Exercise 3: Glaucoma data revisited (2)

a) Fit a random forest using the `cforest` function from package `party`, with either bootstrap sampling with size N or subsampling with size $.632 \cdot N$.

b) Using the `predict()` function, compute the percentage of correctly classified observations — based on all trees and based only on those trees for which the observations are out-of-bag (by adding `OOB = FALSE` or `OOB = TRUE` to the function call) — and compare your results. Determine the predicted response class of each case and create a confusion matrix.

c) Compute and plot the standard permutation importance for the predictor variables.

d) Do the `stabletree()` function and 'cforest()' function give the same 3 most important variables?

Set random seeds everywhere in the code where random sampling is involved.

```
library(party)
data("GlaucomaM", package = "TH.data")
cfor_contr_bs <- cforest_control(replace = TRUE)
cfor_contr_ss <- cforest_control(replace = FALSE, fraction = 0.632)

set.seed(2908)
for_glauc_bs <- cforest(Class ~ ., data = GlaucomaM, control = cfor_contr_bs)
set.seed(21)
for_glauc_ss <- cforest(Class ~ ., data = GlaucomaM, control = cfor_contr_ss)

# training errors
#
# bootstrap sampling
predicted_class <- predict(for_glauc_bs)
table(GlaucomaM$Class, predicted_class)
```

```
##           predicted_class
##            glaucoma normal
##   glaucoma       86     12
##   normal          4     94
```

```
# subsampling
predicted_class <- predict(for_glauc_ss)
table(GlaucomaM$Class, predicted_class)
```

```
##           predicted_class
##            glaucoma normal
##   glaucoma       84     14
##   normal          5     93
```

```
sum(GlaucomaM$Class == predicted_class)/nrow(GlaucomaM)
```

```
## [1] 0.9030612
```

```
# OOB errors
#
# bootstrap sampling
predicted_class <- predict(for_glauc_bs, OOB = TRUE)
table(GlaucomaM$Class, predicted_class)
```

```
##           predicted_class
##            glaucoma normal
##   glaucoma       79     19
```

```
##   normal         15     83
```

```
#
# subsampling
predicted_class <- predict(for_glauc_ss, OOB = TRUE)
table(GlaucomaM$Class, predicted_class)
```

```
##           predicted_class
##            glaucoma normal
##   glaucoma       76     22
##   normal         10     88
```

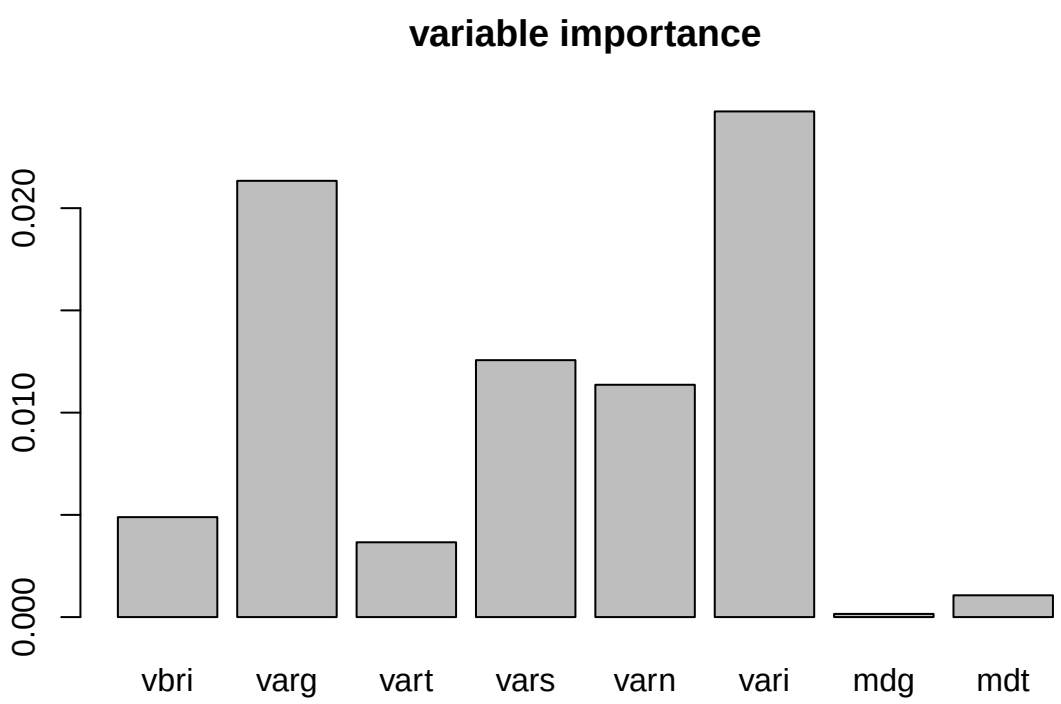
```
sum(GlaucomaM$Class==predicted_class)/nrow(GlaucomaM)
```

```
## [1] 0.8367347
```

