Gopika O - 2048033

R-Laboratory 10

12/04/2021

1.Load the necessary packages for clustering.

```
library(tidyverse)  # data manipulation
```

```
## ── Attaching packages ─────────────────────────────────────────────────────
──────────────────────────────────── tidyverse 1.3.0 ──
```

```
## ✓ ggplot2 3.3.3     ✓ purrr   0.3.4
## ✓ tibble  3.0.3     ✓ dplyr   1.0.4
## ✓ tidyr   1.1.1     ✓ stringr 1.4.0
## ✓ readr   1.4.0     ✓ forcats 0.5.1
```

```
## ── Conflicts ────────────────────────────────────────────────────────────
─────────────────────────────────── tidyverse_conflicts() ──
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(cluster)    # clustering algorithms
library(factoextra) # clustering visualization
```

```
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve
3WBa
```

```
library(dendextend) # for comparing two dendrograms
```

```
##
## ---------------------
## Welcome to dendextend version 1.14.0
## Type citation('dendextend') for how to cite the package.
##
## Type browseVignettes(package = 'dendextend') for the package vignette.
## The github page is: https://github.com/talgalili/dendextend/
##
## Suggestions and bug-reports can be submitted at: https://github.com/talgalili/dend
extend/issues
## Or contact: <tal.galili@gmail.com>
##
##  To suppress this message use:  suppressPackageStartupMessages(library(dendexten
d))
## ---------------------
```

```
##
## Attaching package: 'dendextend'
```

```
## The following object is masked from 'package:stats':
##
##     cutree
```

2.Remove the unnecessary data.

```
df <- USArrests
df
```

	Murder <dbl>	Assault <int>	UrbanPop <int>	Rape <dbl>
Alabama	13.2	236	58	21.2
Alaska	10.0	263	48	44.5
Arizona	8.1	294	80	31.0
Arkansas	8.8	190	50	19.5
California	9.0	276	91	40.6
Colorado	7.9	204	78	38.7
Connecticut	3.3	110	77	11.1
Delaware	5.9	238	72	15.8
Florida	15.4	335	80	31.9
Georgia	17.4	211	60	25.8


```
df <- na.omit(df)
```

3.Scale/Standardise the data.

```
df <- scale(df)
head(df)
```

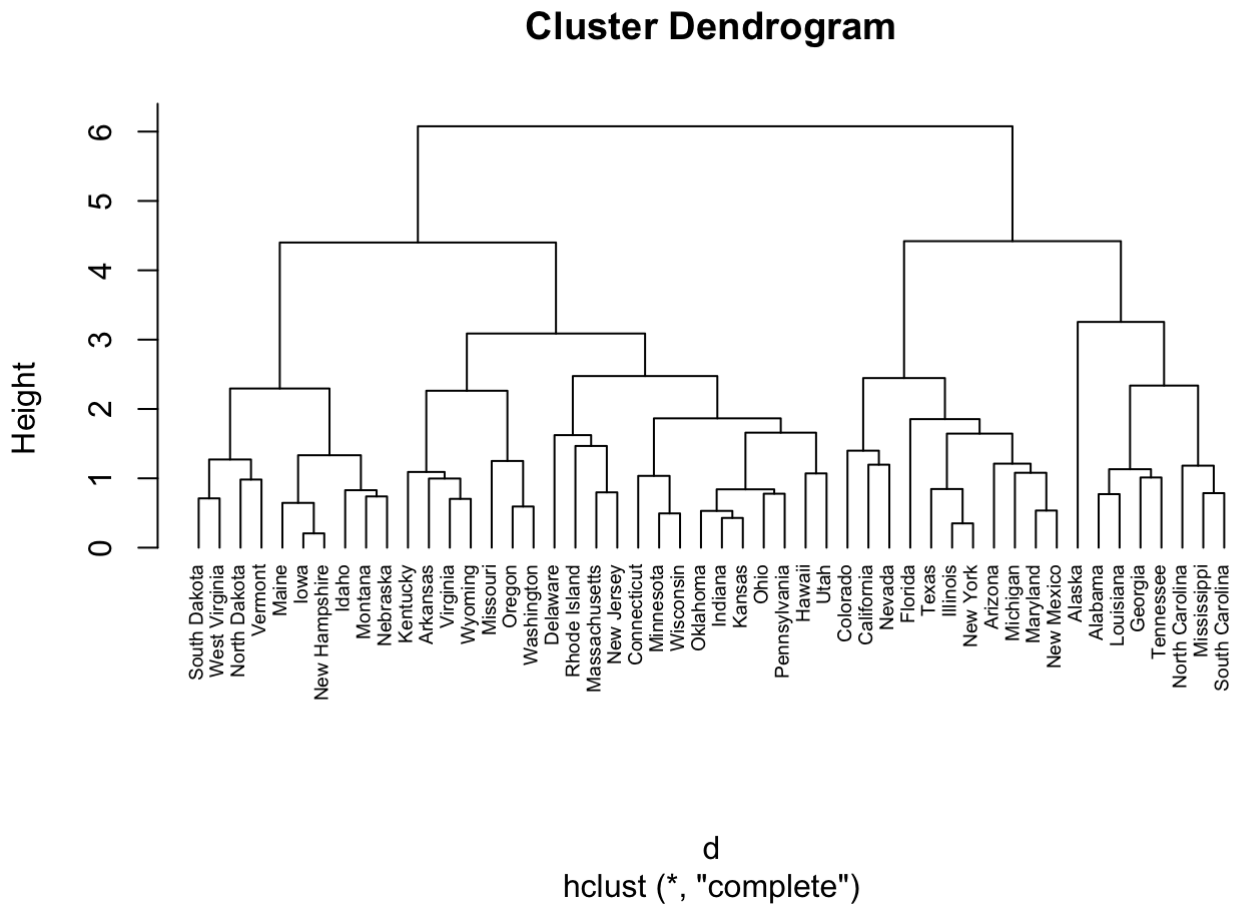
```
##                Murder   Assault   UrbanPop         Rape
## Alabama    1.24256408 0.7828393 -0.5209066 -0.003416473
## Alaska     0.50786248 1.1068225 -1.2117642  2.484202941
## Arizona    0.07163341 1.4788032  0.9989801  1.042878388
## Arkansas   0.23234938 0.2308680 -1.0735927 -0.184916602
## California 0.27826823 1.2628144  1.7589234  2.067820292
## Colorado   0.02571456 0.3988593  0.8608085  1.864967207
```

4.Perform Agglomerative Hierarchical Clustering by computing dissimilarity values and perform any hierarchical clustering method like complete linkage and then plot the dendogram.

```
# Dissimilarity matrix
d <- dist(df, method = "euclidean")

# Hierarchical clustering using Complete Linkage
hc1 <- hclust(d, method = "complete" )

# Plot the obtained dendrogram
plot(hc1, cex = 0.6, hang = -1)
```




```
# Compute with agnes
hc2 <- agnes(df, method = "complete")

# Agglomerative coefficient
hc2$ac
```

```
## [1] 0.8531583
```

```
# methods to assess
m <- c( "average", "single", "complete", "ward")
names(m) <- c( "average", "single", "complete", "ward")

# function to compute coefficient
ac <- function(x) {
  agnes(df, method = x)$ac
}

map_dbl(m, ac)
```

```
##   average    single  complete      ward
## 0.7379371 0.6276128 0.8531583 0.9346210
```

Sub-Group

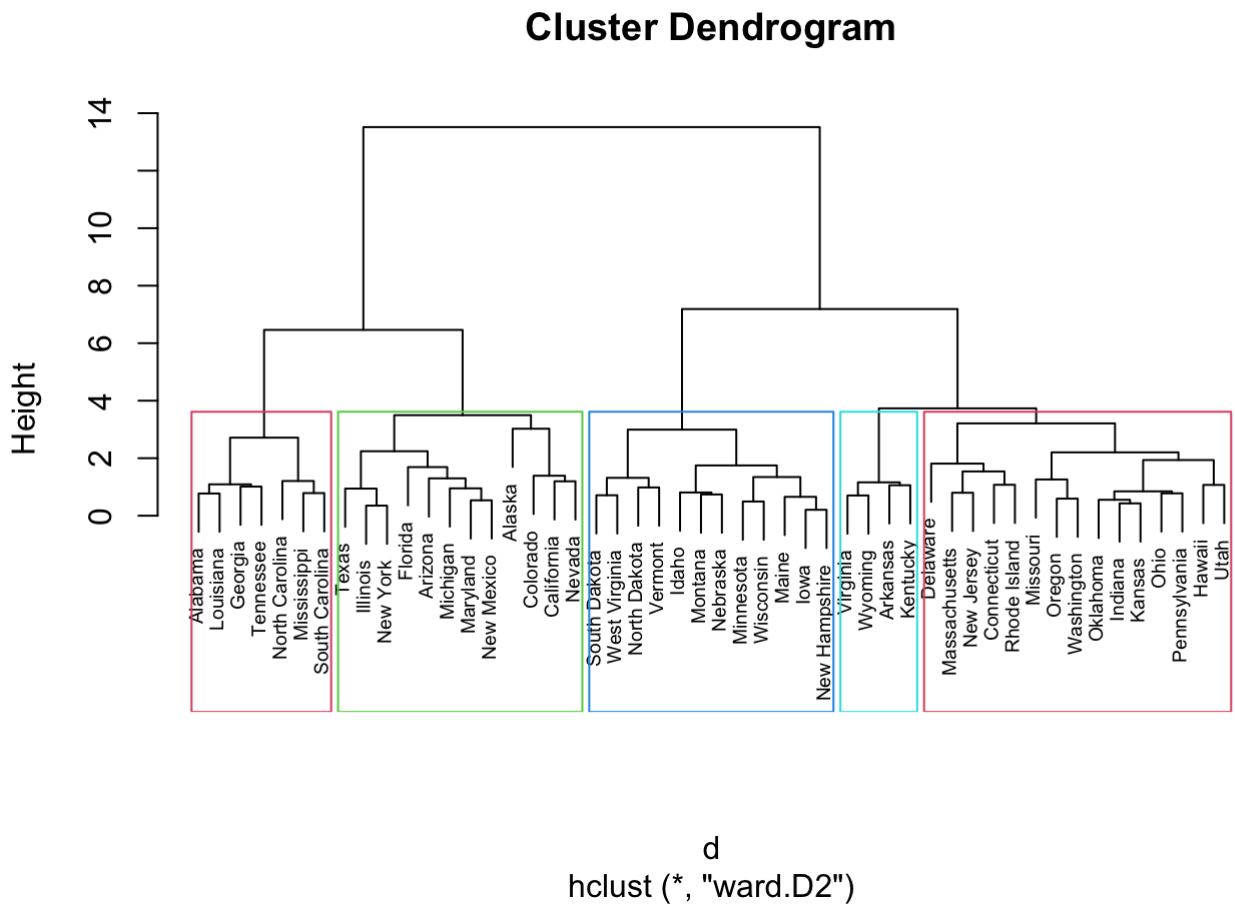
```
# Ward's method
hc5 <- hclust(d, method = "ward.D2" )

# 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
##  7 12 19 12
```

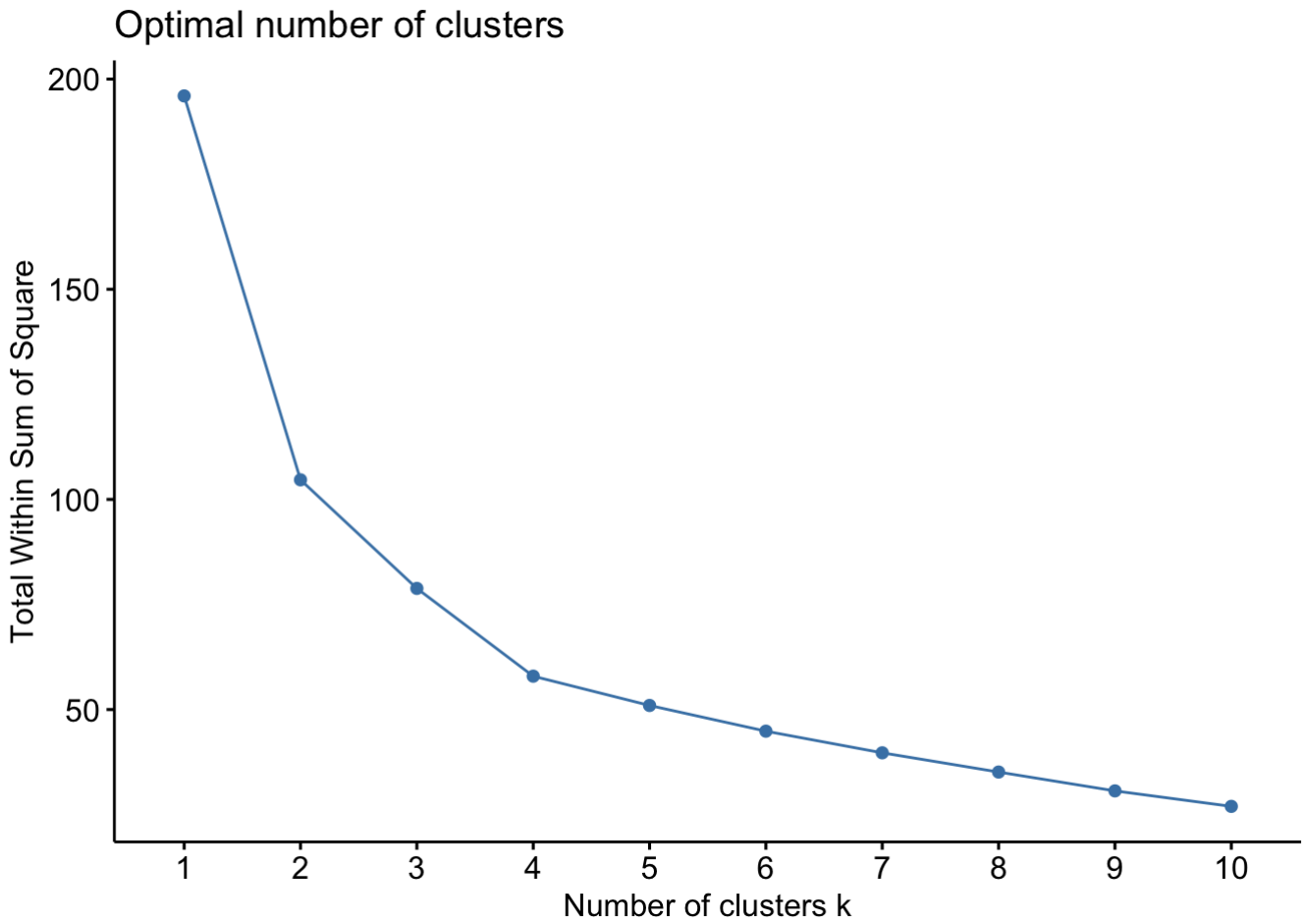
```
plot(hc5, cex = 0.6)
rect.hclust(hc5, k = 5, border = 2:5)
```



