INFS7203 REPORT
HEXIN ZHENG
4501283

Task1

1.1

```
#Extract data and assign a name to data
bcw<-read.table("./data/breast-cancer-wisconsin.data",sep=',')
```

1.2

```
#Assign names to 11 different columns in my dataset.
names(bcw) <- c("Sample.code.number","Clump.Thickness","Uniformity.of.Cell.Size",
                "Uniformity.of.Cell.Shape","Marginal.Adhesion","Single.Epithelial.Cell.Size",
                "Bare.Nuclei","Bland.Chromatin","Normal.Nucleoli","Mitoses","Class")
```

1.3

```
#1.3See Null value
bcw[complete.cases(bcw),]
#Change column “Bare.Nuclei” from factor to integer
bcw$Bare.Nuclei <- as.integer(as.character(bcw$Bare.Nuclei))
#Remove all Null value
bcw1=na.omit(bcw)
```

1.4

```
#Remove the first column.
bcw=bcw[,-1]
```

1.5

```
#see the type of Class
class(bcw$Class)
#"integer"
#Change type integer to factor.
bcw[,'Class']<-factor(bcw[,'Class'])
#see the type of Class after changing
class(bcw$Class)
#factor
```

1.6

```
#save as bcw_processed.Rda
saveRDS(bcw1, file="./data/bcw_processed.Rda")
Save(bcw1, file=”./code/myPreparation.r”)
```

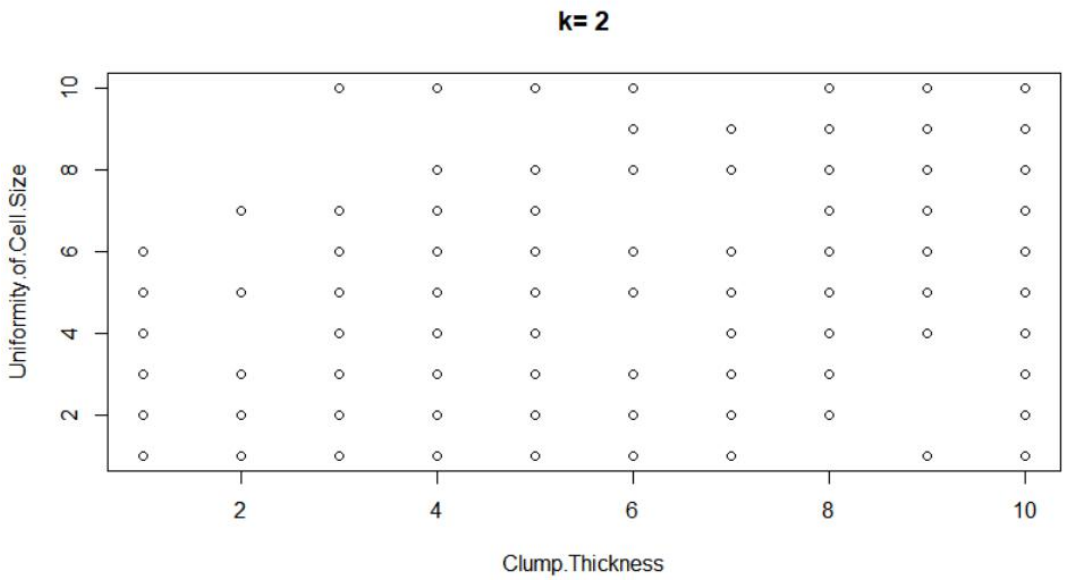
Task2

2.1

```
#Load bcw_processed.Rda
bcw2<-load("bcw_processed.Rda")

#Select first nine variables
bcw3 <- bcw1[,1:9]
#For reproducible result
set.seed(2835)
```

