Assignment 5 suraj gadapa

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

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

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

```
library(dendextend)
```

```
## Warning: package 'dendextend' was built under R version 4.2.2
```

```
##
## ---------------------
## 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)
```

```
## Warning: package 'factoextra' was built under R version 4.2.2
```

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

```
c<-read.csv("C:/Users/suraj/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
```

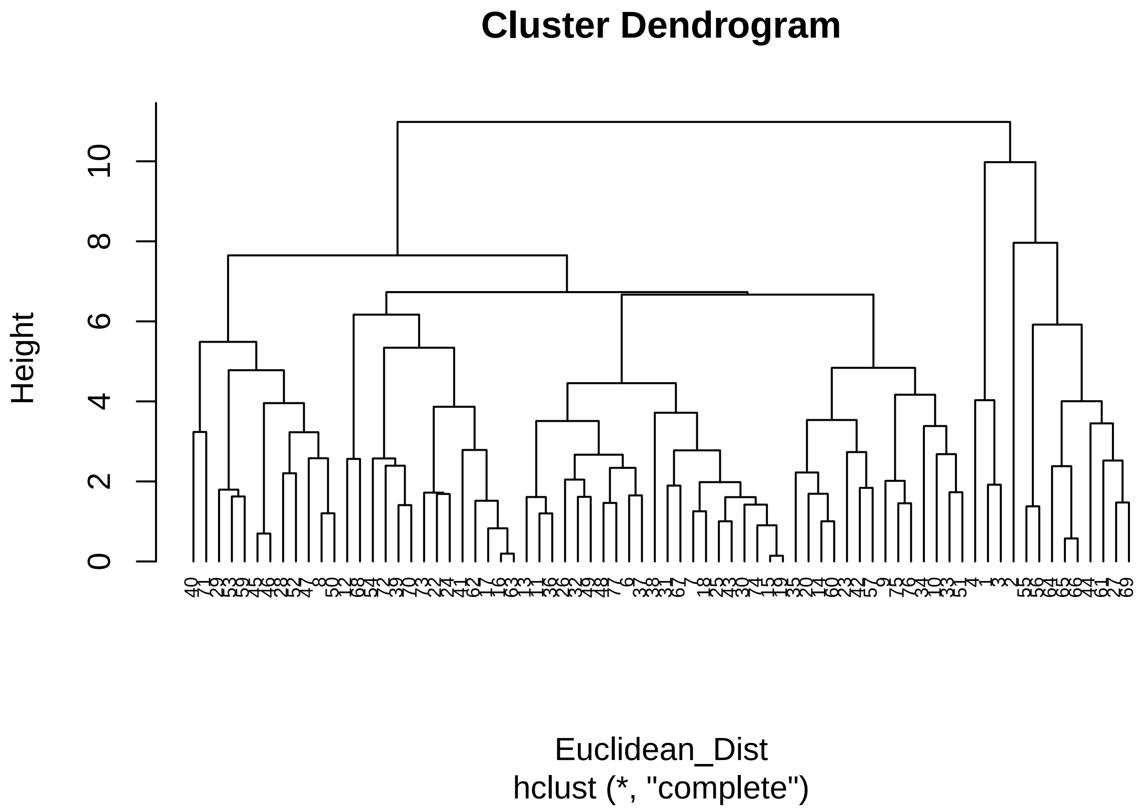
#Normalizing the dataset

```
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.Apply hierarchical clustering to the data using Euclidean distance to the normalized measurements. #Use Agnes to compare the clustering from single linkage, complete #linkage, average linkage, and Ward. Choose the best method.

```
Euclidean_Dist <- dist(c, method = "euclidean")
# Hierarchical clustering using Complete Linkage
cl1 <- hclust(Euclidean_Dist, method = "complete" )
# Plot the obtained dendrogram
plot(cl1, cex = 0.6, hang = -1)
```



