

MachineLearning_Assignment_5

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```
Cereals <- read.csv("C:/Users/HP/Documents/csv file/Cereals.csv")
Cereals <- na.omit(Cereals)
head(Cereals)
```

```
##              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
```

```
#Loading the necessary libraries
```

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

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

```
## Warning in register(): Can't find generic 'scale_type' in package ggplot2 to
## register S3 method.
```

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

```
library(dendextend)
```

```
## Warning: package 'dendextend' was built under R version 4.1.3
```

```
##
```

```
## -----
```

```
## 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(factoextra)
```

```
## Warning: package 'factoextra' was built under R version 4.1.3
```

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

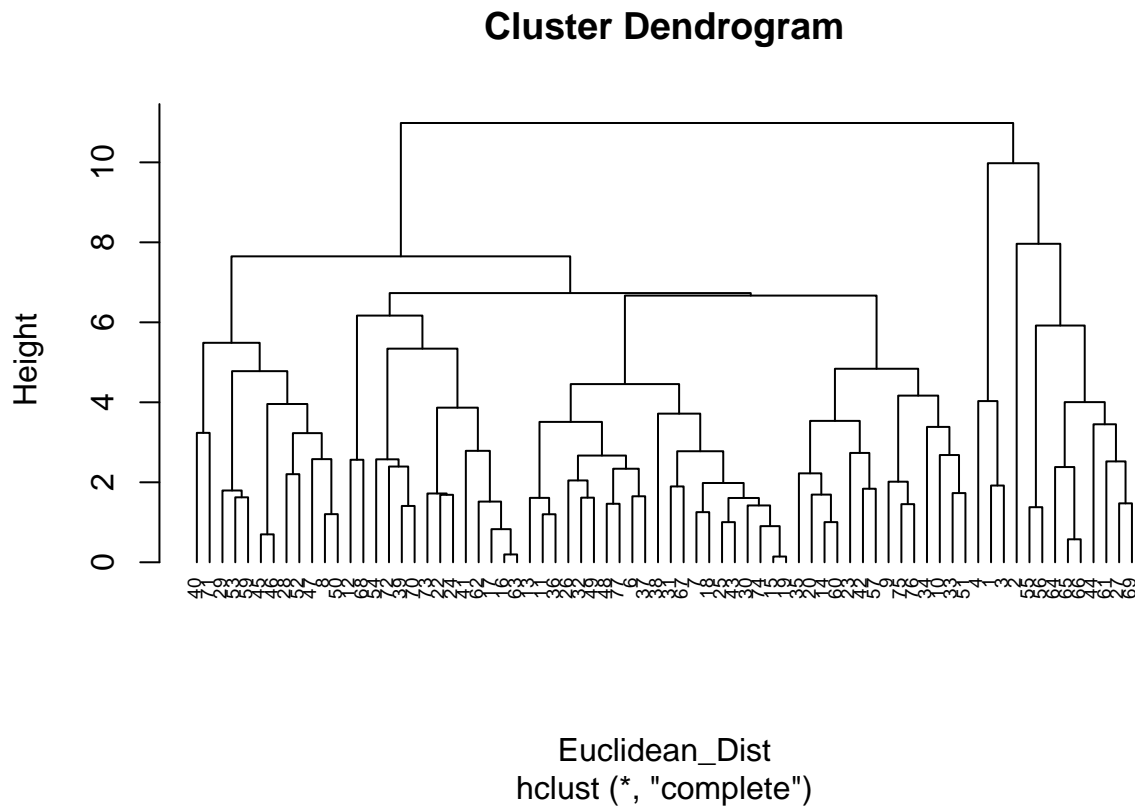
```
#Normalizing the Data
```

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

```
##      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 measure-
ments. #Use Agnes to compare the clustering from single linkage, complete #linkage, average linkage, and
Ward. Choose the best method.
```

