Asignment 5

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2022-11-28

```
library(cluster)
library(caret)
```

```
## Loading required package: ggplot2
```

```
## Loading required package: lattice
```

```
library(dendextend)
```

```
##
## ---------------------
## Welcome to dendextend version 1.16.0
## 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(factoextra)
```

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

```
c<-read.csv("/Users/jay/Downloads/Cereals.csv")
c<- na.omit(c)
head(c)
```

```
##                        name mfr type calories protein fat sodium fiber carbo
## 1                 100%_Bran   N    C       70       4   1    130  10.0   5.0
## 2         100%_Natural_Bran   Q    C      120       3   5     15   2.0   8.0
## 3                   All-Bran   K    C       70       4   1    260   9.0   7.0
## 4 All-Bran_with_Extra_Fiber   K    C       50       4   0    140  14.0   8.0
## 6   Apple_Cinnamon_Cheerios   G    C      110       2   2    180   1.5  10.5
## 7                Apple_Jacks   K    C      110       2   0    125   1.0  11.0
##   sugars potass vitamins shelf weight cups   rating
## 1      6    280       25     3      1 0.33 68.40297
## 2      8    135        0     3      1 1.00 33.98368
## 3      5    320       25     3      1 0.33 59.42551
## 4      0    330       25     3      1 0.50 93.70491
## 6     10     70       25     1      1 0.75 29.50954
## 7     14     30       25     2      1 1.00 33.17409
```

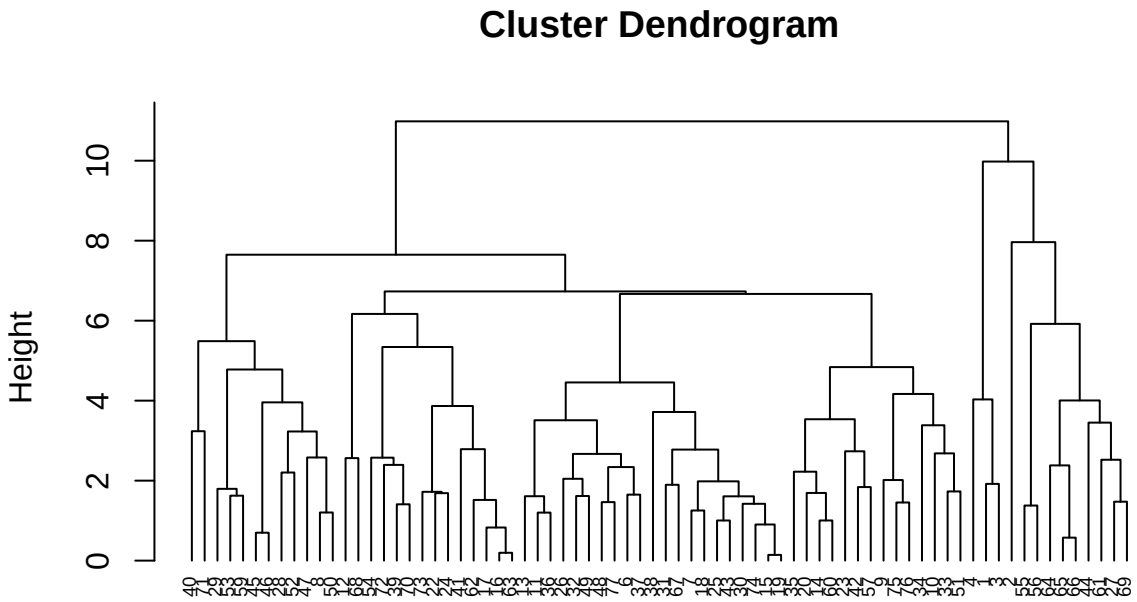
#Normalizing the dataset

```
c<- c[4:16]
c <- scale(c,center = TRUE,scale = TRUE)
head(c)
```

```
##     calories    protein        fat     sodium       fiber      carbo     sugars
## 1 -1.8659155  1.3817478  0.0000000 -0.3910227  3.22866747 -2.5001396 -0.2542051
## 2  0.6537514  0.4522084  3.9728810 -1.7804186 -0.07249167 -1.7292632  0.2046041
## 3 -1.8659155  1.3817478  0.0000000  1.1795987  2.81602258 -1.9862220 -0.4836096
## 4 -2.8737823  1.3817478 -0.9932203 -0.2702057  4.87924705 -1.7292632 -1.6306324
## 6  0.1498180 -0.4773310  0.9932203  0.2130625 -0.27881412 -1.0868662  0.6634132
## 7  0.1498180 -0.4773310 -0.9932203 -0.4514312 -0.48513656 -0.9583868  1.5810314
##       potass   vitamins      shelf     weight       cups     rating
## 1  2.5605229 -0.1818422  0.9419715 -0.2008324 -2.0856582  1.8549038
## 2  0.5147738 -1.3032024  0.9419715 -0.2008324  0.7567534 -0.5977113
## 3  3.1248675 -0.1818422  0.9419715 -0.2008324 -2.0856582  1.2151965
## 4  3.2659536 -0.1818422  0.9419715 -0.2008324 -1.3644493  3.6578436
## 6 -0.4022862 -0.1818422 -1.4616799 -0.2008324 -0.3038480 -0.9165248
## 7 -0.9666308 -0.1818422 -0.2598542 -0.2008324  0.7567534 -0.6553998
```

