

Assignment 5

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```
library(cluster)
library(stats)
library(factoextra)

## Loading required package: ggplot2

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

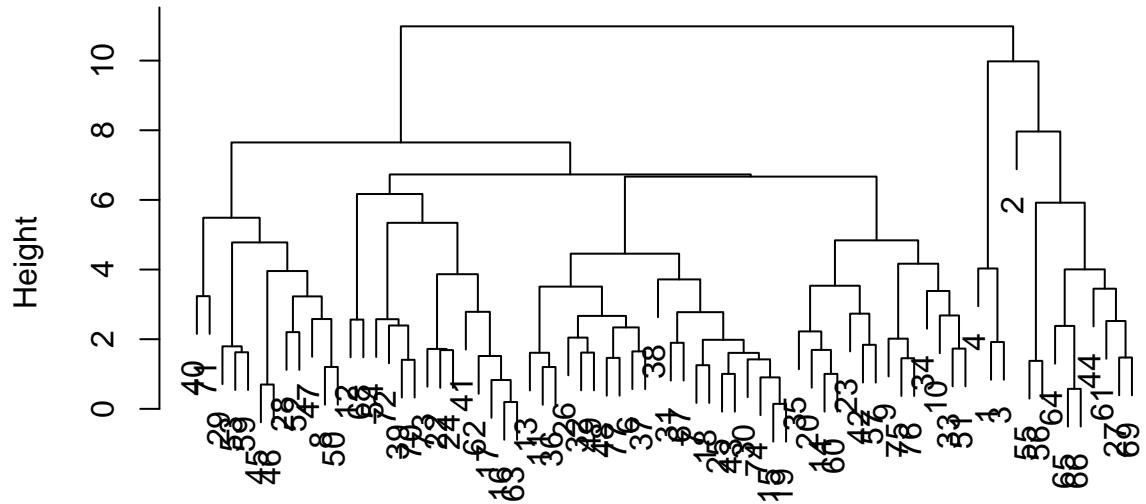
Importing the csv file, pulling out only the numerical data, getting rid of the missing data, and then normalizing the data. The data should be normalized because the weights of the data points are arbitrary and would have to be weighted manually to be useful.

```
cereals<-read.csv("cereals.csv")
numericaldata = data.frame(cereals[,4:16])
OmitMissing = na.omit(numericaldata)
Normalize = scale(OmitMissing)
```

Using the normalized data to do hierarchical clustering.

```
distance<-dist(Normalize, method = "euclidian")
clustering_heirarchical = hclust(distance, method = "complete")
plot(clustering_heirarchical)
```

Cluster Dendrogram



```
distance
hclust (*, "complete")
```

Rounding all of the values to 3 decimal places.

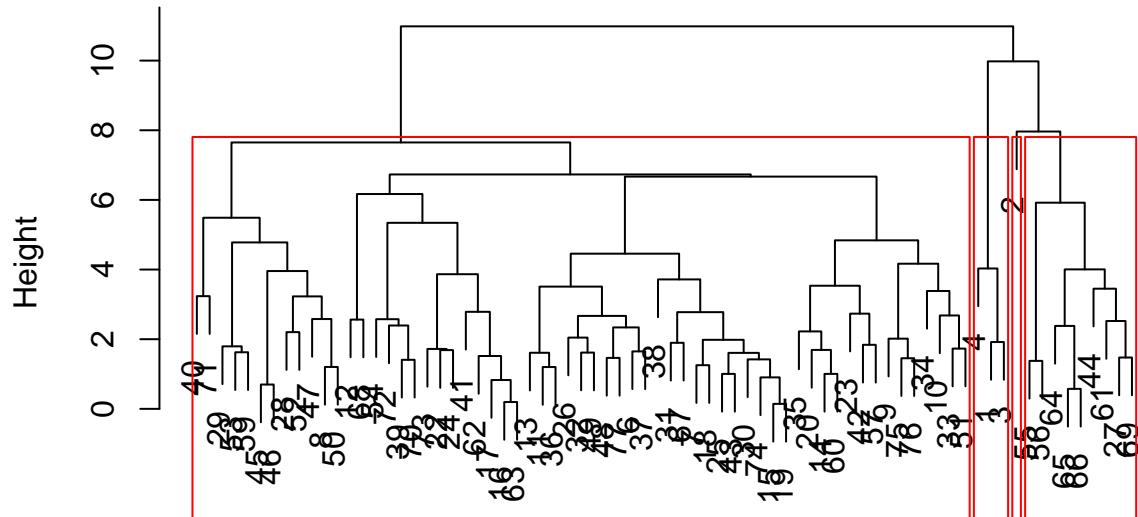
```
round(clustering_heirarchical$height, 3)
```

```
## [1] 0.143 0.196 0.575 0.698 0.828 0.904 1.003 1.004 1.201 1.203
## [11] 1.254 1.378 1.408 1.421 1.454 1.463 1.474 1.517 1.608 1.611
## [21] 1.616 1.625 1.650 1.687 1.692 1.720 1.730 1.795 1.839 1.897
## [31] 1.919 1.982 2.015 2.046 2.203 2.224 2.339 2.381 2.394 2.522
## [41] 2.563 2.574 2.579 2.668 2.682 2.734 2.776 2.787 3.229 3.236
## [51] 3.385 3.451 3.510 3.535 3.717 3.866 3.957 4.005 4.031 4.168
## [61] 4.456 4.779 4.839 5.342 5.488 5.920 6.169 6.669 6.731 7.650
## [71] 7.964 9.979 10.984
```

