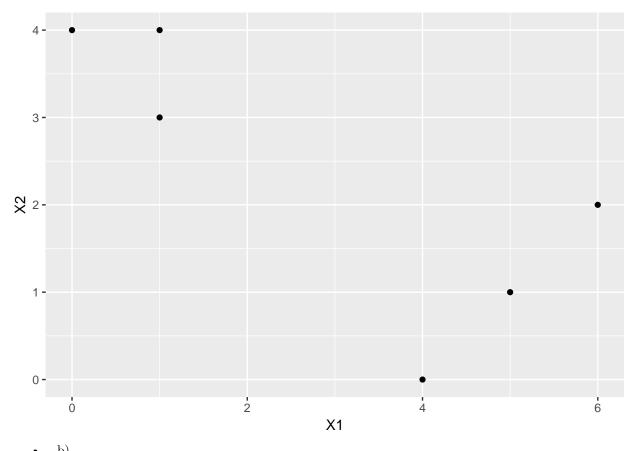
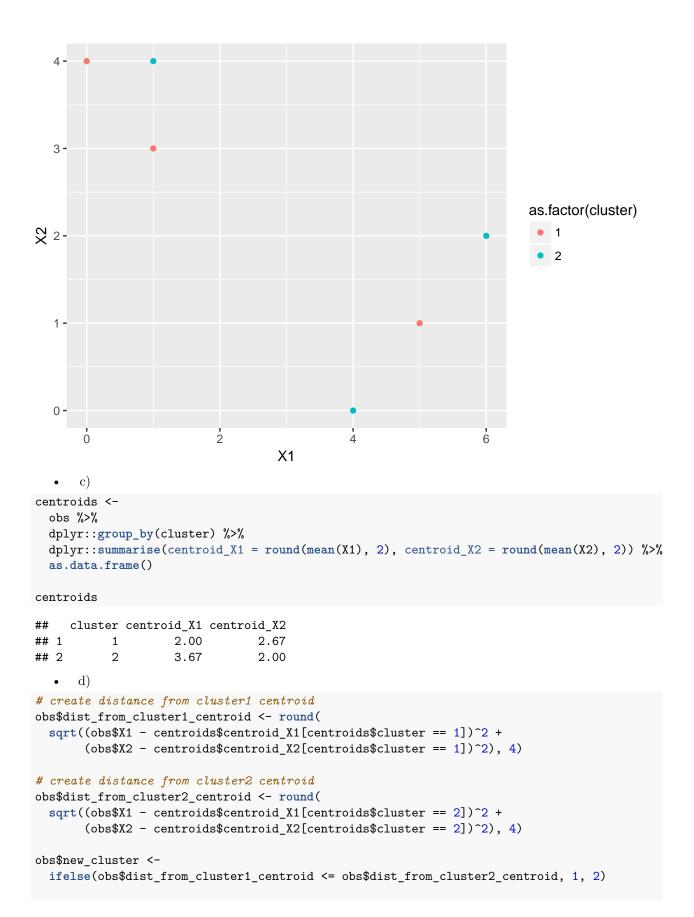
Week 8 Assignment

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```
library(tidyverse)
## Loading tidyverse: ggplot2
## Loading tidyverse: tibble
## Loading tidyverse: tidyr
## Loading tidyverse: readr
## Loading tidyverse: purrr
## Loading tidyverse: dplyr
## Conflicts with tidy packages -----
## filter(): dplyr, stats
## lag():
             dplyr, stats
library(ISLR)
library(maps)
##
## Attaching package: 'maps'
## The following object is masked from 'package:purrr':
##
##
library(ggmap)
library(mapdata)
10.7 \# 3
  • a)
obs <- data.frame(</pre>
 X1 = c(1, 1, 0, 5, 6, 4),
 X2 = c(4, 3, 4, 1, 2, 0)
obs %>%
  ggplot(aes(x = X1, y = X2)) +
geom_point()
```



