

# Untitled

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```
# Helper packages  
library(dplyr)      # for data manipulation
```

## Helper packages and Modeling packages

```
## Warning: package 'dplyr' was built under R version 4.1.3
```

```
##  
## 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
```

```
library(ggplot2)    # for data visualization
```

```
## Warning: package 'ggplot2' was built under R version 4.1.3
```

```
library(stringr)    # for string functionality
```

```
## Warning: package 'stringr' was built under R version 4.1.3
```

```
library(gridExtra)  # for manipulating the grid
```

```
## Warning: package 'gridExtra' was built under R version 4.1.3
```

```
##  
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':  
##  
##   combine
```

```

# Modeling packages
library(tidyverse) # data manipulation

## Warning: package 'tidyverse' was built under R version 4.1.3

## -- Attaching packages ----- tidyverse 1.3.2 --

## v tibble  3.1.8      v purrr  0.3.4
## v tidyr   1.2.0      v forcats 0.5.2
## v readr   2.1.2

## Warning: package 'tibble' was built under R version 4.1.3

## Warning: package 'tidyr' was built under R version 4.1.3

## Warning: package 'readr' was built under R version 4.1.3

## Warning: package 'purrr' was built under R version 4.1.3

## Warning: package 'forcats' was built under R version 4.1.3

## -- Conflicts ----- tidyverse_conflicts() --
## x gridExtra::combine() masks dplyr::combine()
## x dplyr::filter()      masks stats::filter()
## x dplyr::lag()         masks stats::lag()

library(cluster) # for general clustering algorithms
library(factoextra) # for visualizing cluster results

## Warning: package 'factoextra' was built under R version 4.1.3

## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa

data("iris")

#To remove any missing value that might be present in the data, type this:
df <- na.omit(iris)

```

## Loading of Data and Removing of Any Missing Values

```
#we start by scaling/standardizing the data
df <- scale(df[c(1:4)])
head(df)
```

### Scaling/standardizing the data

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width
## 1   -0.8976739   1.01560199   -1.335752   -1.311052
## 2   -1.1392005  -0.13153881   -1.335752   -1.311052
## 3   -1.3807271   0.32731751   -1.392399   -1.311052
## 4   -1.5014904   0.09788935   -1.279104   -1.311052
## 5   -1.0184372   1.24503015   -1.335752   -1.311052
## 6   -0.5353840   1.93331463   -1.165809   -1.048667
```

```
#start at 2 clusters
k2 <- kmeans(df, centers = 2, nstart = 25)
str(k2)
```

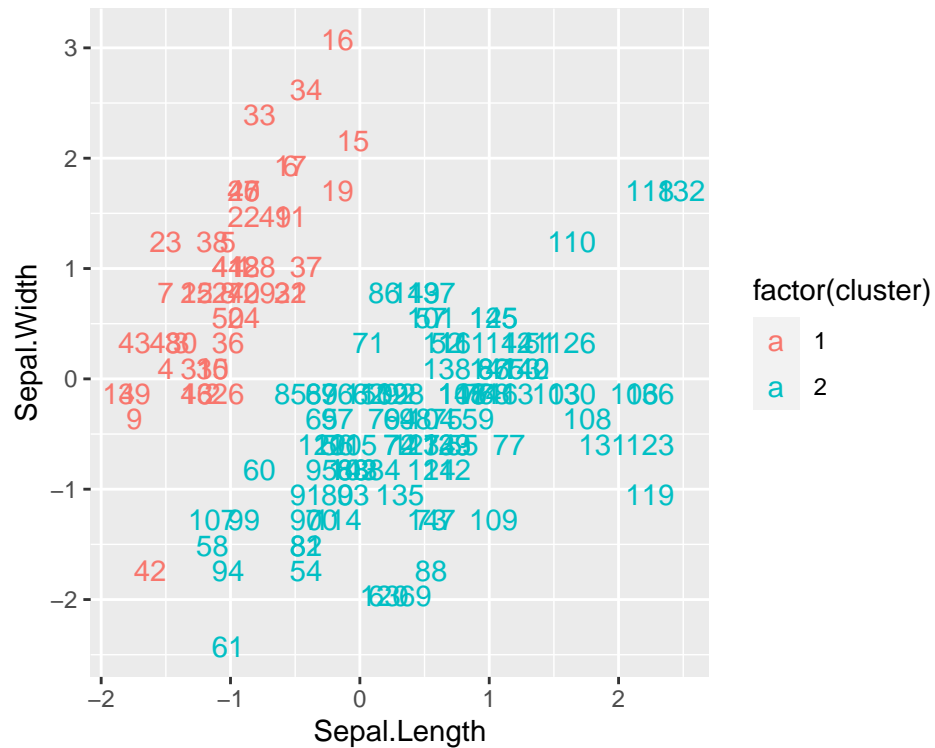
### Start 2 clusters

```
## List of 9
## $ cluster      : Named int [1:150] 1 1 1 1 1 1 1 1 1 1 ...
##   ..- attr(*, "names")= chr [1:150] "1" "2" "3" "4" ...
## $ centers       : num [1:2, 1:4] -1.011 0.506 0.85 -0.425 -1.301 ...
##   ..- attr(*, "dimnames")=List of 2
##     .. ..$ : chr [1:2] "1" "2"
##     .. ..$ : chr [1:4] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width"
## $ totss        : num 596
## $ withinss     : num [1:2] 47.4 173.5
## $ tot.withinss : num 221
## $ betweenss    : num 375
## $ size         : int [1:2] 50 100
## $ iter         : int 1
## $ ifault       : int 0
## - attr(*, "class")= chr "kmeans"
```

```
#plot the 2 clusters
fviz_cluster(k2, data = df)
```

