Non - Hierarchical Cluster

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UTB - Data Science

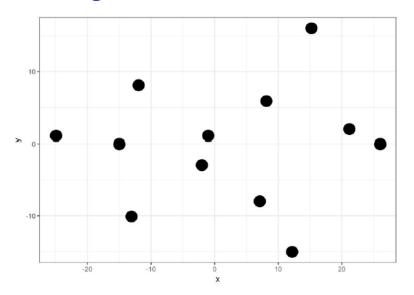


Figure 1:

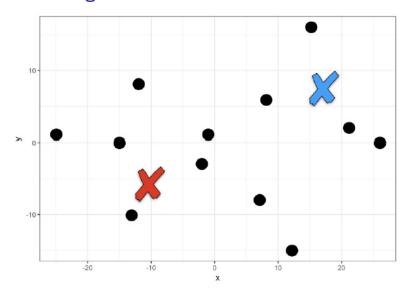


Figure 2:

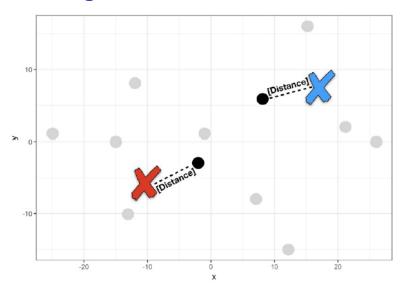


Figure 3:

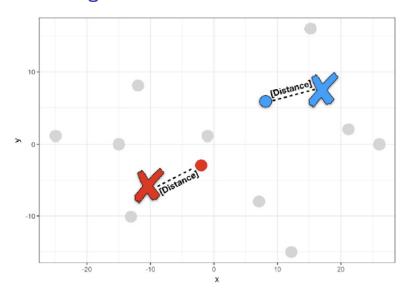


Figure 4:

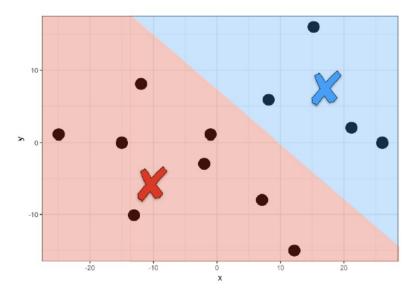
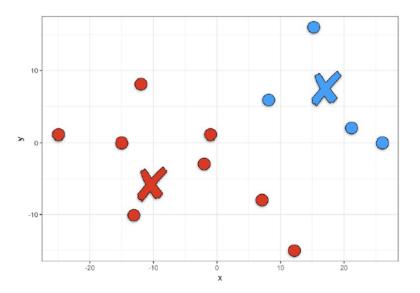


Figure 5:



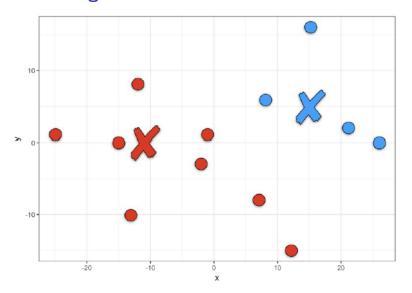


Figure 7:

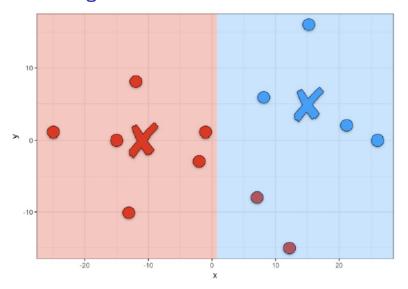


Figure 8:

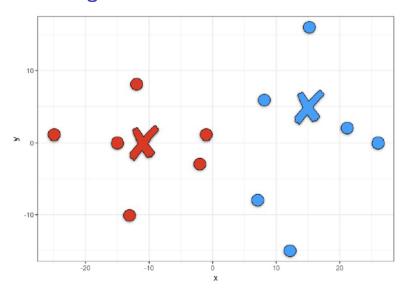


Figure 9:

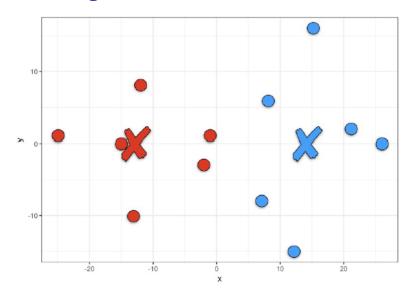


Figure 10:

kmeans in r with function kmeans()

lineup

```
## 1 -1 1
## 2 2 -3
## 3 8 6
## 4 7 -8
## 5 -12 8
## 6 -15 0
```

X Y

```
model <- kmeans(lineup, centers = 2)</pre>
```

Assigning Clusters

model\$cluster

```
library(dplyr)
## Warning: package 'dplyr' was built under R version 3.4.3
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
       filter, lag
##
## The following objects are masked from 'package:base':
##
##
       intersect, setdiff, setequal, union
```

ullet Total Within-Cluster Sum of Squares: k=1

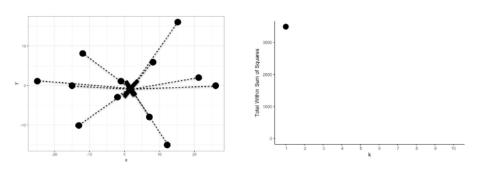


Figure 11:

ullet Total Within-Cluster Sum of Squares: k=2

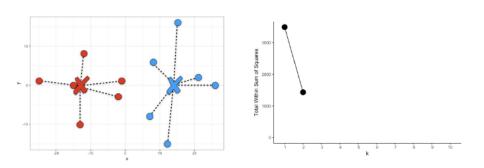


Figure 12:

 \bullet Total Within-Cluster Sum of Squares: k=3

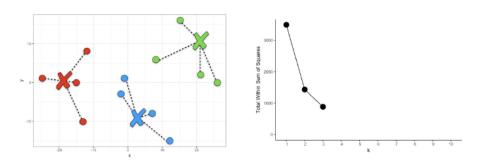


Figure 13:

ullet Total Within-Cluster Sum of Squares: k=4

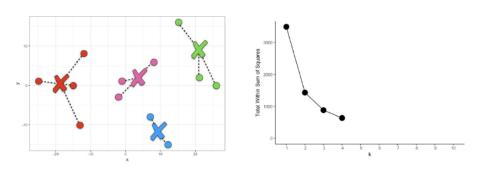


Figure 14:

Elbow Plot

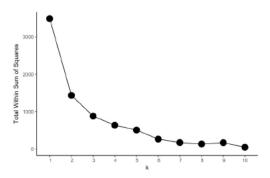


Figure 15:

Elbow Plot

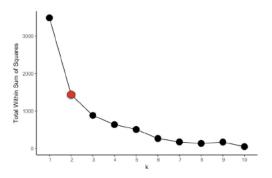


Figure 16:

Generating the Elbow Plot

```
model <- kmeans(x = lineup, centers = 2)
model$tot.withinss</pre>
```

```
## [1] 196.5
```

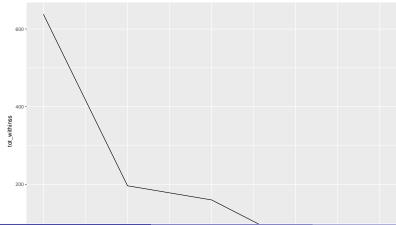
Generating the Elbow Plot

```
library(purrr)
tot withinss <- map dbl(1:5, function(k){
model <- kmeans(x = lineup, centers = k)
model $tot. withinss
})
elbow_df <- data.frame(</pre>
k = 1:5.
tot withinss = tot withinss
elbow df
## k tot_withinss
## 1 1 638.1667
## 2 2 196.5000
```

3 3 160.0000 ## 4 4 49.0000

Plotting the Elbow

```
library(ggplot2)
ggplot(elbow_df, aes(x = k, y = tot_withinss)) +
geom_line() +
scale_x_continuous(breaks = 1:10)
```



Silhouette Analysis

• Soccer Lineup with K = 3

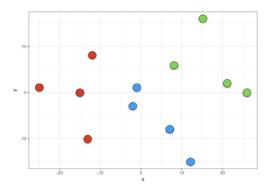


Figure 17:

Within Cluster Distance: C(i)

Closest Neighbor Distance: N(i)

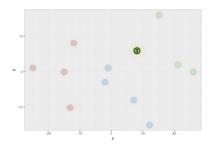


Figure 18:

Within Cluster Distance: C(i)

Closest Neighbor Distance: N(i)

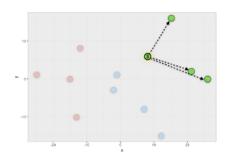


Figure 19:

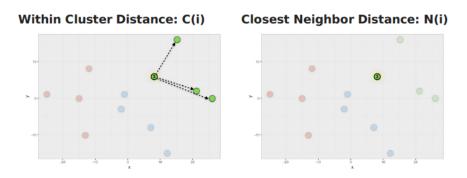


Figure 20:

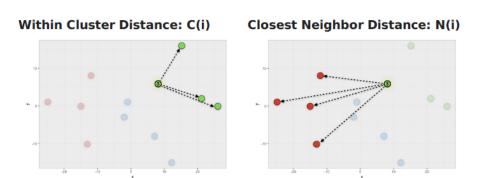


Figure 21:

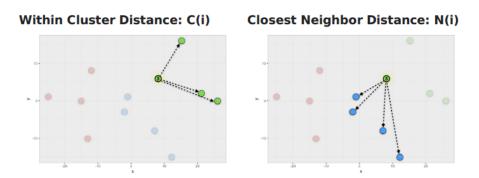
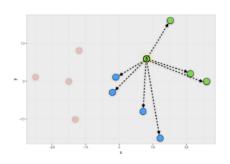


Figure 22:

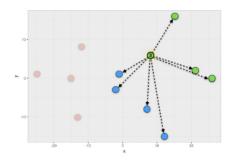
Silhouette Width S(i)



$$s(i) = \begin{cases} 1 - C(i)/N(i), & \text{if } C(i) < N(i) \\ 0, & \text{if } C(i) = N(i) \\ N(i)/C(i) - 1, & \text{if } C(i) > N(i) \end{cases}$$

Figure 23:

Silhouette Width S(i)





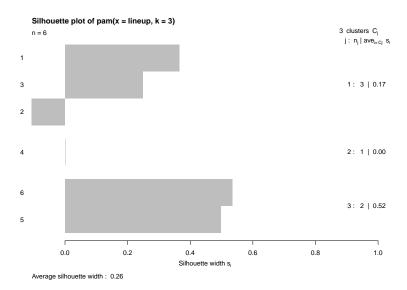
- 1: Well matched to cluster
- 0: On border between two clusters
- -1: Better fit in neighboring cluster

Figure 24:

Calculating S(i) in R

```
library(cluster)
pam_k3 <- pam(lineup, k = 3)
pam_k3$silinfo$widths</pre>
```

Silhouette Plot



Average Silhouette Width

```
## [1] 0.256384
```

- 1: Well matched to each cluster
- 0: On border between clusters
- -1: Poorly matched to each cluster

Highest Average Silhouette Width

```
## k sil_width
## 1 2 0.5021865
## 2 3 0.2563840
## 3 4 0.2845408
## 4 5 0.1345417
```

Choosing K using Average Silhouette Width