```r
round(cl1$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

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

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

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

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

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

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

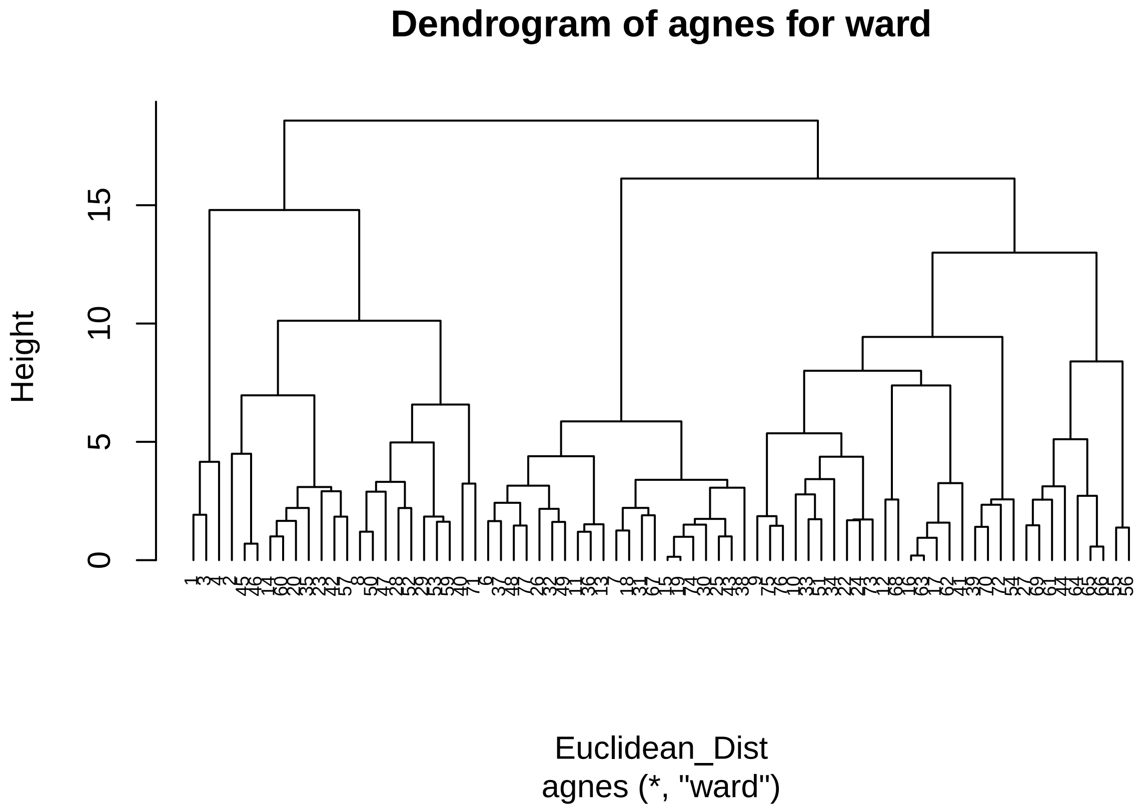
```r
cl_ward <- agnes(c, method = "ward")
print(cl_ward$ac)
```

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

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

#visualizing the dendrogram

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

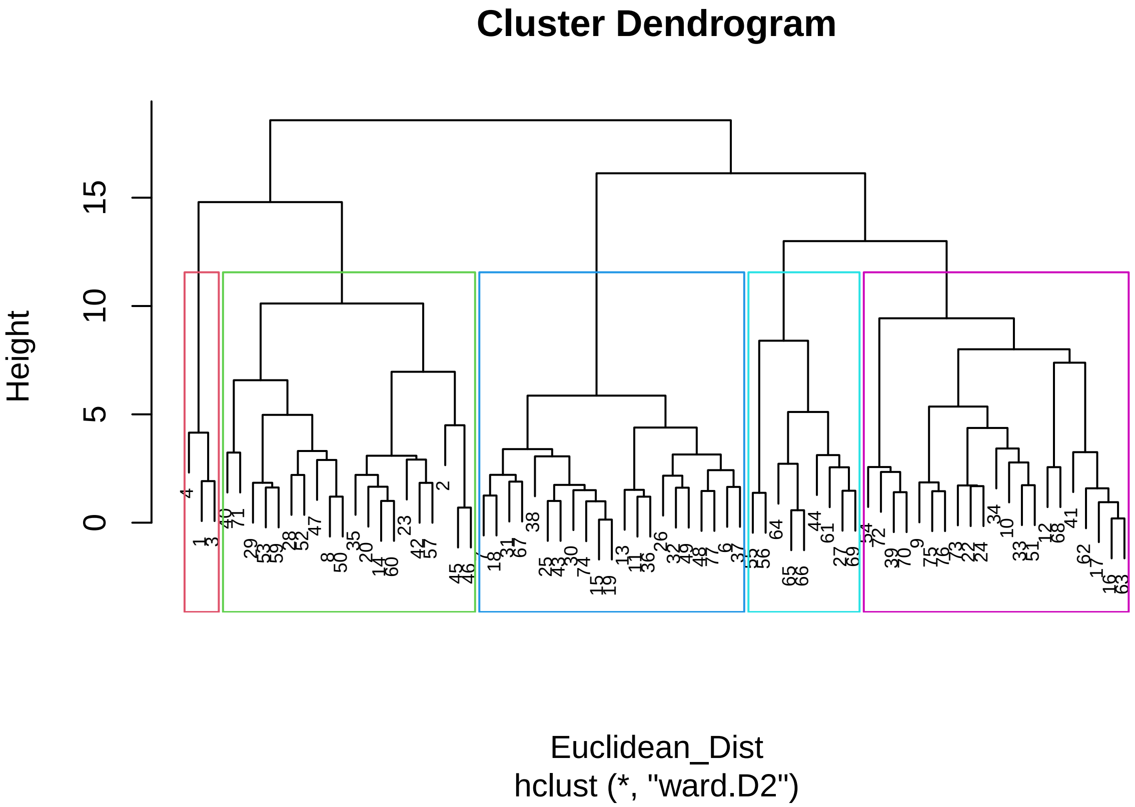


#Task-2.How many clusters would you choose?

