Hierarchical Clustering of the 'mtcars' Data

Michael Levine

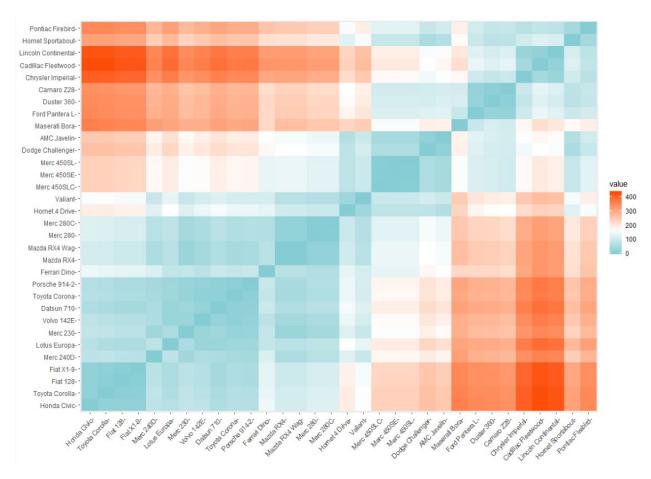
Statistical Learning and Data Mining (STAT 5603-401, Spring 2019)

The R dataset *mtcars* consists of measurements from a collection of 32 automobiles. In the dataset is 11 separate numeric variables. Using 'head', let's look at the first five rows of the dataset:

```
head(mtcars)
                                                wt qsec vs am gear carb
                      mpg cyl disp hp drat
                      21.0 6 160 110 3.90 2.620 16.46 0 1
## Mazda RX4
                                                                        4
## Mazda RX4 Wag
                     21.0 6 160 110 3.90 2.875 17.02 0 1
                                                                        1
## Datsun 710
                     22.8 4 108 93 3.85 2.320 18.61 1 1
## Hornet 4 Drive
                     21.4 6 258 110 3.08 3.215 19.44 1 0
                                                                        1
## Hornet Sportabout 18.7 8 360 175 3.15 3.440 17.02 0 0 ## Valiant 18.1 6 225 105 2.76 3.460 20.22 1 0
                                                                   3
                                                                        2
```

First, let's use the 'dist' function to find the distance between each car. We'll then plot the distance matrix using the *fviz_dist* function.

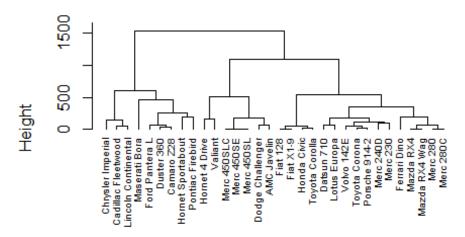
```
distance <- get_dist(mtcars)
fviz_dist(distance, gradient = list(low = "#00AFBB", mid = "white", high = "#FC4E07"))</pre>
```



Next, let's perform a hierarchical clustering using the distance matrix that we created in the previous step. We'll then plot the dendrogram into four separate clusters.

```
df2 <- distance
df <- na.omit(df2)
df <- scale(df2)
d <- dist(df2, method = "euclidean")
hc1 <- hclust(d, method = "complete")
plot(hc1, cex = 0.6, hang = -1)</pre>
```

Cluster Dendrogram



d hclust (*, "complete")

```
# Ward's method
hc5 <- hclust(d, method = "complete" )

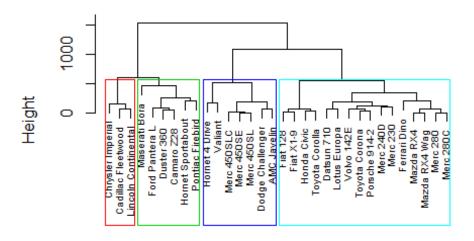
# Cut tree into 4 groups
sub_grp <- cutree(hc5, k = 4)

# Number of members in each cluster
table(sub_grp)

## sub_grp
## 1 2 3 4
## 16 7 6 3

plot(hc5, cex = 0.6)
rect.hclust(hc5, k = 4, border = 2:5)</pre>
```

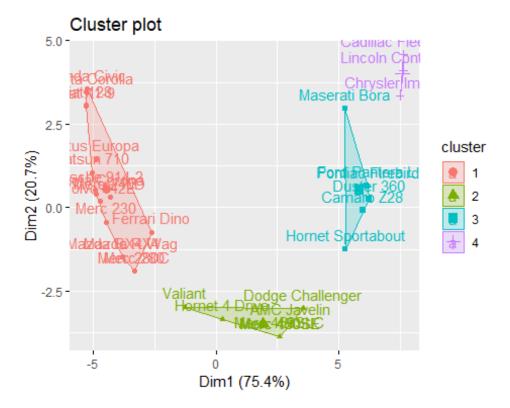
Cluster Dendrogram



d hclust (*, "complete")

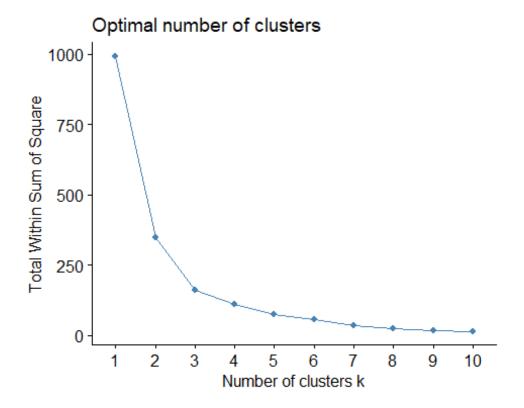
As we can see in our dendrogram, we now have four separate clusters (as we specified in our code). Now let's plot this in an x-y graph.

fviz_cluster(list(data = df, cluster = sub_grp))



Here we can see the clusters in a two-dimensional plane. Now let's use use the Elbow Method to select the optimal number of clusters.

fviz_nbclust(df, FUN = hcut, method = "wss")



Using the Elbow Method, we can see that the optimal number of clusters is three. This is because the 'elbow' of the curve is at three along the x-axis. Now let's cut the dendrogram at three, as well.

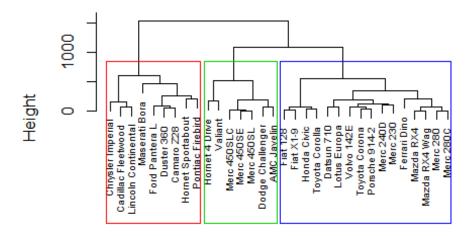
```
hc5 <- hclust(d, method = "complete" )
sub_grp <- cutree(hc5, k = 3)

table(sub_grp)

## sub_grp
## 1 2 3
## 16 7 9

plot(hc5, cex = 0.6)
rect.hclust(hc5, k = 3, border = 2:5)</pre>
```

Cluster Dendrogram



d hclust (*, "complete")

Now let's plot this in a two-dimensional plane.

```
fviz_cluster(list(data = df, cluster = sub_grp))
```

