HW4

Sijia Yue

11/13/2019

Q1

Write two function to generate the results:

```
x_ised_boot = c(0.1,0.15,0.2,0.2,0.55,0.6,0.6,0.65,0.7, 0.75)

majority_clf = function(votes){
  pro_votes = sum(x_ised_boot>0.5)
  majority_is_pro = (length(x_ised_boot)/2) < pro_votes
  return(majority_is_pro)
}
avg_clf = function(votes){
  avg = mean(votes)
  return(avg>0.5)
}

majority_clf(x_ised_boot)
```

```
## [1] TRUE
```

```
avg_clf(x_ised_boot)
```

```
## [1] FALSE
```

When implementing majority vote, the final classification is red.

When calculating the average probability, the final classification is green.

Q2

(a) Create a training set containing a random sample of 800 observations, and a test set containing the remaining observations

```
set.seed(200)
data(OJ)
random_code = sample(1:nrow(OJ), 800, replace = F)
df_train = OJ[random_code,]
df_test = OJ[-random_code,]

dim(df_train)
```

```
## [1] 800  18
```

```
dim(df_test)
```

```
## [1] 270  18
```

(b) Fit a tree to the training data, with Purchase as the response and the other variables as predictors. Use the summary() function to produce summary statistics about the tree, and describe the results obtained. What is the training error rate? How many terminal nodes does the tree have?

```
fit_tree = tree(Purchase ~., df_train)
summary(fit_tree)
```

```
##
## Classification tree:
## tree(formula = Purchase ~ ., data = df_train)
## Variables actually used in tree construction:
## [1] "LoyalCH"       "ListPriceDiff" "PctDiscMM"
## Number of terminal nodes:  6
## Residual mean deviance:  0.7964 = 632.4 / 794
## Misclassification error rate: 0.1713 = 137 / 800
```

3 variables are used in the tree construction. There are 6 terminal nodes and the training error rate is 0.1713.

(c) Type in the name of the tree object in order to get a detailed text output. Pick one of the terminal nodes, and interpret the information displayed.

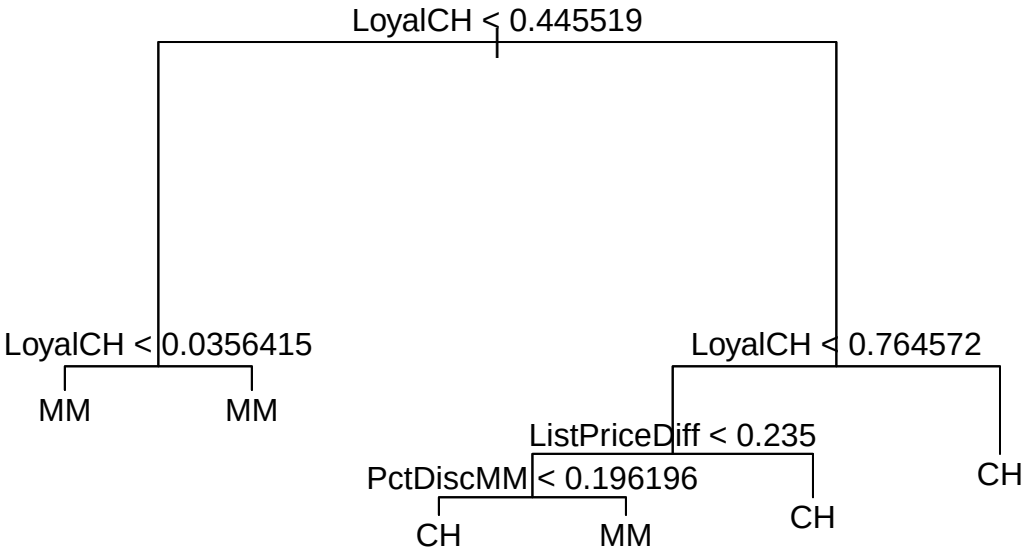
```
fit_tree
```

```
## node), split, n, deviance, yval, (yprob)
##       * denotes terminal node
##
##  1) root 800 1075.000 CH ( 0.60250 0.39750 )
##    2) LoyalCH < 0.445519 279  285.200 MM ( 0.20789 0.79211 )
##      4) LoyalCH < 0.0356415 55    9.996 MM ( 0.01818 0.98182 ) *
##      5) LoyalCH > 0.0356415 224  254.100 MM ( 0.25446 0.74554 ) *
##    3) LoyalCH > 0.445519 521  500.800 CH ( 0.81382 0.18618 )
##      6) LoyalCH < 0.764572 269  338.600 CH ( 0.67658 0.32342 )
##       12) ListPriceDiff < 0.235 110  151.900 MM ( 0.46364 0.53636 )
##         24) PctDiscMM < 0.196196 86  118.100 CH ( 0.55814 0.44186 ) *
##         25) PctDiscMM > 0.196196 24   18.080 MM ( 0.12500 0.87500 ) *
##       13) ListPriceDiff > 0.235 159  148.000 CH ( 0.82390 0.17610 ) *
##      7) LoyalCH > 0.764572 252   84.130 CH ( 0.96032 0.03968 ) *
```

