Tutorial_1

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Exercise 8

In Section 10.2.3, a formula for calculating PVE was given in Equation 10.8. We also saw that the PVE can be obtained using the sdev output of the prcomp() function. On the USArrests data, calculate PVE in two ways:

a. Using the sdev output of the prcomp() function, as was done in Section 10.2.3.

```
#load data
#install.packages('ISLR') #note: may need to install.packages in the console!
library(ISLR)
```

```
## Warning: package 'ISLR' was built under R version 4.3.3
```

```
data("USArrests")

# Note: The variance explained by each principal component:
# pr.var = pr.out$sdev^2

pr.out = prcomp(USArrests, scale = TRUE)
pve =100*pr.out$sdev^2 / sum(pr.out$sdev^2)
pve
```

```
## [1] 62.006039 24.744129  8.914080  4.335752
```

b. By applying Equation 10.8 directly. That is, use the prcomp() function to compute the principal component loadings. Then, use those loadings in Equation 10.8 to obtain the PVE. These two approaches should give the same results.

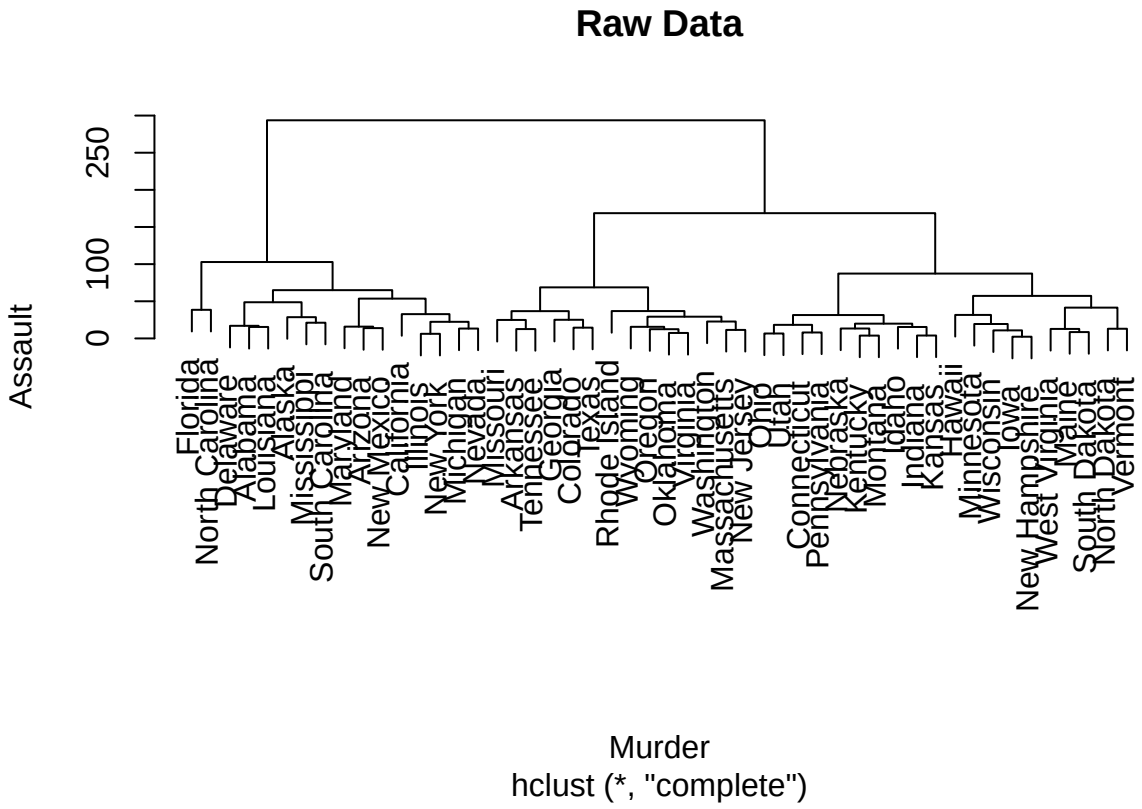
Hint: You will only obtain the same results in (a) and (b) if the same data is used in both cases. For instance, if in (a) you performed prcomp() using centered and scaled variables, then you must center and scale the variables before applying Equation 10.3 in (b).

