# Assignment_5

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## call the libraries

```
library(readr)
```

```
## Warning: package 'readr' was built under R version 4.2.3
```

```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.2.3

## Warning: package 'ggplot2' was built under R version 4.2.3

## Warning: package 'tibble' was built under R version 4.2.3

## Warning: package 'dplyr' was built under R version 4.2.3

## Warning: package 'lubridate' was built under R version 4.2.3

## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.1     v purrr     1.0.1
## v forcats   1.0.0     v stringr   1.5.0
## v ggplot2   3.4.1     v tibble    3.2.1
## v lubridate 1.9.2     v tidyr     1.3.0
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become error
```

```
library(caret)
```

```
## Warning: package 'caret' was built under R version 4.2.3

## Loading required package: lattice
##
## Attaching package: 'caret'
##
## The following object is masked from 'package:purrr':
##
##     lift
```

```r
library(ISLR)
library(dplyr)
library(factoextra)
```

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

```r
library(stats)
library(cluster)
```

```
## Warning: package 'cluster' was built under R version 4.2.3
```

```r
library(ggplot2)
library(knitr)
library(ggcorrplot)
```

```
## Warning: package 'ggcorrplot' was built under R version 4.2.3
```

```r
library(e1071)
```

```
## Warning: package 'e1071' was built under R version 4.2.3
```

```r
library(reshape2)
```

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

```r
library(cowplot)
```

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

```r
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(tidyr)
library(fastDummies)
library(FactoMineR)
```

```
## Warning: package 'FactoMineR' was built under R version 4.2.3
```

## Loading the data

```
cs <- read.csv("E:\\Fundamentals of Machine Learning\\Module 8\\Cereals.csv")
summary(cs)
```

```
##      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  
## 
```

```
row.names(cs) <- cs[,1] #changing column name of Cereals data set to row name
```

## Looking for null values & omitting null values

```r
any(is.na.data.frame(cs))
```

```
## [1] TRUE
```

```r
cs1 <- na.omit(cs) #Remove NA (missing) values
```

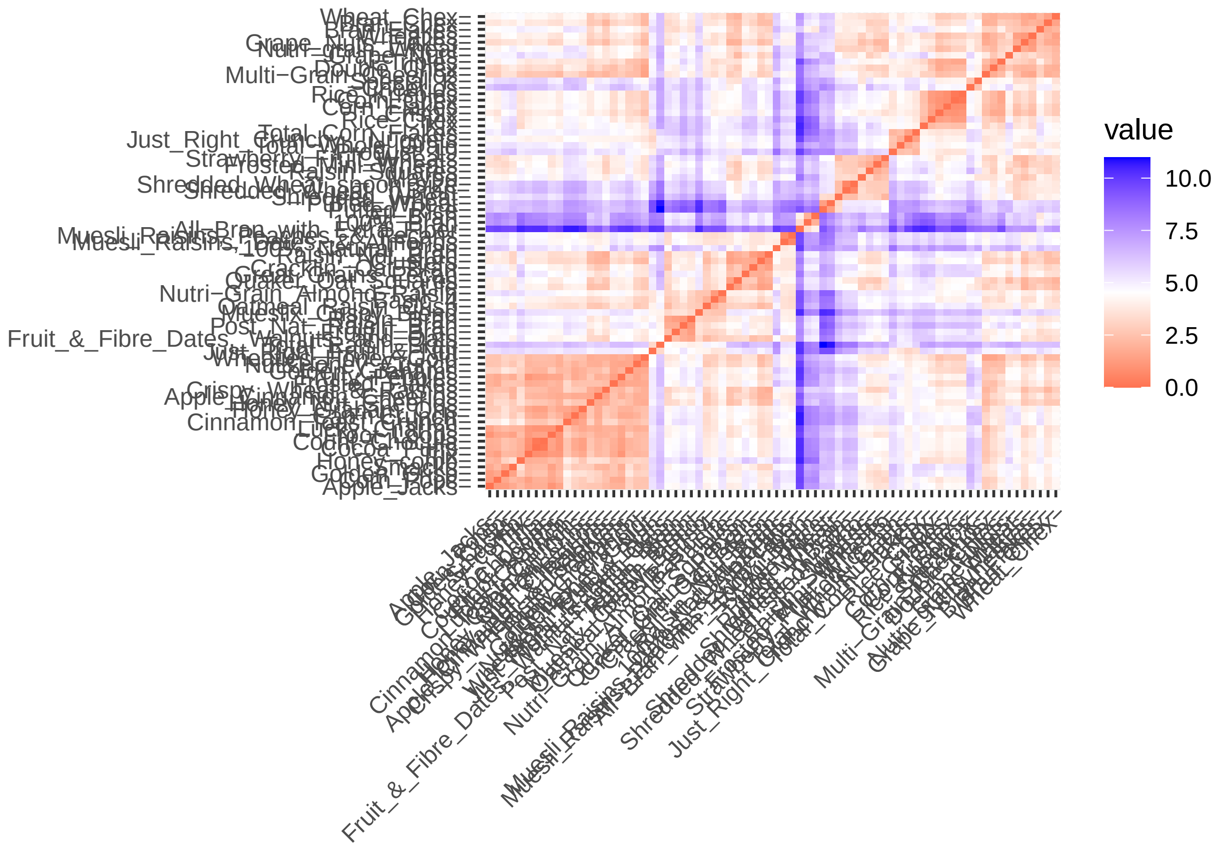
## Normalize the data and finding the optimal k value by Elbow chart & Silhouette method

```r
set.seed(1)
cs2 <- scale(cs1[,-c(1:3,13)])
head(cs2)
```

```
##                            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
```

#Q1:(PartA):Using Euclidean distance to the normalized measurements

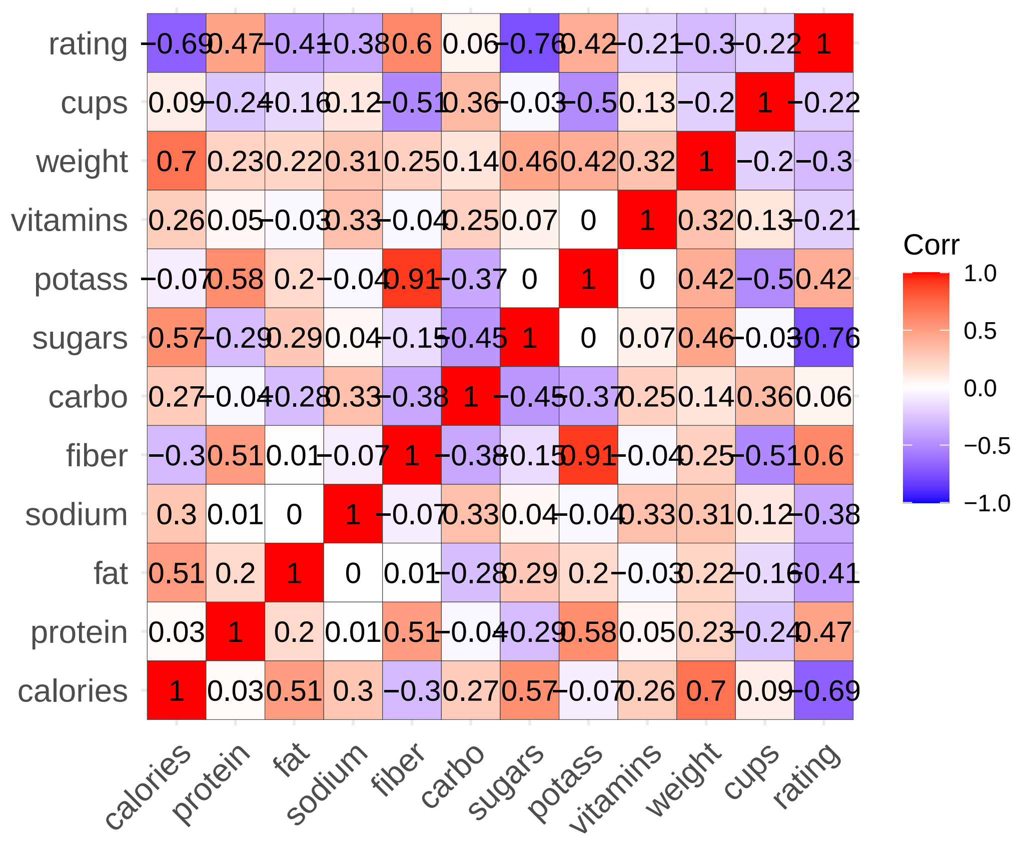
```r
distance_table <- get_dist(cs2) #Compute the distances. Euclidean distance is default.
fviz_dist(distance_table) #fviz_dist() function visualizes a distance matrix
```



#This graph is a distance matrix. As we can see, the diagonal values are zeros (dark orange) because it is showing the distance between any point against itself. The purple and blue represent the furthest distance between any pair of observations.

