lab09

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The Data: The data source for this lab is from UCI Machine Learning Repository - QSAR biodegradation data set.

Import data

Tasks

Training and Test Data

1,Randomly divide the data set into two halves, and save them in two data frames named train and test.

```
set.seed(189)
ind<-sample(1:nrow(biodeg))
train<-biodeg[ind%2==0,]
test<-biodeg[ind%2!=0,]
### teacher's code
n = nrow(biodeg)
i = sample(n, round(n/2))
train = biodeg[i,]
test = biodeg[-i,]
dim(train)</pre>
```

```
## [1] 528 42
```

Classification trees

2, Fit an unpruned classification tree to the data. Plot it(as pretty as you can).

The height of tree decides the deviation difference of each variables. The most important three variables are "SpMaxBm" "F02CN" "SpMaxL". ### Because it is dendrogram, we can use the size of the jump by each split to measure the importance of a split (and thus the variable). Therefore, the three most important variables are.

```
r.tree<-tree(class~., data=train)
r.tree</pre>
```

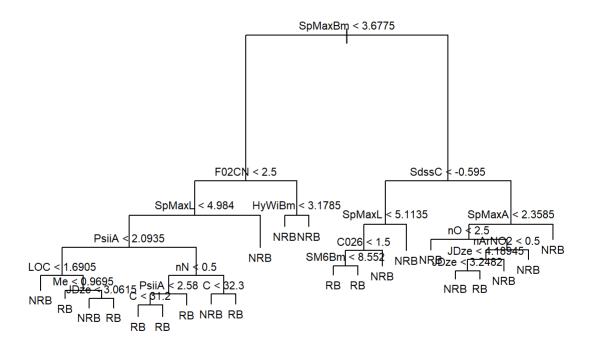
```
## node), split, n, deviance, yval, (yprob)
##
        * denotes terminal node
##
##
     1) root 528 663.500 NRB ( 0.67803 0.32197 )
##
      2) SpMaxBm < 3.6775 222 299.000 RB ( 0.40090 0.59910 )
        4) F02CN < 2.5 189 237.700 RB ( 0.32275 0.67725 )
##
          8) SpMaxL < 4.984 163 181.700 RB ( 0.24540 0.75460 )
##
##
           16) PsiiA < 2.0935 44 60.630 NRB ( 0.54545 0.45455 )
##
             32) LOC < 1.6905 22 20.860 NRB ( 0.81818 0.18182 ) *
             33) LOC > 1.6905 22 25.780 RB ( 0.27273 0.72727 )
##
               66) Me < 0.9695 9
                                  0.000 RB ( 0.00000 1.00000 ) *
##
               67) Me > 0.9695 13 17.940 RB ( 0.46154 0.53846 )
##
##
                134) JDze < 3.0615 8
                                      8.997 NRB ( 0.75000 0.25000 ) *
##
                135) JDze > 3.0615 5
                                      0.000 RB ( 0.00000 1.00000 ) *
##
           17) PsiiA > 2.0935 119 93.950 RB ( 0.13445 0.86555 )
##
             34) nN < 0.5 91 38.730 RB ( 0.05495 0.94505 )
##
               68) PsiiA < 2.58 34 28.390 RB ( 0.14706 0.85294 )
                136) C < 31.2 13 17.320 RB ( 0.38462 0.61538 ) *
##
                                  0.000 RB ( 0.00000 1.00000 ) *
##
                137) C > 31.2 21
##
               69) PsiiA > 2.58 57
                                    0.000 RB ( 0.00000 1.00000 ) *
             35) nN > 0.5 28 37.520 RB ( 0.39286 0.60714 )
##
##
               70) C < 32.3 16 21.170 NRB ( 0.62500 0.37500 ) *
##
               71) C > 32.3 12
                                6.884 RB ( 0.08333 0.91667 ) *
##
          9) SpMaxL > 4.984 26 25.460 NRB ( 0.80769 0.19231 ) *
        5) F02CN > 2.5 33 28.070 NRB ( 0.84848 0.15152 )
##
         10) HyWiBm < 3.1785 20
                                 0.000 NRB ( 1.00000 0.00000 ) *
##
##
         11) HyWiBm > 3.1785 13 17.320 NRB ( 0.61538 0.38462 ) *
##
      3) SpMaxBm > 3.6775 306 225.700 NRB ( 0.87908 0.12092 )
        6) SdssC < -0.595 51 69.740 NRB ( 0.56863 0.43137 )
##
         12) SpMaxL < 5.1135 30 36.650 RB ( 0.30000 0.70000 )
##
           24) C026 < 1.5 25 21.980 RB ( 0.16000 0.84000 )
##
##
             48) SM6Bm < 8.552 10 13.460 RB ( 0.40000 0.60000 ) *
             49) SM6Bm > 8.552 15
                                   0.000 RB ( 0.00000 1.00000 ) *
##
##
           25) C026 > 1.5 5
                             0.000 NRB ( 1.00000 0.00000 ) *
##
         13) SpMaxL > 5.1135 21
                                 8.041 NRB ( 0.95238 0.04762 ) *
##
        7) SdssC > -0.595 255 114.100 NRB ( 0.94118 0.05882 )
         14) SpMaxA < 2.3585 161 99.760 NRB ( 0.90683 0.09317 )
##
##
           28) nO < 2.5 130 54.520 NRB ( 0.94615 0.05385 ) *
##
           29) nO > 2.5 31 35.400 NRB ( 0.74194 0.25806 )
             58) nArNO2 < 0.5 19 25.860 NRB ( 0.57895 0.42105 )
##
##
              ##
                232) JDze < 3.2482 6
                                      7.638 NRB ( 0.66667 0.33333 ) *
##
                233) JDze > 3.2482 6
                                      0.000 RB ( 0.00000 1.00000 ) *
##
              117) JDze > 4.18945 7
                                     0.000 NRB ( 1.00000 0.00000 ) *
##
             59) nArNO2 > 0.5 12
                                 0.000 NRB ( 1.00000 0.00000 ) *
         ##
```