-Using hierarchical clustering and separating the values into 4 groups.

```
plot(clustering_heirarchical)
rect.hclust(clustering_heirarchical, k = 4, border = "red")
```

Cluster Dendrogram



```
distance
hclust (*, "complete")
```

Using agnes to compare the different clustering methods. Because ward's method is the highest value at .90, that means that it is the best of the 4 methods.

```
singleCH = agnes(Normalize, method = "single")
completeCH = agnes(Normalize, method = "complete")
averageCH = agnes(Normalize, method = "average")
wardCH = agnes(Normalize, method = "ward")
print(singleCH$ac)

## [1] 0.6067859

print(completeCH$ac)

## [1] 0.8353712

print(averageCH$ac)

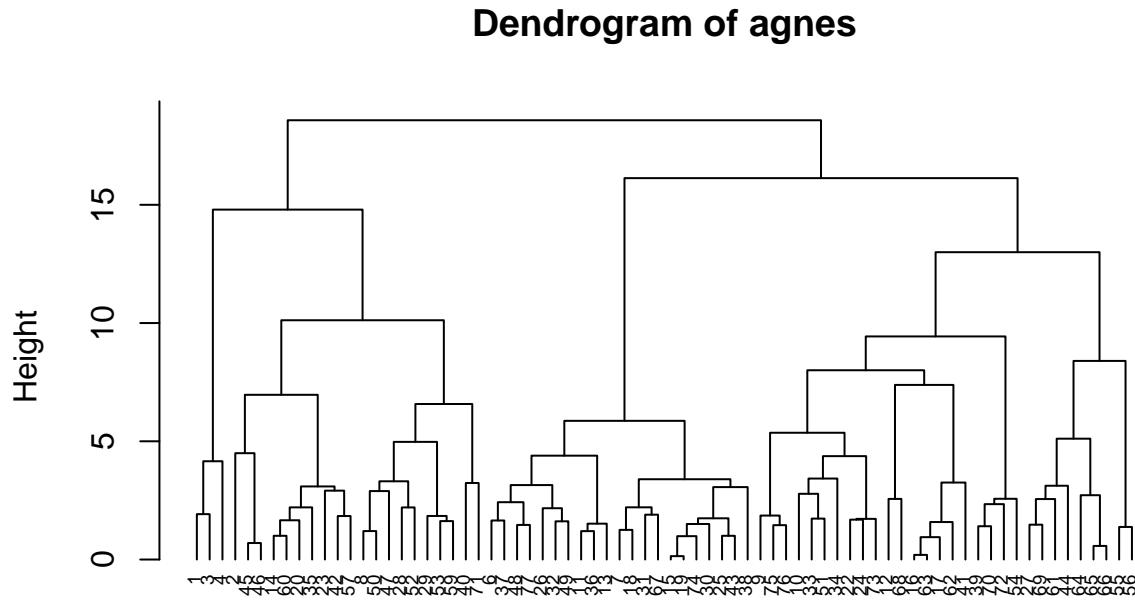
## [1] 0.7766075

print(wardCH$ac)

## [1] 0.9046042
```

Using ward's method for clustering.

```
pltree(wardCH, cex = 0.6, hang = -1, main = "Dendrogram of agnes")
```



Normalize
agnes (*, "ward")

Using ward's method to cluster the data into 4 subgroups.