5.Determine optimal number of clusters

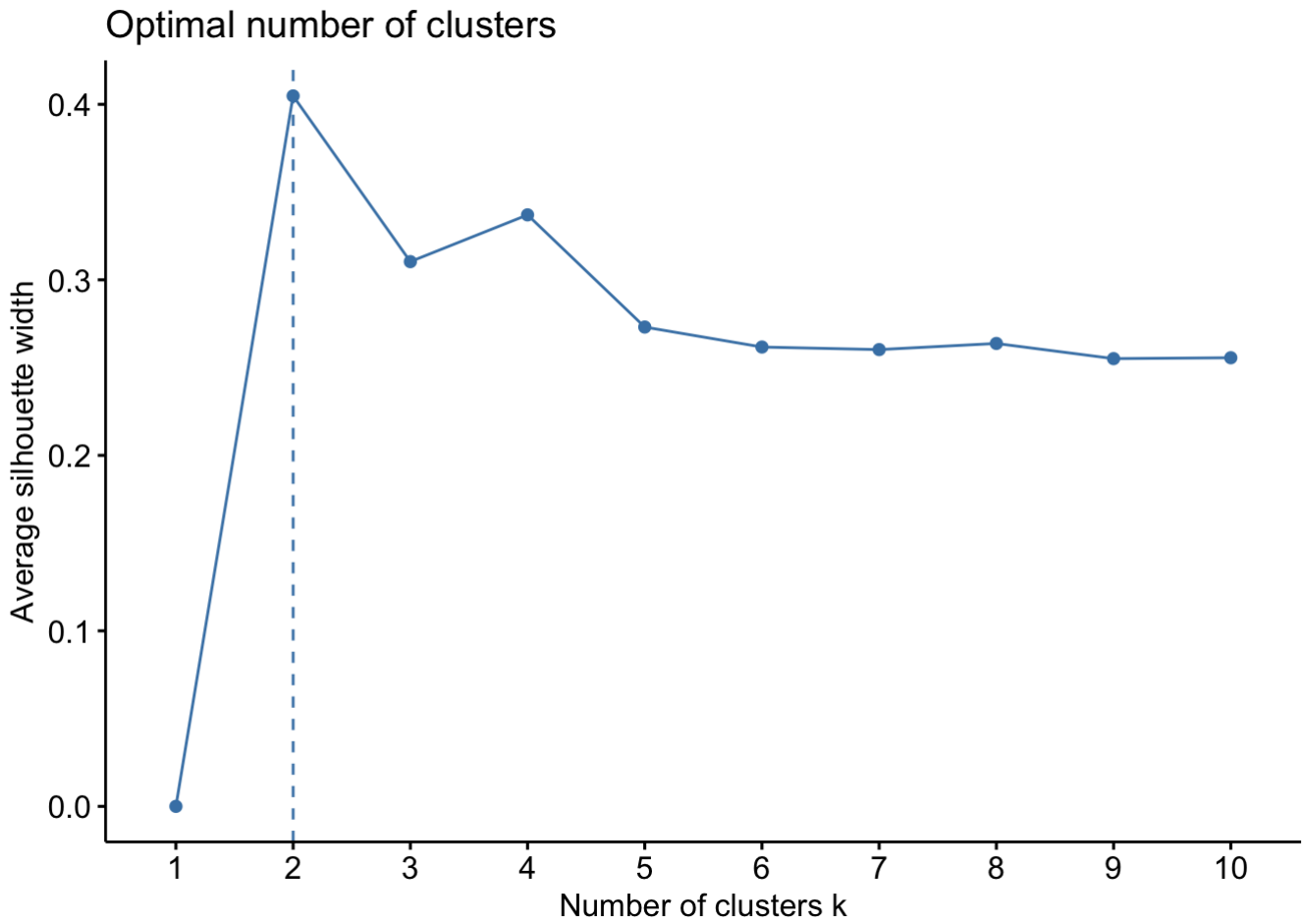
```
# Elbow Method

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




```
# Average Silhouette Method

fviz_nbclust(df, FUN = hcut, method = "silhouette")
```


Optimal number of clusters
Average silhouette width
0.0
0.1
0.2
0.3
0.4
1
2
3
4
5
6
7
8
9
10
Number of clusters k