Assignment5_FML

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Hierarchical Clustering

```
Cereals <- read.csv("C:/Users/mpuru/Downloads/Cereals.csv")
str(Cereals)

## 'data.frame':    77 obs. of  16 variables:
##  $ name    : chr  "100%_Bran" "100%_Natural_Bran" "All-Bran" "All-
Bran_with_Extra_Fiber" ...
##  $ mfr     : chr  "N" "Q" "K" "K" ...
##  $ type    : chr  "C" "C" "C" "C" ...
##  $ calories: int  70 120 70 50 110 110 110 130 90 90 ...
##  $ protein : int  4 3 4 4 2 2 2 3 2 3 ...
##  $ fat     : int  1 5 1 0 2 2 0 2 1 0 ...
##  $ sodium  : int  130 15 260 140 200 180 125 210 200 210 ...
##  $ fiber   : num  10 2 9 14 1 1.5 1 2 4 5 ...
##  $ carbo   : num  5 8 7 8 14 10.5 11 18 15 13 ...
##  $ sugars  : int  6 8 5 0 8 10 14 8 6 5 ...
##  $ potass  : int  280 135 320 330 NA 70 30 100 125 190 ...
##  $ vitamins: int  25 0 25 25 25 25 25 25 25 25 ...
##  $ shelf   : int  3 3 3 3 3 1 2 3 1 3 ...
##  $ weight  : num  1 1 1 1 1 1 1 1.33 1 1 ...
##  $ cups    : num  0.33 1 0.33 0.5 0.75 0.75 1 0.75 0.67 0.67 ...
##  $ rating  : num  68.4 34 59.4 93.7 34.4 ...

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
## 5              Almond_Delight   R    C      110       2   2    200   1.0
14.0
## 6     Apple_Cinnamon_Cheerios   G    C      110       2   2    180   1.5
10.5
##   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
## 5      8     NA       25     3      1 0.75 34.38484
## 6     10     70       25     1      1 0.75 29.50954
```

```
library(DataExplorer)
introduce(Cereals) # Missing values
```

```
##   rows columns discrete_columns continuous_columns all_missing_columns
## 1   77      16                3                  13                   0
##   total_missing_values complete_rows total_observations memory_usage
## 1                    4            74               1232        17296
```

```
Cereals1<-na.omit(Cereals) #Data set with missing values in the rows that
have been omitted
```

Apply hierarchical clustering to the data using normalization measures and Euclidean distance.

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse
1.3.1 --
```

```
## v ggplot2 3.3.5     v purrr   0.3.4
## v tibble  3.1.6     v dplyr   1.0.8
## v tidyr   1.2.0     v stringr 1.4.0
## v readr   2.1.2     v forcats 0.5.1
```

```
## -- Conflicts ------------------------------------------
tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(factoextra)
```

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

```
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(cluster)
library(fastDummies)
```

#Categorical and numerical variables must be identified.

```
Cereals1$name<-as.factor(Cereals1$name)
Cereals1$mfr<-as.factor(Cereals1$mfr)
Cereals1$type<-as.factor(Cereals1$type)
Cereals1$shelf<-as.factor(Cereals1$shelf)

# Creating dummy variables

vaar<-colnames(Cereals1)
n_var<-
c("calories","protein","fat","sodium","fiber","carbo","sugars","potass","vita
mins","weight","cups","rating")
cat_var<-
Cereals1[which(colnames(Cereals1)%in%c('name','mfr','type','shelf'))]
cat_var<-
data.frame(apply((Cereals1[which(colnames(Cereals1)%in%c('name','mfr','type',
'shelf'))]),2,as.factor))
dummy_vars<-fastDummies::dummy_columns(cat_var %>% select(-name))
n_vars<-Cereals1[,c(4:12,14:16)]
Cereals2<-cbind(Cereals1$name,dummy_vars,n_vars)%>% select(-
c(mfr,type,shelf))
```

#Normalizing the data set

