# exercise

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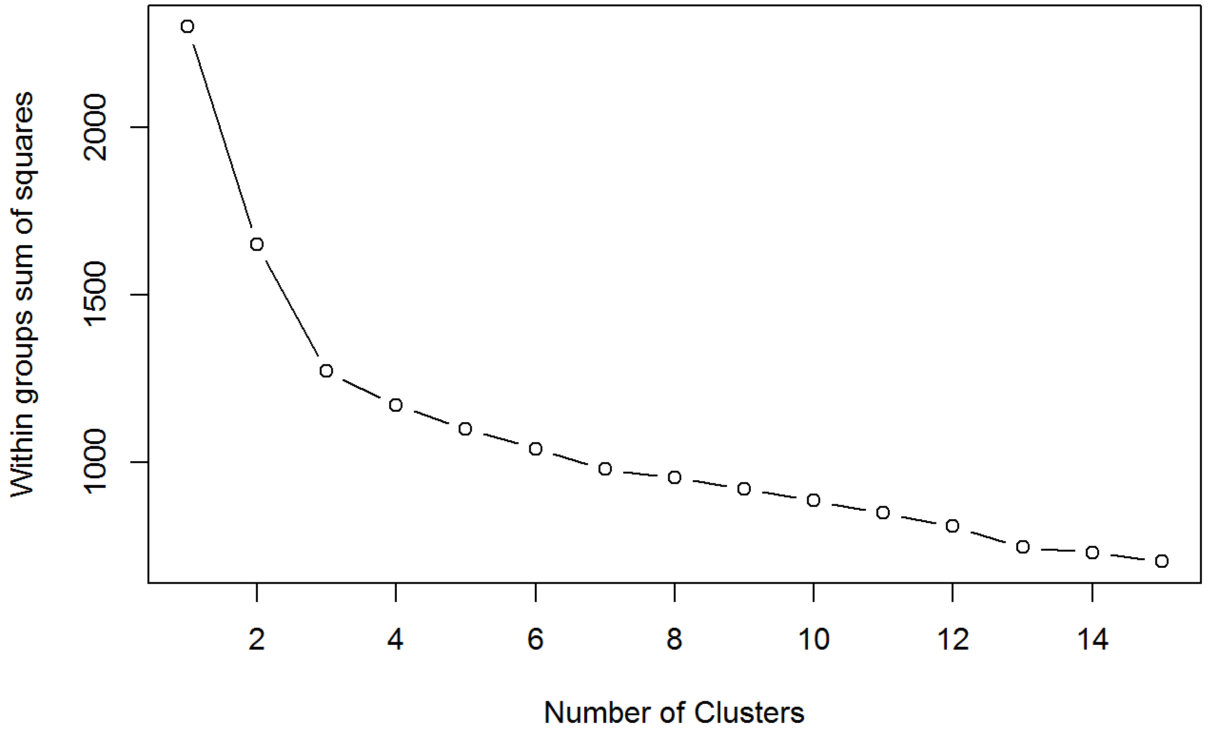
## R Markdown