2.2

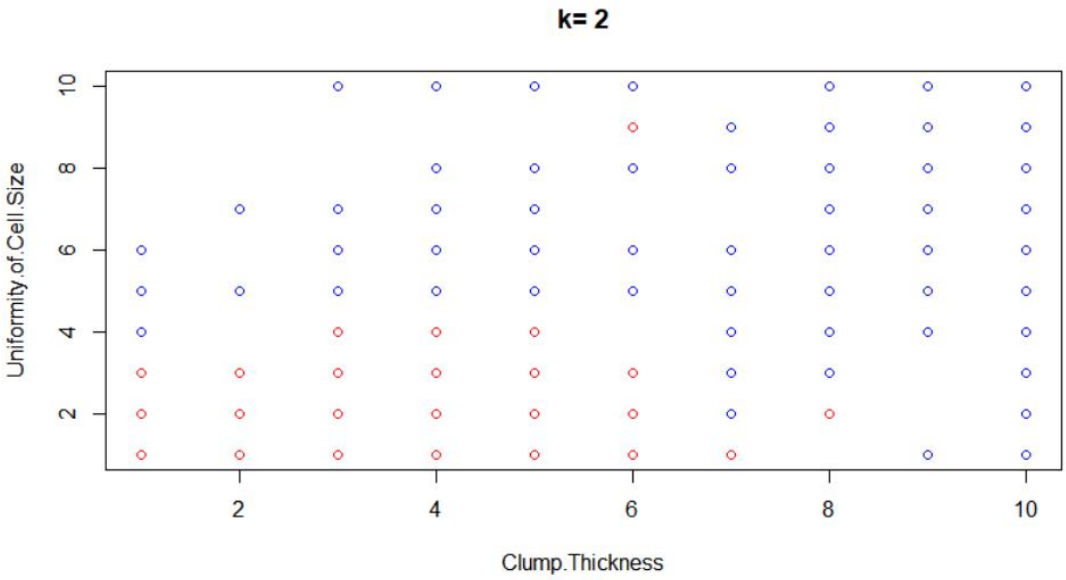
```
#Cluster the data into 2 clusters
nclust = 2
bcw3 <- bcw1[,1:9]
(kmeans.result <- kmeans(bcw3,nclust))

#Plot
plot(bcw1[,c("Clump.Thickness","Uniformity.of.Cell.Size")])
title(paste("k= ",nclust,sep=""))
```



2.3

```
#Color the points according to the Class column
bcw3 <- bcw[,1:9]
nclust = 2
(kmeans.result <- kmeans(bcw3,nclust))
plot(bcw1[,c("Clump.Thickness","Uniformity.of.Cell.Size")],
```

```
        col = bcw1$Class)
title(paste("k=",nclust,sep=""))
```

