

Hierarchical Clustering

In [1]:

```
# Load the data
data("USArrests")

# Standardize the data
df <- scale(USArrests)

# Show the first 6 rows
head(df, nrow = 6)
```

Out[1]:

A matrix: 6 × 4 of type dbl

	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

Similarity measures

In [2]:

```
# Compute the dissimilarity matrix
# df = the standardized data
res.dist <- dist(df, method = "euclidean")
```

To see easily the distance information between objects, we reformat the results of the function `dist()` into a matrix using the `as.matrix()` function.

In [3]:

```
as.matrix(res.dist)[1:6, 1:6]
```

Out[3]:

A matrix: 6 × 6 of type dbl

	Alabama	Alaska	Arizona	Arkansas	California	Colorado
Alabama	0.000000	2.703754	2.293520	1.289810	3.263110	2.651067
Alaska	2.703754	0.000000	2.700643	2.826039	3.012541	2.326519
Arizona	2.293520	2.700643	0.000000	2.717758	1.310484	1.365031
Arkansas	1.289810	2.826039	2.717758	0.000000	3.763641	2.831051
California	3.263110	3.012541	1.310484	3.763641	0.000000	1.287619
Colorado	2.651067	2.326519	1.365031	2.831051	1.287619	0.000000

Linkage

The linkage function takes the distance information, returned by the function `dist()`, and groups pairs

of objects into clusters based on their similarity.

```
In [4]: res.hc <- hclust(d = res.dist, method = "ward.D2")
```

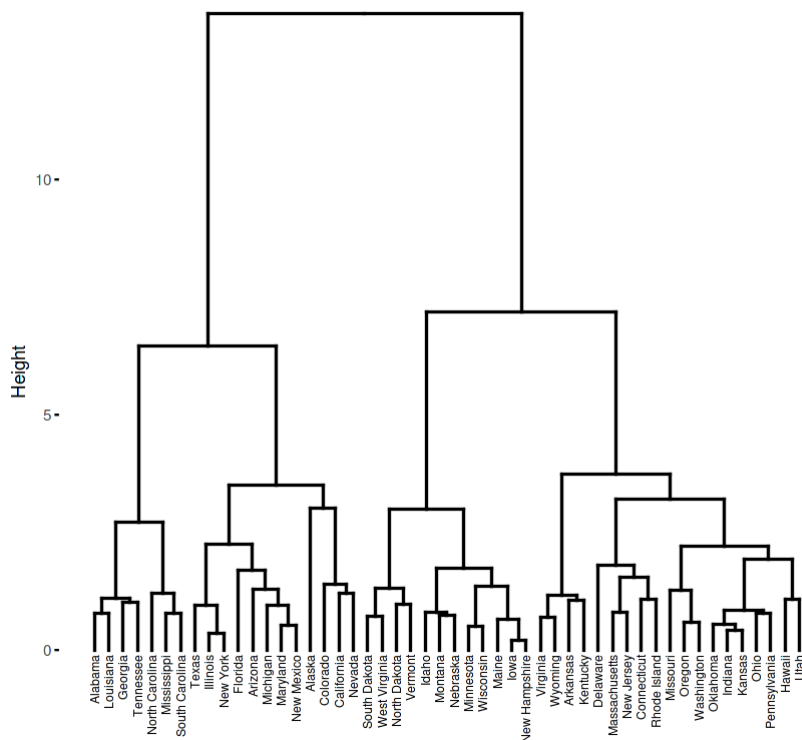
Dendrogram

```
In [5]: # cex: label size
library("factoextra")
fviz_dend(res.hc, cex = 0.5)
```

Loading required package: ggplot2

Welcome! Want to learn more? See two factoextra-related books at <https://goo.gl/ve3Wba>

Out[5]: Cluster Dendrogram



```
In [6]: # Compute cophenetic distance
res.coph <- cophenetic(res.hc)

# Correlation between cophenetic distance and
# the original distance
cor(res.dist, res.coph)
```

Out[6]: 0.697526563237039

```
In [7]: res.hc2 <- hclust(res.dist, method = "average")

cor(res.dist, cophenetic(res.hc2))
```

Out[7]: 0.718038237932047

we see that, the average linkage method gives better correlation.