#Looking at the Correlation between Variables.

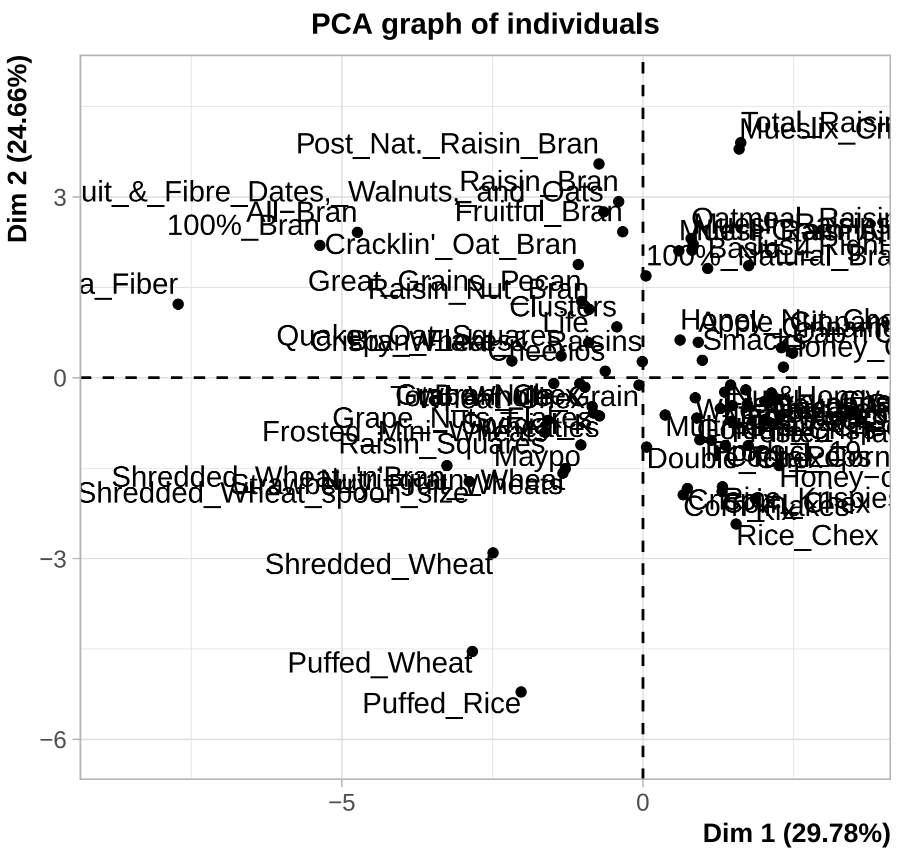
```r
corr <- cor(cs2)
ggcorrplot(corr, outline.color = "grey25", lab = TRUE, hc.order = FALSE, type = "full")
```

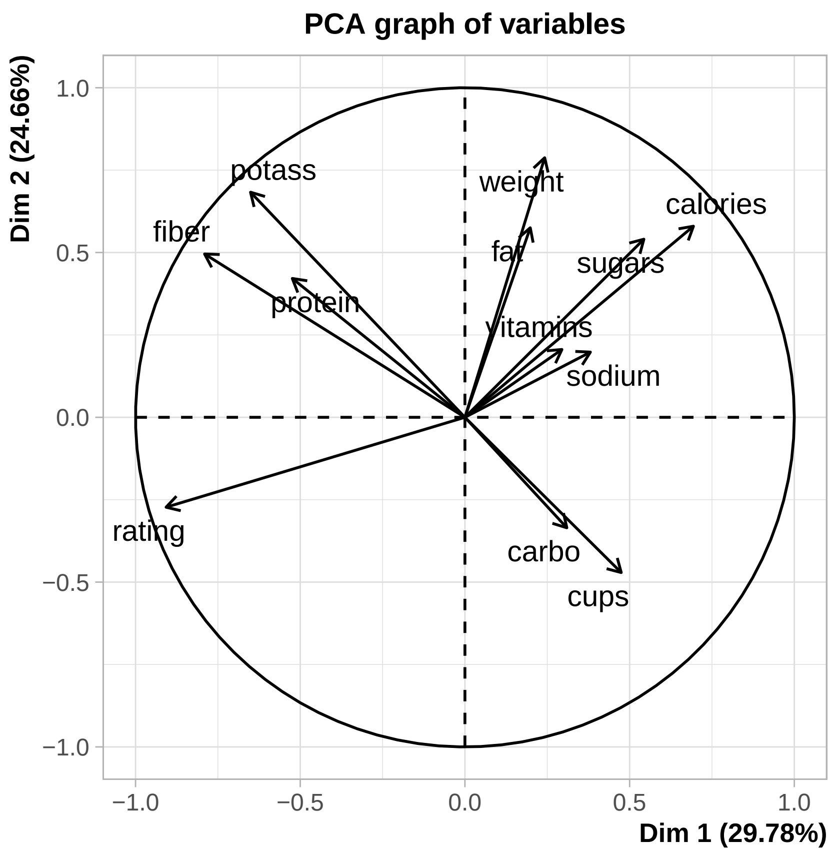


#Sugar and calories are highly negatively correlated with rating. Also, Potass is highly positively correlated with fiber and Protien.

#Trying to Understand the variable variance by performing principle component analysis

```
pca_cereal <- PCA(cs2) #perform principal component analysis
```

