This mini-project is based on the K-Means exercise from ‘R in Action’

Go here for the original blog post and solutions: http://www.r-bloggers.com/k-means-clustering-from-r-in-action/

Exercise 0:

Install these packages if you don’t have them already:

install.packages(c(“cluster”, “rattle.data”,“NbClust”))

Now load the data and look at the first few rows

```
data(wine, package="rattle.data")
head(wine)
```

```
##   Type Alcohol Malic  Ash Alcalinity Magnesium Phenols Flavanoids
## 1    1   14.23  1.71 2.43       15.6       127    2.80       3.06
## 2    1   13.20  1.78 2.14       11.2       100    2.65       2.76
## 3    1   13.16  2.36 2.67       18.6       101    2.80       3.24
## 4    1   14.37  1.95 2.50       16.8       113    3.85       3.49
## 5    1   13.24  2.59 2.87       21.0       118    2.80       2.69
## 6    1   14.20  1.76 2.45       15.2       112    3.27       3.39
##   Nonflavanoids Proanthocyanins Color  Hue Dilution Proline
## 1          0.28            2.29  5.64 1.04     3.92    1065
## 2          0.26            1.28  4.38 1.05     3.40    1050
## 3          0.30            2.81  5.68 1.03     3.17    1185
## 4          0.24            2.18  7.80 0.86     3.45    1480
## 5          0.39            1.82  4.32 1.04     2.93     735
## 6          0.34            1.97  6.75 1.05     2.85    1450
```

Exercise 1:

Remove the first column from the data and scale it using the scale() function

```
df = scale(wine[-1])
```

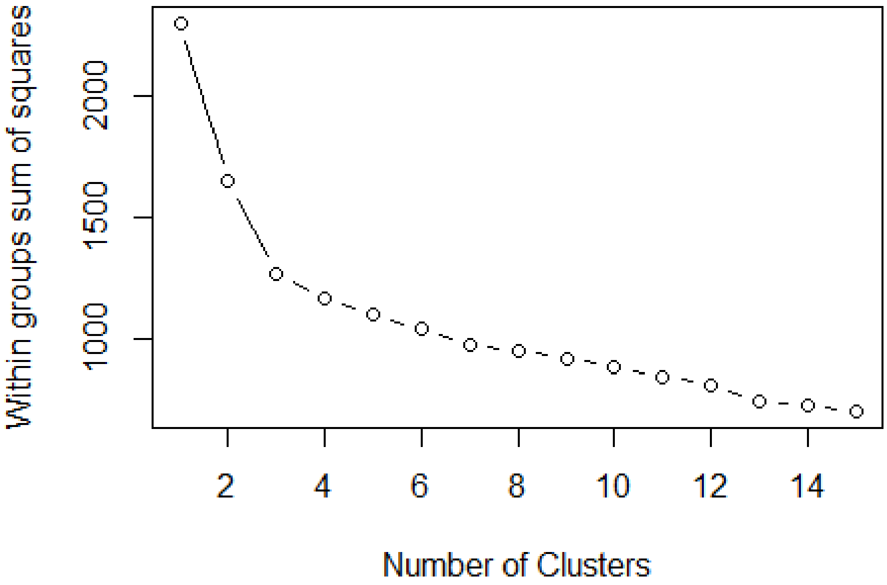
Now we’d like to cluster the data using K-Means. How do we decide how many clusters to use if you don’t know that already? We’ll try two methods.

Method 1: A plot of the total within-groups sums of squares against the number of clusters in a K-means solution can be helpful. A bend in the graph can suggest the appropriate number of clusters.

```
wssplot <- function(data, nc=15, seed=1234){
                  wss <- (nrow(data)-1)*sum(apply(data,2,var))
                      for (i in 2:nc){
                {set.seed(seed)
                    wss[i] <- sum(kmeans(data, centers=i)$withinss)}

              plot(1:nc, wss, type="b", xlab="Number of Clusters",
                            ylab="Within groups sum of squares")
       }

wssplot(df)
```