```
# set random number seed for replicable results
set.seed(2017)
# assign the labels
obs$cluster <- sample(rep(c(1, 2), each = 3), 6, replace = FALSE)</pre>
# print the labels
obs
    X1 X2 cluster
## 1 1 4
## 2 1 3
## 3 0 4
                1
## 4 5 1
                1
## 5 6 2
                2
## 6 4 0
# plot the labels
obs %>%
 dplyr::select(X1, X2, cluster) %>%
 ggplot(aes(x = X1, y = X2, color = as.factor(cluster))) +
geom_point()
```



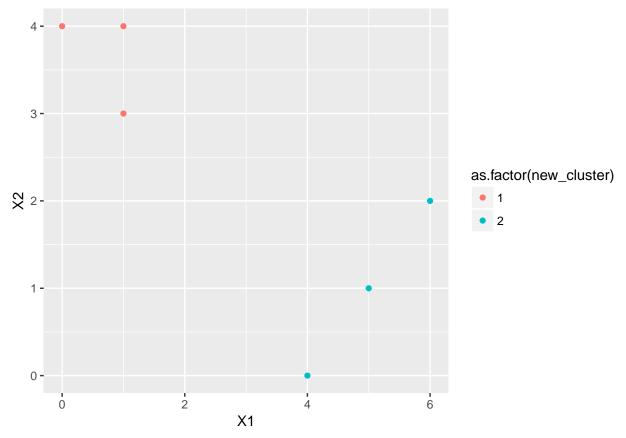
```
X1 X2 cluster dist_from_cluster1_centroid dist_from_cluster2_centroid
## 1 1 4
                                         1.6640
                                                                     3.3360
## 2 1 3
                                         1.0530
                                                                     2.8511
## 3 0 4
                 1
                                        2.4019
                                                                     4.1796
## 4 5 1
                                        3.4335
                                                                     1.6640
## 5 6 2
                                                                     2.3300
                 2
                                        4.0557
## 6 4 0
                                        3.3360
                                                                     2.0270
## new_cluster
## 1
## 2
               1
## 3
               1
## 4
               2
## 5
               2
## 6
      e)
cluster_difference <- FALSE</pre>
while(cluster_difference == FALSE){
# reset obs$cluster to obs$new_cluster
obs$cluster <- obs$new_cluster</pre>
# create distance from cluster1 centroid
obs$dist_from_cluster1_centroid <- round(</pre>
  sqrt((obs$X1 - centroids$centroid_X1[centroids$cluster == 1])^2 +
       (obs$X2 - centroids$centroid_X2[centroids$cluster == 1])^2), 4)
# create distance from cluster2 centroid
obs$dist_from_cluster2_centroid <- round(</pre>
  sqrt((obs$X1 - centroids$centroid_X1[centroids$cluster == 2])^2 +
       (obs$X2 - centroids$centroid_X2[centroids$cluster == 2])^2), 4)
obs$new_cluster <-
  ifelse(obs$dist_from_cluster1_centroid <= obs$dist_from_cluster2_centroid, 1, 2)</pre>
cluster_difference <- all(obs$cluster == obs$new_cluster)</pre>
print(obs)
    X1 X2 cluster dist_from_cluster1_centroid dist_from_cluster2_centroid
## 1 1 4
                                                                     3.3360
                1
                                         1.6640
## 2 1 3
                                         1.0530
                 1
                                                                     2.8511
## 3 0 4
                                        2.4019
                                                                     4.1796
                1
## 4 5 1
                 2
                                        3.4335
                                                                     1.6640
## 5 6 2
                 2
                                         4.0557
                                                                     2.3300
## 6 4 0
                                        3.3360
                                                                     2.0270
## new_cluster
## 1
               1
## 2
               1
```

```
## 3 1
## 4 2
## 5 2
## 6 2
```

The clustering only took one iteration until the algorithm converged.

• f)

```
obs %>%
  dplyr::select(X1, X2, new_cluster) %>%
  ggplot(aes(x = X1, y = X2, color = as.factor(new_cluster))) +
  geom_point()
```



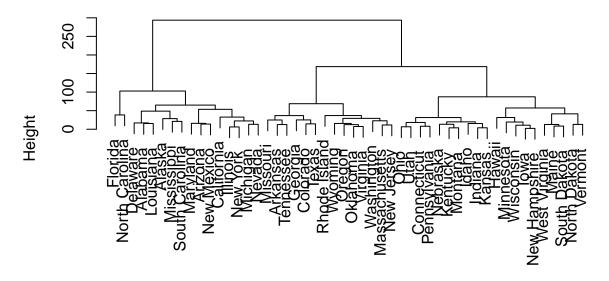
```
10.7 #9
```

• a)

```
# load data
data("USArrests")