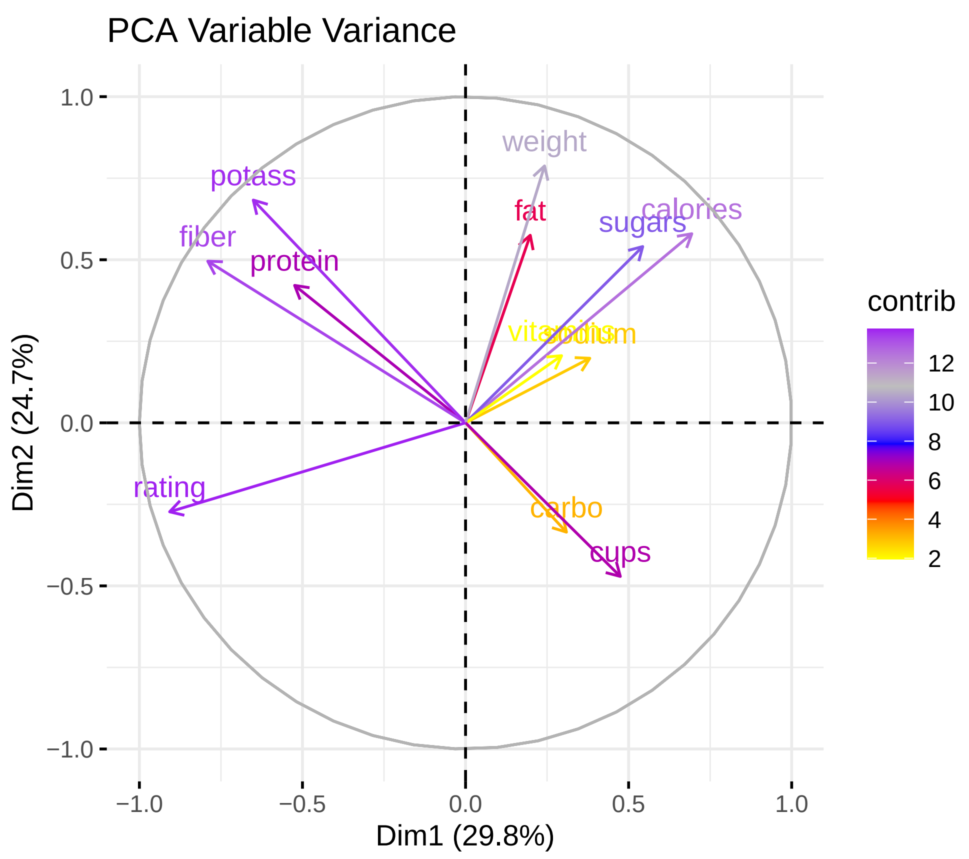

PCA graph of individuals
Dim 2 (24.66%)
Dim 1 (29.78%)
3
0
−3
−6
−5
0
Total_Raisin
Muesli
Post_Nat._Raisin_Bran
Raisin_Bran
uit_&_Fibre_Dates,_Walnuts,_and_Oats
All−Bran
Fruitful_Bran
100%_Bran
Cracklin'_Oat_Bran
100%_Natural_Bra
a_Fiber
Great_Grains_Pecan
Raisin_Nut_Bran
Clusters
Life
Quaker_Oat_Squares
Cheerios
Apple_Cinnam
Smacks
Honey_
Grape_Nuts_Flakes
Frosted_Mini−Wheats
Raisin_Squares
Maypo
Double_Chex
Honey−c
Shredded_Wheat_'n'Bran
Shredded_Wheat_spoon_size
Crispy_Rice
Rice_Krispies
Corn_Flakes
Rice_Chex
Shredded_Wheat
Puffed_Wheat
Puffed_Rice



```
pca_cereal <- prcomp(cs2, scale = TRUE) #variable has mean zero and standard deviation one
loadings <- pca_cereal$rotation #extract loading
print(loadings[, 1:2])#print loading for the first two PCs
```

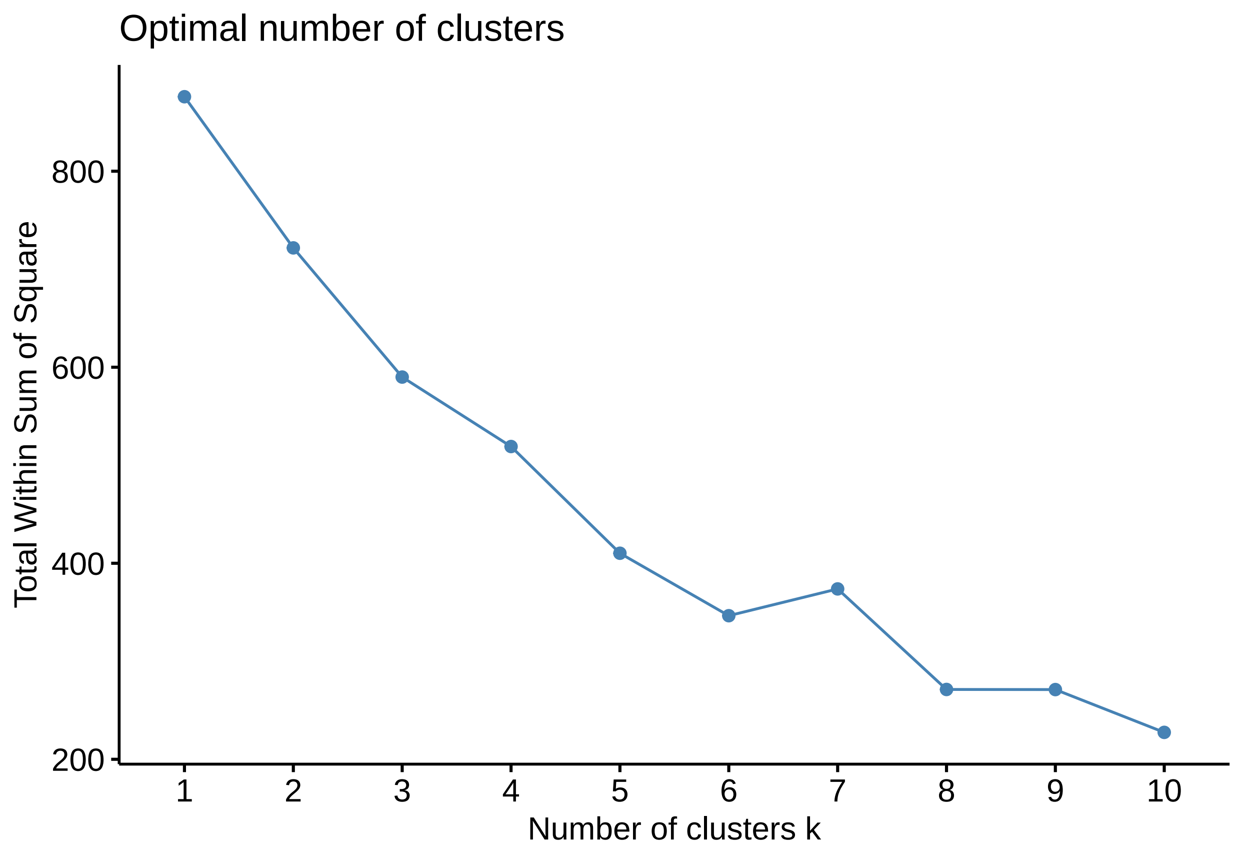
```
##                 PC1        PC2
## calories  0.3670078  0.3370596
## protein  -0.2772241  0.2449194
## fat       0.1049438  0.3343406
## sodium    0.2015610  0.1150253
## fiber    -0.4180964  0.2880965
## carbo     0.1636662 -0.1948813
## sugars    0.2874024  0.3141683
## potass   -0.3443208  0.3970189
## vitamins  0.1557868  0.1196450
## weight    0.1281124  0.4578598
## cups      0.2510333 -0.2738283
## rating   -0.4799624 -0.1586012
```

```
var <- get_pca_var(pca_cereal)
fviz_pca_var(pca_cereal, col.var="contrib",
gradient.cols = c("yellow","red","blue","grey","purple"),
ggrepel = TRUE ) + labs( title = "PCA Variable Variance")
```

