

ISLR | Chapter 10 Exercises

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Conceptual

1

NEED TO COME BACK TOO

- A. 10.12, illustrated below, is showing the the *within-cluster variation* is equal to twice the squared distance between each data point in cluster k (C_k) and that cluster's centroid, summed across all data points.

$$\frac{1}{|C_k|} \sum_{i,i' \in C_k} \sum_{j=1}^P (x_{i,j} - x_{i',j})^2 = 2 \sum_{i \in C_k} \sum_{j=1}^P (x_{i,j} - \bar{x}_{k,j})^2 \quad (1)$$

$$\frac{1}{|C_k|} \sum_{i,i' \in C_k} \sum_{j=1}^P (x_{i,j} - x_{i',j})(x_{i,j} - x_{i',j}) = 2 \sum_{i \in C_k} \sum_{j=1}^P (x_{i,j} - \bar{x}_{k,j})(x_{i,j} - \bar{x}_{k,j}) \quad (2)$$

$$\frac{1}{|C_k|} \sum_{i,i' \in C_k} \sum_{j=1}^P (x_{i,j}^2 - 2x_{i,j}x_{i',j} + x_{i',j}^2) = 2 \sum_{i \in C_k} \sum_{j=1}^P (x_{i,j}^2 - 2\bar{x}_{k,j}x_{i,j} + \bar{x}_{k,j}^2) \quad (3)$$

$$\frac{|C_k|}{|C_k|} \sum_{i,i' \in C_k} \sum_{j=1}^P (x_{i,j}^2 - 2x_{i,j}x_{i',j} + x_{i',j}^2) = 2|C_k| \sum_{i \in C_k} \sum_{j=1}^P (x_{i,j}^2 - 2\bar{x}_{k,j}x_{i,j} + \bar{x}_{k,j}^2) \quad (4)$$

$$\sum_{i,i' \in C_k} \sum_{j=1}^P (x_{i,j}^2 - 2x_{i,j}x_{i',j} + x_{i',j}^2) = 2|C_k| \sum_{i \in C_k} \sum_{j=1}^P (x_{i,j}^2 - 2\bar{x}_{k,j}x_{i,j} + \bar{x}_{k,j}^2) \quad (5)$$

$$\sum_{i \in C_k} \sum_{j=1}^P x_{i,j}^2 - 2 \sum_{i,i' \in C_k} \sum_{j=1}^P x_{i,j}x_{i',j} + \sum_{i' \in C_k} \sum_{j=1}^P x_{i',j}^2 = 2|C_k| \sum_{i \in C_k} \sum_{j=1}^P x_{i,j}^2 - 2|C_k| \sum_{i \in C_k} \sum_{j=1}^P 2\bar{x}_{k,j}x_{i,j} + 2|C_k| \sum_{i \in C_k} \sum_{j=1}^P \bar{x}_{k,j}^2 \quad (6)$$

$$\sum_{i \in C_k} \sum_{j=1}^P x_{i,j}^2 - 2 \sum_{i,i' \in C_k} \sum_{j=1}^P x_{i,j}x_{i',j} + \sum_{i' \in C_k} \sum_{j=1}^P x_{i',j}^2 = 2|C_k| \sum_{i \in C_k} \sum_{j=1}^P x_{i,j}^2 - 4|C_k| \sum_{i \in C_k} \sum_{j=1}^P \bar{x}_{k,j}x_{i,j} + 2|C_k| \sum_{i \in C_k} \sum_{j=1}^P \bar{x}_{k,j}^2 \quad (7)$$

