Assignment_5

2025-11-11

Loading packages

```
library(readr)
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(class)
library(gmodels)
library(tidyverse)
```

```
## ── Attaching core tidyverse packages ──────────────────────── tidyverse
2.0.0 ──
## ✔ forcats   1.0.1     ✔ stringr   1.5.2
## ✔ ggplot2   4.0.0     ✔ tibble    3.3.0
## ✔ lubridate 1.9.4     ✔ tidyr     1.3.1
## ✔ purrr     1.1.0
```

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

```
library(factoextra)
```

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

```
library(flexclust)
library(stats)
library(cluster)
library(caret)
```

```
## Loading required package: lattice
##
## Attaching package: 'lattice'
```

```
##
## The following objects are masked from 'package:flexclust':
##
##     barchart, bwplot, densityplot, histogram
##
##
## Attaching package: 'caret'
##
## The following object is masked from 'package:purrr':
##
##     lift
```

Importing the dataset

```
cereals <- read_csv("./Cereals.csv")
```

```
## Rows: 77 Columns: 16
## ── Column specification
────────────────────────────────────────────────────────
## Delimiter: ","
## chr  (3): name, mfr, type
## dbl (13): calories, protein, fat, sodium, fiber, carbo, sugars, potass,
vita...
##
## ℹ Use `spec()` to retrieve the full column specification for this data.
## ℹ Specify the column types or set `show_col_types = FALSE` to quiet this
message.
```

```
summary(cereals)       #77 observations
```

```
##      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
##
```

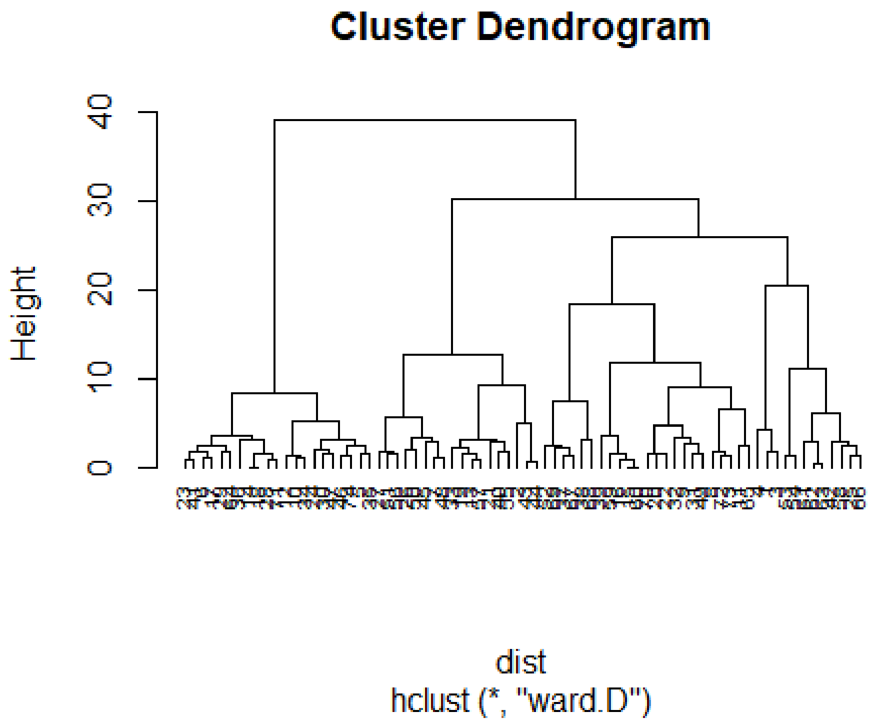
Data procesing

```
cereals <- na.omit(cereals) #removing the observation with null values
summary(cereals)            #3 observations have been removed, now the total
is 74
```

```
##      name               mfr                type              calories
##  Length:74          Length:74          Length:74          Min.   : 50
##  Class :character   Class :character   Class :character   1st Qu.:100
##  Mode  :character   Mode  :character   Mode  :character   Median :110
##                                                           Mean   :107
##                                                           3rd Qu.:110
##                                                           Max.   :160
##     protein           fat        sodium          fiber            carbo
##  Min.   :1.000   Min.   :0   Min.   :  0.0   Min.   : 0.000   Min.   :
5.00
##  1st Qu.:2.000   1st Qu.:0   1st Qu.:135.0   1st Qu.: 0.250   1st
Qu.:12.00
##  Median :2.500   Median :1   Median :180.0   Median : 2.000   Median
:14.50
##  Mean   :2.514   Mean   :1   Mean   :162.4   Mean   : 2.176   Mean
:14.73
##  3rd Qu.:3.000   3rd Qu.:1   3rd Qu.:217.5   3rd Qu.: 3.000   3rd
Qu.:17.00
##  Max.   :6.000   Max.   :5   Max.   :320.0   Max.   :14.000   Max.
:23.00
##      sugars           potass          vitamins          shelf
##  Min.   : 0.000   Min.   : 15.00   Min.   :  0.00   Min.   :1.000
##  1st Qu.: 3.000   1st Qu.: 41.25   1st Qu.: 25.00   1st Qu.:1.250
##  Median : 7.000   Median : 90.00   Median : 25.00   Median :2.000
##  Mean   : 7.108   Mean   : 98.51   Mean   : 29.05   Mean   :2.216
##  3rd Qu.:11.000   3rd Qu.:120.00   3rd Qu.: 25.00   3rd Qu.:3.000
##  Max.   :15.000   Max.   :330.00   Max.   :100.00   Max.   :3.000
##      weight           cups             rating
##  Min.   :0.500   Min.   :0.2500   Min.   :18.04
##  1st Qu.:1.000   1st Qu.:0.6700   1st Qu.:32.45
##  Median :1.000   Median :0.7500   Median :40.25
##  Mean   :1.031   Mean   :0.8216   Mean   :42.37
##  3rd Qu.:1.000   3rd Qu.:1.0000   3rd Qu.:50.52
##  Max.   :1.500   Max.   :1.5000   Max.   :93.70

#from the summary, it is clear that the value of sodium, potassium will
influence the model due to its high magnitude nature, if not normalized

cereals.num <- cereals[, 4:16]  #creating dataset only with numeric variables
```

