ASSIGNMENT 10.2.2

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R Markdown

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --
```

```
## v ggplot2 3.3.4     v purrr   0.3.4
## v tibble  3.1.2     v dplyr   1.0.7
## v tidyr   1.1.3     v stringr 1.4.0
## v readr   2.0.0     v forcats 0.5.1
```

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

```
library(cluster)
library(factoextra)
```

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

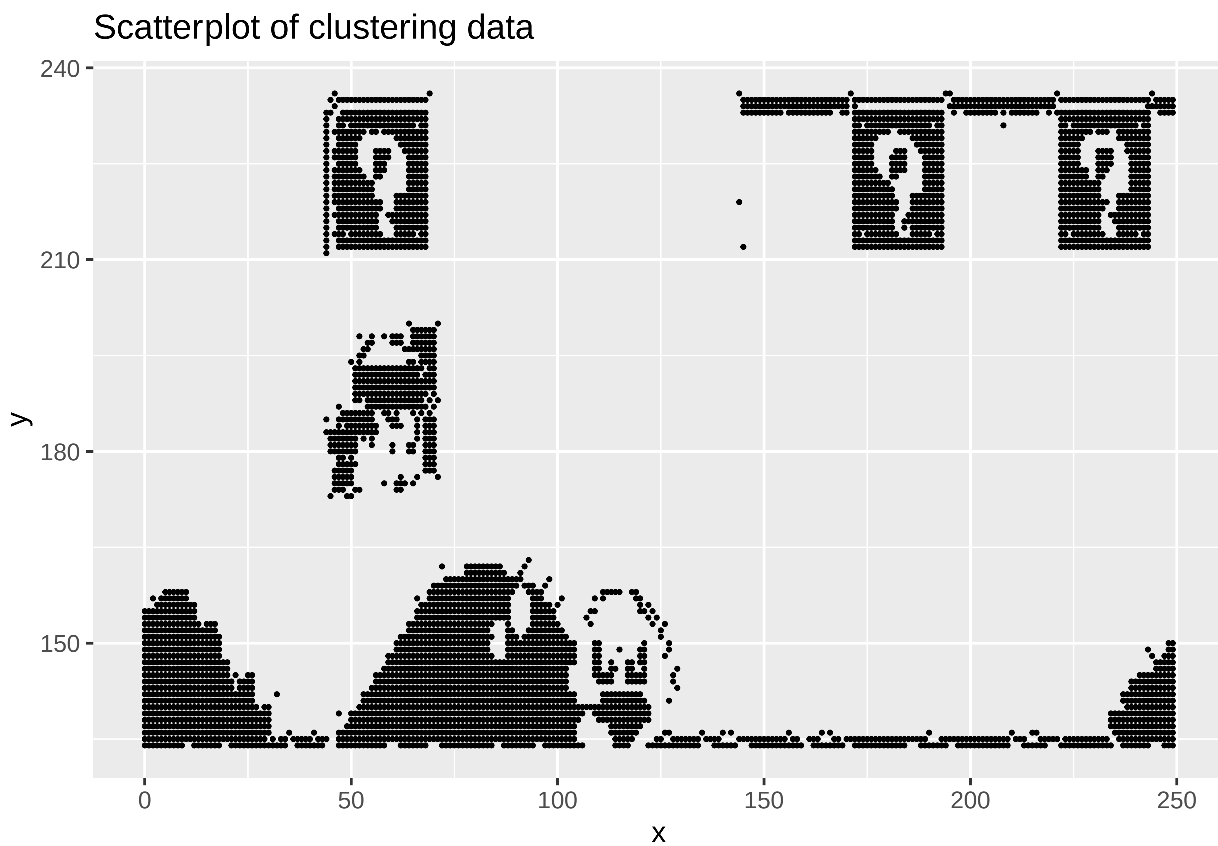
```
setwd('C:/Users/Supraja/dsc520')

# Load the `data/clustering-data.csv` to
cluster_df <- read.csv("data/clustering-data.csv")

# Examine the structure of `clustering-data.csv` using `str()`
str(cluster_df)
```

```
## 'data.frame':    4022 obs. of  2 variables:
##  $ x: int  46 69 144 171 194 195 221 244 45 47 ...
##  $ y: int  236 236 236 236 236 236 236 236 235 235 ...
```

