Assignment-5

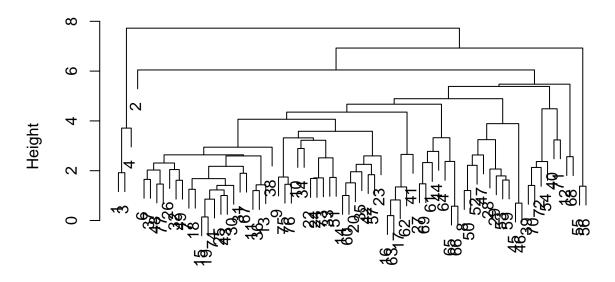
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```
# Load the data
cereals <- read.csv("C:/Users/Anjali/Desktop/Anjali_FML_Assignment 5/Cereals.csv")</pre>
# Remove rows with missing values
cereals <- na.omit(cereals)</pre>
install.packages("cluster")
## Installing package into 'C:/Users/Anjali/AppData/Local/R/win-library/4.3'
## (as 'lib' is unspecified)
##
##
     There is a binary version available but the source version is later:
##
           binary source needs_compilation
## cluster 2.1.4 2.1.5
## installing the source package 'cluster'
## Warning in install.packages("cluster"): installation of package 'cluster' had
## non-zero exit status
install.packages("factoextra")
## Installing package into 'C:/Users/Anjali/AppData/Local/R/win-library/4.3'
## (as 'lib' is unspecified)
\mbox{\tt \#\#} package 'factoextra' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
## C:\Users\Anjali\AppData\Local\Temp\RtmpU33xMs\downloaded_packages
install.packages("tidyverse")
## Installing package into 'C:/Users/Anjali/AppData/Local/R/win-library/4.3'
## (as 'lib' is unspecified)
## package 'tidyverse' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
## C:\Users\Anjali\AppData\Local\Temp\RtmpU33xMs\downloaded_packages
```

```
library(tidyverse)
## Warning: package 'tidyverse' was built under R version 4.3.2
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr 1.1.3 v readr
                                   2.1.4
## v forcats 1.0.0 v stringr 1.5.0
## v ggplot2 3.4.3 v tibble 3.2.1
## v lubridate 1.9.2
                     v tidyr
                                  1.3.0
## v purrr
             1.0.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag() masks stats::lag()
## i Use the conflicted package (<a href="http://conflicted.r-lib.org/">http://conflicted.r-lib.org/</a>) to force all conflicts to become error
library(cluster)
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
# Step 2: Hierarchical Clustering
# Identify numeric columns
numeric_columns <- sapply(cereals, is.numeric)</pre>
# Normalize only the numeric columns
normalized_cereals <- scale(cereals[, numeric_columns])</pre>
# Apply hierarchical clustering with Ward's method
ward_cluster <- agnes(normalized_cereals)</pre>
# Visualize dendrogram for Ward's method
plot(ward_cluster, which.plots = 2, main = "Dendrogram - Ward's Method")
```

Dendrogram - Ward's Method



normalized_cereals Agglomerative Coefficient = 0.78

```
# Step 3: Cluster Stability and Healthy Cereals
\# Create cluster partitions A and B
set.seed(123)
partition_A <- sample(1:2, nrow(normalized_cereals), replace = TRUE)</pre>
partition_B <- 3 - partition_A</pre>
# Fit cluster on partition A
cluster_A <- cutree(ward_cluster, k = 3)</pre>
\# Use cluster centroids from A to assign records in partition B
cluster_B <- cluster_A[partition_B]</pre>
# Assess cluster consistency
consistency <- sum(cluster_A == cluster_B) / length(cluster_B)</pre>
# Identify healthy cereals cluster
# (Based on your analysis and specific criteria for 'healthy')
# Example: Let's assume 'healthy' cereals have low sugar and high fiber
healthy_cereals_cluster <- cluster_A[which(cereals$sugars < 5 & cereals$fiber > 5)]
# Print or visualize the results
cat("Cluster Consistency:", consistency, "\n")
```

Cluster Consistency: 0.5810811

```
cat("Healthy Cereals Cluster:", healthy_cereals_cluster, "\n")
```

Healthy Cereals Cluster: 1