Task 1: Hierarchical clustering and Agnes

```
#Applying hierarchical clustering to the data using Euclidean distance to the
normalized measurements.
df <- scale(cereals.num)   #normalizing data
dist <- dist(df, method="euclidean")   #calculating euclidean distance matrix

hc.ward <- hclust(dist, method="ward")

## The "ward" method has been renamed to "ward.D"; note new "ward.D2"

plot(hc.ward, cex=0.6, hang=-1)
```

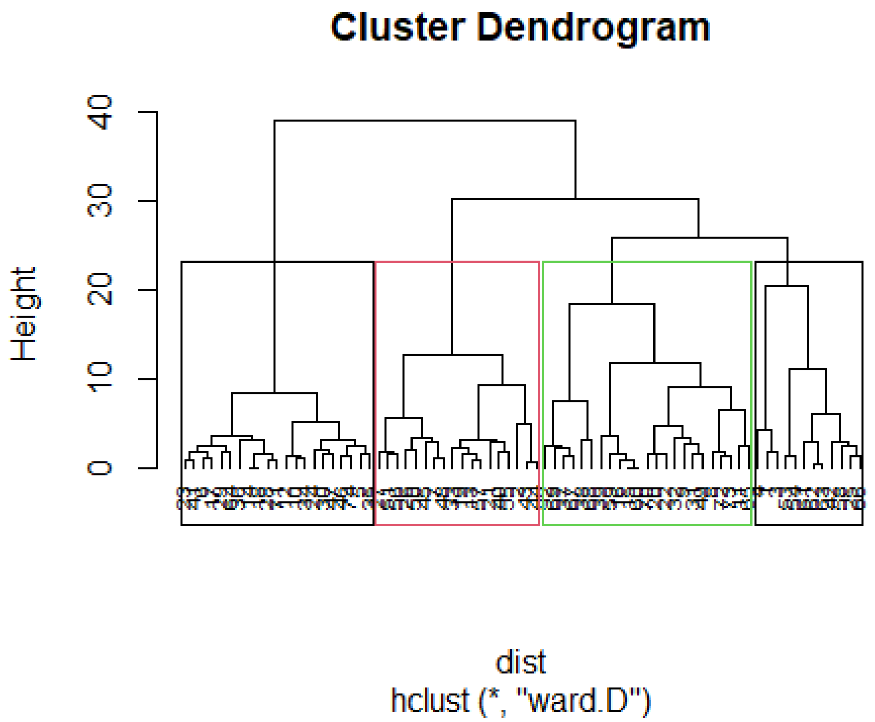


```
#Agnes clustering with different linkage methods, using the normalized data
hc_single <- agnes(df, method="single")
hc_complete <- agnes(df, method="complete")
hc_average <- agnes(df, method="average")
hc_ward <- cluster::agnes(df, method="ward")
#comparing agglomerative coefficients
print(hc_single$ac)
```

```
## [1] 0.6067859

print(hc_complete$ac)

## [1] 0.8353712

print(hc_average$ac)

## [1] 0.7766075

print(hc_ward$ac)

## [1] 0.9046042

#Even if I use the euclidean distance data with agnes instead of the only
normalized data, it shows the same result.
hc_ward1 <- agnes(dist, method="ward")
print(hc_ward1$ac)

## [1] 0.9046042

#From agglomerative coefficient values, ward linkage is the best method for