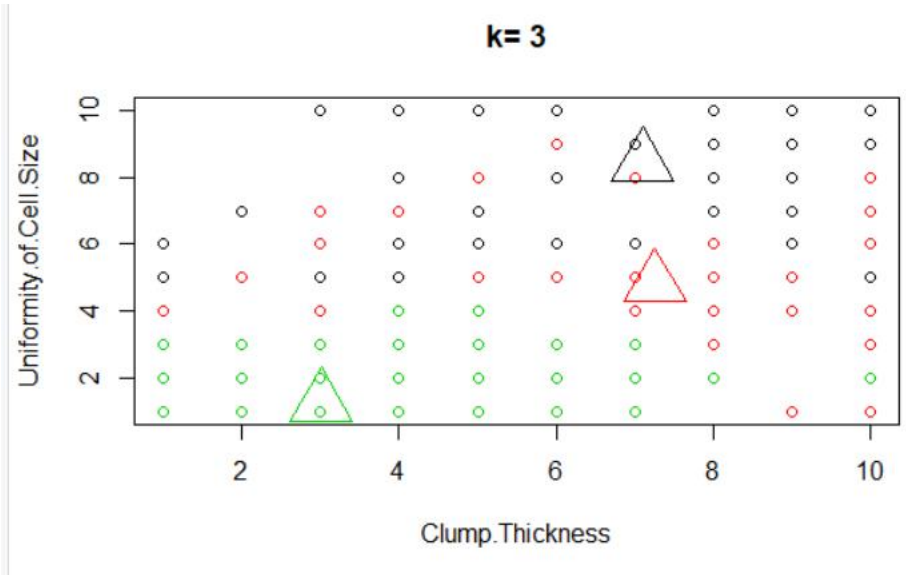


2.4

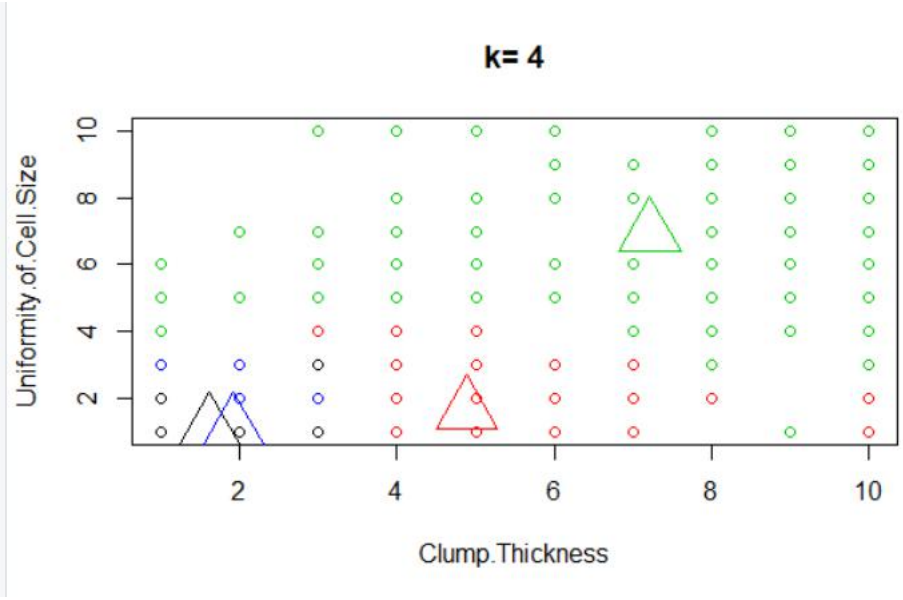
Yes. 2.3 has two colors, which is more obvious. However, before coloring, the graph only has one color and we do not know how to distinguish them.