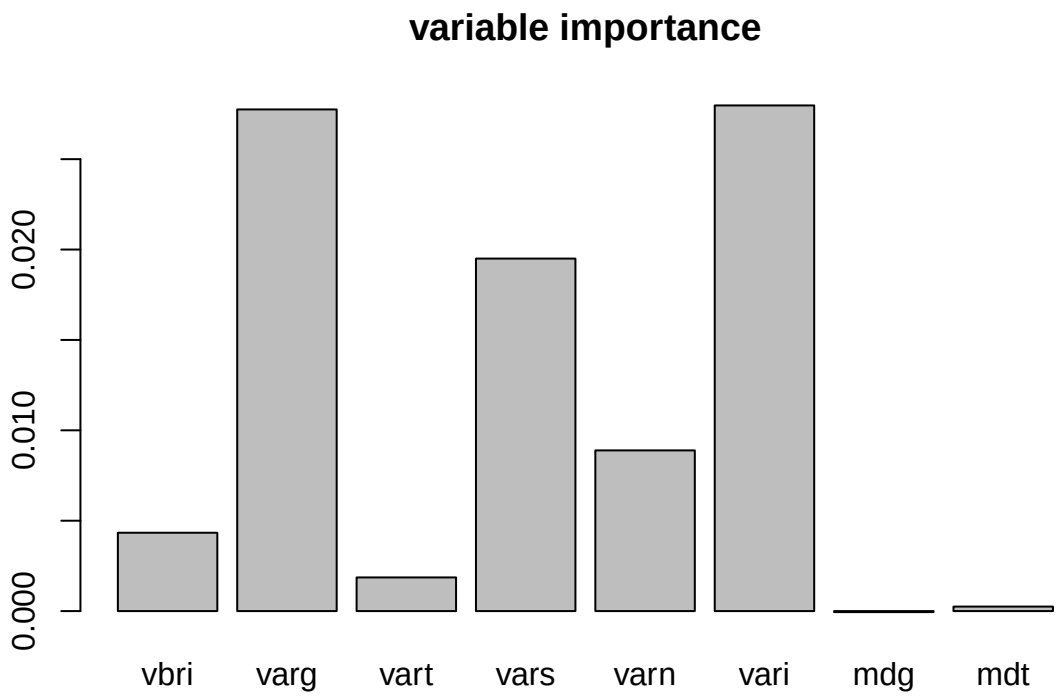
```
set.seed(14)
imp <- varimp(for_glauc_bs)
imp
```

```
##            ag            at            as            an            ai
##  1.395082e-03  1.021327e-03  1.977648e-03  6.317809e-04  1.067874e-03
##           eag           eat           eas           ean           eai
##  3.883825e-04  4.305072e-04  9.937465e-04 -3.556480e-04  3.524894e-04
##          abrg          abrt          abrs          abrn          abri
##  2.475112e-03  3.855851e-04  5.119845e-03  7.697780e-04  6.312554e-03
##           hic          mhcg          mhct          mhcs          mhcn
##  7.904260e-03  4.000060e-03  1.475119e-03  1.204970e-03  5.239234e-04
##          mhci          phcg          phct          phcs          phcn
##  7.385486e-03  6.945339e-03  7.635571e-04  8.209638e-04  3.968590e-03
##          phci           hvc          vbsg          vbst          vbss
##  8.809597e-03  3.077886e-03  8.047762e-04  6.894481e-04  5.154076e-04
##          vbsn          vbsi          vasg          vast          vass
##  6.698471e-05  1.122333e-03  1.041898e-03  3.418676e-04  1.287167e-03
##          vasn          vasi          vbrg          vbrt          vbrs
## -1.915117e-04  5.044782e-04  1.172589e-03  3.186083e-04  1.039984e-03
##          vbrn          vbri          varg          vart          vars
##  5.379197e-04  4.888464e-03  2.133656e-02  3.657933e-03  1.256608e-02
##          varn          vari           mdg           mdt           mds
##  1.136261e-02  2.473086e-02  1.548512e-04  1.066057e-03  1.379876e-04
##           mdn           mdi           tmg           tmt           tms
##  1.114135e-03  5.045643e-04  8.918427e-03  1.218121e-03  6.389034e-03
##           tmn           tmi            mr           rnf          mdic
##  1.088222e-03  7.788858e-03  6.429624e-04  7.355221e-03  5.436358e-03
##           emd            mv
##  2.682900e-03 -1.158468e-04
```

```
# plot importacnes for only a subset of the variables:
barplot(imp[42:49], names.arg = names(GlaucomaM[,42:49]), main = "variable importance")
```




```
set.seed(15)
# plot importacnes for only a subset of the variables:
imp <- varimp(for_glauc_ss)
barplot(imp[42:49], names.arg = names(GlaucomaM[,42:49]), main = "variable importance")
```




```
# Note: Before interpreting any variable importances make sure that
# your results are stable by means of setting two different
# random seeds, before fitting the forest and computing the
# variable importance. If the ranking of the top variable importances
# changes between the two runs, this means that your forest was not
# large enough (as compared to the number of variables) to generate
# stable results and you should increase the number of trees in the
# forest (ntree).
```