Exercise 9

Consider the USArrests data. We will now perform hierarchical clustering on the states.

a. Using hierarchical clustering with complete linkage and Euclidean distance, cluster the states.

```r
#cluster analysis with complete linkage
d = dist(USArrests, method="euclidean") #hclust requires distance
hc = hclust(d, method="complete") #use complete linkage
#plot
plot(hc,ylab="Assault", xlab="Murder",
main="Raw Data")
```



b. Cut the dendrogram at a height that results in three distinct clusters. Which states belong to which clusters?

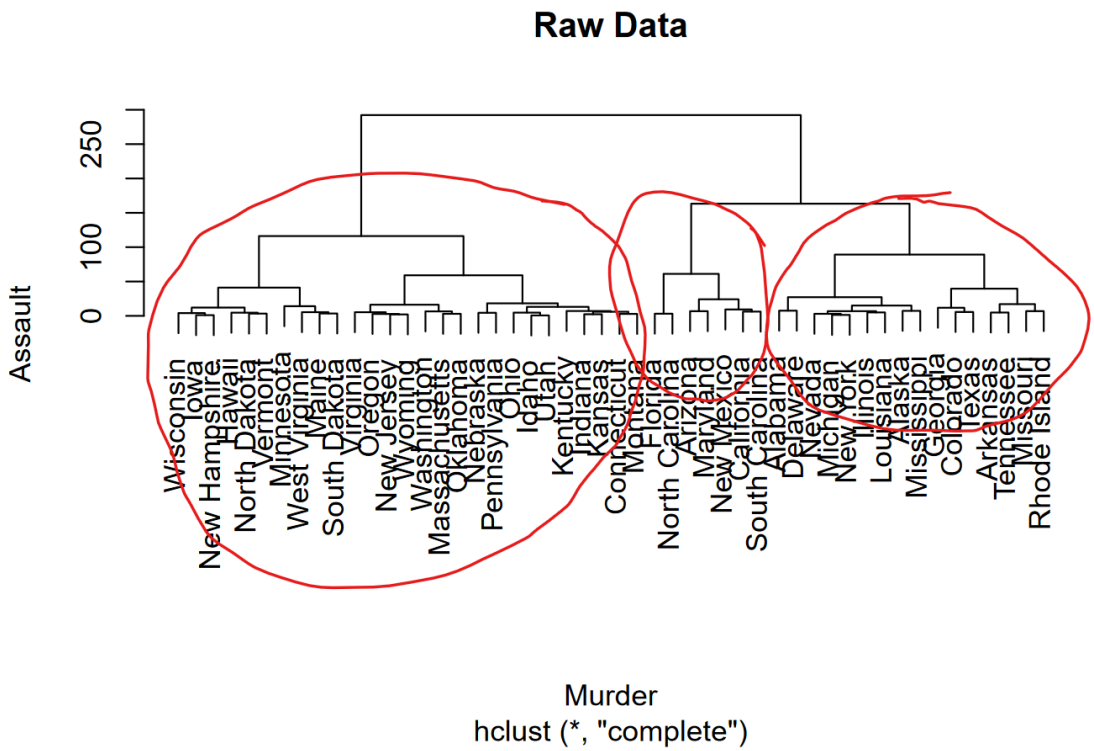
```r
arrests_hclust = cutree(hc, k = 3)
arrests_hclust
```

```
##        Alabama         Alaska        Arizona       Arkansas     California
##              1              1              1              2              1
##       Colorado    Connecticut       Delaware        Florida        Georgia
##              2              3              1              1              2
##         Hawaii          Idaho       Illinois        Indiana           Iowa
##              3              3              1              3              3
##         Kansas       Kentucky      Louisiana          Maine       Maryland
##              3              3              1              3              1
##  Massachusetts       Michigan      Minnesota    Mississippi       Missouri
##              2              1              3              1              2
##        Montana       Nebraska         Nevada New Hampshire     New Jersey
```

```
##              3              3              1              3              2
##     New Mexico       New York North Carolina   North Dakota           Ohio
##              1              1              1              3              3
##       Oklahoma         Oregon   Pennsylvania   Rhode Island South Carolina
##              2              2              3              2              1
##   South Dakota      Tennessee          Texas           Utah        Vermont
##              3              2              2              3              3
##       Virginia     Washington  West Virginia      Wisconsin        Wyoming
##              2              2              3              3              2
```

