Assignment - 5

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```
set.seed(123)

library(cluster)
library(caret)

## Loading required package: ggplot2

## Loading required package: lattice

library(dendextend)

##
## ---------------------
## Welcome to dendextend version 1.15.2
## Type citation('dendextend') for how to cite the package.
##
## Type browseVignettes(package = 'dendextend') for the package vignette.
## The github page is: https://github.com/talgalili/dendextend/
##
## Suggestions and bug-reports can be submitted at:
https://github.com/talgalili/dendextend/issues
## You may ask questions at stackoverflow, use the r and dendextend tags:
##   https://stackoverflow.com/questions/tagged/dendextend
##
##  To suppress this message use:
suppressPackageStartupMessages(library(dendextend))
## ---------------------

##
## Attaching package: 'dendextend'

## The following object is masked from 'package:stats':
##
##     cutree

library(knitr)
library(factoextra)

## Welcome! Want to learn more? See two factoextra-related books at
https://goo.gl/ve3WBa
```

Importing dataset(Cereals)

```
library(readr)
```

```
## Warning: package 'readr' was built under R version 4.1.2

Cereals <- read_csv("Cereals.csv", col_types = cols(calories = col_number(),
                                                    protein = col_number(),
fat = col_number(),
                                                    sodium = col_number(),
fiber = col_number(),
                                                    carbo = col_number(),
sugars = col_number(),
                                                    potass = col_number(),
vitamins = col_number(),
                                                    shelf = col_number(),
weight = col_number(),
                                                    cups = col_number(),
rating = col_number()))

Cereals1 <- data.frame(Cereals[,4:16])
```

Pre-processing data and normalizing the data

```
Cereals1 <- na.omit(Cereals1)
Cereals2 <- scale(Cereals1)
```

Applying hierarchical clustering to the data using Euclidean distance to the normalized measurements.

Calculating Dissimilarity Matrix and performing Hierarchial Clustering.

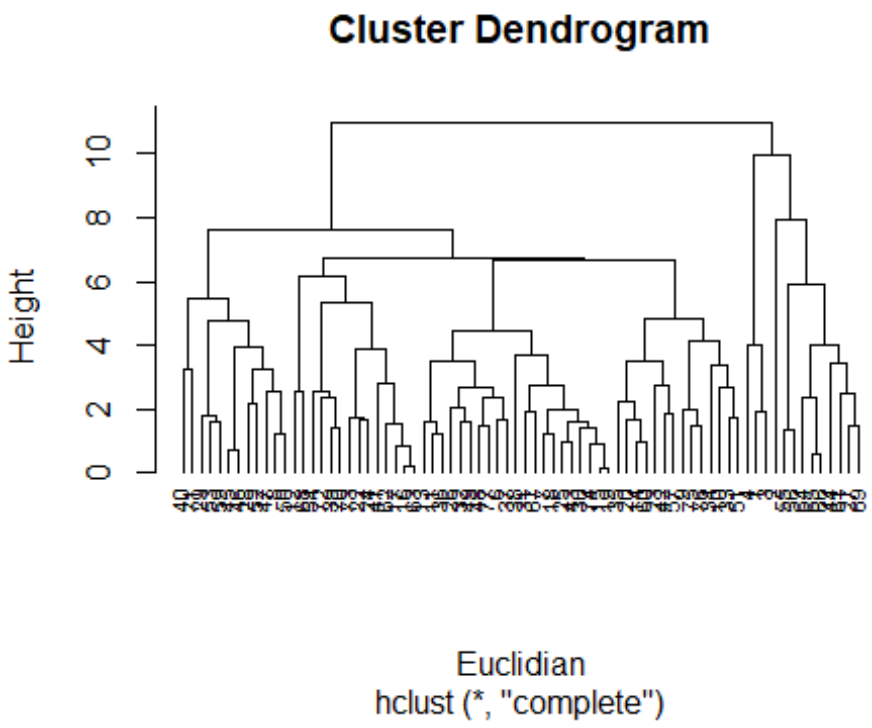
```
Euclidian <- dist(Cereals2, method = "euclidean")

## Clustering the Cereals dataset.

Complete <- hclust(Euclidian, method = "complete")

## Plotting the dendogram.

plot(Complete, cex = 0.7, hang = -1)
```



Using Agnes to compare the clustering.

