

Clustering - Wine

Chinpei Tang

This mini-project is based on the K-Means exercise from ‘R in Action’ - see <http://www.r-bloggers.com/k-means-clustering-from-r-in-action/>.

Exercise 0

- Install these packages if you don't have them already

```
library("cluster")
library("rattle")
```

```
## Rattle: A free graphical interface for data mining with R.
## Version 4.1.0 Copyright (c) 2006-2015 Togaware Pty Ltd.
## Type 'rattle()' to shake, rattle, and roll your data.
```

```
library("NbClust")
library("flexclust")
```

```
## Loading required package: grid
```

```
## Loading required package: lattice
```

```
## Loading required package: modeltools
```

```
## Loading required package: stats4
```

Exercise 1

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

Now load the data and look at the first few rows.

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

```
##   Type Alcohol Malic  Ash Alkalinity 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
```

```
summary(wine)
```

```
## Type      Alcohol      Malic      Ash      Alkalinity
## 1:59 Min. :11.03 Min. :0.740 Min. :1.360 Min. :10.60
## 2:71 1st Qu.:12.36 1st Qu.:1.603 1st Qu.:2.210 1st Qu.:17.20
## 3:48 Median :13.05 Median :1.865 Median :2.360 Median :19.50
##      Mean :13.00 Mean :2.336 Mean :2.367 Mean :19.49
##      3rd Qu.:13.68 3rd Qu.:3.083 3rd Qu.:2.558 3rd Qu.:21.50
##      Max. :14.83 Max. :5.800 Max. :3.230 Max. :30.00
## Magnesium Phenols Flavanoids Nonflavanoids
## Min. : 70.00 Min. :0.980 Min. :0.340 Min. :0.1300
## 1st Qu.: 88.00 1st Qu.:1.742 1st Qu.:1.205 1st Qu.:0.2700
## Median : 98.00 Median :2.355 Median :2.135 Median :0.3400
## Mean : 99.74 Mean :2.295 Mean :2.029 Mean :0.3619
## 3rd Qu.:107.00 3rd Qu.:2.800 3rd Qu.:2.875 3rd Qu.:0.4375
## Max. :162.00 Max. :3.880 Max. :5.080 Max. :0.6600
## Proanthocyanins Color Hue Dilution
## Min. :0.410 Min. : 1.280 Min. :0.4800 Min. :1.270
## 1st Qu.:1.250 1st Qu.: 3.220 1st Qu.:0.7825 1st Qu.:1.938
## Median :1.555 Median : 4.690 Median :0.9650 Median :2.780
## Mean :1.591 Mean : 5.058 Mean :0.9574 Mean :2.612
## 3rd Qu.:1.950 3rd Qu.: 6.200 3rd Qu.:1.1200 3rd Qu.:3.170
## Max. :3.580 Max. :13.000 Max. :1.7100 Max. :4.000
## Proline
## Min. : 278.0
## 1st Qu.: 500.5
## Median : 673.5
## Mean : 746.9
## 3rd Qu.: 985.0
## Max. :1680.0
```

```
str(wine)
```

```
## 'data.frame': 178 obs. of 14 variables:
## $ Type : Factor w/ 3 levels "1","2","3": 1 1 1 1 1 1 1 1 1 1 ...
## $ Alcohol : num 14.2 13.2 13.2 14.4 13.2 ...
## $ Malic : num 1.71 1.78 2.36 1.95 2.59 1.76 1.87 2.15 1.64 1.35 ...
## $ Ash : num 2.43 2.14 2.67 2.5 2.87 2.45 2.45 2.61 2.17 2.27 ...
## $ Alkalinity : num 15.6 11.2 18.6 16.8 21 15.2 14.6 17.6 14 16 ...
## $ Magnesium : int 127 100 101 113 118 112 96 121 97 98 ...
## $ Phenols : num 2.8 2.65 2.8 3.85 2.8 3.27 2.5 2.6 2.8 2.98 ...
## $ Flavanoids : num 3.06 2.76 3.24 3.49 2.69 3.39 2.52 2.51 2.98 3.15 ...
## $ Nonflavanoids : num 0.28 0.26 0.3 0.24 0.39 0.34 0.3 0.31 0.29 0.22 ...
## $ Proanthocyanins: num 2.29 1.28 2.81 2.18 1.82 1.97 1.98 1.25 1.98 1.85 ...
## $ Color : num 5.64 4.38 5.68 7.8 4.32 6.75 5.25 5.05 5.2 7.22 ...
## $ Hue : num 1.04 1.05 1.03 0.86 1.04 1.05 1.02 1.06 1.08 1.01 ...
```

```
## $ Dilution      : num  3.92 3.4 3.17 3.45 2.93 2.85 3.58 3.58 2.85 3.55 ...
## $ Proline        : int   1065 1050 1185 1480 735 1450 1290 1295 1045 1045 ...
```

There are 178 observations and 13 different chemical measurements of each of the wines.