```
## Euclidean distance to measure the Distance
Euclidean_Dist <- dist(Cereals, 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(Cereals, method = "single")
print(hc_single$ac)
```

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

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

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

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

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

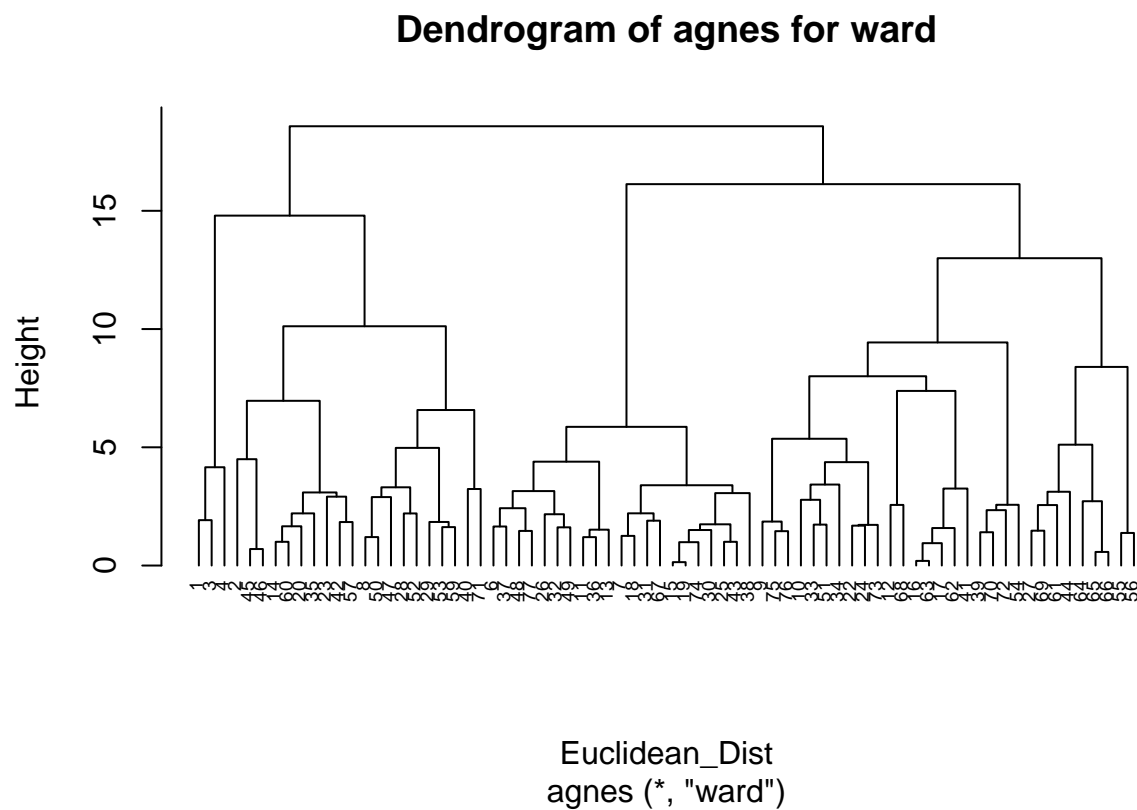
```
hc_ward <- agnes(Cereals, method = "ward")
print(hc_ward$ac)
```

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

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

#visualizing the dendrogram