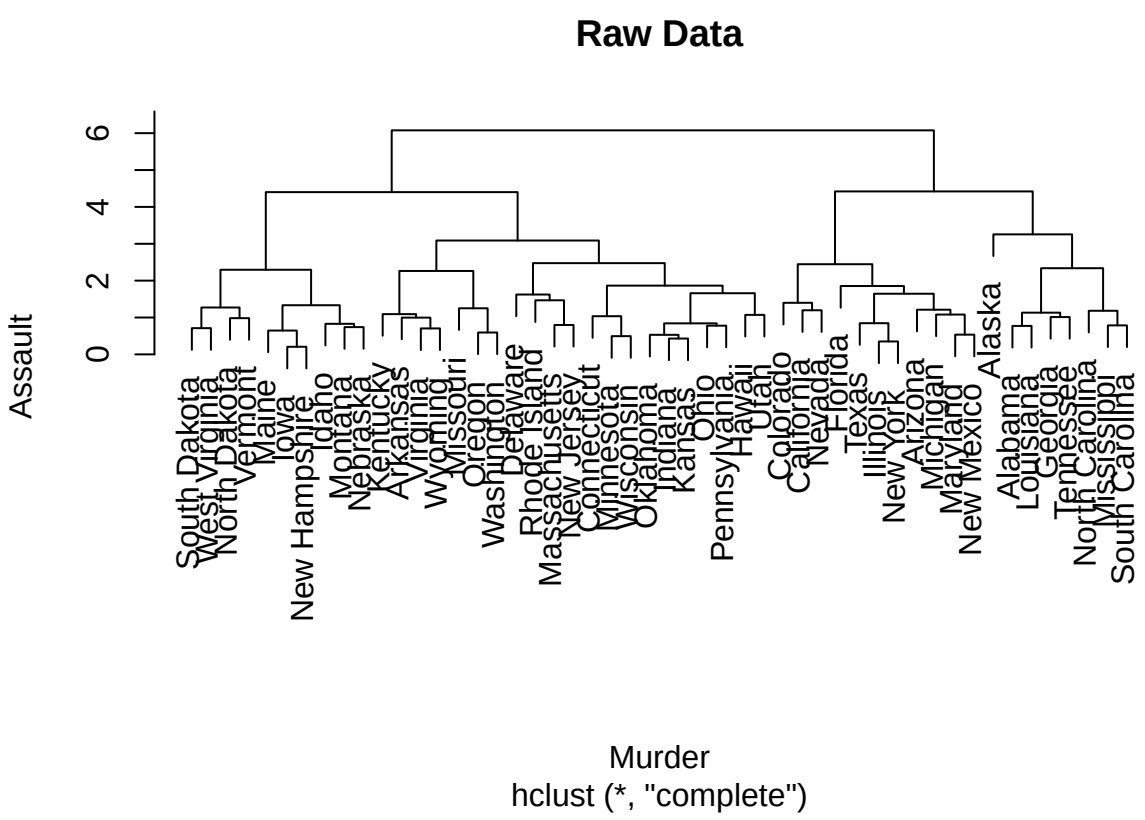
```
arrests_hclust = cutree(hc, k = 3) -> cluster_a
table(cluster_a)
```

```
## cluster_a
##  1  2  3
## 16 14 20
```



c. Hierarchically cluster the states using complete linkage and Eu- clidean distance, after scaling the variables to have standard de- viation one.

```
#scale variables to have standard deviation one
df = scale(USArrests)
#cluster analysis with complete linkage
d = dist(df, method="euclidean") #hclust requires dist.
hc = hclust(d, method="complete") #use complete linkage
#plot
plot(hc,ylab="Assault", xlab="Murder",
main="Raw Data")
```



d. What effect does scaling the variables have on the hierarchical clustering obtained? In your opinion, should the variables be scaled before the inter-observation dissimilarities are computed? Provide a justification for your answer.

The scaling appears to increase the dissimilarity (in a relative sense) of the observations, as the linkages are higher up in the dendrogram. The variables should be scaled as the UrbanPop variable is in different units to the other variables.

