422 0.3946062 0.4045918 0.4198322    0
## lasso    0.3711375 0.3801672 0.3895606 0.3905287 0.3973617 0.4166310    0
## enet     0.3711532 0.3801696 0.3895537 0.3905287 0.3973633 0.4166282    0
## pls      0.3714900 0.3799257 0.3891460 0.3905299 0.3973980 0.4169598    0
## gam      0.3563440 0.3714600 0.3789665 0.3798054 0.3835986 0.4138882    0
## mars     0.3544547 0.3736366 0.3756004 0.3794879 0.3851627 0.4114350    0
## reg.tree 0.3683618 0.3840758 0.3895214 0.3920198 0.3996331 0.4230047    0
## rt       0.3574498 0.3787421 0.3839666 0.3858224 0.3931670 0.4154785    0
## boosting 0.3547992 0.3734574 0.3788330 0.3804563 0.3846729 0.4107268    0
##
## RMSE
##                Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## lm       0.4877568 0.5282710 0.5377199 0.5379234 0.5550979 0.5911010    0
## ridge    0.4832580 0.5336716 0.5528909 0.5447716 0.5625358 0.5886115    0
## lasso    0.4873377 0.5284287 0.5377526 0.5379422 0.5549924 0.5907703    0
## enet     0.4873523 0.5284252 0.5377535 0.5379415 0.5549939 0.5907646    0
## pls      0.4874998 0.5282229 0.5377011 0.5378712 0.5551181 0.5911807    0
## gam      0.4582162 0.5116572 0.5190892 0.5195132 0.5244718 0.5884876    0
## mars     0.4555906 0.5116768 0.5174001 0.5183330 0.5236598 0.5863775    0
## reg.tree 0.4697322 0.5212018 0.5306794 0.5330292 0.5481066 0.5960468    0
## rt       0.4645553 0.5195229 0.5348479 0.5312617 0.5502635 0.5926060    0
## boosting 0.4600815 0.5101843 0.5211270 0.5219467 0.5289549 0.5928327    0
##
## Rsquared
##                 Min.    1st Qu.     Median       Mean   3rd Qu.      Max. NA's
## lm       0.07232202 0.08974674 0.10383362 0.11176919 0.1148894 0.1869123    0
## ridge    0.04866936 0.07546233 0.09240669 0.08803606 0.1037300 0.1154734    0
## lasso    0.07186500 0.09029708 0.10464976 0.11155582 0.1154413 0.1835720    0
## enet     0.07185371 0.09027505 0.10465331 0.11156003 0.1154374 0.1836312    0
## pls      0.07234132 0.09032163 0.10396846 0.11191446 0.1156243 0.1867030    0
## gam      0.10946228 0.11793949 0.17278765 0.17183125 0.2129779 0.2538031    0
## mars     0.11528609 0.12615126 0.17235247 0.17567557 0.2128120 0.2518032    0
## reg.tree 0.05815617 0.08599073 0.12448333 0.13064566 0.1460979 0.2345080    0
## rt       0.07965616 0.10426967 0.13226751 0.13957112 0.1801431 0.2003045    0
## boosting 0.09382376 0.10886935 0.16338729 0.16429301 0.2016713 0.2678397    0
```

```
bwplot(res_pri, metric = "RMSE")
```



Select final model

Since MARS model has the lowest mean RMSE, we selected it as our final model.

Test error

```
mars.pred <- predict(mars.fit, newdata = x2)

mars.testerror = mean((mars.pred - y2)^2)

mars.testerror
```

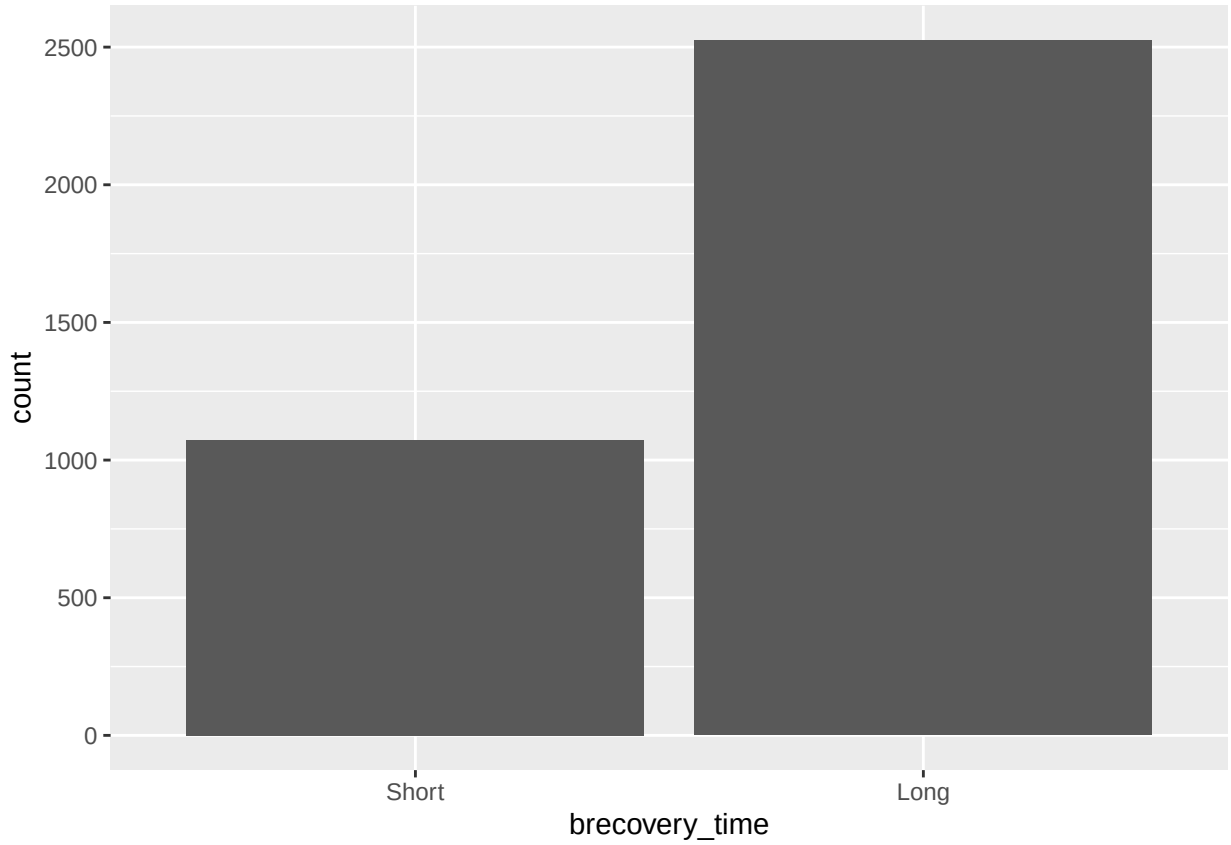
```
## [1] 0.2915917
```

Secondary analysis: binary time to recovery

Set up

