Hierarchical Clustering

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#Loading the dataset

```
data=read.csv("C:\\Users\\Osama Zahir\\Downloads\\Cereals.csv")
head(data)
```

```
##                        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
```

#Viewing the summary and structure of that dataset

```
summary(data)
```

```
##      name               mfr                type              calories    
##  Length:77          Length:77          Length:77          Min.   : 50.0  
##  Class :character   Class :character   Class :character   1st Qu.:100.0  
##  Mode  :character   Mode  :character   Mode  :character   Median :110.0  
##                                                           Mean   :106.9  
##                                                           3rd Qu.:110.0  
##                                                           Max.   :160.0  
##                                                                          
##     protein           fat            sodium          fiber       
##  Min.   :1.000   Min.   :0.000   Min.   :  0.0   Min.   : 0.000  
##  1st Qu.:2.000   1st Qu.:0.000   1st Qu.:130.0   1st Qu.: 1.000  
##  Median :3.000   Median :1.000   Median :180.0   Median : 2.000  
##  Mean   :2.545   Mean   :1.013   Mean   :159.7   Mean   : 2.152  
##  3rd Qu.:3.000   3rd Qu.:2.000   3rd Qu.:210.0   3rd Qu.: 3.000  
##  Max.   :6.000   Max.   :5.000   Max.   :320.0   Max.   :14.000  
##                                                                  
##      carbo          sugars           potass          vitamins     
##  Min.   : 5.0   Min.   : 0.000   Min.   : 15.00   Min.   :  0.00  
##  1st Qu.:12.0   1st Qu.: 3.000   1st Qu.: 42.50   1st Qu.: 25.00  
##  Median :14.5   Median : 7.000   Median : 90.00   Median : 25.00  
##  Mean   :14.8   Mean   : 7.026   Mean   : 98.67   Mean   : 28.25  
##  3rd Qu.:17.0   3rd Qu.:11.000   3rd Qu.:120.00   3rd Qu.: 25.00  
##  Max.   :23.0   Max.   :15.000   Max.   :330.00   Max.   :100.00  
##  NA's   :1      NA's   :1        NA's   :2                        
##      shelf           weight          cups           rating     
##  Min.   :1.000   Min.   :0.50   Min.   :0.250   Min.   :18.04  
##  1st Qu.:1.000   1st Qu.:1.00   1st Qu.:0.670   1st Qu.:33.17  
##  Median :2.000   Median :1.00   Median :0.750   Median :40.40  
##  Mean   :2.208   Mean   :1.03   Mean   :0.821   Mean   :42.67  
##  3rd Qu.:3.000   3rd Qu.:1.00   3rd Qu.:1.000   3rd Qu.:50.83  
##  Max.   :3.000   Max.   :1.50   Max.   :1.500   Max.   :93.70  
## 
```

```
str(data)
```

```
## '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 ...
```

#Loading required packages

```r
library(caret)
```

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

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

```r
library(corrplot)
```

```
## Warning: package 'corrplot' was built under R version 4.3.2
```

```
## corrplot 0.92 loaded
```

```r
library(ggcorrplot)
```

```
## Warning: package 'ggcorrplot' was built under R version 4.3.2
```

```r
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.3.2
```

```
## Warning: package 'forcats' was built under R version 4.3.2
## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──
## ✔ dplyr     1.1.3     ✔ readr     2.1.4
## ✔ forcats   1.0.0     ✔ stringr   1.5.0
## ✔ lubridate 1.9.2     ✔ tibble    3.2.1
## ✔ purrr     1.0.2     ✔ tidyr     1.3.0
```

```
## ── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::lag()    masks stats::lag()
## ✖ purrr::lift()   masks caret::lift()
## ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becom
e errors
```

```
library(tidyr)
library(dplyr)
library(e1071)
library(reshape2)
```

```
##
## Attaching package: 'reshape2'
##
## The following object is masked from 'package:tidyr':
##
##     smiths
```

```
library(factoextra)
```

```
## Warning: package 'factoextra' was built under R version 4.3.2
```

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

```
library(cluster)
library(cowplot)
```

```
## Warning: package 'cowplot' was built under R version 4.3.2
```

```
##
## Attaching package: 'cowplot'
##
## The following object is masked from 'package:lubridate':
##
##     stamp
```

```
library(pander)
library(kernlab)
```

```
##
## Attaching package: 'kernlab'
##
## The following object is masked from 'package:purrr':
##
##     cross
##
## The following object is masked from 'package:ggplot2':
##
##     alpha
```

```
library(FactoMineR)
```

```
## Warning: package 'FactoMineR' was built under R version 4.3.2
```

#Data Preprocessing. Remove all cereals with missing values.

```
dim(data)
```

```
## [1] 77 16
```

```
c_d2=na.omit(data)
dim(c_d2)
```

```
## [1] 74 16
```

#There were 4 missing values in the dataset

#Assigning row names to the cereal column

```
c_d3 = as.data.frame(c_d2)
row.names(c_d3) = c_d3[,1]
c_d4 = c_d3[,-1]
```

#Only selecting numerical values and removing catergorical variables

```
c_d5 = c_d4[, c(3:11,13:15)]
```