```
# Single Linkage Method
Single <- agnes(Cereals2, method = "single")
# Complete Linkage Method
Complete1 <- agnes(Cereals2, method = "complete")
# Average Linkage Method
Average <- agnes(Cereals2, method = "average")
# Ward Method
Ward <- agnes(Cereals2, method = "ward")
```

Comparing the agglomerative coefficients.

Single Linkage vs Complete Linkage vs Average Linkage vs Ward.

```
print(Single$ac)

## [1] 0.6067859

print(Complete1$ac)

## [1] 0.8353712

print(Average$ac)

## [1] 0.7766075

print(Ward$ac)

## [1] 0.9046042
```

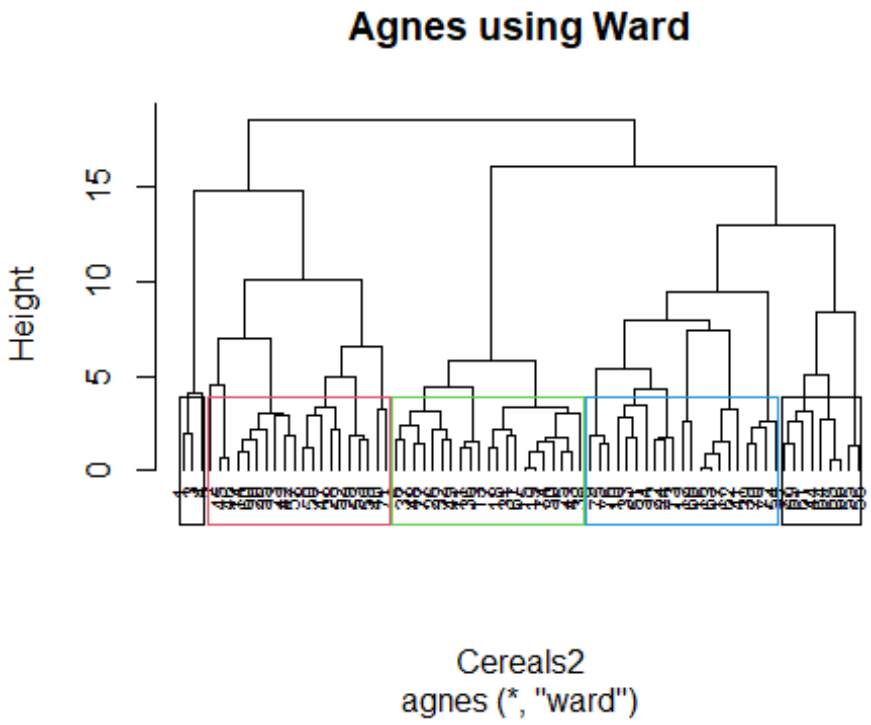
Here we can see that Ward method is best with highest value of 0.9046042.

Choosing the clusters:

Plotting the agnes using ward method and cutting the Dendogram.

We will take 5 clusters (k = 5) based on the distance.

```
pltree(Ward, cex = 0.7, hang = -1, main = "Agnes using Ward")
rect.hclust(Ward, k = 5, border = 1:4)
```




```
Cluster <- cutree(Ward, k=5)
Cluster1 <- as.data.frame(cbind(Cereals2, Cluster))
```

Structure of the clusters and their stability.

Creating Partitions.