summary(r.tree)

```
##
## Classification tree:
## tree(formula = class ~ ., data = train)
## Variables actually used in tree construction:
## [1] "SpMaxBm" "F02CN" "SpMaxL" "PsiiA" "LOC"
                                                        "Me"
                                                                  "JDze"
## [8] "nN"
                 "C"
                           "HyWiBm" "SdssC" "C026"
                                                        "SM6Bm"
                                                                  "SpMaxA"
                 "nArNO2"
## [15] "n0"
## Number of terminal nodes: 22
## Residual mean deviance: 0.3986 = 201.7 / 506
## Misclassification error rate: 0.07955 = 42 / 528
```

```
plot(r.tree)
r.tree
```

```
## node), split, n, deviance, yval, (yprob)
        * denotes terminal node
##
##
    1) root 528 663.500 NRB ( 0.67803 0.32197 )
##
      2) SpMaxBm < 3.6775 222 299.000 RB ( 0.40090 0.59910 )
##
        4) F02CN < 2.5 189 237.700 RB ( 0.32275 0.67725 )
##
##
          8) SpMaxL < 4.984 163 181.700 RB ( 0.24540 0.75460 )
##
           16) PsiiA < 2.0935 44 60.630 NRB ( 0.54545 0.45455 )
             32) LOC < 1.6905 22 20.860 NRB ( 0.81818 0.18182 ) *
##
##
             33) LOC > 1.6905 22 25.780 RB ( 0.27273 0.72727 )
##
               66) Me < 0.9695 9
                                 0.000 RB ( 0.00000 1.00000 ) *
               67) Me > 0.9695 13 17.940 RB ( 0.46154 0.53846 )
##
                134) JDze < 3.0615 8
                                     8.997 NRB ( 0.75000 0.25000 ) *
##
##
                135) JDze > 3.0615 5
                                     0.000 RB ( 0.00000 1.00000 ) *
##
           17) PsiiA > 2.0935 119 93.950 RB ( 0.13445 0.86555 )
             34) nN < 0.5 91 38.730 RB ( 0.05495 0.94505 )
##
               68) PsiiA < 2.58 34 28.390 RB ( 0.14706 0.85294 )
##
                136) C < 31.2 13 17.320 RB ( 0.38462 0.61538 ) *
##
                                 0.000 RB ( 0.00000 1.00000 ) *
                137) C > 31.2 21
##
               69) PsiiA > 2.58 57
                                    0.000 RB ( 0.00000 1.00000 ) *
##
             35) nN > 0.5 28 37.520 RB ( 0.39286 0.60714 )
##
               70) C < 32.3 16 21.170 NRB ( 0.62500 0.37500 ) *
##
               71) C > 32.3 12
                               6.884 RB ( 0.08333 0.91667 ) *
##
          9) SpMaxL > 4.984 26 25.460 NRB ( 0.80769 0.19231 ) *
##
##
        5) F02CN > 2.5 33 28.070 NRB ( 0.84848 0.15152 )
                                0.000 NRB ( 1.00000 0.00000 ) *
         10) HyWiBm < 3.1785 20
##
##
         11) HyWiBm > 3.1785 13 17.320 NRB ( 0.61538 0.38462 ) *
##
      3) SpMaxBm > 3.6775 306 225.700 NRB ( 0.87908 0.12092 )
        6) SdssC < -0.595 51 69.740 NRB ( 0.56863 0.43137 )
##
         12) SpMaxL < 5.1135 30 36.650 RB ( 0.30000 0.70000 )
##
##
           24) C026 < 1.5 25 21.980 RB ( 0.16000 0.84000 )
##
             48) SM6Bm < 8.552 10 13.460 RB ( 0.40000 0.60000 ) *
             49) SM6Bm > 8.552 15
                                  0.000 RB ( 0.00000 1.00000 ) *
##
           25) C026 > 1.5 5
                             0.000 NRB ( 1.00000 0.00000 ) *
##
##
         13) SpMaxL > 5.1135 21
                                 8.041 NRB ( 0.95238 0.04762 ) *
        7) SdssC > -0.595 255 114.100 NRB ( 0.94118 0.05882 )
##
         14) SpMaxA < 2.3585 161 99.760 NRB ( 0.90683 0.09317 )
##
           28) nO < 2.5 130 54.520 NRB ( 0.94615 0.05385 ) *
##
##
           29) nO > 2.5 31 35.400 NRB ( 0.74194 0.25806 )
             58) nArNO2 < 0.5 19 25.860 NRB ( 0.57895 0.42105 )
##
              ##
##
                232) JDze < 3.2482 6
                                     7.638 NRB ( 0.66667 0.33333 ) *
##
                233) JDze > 3.2482 6
                                     0.000 RB ( 0.00000 1.00000 ) *
##
              117) JDze > 4.18945 7
                                    0.000 NRB ( 1.00000 0.00000 ) *
##
             ##
```