this dataset, as it shows the highest value, which is 0.9046042, among all
four methods.
```

Task 2: Choosing the cluster number

```
#From the lecture slides, we learned that agnes ( ) and hclust ( ) functions
behave very similarly, so I am using ward linkage here to find the cluster
number based on euclidean distance matrix
hc.ward <- hclust(dist, method="ward")

## The "ward" method has been renamed to "ward.D"; note new "ward.D2"

plot(hc.ward, cex=0.6, hang=-1)
#visualization of clusters
rect.hclust(hc.ward,k=4,border=1:3)
```



```
#adding the cluster number with the original dataset
df <- as.data.frame(df)
df.clusters <- cutree(hc.ward, k = 4)
df$cluster <- df.clusters
table(df.clusters)
```

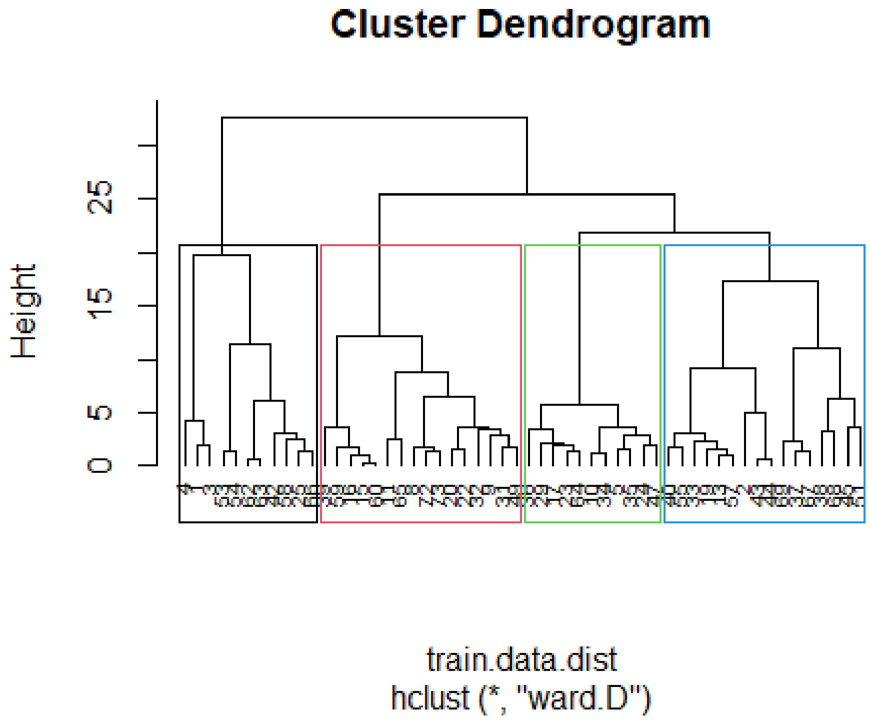
```
## df.clusters
##  1  2  3  4
## 12 18 21 23
```

```
#From the tree structure, 3 or 4 clusters would be a good separation of data.
If cut the tree into 5 or more clusters then the chances of getting small
groups are high. Also, then I will need to jump a larger vertical gaps.
Finally, between those choice, I will proceed with cluster 4.
```

