Assignment 5

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```
# installing required packages
library(ISLR)
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(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union

library(tidyverse)

## -- Attaching packages --------------------------------------- tidyverse 1.
3.1 --

## v tibble  3.1.6     v purrr   0.3.4
## v tidyr   1.2.0     v stringr 1.4.0
## v readr   2.1.2     v forcats 0.5.1

## -- Conflicts ------------------------------------------ tidyverse_conflict
s() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## x purrr::lift()   masks caret::lift()

library(cluster)
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://g
oo.gl/ve3WBa

library(ggplot2)
library(proxy)

##
## Attaching package: 'proxy'

## The following objects are masked from 'package:stats':
##
##     as.dist, dist

## The following object is masked from 'package:base':
##
##     as.matrix

library(NbClust)
library(ppclust)

## Warning: package 'ppclust' was built under R version 4.1.3

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/talgal
ili/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(den
dextend))
## ---------------------

##
## Attaching package: 'dendextend'

## The following object is masked from 'package:stats':
##
##     cutree

# Importing the "cereal" data set
cereals <- read.csv("C:/Users/mavul/Downloads/Cereals.csv")
```

```
# Review
# Reviewing first few rows of the data set
head(cereals)

##                         name mfr type calories protein fat sodium fiber car
bo
## 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

# Analyse the structure
str(cereals)

## 'data.frame':    77 obs. of  16 variables:
##  $ name    : chr  "100%_Bran" "100%_Natural_Bran" "All-Bran" "All-Bran_wit
h_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 ...

# Analyse the summary
summary(cereals)
```

```
##      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  
## 
```

Scaling and removing N/A from the data set

```
# Creating a duplicate of data set for pre processing
cereal_scaled <- cereals
# Scaling the data set before placing it into a clusters
cereal_scaled[ , c(4:16)] <- scale(cereals[ , c(4:16)])
# Removing NA values from data set
cereal_preprocessed <- na.omit(cereal_scaled)
# Review the scaled data set
head(cereal_preprocessed)
```

```
##                         name mfr type   calories    protein         fat
## 1                  100%_Bran   N    C -1.8929836  1.3286071 -0.01290349
## 2          100%_Natural_Bran   Q    C  0.6732089  0.4151897  3.96137277
## 3                   All-Bran   K    C -1.8929836  1.3286071 -0.01290349
## 4 All-Bran_with_Extra_Fiber   K    C -2.9194605  1.3286071 -1.00647256
## 6   Apple_Cinnamon_Cheerios   G    C  0.1599704 -0.4982277  0.98066557
## 7                Apple_Jacks   K    C  0.1599704 -0.4982277 -1.00647256
##        sodium        fiber      carbo      sugars      potass    vitamins
shelf
## 1 -0.3539844  3.29284661 -2.5087829 -0.2343906  2.5753685 -0.1453172  0.95
15734
## 2 -1.7257708 -0.06375361 -1.7409943  0.2223705  0.5160205 -1.2642598  0.95
15734
## 3  1.1967306  2.87327158 -1.9969238 -0.4627711  3.1434645 -0.1453172  0.95
15734
## 4 -0.2346986  4.97114672 -1.7409943 -1.6046739  3.2854885 -0.1453172  0.95
15734
## 6  0.2424445 -0.27354112 -1.1011705  0.6791317 -0.4071355 -0.1453172 -1.45
07595
## 7 -0.4136273 -0.48332864 -0.9732057  1.5926539 -0.9752315 -0.1453172 -0.24
95930
##        weight        cups      rating
## 1 -0.1967771 -2.1100340  1.8321876
## 2 -0.1967771  0.7690100 -0.6180571
## 3 -0.1967771 -2.1100340  1.1930986
## 4 -0.1967771 -1.3795303  3.6333849
## 6 -0.1967771 -0.3052601 -0.9365625
## 7 -0.1967771  0.7690100 -0.6756899
```

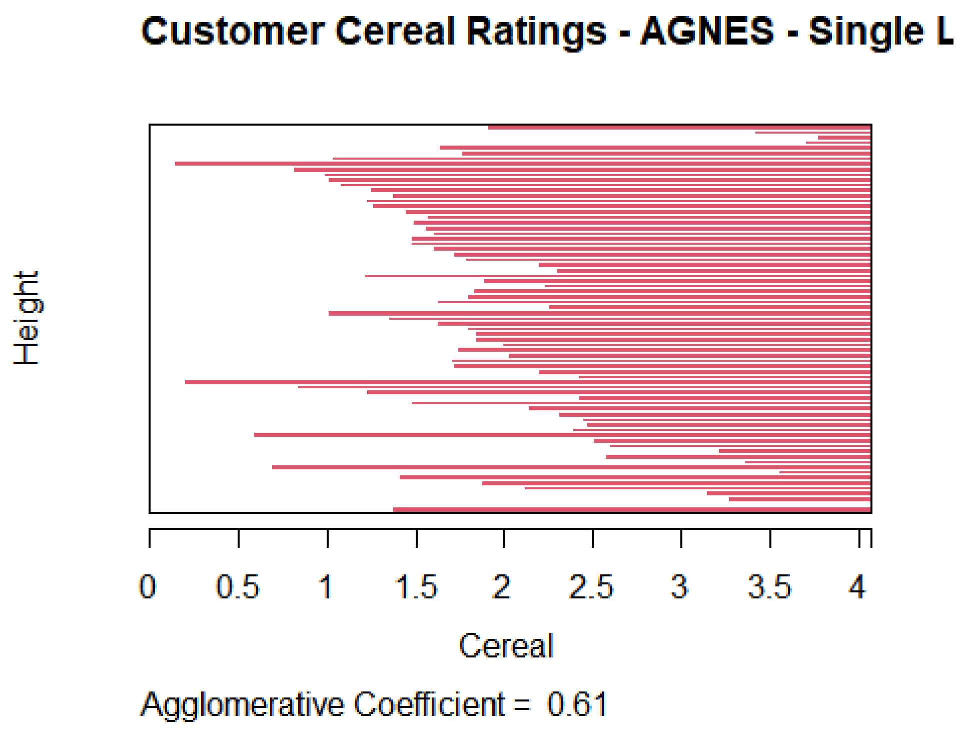
The total number of observations now are 74.

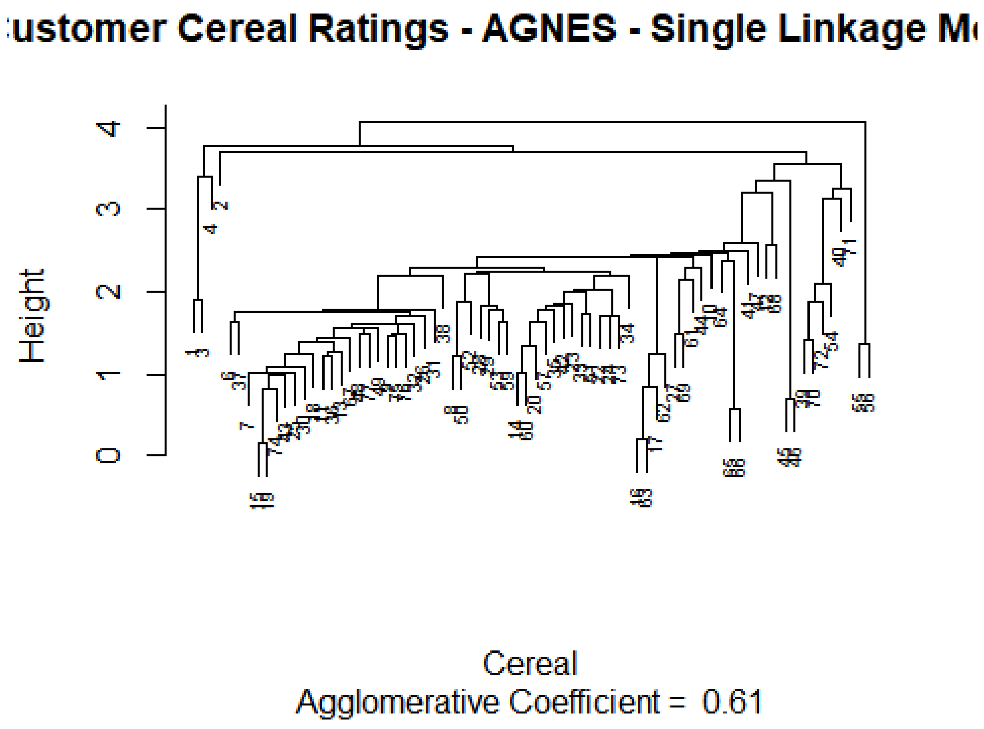
1) Applying hierarchical clustering to the data using Euclidean distance to the normalized measurements

Using Agnes to compare the clustering from single linkage, complete linkage, average linkage, and Ward

Single Linkage:

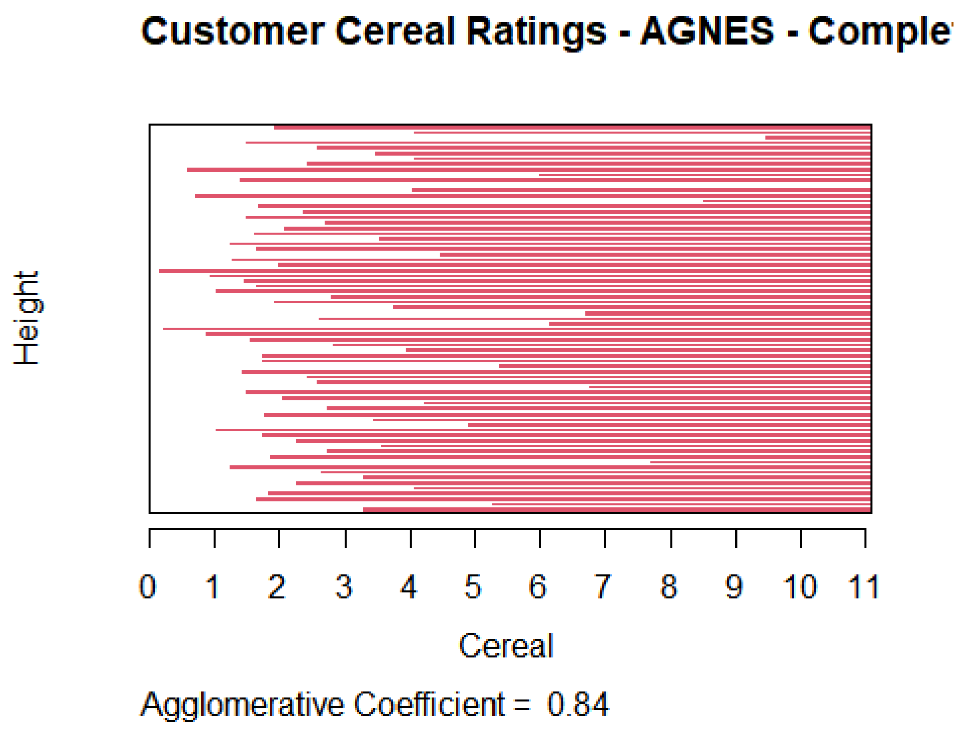
```
# Creating the dissimilarity matrix
cereal_d_euclidean <- dist(cereal_preprocessed[ , c(4:16)], method = "euclide
an")
# Performing hierarchical clustering using the single linkage method
ag_hc_single <- agnes(cereal_d_euclidean, method = "single")
# Ploting the results of the all the methods
plot(ag_hc_single,
     main = "Customer Cereal Ratings - AGNES - Single Linkage Method",
     xlab = "Cereal",
     ylab = "Height",
     cex.axis = 1,
     cex = 0.55)
```

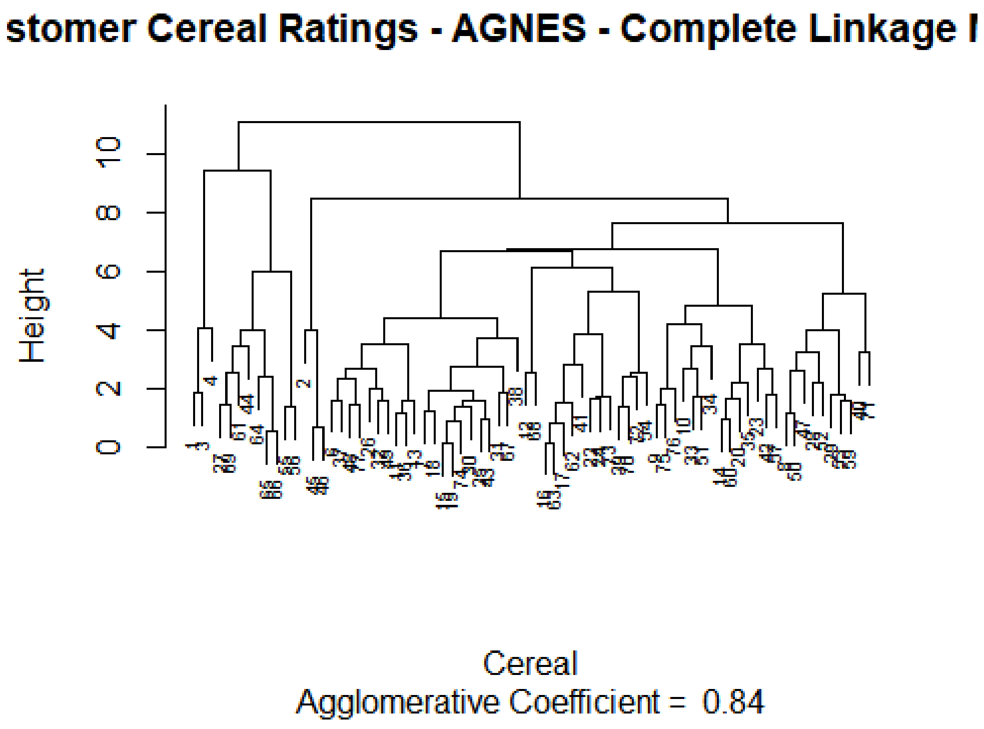

Customer Cereal Ratings - AGNES - Single L
Height