$$(8)$$

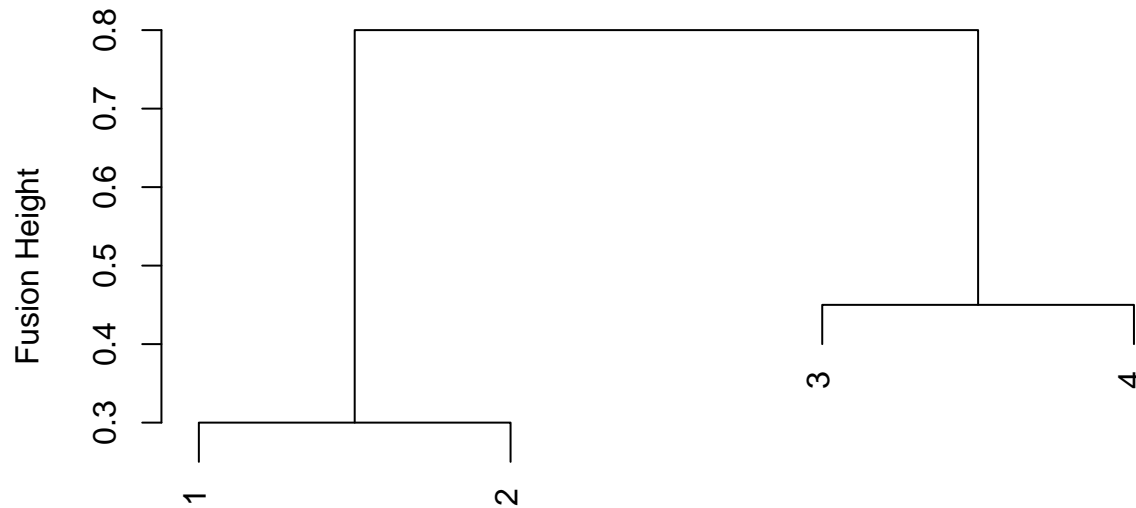
2

- A.

```
x <- matrix(c(0, 0.3, 0.4, 0.7,
              0.3, 0, 0.5, 0.8,
              0.4, 0.5, 0, 0.45,
              0.7, 0.8, 0.45, 0), ncol = 4, nrow = 4)
```

```
plot(hclust(as.dist(x), method = 'complete'),
     xlab = "",
     sub = "",
     ylab = "Fusion Height")
```

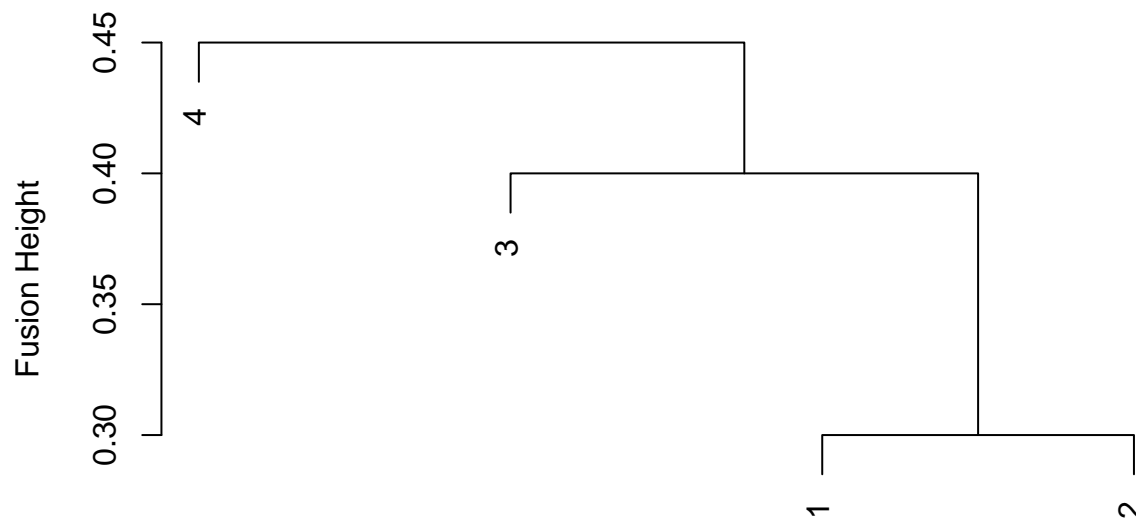
Cluster Dendrogram



- B.

```
plot(hclust(as.dist(x), method = 'single'),
     xlab = "",
     sub = "",
     ylab = "Fusion Height")
```