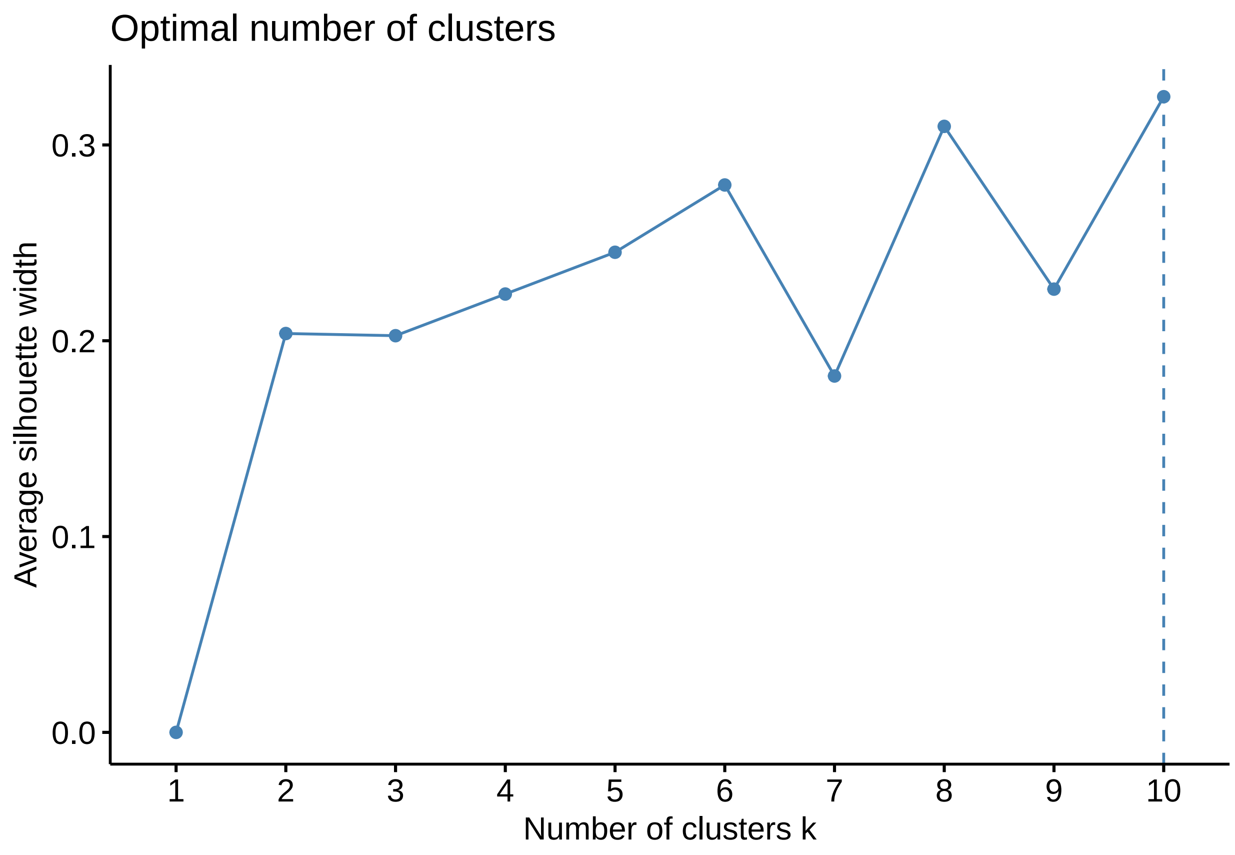


#From PCA Variable Variance, we can infer that Sugar , calories, protien potass and fiber contribute more in the two PCA components/dimensions (Variables)

```
Elbow <- fviz_nbclust(cs2, kmeans, method="wss")
Elbow
```



```
silhouette <- fviz_nbclust(cs2,kmeans,method="silhouette")
silhouette
```



```
set.seed(1)
k10 <- kmeans(cs2, centers = 10, nstart = 25) # k = 10, number of restarts = 25
k5 <- kmeans(cs2, centers = 5, nstart = 25) # k = 5, number of restarts = 25
```

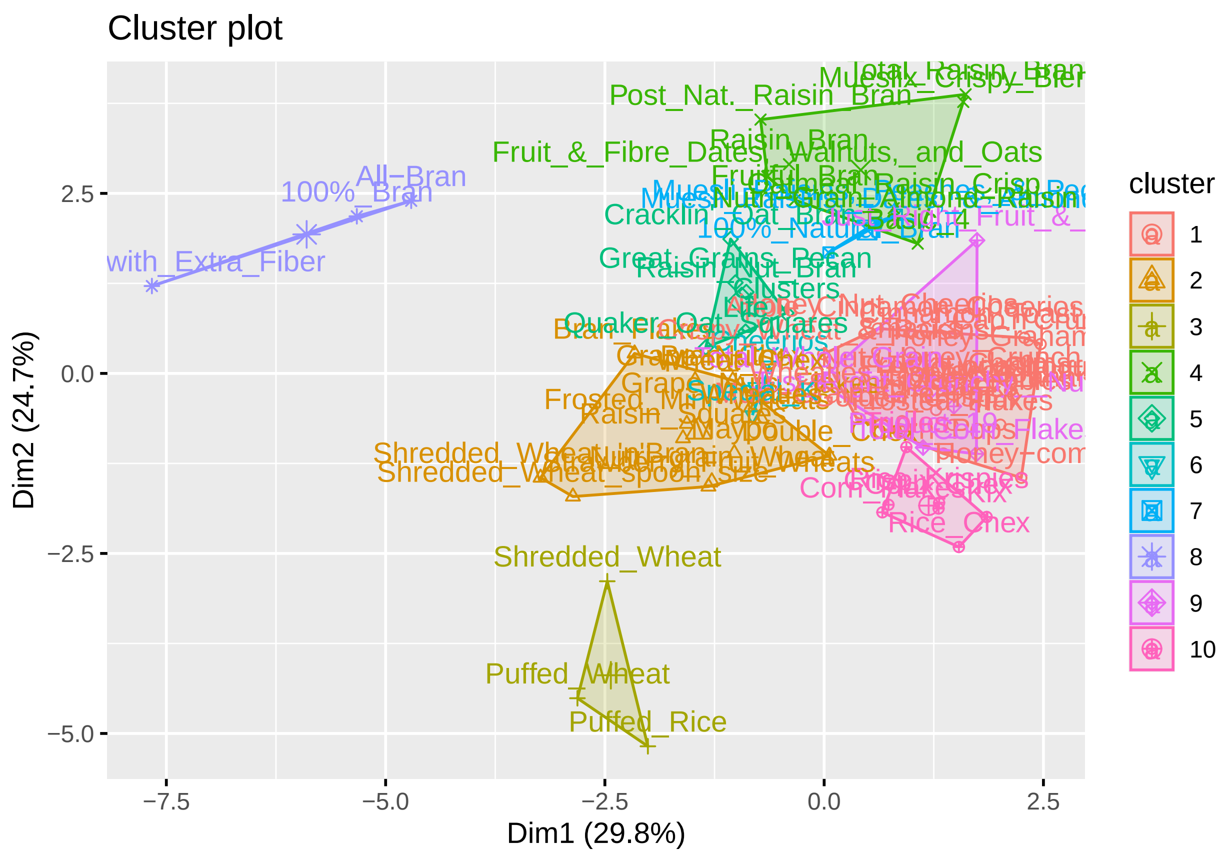
```
k10$centers
```

```
##       calories    protein           fat     sodium      fiber       carbo
## 1   0.17272410 -0.8998490  1.009294e-17  0.1032288 -0.6351893 -0.56126871
## 2  -0.57008680  0.2530213 -6.384987e-01 -0.6456014  0.2812040  0.41817811
## 3  -2.36984887 -0.7871775 -9.932203e-01 -1.9616441 -0.3475883 -0.44446926
## 4   1.21367739  0.4522084  4.414312e-01  0.3875760  0.6840240  0.08372381
## 5  -0.01815976  0.7620548  1.158757e+00 -0.3910227  0.1682179 -0.68001481
## 6   0.14981803  3.2408266  0.000000e+00  1.1795987 -0.2788141  0.45488650
## 7   1.66161818  1.0719013  2.648587e+00 -0.9145632  0.2026049 -0.35881633
## 8  -2.20187108  1.3817478 -3.310734e-01  0.1727901  3.6413124 -2.07187492
## 9   0.25060471  0.0803926 -1.986441e-01  0.5996770 -0.3200786  1.04589172
## 10  0.07782755 -0.6101224 -7.094430e-01  1.1968583 -0.7798829  1.75803465
##        sugars     potass   vitamins     weight       cups      rating
## 1   0.9449551 -0.6940780 -0.1818422 -0.2008324  0.2515215 -0.93991166
## 2  -0.7621723  0.1620584 -0.3420365 -0.2008324 -0.2947571  0.99351683
## 3  -1.6306324 -0.6374297 -1.3032024 -2.7429482  0.7567534  1.54110518
## 4   0.9183071  1.1653377  0.1919445  2.0805535 -0.4923993 -0.43724782
## 5  -0.1777369  0.2796302 -0.1818422 -0.2008324 -1.3644493  0.08281632
## 6  -1.1718233 -0.2612000 -0.1818422 -0.2008324  1.2870541  0.68238355
## 7   0.6634132  0.8439748 -0.5556289 -0.2008324  0.7567534 -0.51910839
## 8  -0.7894824  2.9837813 -0.1818422 -0.2008324 -1.8452553  2.24264794
## 9  -0.5294905 -0.4163948  3.1822385  0.1902623  0.5446331 -0.16904450
## 10 -1.0079629 -0.8759325 -0.1818422 -0.2008324  0.9870554 -0.01518936
```

```
k10$size
```

```
##  [1] 22 14  3  9  6  2  3  3  5  7
```

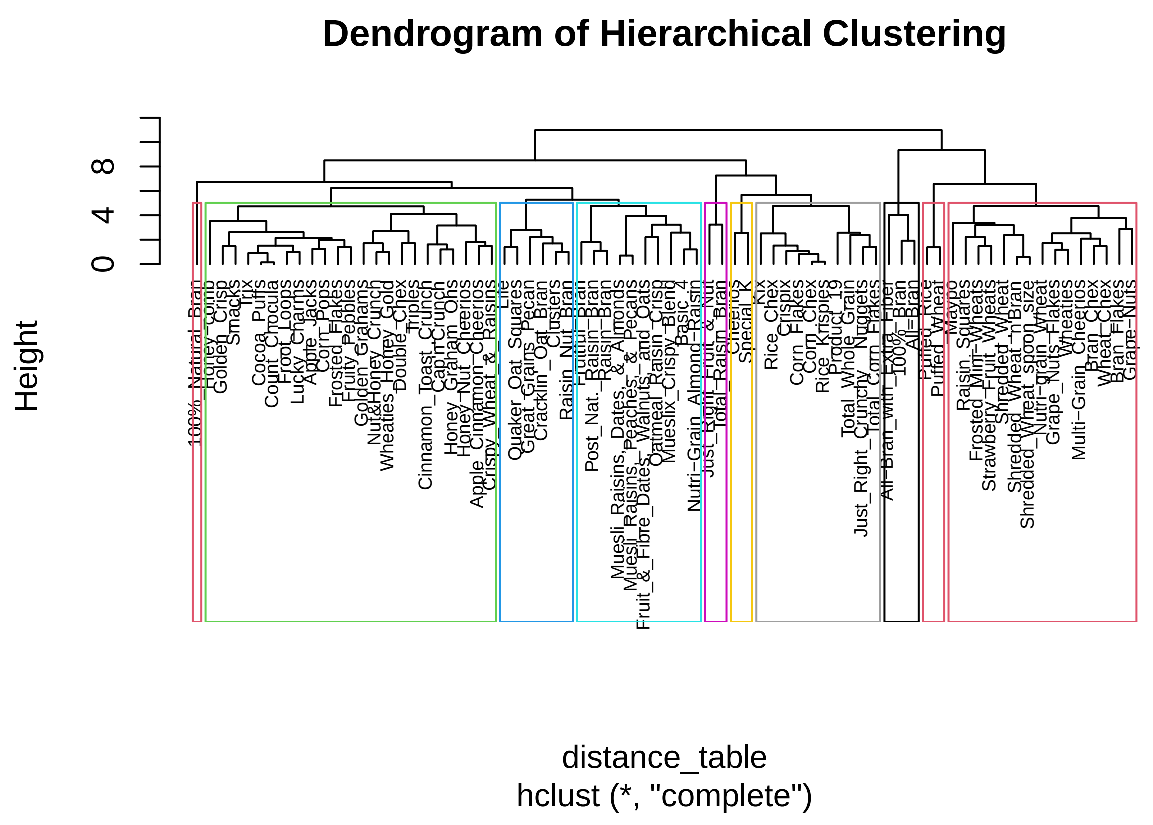
```
fviz_cluster(k10, data = cs2)
```



#After applying both the silhouette method and elbow method, we obtained K value as 10, which we used to plot the 10 clusters. However, upon observing the plot, we noticed that some of the clusters were overlapping, indicating that using only K-means clustering may not be the best option for optimization. Therefore, we will apply hierarchical clustering to obtain an optimal number of clusters.

#Q1:(PartB) Apply hierarchical clustering. Use Agnes to compare the clustering from single linkage, completelinkage, average linkage, and Ward. Choose the best method.

```
set.seed(1)
hierarchical_cluster <- hclust(distance_table, method = "complete") #hierarchical clustering using Comp
plot(hierarchical_cluster, cex = 0.6, hang = -1, main = "Dendrogram of Hierarchical Clustering") #Plot
rect.hclust(hierarchical_cluster, k = 10, border = 2:10)
```



## Compute with agnes and with different linkage methods

```
hc_single<-agnes(distance_table, method ="single")
hc_complete<-agnes(distance_table, method ="complete")
hc_average<-agnes(distance_table, method ="average")
hc_ward <- agnes(distance_table, method = "ward")
```

#Compare Agglomerative coefficients

```
print(hc_single$ac)
```

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

```
print(hc_complete$ac)
```

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

```
print(hc_average$ac)
```

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

```
print(hc_ward$ac)
```

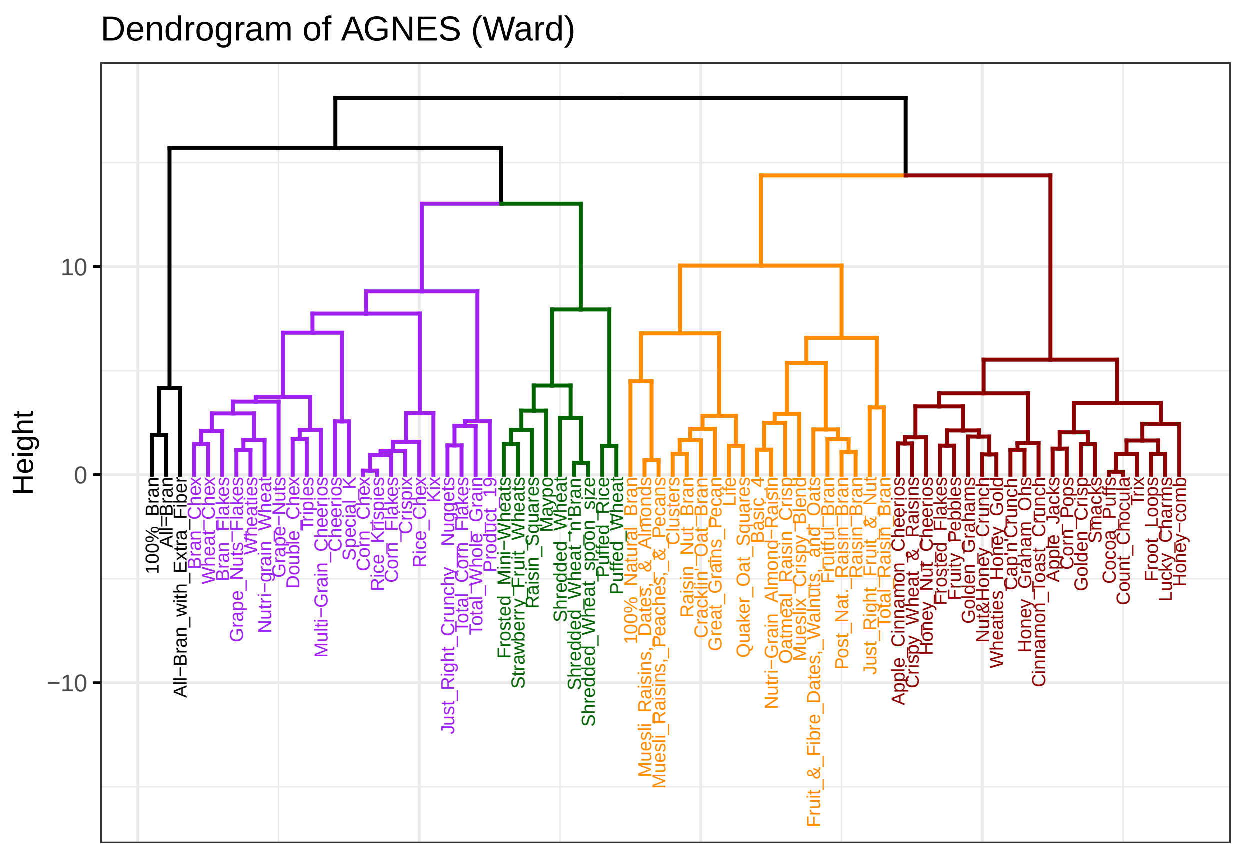
```
## [1] 0.9087265
```

#After comparing the Agglomerative coefficients the best linakage method is ward linkage i.e. 0.90 accuracy

#Q2: How many clusters would you choose?

```
#Utilizing the Ward linkage, 5 clusters seem to be a good number to group the data
set.seed(1)
fviz_dend(hc_ward, k = 5,main = "Dendrogram of AGNES (Ward)",
cex = 0.5, k_colors = c("black", "purple", "darkgreen", "darkorange", "darkred"),
color_labels_by_k = TRUE,labels_track_height = 16,ggtheme = theme_bw()) #Plot the Dendrogram of AGNES
```

```
## 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.
```



```
cs2_5 <- cutree(hc_ward, k = 5)
Clustered_df <-as.data.frame(cbind (cs2, cs2_5 ))
```

#Q3:Comment on the structure of the clusters and their stability. Hint: To check stability, partition the data, and see how well clusters formed based on one part apply to the other part. #Q3: PartA: Cluster partition A

```
#We will partition the dataset into two groups: Training A and Validation B.
set.seed(1) #To get the same random variables
TrainingA <- cs2[1:55,]
nrow(TrainingA)
```

```
## [1] 55
```

```
ValidationB <- cs2[56:74,]
nrow(ValidationB)
```

```
## [1] 19
```

# Compute the distances. Euclidean distance is used by default. Looking at the cluster of trainingA and ValidationB data set.

```
set.seed(1) # To maintain same values
distance_TrainA <- get_dist(TrainingA)
# Compute with AGNES and with different linkage methods For Training Dataset
hc_single_TrainA <- agnes(distance_TrainA, method = "single")
hc_complete_TrainA <- agnes(distance_TrainA, method = "complete")
hc_average_TrainA <- agnes(distance_TrainA, method = "average")
hc_ward_TrainA <- agnes(distance_TrainA, method = "ward")
print(hc_single_TrainA$ac)
```

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

```
print(hc_complete_TrainA$ac)
```

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

```
print(hc_average_TrainA$ac)
```

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

```
print(hc_ward_TrainA$ac)
```

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

#It allows us to determine that the best linkage is Ward with 88.91% accuracy for validationA

## Compute with AGNES and with different linkage methods For Training Dataset

```r
set.seed(1) # To maintain same values
distance_ValidB <- get_dist(ValidationB)

# Compare AGNES (agglomerative) coefficients
hc_single_ValidB <- agnes(distance_ValidB, method = "single")
hc_complete_ValidB <- agnes(distance_ValidB, method = "complete")
hc_average_ValidB <- agnes(distance_ValidB, method = "average")
hc_ward_ValidB <- agnes(distance_ValidB, method = "ward")
print(hc_single_ValidB$ac)
```

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

```r
print(hc_complete_ValidB$ac)
```

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

```r
print(hc_average_ValidB$ac)
```

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

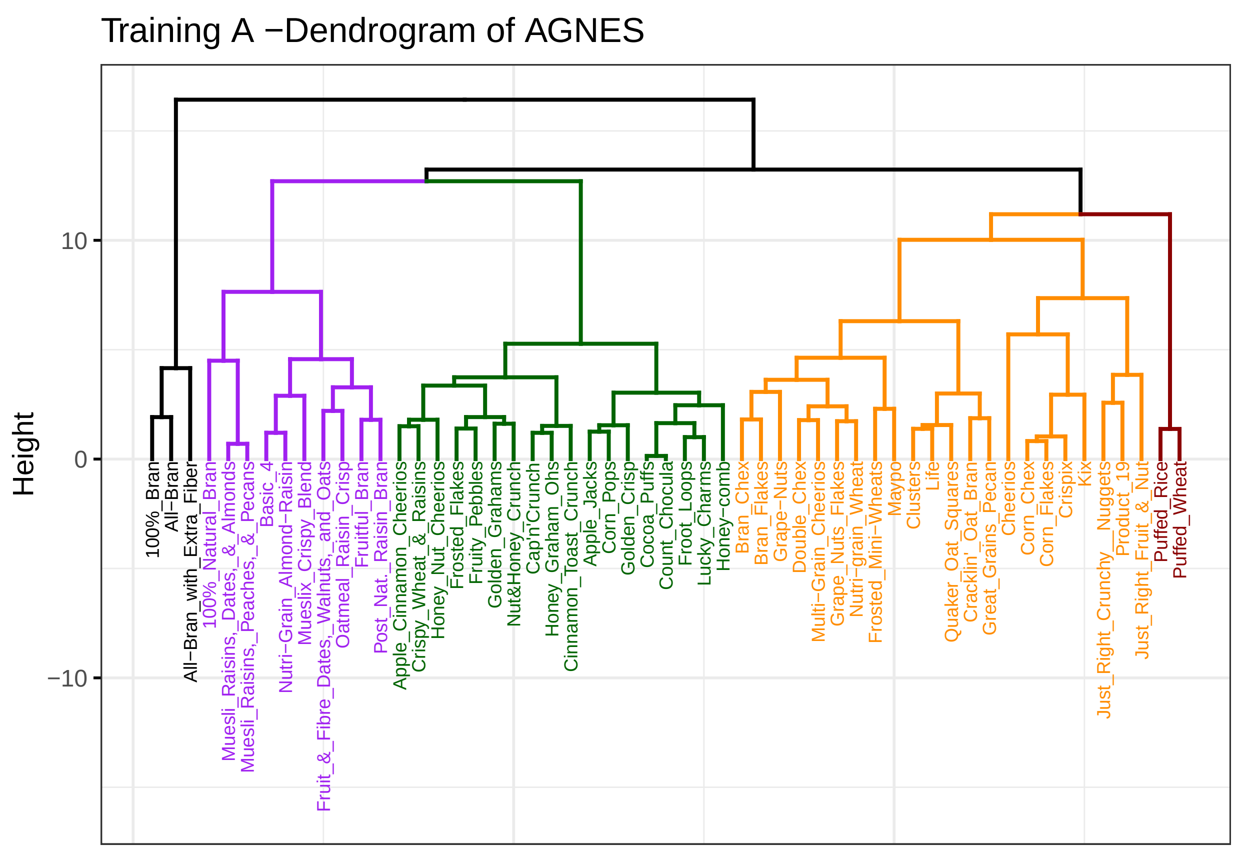
```r
print(hc_ward_ValidB$ac)
```

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

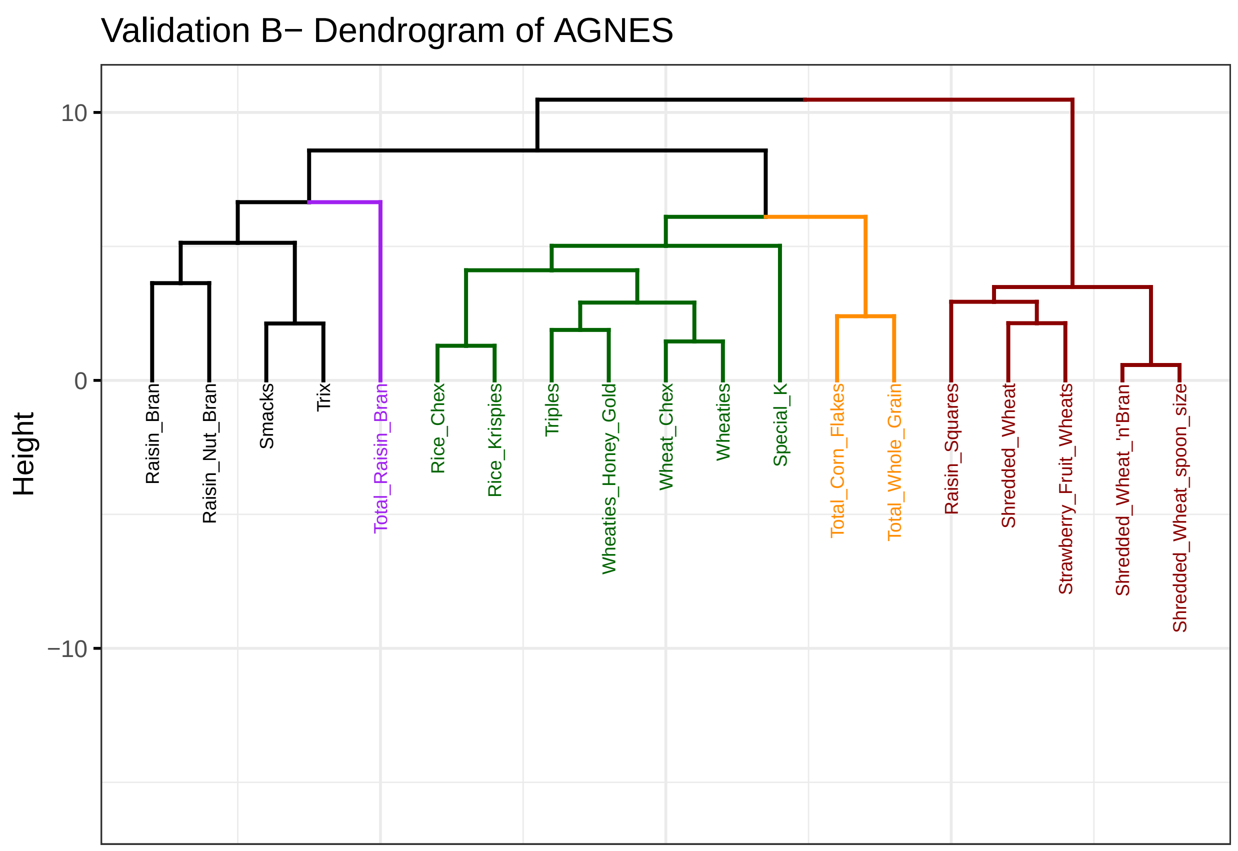
#It allows us to determine that the best linkage is Ward with 77.10% accuracy for validationB

#Dendrogram for TrainingA and ValidationB dataset

```r
fviz_dend(hc_ward_TrainA, k = 5,main = "Training A -Dendrogram of AGNES",
cex = 0.5, k_colors = c("black", "purple", "darkgreen", "darkorange", "darkred"),
color_labels_by_k = TRUE,labels_track_height = 16,ggtheme = theme_bw()) #Plot the Dendrogram of AGNES
```



```
fviz_dend(hc_ward_ValidB, k = 5,main = "Validation B- Dendrogram of AGNES",
cex = 0.5, k_colors = c("black", "purple", "darkgreen", "darkorange", "darkred"),
color_labels_by_k = TRUE,labels_track_height = 16,ggtheme = theme_bw()) #Plot the Dendrogram of AGNES
```



#Q3:PartB: Method1 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_TrainA, k=5)
Clusters_A <-as.data.frame(cbind(TrainingA, Clustered_df_A))
nrow(Clusters_A)#55
```

```
## [1] 55
```

```
Clust_1 <- colMeans (Clusters_A [Clusters_A$ Clustered_df_A == "1" ,]) #This results in a vector of mea
Clustered_df_B <-cutree (hc_ward_ValidB, k=5)
Clusters_B <-as.data.frame(cbind(ValidationB, Clustered_df_B))
nrow(Clusters_B)#55
```

```
## [1] 19
```

```
Clust_2 <- colMeans (Clusters_B [Clusters_B$ Clustered_df_B == "1" ,]) #This results in a vector of mea
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
```

#On overall level the both the cluster seems fine but also a slight difference is - #Cluster_1 has a higher fiber and potassium content compared to Cluster_2, which may suggest that cereals in this cluster are healthier or more nutrient-dense. #Cluster_2 has a higher sugar content compared to Cluster_1, which may suggest that cereals in this cluster are less healthy or have more added sugars.

#Q3:PartB: Method2 Use the cluster centroids from A to assign each record in partition B (each record is assigned to the cluster with the closest centroid)

#In order to predict the calculate distances between each record in data set B and the cluster centroids

```
distances <- dist(ValidationB[, -1], TrainingA, method = "euclidean") #This line calculates the pairwis
hc <- hclust(distances) #This line performs hierarchical clustering on the distances object, using the
clusterB <- cutree(hc, k = 5) #This line cuts the hierarchical tree into five clusters based on the hc
ValidationB$cluster <- clusterB #This line adds a new column to the ValidationB data frame called "clus
```

```
## Warning in ValidationB$cluster <- clusterB: Coercing LHS to a list
```

```
ValidationB$cluster
```

```
##                Raisin_Bran            Raisin_Nut_Bran            Raisin_Squares
##                          1                          1                         2
##                  Rice_Chex               Rice_Krispies             Shredded_Wheat
##                          3                          3                         2
##     Shredded_Wheat_'n'Bran Shredded_Wheat_spoon_size                     Smacks
##                          2                          2                         1
##                  Special_K    Strawberry_Fruit_Wheats          Total_Corn_Flakes
##                          4                          2                         3
##          Total_Raisin_Bran          Total_Whole_Grain                    Triples
##                          5                          3                         3
##                       Trix                 Wheat_Chex                   Wheaties
##                          1                          3                         3
##        Wheaties_Honey_Gold
##                          3
```

#The predicted clusters of B on the basis of centroids of A almost classified same except 3 cereals which are “special_K”, “Total_CF” and “Total_WG”. Out of 19 only 3 observation changed their cluster after comparing the validation data set with Training dataset.It means the stability of clusters are really high.

#Q3:PartC: Assess how consistent the cluster assignments are compared to the assignments based on all the data

#Method 1: We are comparing the mean values of each feature for the two clusters identified in the two datasets. These centroids can be used to compare the features of the two clusters and explore differences or similarities between them.Here we can see that Cluster_1 has a higher fiber and potassium content compared to Cluster_2, which may suggest that cereals in this cluster are healthier or more nutrient-dense.Cluster_2 has a higher sugar content compared to Cluster_1, which may suggest that cereals in this cluster are less healthy or have more added sugars hence cluster 2 rating is really low compared to cluster 1.

#Method 2:This method calculates the pairwise Euclidean distances between the records in the ValidationB dataset and the cluster centroids obtained from the TrainingA dataset using hierarchical clustering with complete linkage method.This enables the prediction of the cluster labels for the validation dataset using the centroids obtained from the training dataset. hence we can see the stability of validation data set on the basis of training dataset. We can see the cereals are cluster exactly the same except "special_K", "Total_CF" and "Total_WG". Out of 19 only 3 observation changed their cluster after comparing the validation data set with Training dataset.It means the stability of clusters are really high.

#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?

#To analyze which group of cereals are healthier to distribute daily in cafeterias in elementary public schools,we will use the non-standardized dataset. In my opinion, it is more meaningful and easier to compare if we look at the variables in their original scale.Here is a table summarizing the number of cereals per cluster:

```
Healthy_data <-as.data.frame(cbind (cs1, cs2_5 ))
Healthy_data_sort <- Healthy_data[order(Healthy_data$cs2_5),c(1,17)]
Count_cluster <- Healthy_data_sort %>% group_by(cs2_5) %>% summarise(count = n())
print(Count_cluster)
```

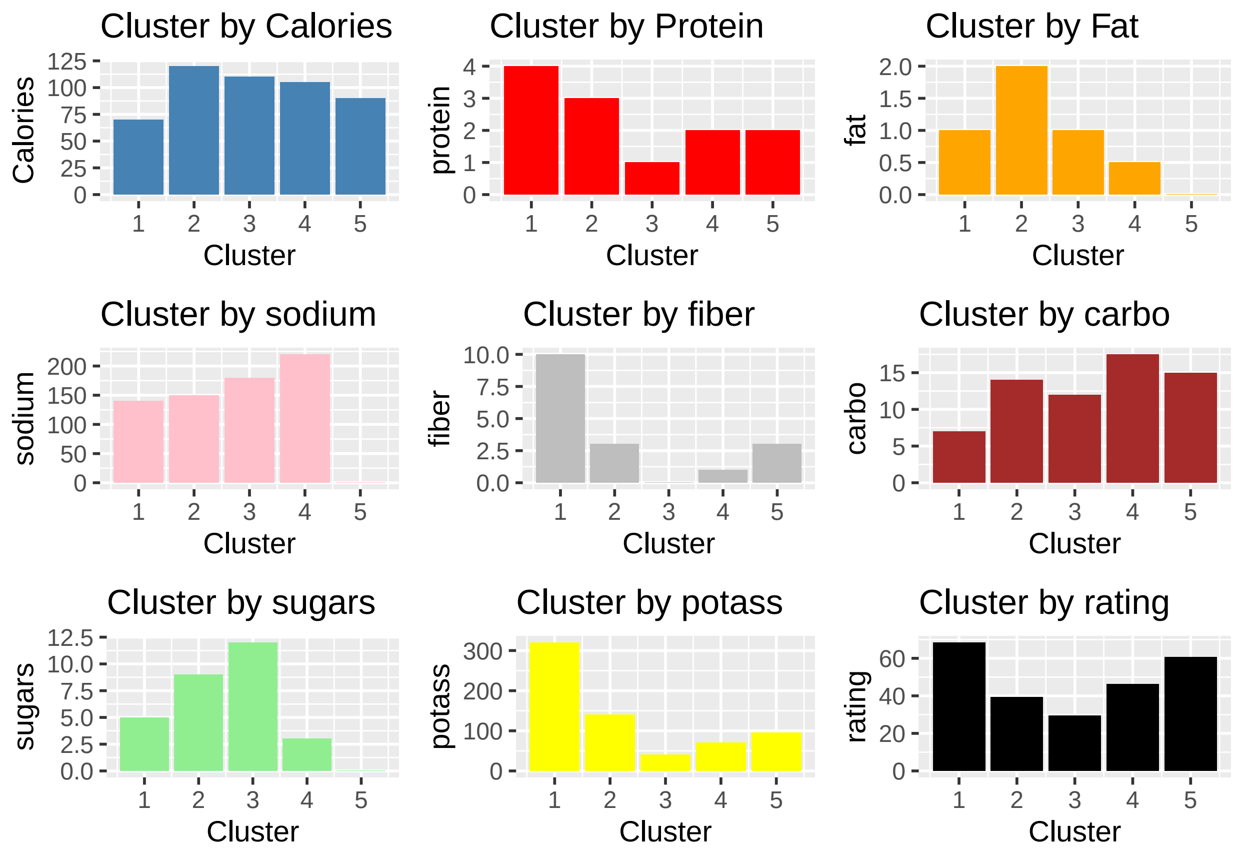
```
## # A tibble: 5 x 2
##   cs2_5 count
##   <int> <int>
## 1     1     3
## 2     2    19
## 3     3    21
## 4     4    22
## 5     5     9
```

```
#Summary table showing the median of each variable
Healthy_data_Var <- Healthy_data [,4:17]
cluster_table <- Healthy_data_Var %>% group_by(cs2_5) %>%
summarize(across(.cols = everything(), .fns = median))
print(cluster_table)
```

```
## # A tibble: 5 x 14
##   cs2_5 calories protein   fat sodium fiber carbo sugars potass vitamins shelf
##   <int>    <dbl>   <dbl> <dbl>  <dbl> <dbl> <dbl>  <dbl>  <dbl>    <dbl> <dbl>
## 1     1       70       4   1      140    10   7        5    320       25   3
## 2     2      120       3   2      150     3  14        9    140       25   3
## 3     3      110       1   1      180     0  12       12     40       25   2
## 4     4      105       2   0.5    220     1  17.5      3     70       25   2.5
## 5     5       90       2   0        0     3  15        0     95        0   2
## # i 3 more variables: weight <dbl>, cups <dbl>, rating <dbl>
```

## Create bar graph

```
calories <- ggplot(cluster_table, aes(x = cs2_5, y = calories)) +
  geom_bar(stat = "identity", fill = "steelblue") +
  labs(x = "Cluster", y = "Calories") +
  ggtitle("Cluster by Calories")

protein <- ggplot(cluster_table, aes(x = cs2_5, y = protein)) +
  geom_bar(stat = "identity", fill = "red") +
  labs(x = "Cluster", y = "protein") +
  ggtitle("Cluster by Protein")

fat <- ggplot(cluster_table, aes(x = cs2_5, y = fat)) +
  geom_bar(stat = "identity", fill = "orange") +
  labs(x = "Cluster", y = "fat") +
  ggtitle("Cluster by Fat")

sodium <- ggplot(cluster_table, aes(x = cs2_5, y = sodium)) +
  geom_bar(stat = "identity", fill = "pink") +
  labs(x = "Cluster", y = "sodium") +
  ggtitle("Cluster by sodium")

fiber <- ggplot(cluster_table, aes(x = cs2_5, y = fiber)) +
  geom_bar(stat = "identity", fill = "gray") +
  labs(x = "Cluster", y = "fiber") +
  ggtitle("Cluster by fiber")

carbo <- ggplot(cluster_table, aes(x = cs2_5, y = carbo)) +
  geom_bar(stat = "identity", fill = "brown") +
  labs(x = "Cluster", y = "carbo") +
  ggtitle("Cluster by carbo")

sugars <- ggplot(cluster_table, aes(x = cs2_5, y = sugars)) +
  geom_bar(stat = "identity", fill = "lightgreen") +
  labs(x = "Cluster", y = "sugars") +
  ggtitle("Cluster by sugars")

potass <- ggplot(cluster_table, aes(x = cs2_5, y = potass)) +
  geom_bar(stat = "identity", fill = "yellow") +
  labs(x = "Cluster", y = "potass") +
  ggtitle("Cluster by potass")

rating <- ggplot(cluster_table, aes(x = cs2_5, 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)
```



#Based on the graphs, we can see that Cluster 1 has the lowest values for calories, fat, and sugars and the highest values for protein, fiber, and vitamins, which suggests that it may contain cereals that are generally considered healthier options and thats why it has very high rating as well. That why Cluster 1 fits the needs of our client! Nevertheless, part of our client's petition is to have a different cereal per day, which this cluster does not satisfy this need. For this reason, we will also recommend cluster 5 to satisfy this request. Cluster 5 has zero fats, Zero sugars, and it has the second-lowest number of calories after cluster 1. It also has a good number of proteins and fiber.On the other hand, Cluster 3 has the highest values for calories and sugars and the lowest values for protein, fiber, and vitamins, which suggests that it may contain cereals that are generally considered less healthy. we saw the same insight from our correlation plot high sugar less rating because its less healthy. However, it's important to note that this is just a general observation and individual cereals within each cluster may vary in terms of their nutritional value.