```
# make binary outcome
dat_bind_secondary = dat_bind %>%
  na.omit(dat_bind) %>%
  mutate(brecovery_time = ifelse(recovery_time > 30, 1, 0)) %>%
  mutate(brecovery_time = as.factor(brecovery_time)) %>%
  mutate(brecovery_time = dplyr::recode(brecovery_time,
                                        "1" = "Long", "0" = "Short")) %>%
  dplyr::select(-recovery_time, -id)
```

```
# lets check the distribution
binary = dat_bind_secondary %>%
  ggplot(aes(x = brecovery_time)) + geom_bar()

binary
```



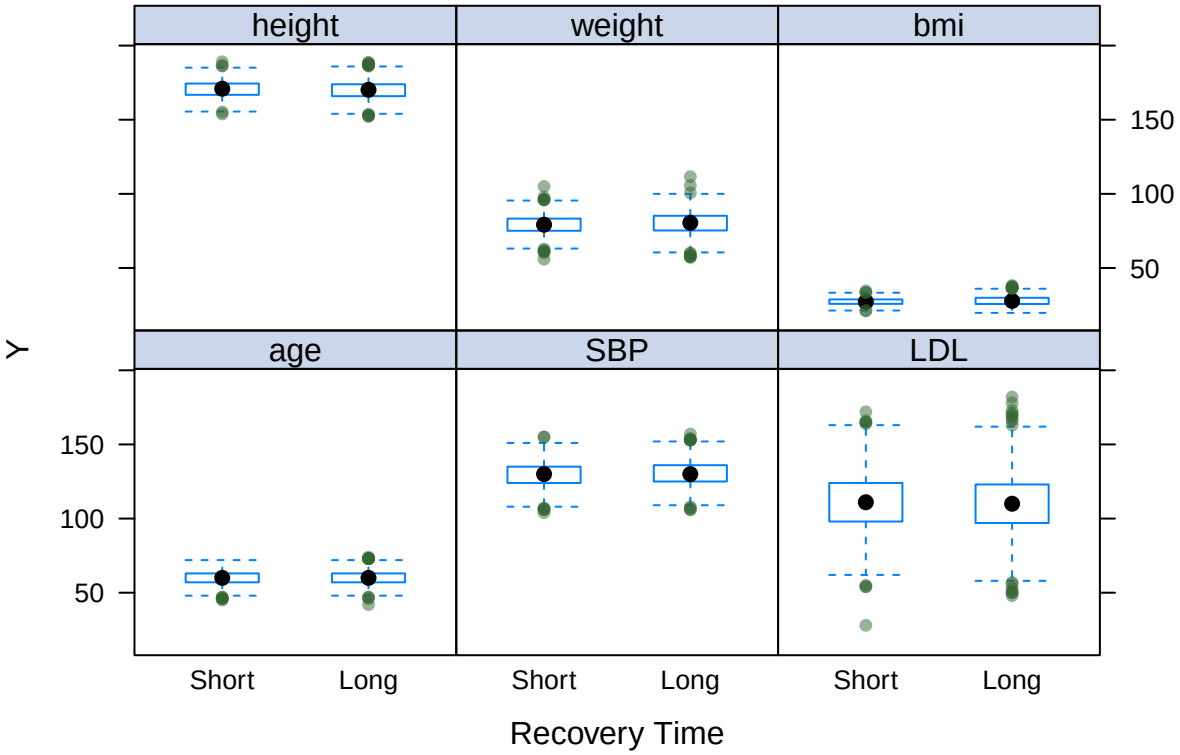

```
# partition again based on the new outcome variable
set.seed(2460)

trainRows_sec <- createDataPartition(y = dat_bind_secondary$brecovery_time, p = 0.8, list = FALSE)

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

contrasts(dat_bind_secondary$brecovery_time)
```

```
##       Long
## Short    0
## Long     1
```

Understand the relationship between continuous predictors and the binary outcome