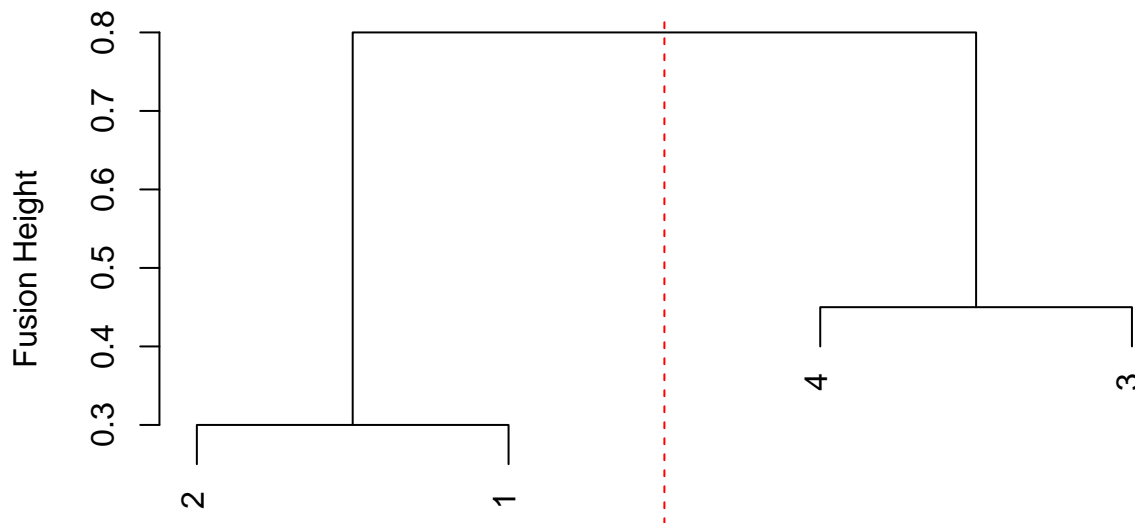
Cluster Dendrogram



- C. Observations 1 & 2 will be in cluster *A* and observations 3 & 4 will be in cluster *B* (assuming one cuts the dendrogram at a height greater than 0.45).
- D. Although the answer to this question depends on where one cuts the dendrogram, the most likely clusters would contain observations 1 & 2 in cluster *A* and observations 3 & 4 in cluster *B*. This would result from a cut at a height greater than 0.3 and less than 0.4, which is the largest vertical distance on the dendrogram. If one were to make a cut between 0.4 and 0.45, then cluster *A* would contain observations 1, 2 & 3, while cluster *B* would consist of only observation 4. However, with the distance being greater between clusters for the first grouping, that would be the more probable grouping.
- E. As shown below, one can simply switch the labels of the observations within each cluster to change the dendrogram without changing the meaning of the dendrogram. In addition, one could take the mirror image of the plot displayed along the dotted red line, producing a “new” dendrogram that has the same meaning.

```
plot(hclust(as.dist(x), method = 'complete'),
     xlab = "",
     sub = "",
     ylab = "Fusion Height", labels = c(2,1,4,3))
abline(v = 2.5, col = 'red', lty = 2)
```