```
PartA <- Cereals1[1:50,]
PartB <- Cereals1[51:74,]
```

Performing Hierarchial Clustering, plotting and cutting the dendogram with k=5.

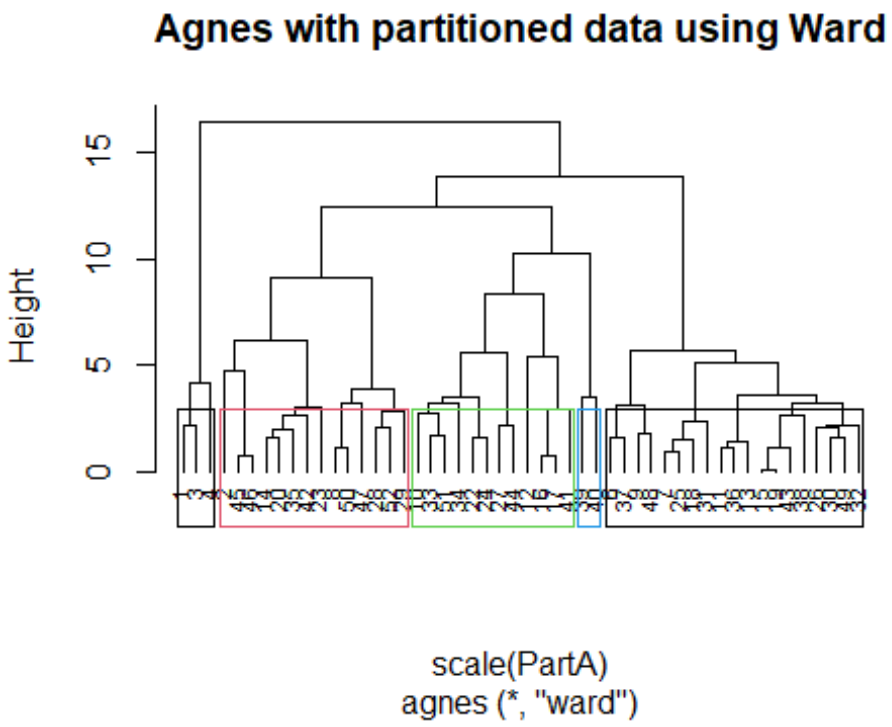
```
# Single Linkage Method of Part A
Single1 <- agnes(scale(PartA), method = "single")
# Complete Linkage Method of Part A
Complete2 <- agnes(scale(PartA), method = "complete")
# Average Linkage Method of Part A
Average1 <- agnes(scale(PartA), method = "average")
# Ward Method of Part A
```

```
Ward1 <- agnes(scale(PartA), method = "ward")

cbind(Single= Single1$ac , Complete=Complete2$ac , Average= Average1$ac ,
Ward= Ward1$ac)

##         Single  Complete   Average      Ward
## [1,] 0.6393338 0.8138238 0.7408904 0.8764323

pltree(Ward1, cex = 0.7, hang = -1, main = "Agnes with partitioned data using
Ward")
# Clustering Part A of the data set
rect.hclust(Ward1, k = 5, border = 1:4)
```




```
# Cutting the dendrogram
Cluster2 <- cutree(Ward1, k = 5)
```

Calculating the centeroids.

```
Centroids <- as.data.frame(cbind(PartA, Cluster2))
Centroids[Centroids$Cluster2==1,]

##   calories protein fat sodium fiber carbo sugars potass vitamins shelf
weight
## 1       70       4   1    130    10     5      6    280       25     3
1
## 3       70       4   1    260     9     7      5    320       25     3
1
## 4       50       4   0    140    14     8      0    330       25     3
```

```
1
##   cups   rating Cluster2
## 1 0.33 68.40297        1
## 3 0.33 59.42551        1
## 4 0.50 93.70491        1