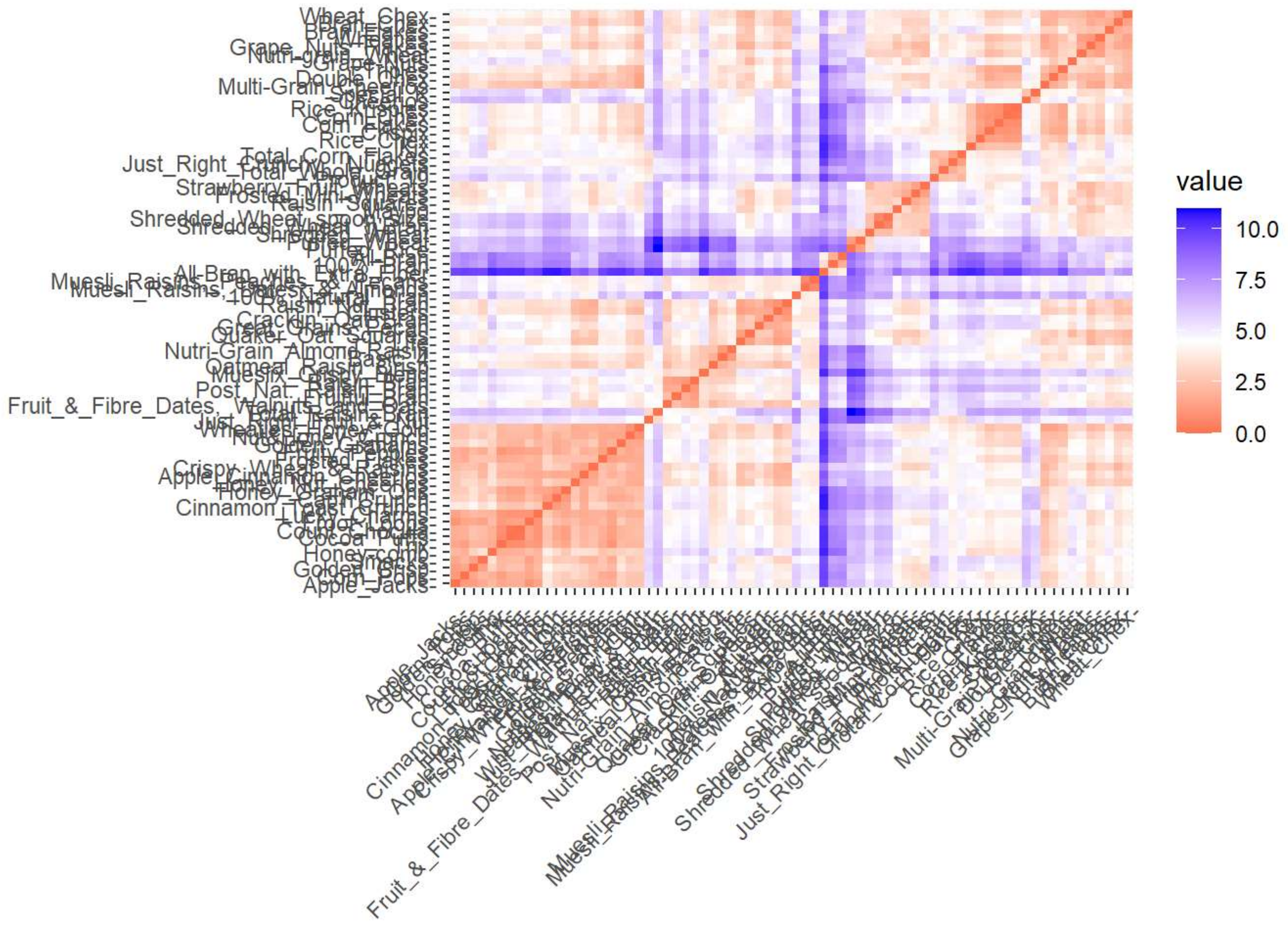
#Normalizing the data using the scale function

```
c_d5 = scale(c_d5)
head(c_d5)
```

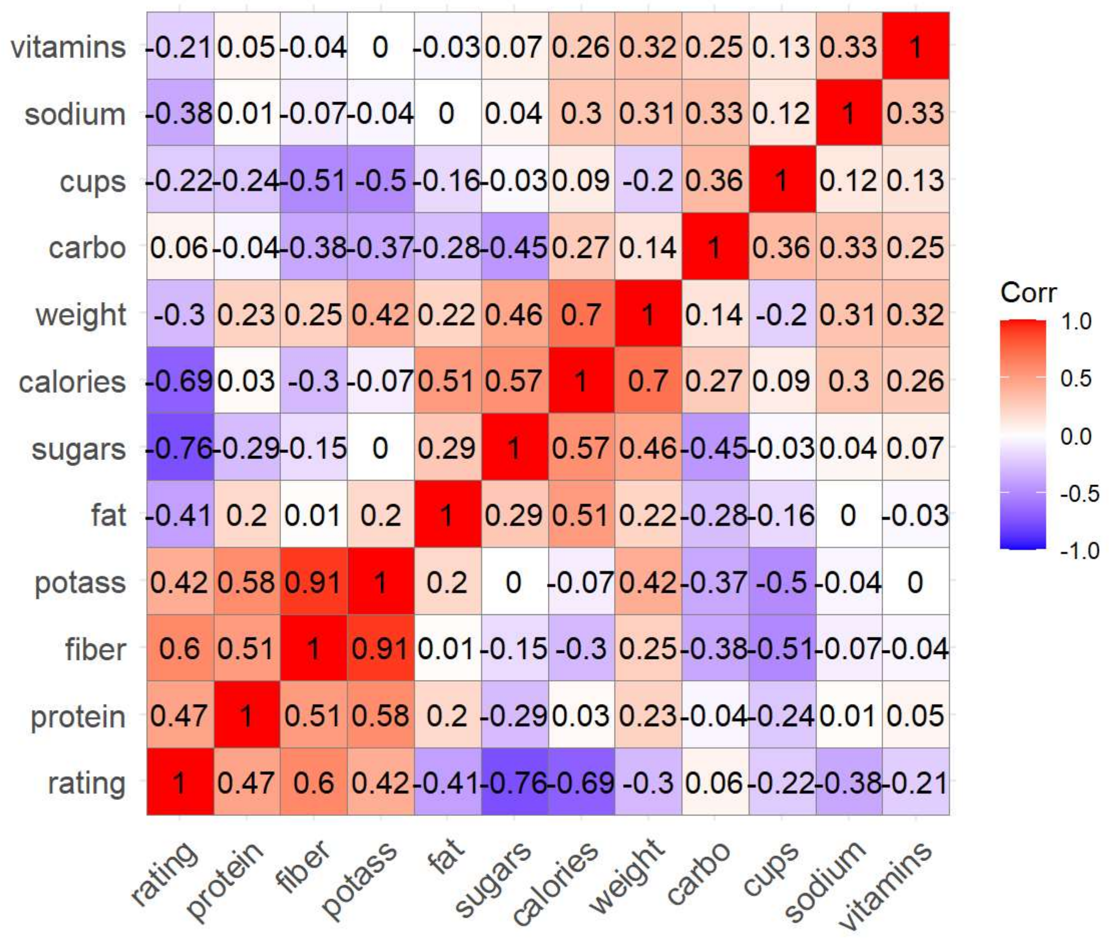
```
##                              calories    protein        fat     sodium
## 100%_Bran                   -1.8659155  1.3817478  0.0000000 -0.3910227
## 100%_Natural_Bran            0.6537514  0.4522084  3.9728810 -1.7804186
## All-Bran                    -1.8659155  1.3817478  0.0000000  1.1795987
## All-Bran_with_Extra_Fiber -2.8737823  1.3817478 -0.9932203 -0.2702057
## Apple_Cinnamon_Cheerios      0.1498180 -0.4773310  0.9932203  0.2130625
## Apple_Jacks                  0.1498180 -0.4773310 -0.9932203 -0.4514312
##                                  fiber      carbo     sugars     potass
## 100%_Bran                    3.22866747 -2.5001396 -0.2542051  2.5605229
## 100%_Natural_Bran           -0.07249167 -1.7292632  0.2046041  0.5147738
## All-Bran                     2.81602258 -1.9862220 -0.4836096  3.1248675
## All-Bran_with_Extra_Fiber  4.87924705 -1.7292632 -1.6306324  3.2659536
## Apple_Cinnamon_Cheerios     -0.27881412 -1.0868662  0.6634132 -0.4022862
## Apple_Jacks                 -0.48513656 -0.9583868  1.5810314 -0.9666308
##                              vitamins     weight       cups     rating
## 100%_Bran                   -0.1818422 -0.2008324 -2.0856582  1.8549038
## 100%_Natural_Bran           -1.3032024 -0.2008324  0.7567534 -0.5977113
## All-Bran                    -0.1818422 -0.2008324 -2.0856582  1.2151965
## All-Bran_with_Extra_Fiber -0.1818422 -0.2008324 -1.3644493  3.6578436
## Apple_Cinnamon_Cheerios     -0.1818422 -0.2008324 -0.3038480 -0.9165248
## Apple_Jacks                 -0.1818422 -0.2008324  0.7567534 -0.6553998
```