Dim1 (73%)

```
#get the each clusters data
df %>%
  as_tibble() %>%
  mutate(cluster = k2$cluster,
         Species = row.names(iris)) %>%
  ggplot(aes(Sepal.Length, Sepal.Width, color = factor(cluster), label = Species)) +
  geom_text()
```

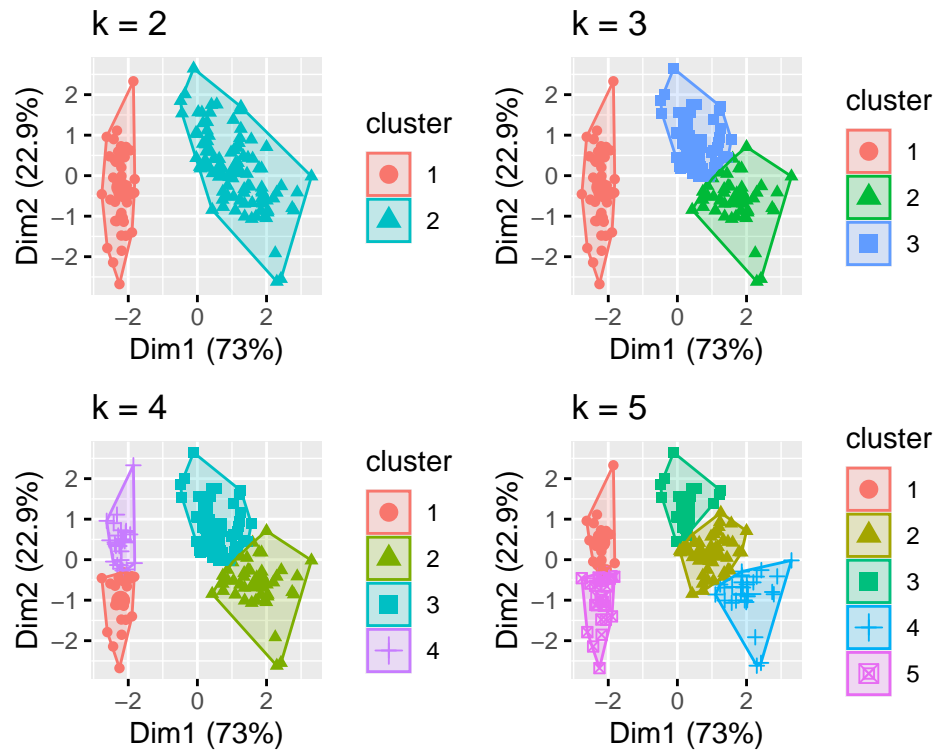


Each clusters data

```
k3 <- kmeans(df, centers = 3, nstart = 25)
k4 <- kmeans(df, centers = 4, nstart = 25)
k5 <- kmeans(df, centers = 5, nstart = 25)
```

```
# plots to compare
p1 <- fviz_cluster(k2, geom = "point", data = df) + ggtitle("k = 2")
p2 <- fviz_cluster(k3, geom = "point", data = df) + ggtitle("k = 3")
p3 <- fviz_cluster(k4, geom = "point", data = df) + ggtitle("k = 4")
p4 <- fviz_cluster(k5, geom = "point", data = df) + ggtitle("k = 5")

grid.arrange(p1, p2, p3, p4, nrow = 2)
```