#Task 1: Use Euclidean distance to apply hierarchical clustering to the data using the normalized measurements.Agnes can be used to compare the clustering from Ward, complete linkage, average linkage, and single linkage. Pick the best approach.

```
Euclidean_Dist <- dist(c, method = "euclidean")
# Hierarchical clustering using Complete Linkage
hc1 <- hclust(Euclidean_Dist, method = "complete" )
# Plot the obtained dendrogram
plot(hc1, cex = 0.6, hang = -1)
```




```
round(hc1$height, 3)
```

```
##  [1]  0.143  0.196  0.575  0.698  0.828  0.904  1.003  1.004  1.201  1.203
## [11]  1.254  1.378  1.408  1.421  1.454  1.463  1.474  1.517  1.608  1.611
## [21]  1.616  1.625  1.650  1.687  1.692  1.720  1.730  1.795  1.839  1.897
## [31]  1.919  1.982  2.015  2.046  2.203  2.224  2.339  2.381  2.394  2.522
## [41]  2.563  2.574  2.579  2.668  2.682  2.734  2.776  2.787  3.229  3.236
## [51]  3.385  3.451  3.510  3.535  3.717  3.866  3.957  4.005  4.031  4.168
## [61]  4.456  4.779  4.839  5.342  5.488  5.920  6.169  6.669  6.731  7.650
## [71]  7.964  9.979 10.984
```

Compute with agnes and with different linkage methods

```
hc_single <- agnes(c, method = "single")
print(hc_single$ac)
```

```
## [1] 0.6067859
```

```
hc_complete <- agnes(c, method = "complete")
print(hc_complete$ac)
```

```
## [1] 0.8353712
```

```r
hc_average <- agnes(c, method = "average")
print(hc_average$ac)
```

```
## [1] 0.7766075
```

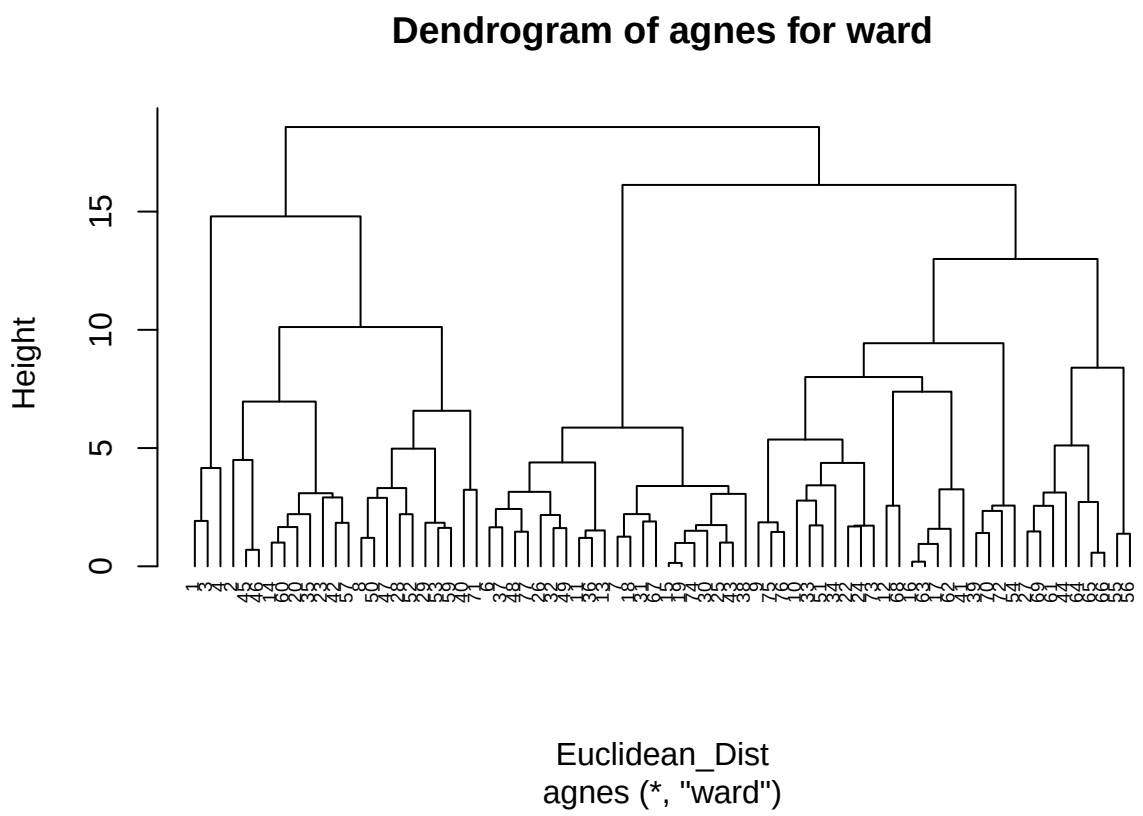
```r
hc_ward <- agnes(c, method = "ward")
print(hc_ward$ac)
```

```
## [1] 0.9046042
```