I pick the first node. The node is separated according to `LoyalCH` < 0.0356415. There are 55 subjects in the class that `LoyalCH` < 0.0356415 and the deviance is 9.996. The prediction for this group is MM and the proportion of data points in this group having class MM is 0.98182.

(d) Create a plot of the tree, and interpret the results.

```
plot(fit_tree)
text(fit_tree)
```



The tree only uses `LoyalCH`, `ListPriceDiff`, and `PctDiscMM` for splitting. The root is splitted base on `LoyalCH` < 0.445519. Three out of four leaves on the right branch give the prediction `CH`, while both nodes on the left brance give the prediction `MM`.

(e) Predict the response on the test data, and produce a confusion matrix comparing the test labels to the predicted test labels. What is the test error rate?

```
pred_tree = predict(fit_tree, df_test, type = 'class')
confusionMatrix(pred_tree,df_test$Purchase)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  CH  MM
##         CH 147  24
##         MM  24  75
##
##                Accuracy : 0.8222
##                  95% CI : (0.7713, 0.8659)
##     No Information Rate : 0.6333
##     P-Value [Acc > NIR] : 8.433e-12
##
##                   Kappa : 0.6172
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.8596
##             Specificity : 0.7576
##          Pos Pred Value : 0.8596
##          Neg Pred Value : 0.7576
##              Prevalence : 0.6333
##          Detection Rate : 0.5444
##    Detection Prevalence : 0.6333
##       Balanced Accuracy : 0.8086
##
```

```
##        'Positive' Class : CH
##
```

```
1 - sum(pred_tree == df_test$Purchase)/nrow(df_test)
```

```
## [1] 0.1777778
```

The test error rate is 0.178.