Task 3: Stability checking

```
set.seed(246)
#Partitioning the data (e.g., 70% training, 30% test)
train.index <- createDataPartition(1:nrow(df), p = 0.7, list = FALSE)
train.data=df[train.index,]      #70%
test.data=df[-train.index,]    #30%

#clustering partition A (training data)
train.data.dist <- dist(train.data, method="euclidean")
hc.clusterA <- hclust(train.data.dist, method="ward")  #making cluster
partition A using Ward linkage
```

```
## The "ward" method has been renamed to "ward.D"; note new "ward.D2"

#doing this part for my visualization
plot(hc.clusterA, cex=0.6, hang=-1)
rect.hclust(hc.clusterA,k=4,border=1:4)
```



```
#calculating training data cluster centroids
train_clusters <- cutree(hc.clusterA, k = 4)
train.data <- as.data.frame(train.data)
train.data$cluster <- train_clusters
centroid.A <- aggregate(train.data, by = list(Cluster = train_clusters),
mean)

#****I couldn't solve the next part. I think this part is not covered in the
class****#
```

Task 4: Healthy diet cereal clustering

```
#To make the cluster of healthy diets, I am using the hierarchical clustering
and ward linkage method. The code will be almost same as task-1
diet <- cereals
diet <- na.omit(diet) #removing the observation with null values
summary(diet)       #from the summary, it is clear that the value of
potassium will influence the model due to its high magnitude nature, if not
normalized
```

```
##      name               mfr                type              calories
##  Length:74          Length:74          Length:74          Min.   : 50
##  Class :character   Class :character   Class :character   1st Qu.:100
##  Mode  :character   Mode  :character   Mode  :character   Median :110
##                                                           Mean   :107
##                                                           3rd Qu.:110
##                                                           Max.   :160
##     protein           fat        sodium          fiber           carbo
##  Min.   :1.000   Min.   :0   Min.   :  0.0   Min.   : 0.000   Min.   :
5.00
##  1st Qu.:2.000   1st Qu.:0   1st Qu.:135.0   1st Qu.: 0.250   1st
Qu.:12.00
##  Median :2.500   Median :1   Median :180.0   Median : 2.000   Median
:14.50
##  Mean   :2.514   Mean   :1   Mean   :162.4   Mean   : 2.176   Mean
:14.73
##  3rd Qu.:3.000   3rd Qu.:1   3rd Qu.:217.5   3rd Qu.: 3.000   3rd
Qu.:17.00
##  Max.   :6.000   Max.   :5   Max.   :320.0   Max.   :14.000   Max.
:23.00
##      sugars          potass          vitamins         shelf
##  Min.   : 0.000   Min.   : 15.00   Min.   :  0.00   Min.   :1.000
##  1st Qu.: 3.000   1st Qu.: 41.25   1st Qu.: 25.00   1st Qu.:1.250
##  Median : 7.000   Median : 90.00   Median : 25.00   Median :2.000
##  Mean   : 7.108   Mean   : 98.51   Mean   : 29.05   Mean   :2.216
##  3rd Qu.:11.000   3rd Qu.:120.00   3rd Qu.: 25.00   3rd Qu.:3.000
##  Max.   :15.000   Max.   :330.00   Max.   :100.00   Max.   :3.000
##      weight          cups            rating
##  Min.   :0.500   Min.   :0.2500   Min.   :18.04
##  1st Qu.:1.000   1st Qu.:0.6700   1st Qu.:32.45
##  Median :1.000   Median :0.7500   Median :40.25
##  Mean   :1.031   Mean   :0.8216   Mean   :42.37
##  3rd Qu.:1.000   3rd Qu.:1.0000   3rd Qu.:50.52
##  Max.   :1.500   Max.   :1.5000   Max.   :93.70
```