# Centroid 1
centroid1 <- colMeans(Centroids[Centroids$Cluster2==1,])
Centroids[Centroids$Cluster2==2,]

##    calories protein fat sodium fiber carbo sugars potass vitamins shelf
weight
## 2       120       3   5     15   2.0   8.0      8    135        0     3
1.00
## 8       130       3   2    210   2.0  18.0      8    100       25     3
1.33
## 14      110       3   2    140   2.0  13.0      7    105       25     3
1.00
## 20      110       3   3    140   4.0  10.0      7    160       25     3
1.00
## 23      100       2   1    140   2.0  11.0     10    120       25     3
1.00
## 28      120       3   2    160   5.0  12.0     10    200       25     3
1.25
## 29      120       3   0    240   5.0  14.0     12    190       25     3
1.33
## 35      120       3   3     75   3.0  13.0      4    100       25     3
1.00
## 42      100       4   2    150   2.0  12.0      6     95       25     2
1.00
## 45      150       4   3     95   3.0  16.0     11    170       25     3
1.00
## 46      150       4   3    150   3.0  16.0     11    170       25     3
1.00
## 47      160       3   2    150   3.0  17.0     13    160       25     3
1.50
## 50      140       3   2    220   3.0  21.0      7    130       25     3
1.33
## 52      130       3   2    170   1.5  13.5     10    120       25     3
1.25
##    cups   rating Cluster2
## 2  1.00 33.98368        2
## 8  0.75 37.03856        2
## 14 0.50 40.40021        2
## 20 0.50 40.44877        2
## 23 0.75 36.17620        2
## 28 0.67 40.91705        2
## 29 0.67 41.01549        2
## 35 0.33 45.81172        2
## 42 0.67 45.32807        2
```

```
## 45 1.00 37.13686        2
## 46 1.00 34.13977        2
## 47 0.67 30.31335        2
## 50 0.67 40.69232        2
## 52 0.50 30.45084        2
```

```
# Centroid 2
centroid2 <- colMeans(Centroids[Centroids$Cluster2==2,])
Centroids[Centroids$Cluster2==3,]
```

```
##    calories protein fat sodium fiber carbo sugars potass vitamins shelf
weight
## 6       110       2   2    180   1.5  10.5     10     70       25     1
1
## 7       110       2   0    125   1.0  11.0     14     30       25     2
1
## 9        90       2   1    200   4.0  15.0      6    125       25     1
1
## 11      120       1   2    220   0.0  12.0     12     35       25     2
1
## 13      120       1   3    210   0.0  13.0      9     45       25     2
1
## 15      110       1   1    180   0.0  12.0     13     55       25     2
1
## 18      110       1   0     90   1.0  13.0     12     20       25     2
1
## 19      110       1   1    180   0.0  12.0     13     65       25     2
1
## 25      110       2   1    125   1.0  11.0     13     30       25     2
1
## 26      110       1   0    200   1.0  14.0     11     25       25     1
1
## 30      110       1   1    135   0.0  13.0     12     25       25     2
1
## 31      100       2   0     45   0.0  11.0     15     40       25     1
1
## 32      110       1   1    280   0.0  15.0      9     45       25     2
1
## 36      120       1   2    220   1.0  12.0     11     45       25     2
1
## 37      110       3   1    250   1.5  11.5     10     90       25     1
1
## 38      110       1   0    180   0.0  14.0     11     35       25     1
1
## 43      110       2   1    180   0.0  12.0     12     55       25     2
1
## 48      100       2   1    220   2.0  15.0      6     90       25     1
1
## 49      120       2   1    190   0.0  15.0      9     40       25     2
1
```

```
##    cups   rating Cluster2
## 6  0.75 29.50954        3
## 7  1.00 33.17409        3
## 9  0.67 49.12025        3
## 11 0.75 18.04285        3
## 13 0.75 19.82357        3
## 15 1.00 22.73645        3
## 18 1.00 35.78279        3
## 19 1.00 22.39651        3
## 25 1.00 32.20758        3
## 26 0.75 31.43597        3
## 30 0.75 28.02576        3
## 31 0.88 35.25244        3
## 32 0.75 23.80404        3
## 36 1.00 21.87129        3
## 37 0.75 31.07222        3
## 38 1.33 28.74241        3
## 43 1.00 26.73452        3
## 48 1.00 40.10597        3
## 49 0.67 29.92429        3
```

```
# Centroid 3
centroid3 <- colMeans(Centroids[Centroids$Cluster2==3,])
Centroids[Centroids$Cluster2==4,]
```