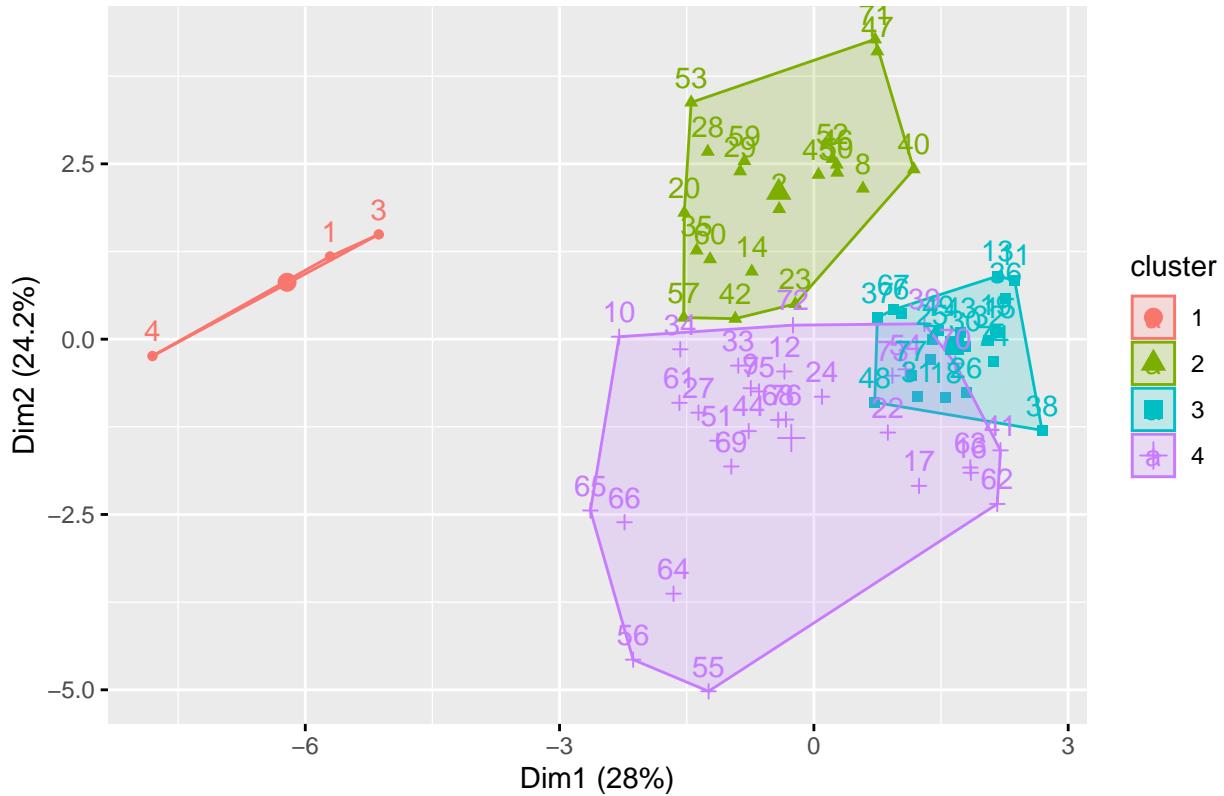
```
Hcluster1 <- hclust(distance, method = "ward.D2")
subgrp <- cutree(Hcluster1, k = 4)
table(subgrp)
```

```
## subgrp
## 1 2 3 4
## 3 20 21 30
```

A visualization of the clusters.

```
cereals <- as.data.frame(cbind(Normalize, subgrp))
fviz_cluster(list(data = Normalize, cluster = subgrp))
```

Cluster plot



```
mean(Clust[Clust$subgrp==2, "rating"])
```

```
## [1] 38.26161
```

```
mean(Clust[Clust$subgrp==3, "rating"])
```

```
## [1] 28.84825
```

```
mean(Clust[Clust$subgrp==4, "rating"])
```

```
## [1] 51.43111
```