Cluster Dendrogram

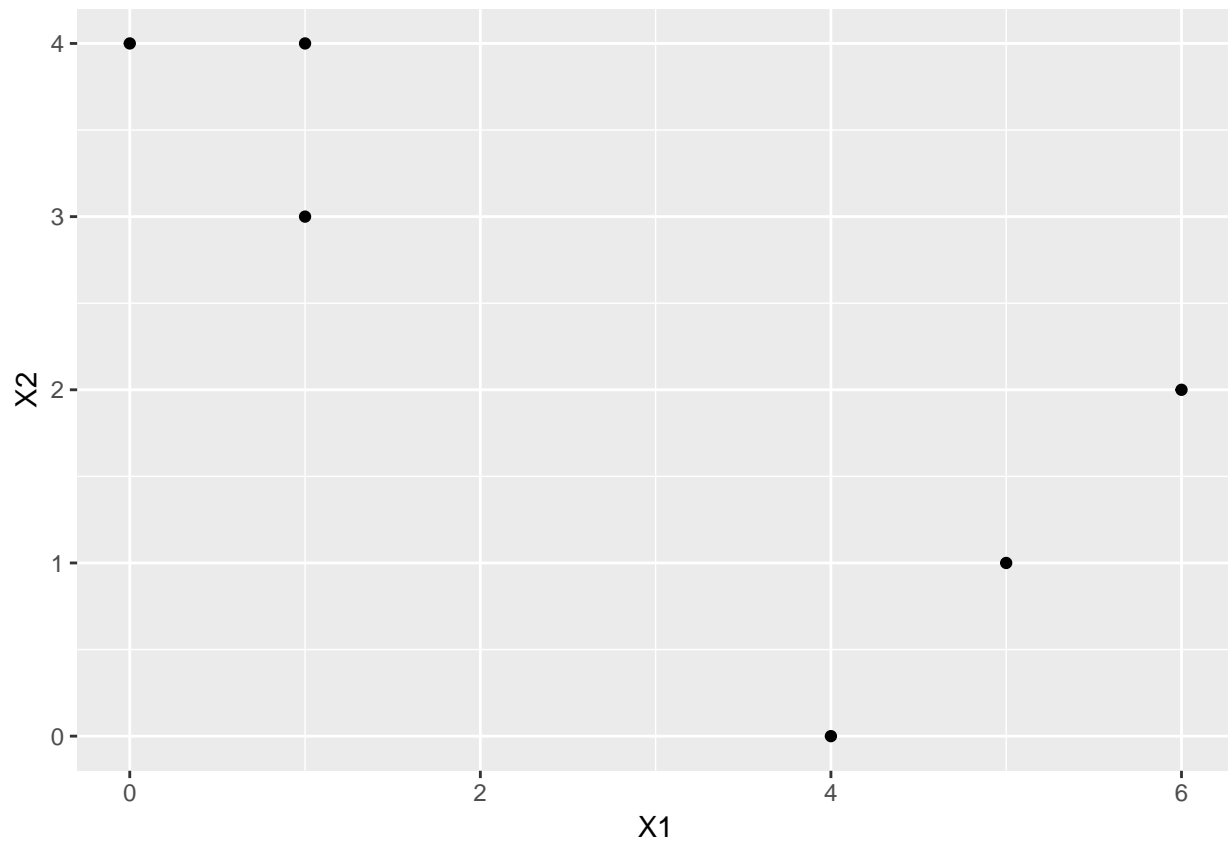


3

- A.

```
suppressPackageStartupMessages(library(ggplot2))
df <- data.frame(x1 = c(1,1,0,5,6,4),
```

```
x2 = c(4,3,4,1,2,0)
qplot(df$x1, df$x2, xlab = 'X1', ylab = 'X2')
```



• B.

```
suppressPackageStartupMessages(library(knitr))
df$group <- sample(c('A','B'), 6, replace = TRUE)
knitr::kable(df, caption = 'Sample Data with Group Assignments')
```

Table 1: Sample Data with Group Assignments

x1	x2	group
1	4	B
1	3	A
0	4	B
5	1	B
6	2	B
4	0	A

• C.

```

group.a <- subset(df, group == 'A')
group.b <- subset(df, group == 'B')

# centroid calculation
calculate.centroid <- function(df, variables=c('x1','x2')) {

  coordinates <- NULL

  for (variable in variables) {
    column.mean <- mean(df[, variable])
    coordinates <- c(column.mean, coordinates)
  }

  return(coordinates)
}
group.a.centroid <- calculate.centroid(group.a)
group.b.centroid <- calculate.centroid(group.b)
print(paste("Group A centroid at coordinates",
            round(group.a.centroid[1], 2), 'and', round(group.a.centroid[2], 2)))

## [1] "Group A centroid at coordinates 1.5 and 2.5"
print(paste("Group B centroid at coordinates",
            round(group.b.centroid[1], 2), 'and', round(group.b.centroid[2], 2)))

## [1] "Group B centroid at coordinates 2.75 and 3"

```

- D.

```

centroid.matrix <- matrix(c(group.a.centroid, group.b.centroid),
                          nrow = 2,
                          ncol = 2)

reassign.cluster <- function(df,
                              col.idx=c(1,2),
                              cluster.column='group',
                              cluster.labels=c('A','B'),
                              centroids=centroid.matrix) {

  df.matrix <- as.matrix(df[, col.idx])

  updated.labels <- NULL
  for (i in 1:dim(df.matrix)[1]) {

    sqr.manhattan.dist <- (df.matrix[i, ] - centroids)^2
    euclidean.dist <- sqrt(colSums(sqr.manhattan.dist))
    closest.centroid <- which.min(euclidean.dist)
    updated.labels <- c(updated.labels, cluster.labels[closest.centroid])

  }

  return(data.frame(df.matrix, group = updated.labels))
}

```

```

}
updated.df <- reassign.cluster(df)
knitr::kable(updated.df, caption = "Sample Data After One Reassignment Iteration")