Remove the type of wine so that we can use clustering algorithm to cluster the types.

```
wine.noType <- wine
wine.noType$Type <- NULL
summary(wine.noType)
```

```
##      Alcohol      Malic      Ash      Alcalinity
## Min.   :11.03   Min.   :0.740   Min.   :1.360   Min.   :10.60
## 1st Qu.:12.36   1st Qu.:1.603   1st Qu.:2.210   1st Qu.:17.20
## Median :13.05   Median :1.865   Median :2.360   Median :19.50
## Mean   :13.00   Mean   :2.336   Mean   :2.367   Mean   :19.49
## 3rd Qu.:13.68   3rd Qu.:3.083   3rd Qu.:2.558   3rd Qu.:21.50
## Max.   :14.83   Max.   :5.800   Max.   :3.230   Max.   :30.00
##      Magnesium      Phenols      Flavanoids      Nonflavanoids
## Min.   : 70.00   Min.   :0.980   Min.   :0.340   Min.   :0.1300
## 1st Qu.: 88.00   1st Qu.:1.742   1st Qu.:1.205   1st Qu.:0.2700
## Median : 98.00   Median :2.355   Median :2.135   Median :0.3400
## Mean   : 99.74   Mean   :2.295   Mean   :2.029   Mean   :0.3619
## 3rd Qu.:107.00   3rd Qu.:2.800   3rd Qu.:2.875   3rd Qu.:0.4375
## Max.   :162.00   Max.   :3.880   Max.   :5.080   Max.   :0.6600
##      Proanthocyanins      Color      Hue      Dilution
## Min.   :0.410   Min.   : 1.280   Min.   :0.4800   Min.   :1.270
## 1st Qu.:1.250   1st Qu.: 3.220   1st Qu.:0.7825   1st Qu.:1.938
## Median :1.555   Median : 4.690   Median :0.9650   Median :2.780
## Mean   :1.591   Mean   : 5.058   Mean   :0.9574   Mean   :2.612
## 3rd Qu.:1.950   3rd Qu.: 6.200   3rd Qu.:1.1200   3rd Qu.:3.170
## Max.   :3.580   Max.   :13.000   Max.   :1.7100   Max.   :4.000
##      Proline
## Min.   : 278.0
## 1st Qu.: 500.5
## Median : 673.5
## Mean   : 746.9
## 3rd Qu.: 985.0
## Max.   :1680.0
```

Since the data are of different scales, use `scale()` function to appropriately scale the data.

```
wine.noType.scaled <- scale(wine.noType)
summary(wine.noType.scaled)
```

```
##      Alcohol      Malic      Ash
## Min.   :-2.42739   Min.   :-1.4290   Min.   :-3.66881
## 1st Qu.: -0.78603   1st Qu.: -0.6569   1st Qu.: -0.57051
## Median : 0.06083   Median : -0.4219   Median : -0.02375
## Mean   : 0.00000   Mean   : 0.00000   Mean   : 0.00000
## 3rd Qu.: 0.83378   3rd Qu.: 0.6679    3rd Qu.: 0.69615
## Max.   : 2.25341   Max.   : 3.1004    Max.   : 3.14745
##      Alcalinity      Magnesium      Phenols
```

```
## Min.      :-2.663505   Min.      :-2.0824   Min.      :-2.10132
## 1st Qu.: -0.687199   1st Qu.: -0.8221   1st Qu.: -0.88298
## Median : 0.001514   Median : -0.1219   Median : 0.09569
## Mean    : 0.000000   Mean    : 0.0000   Mean    : 0.00000
## 3rd Qu.: 0.600395   3rd Qu.: 0.5082   3rd Qu.: 0.80672
## Max.    : 3.145637   Max.    : 4.3591   Max.    : 2.53237
##   Flavanoids      Nonflavanoids      Proanthocyanins      Color
## Min.      :-1.6912   Min.      :-1.8630   Min.      :-2.06321   Min.      :-1.6297
## 1st Qu.: -0.8252   1st Qu.: -0.7381   1st Qu.: -0.59560   1st Qu.: -0.7929
## Median : 0.1059   Median : -0.1756   Median : -0.06272   Median : -0.1588
## Mean    : 0.0000   Mean    : 0.0000   Mean    : 0.00000   Mean    : 0.0000
## 3rd Qu.: 0.8467   3rd Qu.: 0.6078   3rd Qu.: 0.62741   3rd Qu.: 0.4926
## Max.    : 3.0542   Max.    : 2.3956   Max.    : 3.47527   Max.    : 3.4258
##   Hue              Dilution          Proline
## Min.      :-2.08884   Min.      :-1.8897   Min.      :-1.4890
## 1st Qu.: -0.76540   1st Qu.: -0.9496   1st Qu.: -0.7824
## Median : 0.03303   Median : 0.2371   Median : -0.2331
## Mean    : 0.00000   Mean    : 0.0000   Mean    : 0.0000
## 3rd Qu.: 0.71116   3rd Qu.: 0.7864   3rd Qu.: 0.7561
## Max.    : 3.29241   Max.    : 1.9554   Max.    : 2.9631
```