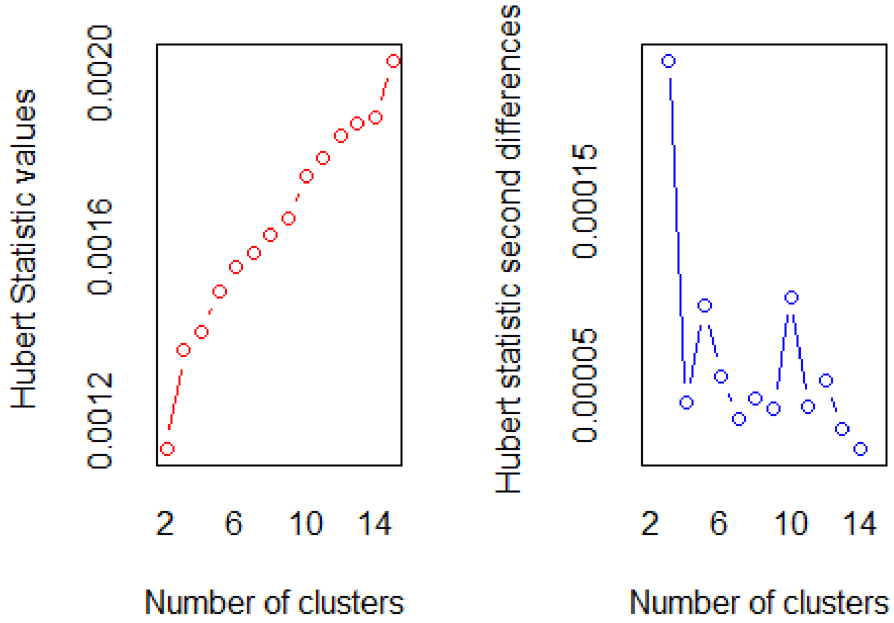
Exercise 2:

* How many clusters does this method suggest?
* Why does this method work? What's the intuition behind it?
* Look at the code for wssplot() and figure out how it works

This method suggests 3 clusters. The function for wssplot iterates the kmeans function across all columns within the df and extracts the $withinss value. Then, this figure is applied to each column and plotted.

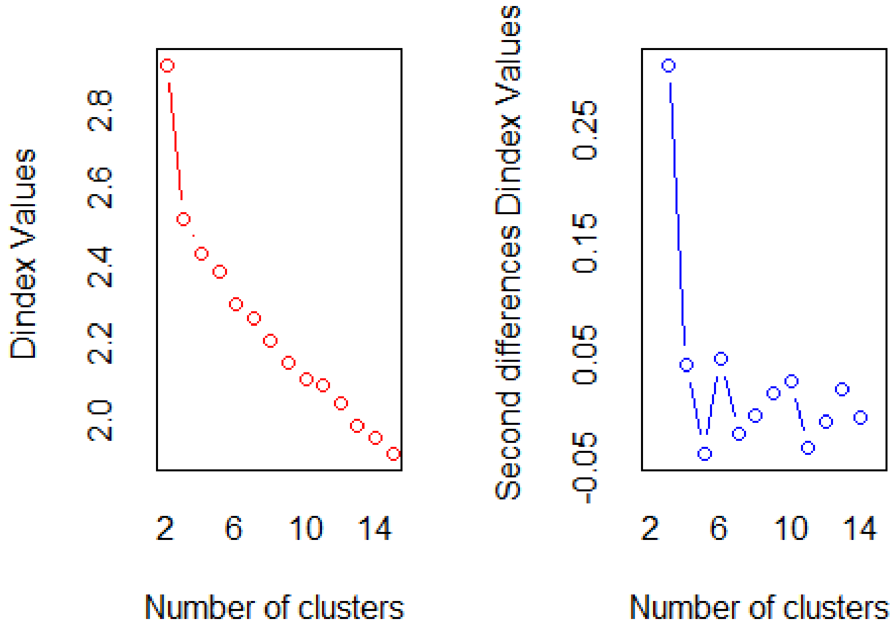
Method 2: Use the NbClust library, which runs many experiments and gives a distribution of potential number of clusters.

```
library(NbClust)
set.seed(1234)
nc <- NbClust(df, min.nc=2, max.nc=15, method="kmeans")
```



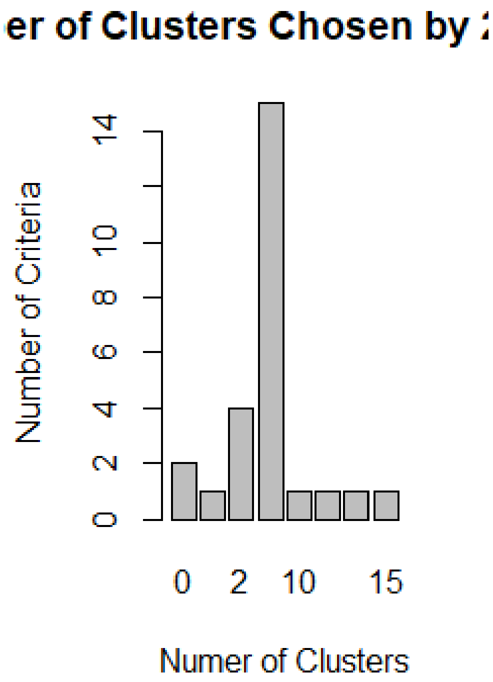
```
## *** : The Hubert index is a graphical method of determining the number of
clusters.
##                 In the plot of Hubert index, we seek a significant knee
that corresponds to a
##                 significant increase of the value of the measure i.e the
significant peak in Hubert
```

```
##                  index second differences plot.
##
```



```
## *** : The D index is a graphical method of determining the number of
clusters.
##                  In the plot of D index, we seek a significant knee (the
significant peak in Dindex
##                  second differences plot) that corresponds to a significant
increase of the value of
##                  the measure.
##
## *******************************************************************
## * Among all indices:
## * 4 proposed 2 as the best number of clusters
## * 15 proposed 3 as the best number of clusters
## * 1 proposed 10 as the best number of clusters
## * 1 proposed 12 as the best number of clusters
## * 1 proposed 14 as the best number of clusters
## * 1 proposed 15 as the best number of clusters
##
##                     ***** Conclusion *****
##
## * According to the majority rule, the best number of clusters is  3
##
##
## *******************************************************************
```

```
barplot(table(nc$Best.n[1,]),
              xlab="Numer of Clusters", ylab="Number of Criteria",
                    main="Number of Clusters Chosen by 26 Criteria")
```



Exercise 3:

How many clusters does this method suggest?

This method suggested 3 clusters according to majority rule from 15 indices.

Exercise 4:

Once you’ve picked the number of clusters, run k-means using this number of clusters. Output the result of calling kmeans() into a variable fit.km

```
fit.km <- kmeans(df, 3, nstart=25)
```

Now we want to evaluate how well this clustering does.

Exercise 5:

*Using the table() function, show how the clusters in fit.km$clusters # compares to the actual wine types in wine$Type.
*Would you consider this a good clustering?

```
wine_val = table(wine$Type, fit.km$cluster)
```

After reviewing the attached link, my numbers are in reverse order, but the actual figures are correct. After reviewing the table, 6 predictions were incorrect, mainly in the second cluster.

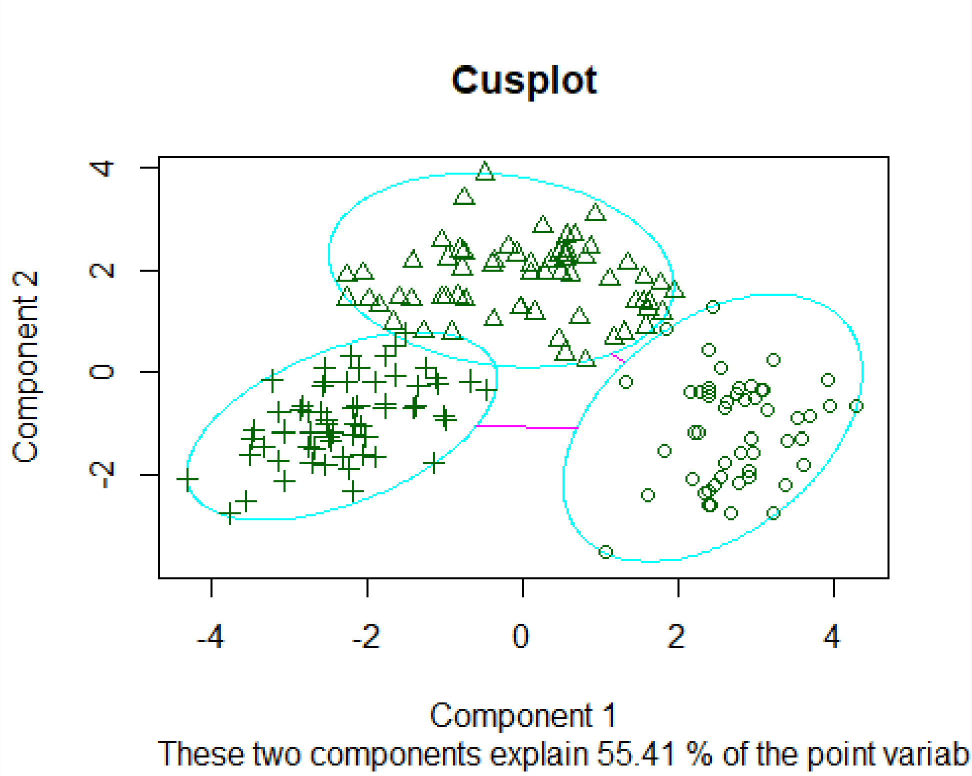
Exercise 6:

* Visualize these clusters using function clusplot() from the cluster library
* Would you consider this a good clustering?

```
library(cluster)

## Warning: package 'cluster' was built under R version 3.4.4

clusplot(df, fit.km$cluster, main = "Cusplot")
```


Cusplot
Component 2
Component 1
These two components explain 55.41 % of the point variab