```

Table 2: Sample Data After One Reassignment Iteration

x1	x2	group
1	4	A
1	3	A
0	4	A
5	1	B
6	2	B
4	0	B

- E.

```

for (i in 1:20) {
  # split data
  group.a <- subset(df, group == 'A')
  group.b <- subset(df, group == 'B')

  # recalculate centroid
  group.a.centroid <- calculate.centroid(group.a)
  group.b.centroid <- calculate.centroid(group.b)

  # create centroid matrix
  centroid.matrix <- matrix(c(group.a.centroid, group.b.centroid), nrow = 2, ncol = 2)

  # re-assign group labels
  df <- reassign.cluster(df)
}

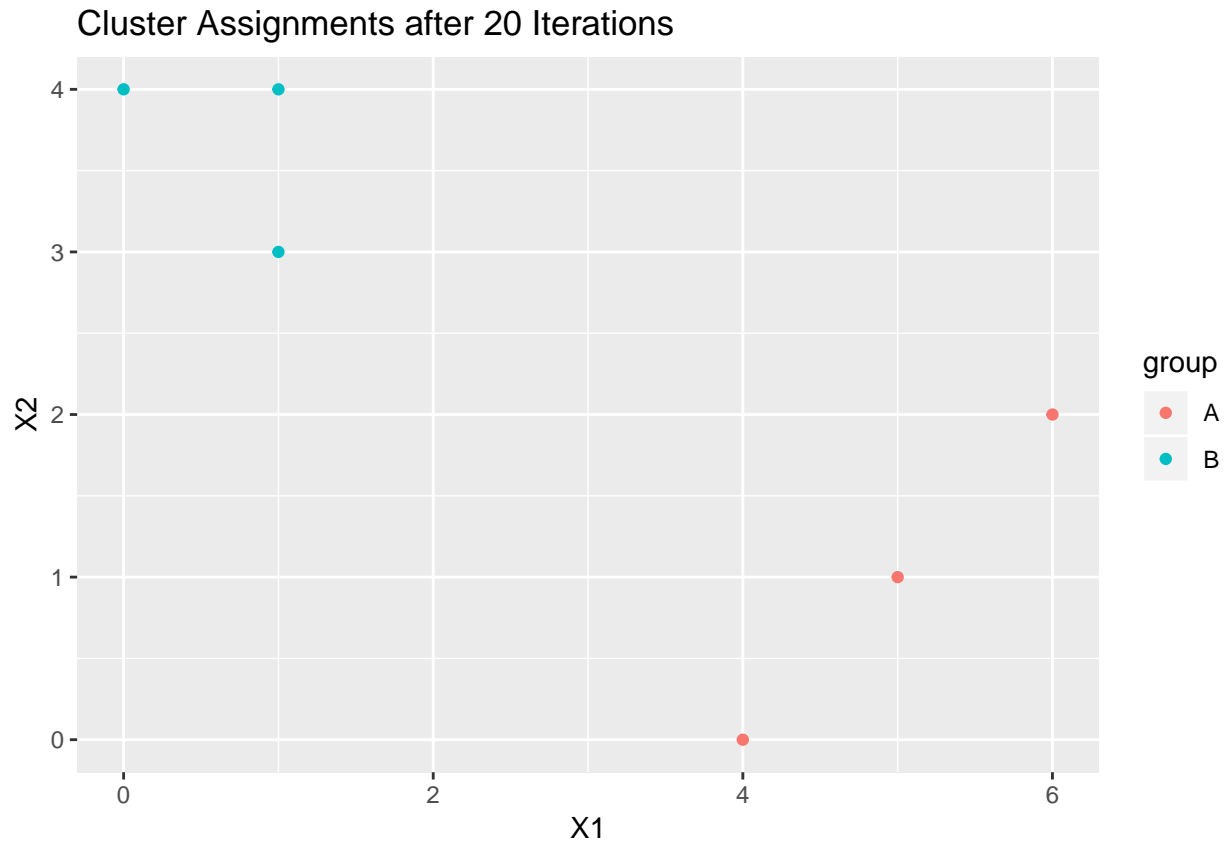
```

- F.

```

ggplot(df, aes(x = x1, y = x2, color = group)) +
  geom_point() +
  xlab('X1') +
  ylab('X2') +
  ggtitle('Cluster Assignments after 20 Iterations')

```



4

- **A.** Assuming the maximal intercluster dissimilarity is **not equal** to the minimal intercluster dissimilarity, the clusters $\{1, 2, 3\}$ and $\{4, 5\}$ will be fused higher on the dendrogram when complete linkage is used. While complete linkage uses the *maximal* intercluster dissimilarity, single linkage uses the *minimal* intercluster dissimilarity. So, if the first assumption is held, using complete linkage will lead to the fusion occurring higher on the dendrogram. However, if the maximal intercluster dissimilarity is equal to the minimal intercluster dissimilarity, then they would fuse at the same height, regardless of the linkage method used.

Resources

[Dendrograms in R](#)