#The agglomerative coefficient obtained by Ward's method is the largest.

#visualizing the dendrogram

```r
hc_Ward <- agnes(Euclidean_Dist, method = "ward")
pltree(hc_Ward, cex = 0.6, hang = -1, main = "Dendrogram of agnes for ward")
```

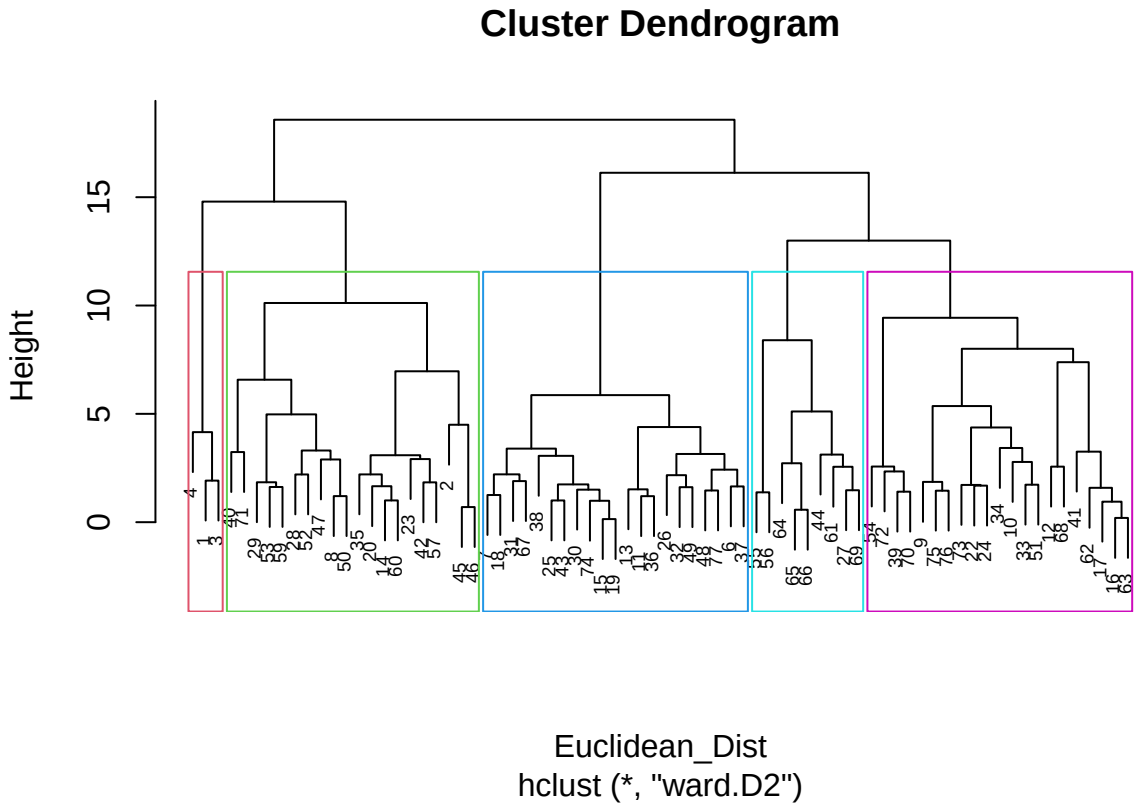


#Task 2.How many clusters would you choose?