```
# Show the top rows of clustering-data.csv
head(cluster_df)
```

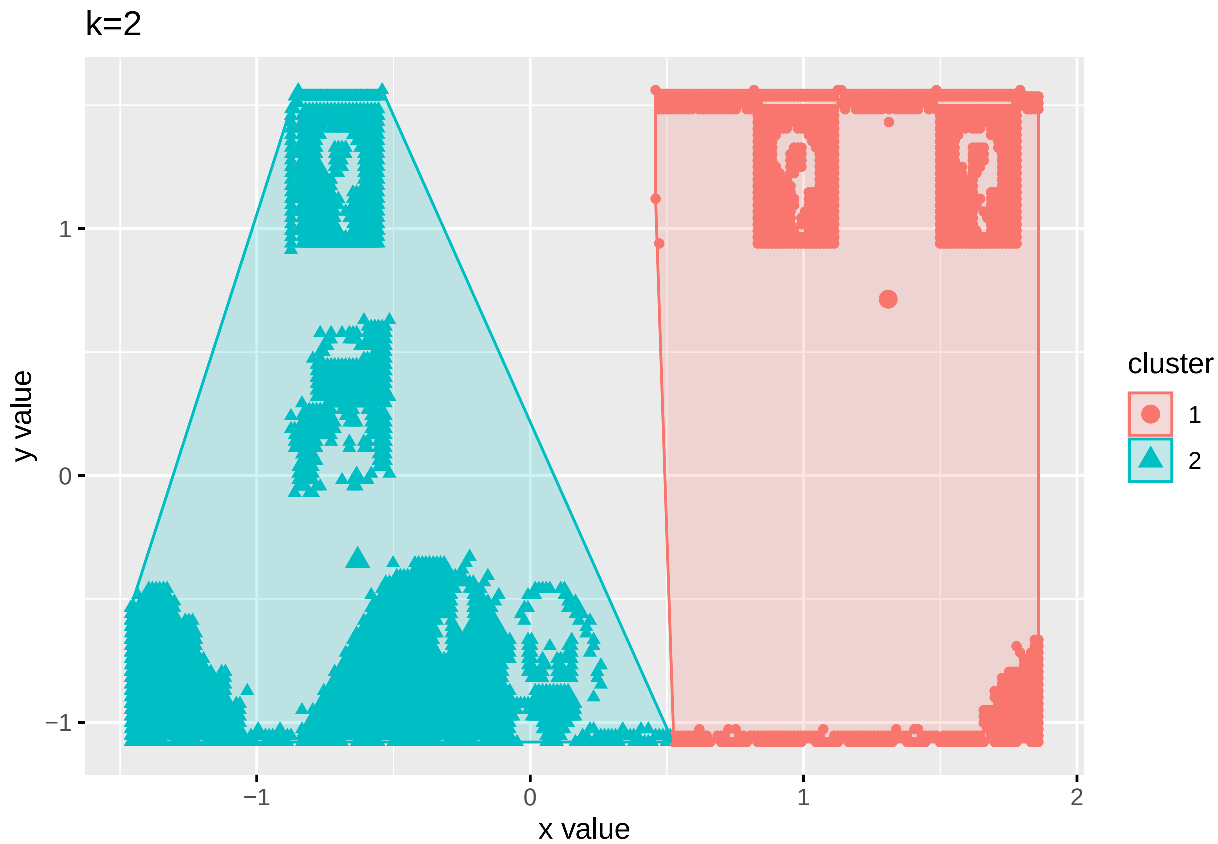
```
##     x   y
## 1  46 236
## 2  69 236
## 3 144 236
## 4 171 236
## 5 194 236
## 6 195 236
```

```r
# i.Plot the dataset using a scatter plot.
# scatter plot of data
library(ggplot2)
ggplot(data = cluster_df, aes(x=x, y=y)) +
 geom_point(size = 0.4) +
 ggtitle("Scatterplot of clustering data")
```

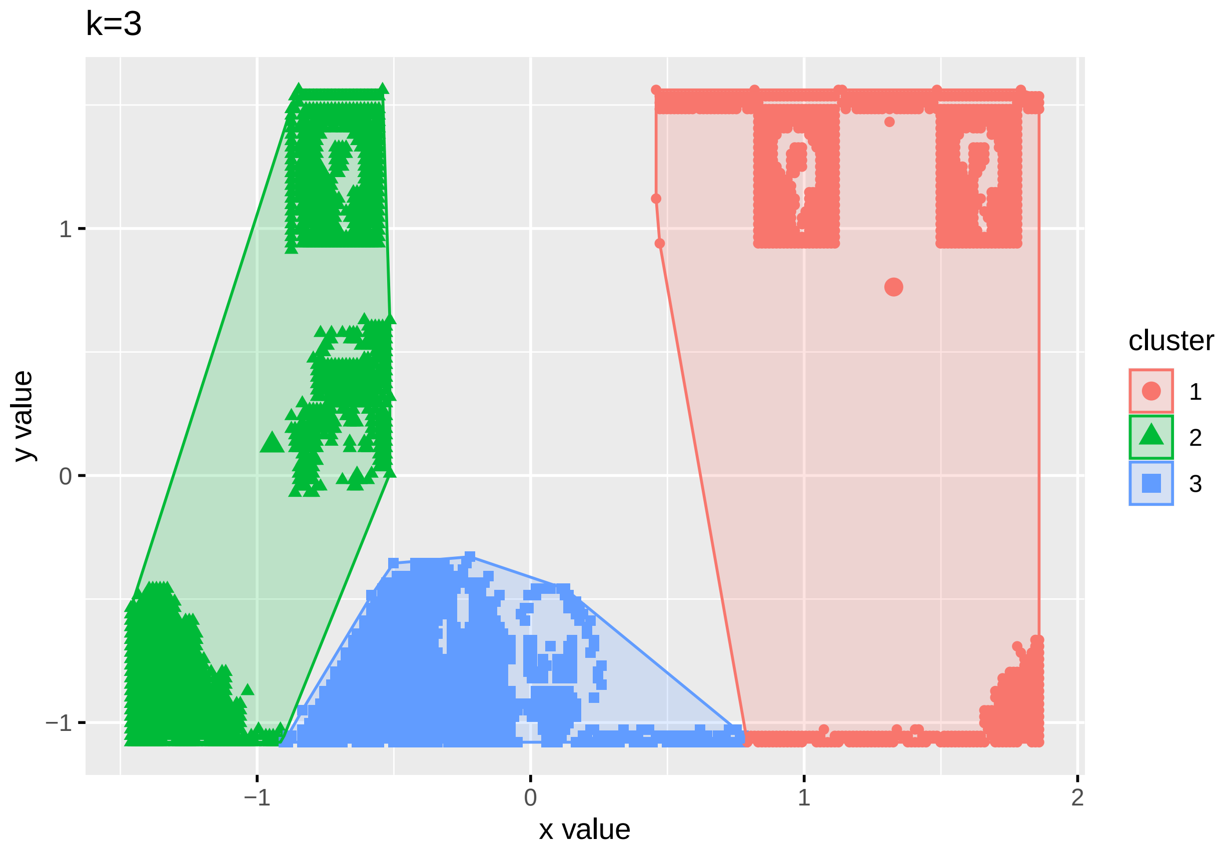



```r
# ii.Fit the dataset using the k-means algorithm from k=2 to k=12.
# Create a scatter plot of the resultant clusters for each value of k.