```
##    calories protein fat sodium fiber carbo sugars potass vitamins shelf
weight
## 10       90       3   0    210     5    13      5    190       25     3
1
## 12      110       6   2    290     2    17      1    105       25     1
1
## 16      110       2   0    280     0    22      3     25       25     1
1
## 17      100       2   0    290     1    21      2     35       25     1
1
## 22      110       2   0    220     1    21      3     30       25     3
1
## 24      100       2   0    190     1    18      5     80       25     3
1
## 27      100       3   0      0     3    14      7    100       25     2
1
## 33      100       3   1    140     3    15      5     85       25     3
1
## 34      110       3   0    170     3    17      3     90       25     3
1
## 41      110       2   1    260     0    21      3     40       25     2
1
## 44      100       4   1      0     0    16      3     95       25     2
1
## 51       90       3   0    170     3    18      2     90       25     3
```

```
1
##    cups   rating Cluster2
## 10 0.67 53.31381        4
## 12 1.25 50.76500        4
## 16 1.00 41.44502        4
## 17 1.00 45.86332        4
## 22 1.00 46.89564        4
## 24 0.75 44.33086        4
## 27 0.80 58.34514        4
## 33 0.88 52.07690        4
## 34 0.25 53.37101        4
## 41 1.50 39.24111        4
## 44 1.00 54.85092        4
## 51 1.00 59.64284        4

# Centroid 4
centroid4 <- colMeans(Centroids[Centroids$Cluster2==4,])
Centroids1 <- rbind(centroid1, centroid2, centroid3, centroid4)
Centroids2 <- as.data.frame(rbind(Centroids[,-14], PartB))
```

Calculating the Distance.

```
Distance <- get_dist(Centroids2)
Matrix <- as.matrix(Distance)
Distance1 <- data.frame(data=seq(1,nrow(PartB),1), Clusters =
rep(0,nrow(PartB)))
for(i in 1:nrow(PartB))
  {Distance1[i,2] <- which.min(Matrix[i+4, 1:4])}
Distance1

##    data Clusters
## 1     1        2
## 2     2        2
## 3     3        2
## 4     4        1
## 5     5        1
## 6     6        2
## 7     7        3
## 8     8        2
## 9     9        2
## 10   10        2
## 11   11        2
## 12   12        3
## 13   13        2
## 14   14        2
## 15   15        1
## 16   16        2
## 17   17        2
## 18   18        2
## 19   19        2
## 20   20        2
```

```
## 21   21        2
## 22   22        1
## 23   23        3
## 24   24        2
```

```
cbind(Cluster1$Cluster[51:74], Distance1$Clusters)
```

```
##       [,1] [,2]
##  [1,]    2    2
##  [2,]    4    2
##  [3,]    5    2
##  [4,]    5    1
##  [5,]    2    1
##  [6,]    2    2
##  [7,]    2    3
##  [8,]    5    2
##  [9,]    4    2
## [10,]    4    2
## [11,]    5    2
## [12,]    5    3
## [13,]    5    2
## [14,]    3    2
## [15,]    4    1
## [16,]    5    2
## [17,]    4    2
## [18,]    2    2
## [19,]    4    2
## [20,]    4    2
## [21,]    3    2
## [22,]    4    1
## [23,]    4    3
## [24,]    3    2
```

```
# Tabulating the results
table(Cluster1$Cluster[51:74] == Distance1$Clusters)
```

```
##
## FALSE  TRUE
##    12    12
```

We are getting 12 FALSE and 12 TRUE, so we can conclude that the model is partially stable.

Finding a cluster of "healthy cereals."

Clustering Healthy Cereals

```
Healthy <- Cereals
Healthy <- na.omit(Healthy)
Healthy1 <- cbind(Healthy, Cluster)
Healthy1[Healthy1$Cluster==1,]
Healthy1[Healthy1$Cluster==2,]
```

```
Healthy1[Healthy1$Cluster==3,]
Healthy1[Healthy1$Cluster==4,]
```

Mean ratings to determine the best cluster.

```
mean(Healthy1[Healthy1$Cluster==1,"rating"])

## [1] 73.84446

mean(Healthy1[Healthy1$Cluster==2,"rating"])

## [1] 38.26161

mean(Healthy1[Healthy1$Cluster==3,"rating"])

## [1] 28.84825

mean(Healthy1[Healthy1$Cluster==4,"rating"])

## [1] 46.46513
```

As we can se that the mean rating of the cluster 1 is the highest(i.e. 73.84446), we will choose cluster 1.