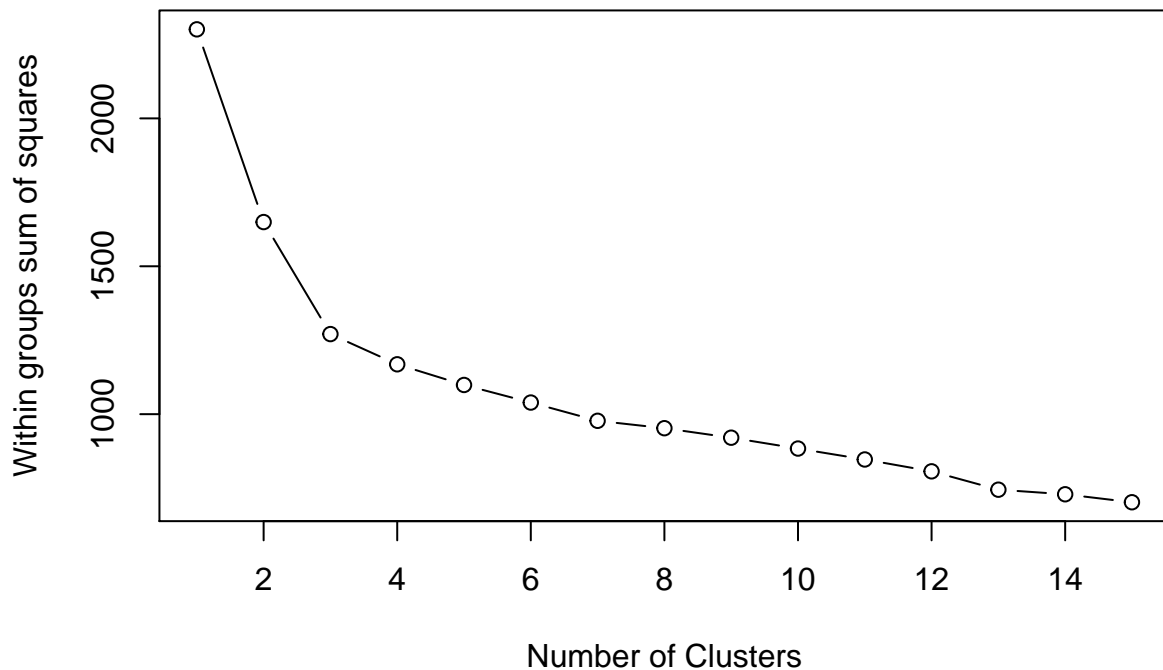
Now we'd like to cluster the data using k-means method. k-means method requires the specification of the number of clusters, so we need to first decide how many clusters to use.