Question 1 (part A): Apply hierarchical clustering to the data using Euclidean distance to the normalized measurements and looking at the correaltion values by plotting the corrplot

```
distance_table <- get_dist(c_d5)
fviz_dist(distance_table)
```



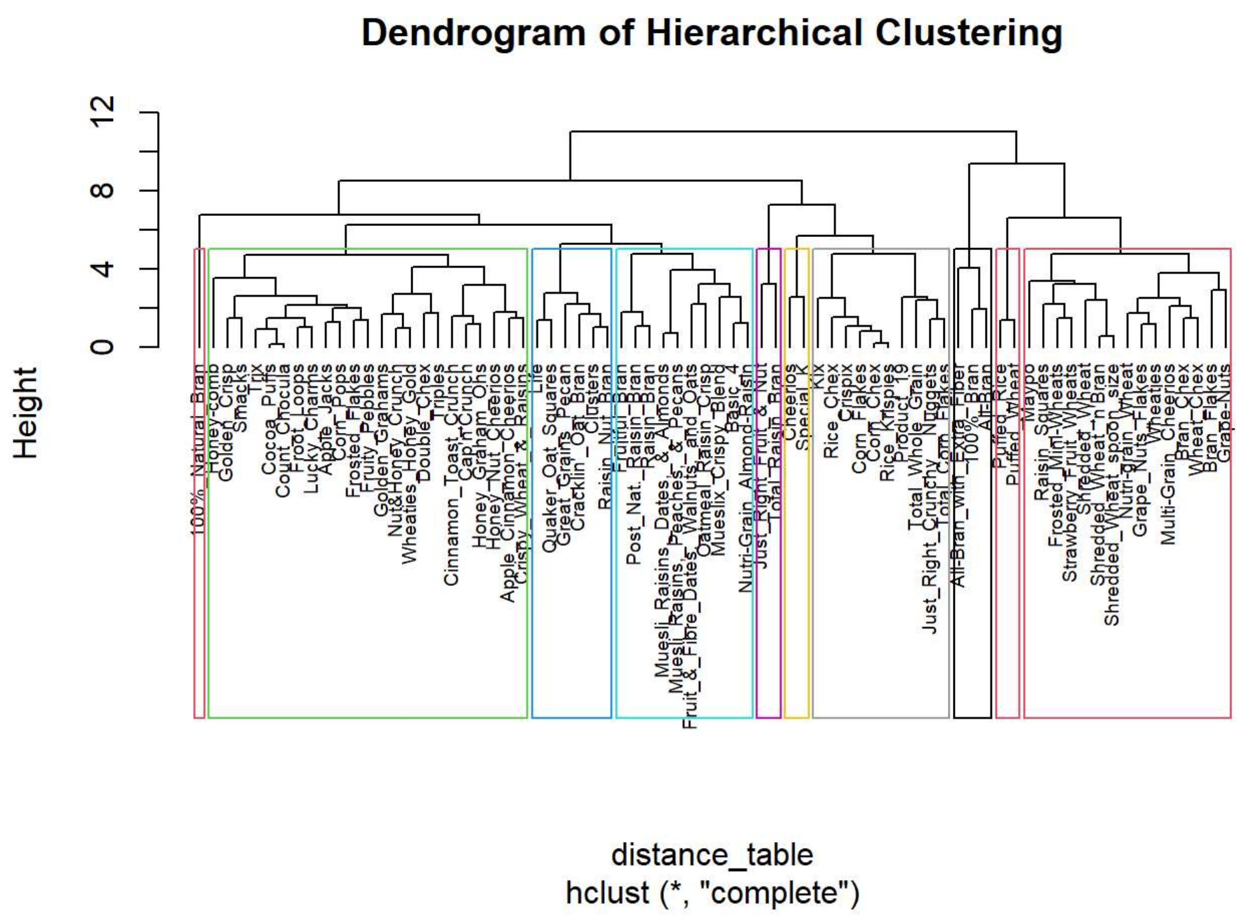
```
corr_plot = cor(c_d5)
ggcorrplot(corr_plot, outline.color = "grey50", lab = TRUE, hc.order = TRUE, type = "full")
```



```
#Sugar and calories are highly negatively correlated with rating. Also, Potass is highly positiv
ely correlated with fiber and Protien.
```

Question 1 (part B): comparing hierarchical clustering with different linkages: single, average, complete and ward.

```
# Hierarchical clustering using Complete Linkage
hc1 <- hclust(distance_table, method = "complete" )
# Plot the obtained dendrogram
plot(hc1, cex = 0.6, hang = -1, main = "Dendrogram of Hierarchical Clustering")
rect.hclust(hc1, k = 10, border = 2:10)
```