3, Compute the training and test errors.

This function fhat.tree computes yhat according to fit and data, errors() function computes classification errors.

```
errors<- function(fit,f,train,test) {
  train_class = f(fit, train)
  test_class = f(fit,test)
  c(training.error=mean(train$class != train_class), test.error=mean(test$class != test_class))
}
fhat.tree <- function(fit,data){
  yhat<-predict(fit,data)
  yhat.class<-levels(data$class)[apply(yhat, 1, which.max)]
}</pre>
```

training and test error for unpruned tree

```
yhat.class<-fhat.tree(r.tree,train) ## converting probability to class index
head(yhat.class)</pre>
```

```
## [1] "RB" "NRB" "NRB" "NRB" "NRB"
```

```
errors(r.tree, fhat.tree, train, test) ## classification errors
```

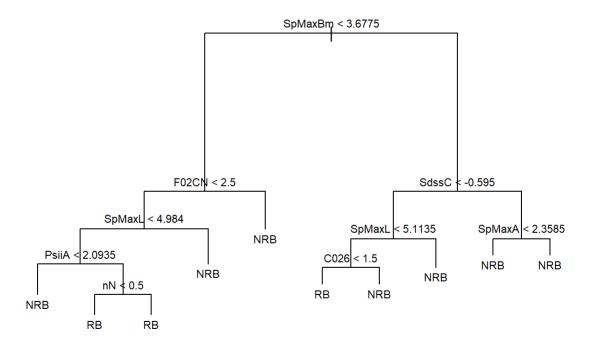
```
## training.error test.error
## 0.07954545 0.20683112
```

4, Consider pruning the tree using cross-validation with deviance. Produce a pruned tree based by selecting a cost-complexity parameter value, and plot it.

The results shows training & test errors do not improve with pruning. Prunning is a data-compression method of reducing size of decision tree to prevent over-fitting,(T) This is the same as returned by function errors(). The test error is much higher than the training error.

(T)While it is understandable that the training error will increase, the test error has also increased a little, from 0.197 to 0.207. The pruning does not help much in terms of reducing the misclassification rate, but it does produce a smaller tree. The pruning should likely have helped in terms of reducing the (test set) deviance.

```
cv.r = cv.tree(r.tree)
j.min<-which.min(cv.r$dev)
k = cv.r$k[j.min]
r2 = prune.tree(r.tree, k=k) # tree pruning, based on cost-complexity
plot(r2)
text(r2, pretty=0,cex=0.7)</pre>
```



```
#### training & test errors
errors(r2,fhat.tree,train,test)

## training.error test.error
## 0.1250000 0.2106262
```

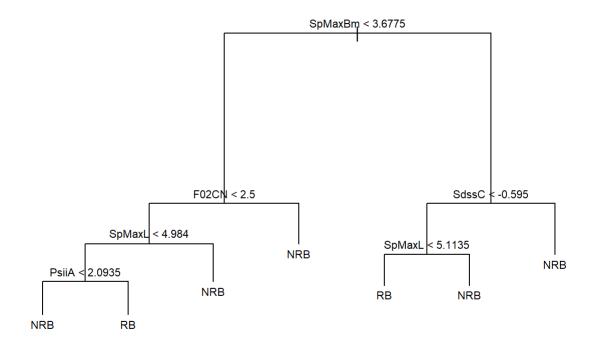
5, Consider pruning the tree using cross-validation with misclassification rates. Produce a pruned tree by selecting a tree size, and plot it.