# perform clustering and plot
hc_complete_no_scale <- hclust(dist(USArrests), method = "complete")
plot(hc_complete_no_scale, main = "Complete Linkage \n No Scaling")</pre>
```

Complete Linkage No Scaling



dist(USArrests) hclust (*, "complete")

• b)

use cutree, specifying 3 clusters
cutree(hc_complete_no_scale, k = 3)

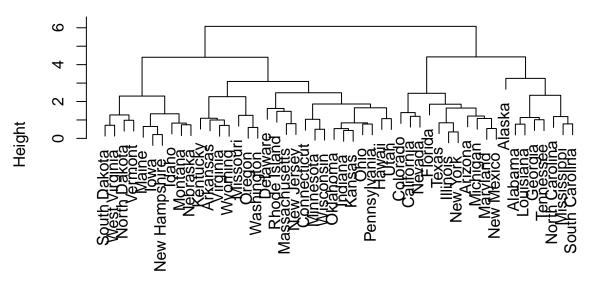
## 2 3 1 1 1 ## Hawaii Idaho Illinois Indiana ## 3 3 1 3 ## Kansas Kentucky Louisiana Maine Mary ## 3 3 1 3	1 orgia 2 Iowa 3 yland 1
## Colorado Connecticut Delaware Florida Geo ## 2 3 1 1 ## Hawaii Idaho Illinois Indiana ## 3 3 1 3 ## Kansas Kentucky Louisiana Maine Mary ## 3 3 1 3	2 Iowa 3 yland 1
## 2 3 1 1 1 ## Hawaii Idaho Illinois Indiana ## 3 3 1 3 1 3 ## Kansas Kentucky Louisiana Maine Mary ## 3 3 1 3	2 Iowa 3 yland 1
## Hawaii Idaho Illinois Indiana ## 3 3 1 3 ## Kansas Kentucky Louisiana Maine Mary ## 3 3 1 3	3 yland 1
## 3 3 1 3 ## Kansas Kentucky Louisiana Maine Mary ## 3 3 1 3	3 yland 1
## Kansas Kentucky Louisiana Maine Mary ## 3 3 1 3	yland 1
## 3 3 1 3	1
	1
## Managharatta Mishima Minagharata Minajadani Mina	
## Massachusetts Michigan Minnesota Mississippi Miss	souri
## 2 1 3 1	2
## Montana Nebraska Nevada New Hampshire New Je	ersey
## 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 Card	olina
## 2 2 3 2	1
## South Dakota Tennessee Texas Utah Ver	rmont
## 3 2 2 3	3
## Virginia Washington West Virginia Wisconsin Wyo	oming
## 2 2 3 3	2

• c)

```
# scale the USArrests data set
USArrests_scaled <- scale(USArrests)

# perform clustering on scaled data
hc_complete_scaled <- hclust(dist(USArrests_scaled), method = "complete")
plot(hc_complete_scaled, main = "Complete Linkage \n With Scaling")</pre>
```

Complete Linkage With Scaling



dist(USArrests_scaled) hclust (*, "complete")

use cutree, specifying 3 clusters cutree(hc_complete_scaled, k = 3)

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

```
## Virginia Washington West Virginia Wisconsin Wyoming
## 3 3 3 3 3
• d)
```

As can be seen from the results below, clustering on scaled data can create much different results than clustering on non-scaled data. The non-scaled data more evenly distributes the cluster assignments between 1, 2, and 3 while the scaled data creates far more cluster 3 labels (31) than cluster 1 or 2 labels (8 and 11 respectively). Furthermore, in examining in the scale of the variables, we see that Murder ranges from 0.80 to 17.40, Assault ranges from 45.0 to 337.0, UrbanPop ranges from 32.00 to 91.00, and Rape ranges from 7.30 to 46.00. Given the varying scales of these variables and because we are using Euclidean Distance, we expect Assault to dominate the clustering, followed by UrbanPop and Rape. Murder will have less of an effect because it is on a much smaller scale than the other variables. For example, a difference of 15 is significant for the Murder variable while it is fairly small for the Assault variable. In fact, 15 almost covers the entire range of Murder while it covers hardly any of the range for Assault.

```
# create data frame for comparison
no_scale <- data.frame(not_scaled_clusters = cutree(hc_complete_no_scale, k = 3))</pre>
with_scale <- data.frame(with_scaled_clusters = cutree(hc_complete_scaled, k = 3))</pre>
both_clusters <- cbind(no_scale, with_scale)</pre>
both_clusters$clusters_match <-
  ifelse(both_clusters$not_scaled_clusters == both_clusters$with_scaled_clusters,
         TRUE,
         FALSE)
# determine percentage of states whose clusters match between scaled and non-scaled data
round(mean(both_clusters$clusters_match), 4)
## [1] 0.56
# get counts of clusters per method
table(both_clusters$not_scaled_clusters)
##
##
   1 2 3
## 16 14 20
table(both_clusters$with_scaled_clusters)
##
##
    1 2 3
    8 11 31
# create a table comparison of the two clustering methods
table(both_clusters$not_scaled_clusters, both_clusters$with_scaled_clusters)
##
             3
##
           2
           9
##
        6
             1
     1
##
     2
        2
           2 10
       0
          0 20
##
# create summary of USArrests data set
summary(USArrests)
```

Mean : 7.788 Mean :170.8 Mean :65.54 Mean :21.23 ## 3rd Qu::11.250 3rd Qu::249.0 3rd Qu::77.75 3rd Qu::26.18 ## Max :17.400 Max :337.0 Max :91.00 Max :46.00