#Computing with AGNES and with different linkage methods

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

```
## [1] 0.6072384
```

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

```
## [1] 0.8469328
```

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

```
## [1] 0.7881955
```

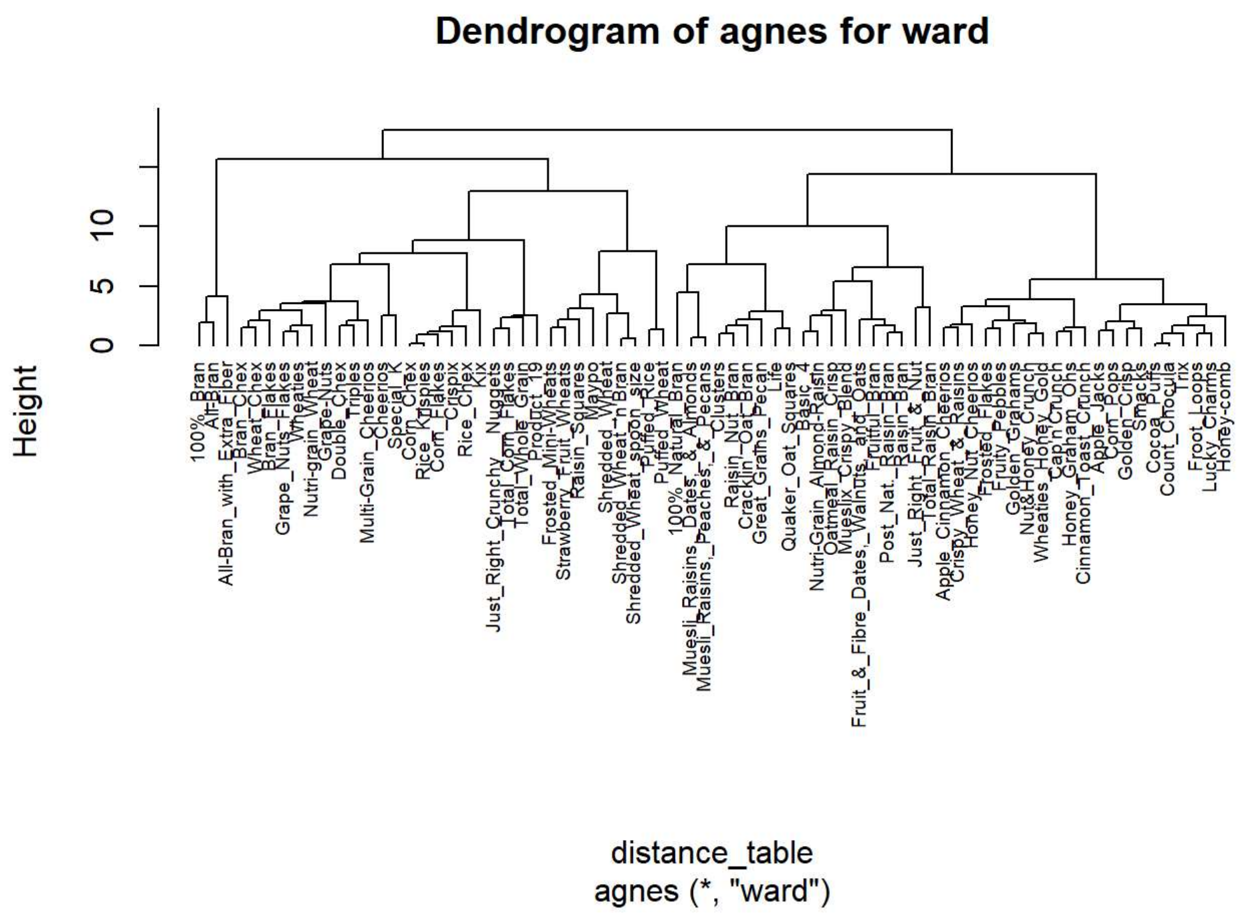
```
hc_ward <- agnes(distance_table, method = "ward")
print(hc_ward$ac)
```

```
## [1] 0.9087265
```

```
#These results confirm that the Ward linkage, which provides 90.87% accuracy, is the optimal agg
lomerative (AGNES) linkage to use.
```

#Visualizing the dendogram

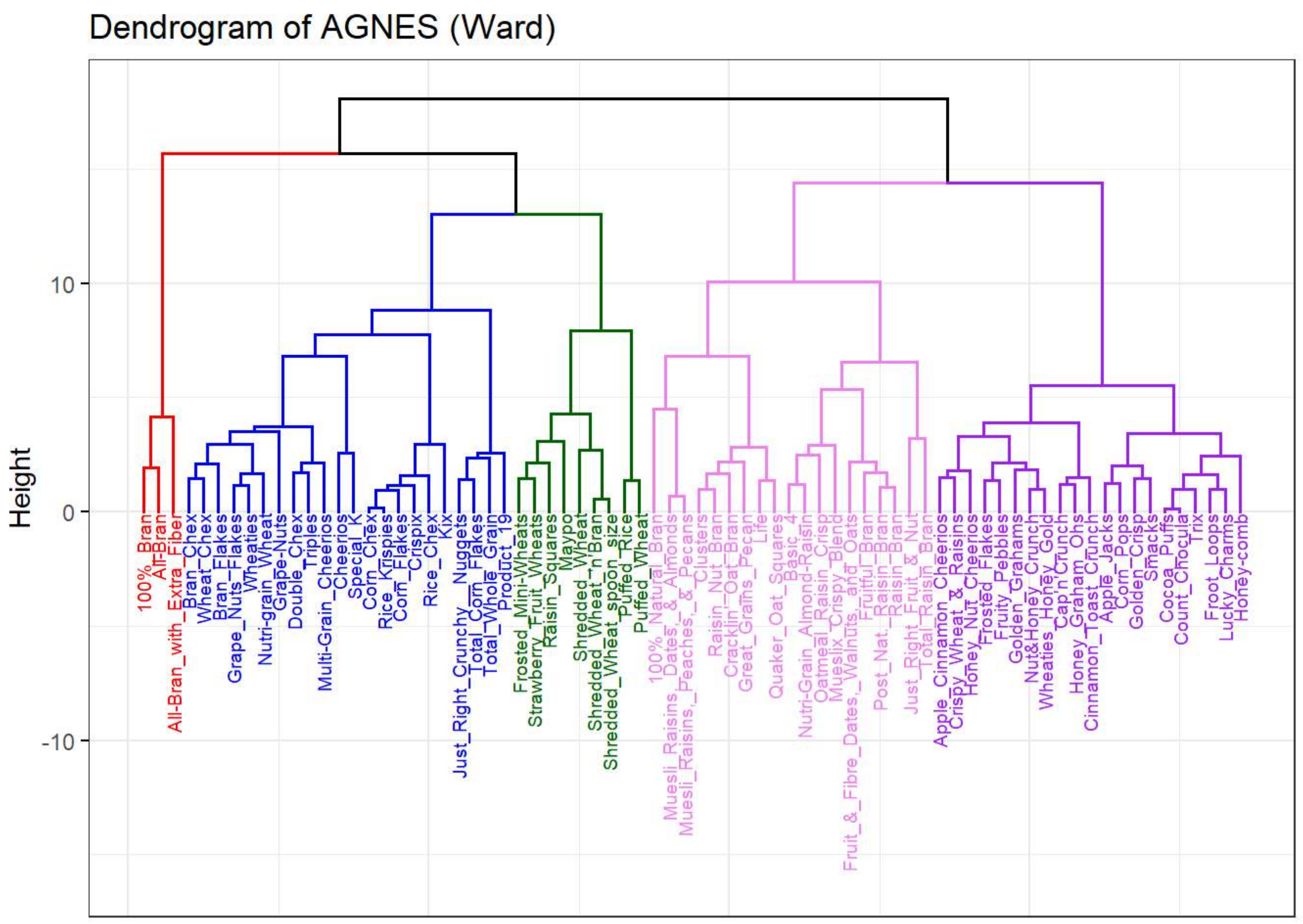
```
hc_Ward <- agnes(distance_table, method = "ward")
pltree(hc_Ward, cex = 0.6, hang = -1, main = "Dendrogram of agnes for ward")
```