The results shows training & test errors increase. Pruning can help with simplify decision tree by removing less-important nodes, sometimes it may increase classification accuracy, but not with this sample.

```
(cv.r = cv.tree(r.tree)) # Cross-validation
```

```
## $size
   [1] 22 21 19 18 17 14 12 11 10 9 8 7 6 5 4 3 2 1
##
##
## $dev
   [1] 736.6644 671.4829 651.9426 654.2912 632.7191 629.4700 602.8071 602.8071
##
   [9] 573.7172 574.4742 555.2797 512.8777 521.3702 524.8104 541.3779 555.9796
## [17] 552.2203 664.7430
##
## $k
##
   [1]
             -Inf
                    7.638170 8.392276
                                         8.523261 9.466416
                                                                9.987454
   [7] 10.705538 10.748428 13.988768 14.338653 14.668364 17.699562
##
## [13] 25.044679 27.067664 30.622457 33.172936 41.838027 138.882538
##
## $method
## [1] "deviance"
##
## attr(,"class")
## [1] "prune"
                       "tree.sequence"
(j.min = which.min(cv.r$dev))
                                      # smallest CV deviance
## [1] 12
(size = cv.r$size[j.min])
## [1] 7
(r3 = prune.tree(r.tree, best=size))
                                      # tree pruning, based on the best size
## node), split, n, deviance, yval, (yprob)
##
         * denotes terminal node
##
   1) root 528 663.500 NRB ( 0.67803 0.32197 )
##
      2) SpMaxBm < 3.6775 222 299.000 RB ( 0.40090 0.59910 )
##
##
        4) F02CN < 2.5 189 237.700 RB ( 0.32275 0.67725 )
##
          8) SpMaxL < 4.984 163 181.700 RB ( 0.24540 0.75460 )
          16) PsiiA < 2.0935 44 60.630 NRB ( 0.54545 0.45455 ) *
##
##
          17) PsiiA > 2.0935 119 93.950 RB ( 0.13445 0.86555 ) *
          9) SpMaxL > 4.984 26 25.460 NRB ( 0.80769 0.19231 ) *
##
##
        5) F02CN > 2.5 33 28.070 NRB ( 0.84848 0.15152 ) *
      3) SpMaxBm > 3.6775 306 225.700 NRB ( 0.87908 0.12092 )
##
        6) SdssC < -0.595 51 69.740 NRB ( 0.56863 0.43137 )
##
         12) SpMaxL < 5.1135 30 36.650 RB ( 0.30000 0.70000 ) *
##
##
         13) SpMaxL > 5.1135 21 8.041 NRB ( 0.95238 0.04762 ) *
        7) SdssC > -0.595 255 114.100 NRB ( 0.94118 0.05882 ) *
##
```

```
plot(r3)
text(r3, pretty=0,cex=0.7)
```



```
##### training & test classification errors
errors(r3,fhat.tree,train,test)

## training.error test.error
## 0.1344697 0.2201139
```

Bagging

6, Produce a Bagging model with 500 trees construnted.

For bagging, mtry is number of variables. According to "Mean decrease Gini", the three most important variables are SpMaxBm, SpPosABp, SpMaxL.

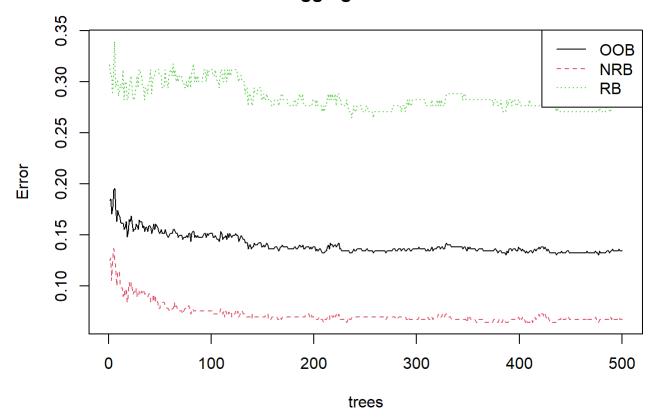
(T)The test error is 0.148, which is very similar to the OOB estimate of the test error: 0.140. Bagging helps prediction here. It reduces the test error from 0.203 of a pruned tree to 0.148. The test error is 0.146, which is also very similar to the OOB estimate of the test error: 0.140. Random Forest helps prediction here, if compared with the pruned tree (test error 0.203), but not much if compared with Bagging (0.148).

```
set.seed(289)
(r.bag = randomForest(class ~ ., data=train, mtry=41, importance=TRUE))
```

```
##
## Call:
   randomForest(formula = class ~ ., data = train, mtry = 41, importance = TRUE)
##
                  Type of random forest: classification
##
##
                        Number of trees: 500
## No. of variables tried at each split: 41
##
           OOB estimate of error rate: 13.45%
##
## Confusion matrix:
       NRB RB class.error
##
## NRB 334 24 0.06703911
## RB
      47 123 0.27647059
```

```
plot(r.bag, main="Bagging Error rates") # error rates
legend("topright", leg=colnames(r.bag$err.rate), lty=1:3, col=1:3)
```

Bagging Error rates



Mean decrease Gini
round(importance(r.bag),2) # show importance of variables - higher values mean more important