Exercise 2

Suppose that we have four observations, for which we compute a dissimilarity matrix, given by

$$\begin{bmatrix} & 0.3 & 0.4 & 0.7 \\ 0.3 & & 0.5 & 0.8 \\ 0.4 & 0.5 & & 0.45 \\ 0.7 & 0.8 & 0.45 & \end{bmatrix}.$$

For instance, the dissimilarity between the first and second observations is 0.3, and the dissimilarity between the second and fourth observations is 0.8.

a. On the basis of this dissimilarity matrix, sketch the dendrogram that results from hierarchically clustering these four observa- tions using complete linkage. Be sure to indicate on the plot the height at which each fusion occurs, as well as the observations corresponding to each leaf in the dendrogram.

b. Repeat (a), this time using single linkage clustering.

c. Suppose that we cut the dendogram obtained in (a) such that two clusters result. Which observations are in each cluster?

d. Suppose that we cut the dendogram obtained in (b) such that two clusters result. Which observations are in each cluster?

e. It is mentioned in the chapter that at each fusion in the den- drogram, the position of the two clusters being fused can be swapped without changing the meaning of the dendrogram. Draw a dendrogram that is equivalent to the dendrogram in (a), for which two or more of the leaves are repositioned, but for which the meaning of the dendrogram is the same.

Exercise 3

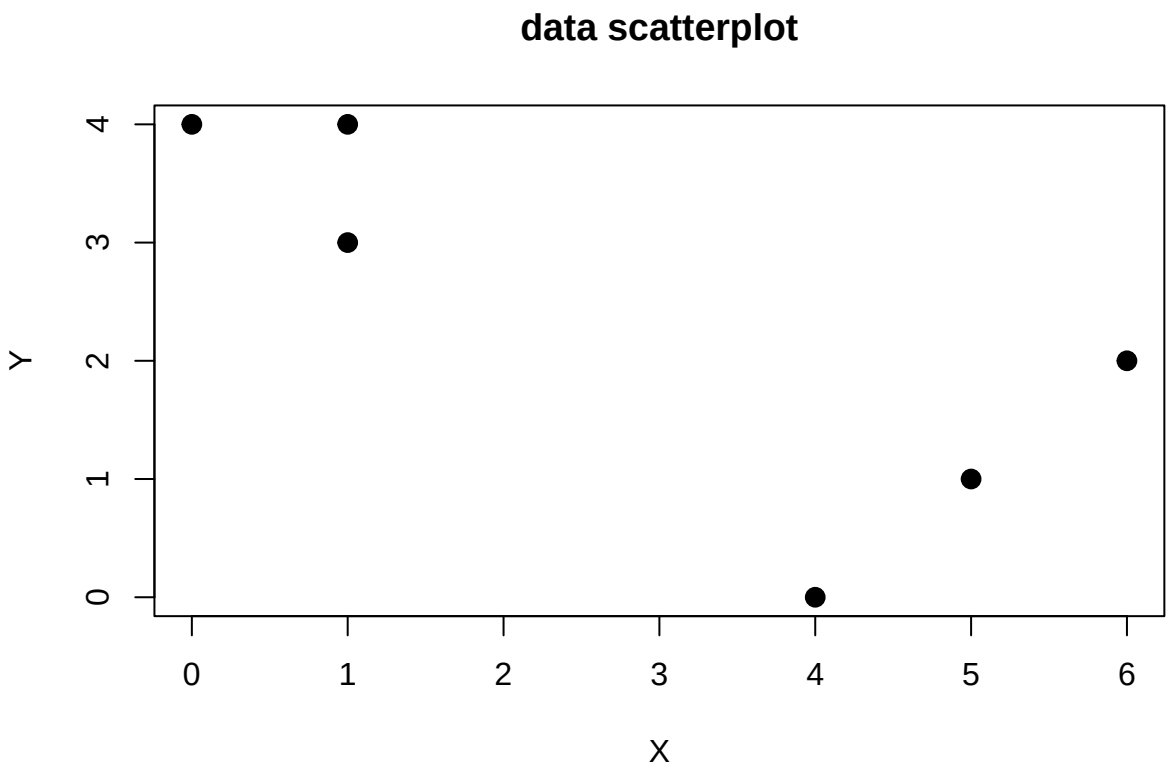
n this problem, you will perform K-means clustering manually, with K = 2, on a small example with n = 6 observations and p = 2 features. The observations are as follows.