Cut the dendrogram into different groups

```
In [8]: # Cut tree into 4 groups
grp <- cutree(res.hc, k = 4)
head(grp, n = 4)
```

Out[8]: Alabama: 1 Alaska: 2 Arizona: 2 Arkansas: 3

```
In [9]: # Number of members in each cluster
table(grp)
```

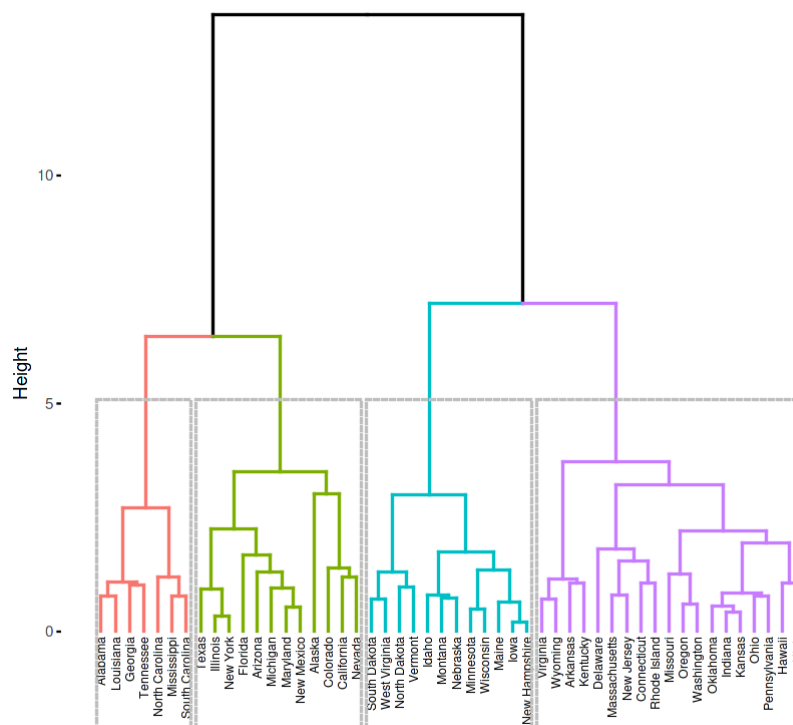
```
Out[9]: grp
 1  2  3  4
 7 12 19 12
```

```
In [10]: # Get the names for the members of cluster 1
rownames(df)[grp == 1]
```

Out[10]: 'Alabama' · 'Georgia' · 'Louisiana' · 'Mississippi' · 'North Carolina' · 'South Carolina' · 'Tennessee'

```
In [11]: fviz_dend(res.hc, cex = 0.5, k = 4,
  color_labels_by_k = FALSE, rect = TRUE)
```

Out[11]: Cluster Dendrogram



Non Hierarchical Clustering

Computing K-means clustering

```
In [12]: data("USArrests")      # Loading the data set
df <- scale(USArrests) # Scaling the data

# View the first 3 rows of the data
head(df, n = 3)
```

```
Out[12]:
```