Question 2: How many cluster would you choose?

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

fviz_dend(hc_ward, k = 5,main = "Dendrogram of AGNES (Ward)",cex = 0.5, k_colors = c("red", "blu
e", "darkgreen", "violet", "purple"), color_labels_by_k = TRUE,labels_track_height = 16,ggtheme
= theme_bw())
```

```
## Warning: The `<scale>` argument of `guides()` cannot be `FALSE`. Use "none" instead as
## of ggplot2 3.3.4.
## ℹ The deprecated feature was likely used in the factoextra package.
##   Please report the issue at <https://github.com/kassambara/factoextra/issues>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



```
c_d6 <- cutree(hc_ward, k = 5)
Clustered_df <-as.data.frame(cbind ( c_d5, c_d6 ))
```

Question 3: Comment on the structure of the clusters and on their stability. Hint: To check stability, partition the data and see how well clusters formed based on one part apply to the other part

#For the stability of the clusters, We will partition the data into A and B.

```
cereal_a = c_d5[1:55,]
cereal_b = c_d5[56:74,]
```

#Computing the distances of cereal_a

```
distance_cereal_a = get_dist(cereal_a)
```

#Compute with AGNES and with different linkage methods for cereal_a

```
hc_single_cereal_a <- agnes(distance_cereal_a, method = "single")
print(hc_single_cereal_a$ac)
```

```
## [1] 0.6663587
```

```
hc_complete_cereal_a <- agnes(distance_cereal_a, method = "complete")
print(hc_complete_cereal_a$ac)
```

```
## [1] 0.8285192
```

```
hc_average_cereal_a <- agnes(distance_cereal_a, method = "average")
print(hc_average_cereal_a$ac)
```

```
## [1] 0.7646836
```

```
hc_ward_cereal_a <- agnes(distance_cereal_a, method = "ward")
print(hc_ward_cereal_a$ac)
```

```
## [1] 0.8891086
```

#With 88.91% accuracy, it enables us to establish that the best linkage for cereal_a is Ward.

#Computing the distances of cereal_a

```
distance_cereal_b = get_dist(cereal_b)
```

#Compute with AGNES and with different linkage methods for cereal_b

```
hc_single_cereal_b <- agnes(distance_cereal_b, method = "single")
print(hc_single_cereal_b$ac)
```

```
## [1] 0.4805129
```

```
hc_complete_cereal_b <- agnes(distance_cereal_b, method = "complete")
print(hc_complete_cereal_b$ac)
```

```
## [1] 0.71298
```

```
hc_average_cereal_b <- agnes(distance_cereal_b, method = "average")
print(hc_average_cereal_b$ac)
```

```
## [1] 0.6232053
```

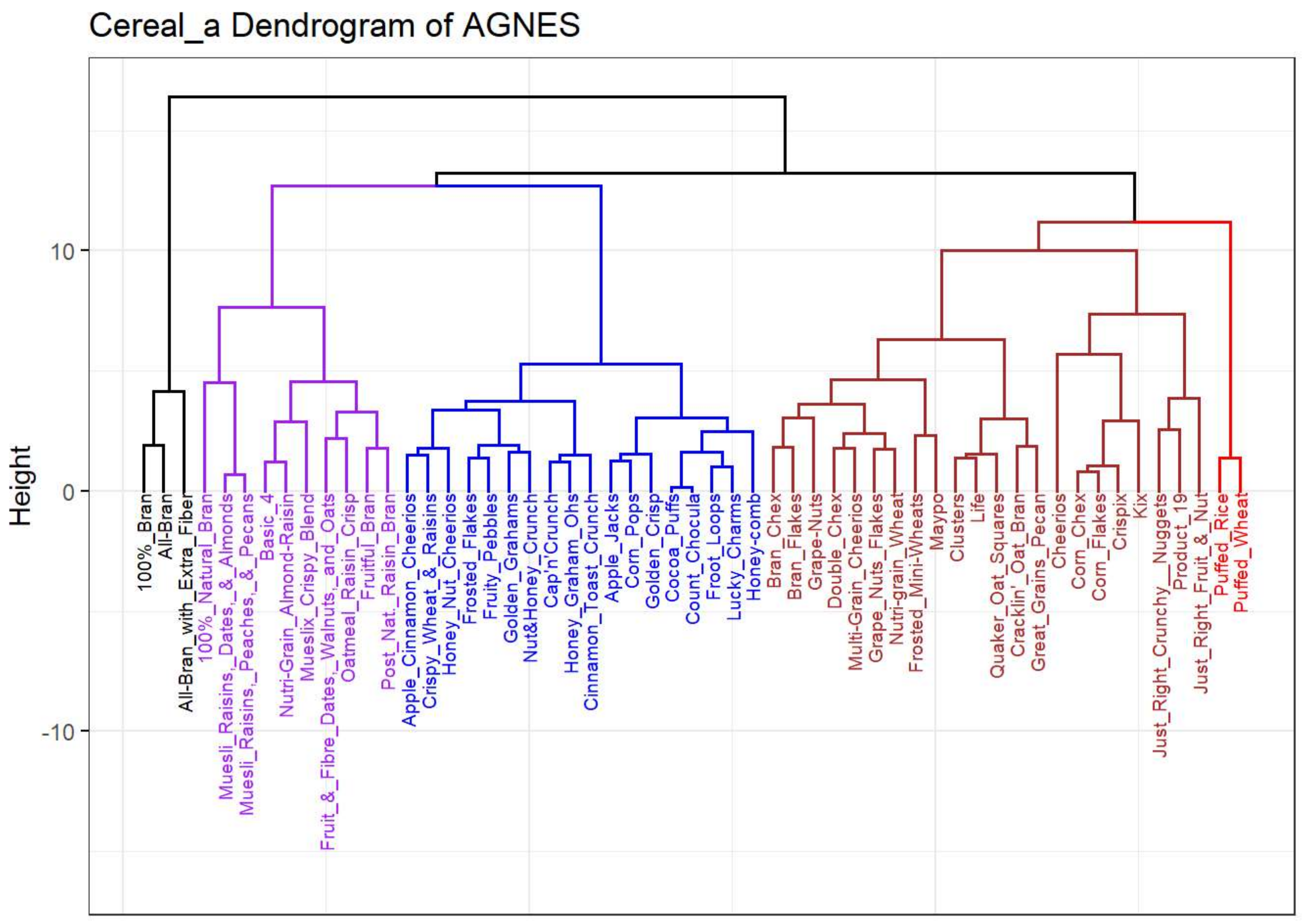
```
hc_ward_cereal_b <- agnes(distance_cereal_b, method = "ward")
print(hc_ward_cereal_b$ac)
```

```
## [1] 0.7710122
```

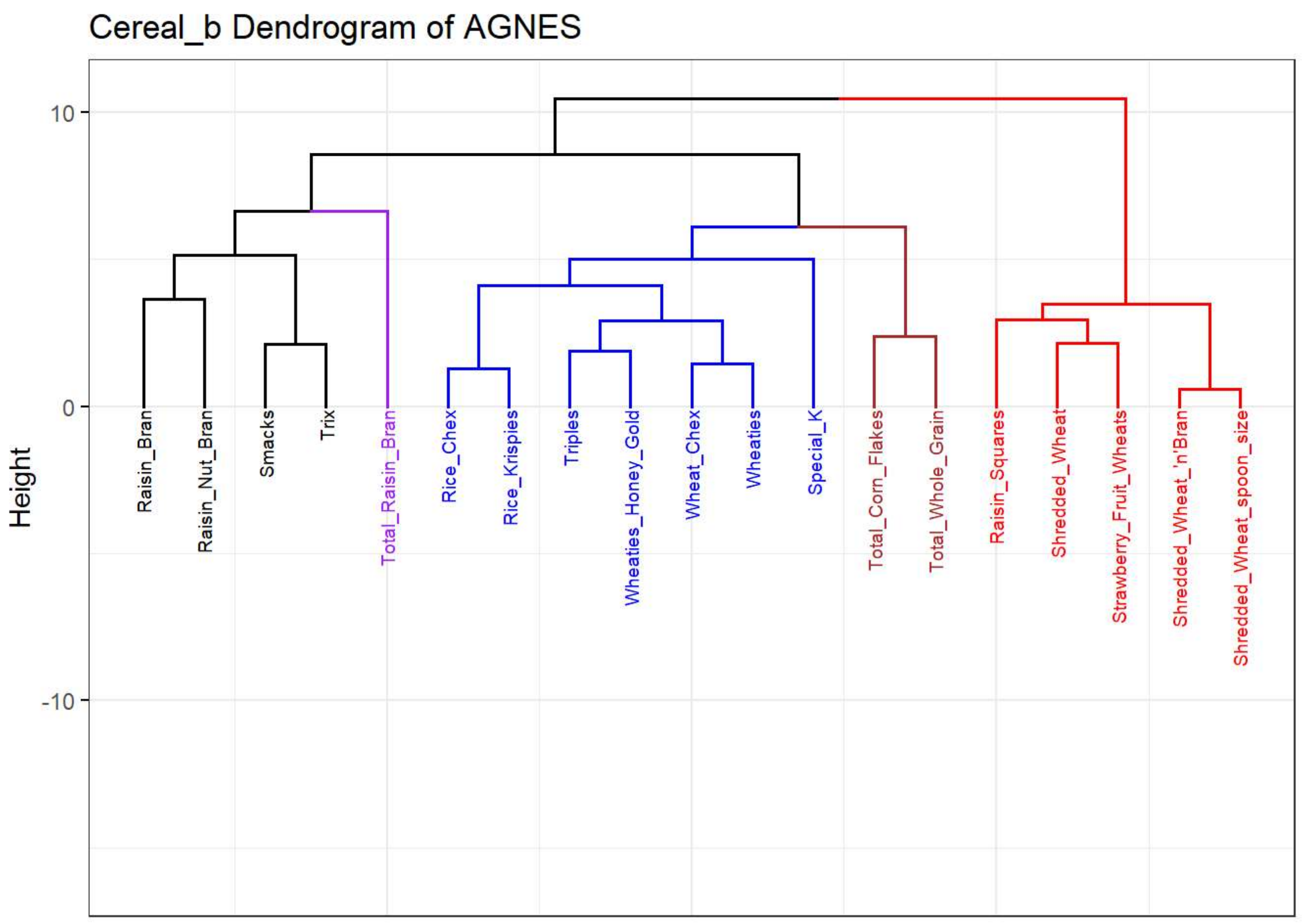
#With 77.10% accuracy, it enables us to establish that the best linkage for cereal_a is Ward.

#Plotting dendogram of cereal_a and cereal_b

```
fviz_dend(hc_ward_cereal_a, k = 5,main = "Cereal_a Dendrogram of AGNES",cex = 0.5, k_colors = c
("black", "purple", "blue", "brown", "red"), color_labels_by_k = TRUE,labels_track_height = 16,g
gtheme = theme_bw())
```



```
fviz_dend(hc_ward_cereal_b, k = 5,main = "Cereal_b Dendrogram of AGNES",cex = 0.5, k_colors = c
("black", "purple", "blue", "brown", "red"), color_labels_by_k = TRUE,labels_track_height = 16,g
gtheme = theme_bw())
```