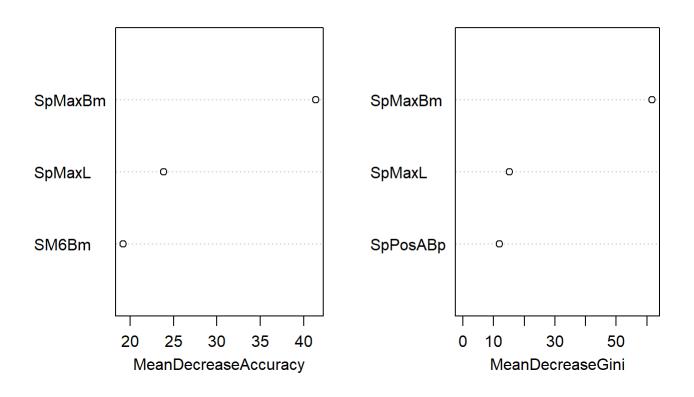
##		NRB	RB	MeanDecreaseAccuracy	MeanDecreaseGini
##	SpMaxL	8.35	23.33	23.86	15.15
##	JDze	8.77	1.65	8.66	5.97
##	nHM	0.39	9.07	9.79	1.05
##	F01NN	0.54	1.60	1.88	0.09
##	F04CN	-1.96	8.64	8.13	1.46
##	NssssC	7.68	9.31	10.53	3.38
##	nCb	4.08	3.06	5.42	0.85
##	С	7.05	-0.67	6.07	5.23
##	nCp	3.33	11.82	10.96	3.28
##	n0	4.40	5.49	7.77	3.33
##	F03CN	3.89	10.44	10.36	3.00
##	SdssC	9.86	11.09	14.52	8.39
	HyWiBm		4.51	11.07	
	LOC		10.18	11.64	
	SM6L		7.91	12.60	
	F03C0		9.36	13.18	
	Me		6.77	13.06	
	Mi		0.31	9.26	
	nNN	0.00		0.00	
	nArNO2		2.55	3.09	
	nCRX3		1.00	1.00	
	SpPosABp			17.62	
	nCIR		5.36	5.58	
	B01CBr	2.47		2.50	
	B03CCl		2.05	1.23	
	N073	-1.00		-1.00	
		7.66		13.34	
	Psii1d		-2.99	9.14	
	B04CBr		-0.87	-3.96	
	Sd0		6.79	9.05	
	TI2L		5.11	8.50	
	nCrt C026		8.48 2.47	8.86 4.18	
	F02CN		14.62	13.66	
	nHDon		0.92	1.75	
	SpMaxBm			41.38	
	PsiiA		8.76	16.06	
	nN CMCD:::		14.07	15.61	
	SM6Bm		6.94	19.22	
	nArCOOR			19.03	
##	nX	-0.25	9.62	9.76	1.19

sort(importance(r.bag)[,4],decreasing =TRUE) # Gini index ranking, max -> min important variable

##	SpMaxBm	SpMaxL	SpPosABp	PsiiA	SM6Bm	nArCOOR
##	61.680985612	15.148565258	11.959512038	11.395871186	10.433418194	8.448168365
##	SdssC	Me	nN	FØ2CN	LOC	SpMaxA
##	8.390369740	8.000780939	7.545341927	6.943576476	6.647890360	6.394527205
##	JDze	Mi	F03C0	C	Psii1d	SM6L
##	5.967641782	5.937843088	5.295158442	5.228120736	4.890491922	4.766519425
##	TI2L	HyWiBm	SdO	NssssC	n0	nCp
##	4.743215356	4.316582028	3.401054025	3.384234052	3.328450287	3.282389808
##	F03CN	nCrt	F04CN	nHDon	nX	nHM
##	2.995905269	1.615628233	1.462584684	1.402257402	1.190961236	1.045300914
##	C026	nCb	nCIR	B03CC1	nArNO2	B04CBr
##	1.005638861	0.854898683	0.606116445	0.239236157	0.144502021	0.124249887
##	F01NN	B01CBr	nNN	N073	nCRX3	
##	0.087566202	0.083739880	0.035839514	0.011333333	0.007108782	

varImpPlot(r.bag,sort=T,n.var = 3,main = "Top 3 variables importance") # importance plot

Top 3 variables importance



7, Compute both the training and test errors of this Bagging predictor.

Because model is fitted with training set, training error is reduced to 0, while the test error is similar to the OOB estimate. The Bagging does not help much with prediction.

```
set.seed(289)
r.bag = randomForest(class ~ ., data=train, mtry=41, importance=TRUE)
table(train$class,predict(r.bag,train)) ## confusion table train
##
##
         NRB RB
##
    NRB 358 0
    RB
##
           0 170
table(test$class,predict(r.bag,test)) ## confusion table test
##
##
         NRB RB
##
    NRB 316 25
##
    RB
         48 138
##### training & test classification errors
errors(r.bag,predict,train,test) ##
## training.error
                      test.error
##
        0.0000000
                       0.1366224
```

Random Forests

8, Produce a Random Forest model with 500 trees constructed.