```
Cereals2[,c(2:25)]<-scale(Cereals2[,c(2:25)],scale = TRUE, center = TRUE)
```

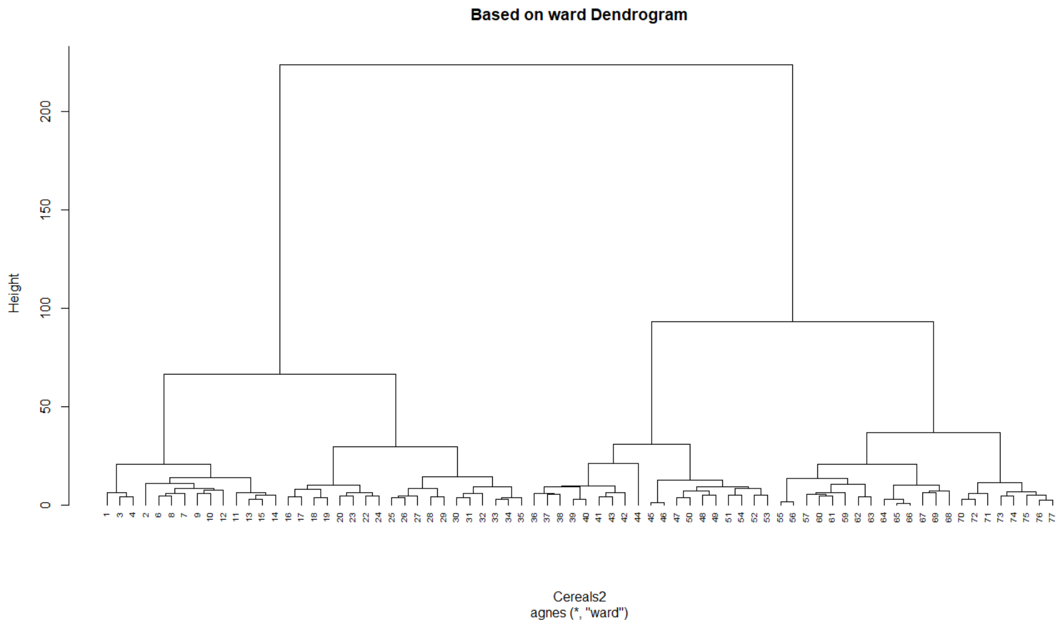
#Q1.Use Agnes to compare the clustering from single linkage, complete linkage, average linkage, and Ward. Choose the best method.

```
Hclustering1<- agnes(Cereals2, method="complete")
Hclustering2<- agnes(Cereals2, method = "average")
Hclustering3<- agnes(Cereals2, method="single")
Hclustering4<- agnes(Cereals2, method="ward")
```

```
ac<-c(Hclustering1$ac,Hclustering2$ac,Hclustering3$ac,Hclustering4$ac)
ac_method<-
c(Hclustering1$method,Hclustering2$method,Hclustering3$method,Hclustering4$me
thod)
ac_df<-data.frame(ac_method, ac)
ac_df
```

```
##   ac_method        ac
## 1  complete 0.9357221
## 2   average 0.8777588
## 3    single 0.7192344
## 4      ward 0.9787001
```

```
pltree(Hclustering4,cex=0.6,hang=-1,main="Based on ward
Dendrogram",labels=Cereals2$'C_df1$name')
```



#According to the table above,the ward technique has the highest agglomerative coefficient,meaning it is the closest to one.As a result it produces the most clusters.

#2.How many clusters would you choose?

```
fviz_nbclust(Cereals2,hcut,method="wss")+geom_vline(xintercept=2,linetype=5)
```

```
## Warning in stats::dist(x): NAs introduced by coercion

## Warning in stats::dist(x, method = method, ...): NAs introduced by
coercion

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```

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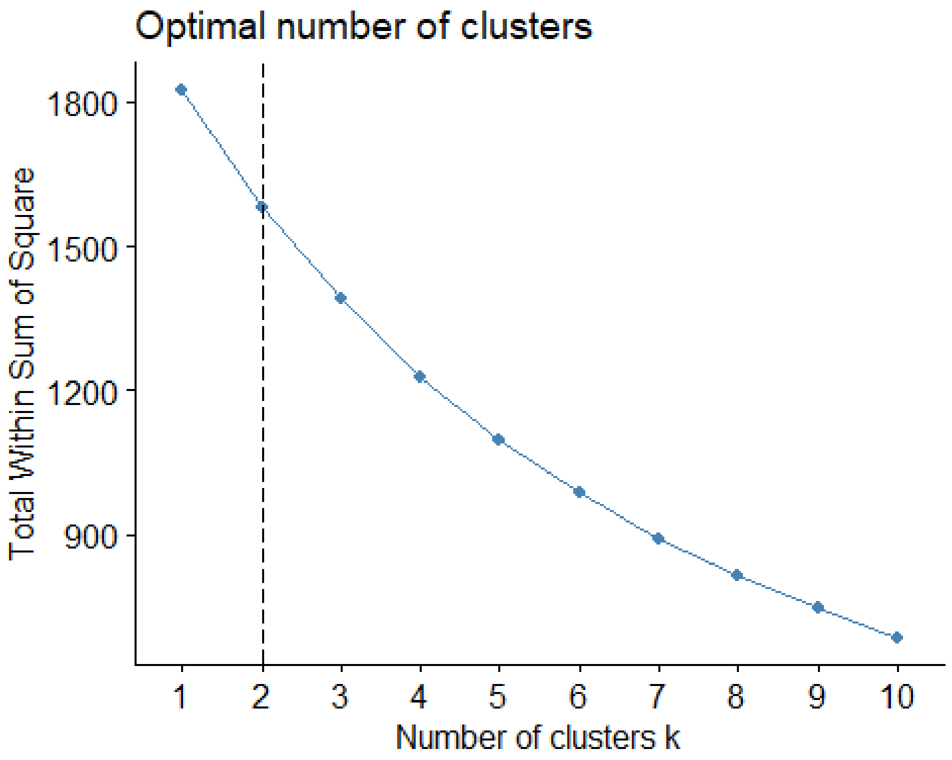
coercion
```



