# Project 4

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#### Tree-based methods

We study the German credit data set from the UC Irvine machine learning repository. A set of 20 covariates (attributes) are available (7 numerical, 13 categorical) for 300 customers with bad credit risk and 700 customers with good credit risk (0 = Good, 1 = Bad).

We aim to classify a customer as *good* or *bad* with respect to credit risk. It is worse to class a customer as good when they are bad, than it is to class a customer as bad when they are good.

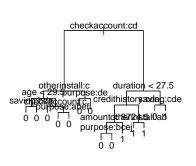
```
#read data, divide into train and test
German.credit <- read.table("http://archive.ics.uci.edu/ml/machine-learning-databases/statlog/german/ge</pre>
 \hbox{\it\# You can also find a doc file with a brief description of the German credit dataset on the web. } \\
colnames(German.credit) = c("checkaccount", "duration", "credithistory", "purpose",
                              "amount", "saving", "presentjob", "installmentrate",
                              "sexstatus", "otherdebtor", "resident", "property",
                              "age", "otherinstall", "housing", "ncredits", "job",
                              "npeople", "telephone", "foreign", "response")
German.credit$response <- ifelse(German.credit$response==1,0,1)</pre>
German.credit$response = as.factor(German.credit$response) # 2 = bad
table(German.credit$response)
##
##
     0
## 700 300
# str(German.credit) # to see factors and integers, numerics
set.seed(1234)
n <- nrow(German.credit)</pre>
in.train \leftarrow sample(1:n,0.75*n)
train <- German.credit[in.train,]</pre>
test <- German.credit[-in.train,]</pre>
```

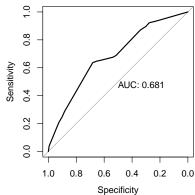
We want to try all 4 tree methods: single classification tree, bagging, random forest, boosting

- 1. Classification tree
- (a) Full classification tree

Modify the setting in the following R chunk for "eval" to be eval=TRUE to see the results.

```
set.seed(100)
fulltree=tree(response~.,train,split="deviance")
summary(fulltree)
##
## Classification tree:
## tree(formula = response ~ ., data = train, split = "deviance")
## Variables actually used in tree construction:
## [1] "checkaccount" "otherinstall" "age"
                                                       "saving"
## [5] "purpose"
                       "duration"
                                       "credithistory" "amount"
## Number of terminal nodes: 14
## Residual mean deviance: 0.8658 = 637.2 / 736
## Misclassification error rate: 0.2067 = 155 / 750
par(mfrow=c(1,2))
plot(fulltree)
text(fulltree)
# print(fulltree)
fullpred=predict(fulltree,test,type="class")
testres = table(test$response,fullpred) # confusion matrix, rows=true, columns = predictions
print(testres)
##
      fullpred
##
         0
           1
     0 156 17
##
     1 58 19
1-sum(diag(testres))/(sum(testres)) # Classification error rate
## [1] 0.3
predfulltree = predict(fulltree,test, type = "vector")
testfullroc=roc(test$response == "1", predfulltree[,2])
auc(testfullroc)
## Area under the curve: 0.6808
par(pty="s") # "s" generates a square plotting region
plot.roc(testfullroc,xlim=c(1,0),asp=1,print.auc=TRUE)
```





#### (b) Pruned classification tree

Modify the setting in the following R chunk for "eval" to be eval=TRUE to see the results.

```
# prune the full tree
set.seed(1234)
fullcv=cv.tree(fulltree,FUN=prune.misclass,K=5)
par(mfrow=c(1,3))
par(pty="s")
plot(fullcv$size,fullcv$dev,type="b", xlab="Terminal nodes",ylab="misclassifications")
# print(fullcv)
prunesize=fullcv$size[which.min(fullcv$dev)]
prunetree=prune.misclass(fulltree,best=prunesize)
plot(prunetree,type="proportional")
text(prunetree,pretty=1)
predprunetree = predict(prunetree,test, type = "class")
prunetest=table(test$response,predprunetree)
print(prunetest)# rows are true; columns are predictions
1-sum(diag(prunetest))/(sum(prunetest))
predprunetree = predict(prunetree,test, type = "vector")
testpruneroc=roc(test$response == "1", predprunetree[,2])
auc(testpruneroc)
par(pty="s")
plot(testpruneroc,xlim=c(1,0),print.auc=TRUE)
```

### Question 1: Why do we want to prune the full tree?

**Answer**: Pruning is done to reduce the chances of overfitting the tree to the training data and reduce the overall complexity of the tree.

#### 2. Bagged trees

Modify the setting in the following R chunk for "eval" to be eval=TRUE to see the results.

```
library(randomForest)
set.seed(1234)
bag=randomForest(response~., data=German.credit,subset=in.train,
                 mtry=20,ntree=500,importance=TRUE)
bag$confusion # for training data
yhat.bag=predict(bag,newdata=test)
misclass.bag=table(test$response,yhat.bag) # rows are true; columns are predictions
print(misclass.bag)
1-sum(diag(misclass.bag))/(sum(misclass.bag)) # test error rate
predbag = predict(bag,test, type = "prob") # to AUC of ROC curves
testbagroc=roc(test$response == "1", predbag[,2])
auc(testbagroc)
# make plots
layout(matrix(c(1,1,1), ncol=3, byrow = TRUE), widths = c(1,4))
par(mfrow=c(1,3))
par(pty="s")
plot.roc(testbagroc,xlim=c(1,0),print.auc=TRUE)
varImpPlot(bag,pch=20,type=1)
varImpPlot(bag,pch=20,type=2)
```

Question 2: What is the main motivation behind bagging?

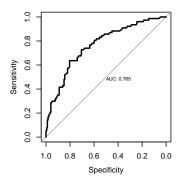
**Answer**: the main motivation behind bagging is to decrease the variance through building more advanced models of data sets.

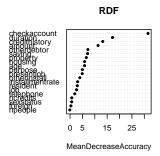
#### 3. Random forest

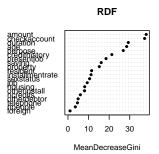
#### Question 3:

- 1. Plug in your code in the following R chunk for using random forest method to the train and make predictions for test, calculate ROC curves, etc.
- 2. The code will be similar to code for bagging method with only one parameter 'mtry' being different (use the number for 'mtry' suggested in the book or notes).
- 3. Please use your own name for the returned random forest model, predictions, etc.

```
library(randomForest)
set.seed(1234)
RDF = randomForest(response~., data=German.credit,subset=in.train,
                 mtry=4,ntree=500,importance=TRUE) #We choose mtry=4 because sqrt(20) = 4 approximately.
RDF$confusion # for training data
##
       0 1 class.error
## 0 488 39
              0.0740038
## 1 140 83
              0.6278027
yhat.RDF=predict(RDF,newdata=test)
misclass.RDF=table(test$response,yhat.RDF) # rows are true; columns are predictions
print(misclass.RDF)
##
      yhat.RDF
##
         0
##
     0 160 13
     1 53 24
1-sum(diag(misclass.RDF))/(sum(misclass.RDF)) # test error rate
## [1] 0.264
predRDF = predict(RDF,test, type = "prob") # to AUC of ROC curves
testRDFroc=roc(test$response == "1", predRDF[,2])
auc(testRDFroc)
## Area under the curve: 0.7649
# make plots
layout(matrix(c(1,1,1), ncol=3, byrow = TRUE), widths = c(1,4))
par(mfrow=c(1,3))
par(pty="s")
plot.roc(testRDFroc,xlim=c(1,0),print.auc=TRUE)
varImpPlot(RDF,pch=20,type=1)
varImpPlot(RDF,pch=20,type=2)
```







Question 4: The value of the parameter mtry is the only difference between bagging and random forest. What does this parameter mean? What is the good effect of choosing mtry to be a value less than the number of covariates?

Answer: mtry means the Number of variables randomly sampled as candidates at each split. By doing so, there are only at most m very correlated predictors across any two splits. the good effect of choosing mtry to be a value less than the number of covariates it is correlate the tree hence will help improve the variance reduction of bagging

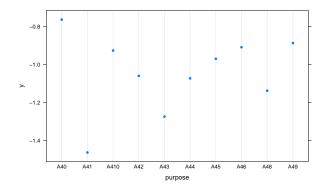
### 4. Boosting

Modify the setting in the following R chunk for "eval" to be eval=TRUE to see the results.

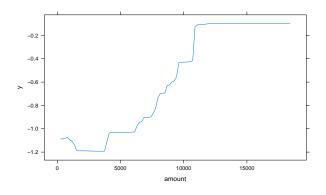
```
##
                                var
                                         rel.inf
## checkaccount
                      checkaccount 31.048947678
## credithistory
                     credithistory 12.383104160
## amount
                            amount 11.791325649
## duration
                          duration 10.917186437
## purpose
                           purpose
                                    8.510126568
## age
                                age
                                    5.582791507
## saving
                            saving
                                    5.567498296
## property
                          property
                                    2.611584544
## presentjob
                        presentjob
                                    2.407915227
## otherinstall
                      otherinstall
                                    2.090040115
## housing
                           housing
                                    2.029122406
## installmentrate installmentrate
                                    2.012068991
## otherdebtor
                       otherdebtor 1.138581958
                                    0.918719445
## sexstatus
                         sexstatus
## resident
                                    0.658115877
                          resident
## job
                                job
                                    0.200007991
## telephone
                         telephone
                                    0.087931571
```

```
## foreign foreign 0.039202985
## ncredits ncredits 0.005728594
## npeople npeople 0.00000000

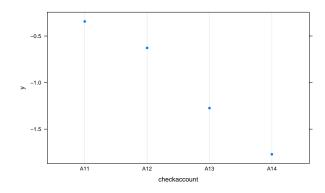
par(pty="s")
par(mfrow=c(1,4))
plot(boost,i="purpose")
```



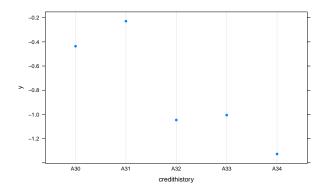
# plot(boost,i="amount")



plot(boost,i="checkaccount")



plot(boost,i="credithistory")



```
library(gbm)
# make predictions
test$response <- as.character(test$response)
yhat.boost=predict(boost,newdata=test,n.trees=8000,type="response")
boost.pred <- ifelse(yhat.boost>=0.5,1,0)

misclass.boost <- table(test$response,boost.pred)
print(misclass.boost)
1-sum(diag(misclass.boost))/(sum(misclass.boost))

testrfroc=roc(test$response == "1",yhat.boost)
auc(testrfroc)
par(pty="s")
plot(testrfroc,xlim=c(1,0),print.auc=TRUE)</pre>
```

Question 5: What is the main difference between boosting and random forest (or bagging)?

**Answer**: The main difference between boosting and random forest is the random forests builds each tree independently while boosting builds one tree at a time.

Question 6: Compare among the above 4 methods: classification tree, bagging, random forest, boosted trees, using the above results and/or plots, such as the test misclassification error rates, AUC, etc.

Answer: for classification method the misclassification error is 0.3 and the area under the curve 0.68. the classification error for bagging is 0.284 and the area under the curve is 0.7561.the classification method gives 14 terminal nodes. However, after pruning the tree using cross validation we got 7 terminal node which is a better ternimal node, the random Forrest misclassification error is 0.264 and the AUC is 0.7649 also the predictors that contribute the most in the tree are checkacount and amount boosting misclassification error is 0.296 and the AUC is 0.7493, the best method is the one with small misclassification error and big AUC. Therefore, the random forrest method is the best method to use in this case.