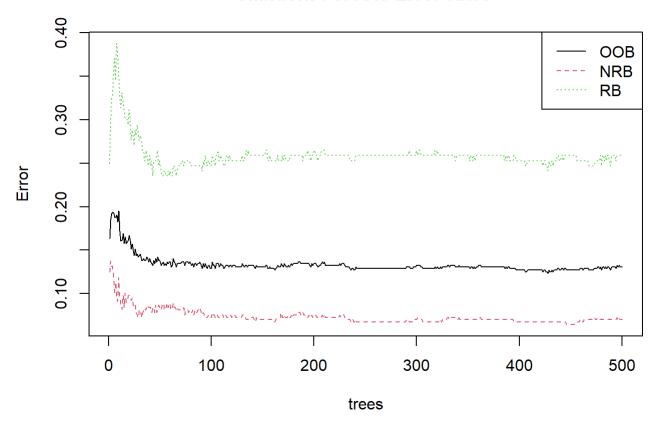
For random forest, we take m = sqrt(number of variables), sqrt(41)~6. The three most important variables are SpMaxL,SpMaxBm and SM6Bm in terms of mean decrease accuracy-the deviance. This OOB of Random Forest is slightly better than bagging method.

```
set.seed(289)
(r.RF = randomForest(class ~ ., data=train, mtry=6, importance=TRUE))
```

```
##
## Call:
##
    randomForest(formula = class ~ ., data = train, mtry = 6, importance = TRUE)
##
                  Type of random forest: classification
                        Number of trees: 500
##
## No. of variables tried at each split: 6
##
##
           OOB estimate of error rate: 13.07%
## Confusion matrix:
##
       NRB RB class.error
## NRB 333 25
                 0.0698324
## RB
        44 126
                 0.2588235
```

```
plot(r.RF, main="Random Forests Error rates") # error rates
legend("topright", leg=colnames(r.RF$err.rate), lty=1:3, col=1:3)
```

Random Forests Error rates



importance of variables matrix
round(importance(r.RF),2)

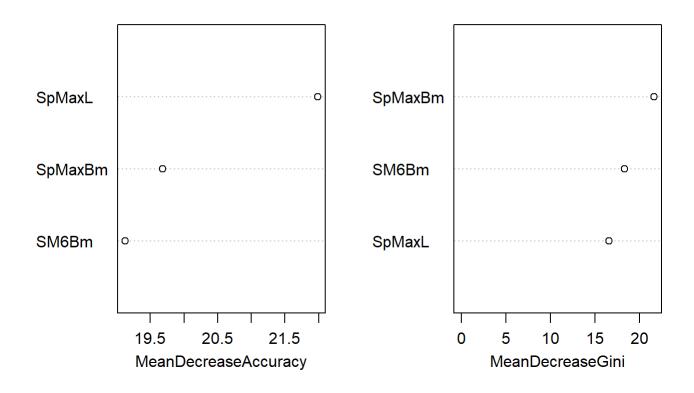
##		NRB	RB	MeanDecreaseAccuracy	MeanDecreaseGini
##	SpMaxL	13.03	18.62	21.99	16.55
##	JDze	8.36	3.65	9.06	6.36
##	nHM	7.05	8.58	9.97	3.62
##	F01NN	-0.75	1.03	-0.02	0.27
##	F04CN	5.55	9.68	10.28	2.92
##	NssssC	8.13	9.51	10.64	3.16
##	nCb	6.48	6.05	9.02	3.98
##	С	7.26	3.86	8.75	6.31
##	nCp	3.58	7.27	7.76	3.55
##	n0	9.76	12.18	15.07	6.89
##	F03CN	6.10	11.93	13.20	4.78
##	SdssC	8.22	9.98	12.06	7.56
			8.01	13.00	
	-		8.83		
			10.42	15.81	
			10.00	14.31	
	Me		7.55		
	Mi		3.82	9.40	
	nNN		0.00	1.74	
	nArNO2		2.64		
	nCRX3		1.00	0.65	
	SpPosABp			16.61	
	nCIR		5.43	6.86	
			-0.80	-1.00	
			3.88	4.34	
			-1.41		
			11.48		
	•		1.87	7.57	
			-0.73	-0.58	
	SdO		7.35	10.97	
	TI2L		7.80	10.79	
	nCrt		3.97	4.91	
	C026		3.92	8.50	
	FØ2CN		12.83	13.13	
	nHDon		2.55	3.38	
			13.33	19.68	
	•		8.85	13.70	
	nN		12.22	13.79	
			13.67	19.13	
	nArCOOR		9.86	10.56	
##	nX	5.32	7.54	8.60	2.65

ranking of mean decrease accuracy (deviance) from max to min
sort(round(importance(r.RF)[,3],2),decreasing = TRUE)

##	SpMaxL	SpMaxBm	SM6Bm	SpPosABp	SM6L	SpMaxA	n0	F03C0
##	21.99	19.68	19.13	16.61	15.81	15.36	15.07	14.31
##	nN	PsiiA	F03CN	F02CN	HyWiBm	Me	SdssC	Sd0
##	13.79	13.70	13.20	13.13	13.00	12.81	12.06	10.97
##	LOC	TI2L	NssssC	nArCOOR	F04CN	nHM	Mi	JDze
##	10.82	10.79	10.64	10.56	10.28	9.97	9.40	9.06
##	nCb	C	nX	C026	nCp	Psii1d	nCIR	nCrt
##	9.02	8.75	8.60	8.50	7.76	7.57	6.86	4.91
##	B03CCl	nArNO2	nHDon	nNN	nCRX3	F01NN	B04CBr	B01CBr
##	4.34	3.84	3.38	1.74	0.65	-0.02	-0.58	-1.00
##	N073							
##	-1.19							

```
### variable importance plot
varImpPlot(r.RF,sort=T,n.var = 3,main = "Top 3 variables importance") # importance plot
```

Top 3 variables importance



9, Compute both the training and test errors of this Random Forest predictor.

The test error is similar to the OOB estimate 13.4%. The tweak used by Random Forest does not help prediction here.

```
### errors of train and test
errors(r.RF, predict,train,test)
```

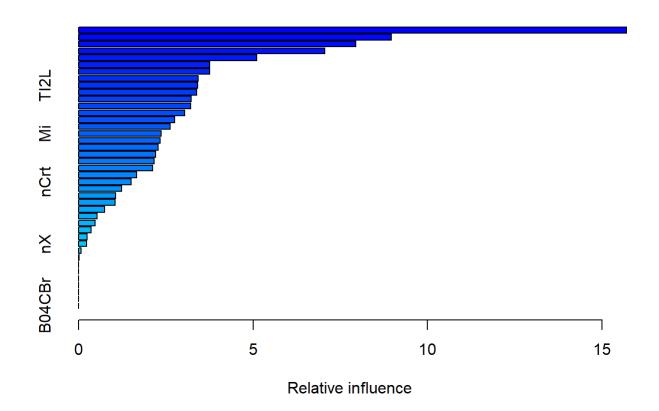
```
## training.error test.error
## 0.0000000 0.1574953
```

Boosting

10, Produce a Boosting model, with 500 trees constructed.

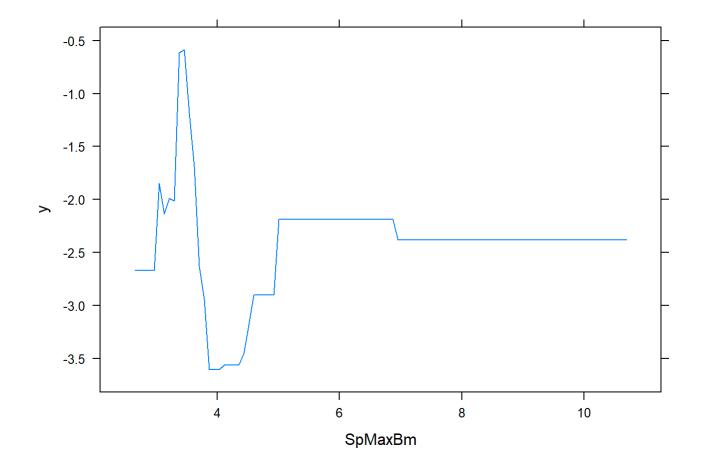
The three most important variables are SpMaxBm,SpPosABp and SM6Bm according to relative influence value (rel.inf).

```
set.seed(289)
# use distribution="bernoulli" for a two-class classification problem
train2 = cbind(train, class2=as.integer(train$class)-1) # convert class to integer class
test2 = cbind(test, class2=as.integer(test$class)-1) # convert class to integer class 2
r.boo = gbm(class2 ~ . - class, data=train2, distribution="bernoulli", n.trees=500, interaction.
depth=3)
summary(r.boo)
```



```
##
                 var
                          rel.inf
## SpMaxBm
             SpMaxBm 15.696686603
## SpPosABp SpPosABp
                      8.959091051
                     7.944346203
## SpMaxL
              SpMaxL
## SM6Bm
                     7.060195664
              SM6Bm
## PsiiA
              PsiiA 5.105365920
## nN
                  nN 3.758154886
## C
                  C 3.756462023
## F02CN
              F02CN 3.421308727
## TI2L
               TI2L
                     3.406940535
## SdssC
               SdssC
                     3.381051656
## HyWiBm
             HyWiBm 3.228784925
## JDze
                     3.209986617
                JDze
## SM6L
                SM6L
                     3.036339030
                 Me 2.752224411
## Me
## Psii1d
              Psii1d 2.623964969
## Mi
                     2.364063499
                  Μi
## F03C0
              F03C0
                      2.333888290
## SpMaxA
             SpMaxA 2.286668931
                 n0
## n0
                      2.211646432
## LOC
                 LOC
                      2.165157794
                Sd0
## Sd0
                     2.118978679
## NssssC
             NssssC
                     1.668535061
## nCrt
                nCrt
                     1.508725206
## nArCOOR
             nArCOOR
                     1.240192801
## F03CN
              F03CN
                     1.055786379
## C026
                C026
                     1.050270582
## nHDon
              nHDon
                     0.753652774
## nCp
                nCp
                      0.531574980
## nCb
                      0.470227089
                nCb
## nCIR
                nCIR
                     0.353771746
## nHM
                 nHM
                      0.239405063
## nX
                  nΧ
                      0.224196521
## F04CN
              F04CN 0.072838972
## B01CBr
              B01CBr
                      0.009515978
## F01NN
              F01NN
                      0.000000000
## nNN
                 nNN
                      0.000000000
             nArNO2
## nArNO2
                     0.000000000
## nCRX3
              nCRX3
                      0.000000000
## B03CCl
              B03CCl
                      0.000000000
## N073
                N073
                      0.000000000
## B04CBr
              B04CBr
                      0.000000000
```

plot(r.boo, "SpMaxBm") # how SpMaxBm changes would affect prediction of y values



11, Compute both the training and test errors of this Boosting predictor.