#Kmeans for k=2
set.seed(123)
kmeans_2 <- kmeans(cluster_df, 2, iter.max = 300, nstart = 10)
#Kmeans for k=3
set.seed(123)
kmeans_3 <- kmeans(cluster_df, 3, iter.max = 300, nstart = 10)
#Kmeans for k=4
```

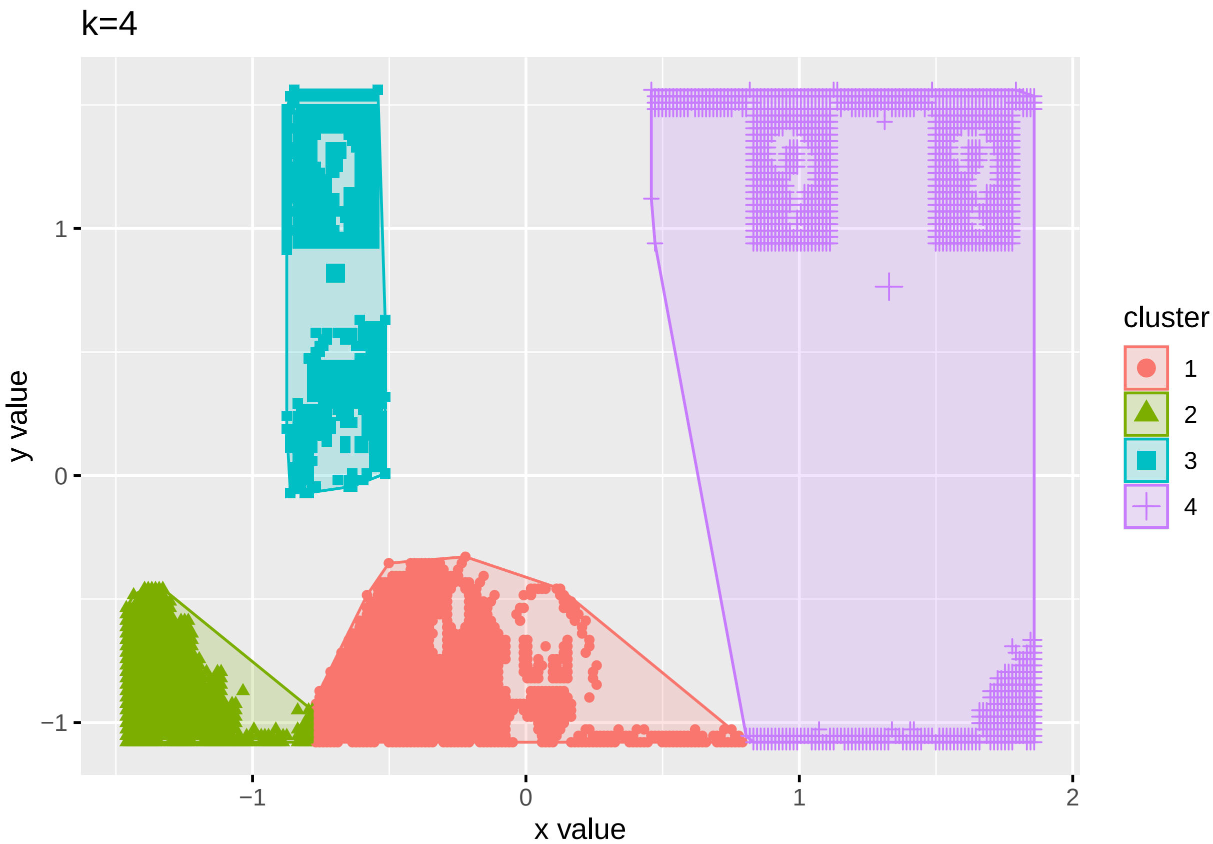
```r
set.seed(123)
kmeans_4 <- kmeans(cluster_df, 4, iter.max = 300, nstart = 10)
#Kmeans for k=5
set.seed(123)
kmeans_5 <- kmeans(cluster_df, 5, iter.max = 300, nstart = 10)
#Kmeans for k=6
set.seed(123)
kmeans_6 <- kmeans(cluster_df, 6, iter.max = 300, nstart = 10)
#Kmeans for k=7
set.seed(123)
kmeans_7 <- kmeans(cluster_df, 7, iter.max = 300, nstart = 10)
#Kmeans for k=8
set.seed(123)
kmeans_8 <- kmeans(cluster_df, 8, iter.max = 300, nstart = 10)
#Kmeans for k=9
set.seed(123)
kmeans_9 <- kmeans(cluster_df, 9, iter.max = 300, nstart = 10)
#Kmeans for k=10
set.seed(123)
kmeans_10 <- kmeans(cluster_df, 10, iter.max = 300, nstart = 10)
#Kmeans for k=11
set.seed(123)
kmeans_11 <- kmeans(cluster_df, 11, iter.max = 300, nstart = 10)
#Kmeans for k=12
set.seed(123)
kmeans_12 <- kmeans(cluster_df, 12, iter.max = 300, nstart = 10)