```
theme1 <- trellis.par.get()
theme1$plot.symbol$col <- rgb(.2, .4, .2, .5)
theme1$plot.symbol$pch <- 16
```

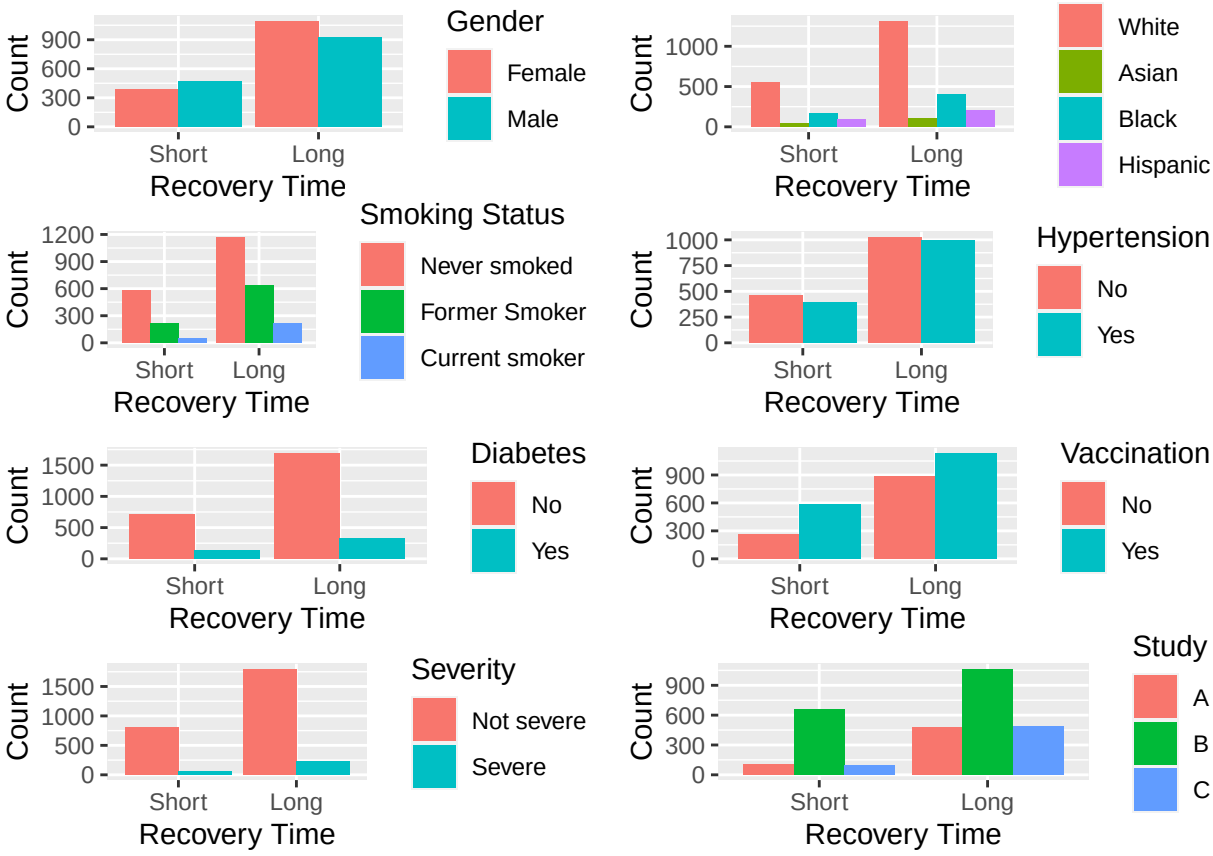
```
theme1$plot.line$col <- rgb(.8, .1, .1, 1)
theme1$plot.line$lwd <- 2
theme1$strip.background$col <- rgb(.0, .2, .6, .2)
trellis.par.set(theme1)

# plotting continuous predictors
featurePlot(x = model.matrix(brecovery_time ~ ., dat_bind_secondary)[trainRows_sec,c("age", "SBP", "LDL
            y = dat_bind_secondary$brecovery_time[trainRows_sec],
            plot = "box",
            span = .5,
            labels = c("Recovery Time","Y"),
            layout = c(3,2))
```



Understand the relationship between categorical predictors and the binary outcome

```
gender2 = (dat_bind_secondary[trainRows_sec, -1]) %>%
  ggplot(aes(x = brecovery_time, fill = as.factor(gender), group = as.factor(gender))) + geom_bar(posit
  scale_fill_discrete(labels = c("Female", "Male"))


race2 = (dat_bind_secondary[trainRows_sec, -1]) %>%
  ggplot(aes(x = brecovery_time, fill = as.factor(race), group = as.factor(race))) + geom_bar(position =
  scale_fill_discrete(labels = c("White", "Asian", "Black", "Hispanic"))

smoking2 = (dat_bind_secondary[trainRows_sec, -1]) %>%
  ggplot(aes(x = brecovery_time, fill = as.factor(smoking), group = as.factor(smoking))) + geom_bar(posi
  scale_fill_discrete(labels = c("Never smoked", "Former Smoker", "Current smoker"))
```

```r
hypertension2 = (dat_bind_secondary[trainRows_sec, -1]) %>%
  ggplot(aes(x = brecovery_time, fill = as.factor(hypertension), group = as.factor(hypertension))) + ge
  scale_fill_discrete(labels = c("No", "Yes"))

diabetes2 = (dat_bind_secondary[trainRows_sec, -1]) %>%
  ggplot(aes(x = brecovery_time, fill = as.factor(diabetes), group = as.factor(diabetes))) + geom_bar(p
  scale_fill_discrete(labels = c("No", "Yes"))

vaccine2 = (dat_bind_secondary[trainRows_sec, -1]) %>%
  ggplot(aes(x = brecovery_time, fill = as.factor(vaccine), group = as.factor(vaccine))) + geom_bar(pos
  scale_fill_discrete(labels = c("No", "Yes"))

severity2 = (dat_bind_secondary[trainRows_sec, -1]) %>%
  ggplot(aes(x = brecovery_time, fill = as.factor(severity), group = as.factor(severity))) + geom_bar(p
  scale_fill_discrete(labels = c("Not severe", "Severe"))

study2 = (dat_bind_secondary[trainRows_sec, -1]) %>%
  ggplot(aes(x = brecovery_time, fill = as.factor(study), group = as.factor(study))) + geom_bar(positio

cat_combined_plot2 = ggarrange(gender2, race2, smoking2, hypertension2,
                               diabetes2, vaccine2, severity2, study2,
                          ncol = 2, nrow = 4)

cat_combined_plot2
```



Make dummy variables

```
# dummy variable creation

secondary = dat_bind_secondary %>%
  mutate(
  # create dummy variables for categorical variables
    # set up 3 dummy variables for `race`, reference = White:
         race_2 = ifelse(race == 2, 1, 0),
         race_3 = ifelse(race == 3, 1, 0),
         race_4 = ifelse(race == 4, 1, 0),
    # set up 2 dummy variables for `smoking`, reference = Never smoked:
         smoking_1 = ifelse(smoking == 1, 1, 0),
         smoking_2 = ifelse(smoking == 2, 1, 0))