Question 3 (part B): Use the cluster centroids from A to assign each record in partition B (each record is assigned to the cluster with the closest centroid)

```
Clustered_df_A <-cutree (hc_ward_cereal_a, k=5)
Clusters_A <-as.data.frame(cbind(cereal_a, Clustered_df_A))
Clust_1 <- colMeans (Clusters_A [Clusters_A$ Clustered_df_A == "1" ,])
# The centroid of cluster 1 is represented by a vector of mean values for each column of the dat
a as a result.
```

```
Clustered_df_B <-cutree (hc_ward_cereal_b, k=5)
Clusters_B <-as.data.frame(cbind(cereal_b, Clustered_df_B))
Clust_2 <- colMeans (Clusters_B [Clusters_B$ Clustered_df_B == "1" ,])
# The centroid of cluster 2 is represented by a vector of mean values for each column of the dat
a as a result.
```

```
Centroid <-rbind(Clust_1, Clust_2)
Centroid
```

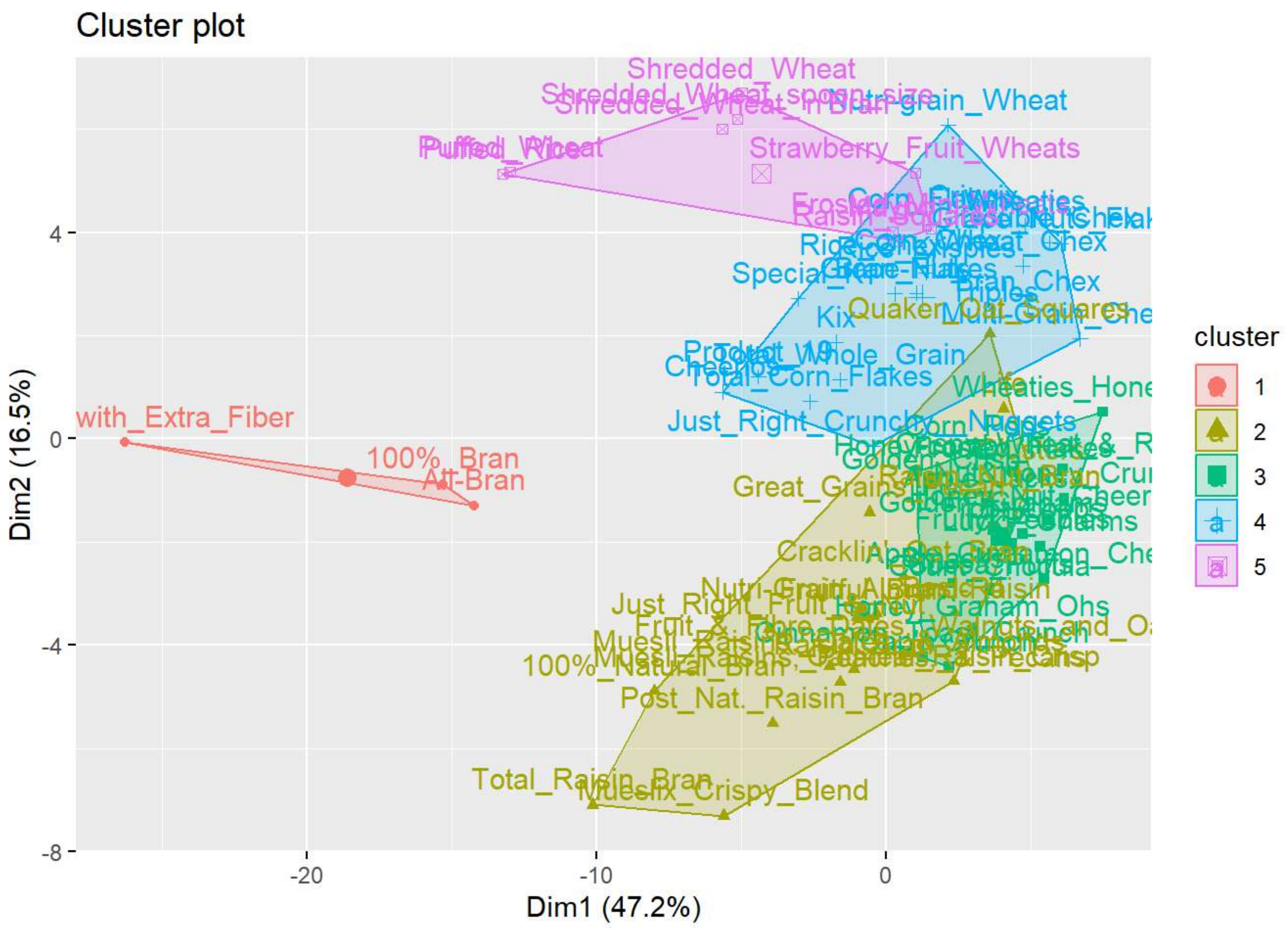
```
##          calories    protein        fat     sodium       fiber      carbo
## Clust_1 -2.201871  1.3817478 -0.3310734  0.1727901  3.64131237 -2.0718749
## Clust_2  0.149818 -0.2449462  0.2483051 -0.2702057 -0.02091106 -0.7977876
##             sugars    potass   vitamins     weight      cups     rating
## Clust_1 -0.7894824 2.9837813 -0.1818422 -0.2008324 -1.845255  2.2426479
## Clust_2  1.0648712 0.1796942 -0.1818422  0.3369228 -0.303848 -0.5618826
##         Clustered_df_A
## Clust_1              1
## Clust_2              1
```

Question 3 (part C): Assess how consistent the cluster assignments are compared to the assignments based on all the data.

```
# After reviewing the centroid, it shows that cluster 1 is high in protein, fiber, and potassiu
m. It means that the cereals in cluster 1 is more healthier than cluster 2. It can also be suppo
rted by looking at calories, fat, carbs, and sugar levels which are higher in cluster 2 as compa
red to cluster 1. Thus cereals in cluster 1 are healthier.
```

Q4: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.”Should the data be normalized? If not, how should they be used in the cluster analysis?

```
#Visualizing the clusters in Scatter plot
fviz_cluster(list(data=distance_table, cluster = c_d6))
```



```
Healthy_cereal<- cbind(c_d2,c_d6)
mean(Healthy_cereal[Healthy_cereal$c_d6==1,"rating"])
```

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

```
mean(Healthy_cereal[Healthy_cereal$c_d6==2,"rating"])
```

```
## [1] 38.37137
```

```
mean(Healthy_cereal[Healthy_cereal$c_d6==3,"rating"])
```

```
## [1] 28.66112
```

```
mean(Healthy_cereal[Healthy_cereal$c_d6==4,"rating"])
```

```
## [1] 46.17608
```