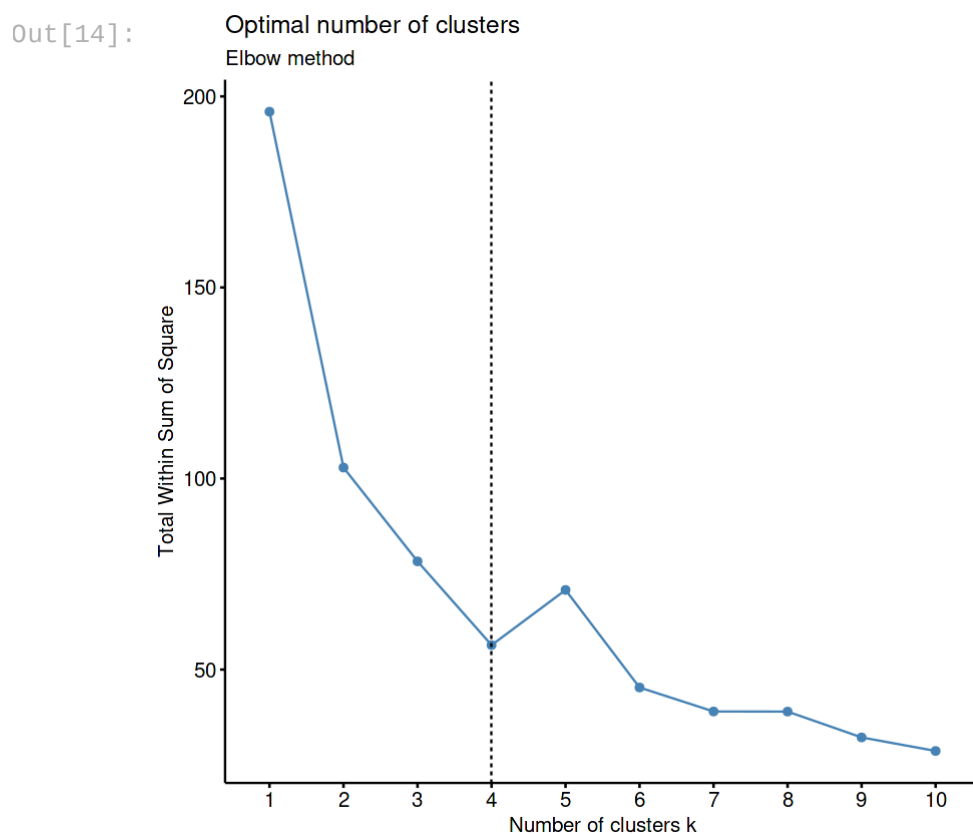
A matrix: 3 × 4 of type dbl

	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

```
In [13]: library(factoextra)
```

Determine the optimal number of clusters for k-means clustering:

```
In [14]: # Elbow method
fviz_nbclust(df, kmeans, method = "wss") +
geom_vline(xintercept = 4, linetype = 2) +
labs(subtitle = "Elbow method")
```



```
In [15]:
```

```
# Compute k-means with k = 4
set.seed(123)
km.res <- kmeans(df, 4, nstart = 25)
```

In [16]:

```
# Print the results
print(km.res)
```

K-means clustering with 4 clusters of sizes 8, 13, 16, 13

Cluster means:

	Murder	Assault	UrbanPop	Rape
1	1.4118898	0.8743346	-0.8145211	0.01927104
2	-0.9615407	-1.1066010	-0.9301069	-0.96676331
3	-0.4894375	-0.3826001	0.5758298	-0.26165379
4	0.6950701	1.0394414	0.7226370	1.27693964

Clustering vector:

Alabama	Alaska	Arizona	Arkansas	California
1	4	4	1	4
Colorado	Connecticut	Delaware	Florida	Georgia
4	3	3	4	1
Hawaii	Idaho	Illinois	Indiana	Iowa
3	2	4	3	2
Kansas	Kentucky	Louisiana	Maine	Maryland
3	2	1	2	4
Massachusetts	Michigan	Minnesota	Mississippi	Missouri
3	4	2	1	4
Montana	Nebraska	Nevada	New Hampshire	New Jersey
2	2	4	2	3
New Mexico	New York	North Carolina	North Dakota	Ohio
4	4	1	2	3
Oklahoma	Oregon	Pennsylvania	Rhode Island	South Carolina
3	3	3	3	1
South Dakota	Tennessee	Texas	Utah	Vermont
2	1	4	3	2
Virginia	Washington	West Virginia	Wisconsin	Wyoming
3	3	2	2	3

Within cluster sum of squares by cluster:

```
[1] 8.316061 11.952463 16.212213 19.922437
(between_SS / total_SS = 71.2 %)
```

Available components:

```
[1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
[6] "betweenss"    "size"         "iter"         "ifault"       "
```

In [17]:

```
aggregate(USArrests, by=list(cluster=km.res$cluster), mean)
```

Out[17]:

A data.frame: 4 × 5

cluster	Murder	Assault	UrbanPop	Rape
<int>	<dbl>	<dbl>	<dbl>	<dbl>
1	13.93750	243.62500	53.75000	21.41250
2	3.60000	78.53846	52.07692	12.17692
3	5.65625	138.87500	73.87500	18.78125
4	10.81538	257.38462	76.00000	33.19231

```
In [18]: dd <- cbind(USArrests, cluster = km.res$cluster)
          head(dd)
```

```
Out[18]:
```