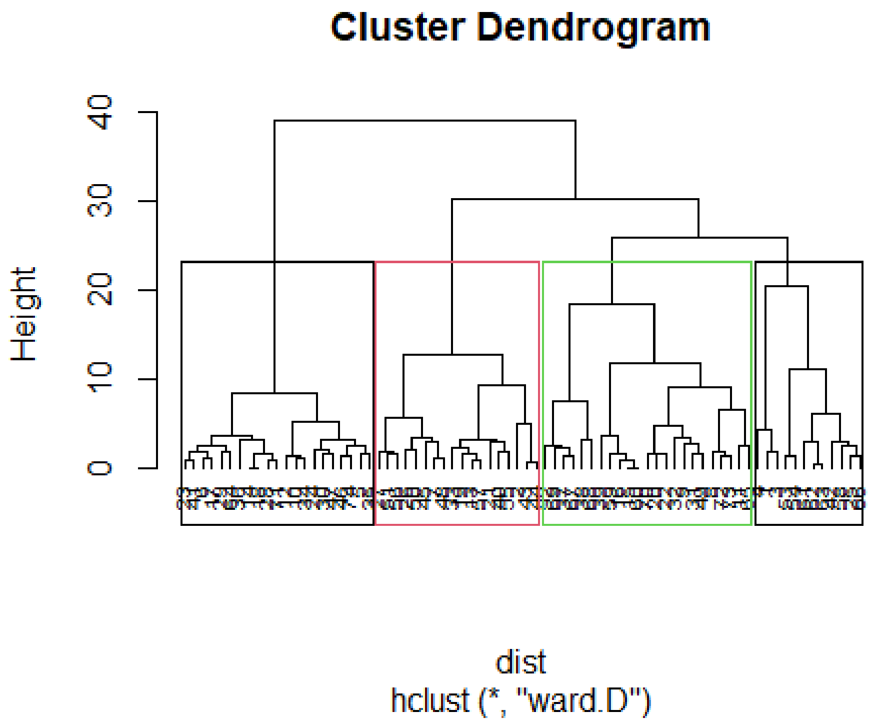
```
diet.num <- diet[, 4:16] #removing the non-numeric variables

diet <- scale(diet.num)   #normalizing data
summary(diet)            # now all variables are in same scale
```

```
##     calories          protein             fat              sodium
##  Min.   :-2.8738   Min.   :-1.40687   Min.   :-0.9932   Min.   :-1.9616
##  1st Qu.:-0.3541   1st Qu.:-0.47733   1st Qu.:-0.9932   1st Qu.:-0.3306
##  Median : 0.1498   Median :-0.01256   Median : 0.0000   Median : 0.2131
##  Mean   : 0.0000   Mean   : 0.00000   Mean   : 0.0000   Mean   : 0.0000
##  3rd Qu.: 0.1498   3rd Qu.: 0.45221   3rd Qu.: 0.0000   3rd Qu.: 0.6661
##  Max.   : 2.6695   Max.   : 3.24083   Max.   : 3.9729   Max.   : 1.9045
##      fiber            carbo              sugars            potass
##  Min.   :-0.89778   Min.   :-2.50014   Min.   :-1.6306   Min.   :-1.1783
##  1st Qu.:-0.79462   1st Qu.:-0.70143   1st Qu.:-0.9424   1st Qu.:-0.8079
##  Median :-0.07249   Median :-0.05903   Median :-0.0248   Median :-0.1201  
##  Mean   : 0.00000   Mean   : 0.00000   Mean   : 0.0000   Mean   : 0.0000  
##  3rd Qu.: 0.34015   3rd Qu.: 0.58337   3rd Qu.: 0.8928   3rd Qu.: 0.3031  
##  Max.   : 4.87925   Max.   : 2.12512   Max.   : 1.8104   Max.   : 3.2660  
##     vitamins            shelf              weight              cups        
##  Min.   :-1.3032   Min.   :-1.4617   Min.   :-3.4600   Min.   :-2.4251  
##  1st Qu.:-0.1818   1st Qu.:-1.1612   1st Qu.:-0.2008   1st Qu.:-0.6432  
##  Median :-0.1818   Median :-0.2599   Median :-0.2008   Median :-0.3038  
##  Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000   Mean   : 0.0000  
##  3rd Qu.:-0.1818   3rd Qu.: 0.9420   3rd Qu.:-0.2008   3rd Qu.: 0.7568  
##  Max.   : 3.1822   Max.   : 0.9420   Max.   : 3.0583   Max.   : 2.8780  
##      rating       
##  Min.   :-1.7336  
##  1st Qu.:-0.7071  
##  Median :-0.1510  
##  Mean   : 0.0000  
##  3rd Qu.: 0.5807  
##  Max.   : 3.6578
```

```r
dist <- dist(diet, method="euclidean")   #calculating euclidean distance matrix

#performing hierarchical clustering with ward linkage as it's agglomerative coefficient value is high (got from task-1)
hc.ward <- hclust(dist, method="ward")