# plots to compare
#Scatter plot for k=2
fviz_cluster(kmeans_2, geom = "point", data =cluster_df)+ggtitle("k=2")
```



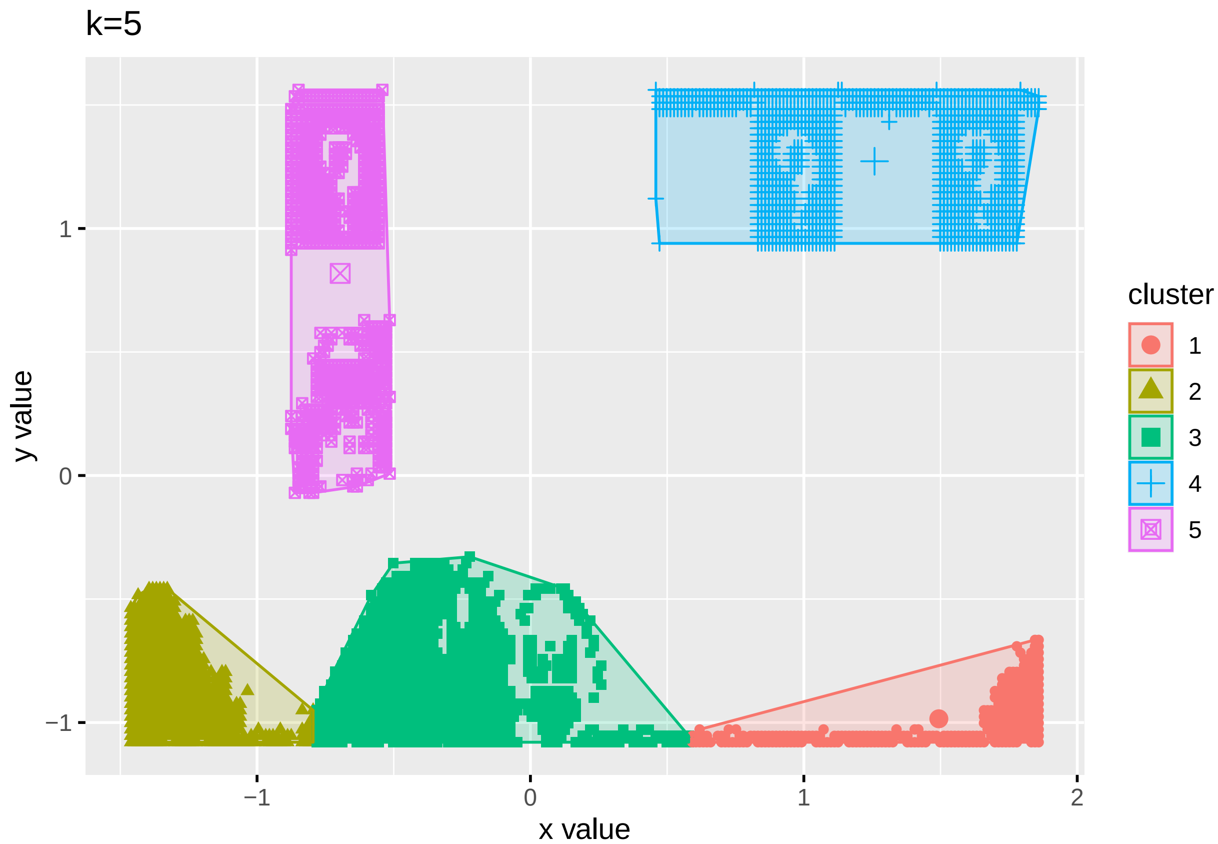

```
#Scatter plot for k=3
fviz_cluster(kmeans_3, geom = "point", data =cluster_df)+ggtitle("k=3")
```



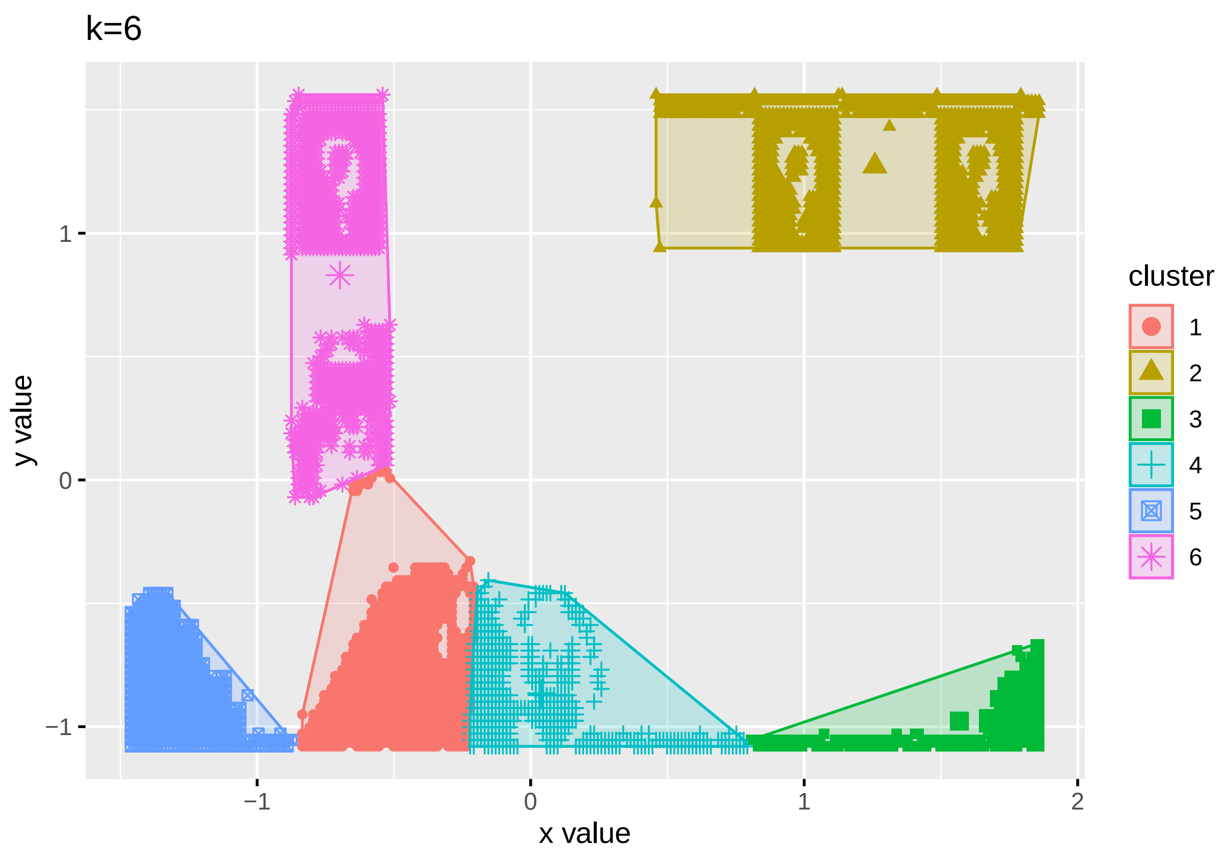