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



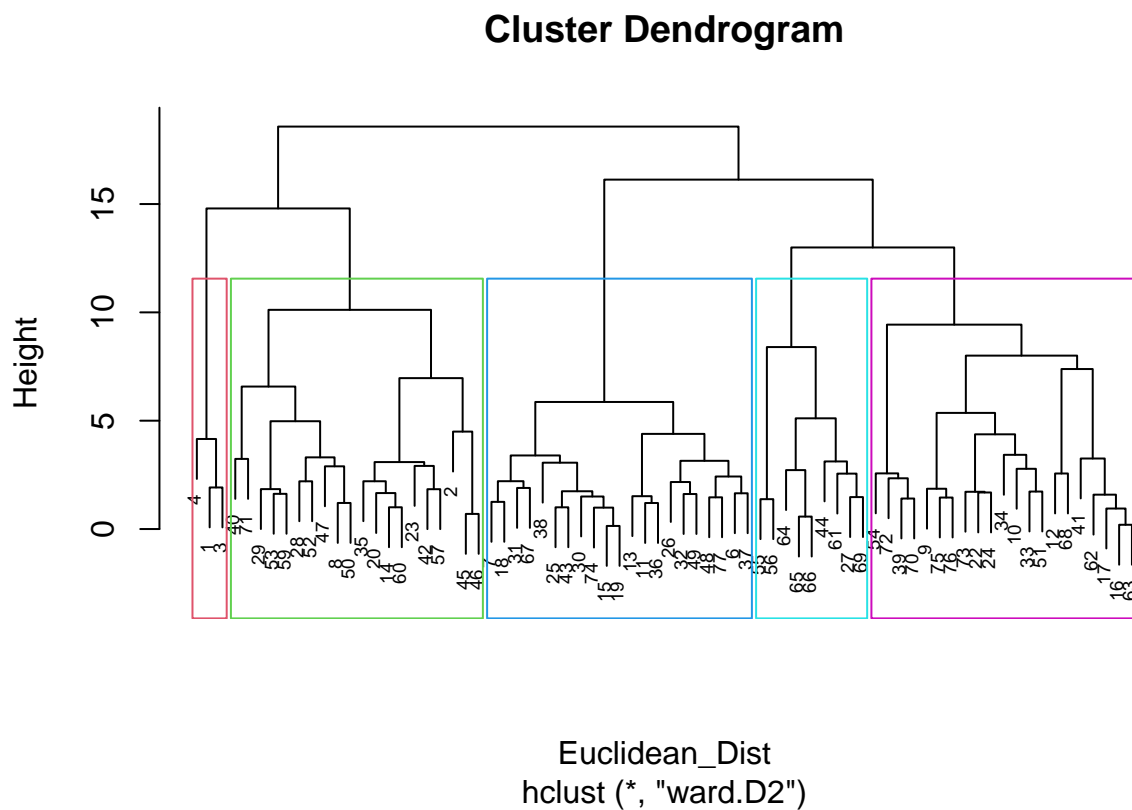
##Task-2.How many clusters would you choose?

#The largest difference in height can be used to determine the k value, hence K =5 is the best option.

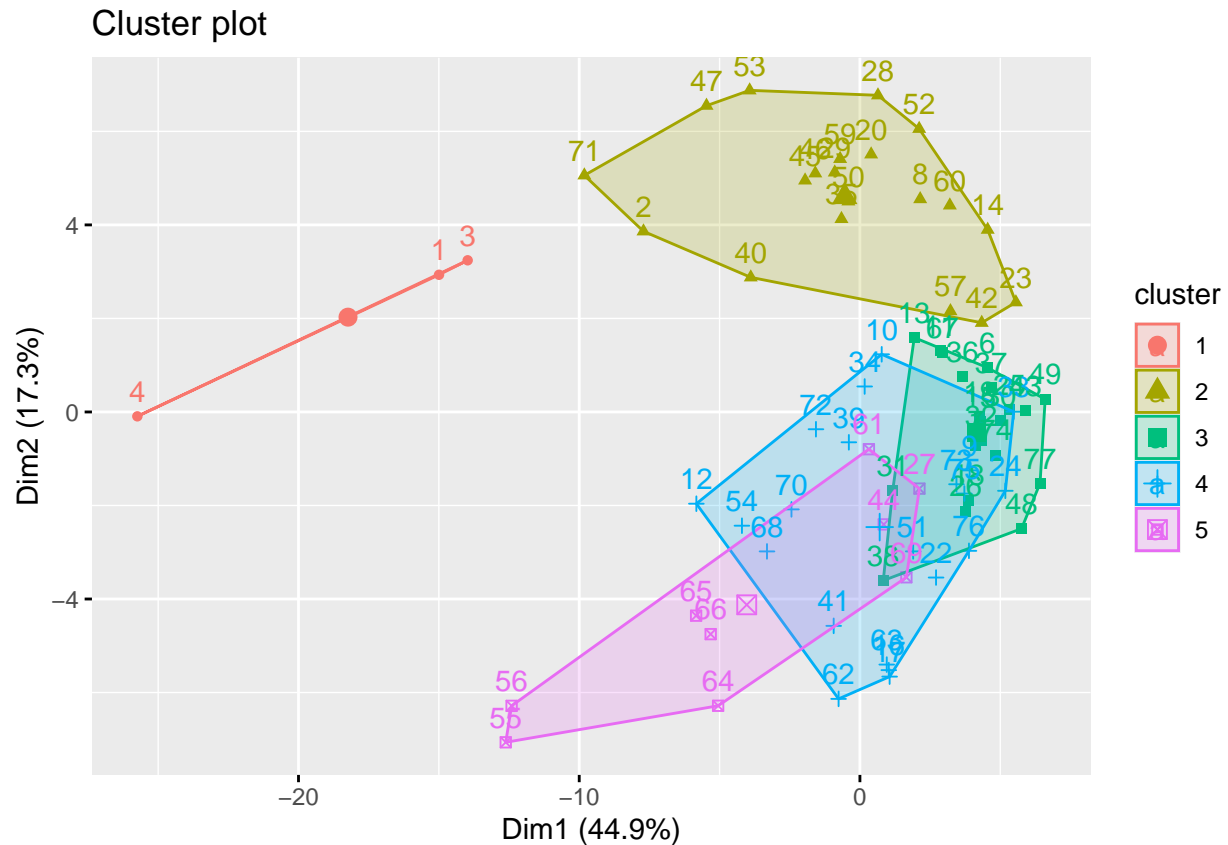
```
hc_Ward <- hclust(Euclidean_Dist,method = "ward.D2")
clust_comp <- cutree(hc_Ward, k=5)
table(clust_comp)
```

```
## 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(Cereals,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/HP/Documents/csv file/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
```

#It is Clear that Cluster1 has maximum rating i.e.73.84446,hence we'll choose it as an healthy cereal.