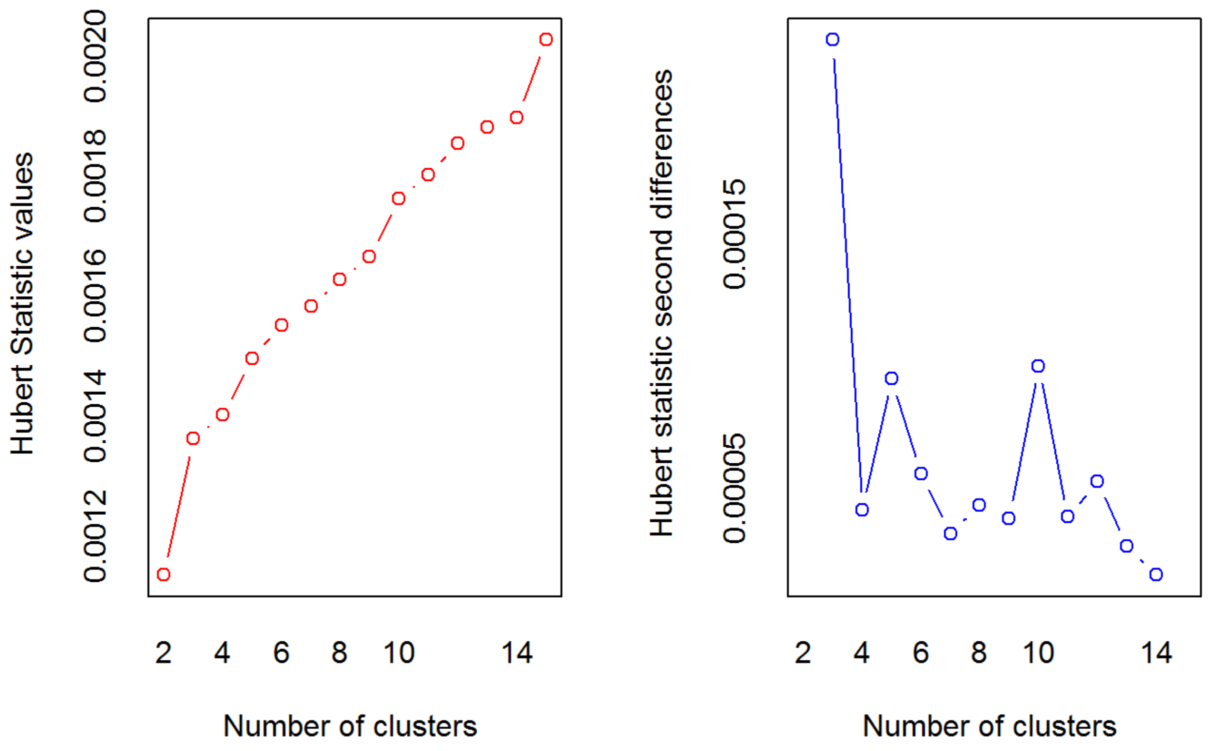
```
library("cluster", lib.loc="~/R/win-library/3.4")
library("NbClust", lib.loc="~/R/win-library/3.4")
library("rattle.data", lib.loc="~/R/win-library/3.4")
data(wine, package="rattle.data")
head(wine)
```

```
##   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
```

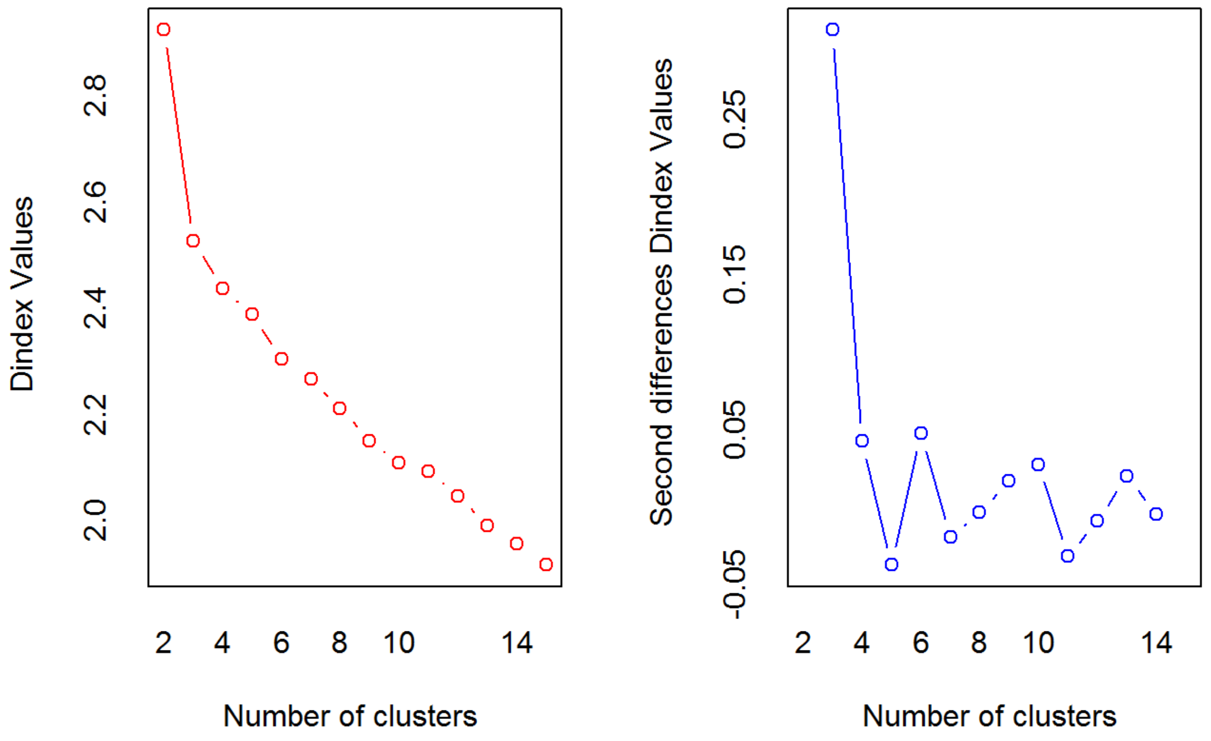
```
df <- scale(wine[-1])

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)
```



```
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 Huber
t
##                 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 o
f
##                 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
##
##
## *******************************************************************
```

```
table(nc$Best.n[1,])
```

```
##
##  0  1  2  3 10 12 14 15
##  2  1  4 15  1  1  1  1
```