2.5 #Cluster more

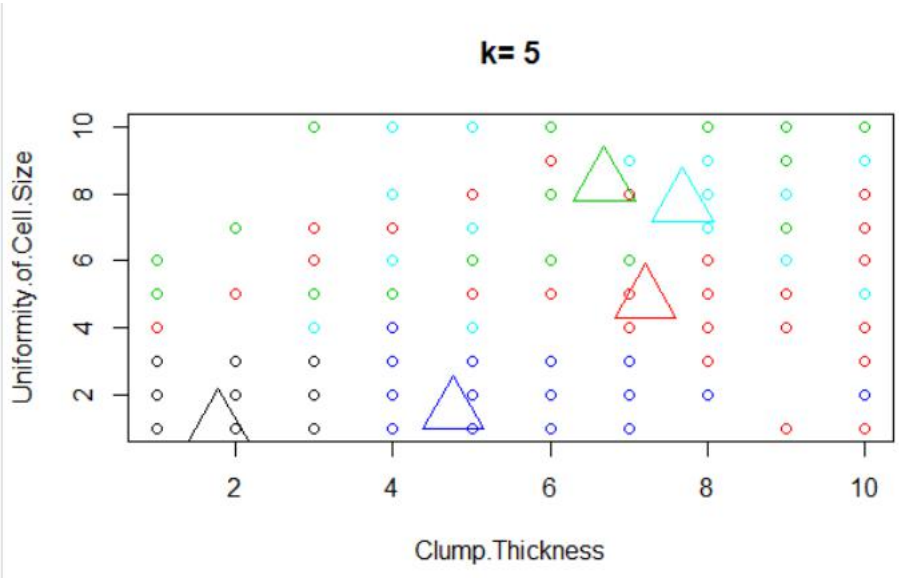
When k=3



When k=4



When k=5



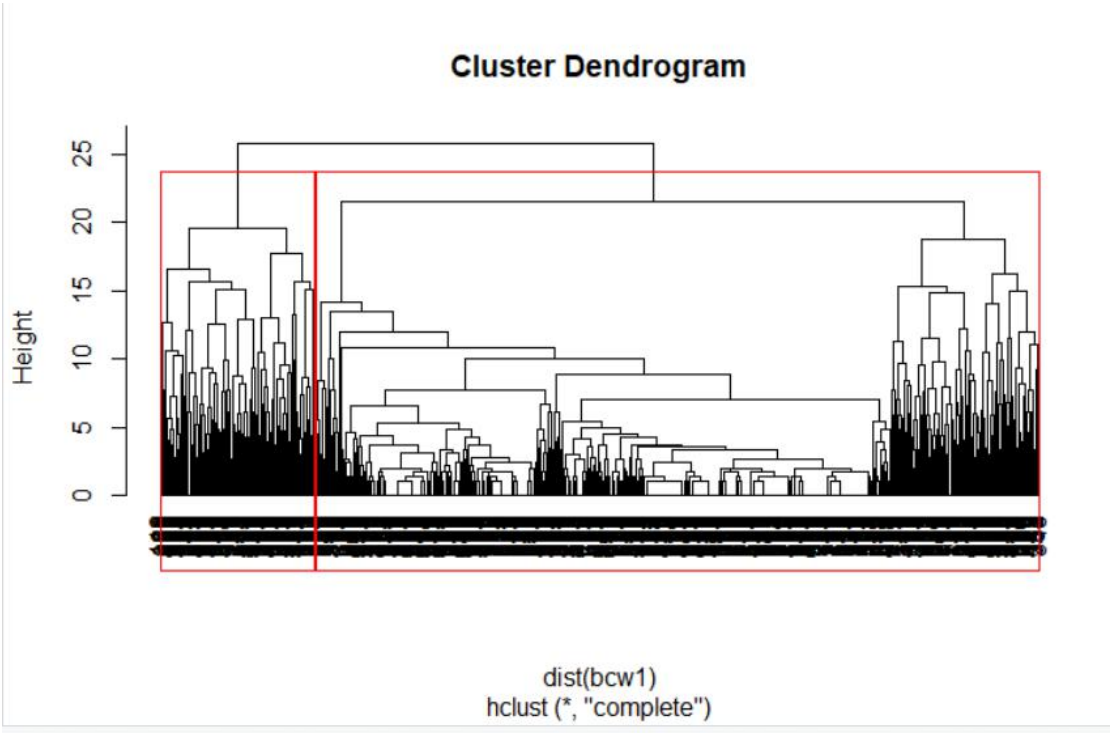
2.6

According to the plot with k=2,3,4,5. In my opinion, it is not a good choice if we set too many clusters. As k=5, the centroid is very close between two clusters and it looks a little messy, which is not necessary. On the other hand, when there are two or three clusters, it is convenient for us to observe.

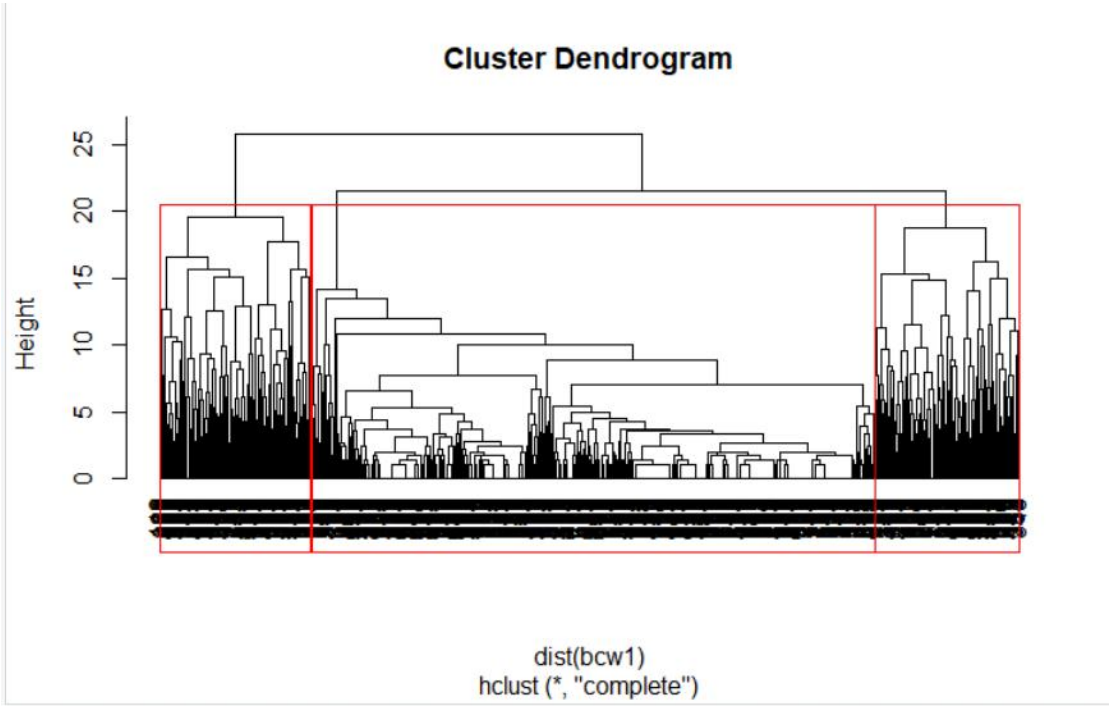
2.7 hierarchical clustering

```
#hierarchical clustering with hclust function
hc <- hclust(dist(bcw1))
#plot the obtained dendrogram
plot(hc,hang=-1)

#Cluster the dendrogram into nclust clusters
#when n =2
nclust = 2
rect.hclust(hc,k=nclust)
groups <- cutree(hc,k=nclust)
```