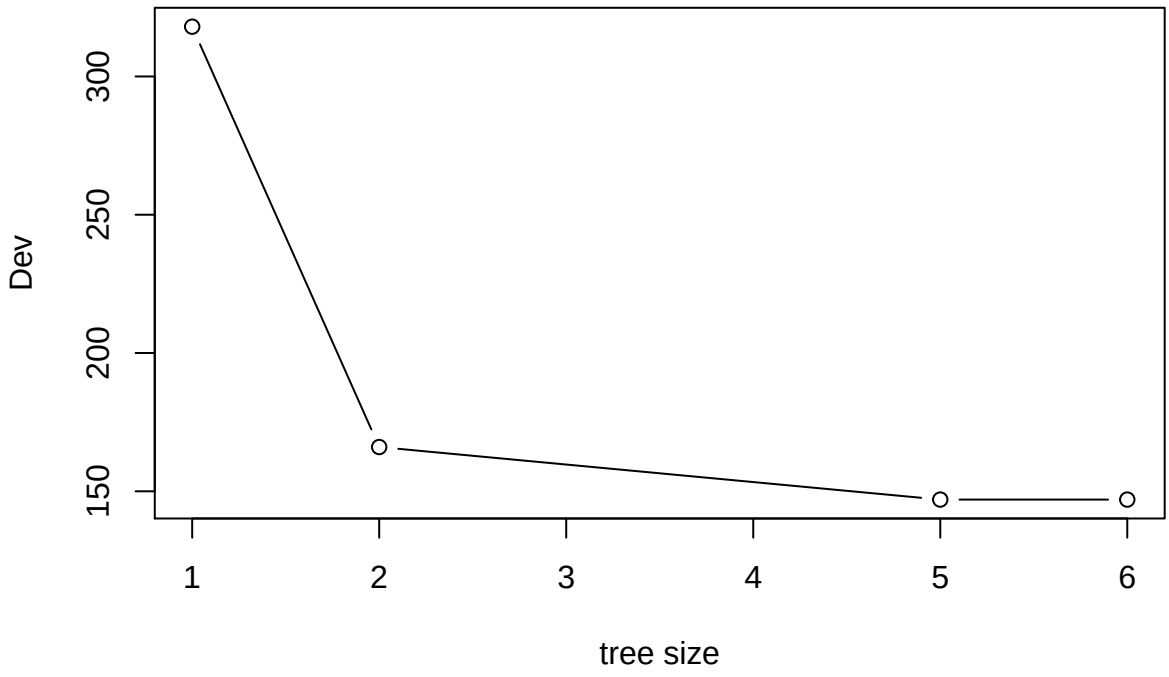
(f) Apply the cv.tree() function to the training set in order to determine the optimal tree size.

```
set.seed(200)
cv_tree = cv.tree(fit_tree)
cv_tree
```

```
## $size
## [1] 6 5 4 3 2 1
##
## $dev
## [1]  726.0312  724.5895  736.9482  746.1978  807.8629 1077.4384
##
## $k
## [1]      -Inf  15.76919  21.12084  38.71184  78.06067 289.13544
##
## $method
## [1] "deviance"
##
## attr(,"class")
## [1] "prune"         "tree.sequence"
```

(g) Produce a plot with tree size on the x-axis and cross-validated classification error rate on the y-axis.

```
set.seed(200)
cv_tree2 = cv.tree(fit_tree, method="misclass")
plot(x = cv_tree2$size, y = cv_tree2$dev, xlab = "tree size", ylab = "Dev", type = "b")
```



(h) Which tree size corresponds to the lowest cross-validated classification error rate?

```
cv_tree2$size[which(cv_tree2$dev == min(cv_tree2$dev))]
```

```
## [1] 6 5
```

Tree size equals to 6 and 5 correspond to the lowest cross-validation error rate.

(i) Produce a pruned tree corresponding to the optimal tree size obtained using cross-validation. If cross-validation does not lead to selection of a pruned tree, then create a pruned tree with five terminal nodes.

```
set.seed(200)
prune_tree = prune.misclass(fit_tree)
prune_tree$size[which(prune_tree$dev == min(prune_tree$dev))]
```

```
## [1] 6 5
```

```
prune_tree = prune.misclass(fit_tree, best = 5)
```

Since tree sizes 5 and 6 both have the lowest CV error rate, we use 5 nodes based on the parsinomy principle.

(k) Compare the test error rates between the pruned and unpruned trees. Which is higher?

```
pred_prune_tree = predict(prune_tree, df_test, type ='class')
1 - sum(pred_prune_tree == df_test$Purchase)/nrow(df_test)
```

```
## [1] 0.1777778
```

They are the same.

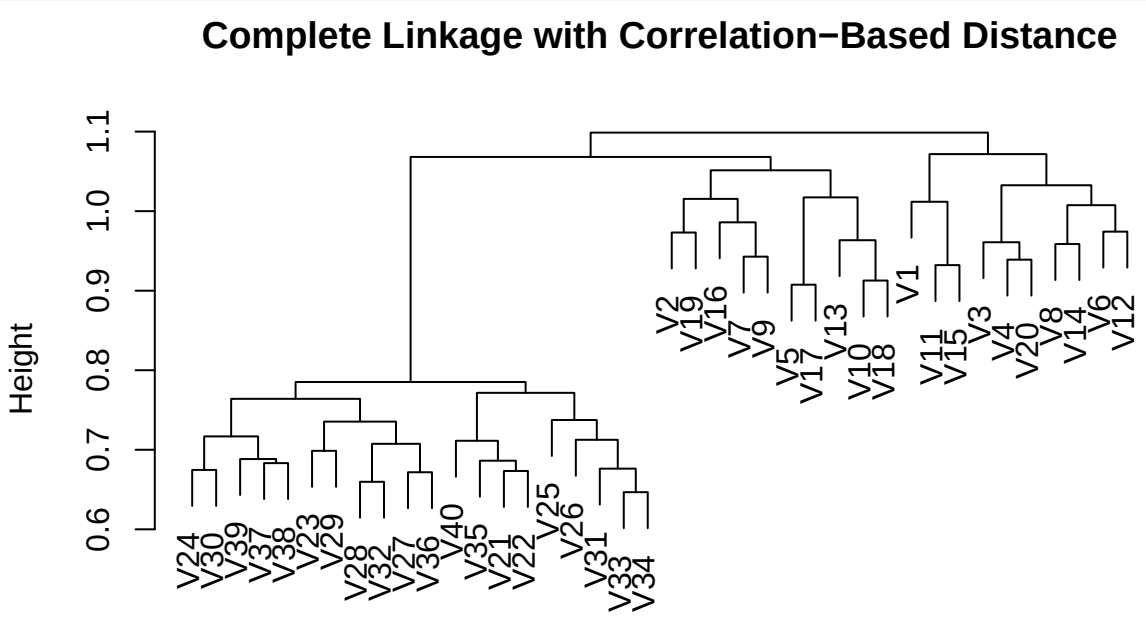
Q3

(a) Read data

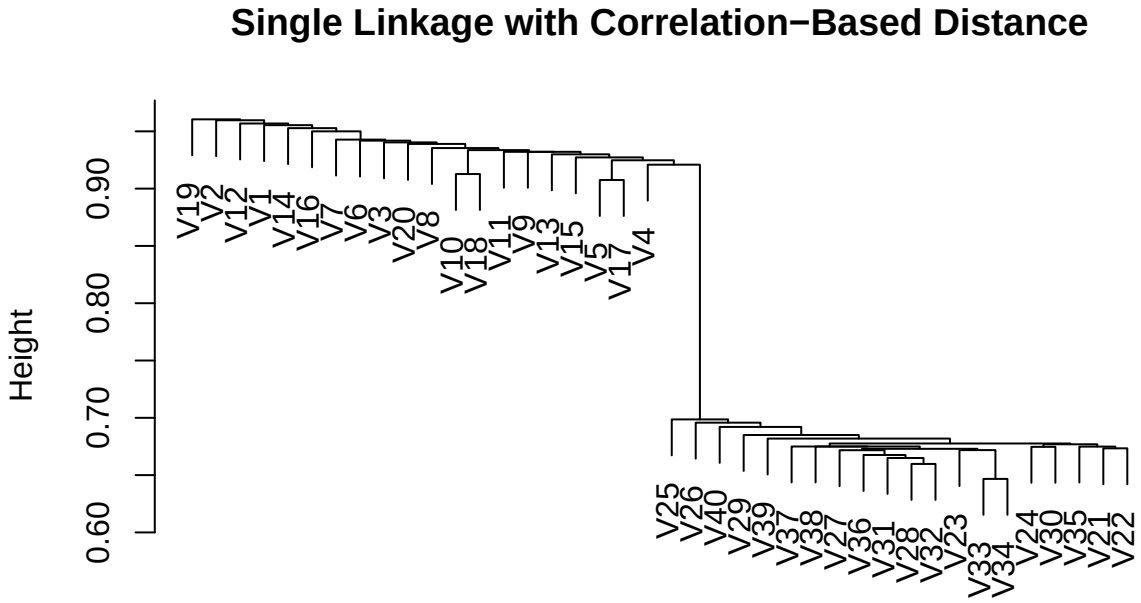
```
gene = read.csv("Ch10Ex11.csv", header = F)
```

(b) Apply hierarchical clustering to the samples using correlation based distance, and plot the dendrogram. Does the genes separate the samples into the two groups? Do your results depend on the type of linkage used?

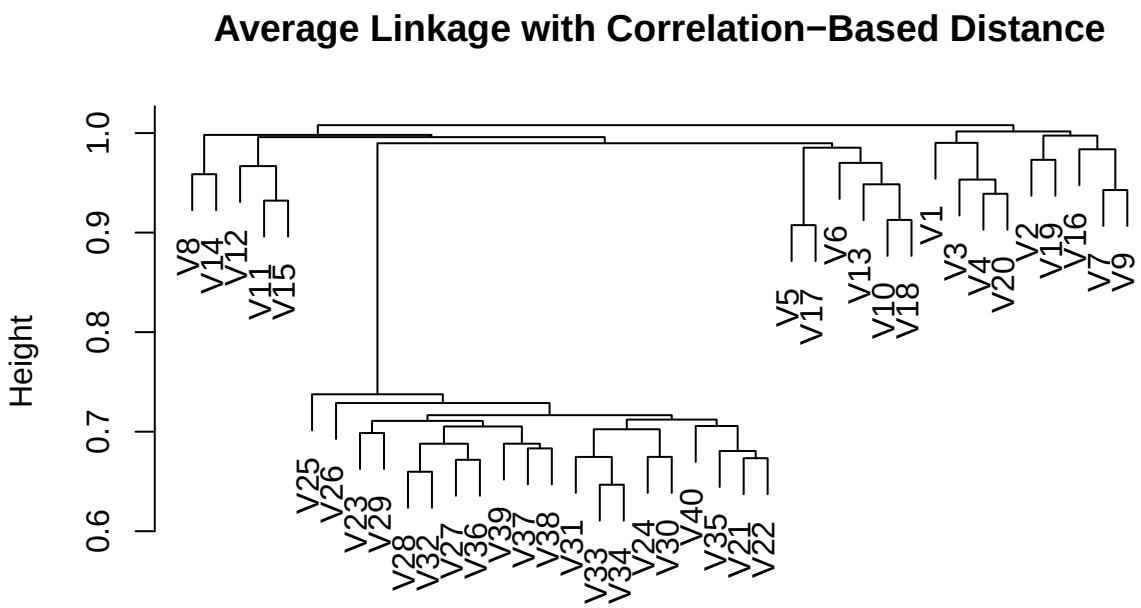
```
set.seed(200)
dis = as.dist(1 - cor(gene))
d_comp = hclust(dis, method = 'complete')
d_single = hclust(dis, method = 'single')
d_avg = hclust(dis, method = 'average')
plot(d_comp, main = "Complete Linkage with Correlation-Based Distance",xlab = "", sub="")
```




```
plot(d_single, main = "Single Linkage with Correlation-Based Distance",xlab = "", sub="")
```




```
plot(d_avg, main = "Average Linkage with Correlation-Based Distance",xlab = "", sub="")
```



My results depend on the type of linkage used. In complete linkage, the genes separate the samples into 2 groups. In single linkage, the genes separate the samples into 2 groups. In average linkage, the genes separate the samples into 3 groups.

(c) Find which genes differ the most across the two groups.

I will use PCA to find the genes differ the most.

```
gene_pca = prcomp(t(gene))

df_pca = gene_pca$rotation %>%
  as_tibble()
```

```r
tibble(
    gene_id = 1:1000,
   sum_loading = apply(df_pca[1:10], 1, sum)) %>%
  arrange(desc(abs(sum_loading))) %>%
  head(15) %>%
  knitr::kable(digits = 2)
```

gene_id	sum_loading
529	0.37
533	0.32
575	0.31
865	0.29
631	0.29
783	-0.28
573	0.28
564	0.28
593	0.28
551	0.28
861	0.27
364	-0.27
660	-0.27
570	0.26
192	0.26

```r
tibble(
    gene_id = 1:1000,
   sum_loading = apply(df_pca, 1, sum)) %>%
  arrange(desc(abs(sum_loading))) %>%
  head(15) %>%
  knitr::kable(digits = 2)
```

gene_id	sum_loading
865	0.78
68	0.71
911	-0.71
428	-0.64
624	-0.62
11	0.59
524	0.56
803	0.55
980	-0.52
822	0.50
529	0.49
765	0.48
801	0.48
771	-0.48
570	0.48

The first table shows the top 15 genes based on the sum of PC1 to PC10.

The second table shows the top 15 genes based on the sum of all PCs.