Exercise 4: Carseat sales revisited

Using the `cforest()` function from the `party` package, fit a random forest and a bagged ensemble to the 300 training observations. Using the `predict()` function, calculate the mean squared error (MSE) for:

$$MSE = \frac{1}{N}\sum_i (y_i - \hat{y}_i)^2$$

a) The training observations

```
data("Carseats", package = "ISLR")
set.seed(42)
train <- sample(1:400, 300)
library(party)
bagged_cs <- cforest(Sales ~ ., data = Carseats[train,], controls = cforest_unbiased(mtry = NULL))
ranfor_cs <- cforest(Sales ~ ., data = Carseats[train,])
```

```
mean((Carseats[train,"Sales"] - predict(bagged_cs))^2)
```

```
## [1] 2.10367
```

```
mean((Carseats[train,"Sales"] - predict(ranfor_cs))^2)
```

```
## [1] 2.241822
```

b) The OOB predictions for training observations (add `OOB = TRUE` to the function call)

```
mean((Carseats[train,"Sales"] - predict(bagged_cs, OOB = TRUE))^2)
```

```
## [1] 3.204182
```

```
mean((Carseats[train,"Sales"] - predict(ranfor_cs, OOB = TRUE))^2)
```

```
## [1] 3.174919
```

c) The test observations (specify `newdata` argument)

```
mean((Carseats[-train,"Sales"] - predict(bagged_cs, newdata = Carseats[-train,]))^2)
```

```
## [1] 3.237652
```

```
mean((Carseats[-train,"Sales"] - predict(ranfor_cs, newdata = Carseats[-train,]))^2)
```

```
## [1] 3.389324
```

d) Are the OOB training error estimates indeed less optimistic / more realistic estimates of the test error?

```
# Yes, the error estimated based on OOB observations more closely resembles the error on test data
```

Exercise 5: Boston housing data

Fit a random forest and bagged ensemble of CART trees to the Boston housing data. This dataset reports the median value (`medv`) of owner-occupied homes in 506 districts in the Boston area (USA), together with 13 potential predictor variables reporting sociodemographic and other characteristics of the districts:

```
library("randomForest")
```

```
## randomForest 4.6-12
```

```
## Type rfNews() to see new features/changes/bug fixes.
```

```
?randomForest
```

```
## starting httpd help server ...
```

```
##  done
```

```
data("Boston", package = "MASS")
?MASS::Boston
```

Use the `randomForest()` function from the `randomForest` package to predict the median value of owner occupied home. Fit bth a random forest and a bagged ensemble. You could create the ensembles using a formula statement (i.e., `medv ~ .`), but if you supply arguments `x`, `y`, `xtest` and `ytest`, you can evaluate the test error for random forests consisting of 1 through the specified number of trees to grow. You will use these estimates to evaluate the effect of the number of trees on accuracy and to compare the OOB error estimates with the error estimated on test data. Therefore, first separate the data into a training and test set:

```
set.seed(1)
train <- sample(1:nrow(Boston), nrow(Boston)/4)
```