# remove variables that will not be used
secondary = secondary %>%
  dplyr::select(-study, -race, -smoking) %>%
  dplyr::select(brecovery_time, everything()) #arrange variable orders
```

Model 1: Logistic regression

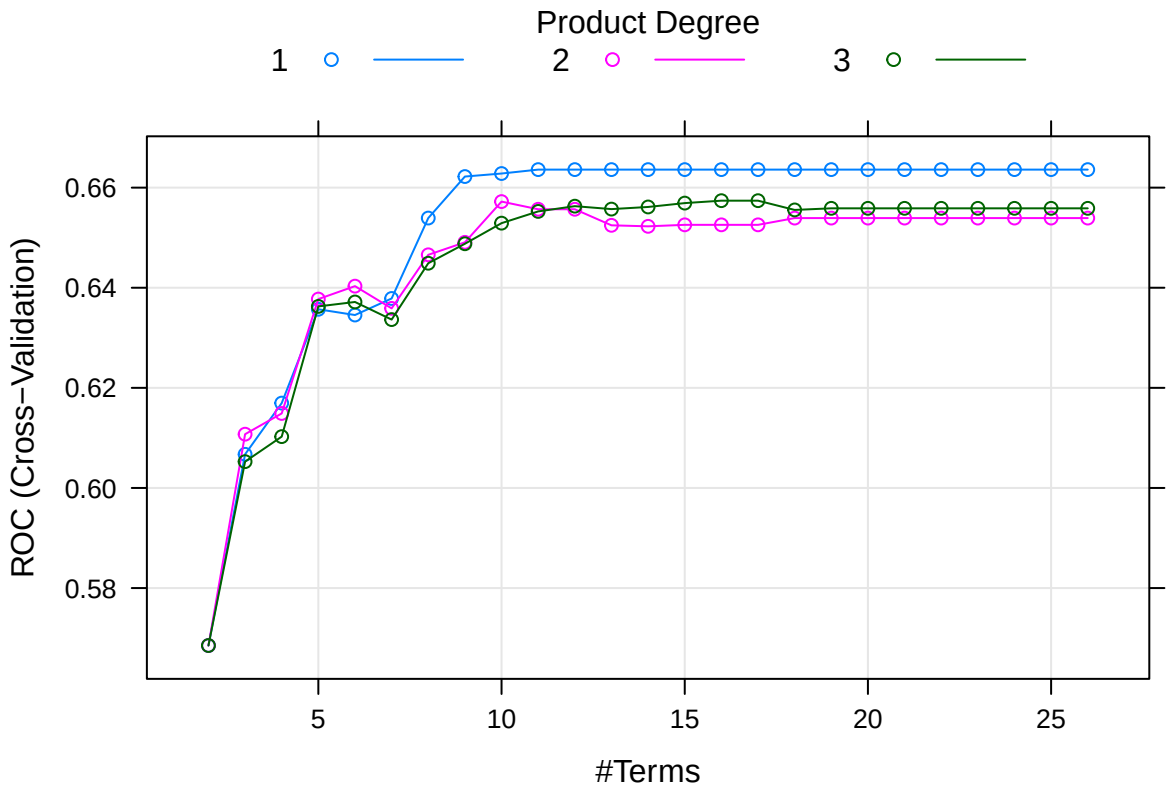
```
set.seed(2460)

model.glm <- train(x = secondary[trainRows_sec,2:17],
                   y = secondary$brecovery_time[trainRows_sec],
                   method = "glm",
                   metric = "ROC",
                   trControl = ctrl2,
                   preProcess = c("center", "scale"))

summary(model.glm)
```

```
##
## Call:
## NULL
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.2831  -1.2567   0.6816   0.8716   1.4994
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.926893   0.043431  21.342  < 2e-16 ***
## age           0.168966   0.047345   3.569 0.000359 ***
## gender       -0.193910   0.042180  -4.597 4.28e-06 ***
## height        2.142077   0.468179   4.575 4.75e-06 ***
## weight       -2.740050   0.594517  -4.609 4.05e-06 ***
## bmi           3.330127   0.677136   4.918 8.74e-07 ***
## hypertension -0.009330   0.070639  -0.132 0.894924
## diabetes     -0.014487   0.041995  -0.345 0.730121
## SBP           0.051686   0.074248   0.696 0.486350
## LDL          -0.084622   0.043824  -1.931 0.053489 .
## vaccine      -0.277714   0.043300  -6.414 1.42e-10 ***
```

```
## severity      0.199213   0.047867   4.162 3.16e-05 ***
## race_2       -0.014534   0.042492  -0.342 0.732321
## race_3       -0.002099   0.043042  -0.049 0.961097
## race_4       -0.021811   0.042819  -0.509 0.610494
## smoking_1     0.174926   0.043862   3.988 6.66e-05 ***
## smoking_2     0.202077   0.047815   4.226 2.38e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3506.9  on 2877  degrees of freedom
## Residual deviance: 3323.4  on 2861  degrees of freedom
## AIC: 3357.4
##
## Number of Fisher Scoring iterations: 4
```

Model 2: MARS

```
set.seed(2460)

model.mars <- train(x = secondary[trainRows_sec,2:17],
                    y = secondary$brecovery_time[trainRows_sec],
                    method = "earth",
                    tuneGrid = expand.grid(degree = 1:3,
                                           nprune = 2:26),
                    metric = "ROC",
                    trControl = ctrl2,
                    preProcess = c("center", "scale"))

plot(model.mars)
```




```
model.mars$bestTune
```

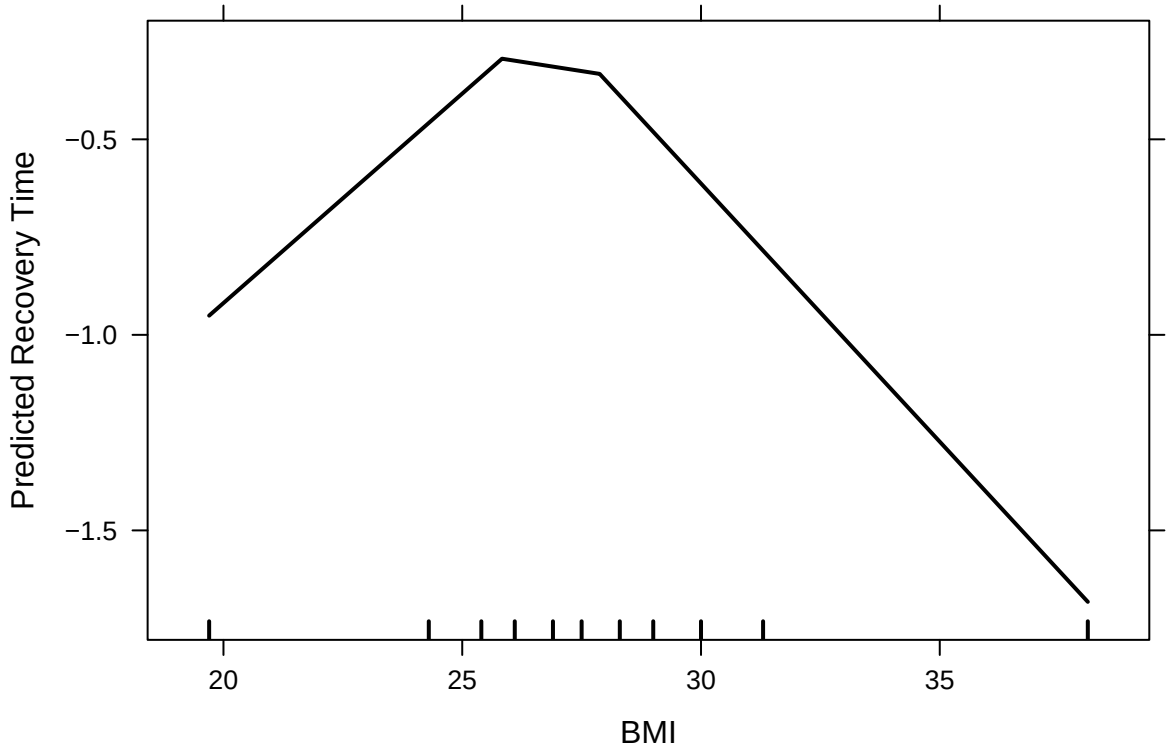
```
##    nprune degree
## 10     11      1
```

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

```
##       (Intercept) h(bmi- -0.320384)  h(-0.320384-bmi)           vaccine
##         0.06779826        0.73070555        0.59261712       -0.28696690
##             gender  h(age- -1.83762)   h(-1.83762-age)          severity
##        -0.20048727        0.15362456       -0.82201440        0.19998994
##          smoking_2          smoking_1  h(-0.675495-LDL)
##         0.20415317        0.18700246        0.27088201
```

Partial dependence

```
pdp2 <- pdp::partial(model.mars,
                     pred.var = c("bmi"),
                     grid.resolution = 10) %>%
  plotPartial(train = secondary[trainRows_sec,], rug = TRUE,
              xlab = "BMI", ylab = "Predicted Recovery Time")

pdp2
```



Model 3: LDA

```
set.seed(2460)

model.lda <- train(x = secondary[trainRows_sec,2:17],
                   y = secondary$brecovery_time[trainRows_sec],
                   method = "lda",
                   metric = "ROC",
                   trControl = ctrl2,
                   preProcess = c("center", "scale"))

summary(model.lda)
```

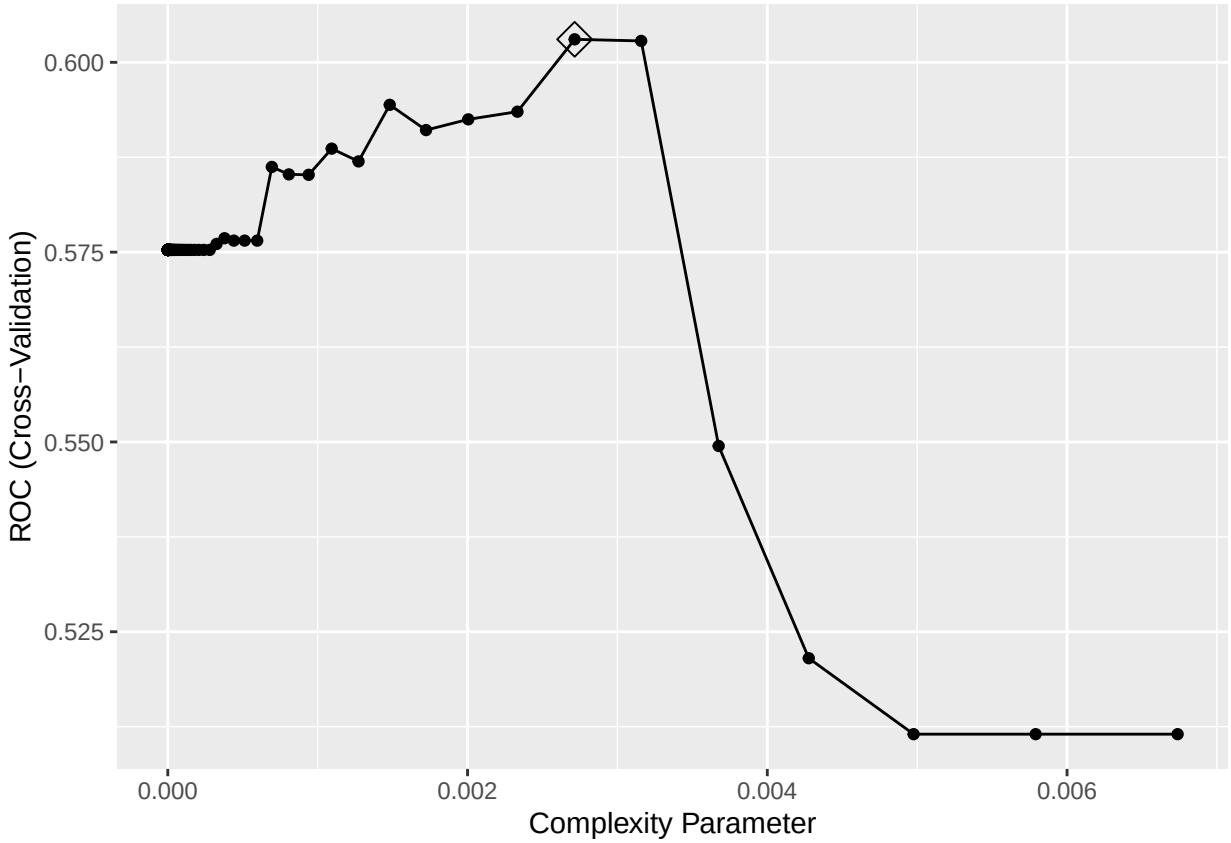
```
##             Length Class      Mode
## prior        2     -none-     numeric
## counts       2     -none-     numeric
## means       32     -none-     numeric
## scaling     16     -none-     numeric
## lev          2     -none-     character
## svd          1     -none-     numeric
## N            1     -none-     numeric
## call         3     -none-     call
## xNames      16     -none-     character
## problemType  1     -none-     character
## tuneValue    1     data.frame list
## obsLevels    2     -none-     character
## param        0     -none-     list
```

Model 4: Classification tree

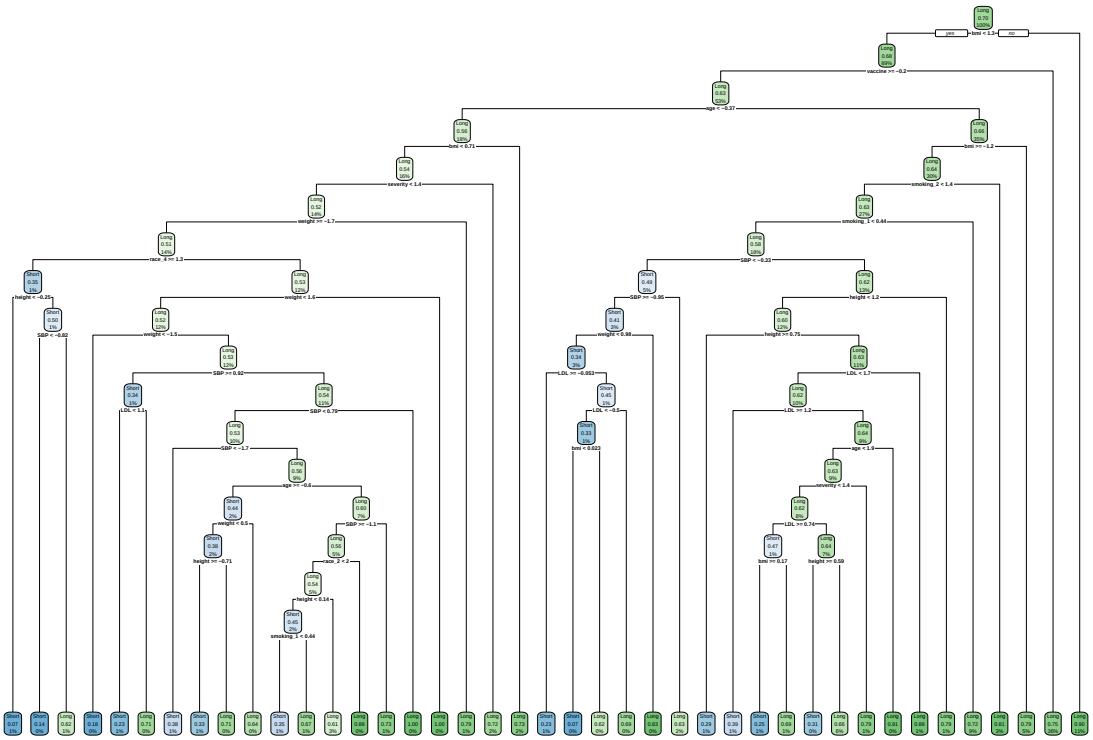
```
set.seed(2460)

model.rpart <- train(brecovery_time ~ . , secondary,
                     subset = trainRows_sec,
                     method = "rpart",
                     tuneGrid = data.frame(cp = exp(seq(-20,-5, len = 100))),
                     trControl = ctrl2,
                     metric = "ROC",
                     preProcess = c("center", "scale"))

model.rpart$bestTune
```

```
##             cp
## 94 0.002714654
```

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

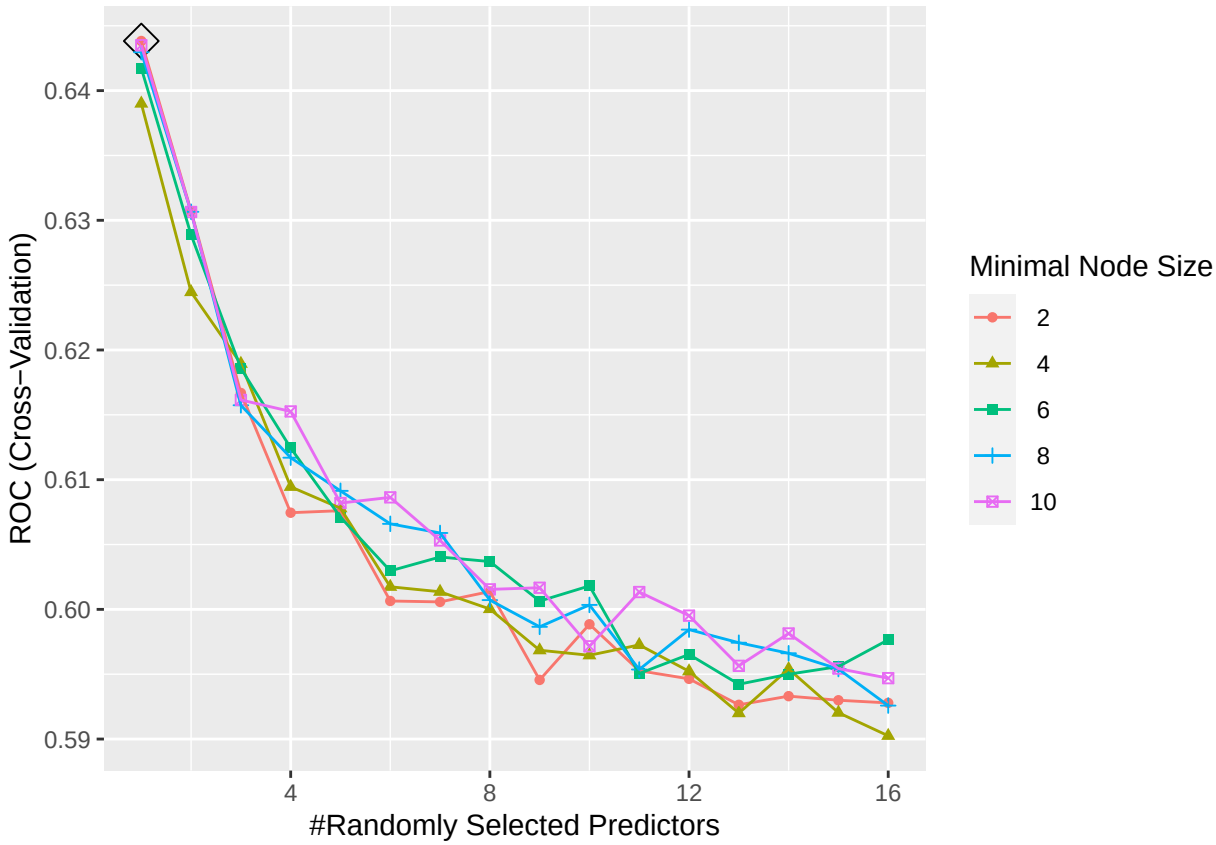



```
rpart.plot(model.rpart$finalModel)
```



Model 5: Random forest

```
rf.grid.sec <- expand.grid(mtry = 1:16,
                           splitrule = "gini",
                           min.node.size = seq(from = 2, to = 10, by = 2))

set.seed(2460)

model.rf <- train(brecovery_time ~ . , secondary,
                  subset = trainRows_sec,
                  method = "ranger",
                  tuneGrid = rf.grid.sec,
                  metric = "ROC",
                  trControl = ctrl2,
                  preProcess = c("center", "scale"))

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

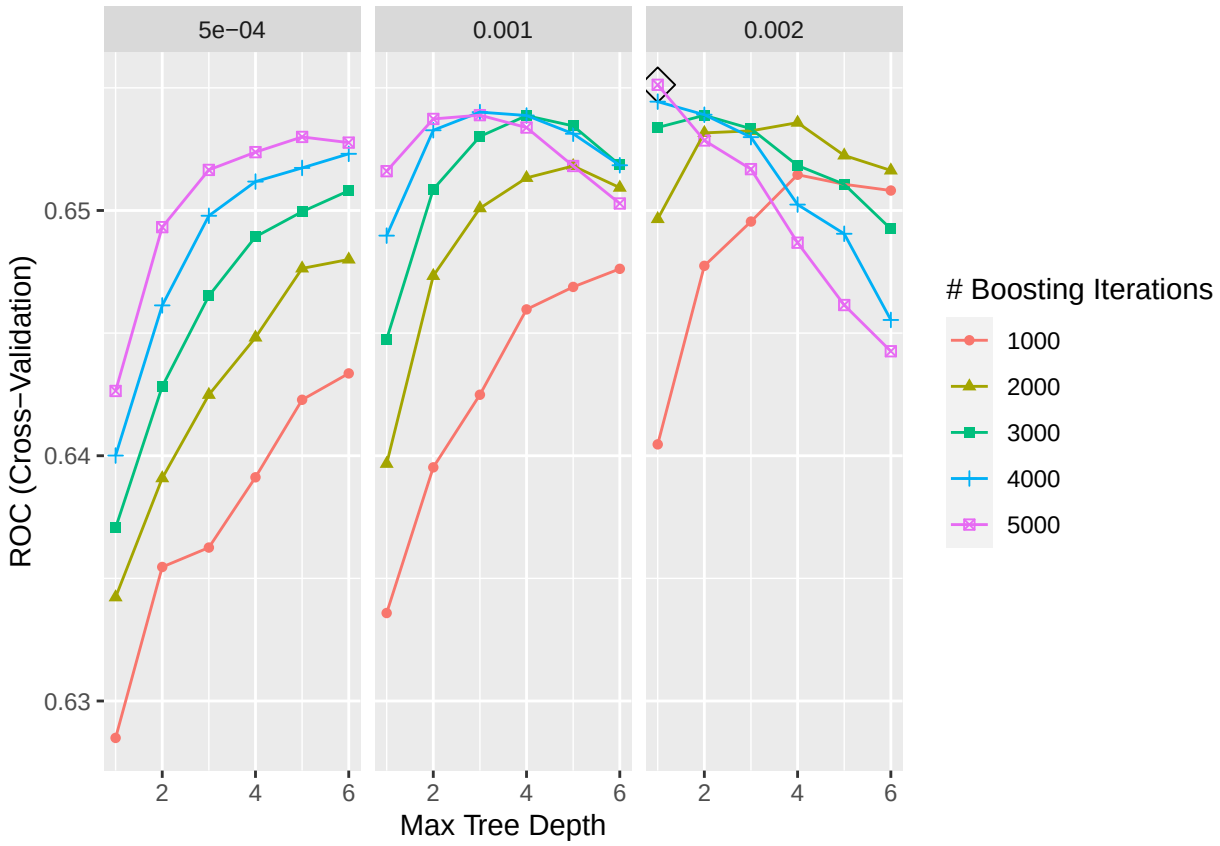



```
model.rf$bestTune
```

```
##   mtry splitrule min.node.size
## 1    1      gini             2
```

Model 6: Boosting

```
gbmA.grid <- expand.grid(n.trees = c(1000,2000,3000,4000,5000),
                         interaction.depth = 1:6,
                         shrinkage = c(0.0005,0.001,0.002),
                         n.minobsinnode = 1)

set.seed(2460)

model.gbmA <- train(brecovery_time ~ . , secondary,
                    subset = trainRows_sec,
                    tuneGrid = gbmA.grid,
                    trControl = ctrl2,
                    method = "gbm",
                    distribution = "adaboost",
                    metric = "ROC",
                    preProcess = c("center", "scale"),
                    verbose = FALSE)

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




```
model.gbmA$bestTune
```

```
##    n.trees interaction.depth shrinkage n.minobsinnode
## 65    5000                 1     0.002              1
```

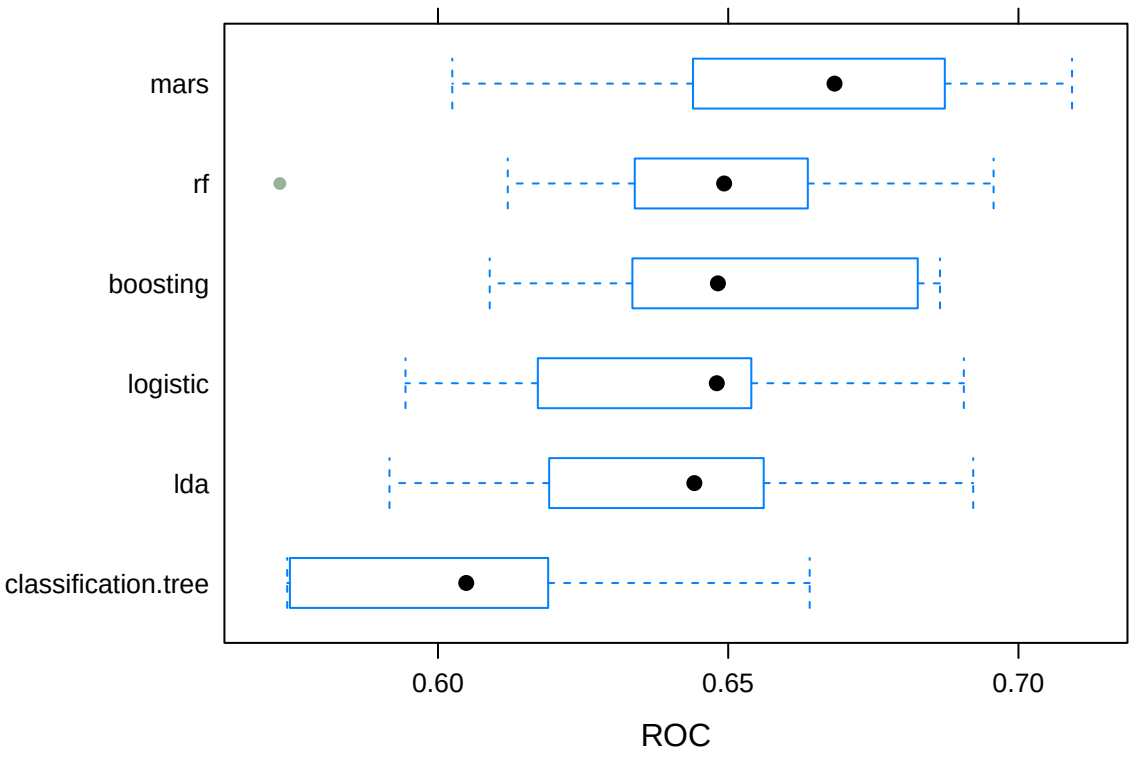
Model comparison

```
res_sec <- resamples(list(logistic = model.glm,
                          mars = model.mars,
                          lda = model.lda,
                          classification.tree = model.rpart,
                          rf = model.rf,
                          boosting = model.gbmA))

summary(res_sec)
```

```
##
## Call:
## summary.resamples(object = res_sec)
##
## Models: logistic, mars, lda, classification.tree, rf, boosting
## Number of resamples: 10
##
## ROC
##                            Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## logistic              0.5944048 0.6244100 0.6480330 0.6437327 0.6534797 0.6905941
## mars                  0.6024637 0.6468383 0.6683168 0.6636018 0.6851687 0.7092312
```

```
## lda                 0.5916417 0.6252159 0.6441691 0.6434160 0.6559550 0.6922058
## classification.tree 0.5740245 0.5764305 0.6048670 0.6030341 0.6173728 0.6640361
## rf                  0.5727608 0.6340663 0.6492998 0.6438254 0.6623590 0.6957172
## boosting            0.6089109 0.6359371 0.6482270 0.6551238 0.6825639 0.6864881
##                     NA's
## logistic               0
## mars                   0
## lda                    0
## classification.tree    0
## rf                     0
## boosting               0
##
## Sens
##                           Min.    1st Qu.     Median       Mean    3rd Qu.
## logistic            0.03488372 0.04664843 0.06429549 0.07105335 0.08720930
## mars                0.06976744 0.08163475 0.09883721 0.12359781 0.15988372
## lda                 0.03488372 0.04664843 0.05841313 0.06522572 0.07848837
## classification.tree 0.10465116 0.15697674 0.19186047 0.18777018 0.22093023
## rf                  0.00000000 0.00000000 0.00000000 0.00000000 0.00000000
## boosting            0.00000000 0.01463748 0.02325581 0.02326949 0.03197674
##                           Max. NA's
## logistic            0.12790698    0
## mars                0.21176471    0
## lda                 0.11627907    0
## classification.tree 0.24705882    0
## rf                  0.00000000    0
## boosting            0.04651163    0
##
## Spec
##                          Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## logistic            0.9306931 0.9616337 0.9678218 0.9618812 0.9702970 0.9702970
## mars                0.9207921 0.9319307 0.9504950 0.9475248 0.9628713 0.9752475
## lda                 0.9356436 0.9628713 0.9702970 0.9663366 0.9752475 0.9851485
## classification.tree 0.8613861 0.8873762 0.9059406 0.9014851 0.9195545 0.9257426
## rf                  1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000
## boosting            0.9752475 0.9876238 0.9950495 0.9925743 0.9987624 1.0000000
##                     NA's
## logistic               0
## mars                   0
## lda                    0
## classification.tree    0
## rf                     0
## boosting               0
```

```
bwplot(res_sec, metric = "ROC")
```



Select final model

Since MARS model has the highest mean AUC ROC, we selected it as our final model.

Test error

```
pred.mars <- predict(model.mars, newdata = secondary[-trainRows_sec,])

confusionMatrix(data = pred.mars, reference = secondary$brecovery_time[-trainRows_sec],
                positive = "Long")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction Short Long
##      Short    16   27
##      Long    198  477
##
##                Accuracy : 0.6866
##                  95% CI : (0.6513, 0.7204)
##     No Information Rate : 0.7019
##     P-Value [Acc > NIR] : 0.8261
##
##                   Kappa : 0.0275
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.94643
##             Specificity : 0.07477
##          Pos Pred Value : 0.70667
```

```
##          Neg Pred Value : 0.37209
##              Prevalence : 0.70195
##          Detection Rate : 0.66435
##    Detection Prevalence : 0.94011
##       Balanced Accuracy : 0.51060
##
##        'Positive' Class : Long
##
```

The accuracy of the MARS model was 0.6866. The misclassification (test error) is calculated as 1 - 0.6866 = 0.3134.