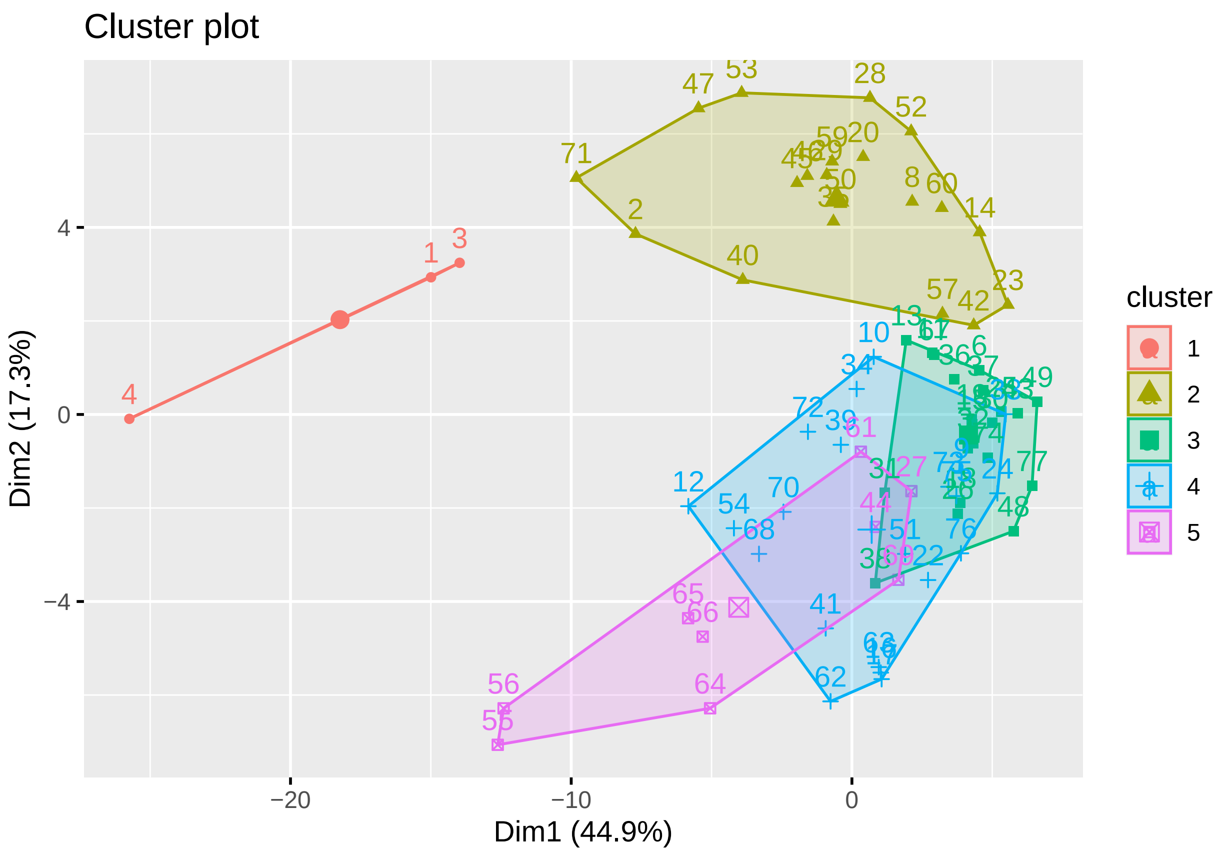
```r
#The largest difference in height can be used to determine the k value, hence K =5 is the best option.
cl_Ward <- hclust(Euclidean_Dist,method = "ward.D2")
clust_comp <- cutree(cl_Ward, k=5)
table(clust_comp)
```

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

```
plot(cl_Ward,cex=0.6)
rect.hclust(cl_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.The elementary public schools would like to choose a set of cereals to include in their #daily cafeterias. Every day a different cereal is offered, but all cereals should support a #healthy diet. For this goal, you are requested to find a cluster of “healthy cereals.”

```
Healthy_cereal <- na.omit(read.csv("C:/Users/suraj/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
```

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

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

Cluster1 has the highest rating (73.84446), so we'll choose it as a healthy cereal.