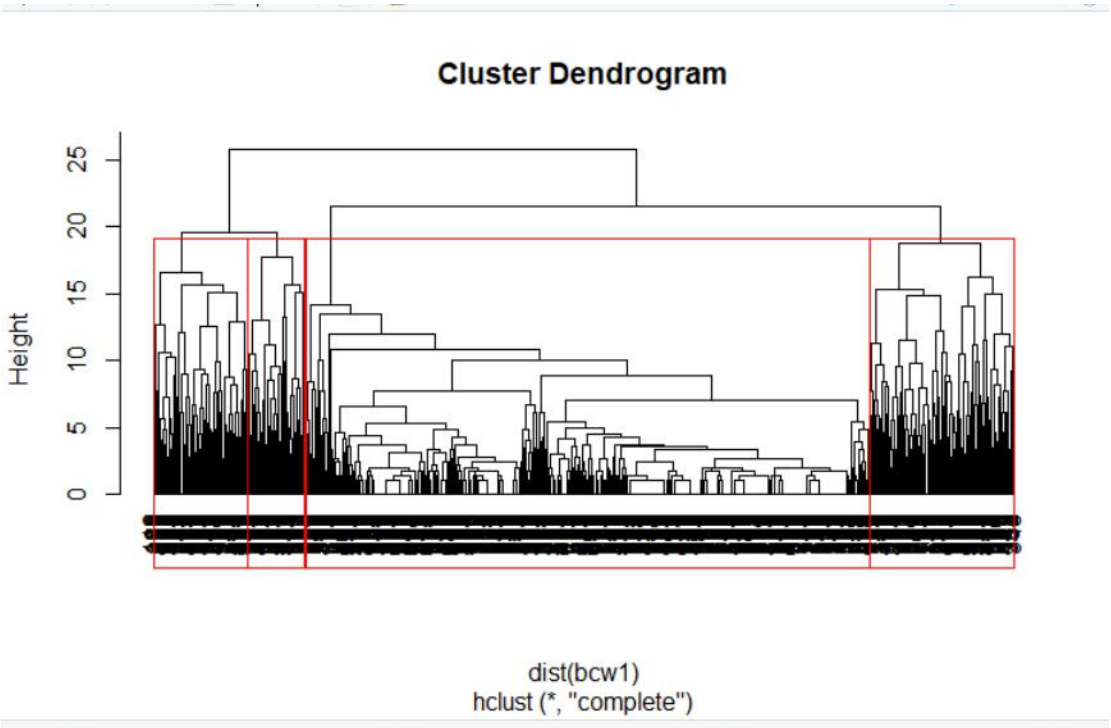
When n=2



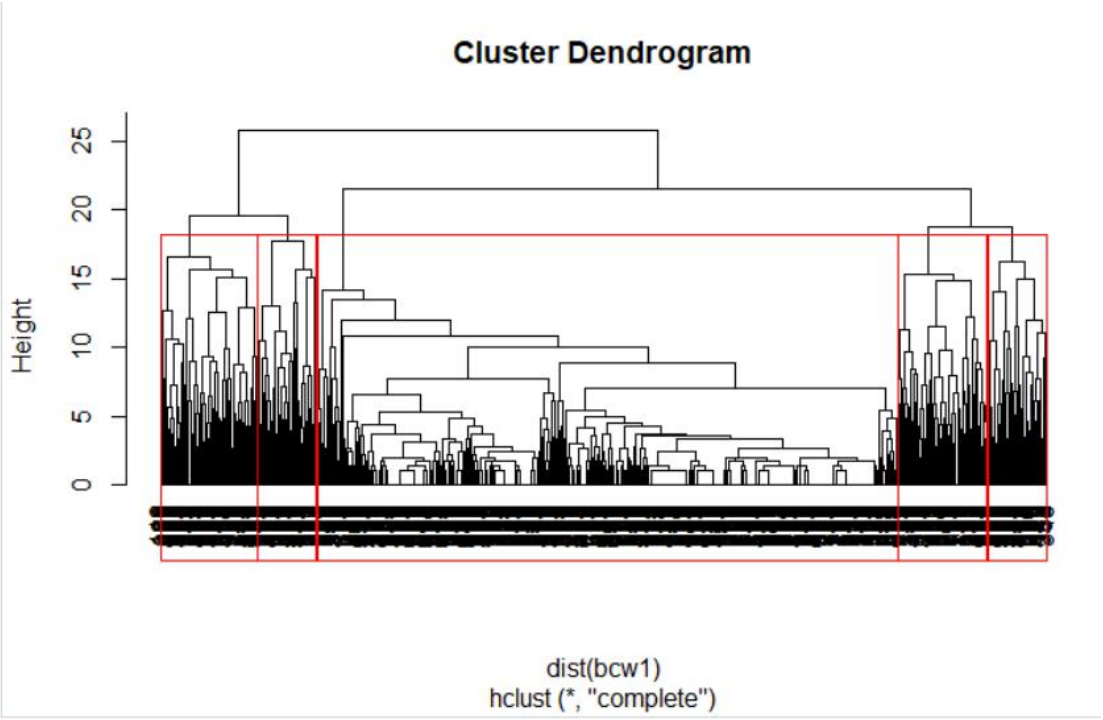
n=3


Cluster Dendrogram
Height
0
5
10
15
20
25
dist(bcw1)
hclust (*, "complete")

n =4


Cluster Dendrogram
Height
0
5
10
15
20
25
dist(bcw1)
hclust (*, "complete")