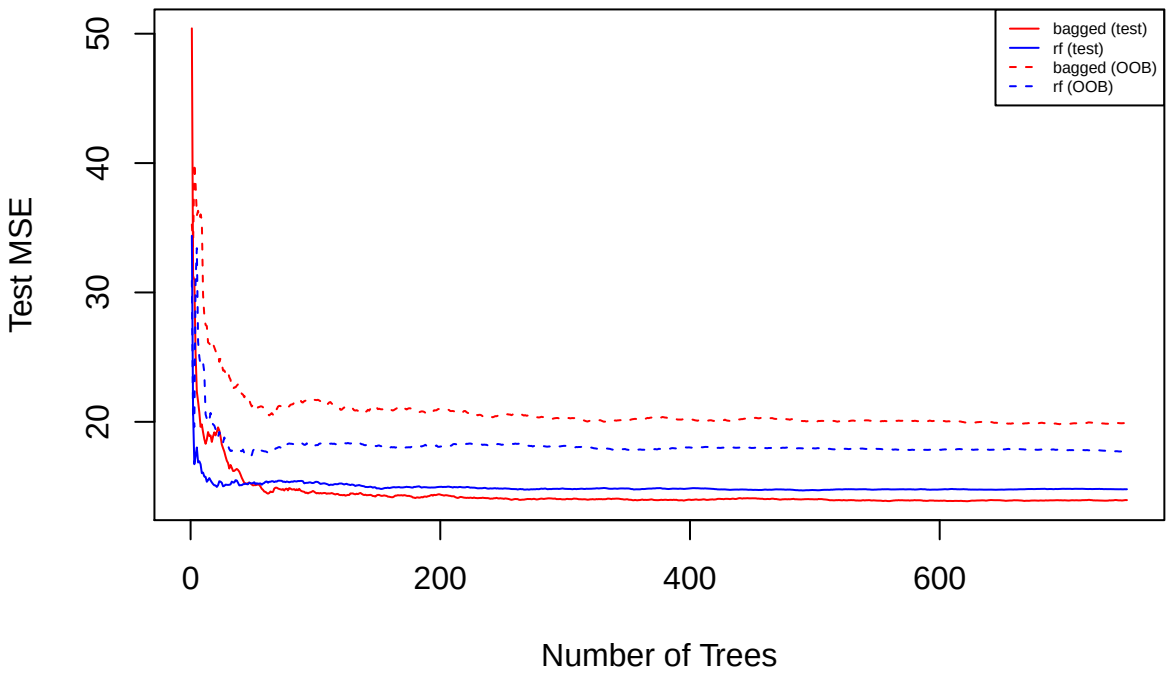
```
x <- Boston[train, -14]
y <- Boston[train, 14]
xtest <- Boston[-train, -14]
ytest <- Boston[-train, 14]
```

a) Set the `ntree` argument to 750, and create two ensembles: a bagged ensemble, using all 13 predictor variables for selecting each split, and a random forest using `sqrt(13)` for selecting each split.

```
set.seed(42)
rf.boston <- randomForest(x = x, y = y, xtest = xtest, ytest = ytest, mtry = sqrt(13),
                          ntree = 750, data = Boston)
bag.boston <- randomForest(x = x, y = y, xtest = xtest, ytest = ytest, mtry = 13,
                           ntree = 750)
```

b) Inspect the test error (which can be found in the `$test$mse` slot of the randomForest object) and the OOB error (which can be found in the `$mse` slot of the randomForest object) for both ensembles. Create a plot where the number of trees in the ensemble is on the x-axis, and the MSE is on the y-axis. Draw different lines for the OOB and test error of the bagged ensemble, as well as the OOB and test error of the random forest. (Hint: use functions `plot()` and `lines()` and the `type`, `lty` and `col` arguments)

```
plot(1:750, rf.boston$test$mse, col = "red", type = "l", xlab = "Number of Trees",
     ylab = "Test MSE")
lines(1:750, rf.boston$mse, col = "red", type = "l", lty = 2)
lines(1:750, bag.boston$test$mse, col = "blue", type = "l")
lines(1:750, bag.boston$mse, col = "blue", type = "l", lty = 2)
legend("topright", paste(rep(c("bagged", "rf"), times=2),
                         rep(c("(test)", "(OOB)"), each = 2)),
       col = rep(c("red", "blue"), times = 2), cex = .5, lty = rep(1:2, each = 2))
```



c) After which number of trees does the MSE start to stabilize?

d) Which of the two ensembles is most accurate on the test data?

e) Does the OOB error give a better estimate of test error for the random forest, or for the bagged ensemble? Can you explain the difference?