Obs.	X_1	X_2
1	1	4
2	1	3
3	0	4
4	5	1
5	6	2
6	4	0

a. Plot the observations.

```
df2 = data.frame(c(1,1,0,5,6,4),
                 c(4,3,4,1,2,0))
colnames(df2)=c('X', 'Y')

plot(df2$X, df2$Y,
     pch=19,
     cex=1.3,
     ylab="Y", xlab="X",
     main="data scatterplot")
```



b. Randomly assign a cluster label to each observation. You can use the sample() command in R to do this. Report the cluster labels for each observation.

```
set.seed(123)
labs <- sample(c(1,2), size=6, replace=T)
df2$labels <- labs
df2$labels
```

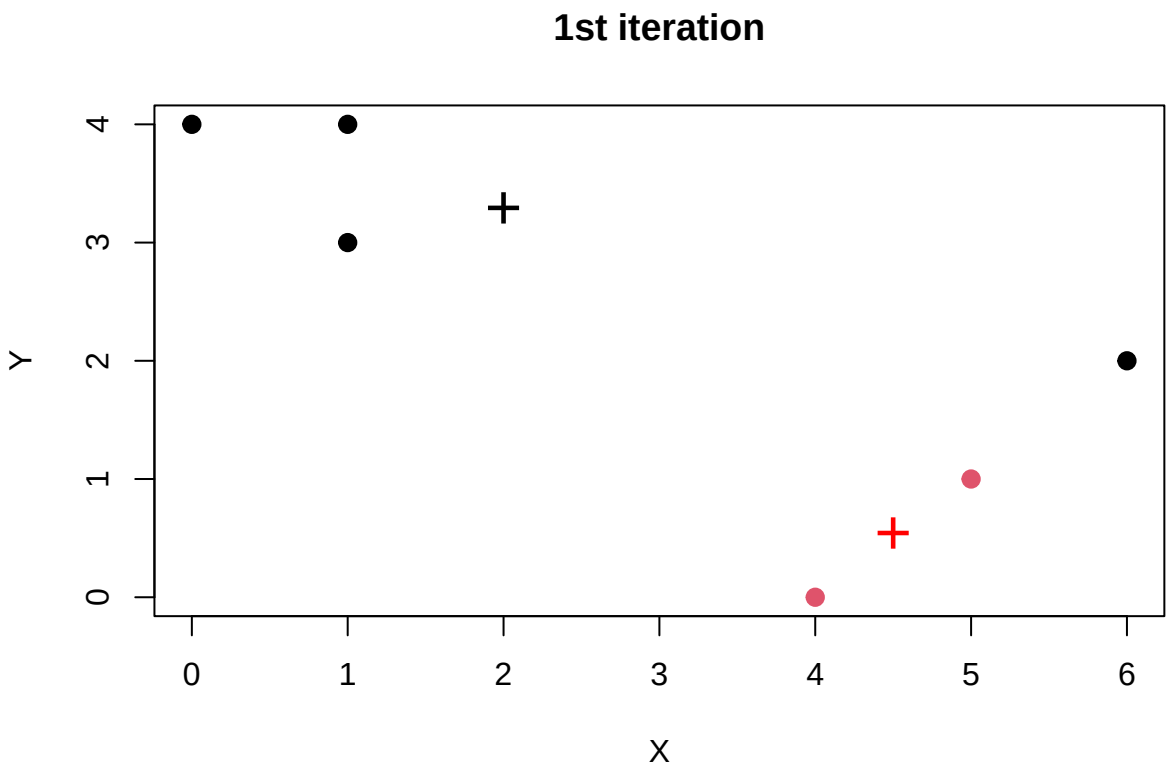
```
## [1] 1 1 1 2 1 2
```

c. Compute the centroid for each cluster

```
x1 = df2[labs==1,c(1,2)]
xc1 = colSums(x1)/4
x2 = df2[labs==2,c(1,2)]
xc2 = colSums(x2)/2
```

d. Assign each observation to the centroid to which it is closest, in terms of Euclidean distance. Report the cluster labels for each observation.

