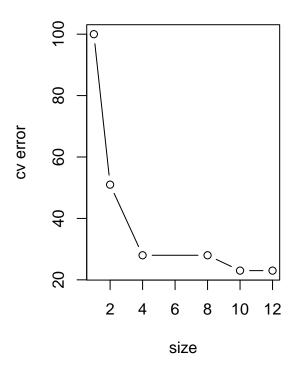
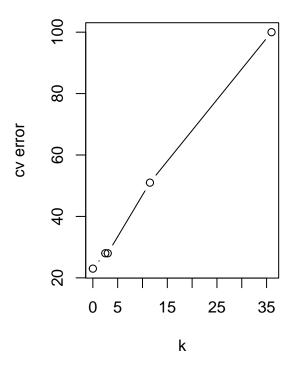
Q2.

```
data(crabs)
head(crabs)
##
     sp sex index
                  FL RW CL
                                 CW BD
## 1 B
              1 8.1 6.7 16.1 19.0 7.0
## 2 B
                2 8.8 7.7 18.1 20.8 7.4
         Μ
## 3 B
         M
               3 9.2 7.8 19.0 22.4 7.7
## 4 B M
               4 9.6 7.9 20.1 23.1 8.2
## 5 B M
               5 9.8 8.0 20.3 23.0 8.2
## 6 B M
               6 10.8 9.0 23.0 26.5 9.8
set.seed(6789)
inTrain <- createDataPartition(crabs$sp, p = 0.8, list = FALSE)</pre>
training <- crabs[inTrain,]</pre>
testing <- crabs[-inTrain,]</pre>
(a)
library(tree)
## Warning: package 'tree' was built under R version 4.0.3
## Registered S3 method overwritten by 'tree':
     method
##
     print.tree cli
set.seed(10)
tree.crabs=tree(sp~. -index, training)
cv.crabs=cv.tree(tree.crabs,FUN=prune.misclass)
names(cv.crabs)
## [1] "size"
                "dev"
                                  "method"
cv.crabs
## $size
## [1] 12 10 8 4 2 1
## $dev
## [1] 23 23 28 28 51 100
##
## [1] -Inf 0.0 2.5 3.0 11.5 36.0
## $method
## [1] "misclass"
##
## attr(,"class")
## [1] "prune"
                       "tree.sequence"
par(mfrow=c(1,2))
plot(cv.crabs$size,cv.crabs$dev / length(train),ylab="cv error", xlab="size",type="b")
plot(cv.crabs$k, cv.crabs$dev / length(train),ylab="cv error", xlab="k",type="b")
```

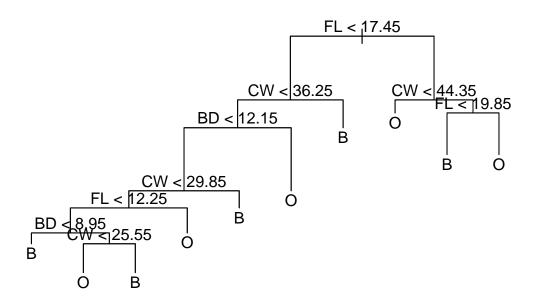




Hence, the lowest test error is obtained when size = 10

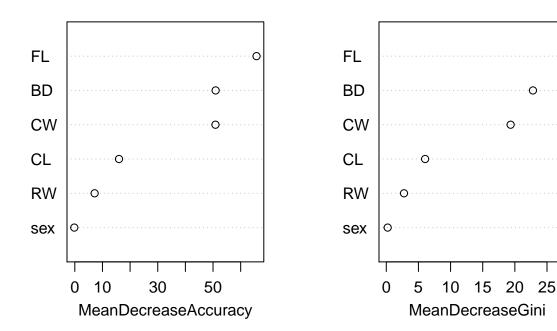
 $\#\mathrm{plot}$

```
prune.crabs=prune.misclass(tree.crabs,best=10)
plot(prune.crabs)
text(prune.crabs,pretty=0)
```



```
#test error
tree.pred=predict(prune.crabs,testing,type="class")
table(tree.pred,testing$sp)
##
## tree.pred B O
##
           B 18 3
           0 2 17
##
(test.err<-(3+2)/40) #test error
## [1] 0.125
#train error
tree.pred_train=predict(prune.crabs,training,type="class")
table(tree.pred_train,training$sp)
##
## tree.pred_train B O
##
                B 78 2
                0 2 78
(train.err<-(2+2)/160) #train error
## [1] 0.025
(b)
library(randomForest)
```

rf.crabs



The two most important variables are FL and BD, however, the result of single tree shows that FL and CW are the two most important variables, which indicates a difference.

```
#train error
rf.train_pred = predict(rf.crabs, training)
table(rf.train_pred,training$sp)
##
## rf.train_pred B 0
```

```
B 80 0
##
               0 0 80
(train.err<-(0+0)/160) #train error
## [1] 0
#test error
rf.test_pred = predict(rf.crabs, testing)
table(rf.test_pred,testing$sp)
## rf.test_pred B O
##
              B 15 2
              0 5 18
##
(test.err<-(5+2)/40) #test error
## [1] 0.175
(C)
library(gbm)
## Warning: package 'gbm' was built under R version 4.0.3
## Loaded gbm 2.1.8
library(adabag)
## Warning: package 'adabag' was built under R version 4.0.3
## Loading required package: rpart
## Loading required package: foreach
##
## Attaching package: 'foreach'
## The following objects are masked from 'package:purrr':
##
##
       accumulate, when
## Loading required package: doParallel
## Warning: package 'doParallel' was built under R version 4.0.3
## Loading required package: iterators
## Loading required package: parallel
crabs$sp01 = ifelse(crabs$sp=="B", 1, 0)
set.seed(6789)
inTrain <- createDataPartition(crabs$sp01, p = 0.8, list = FALSE)</pre>
training <- crabs[inTrain,]</pre>
testing <- crabs[-inTrain,]</pre>
\#crabs.boostcv < -boosting.cv (sp~.-index-sp01, data = training, v = 5, mfinal = 1000)
#The cross-validation step is too slow, so this step is skipped in the result
adaboost.fit = gbm(sp01~.-index-sp, data = training, distribution="adaboost", n.trees=1000)
```

```
#train error
probs.adaboost = predict(adaboost.fit, training, n.trees = 1000, type = 'response')
pred.adaboost = ifelse(probs.adaboost > 0.5, 1, 0)
train_err = mean(pred.adaboost!=training$sp01)
print(train_err)

## [1] 0.0125

#test error
probs.adaboost = predict(adaboost.fit, testing, n.trees = 1000, type = 'response')
pred.adaboost = ifelse(probs.adaboost > 0.5, 1, 0)
test_err = mean(pred.adaboost!=testing$sp01)
print(test_err)
```

[1] 0.075

(d) The results of Adaboost reports the second lowest train error and lowest test error. Hence, for this dataset, we should choose adaboost as our method. The results are non-consistent across methods.