The test error 14.9% is higher than the OOB estimate 13.4% with random forest. The boosting does not help with the prediction for this dataset.(T)The test error is 0.142, an improvement from the pruned tree.

```
# new function to calculate yhat based on probablity and errors based on numeric class2
fhat.boo = function(r,data) {
  p.boo = predict(r,data,type="response")
    yhat.boo = as.integer(p.boo>0.5)
}
errors.boo<- function(r,f,train,test) {
    train_class = f(r, train)
    test_class = f(r,test)
    c(training.error=mean(train$class2 != train_class), test.error=mean(test$class2 != test_class))
}
#### training / test error
errors.boo(r.boo,fhat.boo,train2,test2)</pre>
```

```
## Using 500 trees...
##
## Using 500 trees...
```

```
## training.error test.error
## 0.000000 0.142315
```

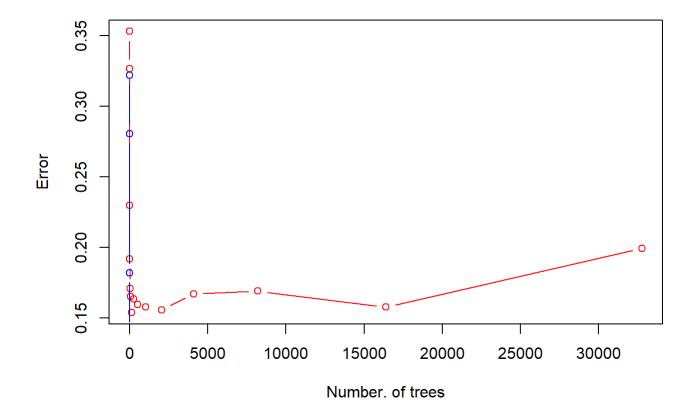
12, Demonstrate that Boosting can overfit.

100-2000 number of trees are attempted in test, the resulting train / test errors are printed. The result shows 500-600 trees have smallest test errors. Number >1000 can cause over-fitting.

```
trees = 2^{(0:15)}
test.error=rep(0,length(trees))
train.error=rep(0,length(trees))
for (i in 1:length(trees)){
  set.seed(189)
  r.over<- gbm(class2 ~ . - class, data=train2, distribution="bernoulli", n.trees=trees[i],inter
action.depth=3)
  ## train2 prediction
  p.boo1 = predict(r.over, train2, type="response")
  yhat.boo1 = as.integer(p.boo1>0.5)
  ## test 2 prediction
  p.boo2 = predict(r.over,test2,type="response")
  yhat.boo2 = as.integer(p.boo2>0.5)
  ## train / test errors
  train.error[i]<-mean(train2$class2 != yhat.boo1)</pre>
  test.error[i]<-mean(test2$class2 != yhat.boo2)</pre>
}
```

```
## Using 1 trees...
##
## Using 1 trees...
## Using 2 trees...
##
## Using 2 trees...
## Using 4 trees...
## Using 4 trees...
## Using 8 trees...
##
## Using 8 trees...
## Using 16 trees...
##
## Using 16 trees...
## Using 32 trees...
##
## Using 32 trees...
## Using 64 trees...
##
## Using 64 trees...
## Using 128 trees...
##
## Using 128 trees...
## Using 256 trees...
##
## Using 256 trees...
## Using 512 trees...
##
## Using 512 trees...
## Using 1024 trees...
##
## Using 1024 trees...
```

```
## Using 2048 trees...
##
## Using 2048 trees...
## Using 4096 trees...
##
## Using 4096 trees...
## Using 8192 trees...
##
## Using 8192 trees...
## Using 16384 trees...
##
## Using 16384 trees...
## Using 32768 trees...
##
## Using 32768 trees...
### GBM train / test errors of trees 100 - 1000
rgbm<-t(rbind(trees=trees,train.error = train.error,test.error = test.error))</pre>
### plot tree & test / train errors
plot(rgbm[,1],rgbm[,3],type = "b",col="red",xlab="Number. of trees",ylab="Error")#,log = "x")
lines(rgbm[,1],rgbm[,2],type = "b", col="blue")
```



Summary

In this class, we learn different tree-based classification/regression methods, including unpruned tree, pruned tree, bagging, random forest and GBM. We use 50% randomly generated orginal data as training data to train the model and test model classfication errors with 50% test dataset. Because the training data is used to generate the model, the test error would reflect more the accuracy of the fitted model. The result shows that the pruned tree models seleted by either Gini index or variance do not reduce the test errors, both \sim 19% test errors. About bagging, the estimated OOB of error rate is 14.04%, the real testing error is 14.4%. For random forest, OOB estimate is 13.5% , the real test error is 14.4%. For GBM, we teseted number of trees from 100- 1000, the lowest test errors have 500-600 trees with 14.7% error rate. Trees over 600 can cause over-fitting of model. Sofar, The bagging / random forest are probably the best methods according to the result of test errors.