0
0.5
1
1.5
2
2.5
3
3.5
4
Cereal
Agglomerative Coefficient = 0.61


ustomer Cereal Ratings - AGNES - Single Linkage M
Height
0
1
2
3
4
Cereal
Agglomerative Coefficient = 0.61

Complete Linkage:

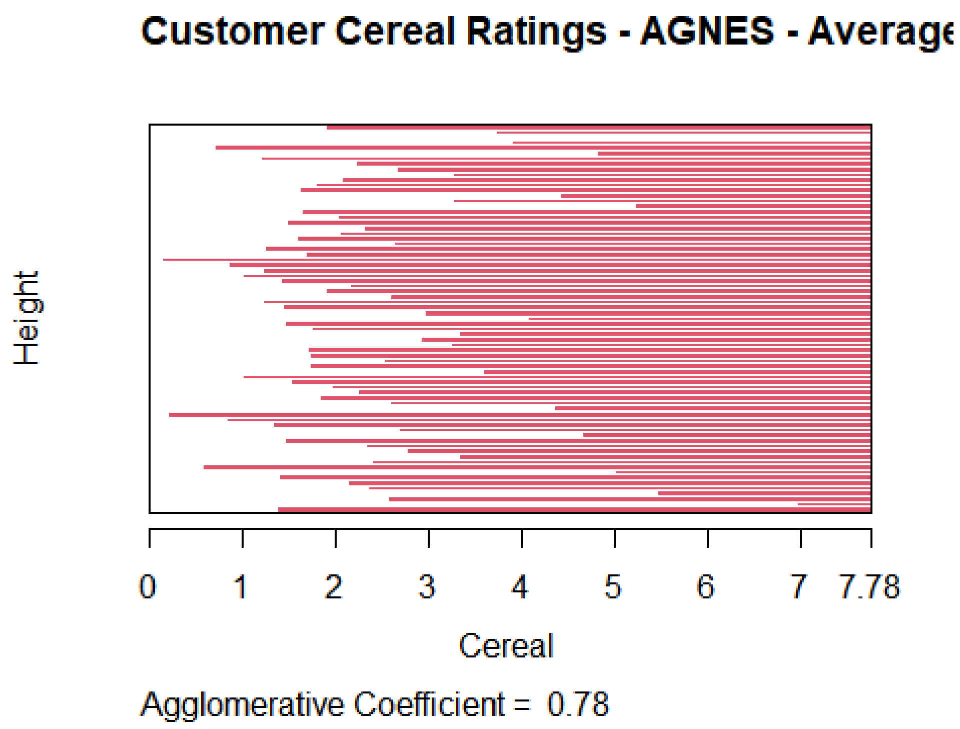
```
# Creating hierarchical clustering using the complete linkage method
ag_hc_complete <- agnes(cereal_d_euclidean, method = "complete")
# Ploting the results of the different methods
plot(ag_hc_complete,
     main = "Customer Cereal Ratings - AGNES - Complete Linkage Method",
     xlab = "Cereal",
     ylab = "Height",
     cex.axis = 1,
     cex = 0.55)
```

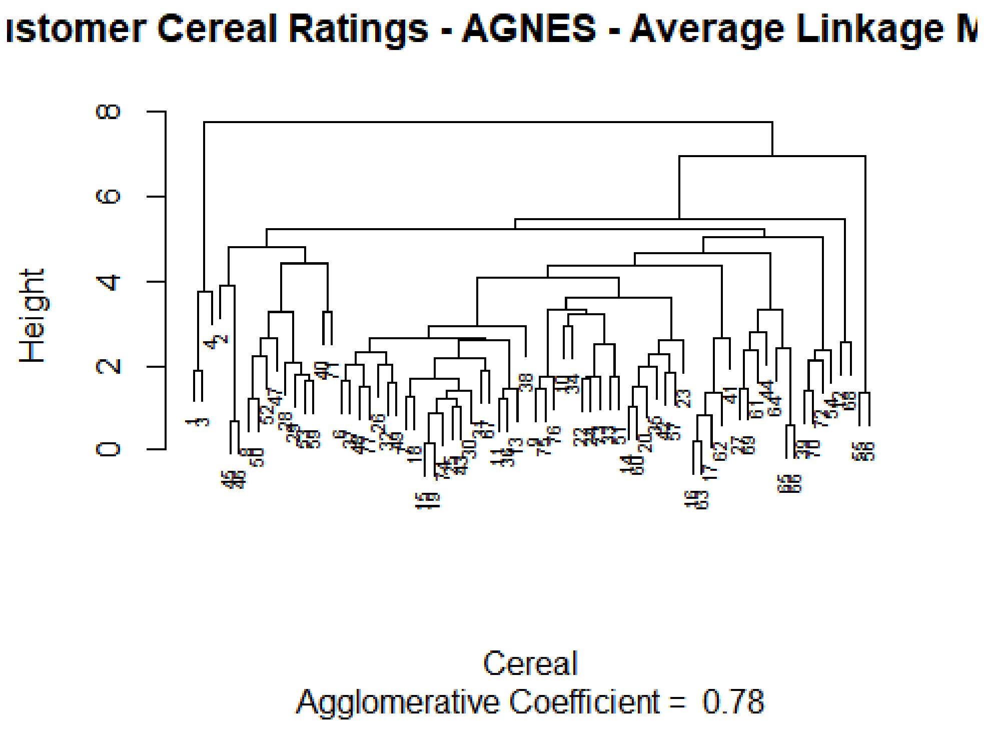

Customer Cereal Ratings - AGNES - Comple
Height
0 1 2 3 4 5 6 7 8 9 10 11
Cereal
Agglomerative Coefficient = 0.84


stomer Cereal Ratings - AGNES - Complete Linkage I
Height
0 2 4 6 8 10
Cereal
Agglomerative Coefficient = 0.84

Average Linkage:

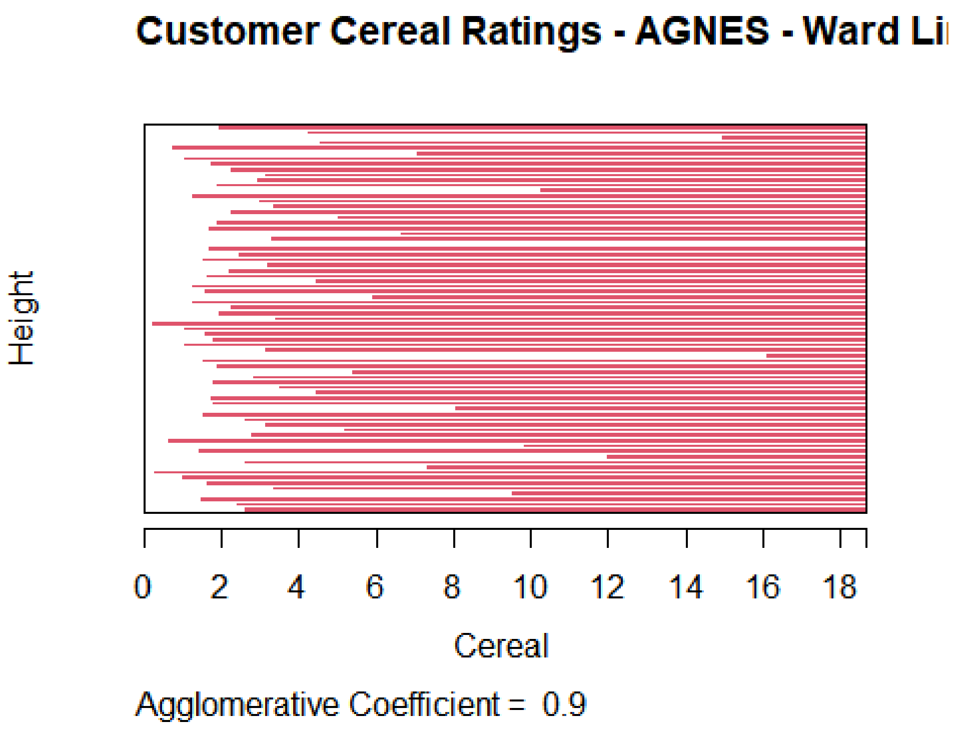
```r
# Creating hierarchical clustering via the average linkage method
ag_hc_average <- agnes(cereal_d_euclidean, method = "average")
# Ploting the results of the different methods
plot(ag_hc_average,
     main = "Customer Cereal Ratings - AGNES - Average Linkage Method",
     xlab = "Cereal",
     ylab = "Height",
     cex.axis = 1,
     cex = 0.55)
```

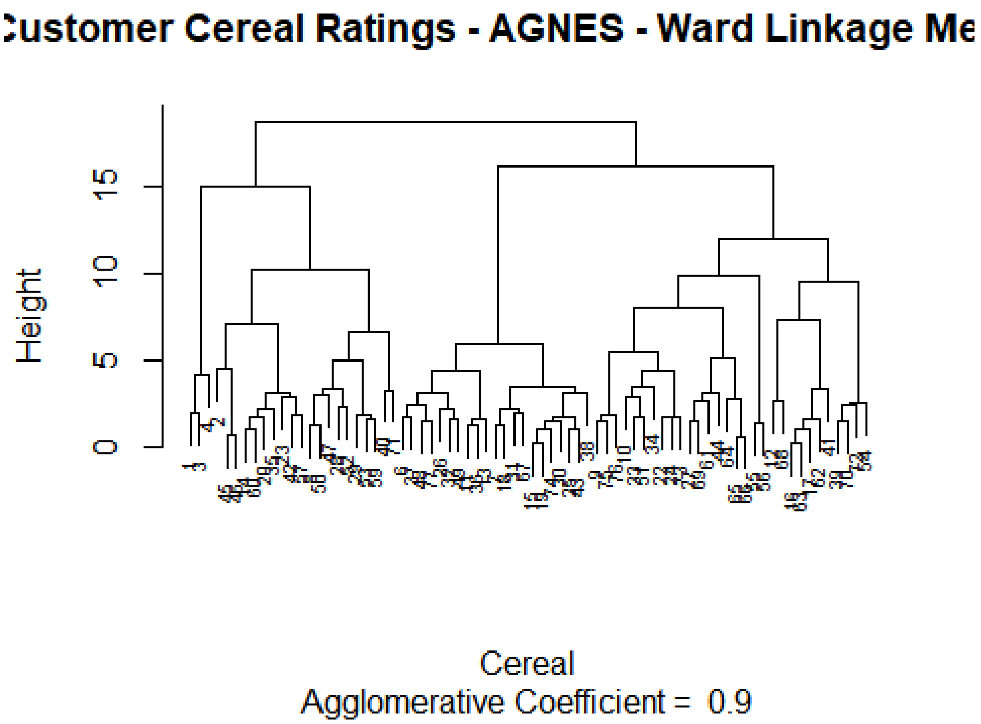

Customer Cereal Ratings - AGNES - Average
Height
0
1
2
3
4
5
6
7
7.78
Cereal
Agglomerative Coefficient = 0.78


istomer Cereal Ratings - AGNES - Average Linkage M
Height
0
2
4
6
8
Cereal
Agglomerative Coefficient = 0.78

Ward Method:

```
# Creating hierarchical clustering via the ward linkage method
ag_hc_ward <- agnes(cereal_d_euclidean, method = "ward")
# Ploting the results of the different methods
plot(ag_hc_ward,
     main = "Customer Cereal Ratings - AGNES - Ward Linkage Method",
     xlab = "Cereal",
     ylab = "Height",
     cex.axis = 1,
     cex = 0.55)
```





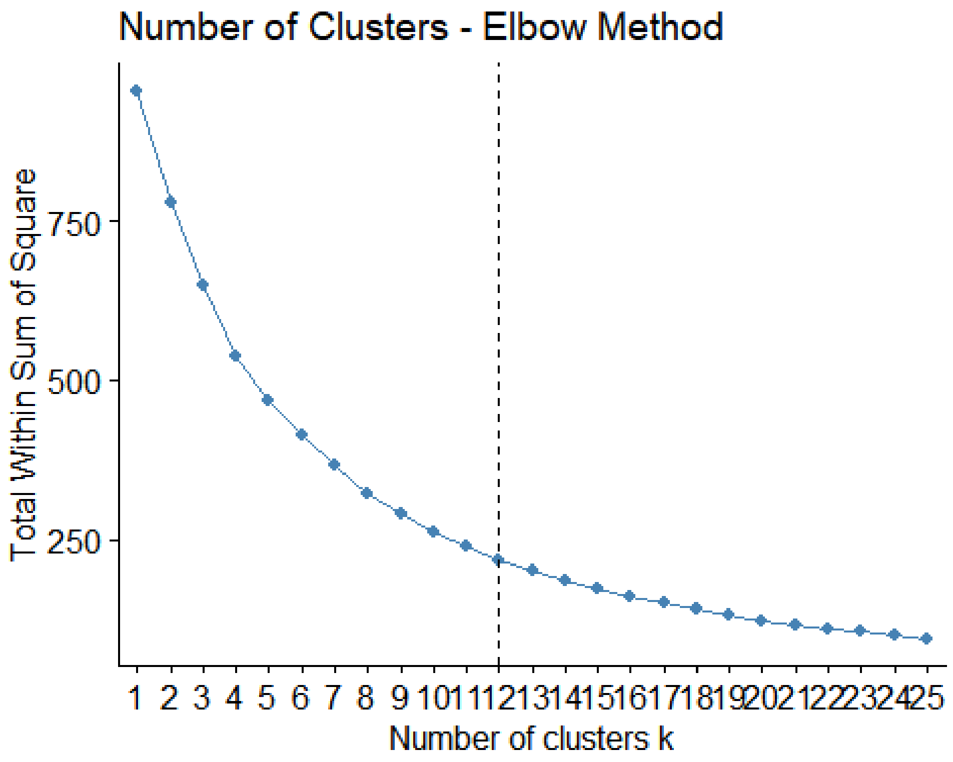
The best clustering method would be based on the agglomerative coefficient that is returned from each method. The closer the value is to 1.0, the closer the clustering structure is. Therefore, we choose the value closest to 1.0.

Single Linkage: 0.61 Complete Linkage: 0.84 Average Linkage: 0.78 Ward Method: 0.90

Therefore, we choose the Ward method as the best clustering model.

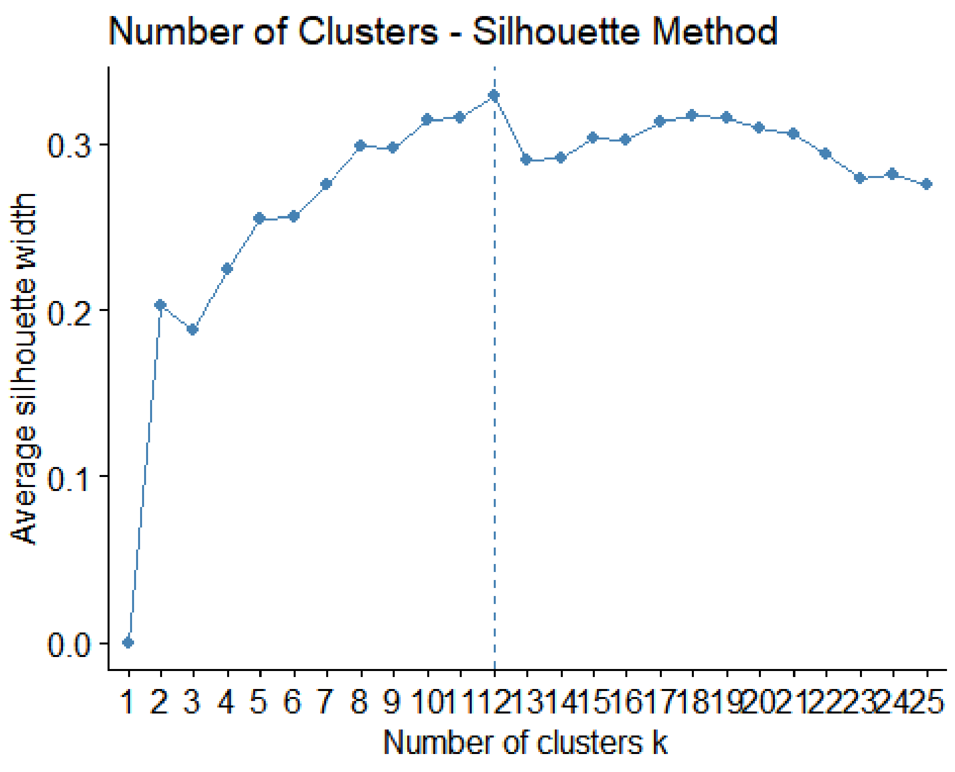
2) How many clusters would you choose?

```
# Determine the optimal number of clusters for the dataset via the Elbow meth
od
fviz_nbclust(cereal_preprocessed[ , c(4:16)], hcut, method = "wss", k.max = 2
5) +
  labs(title = "Number of Clusters - Elbow Method") +
  geom_vline(xintercept = 12, linetype = 2)
```



Silhouette Method:

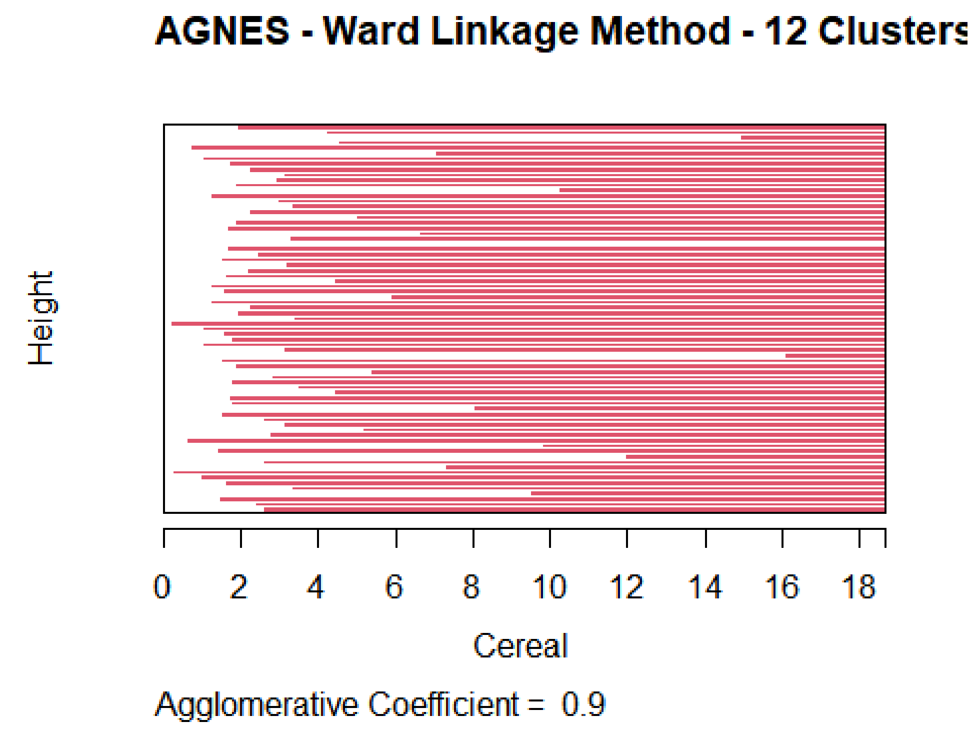
```
# Determine the optimal number of clusters for the dataset via the silhouette
method
fviz_nbclust(cereal_preprocessed[ , c(4:16)],
                               hcut,
                               method = "silhouette",
                               k.max = 25) +
  labs(title = "Number of Clusters - Silhouette Method")
```



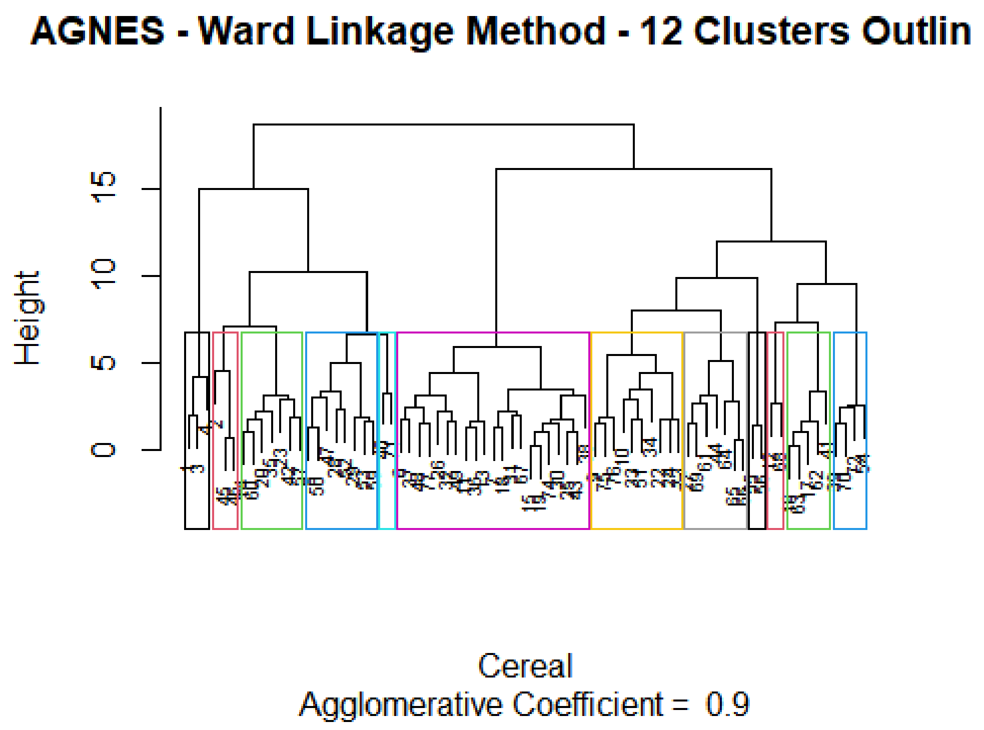
The number of clusters are 12

Making an outline of the 12 clusters on the hierarchical tree

```
# Plot of the Ward hierarchical tree with the 12 clusters outlined for refere
nce
plot(ag_hc_ward,
     main = "AGNES - Ward Linkage Method - 12 Clusters Outlined",
     xlab = "Cereal",
     ylab = "Height",
     cex.axis = 1,
     cex = 0.55,)
```



```
rect.hclust(ag_hc_ward, k = 12, border = 1:12)
```



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

a) In this case, normalizing the data is not suitable because the nutritional information for cereal is normalized based on the sample of cereal being evaluated. As a result, the data has cereals with extremely high sugar content and very little fiber, iron, and other nutritional data. Therefore, we can not determine how much nourishment the cereal will provide a child once it is normalized throughout the sample set. We may infer that cereal with an iron content of 0.99, which is it contains all of the nutritional iron a child needs but could be the best out of the sample set, having nearly no nutritional value.

b) As a result, a better way to preprocess the data would be to convert it to a ratio of daily recommended calories, fiber, carbohydrates, and other nutrients for a child. This allows the analysts to make more precise decisions on clusters preventing larger variables from overriding the distance estimates. An analyst may look at the cluster average to see what percentage of a student's daily needed nutrition would come from a particular cereal. This would enable the employees to make better selections about healthy cereal clusters.