```r
#Scatter plot for k=4
fviz_cluster(kmeans_4, geom = "point", data =cluster_df)+ggtitle("k=4")
```



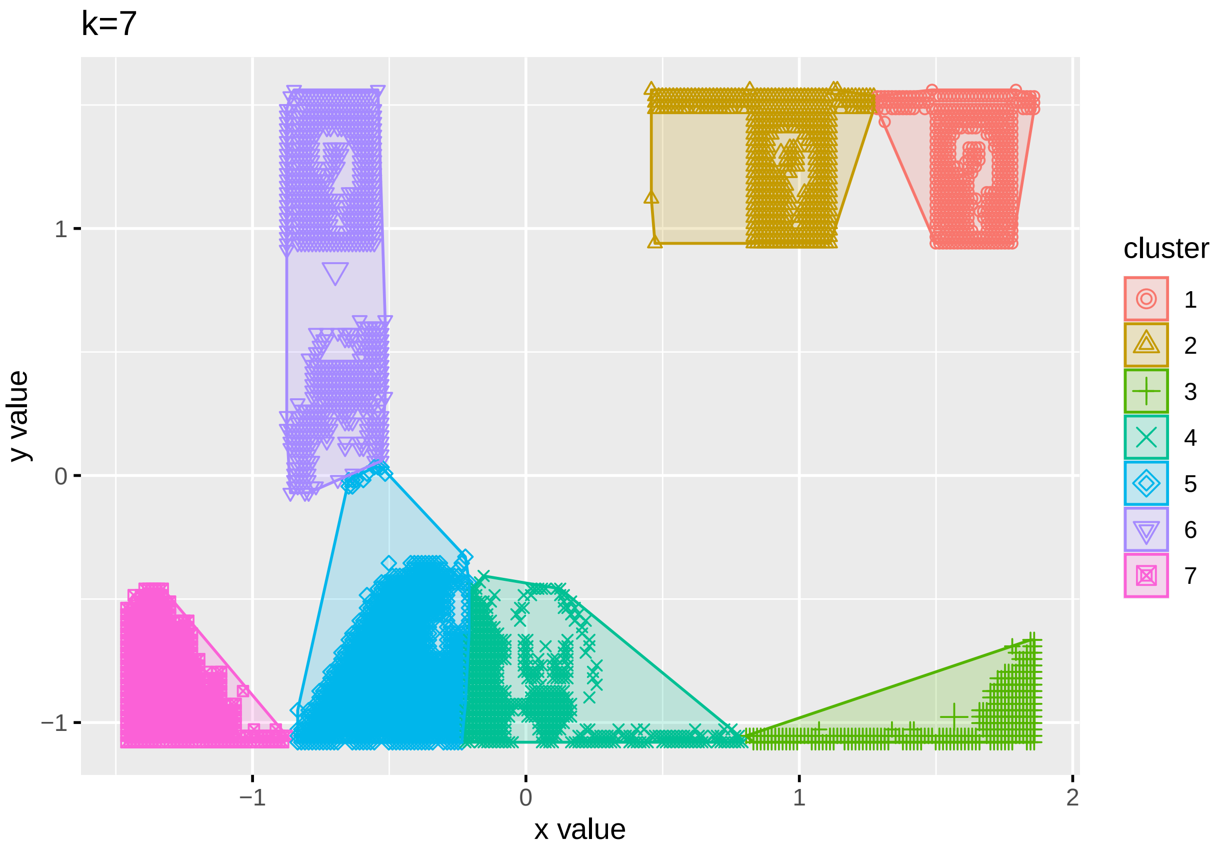

```r
#Scatter plot for k=5
fviz_cluster(kmeans_5, geom = "point", data =cluster_df)+ggtitle("k=5")
```



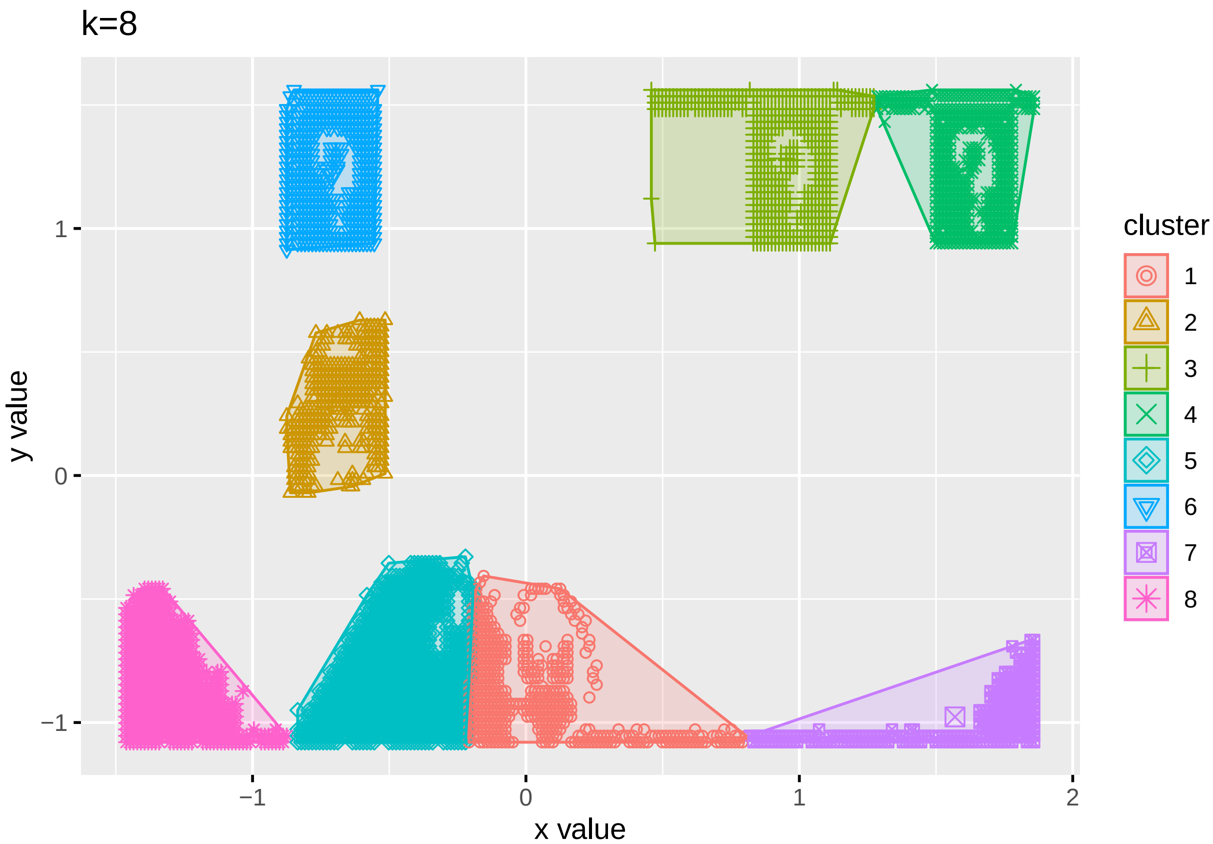

```r
#Scatter plot for k=6
fviz_cluster(kmeans_6, geom = "point", data =cluster_df)+ggtitle("k=6")
```



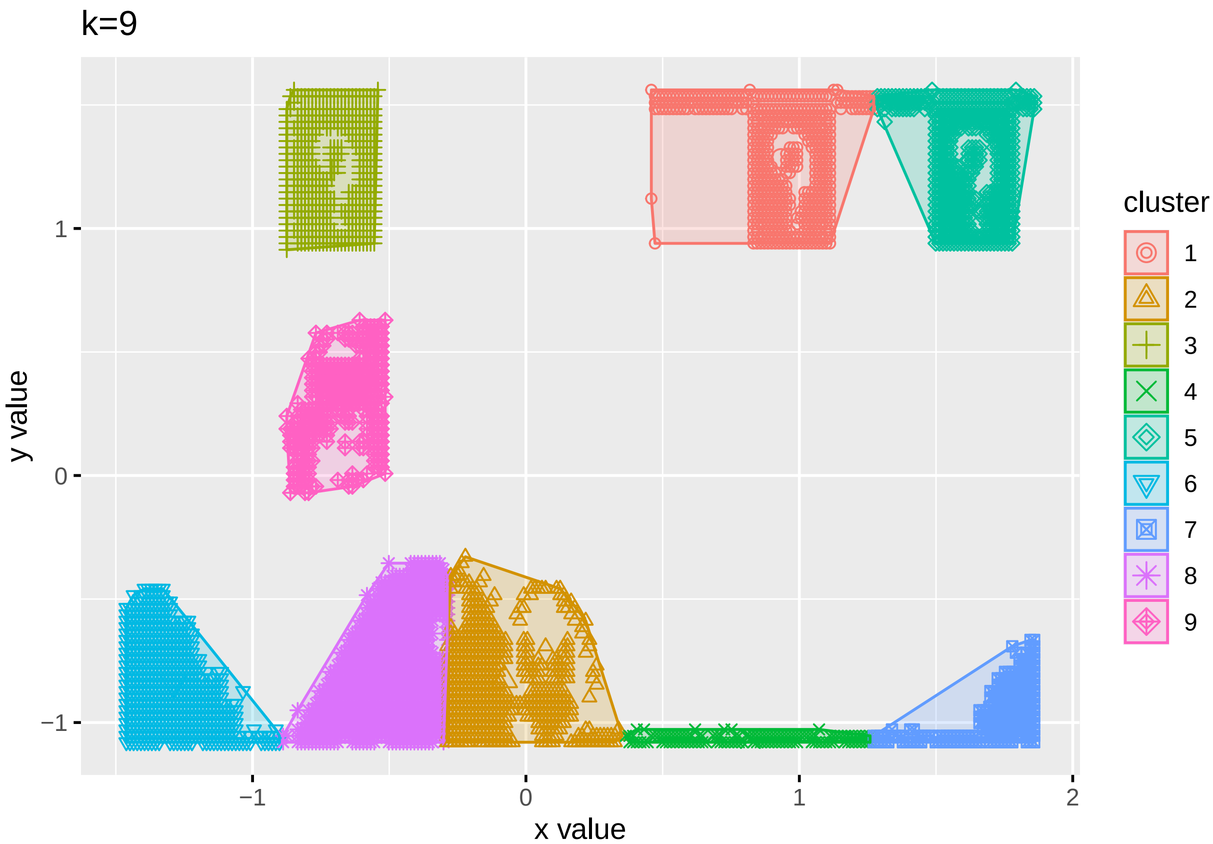

```
#Scatter plot for k=7
fviz_cluster(kmeans_7, geom = "point", data =cluster_df)+ggtitle("k=7")
```



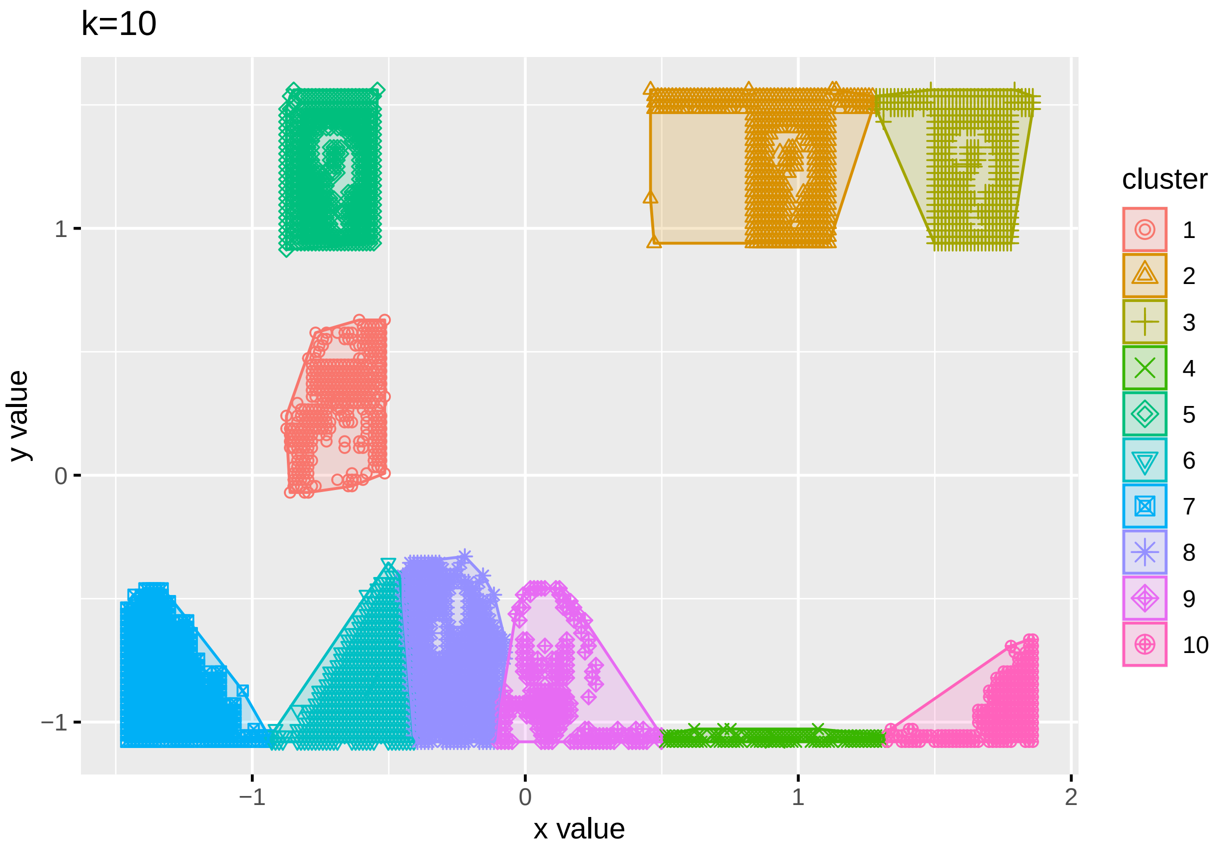