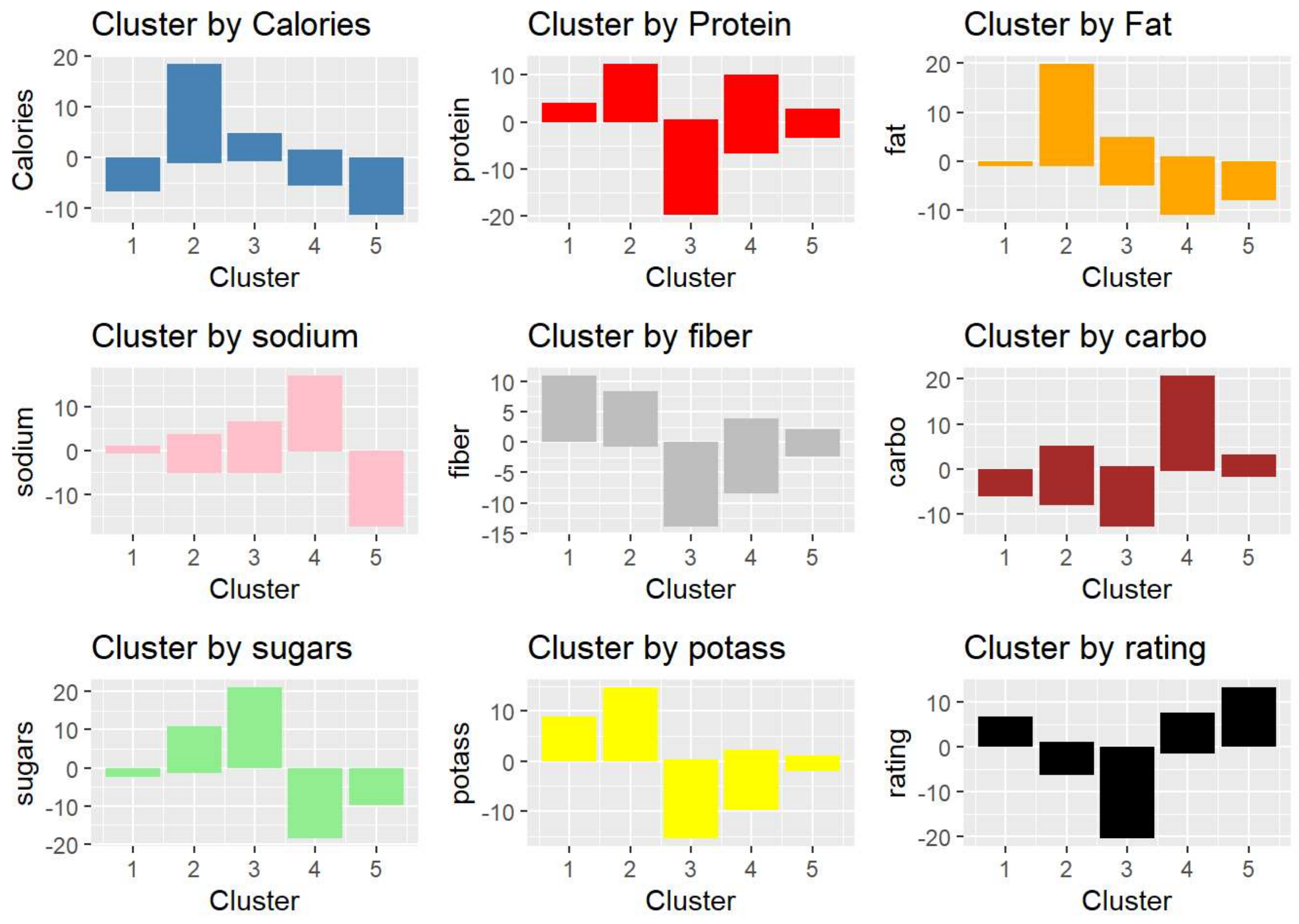
```
mean(Healthy_cereal[Healthy_cereal$c_d6==5,"rating"])
```

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

#It is evident that Cluster1 has the highest rating (73.84446), so we will select it as a nutritious cereal.

#lets also visualize the results by plotting a bar chart

```r
calories <- ggplot(Clustered_df, aes(x = c_d6, y = calories)) +
  geom_bar(stat = "identity", fill = "steelblue") +
  labs(x = "Cluster", y = "Calories") +
  ggtitle("Cluster by Calories")

protein <- ggplot(Clustered_df, aes(x = c_d6, y = protein)) +
  geom_bar(stat = "identity", fill = "red") +
  labs(x = "Cluster", y = "protein") +
  ggtitle("Cluster by Protein")

fat <- ggplot(Clustered_df, aes(x = c_d6, y = fat)) +
  geom_bar(stat = "identity", fill = "orange") +
  labs(x = "Cluster", y = "fat") +
  ggtitle("Cluster by Fat")

sodium <- ggplot(Clustered_df, aes(x = c_d6, y = sodium)) +
  geom_bar(stat = "identity", fill = "pink") +
  labs(x = "Cluster", y = "sodium") +
  ggtitle("Cluster by sodium")

fiber <- ggplot(Clustered_df, aes(x = c_d6, y = fiber)) +
  geom_bar(stat = "identity", fill = "gray") +
  labs(x = "Cluster", y = "fiber") +
  ggtitle("Cluster by fiber")

carbo <- ggplot(Clustered_df, aes(x = c_d6,, y = carbo)) +
  geom_bar(stat = "identity", fill = "brown") +
  labs(x = "Cluster", y = "carbo") +
  ggtitle("Cluster by carbo")

sugars <- ggplot(Clustered_df, aes(x = c_d6,, y = sugars)) +
  geom_bar(stat = "identity", fill = "lightgreen") +
  labs(x = "Cluster", y = "sugars") +
  ggtitle("Cluster by sugars")

potass <- ggplot(Clustered_df, aes(x = c_d6,, y = potass)) +
  geom_bar(stat = "identity", fill = "yellow") +
  labs(x = "Cluster", y = "potass") +
  ggtitle("Cluster by potass")

rating <- ggplot(Clustered_df, aes(x = c_d6,, y = rating)) +
  geom_bar(stat = "identity", fill = "black") +
  labs(x = "Cluster", y = "rating") +
  ggtitle("Cluster by rating")
plot_grid(calories, protein, fat, sodium, fiber, carbo, sugars, potass, rating)
```



#Here we can see that cluster 1 still has the best results. It is low in calories, sugar, and fat. It has higher content of fiber, potassium and protein. Thus we can conclude that cluster 1 can be a set of cereals to include in their daily cafeterias.