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

set.seed(1234)
fit.km <- kmeans(df, 3, nstart=25)
fit.km$size
```

```
## [1] 62 65 51
```

```
fit.km$centers
```

```
##      Alcohol      Malic        Ash Alcalinity   Magnesium     Phenols
## 1  0.8328826 -0.3029551  0.3636801 -0.6084749  0.57596208  0.88274724
## 2 -0.9234669 -0.3929331 -0.4931257  0.1701220 -0.49032869 -0.07576891
## 3  0.1644436  0.8690954  0.1863726  0.5228924 -0.07526047 -0.97657548
##    Flavanoids Nonflavanoids Proanthocyanins      Color        Hue
## 1  0.97506900   -0.56050853      0.57865427  0.1705823  0.4726504
## 2  0.02075402   -0.03343924      0.05810161 -0.8993770  0.4605046
## 3 -1.21182921    0.72402116     -0.77751312  0.9388902 -1.1615122
##     Dilution    Proline
## 1  0.7770551  1.1220202
## 2  0.2700025 -0.7517257
## 3 -1.2887761 -0.4059428
```

```
aggregate(wine[-1], by=list(cluster=fit.km$cluster), mean)
```

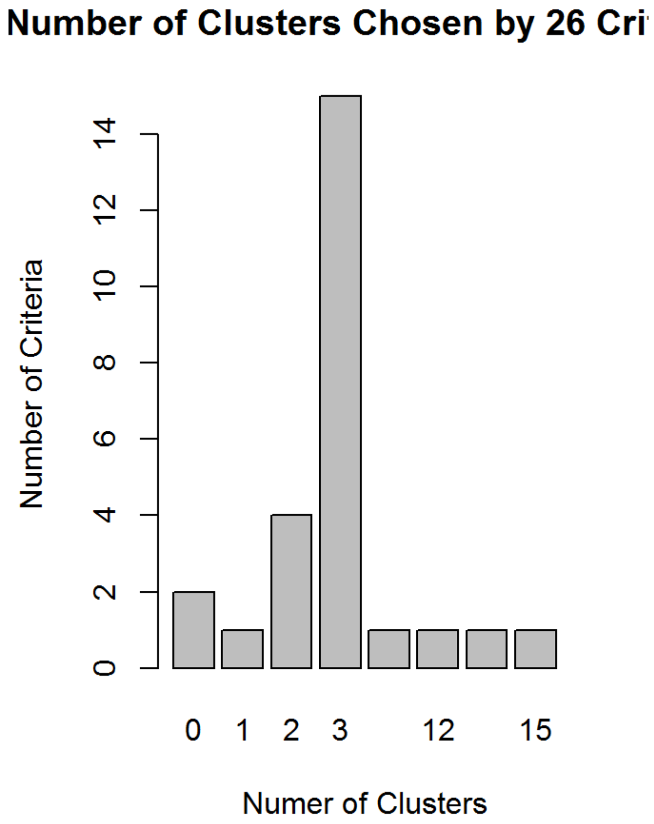
```
##   cluster  Alcohol    Malic      Ash Alcalinity Magnesium  Phenols
## 1       1 13.67677 1.997903 2.466290   17.46290 107.96774 2.847581
## 2       2 12.25092 1.897385 2.231231   20.06308  92.73846 2.247692
## 3       3 13.13412 3.307255 2.417647   21.24118  98.66667 1.683922
##   Flavanoids Nonflavanoids Proanthocyanins    Color       Hue Dilution
## 1  3.0032258     0.2920968        1.922097 5.453548 1.0654839 3.163387
## 2  2.0500000     0.3576923        1.624154 2.973077 1.0627077 2.803385
## 3  0.8188235     0.4519608        1.145882 7.234706 0.6919608 1.696667
##     Proline
## 1 1100.2258
## 2  510.1692
## 3  619.0588
```

```
table(fit.km$clusters)
```

```
## < table of extent 0 >
```

```
table(wine$Type)
```

```
## 
##  1  2  3 
## 59 71 48
```


Number of Clusters Chosen by 26 Cri
Number of Criteria
0
2
4
6
8
10
12
14
0
1
2
3
12
15
Numer of Clusters