```
#Scatter plot for k=8
fviz_cluster(kmeans_8, geom = "point", data =cluster_df)+ggtitle("k=8")
```



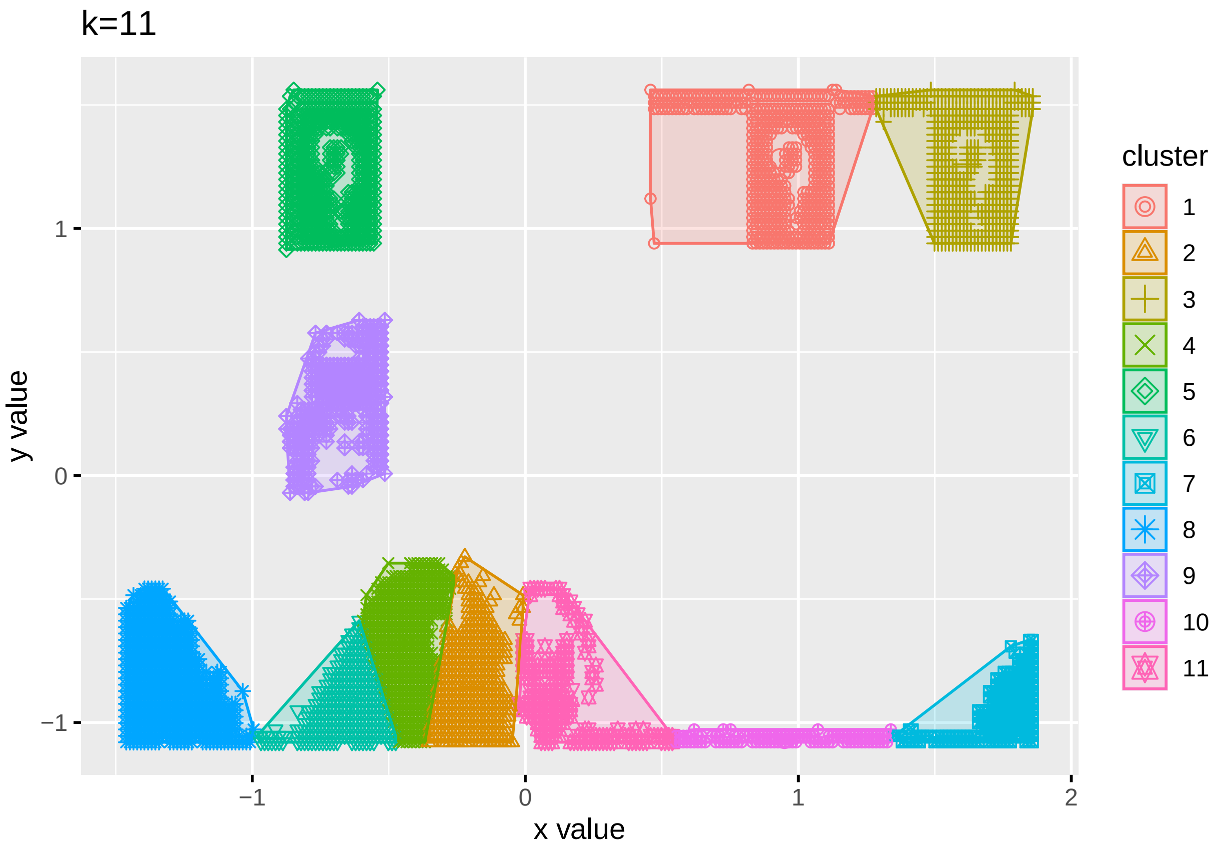

```
#Scatter plot for k=9
fviz_cluster(kmeans_9, geom = "point", data =cluster_df)+ggtitle("k=9")
```



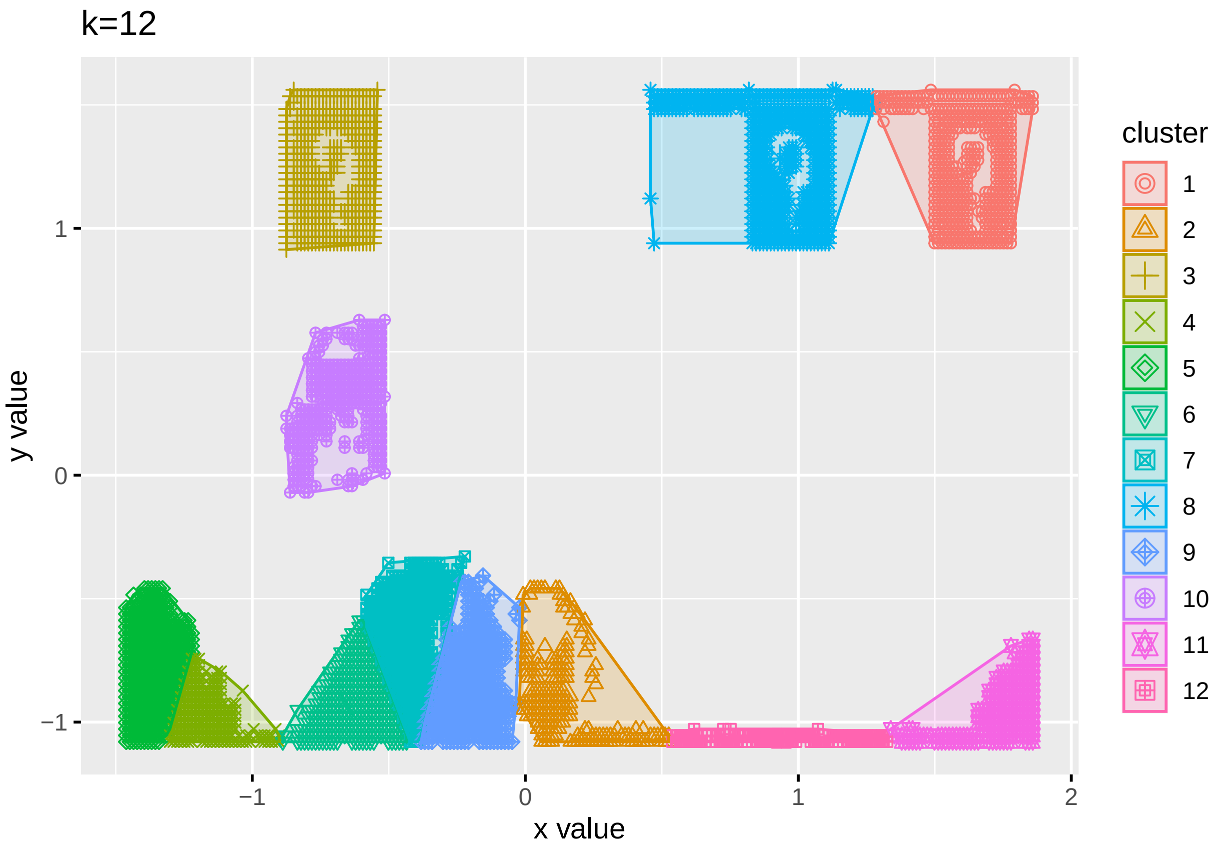

```
#Scatter plot for k=10
fviz_cluster(kmeans_10, geom = "point", data =cluster_df)+ggtitle("k=10")
```



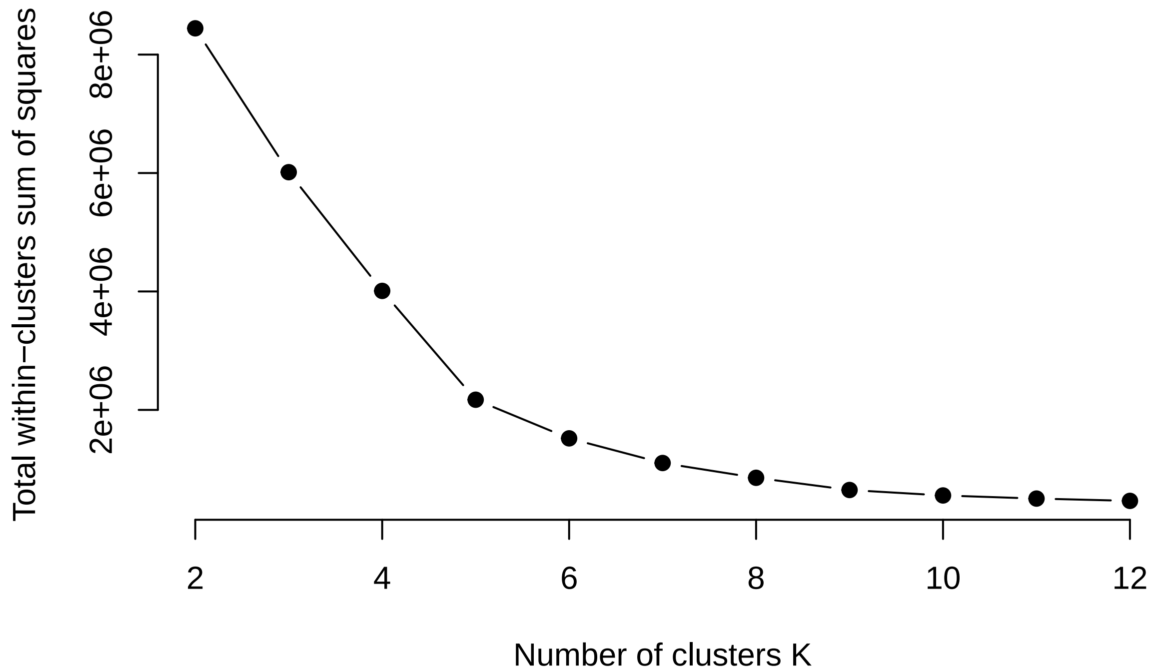

```
#Scatter plot for k=11
fviz_cluster(kmeans_11, geom = "point", data =cluster_df)+ggtitle("k=11")
```




```
#Scatter plot for k=12
fviz_cluster(kmeans_12, geom = "point", data =cluster_df)+ggtitle("k=12")
```




```
set.seed(123)
# function to compute total within-cluster sum of square
wss <- function(k) { kmeans(cluster_df, k, nstart = 25 )$tot.withinss }
# Compute and plot wss for k = 1 to k = 15
k.values <- 2:12

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

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




```
#The results suggest that 6 is the optimal number of clusters as it appears to be the bend in elbow.
```