```
fviz_nbclust(Cereals2,hcut,method = "silhouette")
```

```
## Warning in stats::dist(x): NAs introduced by coercion

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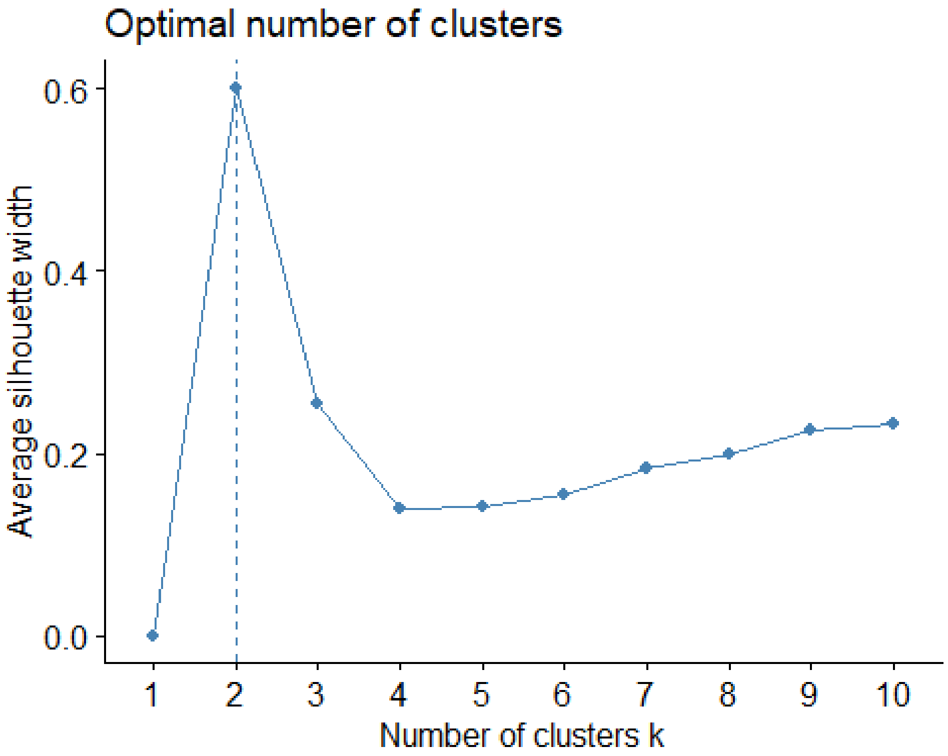
```



```
Cereals2<-Cereals2%>% mutate(cluster=cutree(Hclustering4,k=2))
```

#I will select Two clusters based on the dendogram

#3.Comment on the structure of the clusters and on their stability

```
library(caret)
```

```
## Loading required package: lattice

##
## Attaching package: 'caret'

## The following object is masked from 'package:purrr':
##
##     lift

library(dplyr)
set.seed(12)
split_index<-createDataPartition(Cereals2$rating,p=0.6,times=1,list=FALSE)
C_p1<-Cereals2[ split_index, ]
C_p2<-Cereals2[-split_index, ]
centroid1<-C_p1 %>% select_if(is.numeric) %>% filter(cluster==1) %>%
colMeans()
centroid2<-C_p1 %>% select_if(is.numeric)%>% filter(cluster==2)%>% colMeans()
centroid<-rbind(centroid1,centroid2)
cluster_B<-data.frame(data=seq(1,nrow(C_p2),1),clusterB=rep(0,nrow(C_p2)))
for (x in 1:nrow(C_p2)) {cluster_B$clusterB<-
which.min(as.matrix(get_dist(as.data.frame(rbind(  centroid[,-25],C_p2[x,c(-
1,-26)]))))[3,-3])
}

cluster_B<-cluster_B %>% mutate(orig_clusters=C_p2$cluster)
mean(cluster_B$clusterB==cluster_B$orig_clusters)

## [1] 0.3928571
```

According to the comparison,the clusters are stable.

#4. The elementary public schools would like to choose a set of cereals to include in their daily cafeterias

```
h_cereals<-data.frame(Cereals2 %>% filter(cluster==2) %>%
select_if(is.numeric) %>% colMeans())
```

Cluster Two has cereals that are high in protein,vitamins,carbohydrates and fiber,but low in sodium and sugar.As a result,Cereals in cluster 2 can be used to maintain a healthy diet.