```

```
## The "ward" method has been renamed to "ward.D"; note new "ward.D2"
```

```r
plot(hc.ward, cex=0.6, hang=-1)
rect.hclust(hc.ward,k=4,border=1:3)
```



```
#adding the cluster number with the the scaled dataset
diet <- as.data.frame(df)
diet.clusters <- cutree(hc.ward, k = 4)
diet$cluster <- diet.clusters
#some cluster summary
table(df.clusters)

## df.clusters
##  1  2  3  4
## 12 18 21 23

cereal.diet <- aggregate(diet, by = list(diet$cluster), FUN = mean)

#I will use the protein, fiber, vitamins, fat and potassium variables to
interprate the clusters to select the best set of cereals
cereal.diet %>% group_by(cluster) %>% select(calories, protein, fiber,
vitamins, fat, potass, sodium, sugars, carbo)

## Adding missing grouping variables: `cluster`

## # A tibble: 4 × 10
## # Groups:   cluster [4]
##   cluster calories protein  fiber vitamins    fat potass sodium sugars
carbo
##     <dbl>    <dbl>   <dbl>  <dbl>    <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
<dbl>
## 1       1 -1.49      0.297  0.890   -0.649 -0.745  0.662 -1.41  -1.02  -
```

```
0.402
## 2       2  0.766     0.607  0.386   -0.244  1.05   0.730 -0.123  0.459 -
0.302
## 3       3  0.198    -0.920 -0.662   -0.182  0      -0.742  0.121  0.958 -
0.542
## 4       4 -0.00355   0.210 -0.162    0.696 -0.432 -0.240  0.723 -0.703
0.941

#The following conclusions were obtained based on the averages of each
cluster:
#Cluster 1 = High Protein, High Fiber, High Potassium
#Cluster 2 = High Calories, High Protein, High Fiber,High Fat, High
Potassium, High Sugars
#Cluster 3 = High Calories, No Fat, High Potassium, High Carbohydrates
#Cluster 4 = High Protein, High Vitamins, High Sodium, High Carbohydrates

#The choice of health cereals will depend on what nutrition we want to
provide the children. For example, without no doubt high protein, high
vitamins, high fiber cereals are good for children, at the same time
carbohydrate, calories, sodium, fat are good for children too but to a
certain limit, for which I need expert help.

#Finally, I am in support of normalizing the dataset. Otherwise Variables
with larger numerical ranges (e.g., sodium, potassium) would influence the
distance calculations.
```