Plots to compare

```
#Determining Optimal Number of Clusters
set.seed(123)
```

### Determining Optimal Number of Clusters

```
# Function to compute total within-cluster sum of square
wss <- function(k) {
  kmeans(df, k, nstart = 10)$tot.withinss
}
```

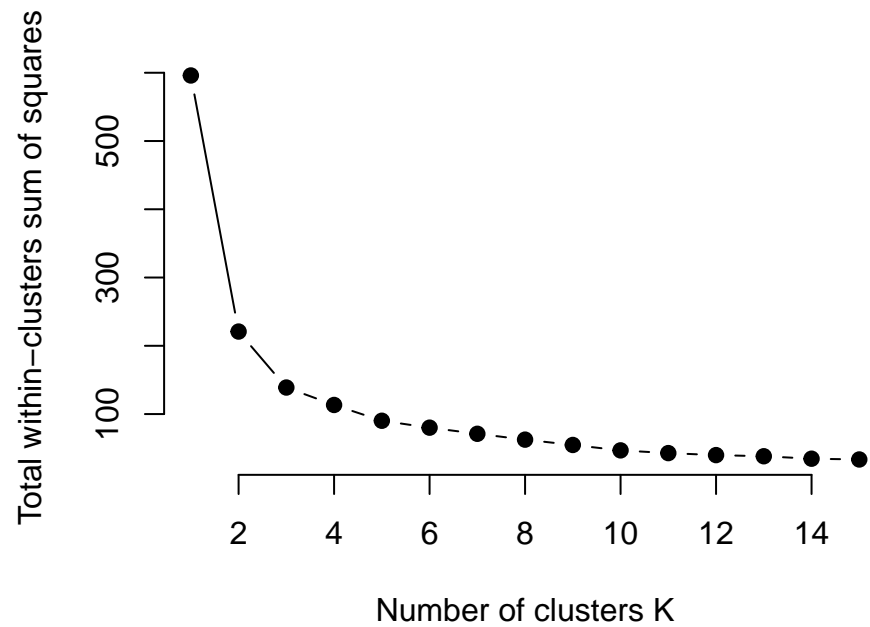
### Function to compute total within-cluster sum of square

```
# Compute and plot wss for k = 1 to k = 15
k.values <- 1:15
```

### Compute and plot wss for k = 1 to k = 15

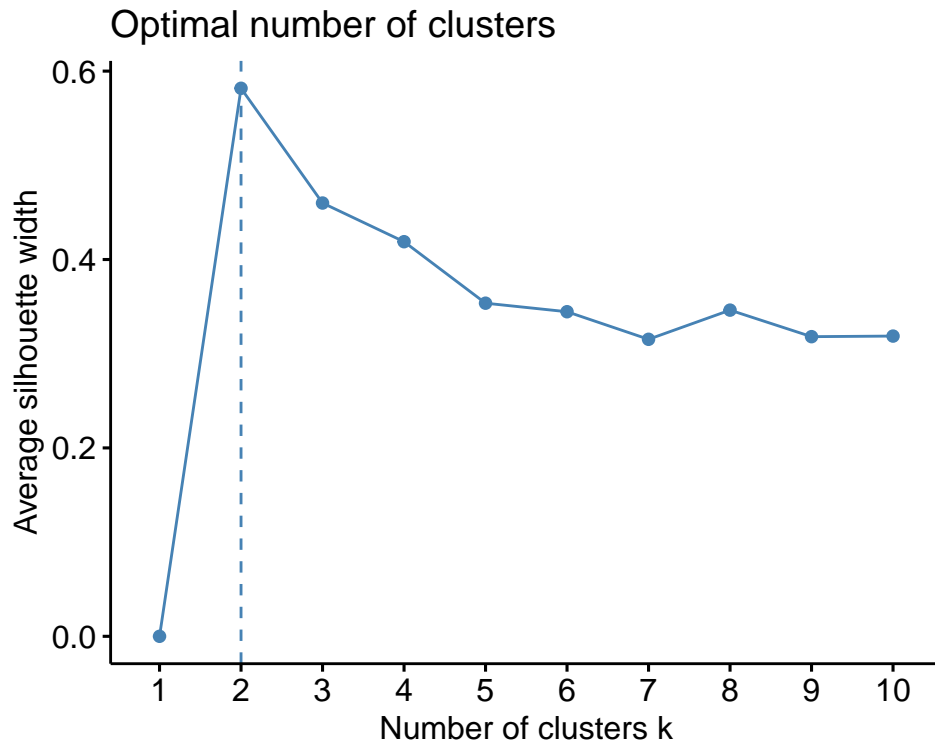
```
# extract wss for 2-15 clusters
wss_values <- map_dbl(k.values, wss)

plot(k.values, wss_values,
     type="b", pch = 19, frame = FALSE,
     xlab="Number of clusters K",
     ylab="Total within-clusters sum of squares")
```



Extract wss for 2-15 clusters

```
#or use this
fviz_nbclust(df, kmeans, method = "silhouette")
```



Or use this

```
# compute gap statistic
set.seed(123)
gap_stat <- clusGap(df, FUN = kmeans, nstart = 25,
                    K.max = 10, B = 50)
```

Compute gap statistic

```
# Print the result
print(gap_stat, method = "firstmax")
```

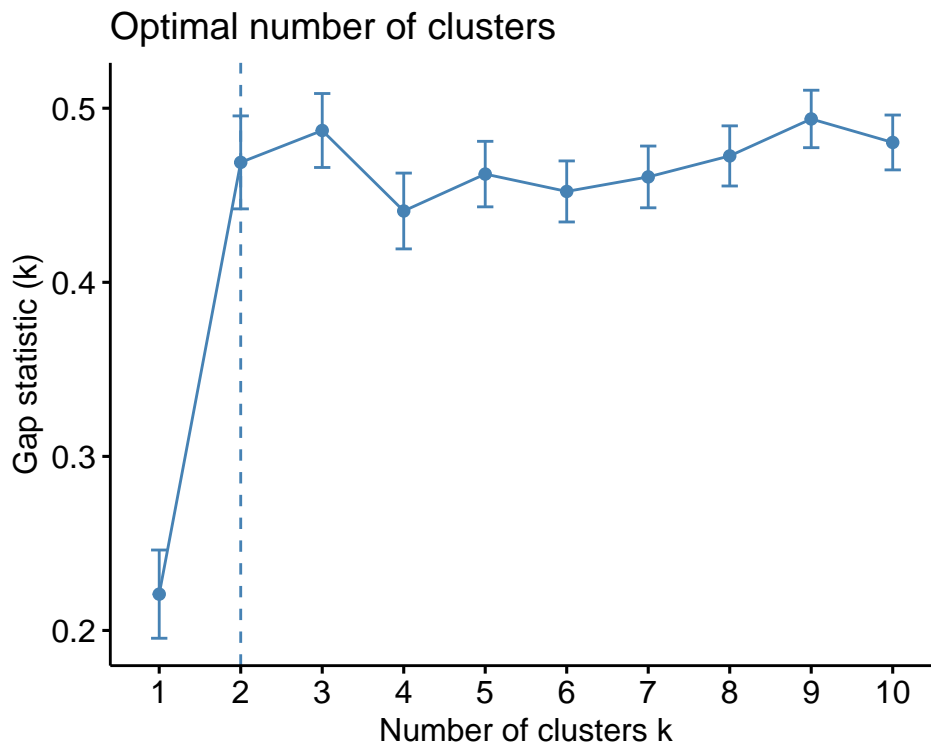
Print the result

```
## Clustering Gap statistic ["clusGap"] from call:
## clusGap(x = df, FUNcluster = kmeans, K.max = 10, B = 50, nstart = 25)
## B=50 simulated reference sets, k = 1..10; spaceH0="scaledPCA"
## --> Number of clusters (method 'firstmax'): 3
##      logW    E.logW      gap    SE.sim
## [1,] 4.534565 4.755428 0.2208634 0.02534324
## [2,] 4.021316 4.490212 0.4688953 0.02670070
## [3,] 3.806577 4.293793 0.4872159 0.02124741
```



```
## [4,] 3.699263 4.140237 0.4409736 0.02177507
## [5,] 3.589284 4.051459 0.4621749 0.01882154
## [6,] 3.522810 3.975009 0.4521993 0.01753073
## [7,] 3.448288 3.908834 0.4605460 0.01774025
## [8,] 3.379870 3.852475 0.4726054 0.01727207
## [9,] 3.310088 3.803931 0.4938436 0.01649671
## [10,] 3.278659 3.759003 0.4803440 0.01576050
```

```
fviz_gap_stat(gap_stat)
```



```
# Compute k-means clustering with k = 2
set.seed(123)
final <- kmeans(df, 2, nstart = 25)
print(final)
```

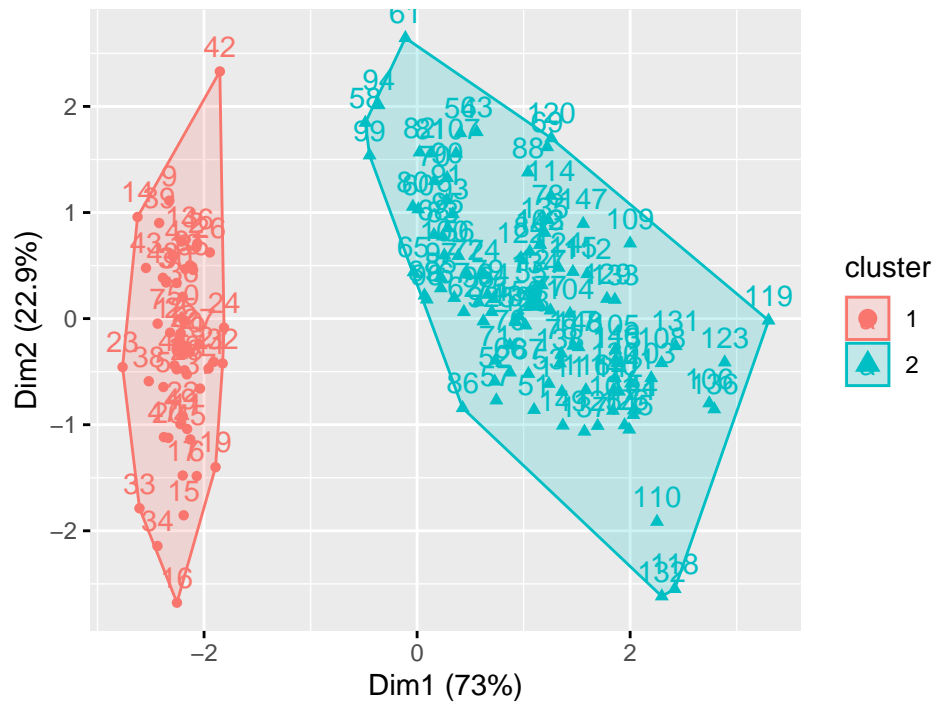
Compute k-means clustering with  $k = 2$

```
## K-means clustering with 2 clusters of sizes 50, 100
```

```
##
## Cluster means:
##   Sepal.Length Sepal.Width Petal.Length Petal.Width
## 1   -1.0111914   0.8504137   -1.300630   -1.2507035
## 2    0.5055957  -0.4252069    0.650315    0.6253518
##
## Clustering vector:
##   1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20
##   1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1
## 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
##   1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1
## 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
##   1  1  1  1  1  1  1  1  1  1  1  2  2  2  2  2  2  2  2  2
## 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
##   2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2
## 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
##   2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2
## 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
##   2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2
## 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140
##   2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2  2
## 141 142 143 144 145 146 147 148 149 150
##   2  2  2  2  2  2  2  2  2  2
##
## Within cluster sum of squares by cluster:
## [1] 47.35062 173.52867
## (between_SS / total_SS = 62.9 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"
```

```
# Final data
fviz_cluster(final, data = df)
```

Cluster plot



Final data