# qz2266_primary_regression tree_random forest

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**Data preparation**

**Data partition**

Next, we split the dataset into two parts: training data (80%) and test data (20%).

```r
set.seed(2266)
trainRows <- createDataPartition(y = covid$recovery_time, p = 0.8, list = FALSE)

# Training data
covid_train = covid[trainRows, ]
x_train = model.matrix(recovery_time~.,covid)[trainRows, -1]
y_train = covid$recovery_time[trainRows]
# Test data
covid_test = covid[-trainRows, ]
x_test = model.matrix(recovery_time~.,covid)[-trainRows, -1]
y_test = covid$recovery_time[-trainRows]

# create cross-validation objects
ctrl1 <- trainControl(method = "cv")
```

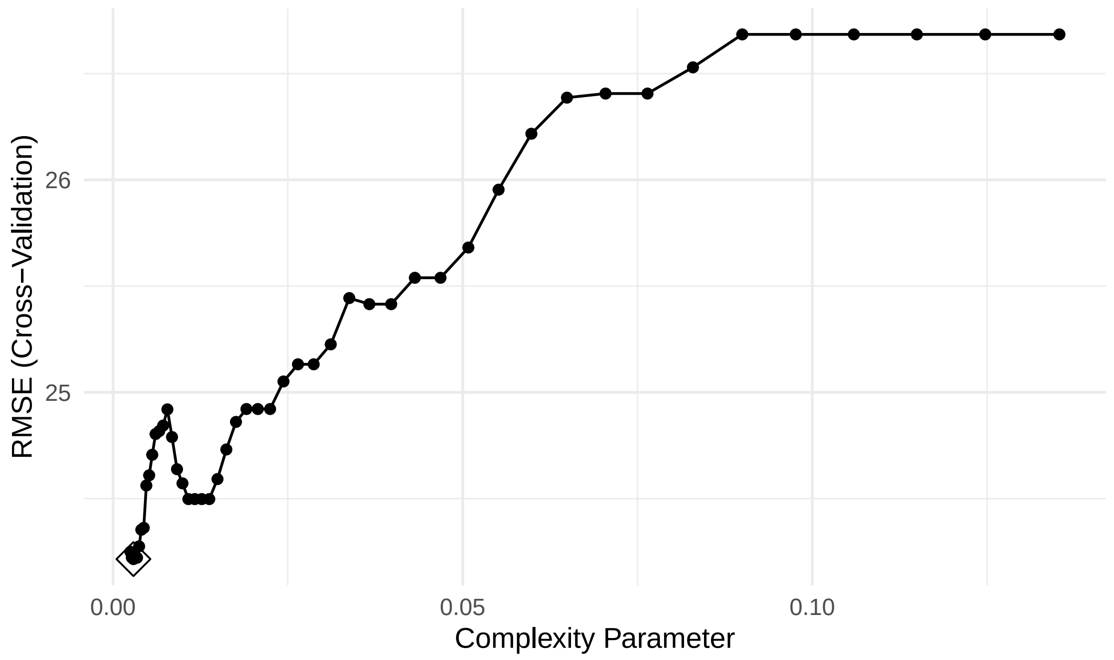
## (a) Regression tree

Build a regression tree on the training data to predict the response. Create a plot of the tree.

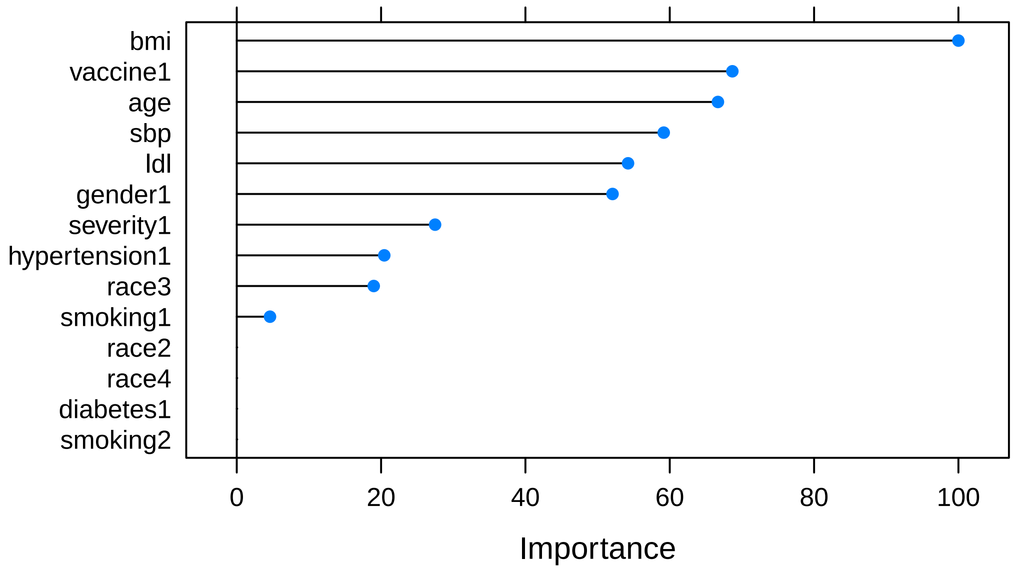
```r
set.seed(2266)

# build a regression tree on the training data
rpart.fit <- train(recovery_time ~ . ,
                   data = covid_train,
                   method = "rpart",
                   tuneGrid = data.frame(cp = exp(seq(-6,-2, length = 50))),
                   trControl = ctrl1)
rpart.fit$bestTune
```

```
##            cp
## 3 0.002918356
```

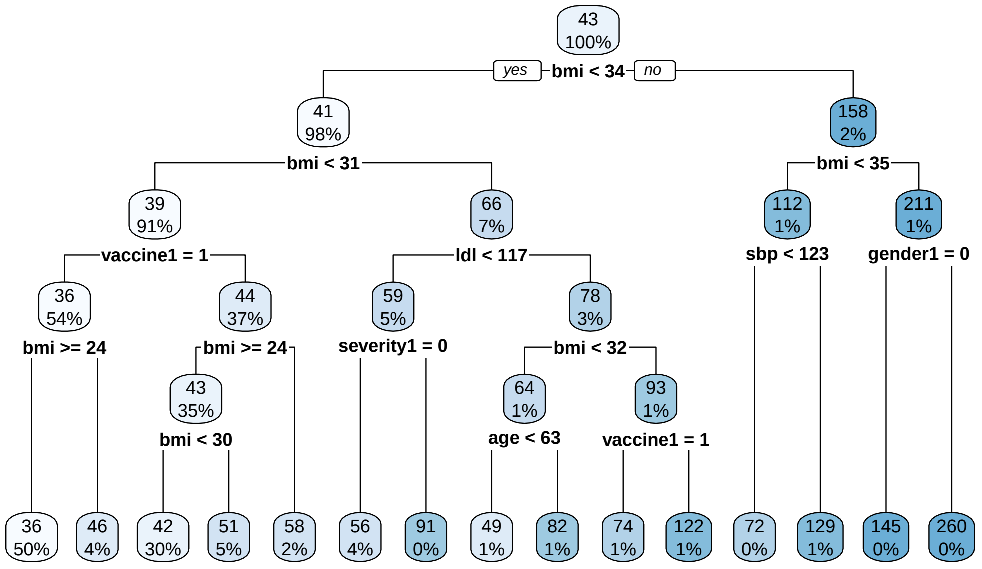
```r
# plot of the complexity parameter
ggplot(rpart.fit, highlight = TRUE)
```



```r
# importance
plot(varImp(rpart.fit, scale = TRUE))
```



```
# create a plot of the tree
rpart.plot(rpart.fit$finalModel)
```

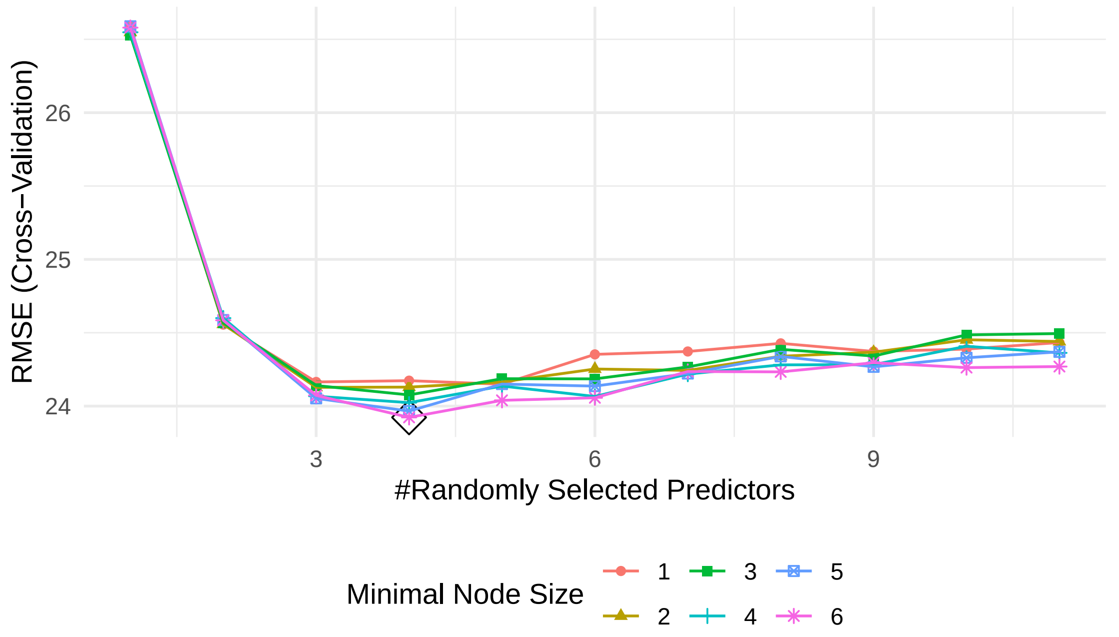


- The root node is `bmi` over or under 34.
- The optimal cp is 0.002918356.
- The pruned tree based on the optimal cp value is plotted as above. It's quite complicated with 15 terminal nodes and 14 splits.
- The model indicated that the variables `bmi` has the highest predictive power, followed by `vaccine1`, `age`, and `sbp`.

## (b) Random forest

Perform random forest on the training data. Report the variable importance and the test error.

```
rf.grid <- expand.grid(mtry = 1:11,
                       splitrule = "variance",
                       min.node.size = 1:6)

set.seed(2266)
# train a random forest model on the training data
rf.fit <- train(recovery_time ~ .,
               data = covid_train,
                method = "ranger",
                tuneGrid = rf.grid,
                trControl = ctrl1)

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

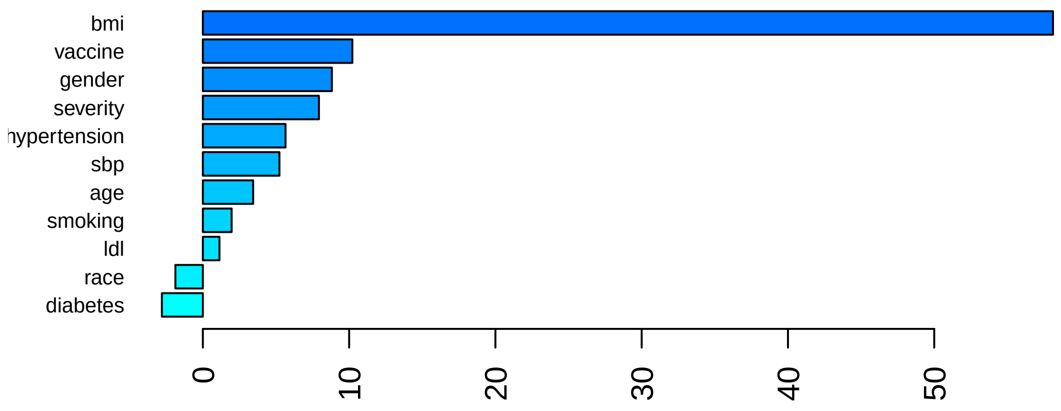


```
rf.fit$bestTune
```

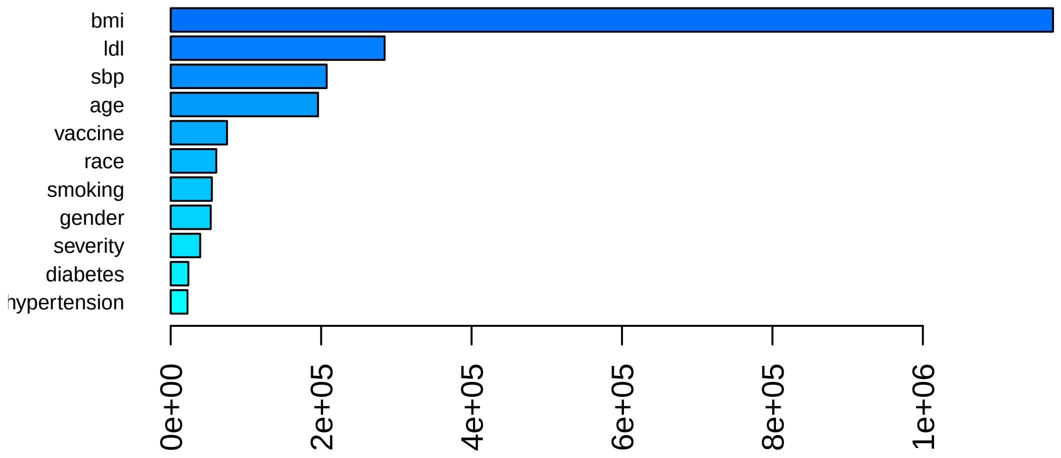
```
##    mtry splitrule min.node.size
## 24    4  variance             6
```

- Using ranger method, we perform Random Forest algorithm with minimum node size 6 and 4 selected predictors.
- It is a common practice to investigate the variables with the greatest predictive power once a random forest model has been trained. These important variables play a crucial role in determining the outcome, and their values can have a substantial impact on the results. Conversely, variables with low importance may be omitted from the model, leading to a streamlined model that is more efficient in terms of fitting and prediction accuracy.

```
# variable importance using permutation methods
set.seed(2266)
rf.perm = ranger(recovery_time ~ .,
                      data = covid_train,
                      mtry = rf.fit$bestTune[[1]],
                      splitrule = "variance",
                      min.node.size = rf.fit$bestTune[[3]],
                      importance = "permutation",
                      scale.permutation.importance = TRUE)
# report variable importance
barplot(sort(ranger::importance(rf.perm), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("cyan", "blue"))(19))
```



```r
# variable importance using impurity methods
set.seed(2266)
rf.impu <- ranger(recovery_time ~ .,
                        data = covid_train,
                        mtry = rf.fit$bestTune[[1]],
                        splitrule = "variance",
                        min.node.size = rf.fit$bestTune[[3]],
                        importance = "impurity")
# report variable importance
barplot(sort(ranger::importance(rf.impu), decreasing = FALSE),
        las = 2, horiz = TRUE, cex.names = 0.7,
        col = colorRampPalette(colors = c("cyan", "blue"))(19))
```



- Calculate and graph variable importance using permutation and impurity metrics.
- The model using impurity method indicated that the variables `bmi` has the highest predictive power, followed by `ldl`, `sbp`, and `age`. Their values were the most significant in determining `recovery_time`. This suggests that these variables play a crucial role in influencing the Covid recovery time. Moreover, vaccinated status, race and smoking or not also contributes to the outcome.
- Similarly, The model using permutation method indicated that the variables `bmi` has the highest predictive power, followed by `vaccine`, `gender` , `severity`, `hypertension` and `sbp`.

```
# test error
pred.rf <- predict(rf.fit, newdata = covid_test)
RMSE(pred.rf, covid_test$recovery_time)
```

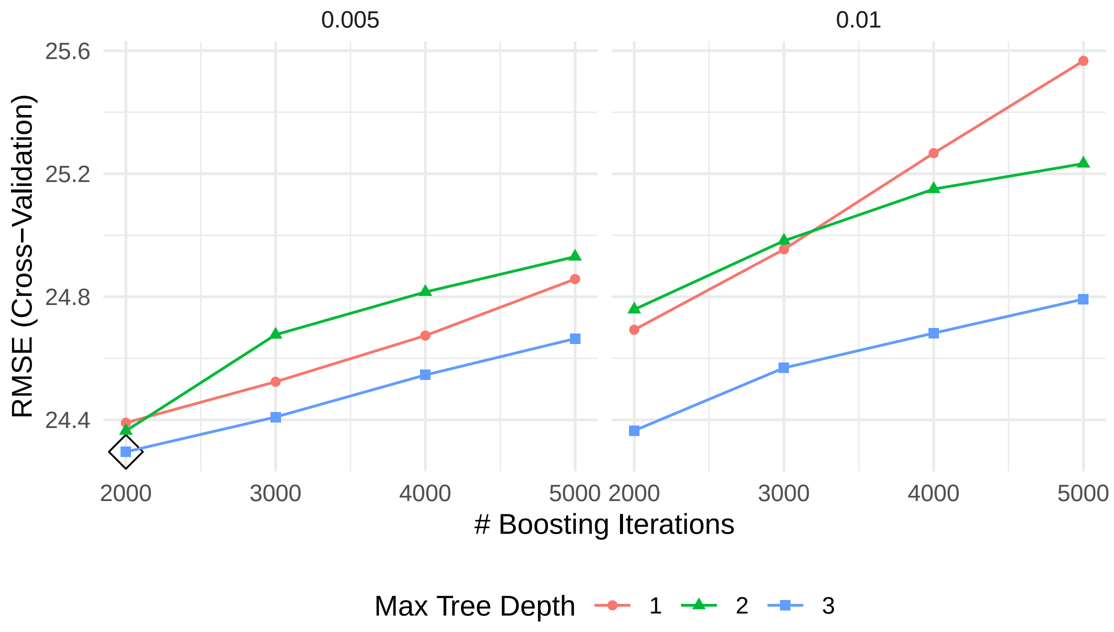
```
## [1] 25.54926
```

- The test error of the model is 25.54926

## (c) Boosting

Perform boosting on the training data. Report the variable importance and the test error.

```
# train model using gbm with grid of tuning parameters
bst.grid = expand.grid(n.trees = c(2000,3000,4000,5000),
                       interaction.depth = 1:3,
                       shrinkage = c(0.005,0.01),
                       n.minobsinnode = c(1))

set.seed(2266)
bst.fit <- train(recovery_time ~.,
                 data = covid_train,
                 method = "gbm",
                 tuneGrid = bst.grid,
                 trControl = ctrl1,
                 verbose = FALSE)

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

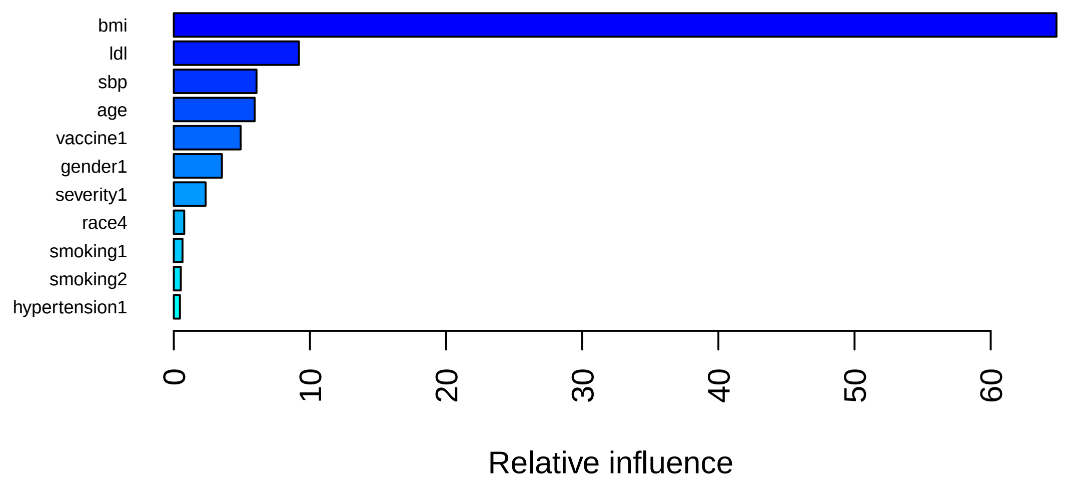


```
bst.fit$bestTune
```

```
##   n.trees interaction.depth shrinkage n.minobsinnode
## 9    2000                 3     0.005              1
```

We use the gradient boosting method implemented with gbm in caret package.

```
# variable importance
summary(bst.fit$finalModel, las = 2, cBars = 11, cex.names = 0.6)
```



```
##                         var     rel.inf
## bmi                     bmi 64.83239479
## ldl                     ldl  9.18542162
## sbp                     sbp  6.07576347
## age                     age  5.93877097
## vaccine1           vaccine1  4.90865739
## gender1             gender1  3.53209189
## severity1         severity1  2.33722407
## race4                 race4  0.77066076
## smoking1           smoking1  0.64037527
## smoking2           smoking2  0.51373728
## hypertension1 hypertension1  0.45089717
## race3                 race3  0.42357711
## race2                 race2  0.36420571
## diabetes1         diabetes1  0.02622248
```

```
# test error
pred.bst <- predict(bst.fit, newdata = covid_test)
RMSE(pred.bst, covid_test$recovery_time)
```

```
## [1] 25.13826
```

- The most important variables for gradient boosting are still `bmi`. Other important variables include `ldl`, `sbp` and `age`.
- The test error for boosting is 25.13826, smaller than the test error for random forest.
-