n=5

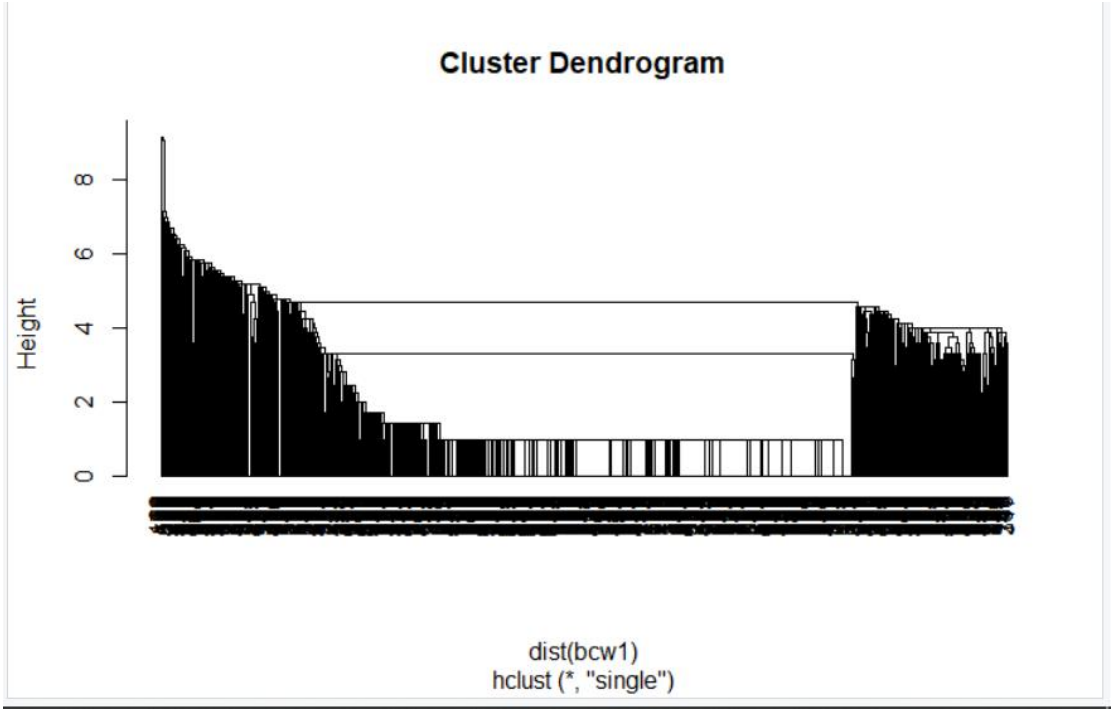


2.8

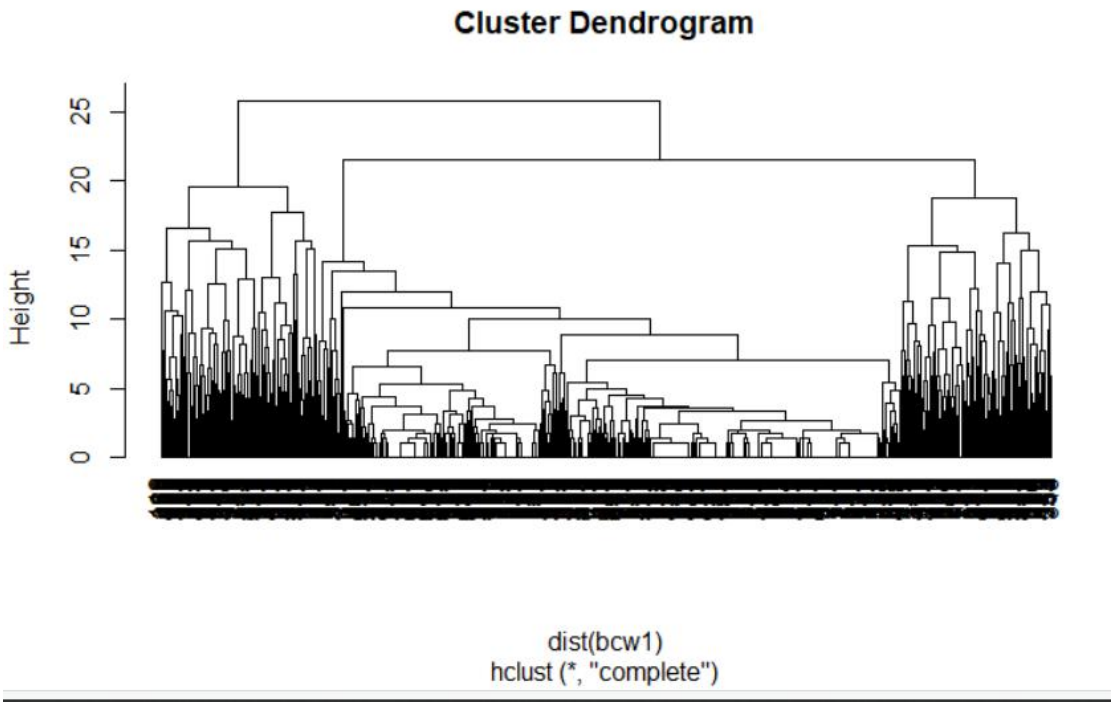
Yes, because the cluster in the middle is too large.

2.9 #Cluster with methods

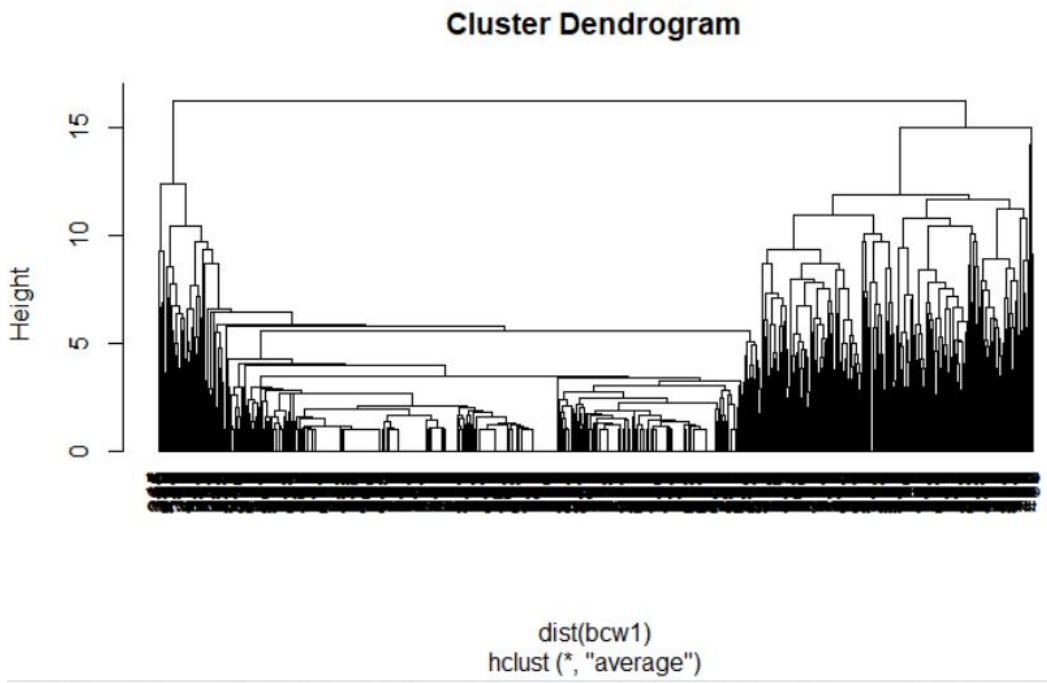
```
hc <- hclust(dist(bcw1),method="single")
plot(hc,hang=-1)
```



"complete"



"average"



Agglomerative function makes clustering work in a bottom-up manner. After using this function, the hierarchical clustering becomes more obvious and easy to help us to find difference.