A data.frame: 6 × 5

	Murder	Assault	UrbanPop	Rape	cluster
	<dbl>	<int>	<int>	<dbl>	<int>
Alabama	13.2	236	58	21.2	1
Alaska	10.0	263	48	44.5	4
Arizona	8.1	294	80	31.0	4
Arkansas	8.8	190	50	19.5	1
California	9.0	276	91	40.6	4
Colorado	7.9	204	78	38.7	4

```
In [19]: # Cluster number for each of the observations
          km.res$cluster
```

```
Out[19]: Alabama: 1 Alaska: 4 Arizona: 4 Arkansas: 1 California: 4 Colorado: 4 Connecticut: 3
          Delaware: 3 Florida: 4 Georgia: 1 Hawaii: 3 Idaho: 2 Illinois: 4 Indiana: 3 Iowa: 2 Kansas: 3
          Kentucky: 2 Louisiana: 1 Maine: 2 Maryland: 4 Massachusetts: 3 Michigan: 4 Minnesota: 2
          Mississippi: 1 Missouri: 4 Montana: 2 Nebraska: 2 Nevada: 4 New Hampshire: 2
          New Jersey: 3 New Mexico: 4 New York: 4 North Carolina: 1 North Dakota: 2 Ohio: 3
          Oklahoma: 3 Oregon: 3 Pennsylvania: 3 Rhode Island: 3 South Carolina: 1 South Dakota: 2
          Tennessee: 1 Texas: 4 Utah: 3 Vermont: 2 Virginia: 3 Washington: 3 West Virginia: 2
          Wisconsin: 2 Wyoming: 3
```

```
In [20]: head(km.res$cluster, 4)
```

```
Out[20]: Alabama: 1 Alaska: 4 Arizona: 4 Arkansas: 1
```

```
In [21]: # Cluster size
          km.res$size
```

```
Out[21]: 8 · 13 · 16 · 13
```

```
In [22]: # Cluster means
          km.res$centers
```

```
Out[22]:
```

A matrix: 4 × 4 of type dbl

	Murder	Assault	UrbanPop	Rape
1	1.4118898	0.8743346	-0.8145211	0.01927104
2	-0.9615407	-1.1066010	-0.9301069	-0.96676331
3	-0.4894375	-0.3826001	0.5758298	-0.26165379
4	0.6950701	1.0394414	0.7226370	1.27693964

```

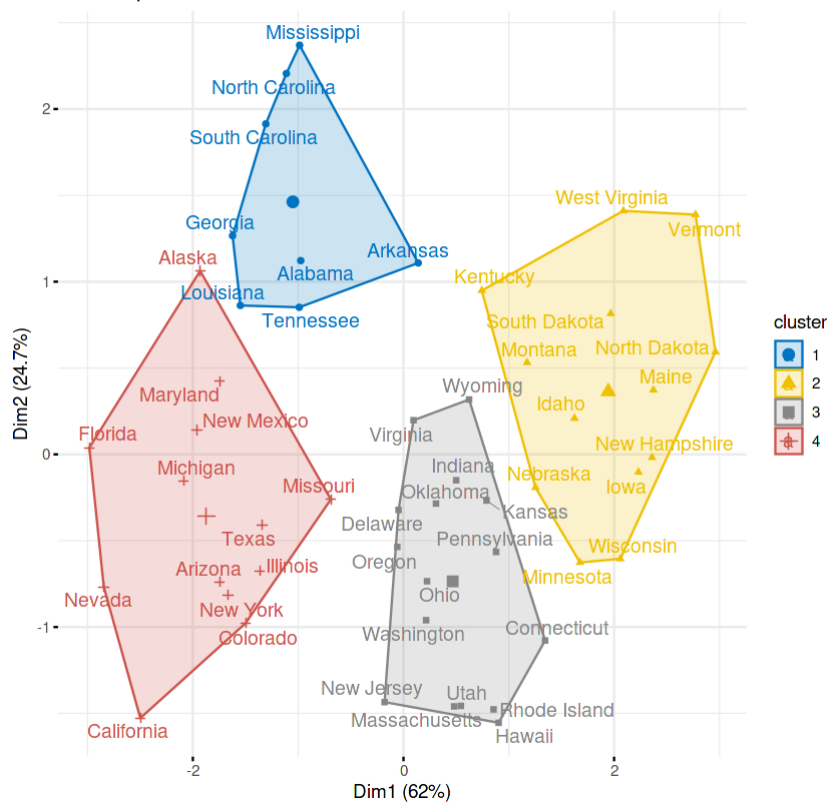
In [24]: set.seed(123)
km.res <- kmeans(df, 4, nstart = 25)

# Visualize
library("factoextra")
fviz_cluster(km.res, data = df,
              ellipse.type = "convex",
              palette = "jco",
              repel = TRUE,
              ggtheme = theme_minimal())

```

Out[24]:

Cluster plot



In [0]: