ML Assignment 5

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```
getwd()
```

```
## [1] "C:/Users/tejar/OneDrive/Desktop/ML Assignments"
```

```
setwd("C:/Users/tejar/OneDrive/Documents")
```

Installing the required packages:

```
library(ISLR)
library(caret)
```

```
## Loading required package: ggplot2

## 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(cluster)
library(factoextra)
```

```
## Warning: package 'factoextra' was built under R version 4.2.2

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

```r
library(NbClust)
library(ppclust)
```

```
## Warning: package 'ppclust' was built under R version 4.2.2
```

```r
library(dendextend)
```

```
## Warning: package 'dendextend' was built under R version 4.2.2
```

```
##
## ---------------------
## Welcome to dendextend version 1.16.0
## 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
```

```r
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.2 --
```

```
## v tibble  3.1.8     v purrr   0.3.4
## v tidyr   1.2.1     v stringr 1.4.1
## v readr   2.1.2     v forcats 0.5.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## x purrr::lift()   masks caret::lift()
```

```r
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
```

```
## The "cereal" data collection import
Cereals <- Info<- read.csv("C:/Users/tejar/Downloads/Cereals.csv")

## Using head, obtaining the first few rows of the data set
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
```

```
## Using str to examine the data set's organization
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 ...
```

```
## Analysing the data set using Summary command
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
##
```

In order to remove NA values from the data set, I am now scaling the data.

```r
## To prepare, I'm creating a copy of this data set here.
Scaled_Cereals <- Cereals

##I'm currently scaling the data set to fit it into a clustering method.
Scaled_Cereals[ , c(4:16)] <- scale(Cereals[ , c(4:16)])

##The NA values are being removed from the data collection in this case using the omit function.
Preprocessed_Cereal <- na.omit(Scaled_Cereals)

##Head is used to display the first few rows after eliminating NA.
head(Preprocessed_Cereal)
```

```
##                          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  0.9515734
## 2 -1.7257708 -0.06375361 -1.7409943  0.2223705  0.5160205 -1.2642598  0.9515734
## 3  1.1967306  2.87327158 -1.9969238 -0.4627711  3.1434645 -0.1453172  0.9515734
## 4 -0.2346986  4.97114672 -1.7409943 -1.6046739  3.2854885 -0.1453172  0.9515734
## 6  0.2424445 -0.27354112 -1.1011705  0.6791317 -0.4071355 -0.1453172 -1.4507595
## 7 -0.4136273 -0.48332864 -0.9732057  1.5926539 -0.9752315 -0.1453172 -0.2495930
##       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 dropped from 77 to 74 after pre-processing and scaling the data. There were only 3 records with the value “NA”

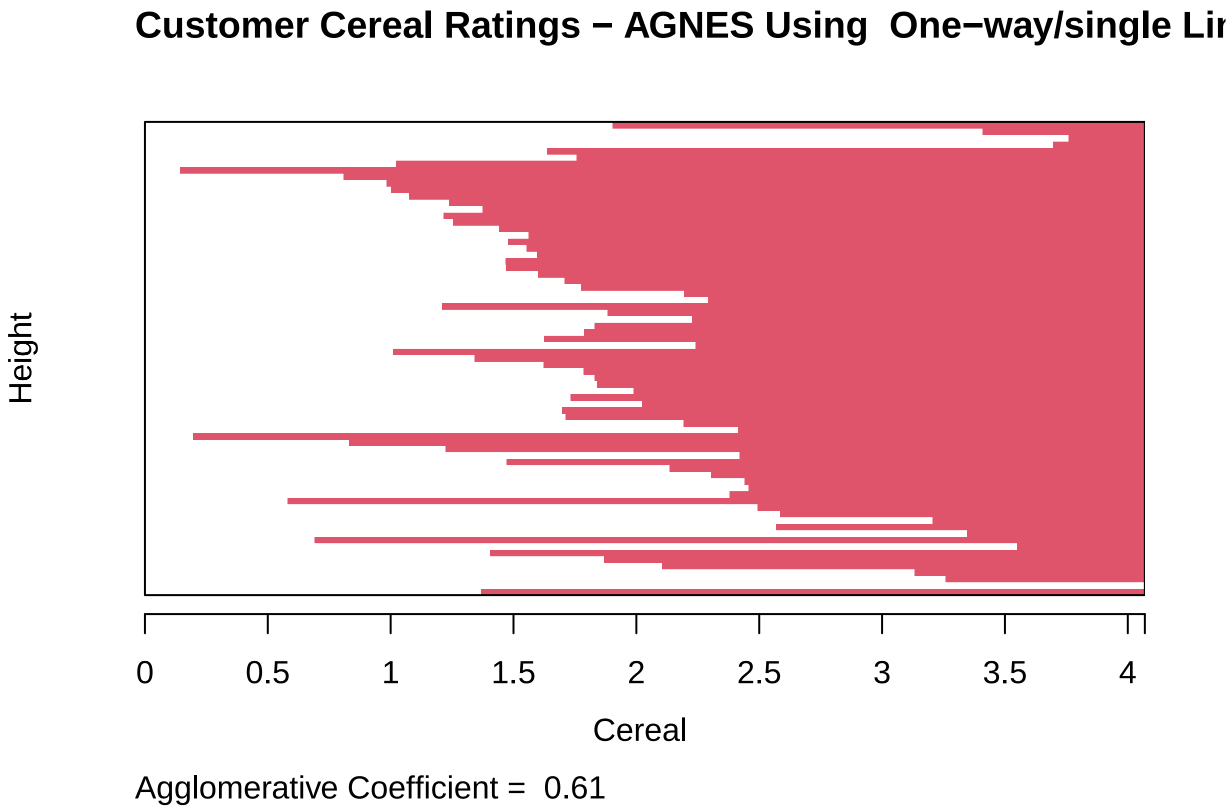
Q) Apply hierarchical clustering to the data using Euclidean distance to the normalized measurements. Use Agnes to compare the clustering from single linkage, complete linkage, average linkage, and Ward. Choose the best method.

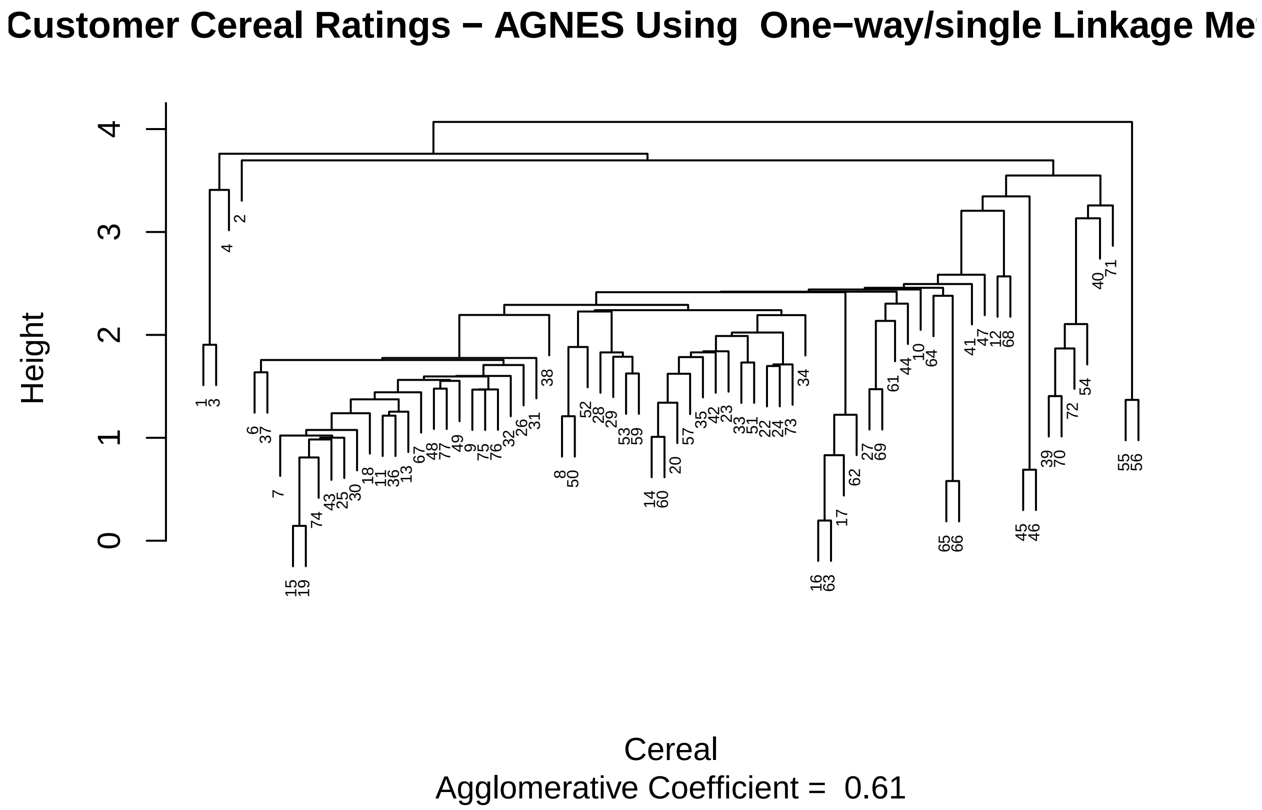
One-way/Single Linkage:

```
##The dissimilarity matrix of all the numerical values in the data set is constructed using Euclidean d
Cereal_Euclidean <- dist(Preprocessed_Cereal[ , c(4:16)], method = "euclidean")

##A hierarchical clustering is carried out utilizing the single linkage method.
HC_Single <- agnes(Cereal_Euclidean, method = "single")

##Here, I'm displaying the results of the various strategies.
plot(HC_Single,
     main = "Customer Cereal Ratings - AGNES Using  One-way/single Linkage Method",
     xlab = "Cereal",
     ylab = "Height",
     cex.axis = 1,
     cex = 0.50)
```


Customer Cereal Ratings − AGNES Using One−way/single Lir
Height
0
0.5
1
1.5
2
2.5
3
3.5
4
Cereal
Agglomerative Coefficient = 0.61

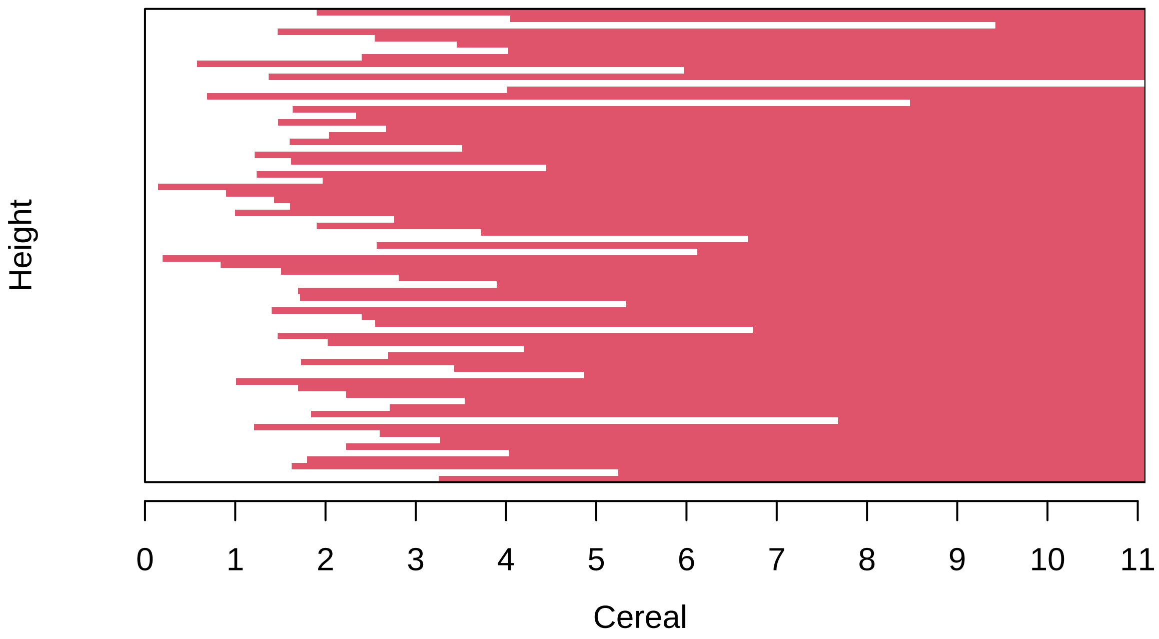


##Complete Linkage

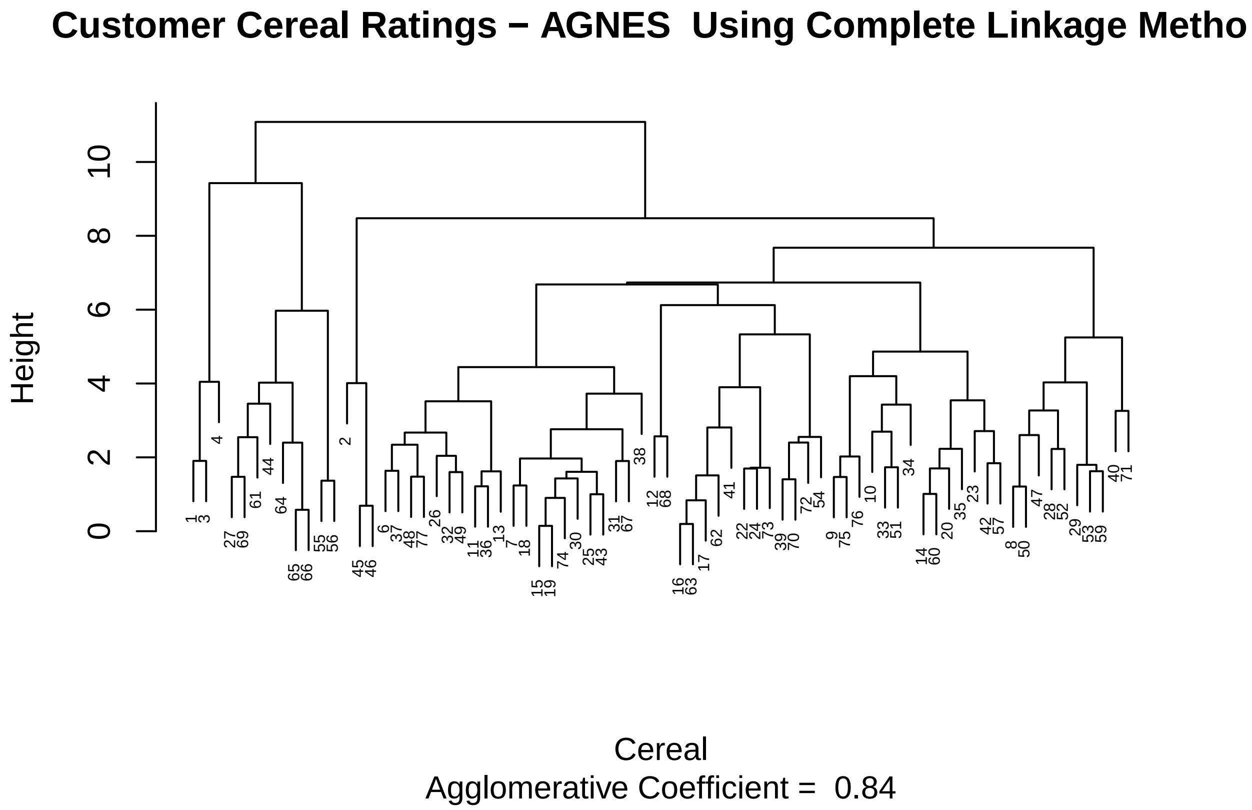
```
##Hierarchical clustering is carried out by utilizing the Complete linkage technique.
HC_Complete <- agnes(Cereal_Euclidean, method = "complete")

##The results of the several methods are plotted here.
plot(HC_Complete,
     main = "Customer Cereal Ratings - AGNES  Using Complete Linkage Method",
     xlab = "Cereal",
     ylab = "Height",
     cex.axis = 1,
     cex = 0.50)
```

Customer Cereal Ratings − AGNES Using Complete Linkage I

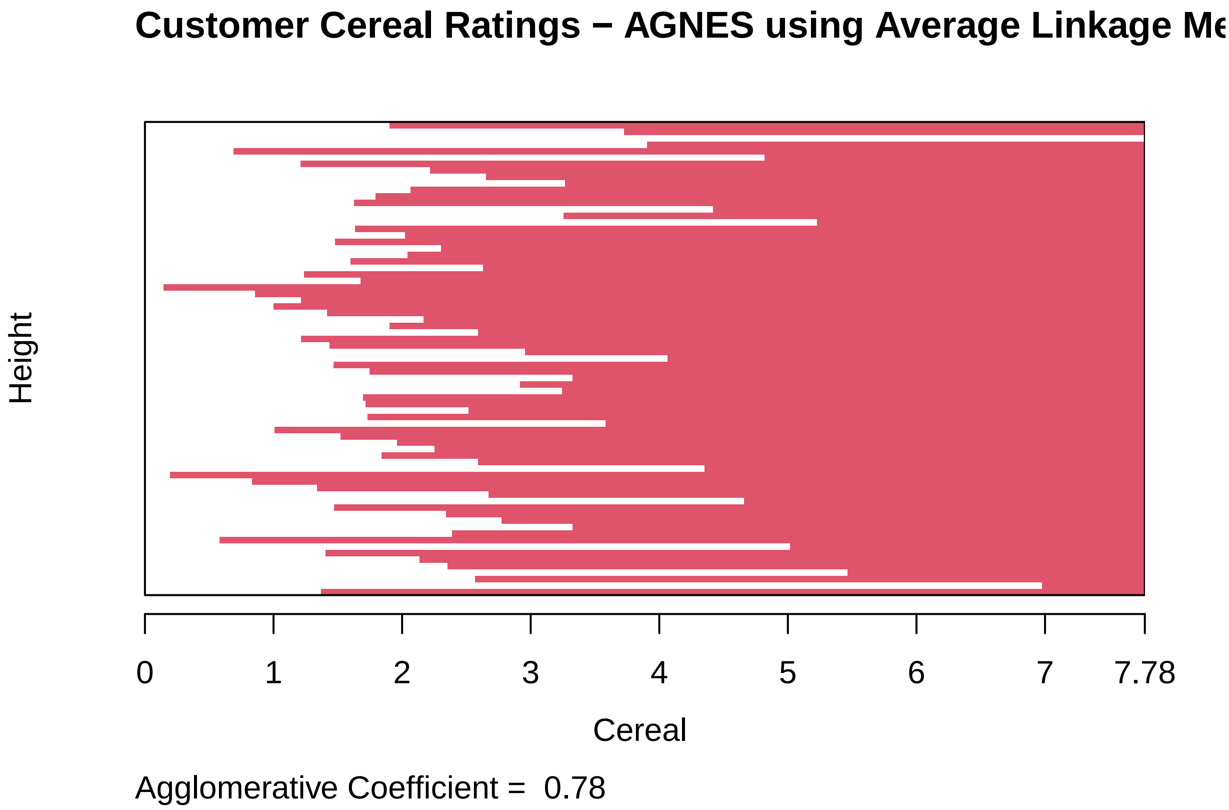


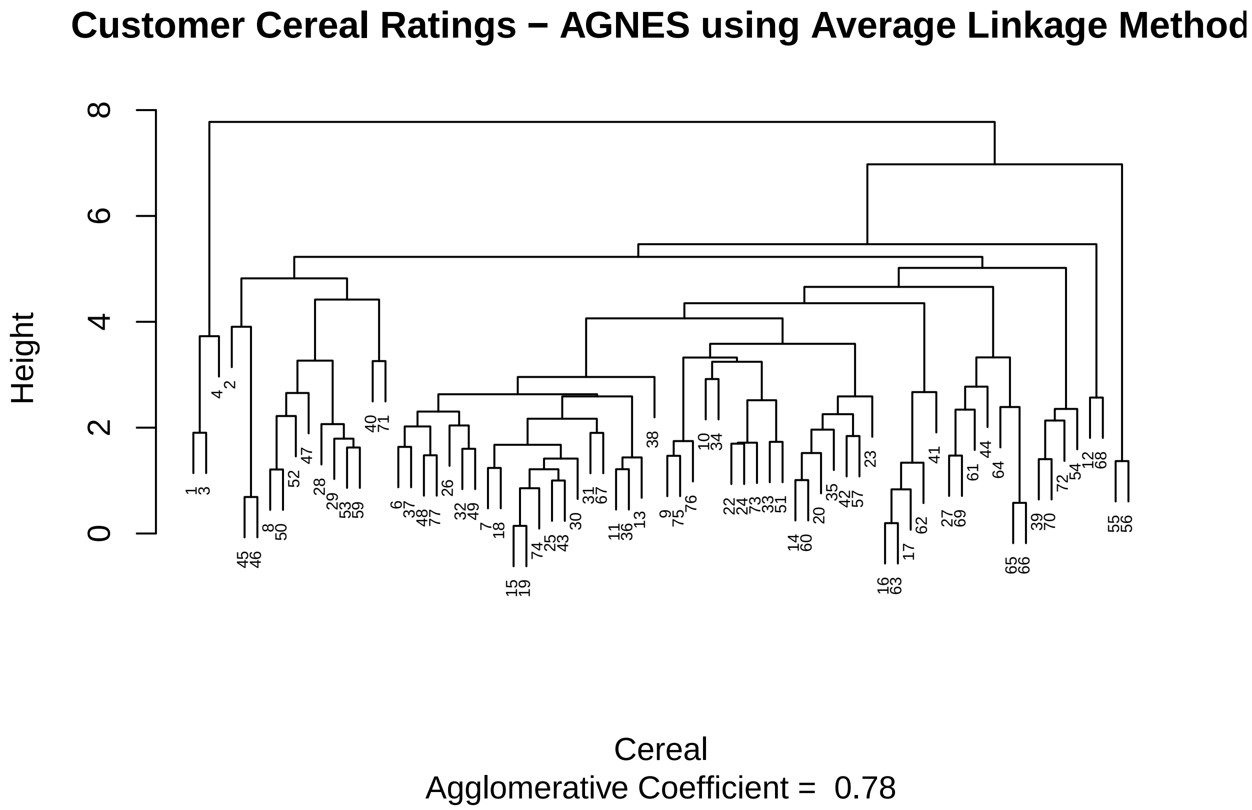
Agglomerative Coefficient = 0.84



##Average Linkage:

```
##applying the average linkage method to hierarchical clustering
HC_Average <- agnes(Cereal_Euclidean, method = "average")
##I'm plotting the outcomes of the various techniques here.
plot(HC_Average,
     main = "Customer Cereal Ratings - AGNES using Average Linkage Method",
     xlab = "Cereal",
     ylab = "Height",
     cex.axis = 1,
     cex = 0.50)
```

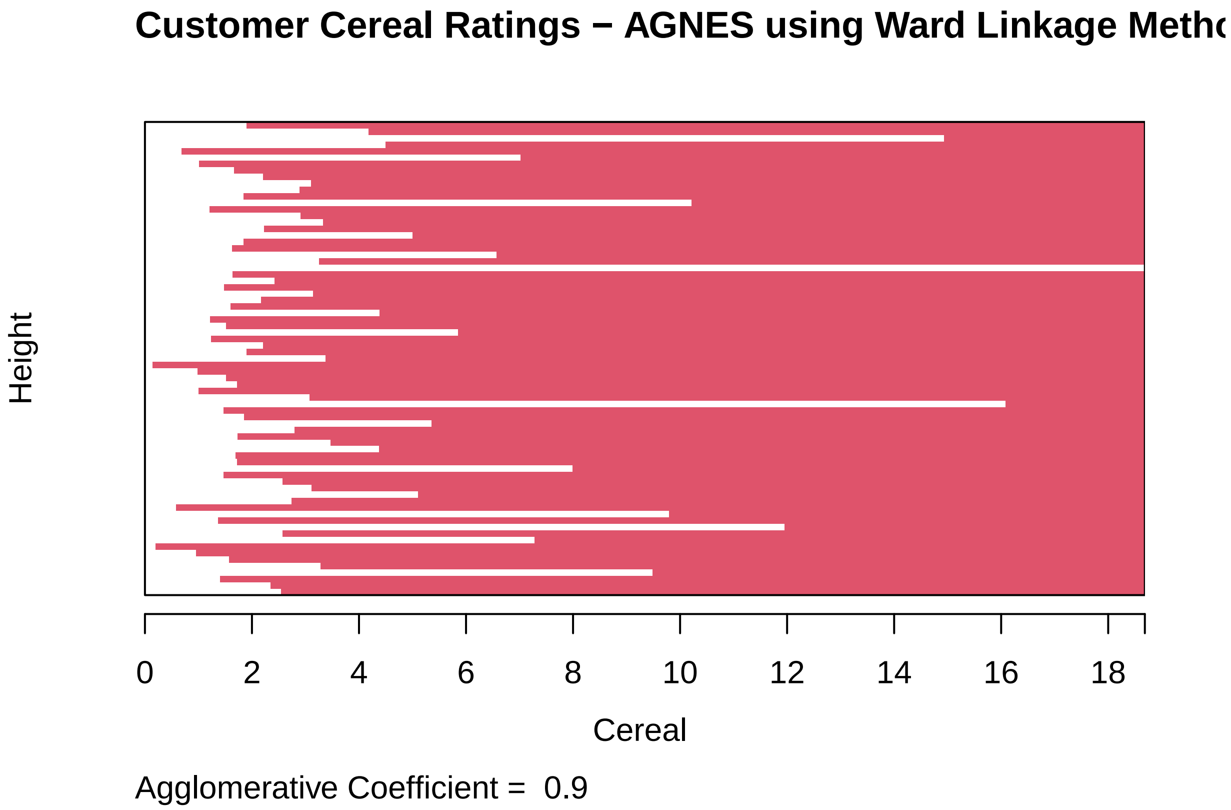

Customer Cereal Ratings − AGNES using Average Linkage Me
Height
0
1
2
3
4
5
6
7
7.78
Cereal
Agglomerative Coefficient = 0.78

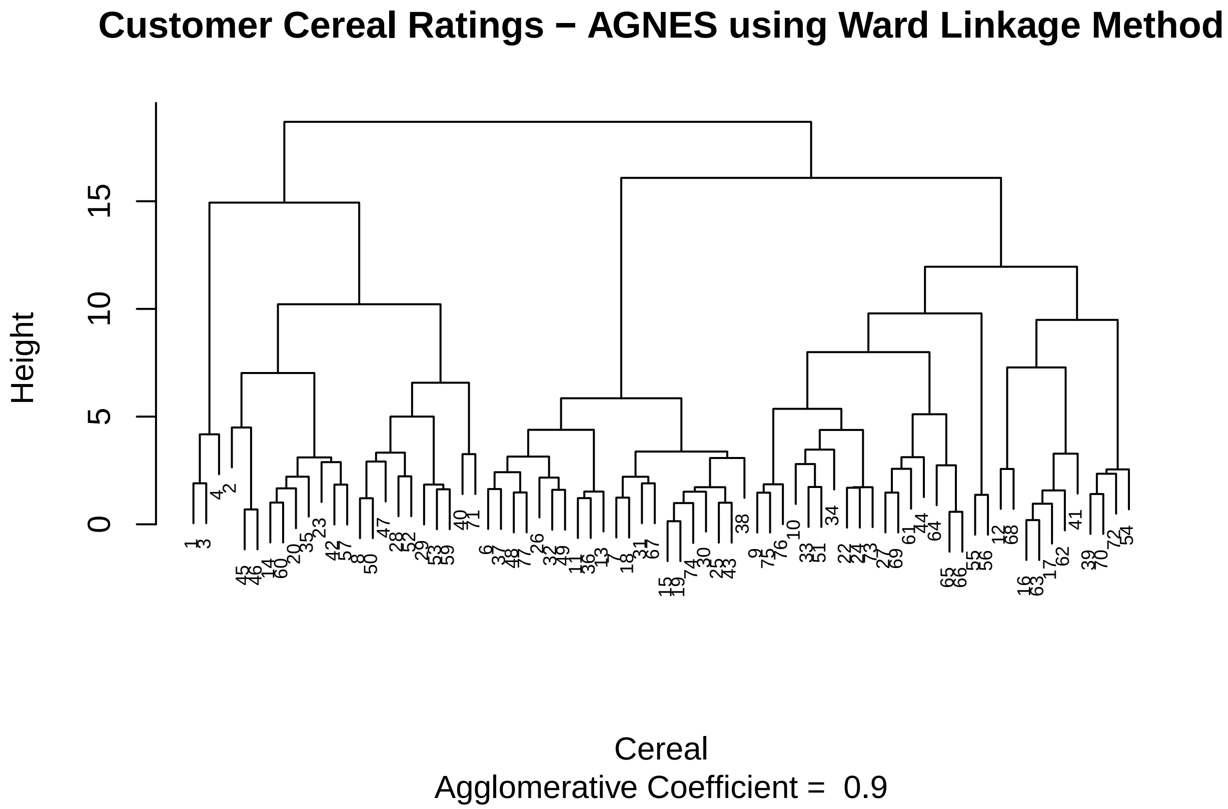


Ward Method:

```
##The ward linkage method of hierarchical clustering
HC_Ward <- agnes(Cereal_Euclidean, method = "ward")

##I am calculating the results of several strategies.
plot(HC_Ward,
     main = "Customer Cereal Ratings - AGNES using Ward Linkage Method",
     xlab = "Cereal",
     ylab = "Height",
     cex.axis = 1,
     cex = 0.55)
```


Customer Cereal Ratings − AGNES using Ward Linkage Metho
Height
0
2
4
6
8
10
12
14
16
18
Cereal
Agglomerative Coefficient = 0.9



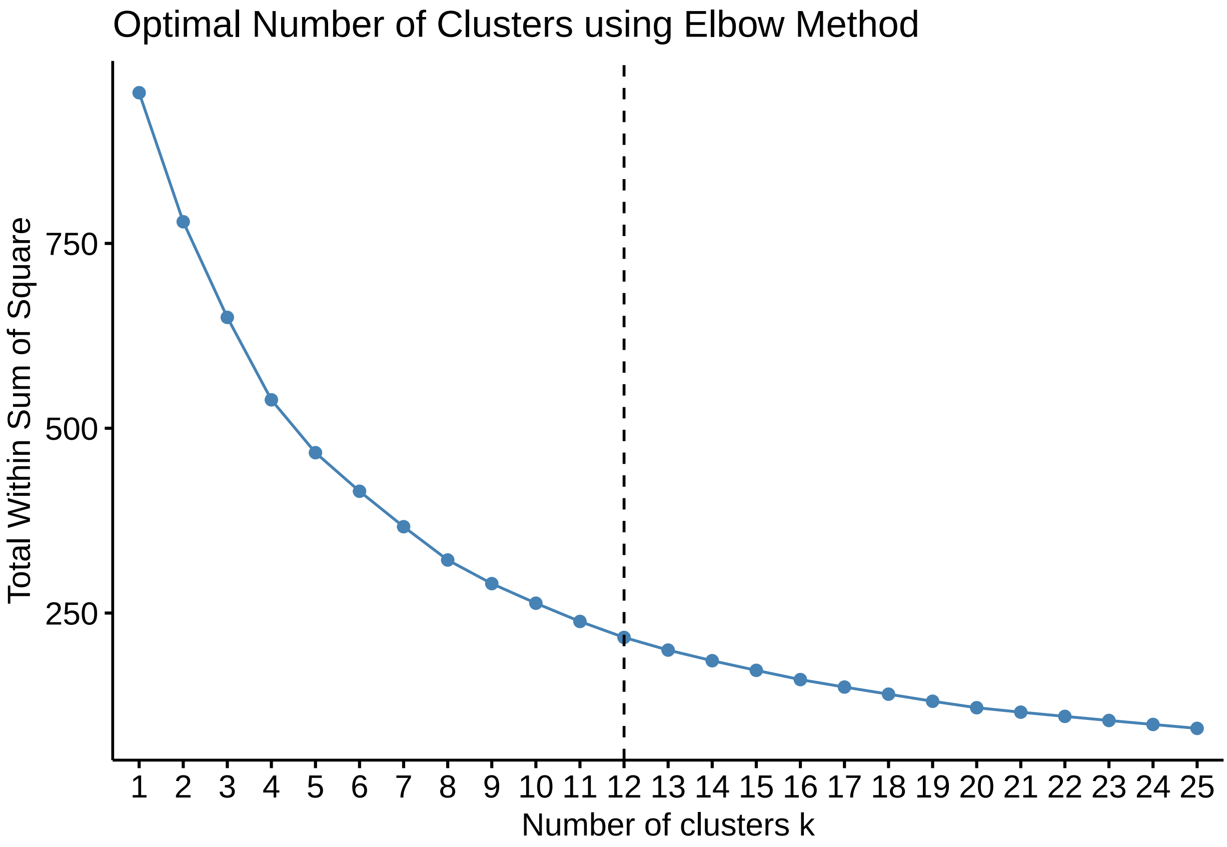
The clustering structure is more likely to be present if the value is close to 1.0. As a result, the strategy with the value that is closest to 1.0 will be chosen. Single Linkage: 0.61 Complete Linkage: 0.84 Average Linkage: 0.78 Ward Method: 0.90 The Ward technique is the most effective clustering model in this case, according to the results.

Q) How many clusters would you choose?

##In this instance, I'm deciding on the right amount of clusters using the elbow and silhouette methods.

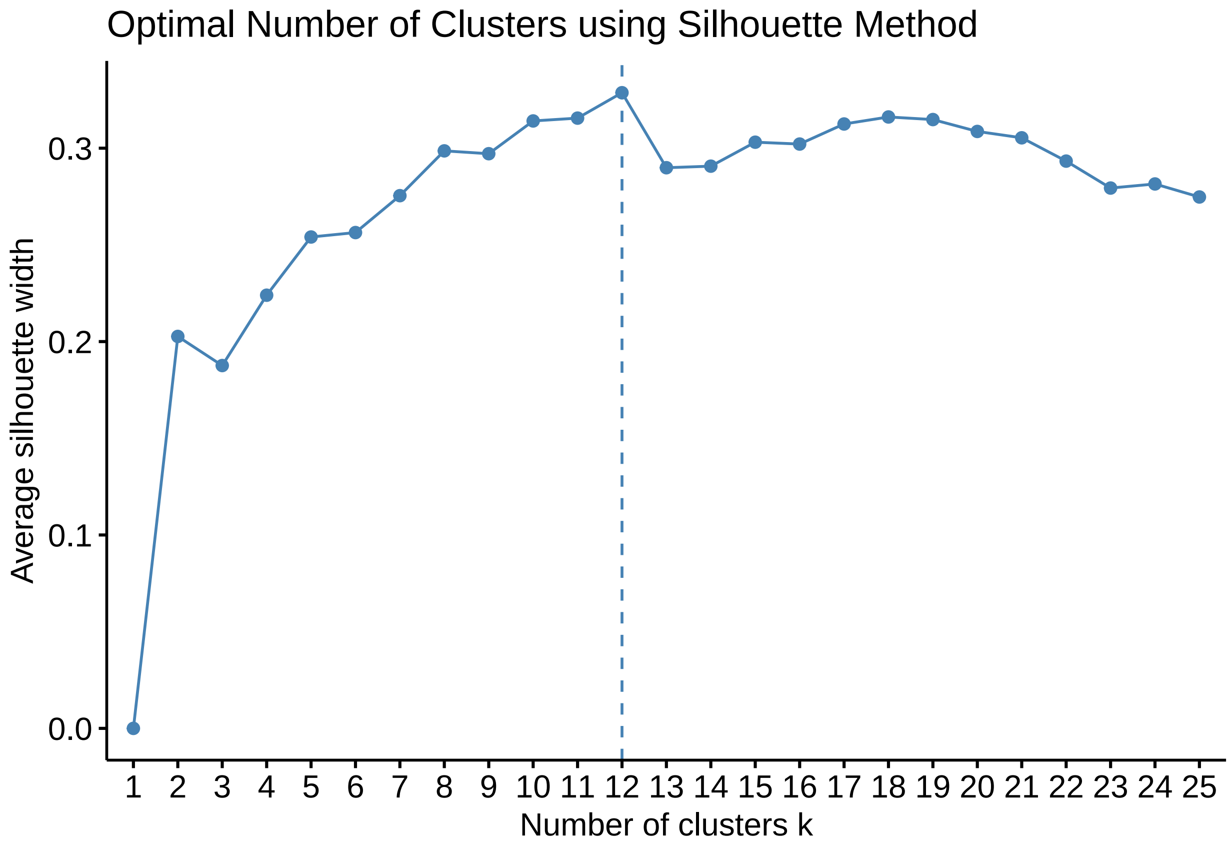
Elbow Method:

```r
fviz_nbclust(Preprocessed_Cereal[ , c(4:16)], hcut, method = "wss", k.max = 25) +
  labs(title = "Optimal Number of Clusters using Elbow Method") +
  geom_vline(xintercept = 12, linetype = 2)
```



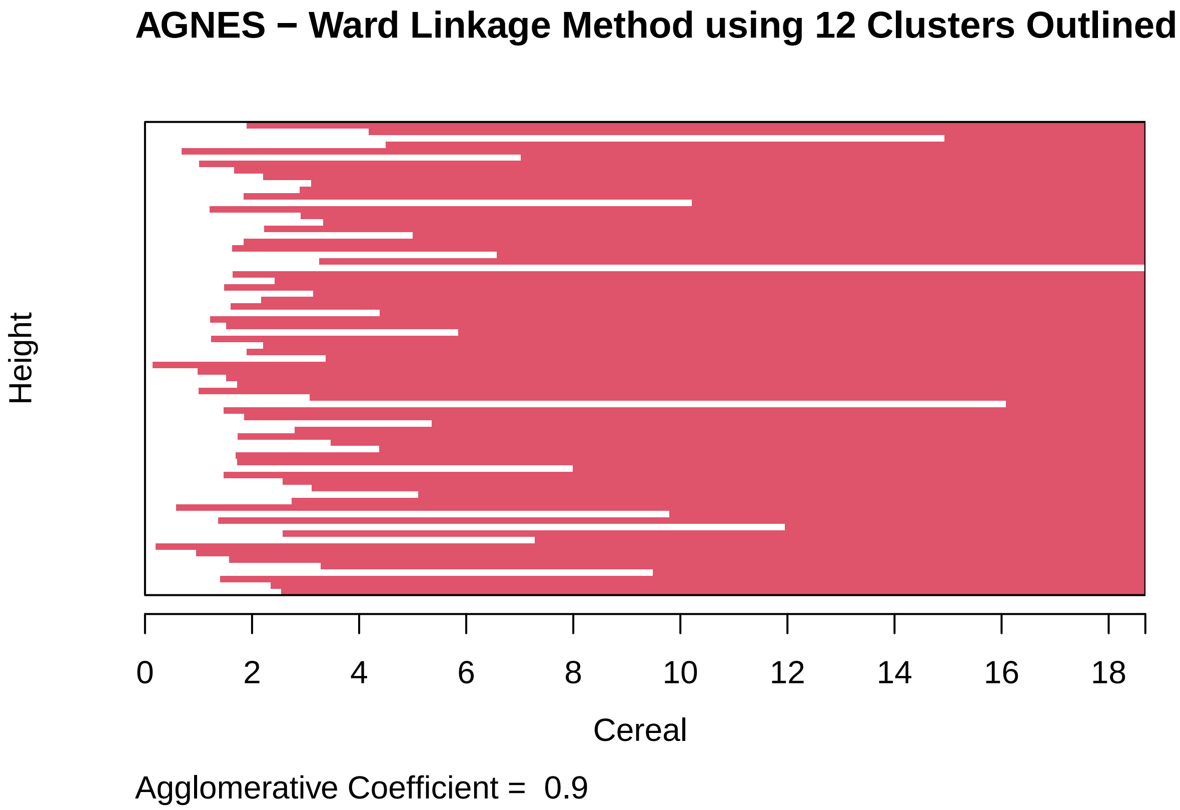
##Silhouette Method:

```
fviz_nbclust(Preprocessed_Cereal[ , c(4:16)],
                               hcut,
                               method = "silhouette",
                               k.max = 25) +
  labs(title = "Optimal Number of Clusters using Silhouette Method")
```

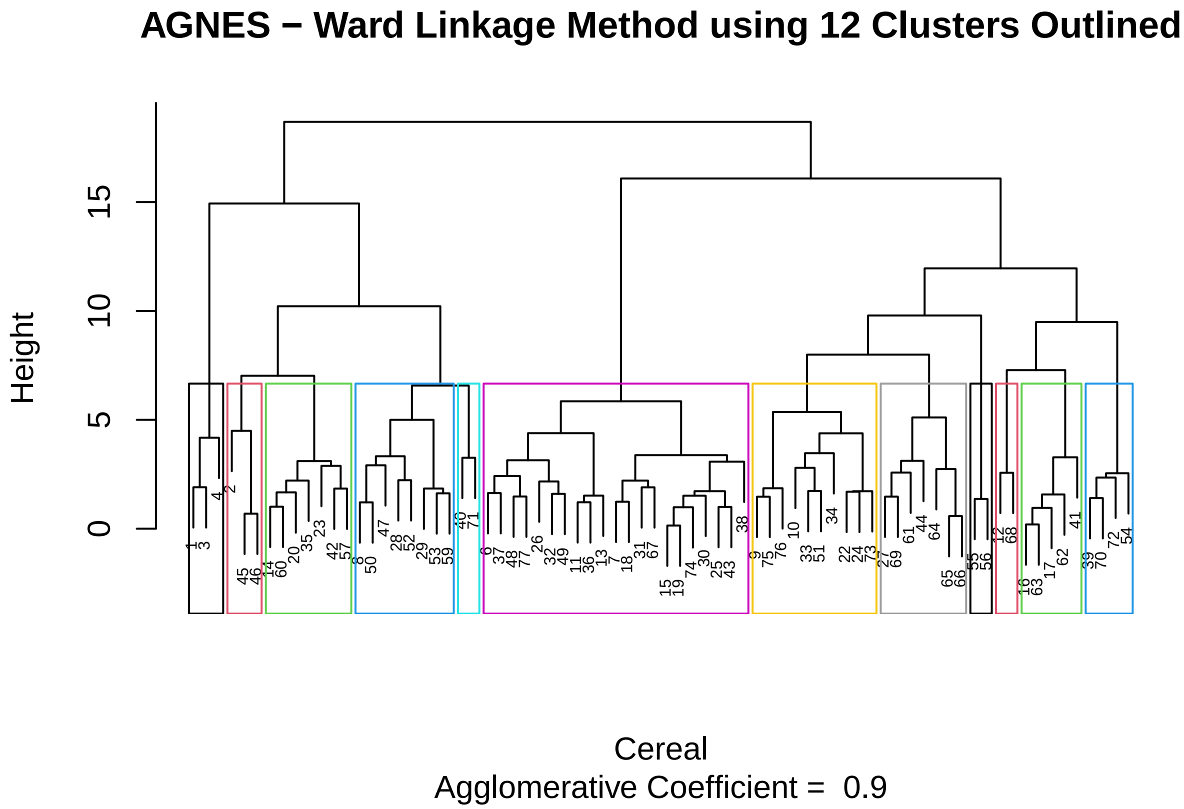


According on the results of the elbow and silhouette techniques, 12 clusters would be the best number.

```
##The 12 groups are marked for easy reference on this map of the Ward hierarchical tree.
plot(HC_Ward,
     main = "AGNES - Ward Linkage Method using 12 Clusters Outlined",
     xlab = "Cereal",
     ylab = "Height",
     cex.axis = 1,
     cex = 0.50,)
```



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



Q) 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?

Since the nutritional facts for the cereal sample under consideration are standardized, normalizing the data would not be appropriate in this situation. Only cereals with extremely high sugar content and very little fiber, iron, or other nutritional information, therefore, could be included in the information acquired. Once the cereal has been averaged over the sample set, it is difficult to forecast how much nutrition the cereal will give a child. But it's possible that a cereal with an iron content of 0.999 is only the best of the worst in the sample set and is completely nutritionally worthless. One would assume that a cereal with an iron content of 0.999 contains nearly all of the dietary iron required for a youngster. The ratio of the daily recommended amounts of calories, fiber, carbs, and other nutrients for a child would be a better approach to preprocess the data. This would allow analysts to make more educated cluster judgments during the review phase by preventing a small number of relevant variables from overriding the distance estimations. In order to determine how much of a student's daily nutritional needs would be satisfied by XX cereal, an analyst may examine the cluster average while examining the clusters. Informed decisions regarding which "healthy" cereal clusters to choose would be made possible by the workers thanks to this.