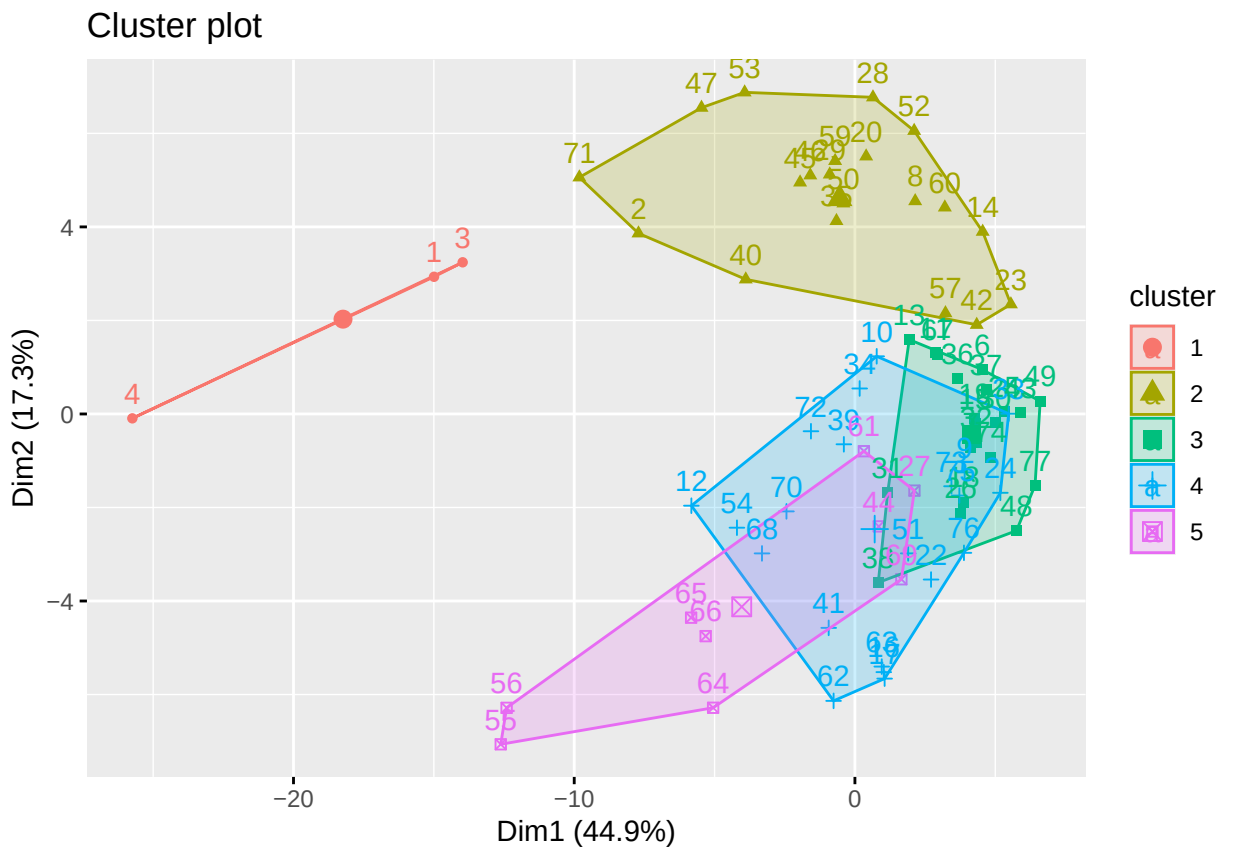
```r
#The largest difference in height can be used to determine the k value, hence K =5 is the best option.
hc_Ward <- hclust(Euclidean_Dist,method = "ward.D2")
clust_comp <- cutree(hc_Ward, k=5)
table(clust_comp)
```

```
## clust_comp
##  1  2  3  4  5
##  3 20 21 21  9
```

```
plot(hc_Ward,cex=0.6)
rect.hclust(hc_Ward, k = 5, border = 2:10,)
```




```
Temp <- cbind(as.data.frame(cbind(c,clust_comp)))
#Visualizing the clusters in Scatter plot
fviz_cluster(list(data=Euclidean_Dist, cluster = clust_comp))
```



#Task 3: Choose a set of cereals for the elementary public schools to stock in their daily cafeterias. There is a different cereal available every day, but they should all promote a healthy diet. To complete this task, you must locate a group of "healthy cereals."

```
Healthy_cereal <- na.omit(read.csv("/Users/Jay/Downloads/Cereals.csv"))
Healthy_cereal<- cbind(Healthy_cereal,clust_comp)
mean(Healthy_cereal[Healthy_cereal$clust_comp==1,"rating"])
```

```
## [1] 73.84446
```

```
mean(Healthy_cereal[Healthy_cereal$clust_comp==2,"rating"])
```

```
## [1] 38.26161
```

```
mean(Healthy_cereal[Healthy_cereal$clust_comp==3,"rating"])
```

```
## [1] 28.84825
```

```
mean(Healthy_cereal[Healthy_cereal$clust_comp==4,"rating"])
```

```
## [1] 46.46513
```

```r
mean(Healthy_cereal[Healthy_cereal$clust_comp==5,"rating"])
```

```
## [1] 63.0184
```

It is clear that Cluster1 has maximum rating (73.84446), therefore we'll choose it as a healthy cereal.