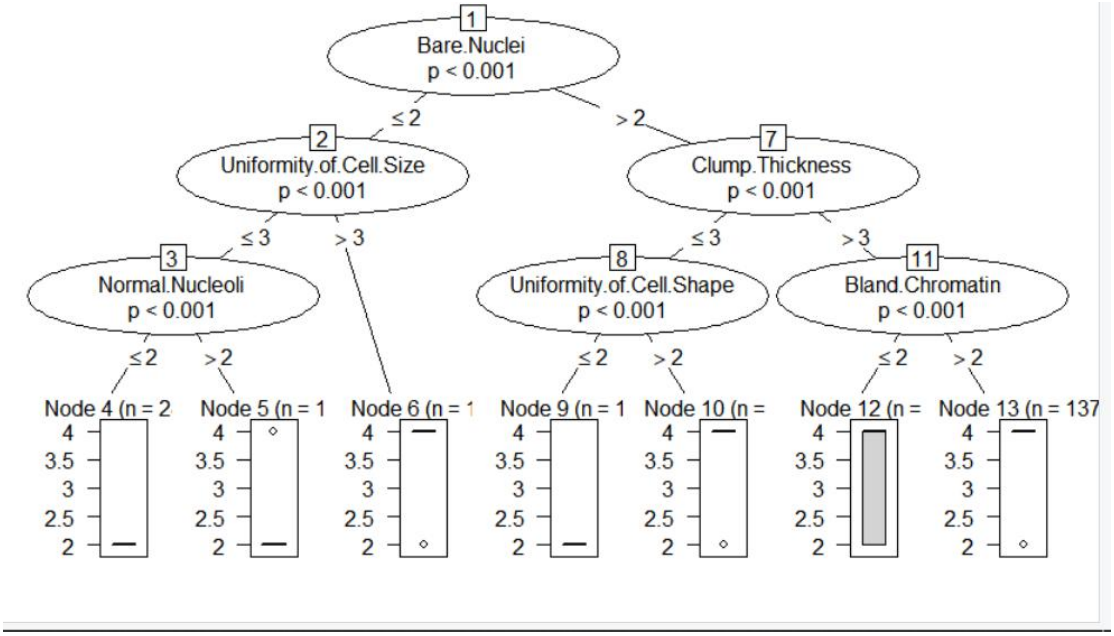
Task3

3.1

```
#3Load bcw_processed.Rda
bcwtask3<-load("bcw_processed.Rda")

#Divde dataset into "training" and "test"
set.seed(2835)

m = nrow(bcwtask3)
training_percentage = 0.7
test_percentage = 0.3

#Sample random index
ind <- sample(2,m,replace = TRUE, prob = c(training_percentage,test_percentage))

#Select training and test data
training_data = bcw1[ind == 1,]
test_data = bcw1[ind == 2,]

#divide features and labels
training_features <- training_data[,1:9]
training_labels <- training_data[,10]
test_features <- test_data[,1:9]
test_labels <- test_data[,10]
```

3.2

```
# install and import "party" library
install.packages("party")
library(party)

#Specify target(class) and predictors(features)
myFormula <- Class ~ Clump.Thickness + Uniformity.of.Cell.Size + Uniformity.of.Cell.Shape +
   Marginal.Adhesion + Single.Epithelial.Cell.Size +
   Bare.Nuclei + Bland.Chromatin + Normal.Nucleoli + Mitoses

#generate classification tree
bcwtask3_ctree <- ctree(myFormula,data=training_data)

#visualise the tree
plot(bcwtask3_ctree)

#predict test labels
ctree_pred<- predict(bcwtask3_ctree, training_data)
```



When we have more than two variables, it is better to use classification tree and it can help us to predict. According to output graph, every middle node needs to depend on corresponding variables and the conditions of splitting has shown on the branches. Leaf nodes can show the number of different sample.

3.4 K-MN

```
#install and import "class" library
install.packages("class")
library(class)

#classify using K-MN
knn_pred <- knn(train = training_features,
                test = test_features,
                cl = training_labels,
                k=1)

# create the confusion matrix
cm = as.matrix(table(Actual = test_labels, Predicted = ctree_pred))

n = sum(cm) #number of instances
nc = nrow(cm) #number of classes
diag = diag(cm) #number of correctly classified instances per class
rowsums = apply(cm,1,sum)#number of instances per class
colsums = apply(cm,2,sum)#number of predictions per class

#compute accruacy, precision, recall and f1
accruacy = sum(diag) / n
precision = diag / colsums
recall = diag / rowsums
f1 = 2 * precision * recall/(precsion + recall)

results <- data.frame(precision,recall,f1)
```