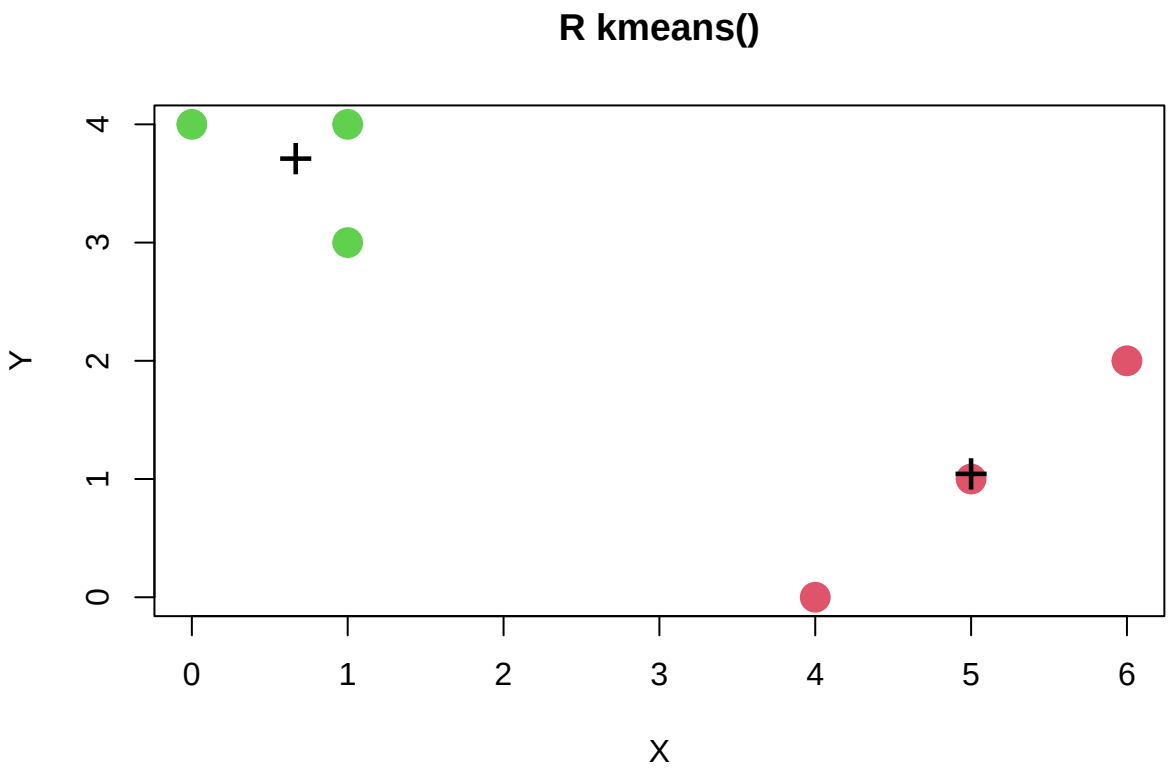
```
plot(df2$X,df2$Y, pch=19, cex=1.2,
ylab="Y", xlab="X", col=labs, main="1st iteration")
points(xc1[1], xc1[2], col='black', pch='+', cex=2)
points(xc2[1],xc2[2], col='red', pch='+', cex=2)
```



e. Repeat (c) and (d) until the answers obtained stop changing

```
#cluster 1
temp1a = (df2[,1] - xc1[1])
temp1b = (df2[,2] - xc1[2])
d1 = sqrt(temp1a^2 + temp1b^2)
#cluster2
temp2a = (df2[,1] - xc2[1])
temp2b = (df2[,2] - xc2[2])
d2 = sqrt(temp2a^2 + temp2b^2)
df2$d1 = round(d1,3)
df2$d2 = round(d2,3)

res <- kmeans(df2, centers=2,nstart=10) # 2 clusters; 10 random sets
plot(df2$X, df2$Y, pch=19,cex=2, col=res$cluster+1,
ylab="Y", xlab="X",
main="R kmeans()")
points(res$centers, pch="+", cex=2)
```



f. In your plot from (a), color the observations according to the cluster labels obtained