Week 7 Lab Solutions

1) `survived` is a numeric value. We need to first transform it to a categorical value and saved it as a new variable survived01. Use `titanic3$survived01 = as.factor(titanic3$survived)` to do so and check that this variable has been included in the dataset.

```
titanic3$survived01 = as.factor(titanic3$survived)
summary(titanic3)
```

```
##  pclass     survived         sex           age               sibsp       
##  1:323   Min.   :0.000   female:466   Min.   : 0.1667   Min.   :0.0000  
##  2:277   1st Qu.:0.000   male  :843   1st Qu.:21.0000   1st Qu.:0.0000  
##  3:709   Median :0.000                Median :28.0000   Median :0.0000  
##          Mean   :0.382                Mean   :29.8811   Mean   :0.4989  
##          3rd Qu.:1.000                3rd Qu.:39.0000   3rd Qu.:1.0000  
##          Max.   :1.000                Max.   :80.0000   Max.   :8.0000  
##                                       NA's   :263                       
##      parch            fare         embarked survived01
##  Min.   :0.000   Min.   :  0.000    :  2    0:809     
##  1st Qu.:0.000   1st Qu.:  7.896   C:270    1:500     
##  Median :0.000   Median : 14.454   Q:123              
##  Mean   :0.385   Mean   : 33.295   S:914              
##  3rd Qu.:0.000   3rd Qu.: 31.275                      
##  Max.   :9.000   Max.   :512.329                      
##                  NA's   :1                            
```

2) Install the package of randomForest and include this package into your code. In order to call the randomForest() function, all the missing value rows need to be dealt with. The simplest way is to remove those rows. Use titanic3 <- na.omit(titanic3) to do that.

```
library(randomForest)
nrow(titanic3)
```

```
## [1] 1309
```

```
titanic3 <- na.omit(titanic3)
nrow(titanic3)
```

```
## [1] 1045
```

3) Use a seed (e.g. set.seed(1)) to set half of the dataset to be training dataset and the other half to be testing dataset.

```
set.seed(1)
train <- sample(1:nrow(titanic3), nrow(titanic3)/2)
test <- titanic3[-train,]  #the testing set
x_test <- test[,-c(2,9)]  #the predictors in the testing set
#-c(2,9) is to remove survived and survived01
# names(titanic3)
#[1] "pclass"     "survived"   "sex"        "age"        "sibsp"
#[6] "parch"      "fare"       "embarked"   "survived01"

survived.test <- titanic3$survived[-train]
survived01.test <- titanic3$survived01[-train]
```

4) Use the training dataset to build a bagged model (with set.seed(1)) for

- y: survived
- x: all the predictors other than survived and survived01.

Compute the mean error rate on the testing dataset.

Remark: You might get a warning message, saying that

In randomForest.default(m, y, ...) : The response has five or fewer unique values. Are you sure you want to do regression?

Ignore the message for now. It's doable and you will get a bagged model anyway.

```
set.seed(1)
bag.titanic <- randomForest(survived ~ .-survived01,
                           data = titanic3,
                           subset = train,
                           mtry=7,
                           importance = TRUE)
```

```
## Warning in randomForest.default(m, y, ...): The response has five or fewer
## unique values. Are you sure you want to do regression?
```

```
print(bag.titanic)
```

```
##
## Call:
##  randomForest(formula = survived ~ . - survived01, data = titanic3,      mtry = 7, importance = TRUE
##                Type of random forest: regression
##                      Number of trees: 500
## No. of variables tried at each split: 7
##
##           Mean of squared residuals: 0.1662624
##                     % Var explained: 31.27
```

```
bag.pred <- predict(bag.titanic, newdata = test)
bag.pred.class <- ifelse(bag.pred <= 0.5, "0", "1")
print(mean(bag.pred.class!=survived.test))
```

```
## [1] 0.2256214
```

5) Using the same training and testing dataset, build a bagged model (with set.seed(1)) for

- y: survived01
- x: all the predictors other than survived and survived01

a) Find out on how many trees your model is built and the OOB error.
b) Compute the mean error rate on the testing dataset.

```
set.seed(1)
bag.titanic01 <- randomForest(survived01 ~ .-survived,
                             data = titanic3,
                             subset = train,
                             mtry = 7,
                             importance = TRUE)
print(bag.titanic01)
```

```
##
## Call:
```

```
##  randomForest(formula = survived01 ~ . - survived, data = titanic3,      mtry = 7, importance = TRUE
##                Type of random forest: classification
##                      Number of trees: 500
## No. of variables tried at each split: 7
##
##         OOB estimate of  error rate: 25.1%
## Confusion matrix:
##     0   1 class.error
## 0 254  54   0.1753247
## 1  77 137   0.3598131
```

```
bag.pred01 <- predict(bag.titanic01, newdata = test, type="class")
print(mean(bag.pred01!=survived.test))
```

```
## [1] 0.2428298
```

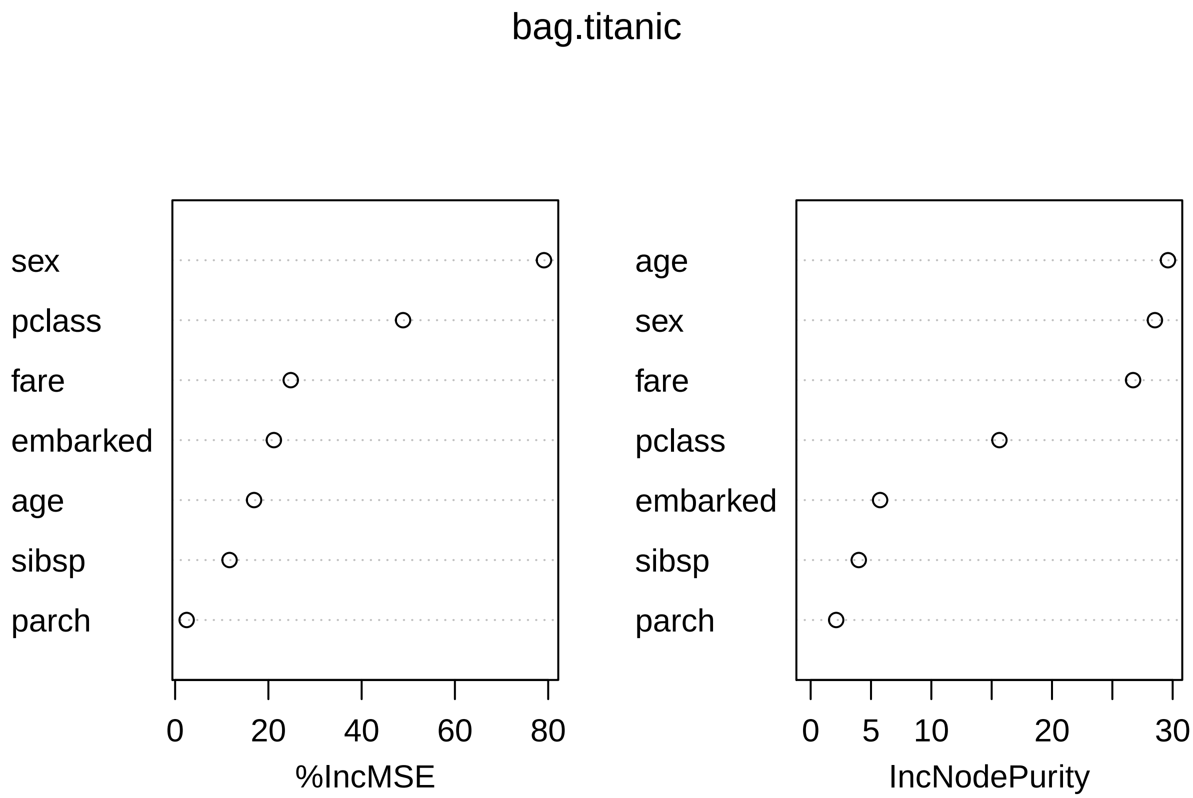
The OOB error is 25.1% and the number of trees grown is 500. Note that OOB error rate is only available for classification trees.

6) Plot the variable importance plot for the two bagged models you built in 4) and 5) and comment whether the importance coincides.

```
importance(bag.titanic)
```

```
##            %IncMSE IncNodePurity
## pclass   48.881139     15.640940
## sex      79.099132     28.526301
## age      16.927281     29.610071
## sibsp    11.669782      3.987307
## parch     2.476521      2.113892
## fare     24.799137     26.719179
## embarked 21.173869      5.754308
```

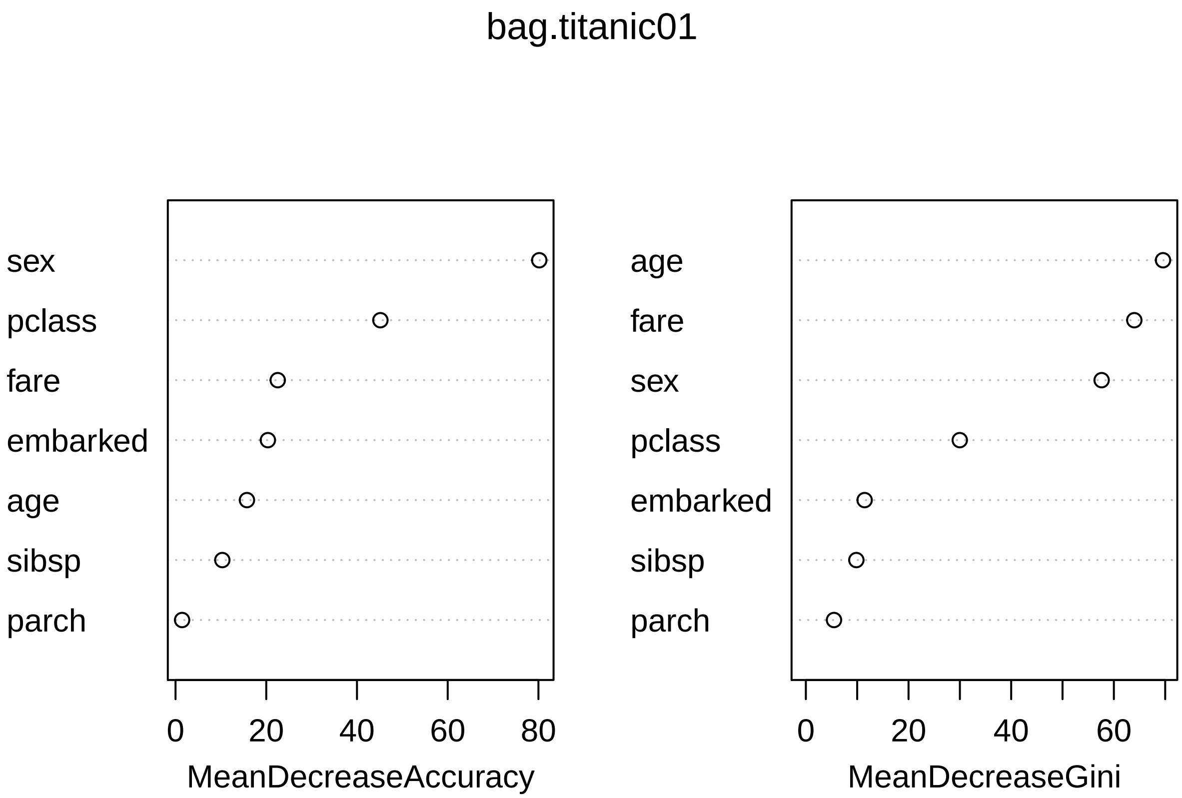
```
varImpPlot(bag.titanic)
```




```r
importance(bag.titanic01)
```

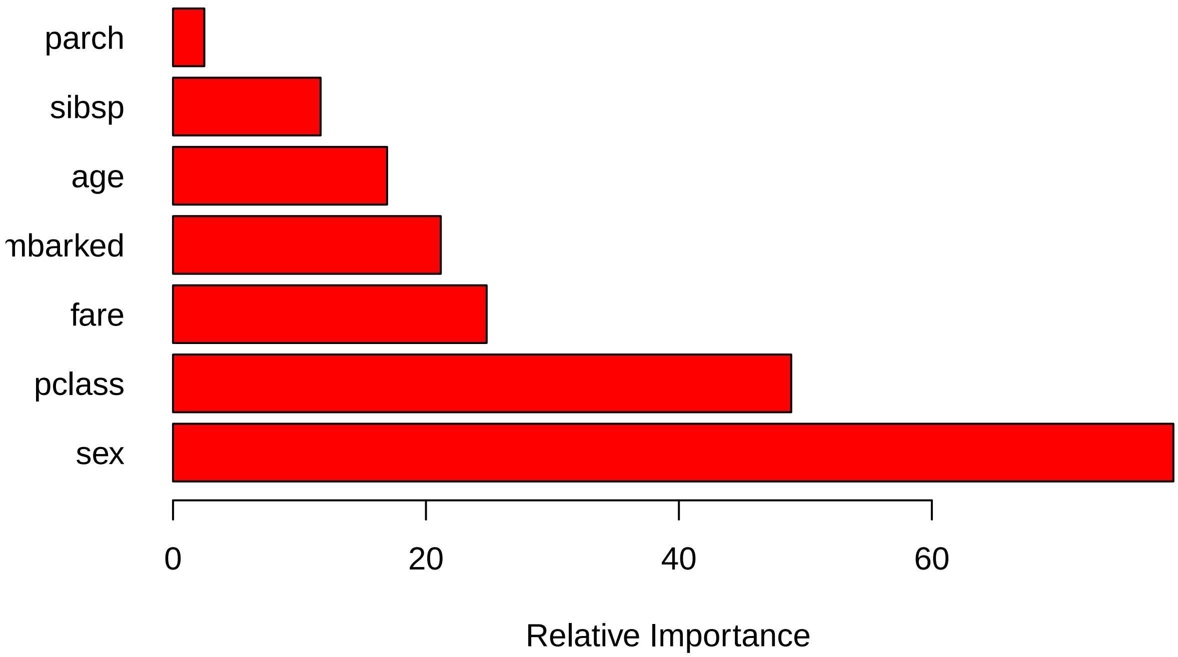
```
##                  0         1 MeanDecreaseAccuracy MeanDecreaseGini
## pclass   20.309513 40.299246            45.159371        29.979668
## sex      51.133866 65.094782            80.185171        57.617711
## age      14.216130  6.490663            15.744389        69.575333
## sibsp    14.949575 -4.753609            10.318365         9.834013
## parch     2.598222 -1.602406             1.449338         5.482502
## fare     10.977157 19.824188            22.532082        63.981122
## embarked 19.820160  6.346271            20.358576        11.447718
```

```r
varImpPlot(bag.titanic01)
```




```r
#The barplot can be:

barplot(sort(importance(bag.titanic)[,1], decreasing = TRUE),
        xlab = "Relative Importance",
        horiz = TRUE,
        col = "red",
        las=1 #The las argument will allow rotation of 90 degrees for labels
        )
```



Yes, the importance of both models coincide if we look at the %IncMSE.

7) Plot a graph that shows the testing error rate of a single tree (red dashed line), the mean testing error rates for majority vote (black curve) and the testing error rates for averaging the probabilities (blue curve), both in relation to the number of trees. Define set.seed(1) and add a legend if you can.

```
set.seed(1)
# calculate the black line:
#Here we insert the testing dataset (xtest and ytest) when building the model.
#Please read the last three slides of Session 7 for more information.
bag.titanic01=randomForest(survived01 ~ .-survived,
                           data=titanic3,
                           subset = train,
                           importance = TRUE,
                           xtest=x_test,
                           ytest=survived01.test,
                           mtry=7,
                           ntree=200)
print(bag.titanic01$test$err.rate[1,1])
```

```
##      Test
## 0.3078394
```

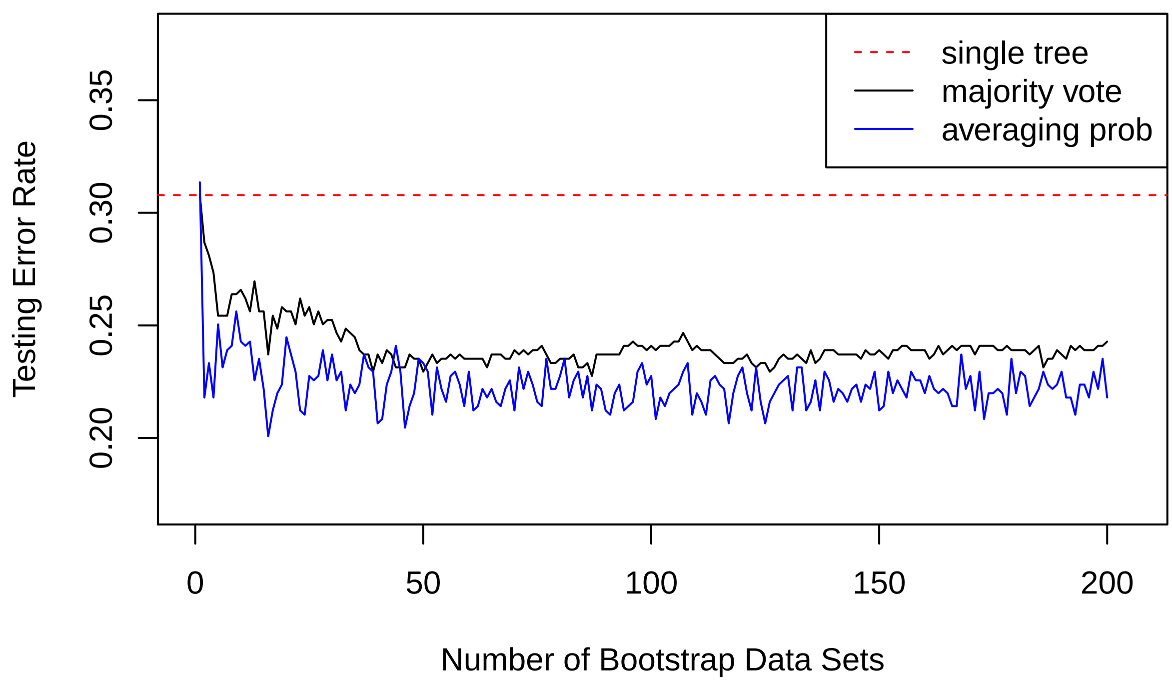
```
#plot the black line
plot(1:200, bag.titanic01$test$err.rate[,1],
     type="l",
     xlab="Number of Bootstrap Data Sets",
     ylab="Testing Error Rate",
     ylim=c(0.17,0.38), xlim=c(0,205))

#plot the red dashed line
abline(h = bag.titanic01$test$err.rate[1,1],lty=2,col="red")
```

```r
yhat.ter.ave <- rep(0,200)      # a vector for Testing Error Rate using averaging
for(j in 1:200){
  #set.seed(6)
  bag.titanic <- randomForest(survived ~ .-survived01,
                              data=titanic3,
                              subset = train,
                              mtry=7,
                              importance = TRUE,
                              ntree=j)
  bag.pred <- predict(bag.titanic, newdata = test)
  bag.pred.class <- ifelse(bag.pred<=0.5, "0", "1")
  yhat.ter.ave[j] <- mean(bag.pred.class!=survived.test)
}

lines(yhat.ter.ave,col="blue")

legend("topright",
       c("single tree","majority vote","averaging prob"),
       lty=c(2,1,1),
       col=c("red","black","blue"))
```

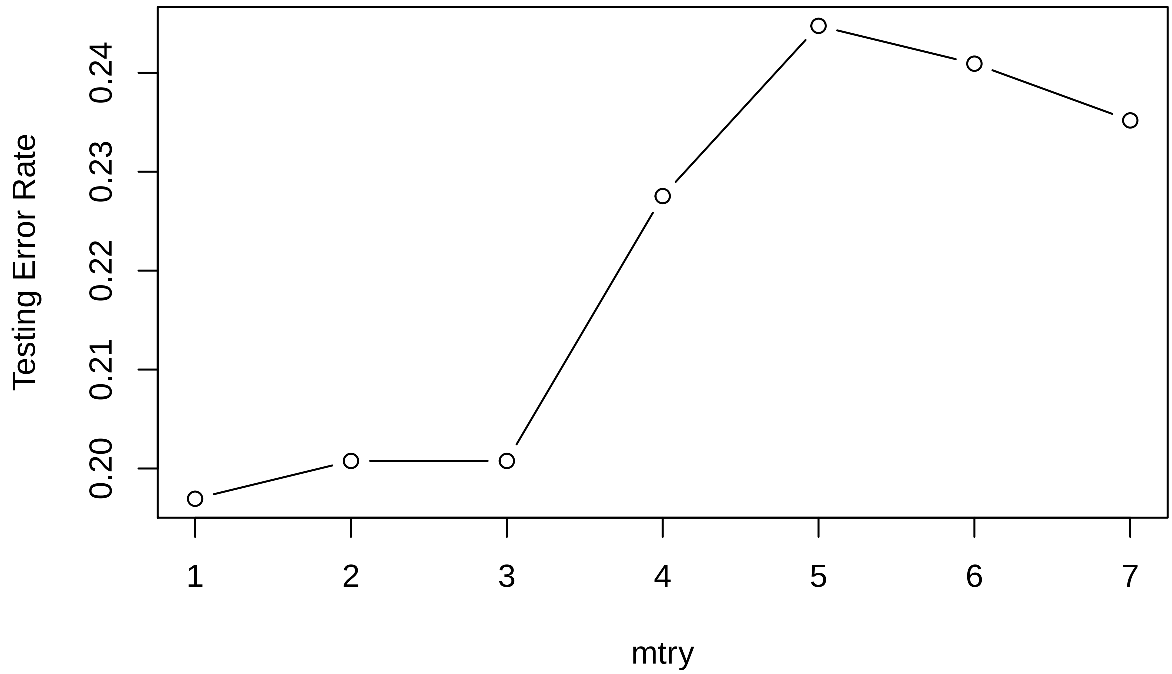


8) Plot a graph that shows the best value of mtry for the random forests model.

- y: survived01
- x: all the predictors other than survived and survived01
- mtry: range from 1 to 7

```r
testErrorRate <- rep(0,7)
for(i in 1:7){
  set.seed(3)
  bag.titanic01 <- randomForest(survived01 ~ .-survived,
```

```
                                data=titanic3,
                                subset=train,
                                mtry=i,
                                importance=TRUE,
                                xtest=x_test,
                                ytest=survived01.test,
                                ntree=500)
  testErrorRate[i] <- bag.titanic01$test$err.rate[500,1]
}
plot(testErrorRate,type="b",xlab="mtry",ylab="Testing Error Rate")
```



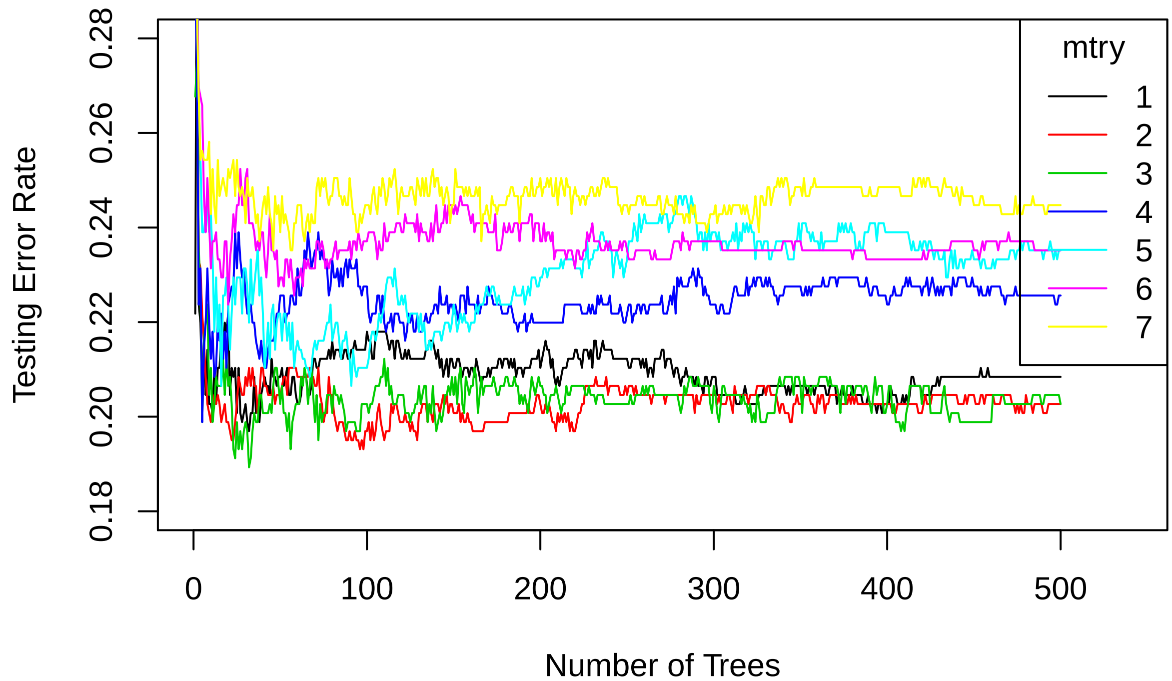
9) Play with mtry and ntree, plot a graph that shows testing error rate vs ntree for different mtry, and find the best/reasonably good combination of mtry and ntree from the plot. Add a legend if you can.

```
plot(0,
     xlab="Number of Trees",ylab="Testing Error Rate",
     xlim=c(1,540), ylim =c(0.18,0.28))


for(i in 1:7){
  # It's also possible to call randomForest using x and y as the training set.
  # bag.titanic01=randomForest(x=x_train, y=y_train01,
  #                             importance = TRUE,
  #                             xtest=x_test, ytest=survived01.test,
  #                             mtry=7,ntree=500)
  bag.titanic01=randomForest(survived01 ~ .-survived,
                              data=titanic3,
                              subset=train,
                              importance = TRUE,
                              xtest=x_test,
                              ytest=survived01.test,
```

```
                              mtry=i,
                              ntree=500)
  lines(bag.titanic01$test$err.rate[,1],col=i,type="l")
}

legend(title = "mtry",
       "topright",
       c("1","2","3","4","5","6","7"),
       lty=rep(1,7),col=1:7)
```



From the plot, we can see that mtry = 2 and 3 are better than the others in the long run. This result coincides with the empirical result: pick `mtry = sqrt(p)` when it is a classification tree. Here `p = 7` and `sqrt(p) = sqrt(7) = 2.65` $\in [2, 3]$.