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(wine.noType.scaled)
```



Looking at the plot, since the sum of squares are significant between 1 and 2, and 2 and 3, then doesn't change much after 3, $k = 3$ is a good number of clusters.

Exercise 2

- How many clusters does this method suggest?

This method suggests $k = 3$ clusters.

- Why does this method work? What's the intuition behind it?

It looks into the sum of squares within the cluster, which is roughly how spreaded out a cluster. We want a reasonably sized cluster, so we want to reduce the sum of squares of within clusters. We can see significant improvement from 1 cluster to 2 clusters, then more improvement from 2 clusters to 3 clusters. However, the improvement from 3 clusters to 4 clusters started to decrease. This means that adding more clusters actually not distinguish too much of some of the clusters. Furthermore, it may be “overfitting” some of the features.

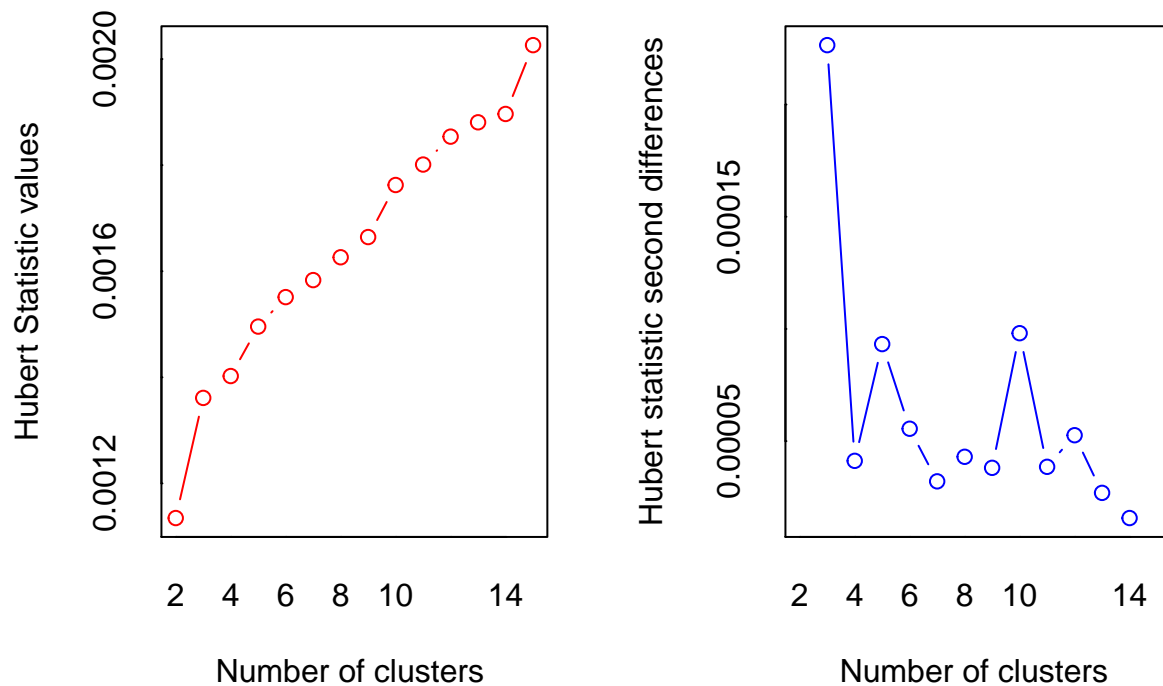
- Look at the code for `wssplot()` and figure out how it works

The `wssplot` functions determine sum of within-cluster sum of squares of varying number of clusters determined by a k-means method from 2 to maximum number of `nc`. The `nc` is the maximum number of clusters to consider, which is 15 in this case. The seed is the random-number seed to ensure reproducible result since k-means require initial random guess of centroids. It plots the sum of the within-cluster sum of squares over the number of clusters k tried.

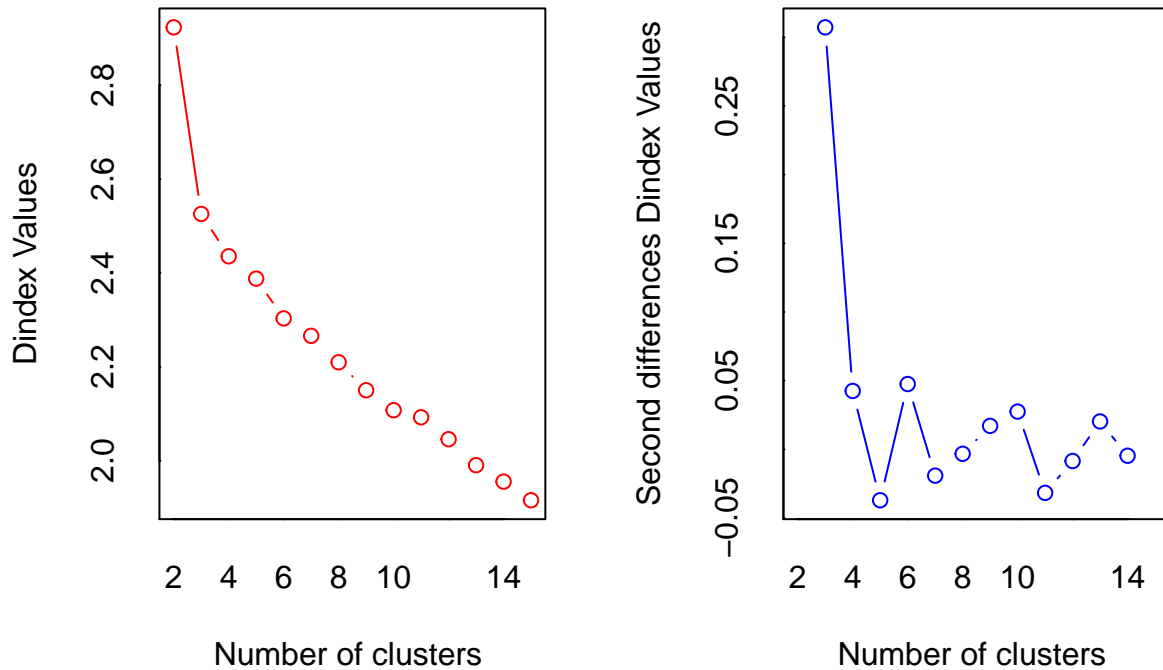
Method 2

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

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



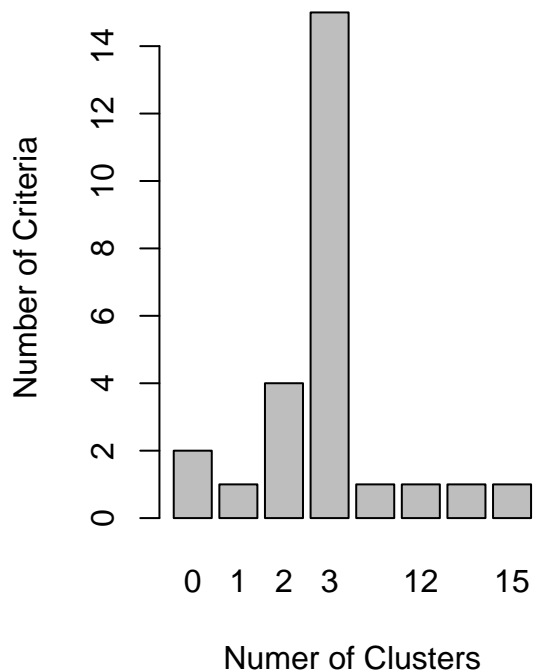
```
## *** : The Hubert index is a graphical method of determining the number of clusters.
##       In the plot of Hubert index, we seek a significant knee that corresponds to a
##       significant increase of the value of the measure i.e the significant peak in Hubert
##       index second differences 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="Number of Clusters", ylab="Number of Criteria",
         main="Number of Clusters Chosen by 26 Criteria")
```

Number of Clusters Chosen by 26 Cr



Exercise 3

- How many clusters does this method suggest?

The NbClust method clearly suggested $k = 3$ clusters.

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(wine.noType.scaled, centers = 3)
fit.km
```

```
## K-means clustering with 3 clusters of sizes 51, 65, 62
##
## Cluster means:
##      Alcohol      Malic      Ash Alkalinity      Magnesium      Phenols
## 1  0.1644436  0.8690954  0.1863726  0.5228924 -0.07526047 -0.97657548
## 2 -0.9234669 -0.3929331 -0.4931257  0.1701220 -0.49032869 -0.07576891
## 3  0.8328826 -0.3029551  0.3636801 -0.6084749  0.57596208  0.88274724
##  Flavanoids Nonflavanoids Proanthocyanins      Color      Hue
```



```
## 1 -1.21182921    0.72402116   -0.77751312  0.9388902 -1.1615122
## 2  0.02075402   -0.03343924    0.05810161 -0.8993770  0.4605046
## 3  0.97506900   -0.56050853    0.57865427  0.1705823  0.4726504
##      Dilution    Proline
## 1 -1.2887761 -0.4059428
## 2  0.2700025 -0.7517257
## 3  0.7770551  1.1220202
##
## Clustering vector:
##  [1] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
## [36] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 2 2 1 2 2 2 2 2 2 2
## [71] 2 2 2 3 2 2 2 2 2 2 2 2 1 2 2 2 2 2 2 2 2 2 3 2 2 2 2 2 2 2
## [106] 2 2 2 2 2 2 2 2 2 2 2 2 1 2 2 3 2 2 2 2 2 2 2 1 1 1 1 1 1 1
## [141] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [176] 1 1 1
##
## Within cluster sum of squares by cluster:
## [1] 326.3537 558.6971 385.6983
## (between_SS / total_SS =  44.8 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
## [5] "tot.withinss" "betweenss"    "size"         "iter"
## [9] "ifault"
```

Now we want to evaluate how well this clustering does.

Exercise 5

- Using the `table()` function, show how the clusters in `ct.km` compares to the actual wine types. Would you consider this a good clustering?

```
ct.km <- table(wine$Type, fit.km$cluster)
ct.km
```

```
##
##      1  2  3
## 1  0  0 59
## 2  3 65  3
## 3 48  0  0
```

```
randIndex(ct.km)
```

```
##      ARI
## 0.897495
```

It predicts 89.75% accuracy, which is pretty good.

Exercise 6

- Visualize these clusters using function `clusplot()` from the `cluster` library.

`clusplot()` can only be used for Partitioning Around Medoids (PAM), Clustering Large Applications (CLARA) and Fuzzy Analysis Clustering (FANNY) methods. So these methods are tried here with the same selection of $k = 3$. However, only PAM and CLARA works since $k = 3$ is too small for the FANNY method.

For PAM method, it predicts about 74.11% accuracy.

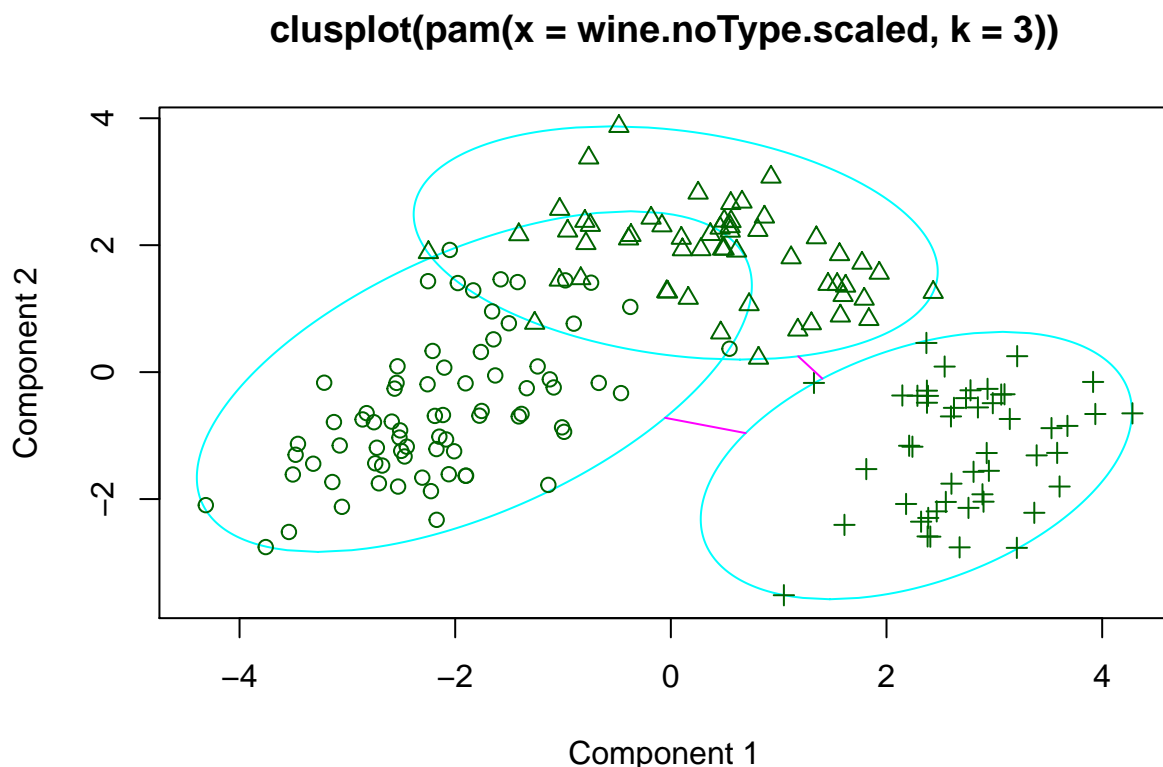
```
fit.pam <- pam(wine.noType.scaled, k = 3)
ct.pam <- table(wine$Type, fit.pam$clustering)
ct.pam
```

```
##
##      1  2  3
##  1 59  0  0
##  2 15 55  1
##  3  0  0 48
```

```
randIndex(ct.pam)
```

```
##      ARI
## 0.7411365
```

```
clusplot(fit.pam)
```



These two components explain 55.41 % of the point variability.

For CLARA method, it predicts about 81.42% accuracy.

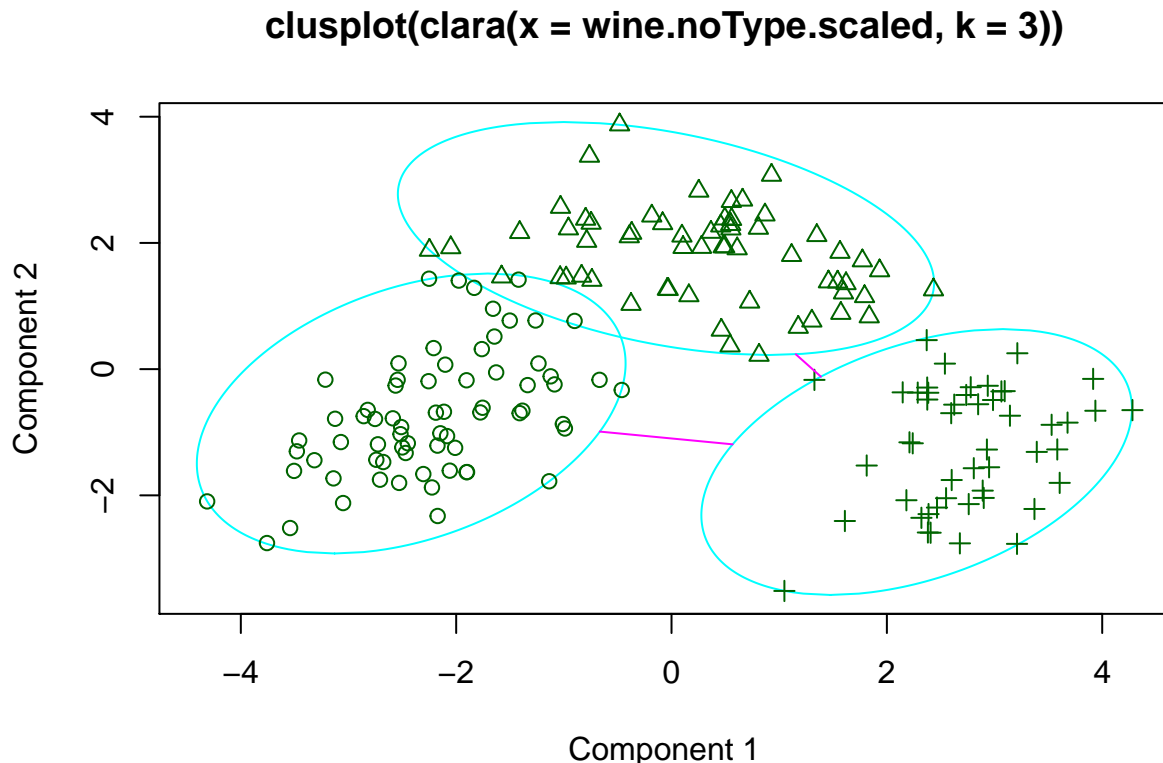
```
fit.clara <- clara(wine.noType.scaled, k = 3)
ct.clara <- table(wine$Type, fit.clara$clustering)
ct.clara
```

```
##
##      1  2  3
##  1 59  0  0
##  2 10 60  1
##  3  0  0 48
```

```
randIndex(ct.clara)
```

```
##      ARI
## 0.8141769
```

```
clusplot(fit.clara)
```



These two components explain 55.41 % of the point variability.

- Would you consider this a good clustering?

We can see that k-means is the best clustering method at 89.75% accuracy. Next best is CLARA at 81.24% accuracy. Worst is PAM at 74.11% accuracy.