Final Project

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R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com (http://rmarkdown.rstudio.com).

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
#install.packages("agplot2")
#install.packages("dplyr")
#install.packages("factoextra")
#install.packages("glmnet")
library(ggplot2)
## Warning: package 'ggplot2' was built under R version 4.3.3
library(dplyr)
## 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(factoextra)
## Warning: package 'factoextra' was built under R version 4.3.3
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
```

```
file_path <- "C:/Users/Asus/OneDrive/Desktop/dataset/Mall_Customers.csv"

mall_customers <- read.csv(file_path, header = TRUE, stringsAsFactors = FALSE)

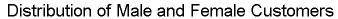
head(mall_customers)</pre>
```

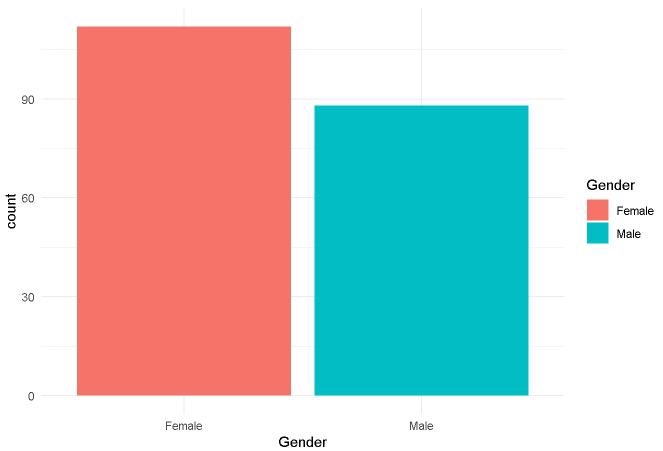
```
##
     CustomerID Gender Age Annual.Income..k.. Spending.Score..1.100.
## 1
              1
                  Male 19
                                           15
## 2
                  Male 21
                                           15
                                                                  81
              3 Female 20
## 3
                                           16
                                                                   6
## 4
              4 Female 23
                                           16
                                                                  77
## 5
              5 Female 31
                                                                  40
                                           17
## 6
              6 Female 22
                                           17
                                                                  76
```

```
colnames(mall_customers)
```

```
## [1] "CustomerID" "Gender" "Age"
## [4] "Annual.Income..k.." "Spending.Score..1.100."
```

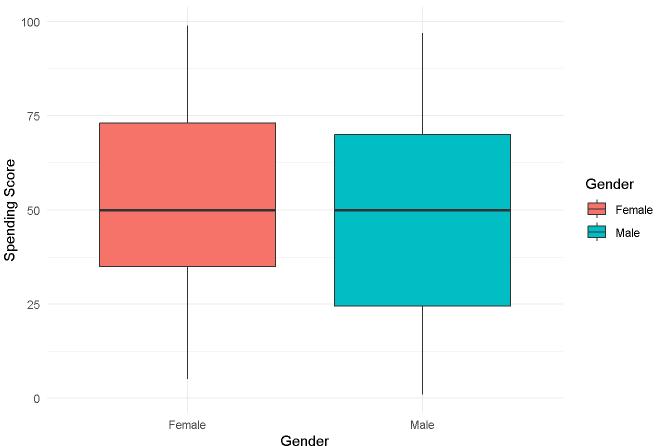
```
ggplot(mall_customers, aes(x = Gender, fill = Gender)) +
  geom_bar() +
  labs(title = "Distribution of Male and Female Customers", x = "Gender", y = "count") +
  theme_minimal()
```





```
ggplot(mall_customers, aes(x = Gender, y = Spending.Score..1.100., fill = Gender)) +
  geom_boxplot() +
  labs(title = "Spending Score Distribution by Gender", x = "Gender", y = "Spending Score") +
  theme_minimal()
```





```
# Load required libraries
library(ggplot2)
library(dplyr)

# Select numeric features: Annual Income, Spending Score
selected_data <- mall_customers %>%
    select(`Annual.Income..k..`, `Spending.Score..1.100.`)

# Perform PCA on selected features
pca <- prcomp(selected_data, center = TRUE, scale. = TRUE)

summary(pca)</pre>
```

```
## Importance of components:
## PC1 PC2
## Standard deviation 1.005 0.995
## Proportion of Variance 0.505 0.495
## Cumulative Proportion 0.505 1.000
```

```
pca_data <- as.data.frame(pca$x)

pca_data$Gender <- mall_customers$Gender

# View the new dataset
head(pca_data)</pre>
```

```
## PC1 PC2 Gender

## 1 -1.5332616 -0.91989864 Male

## 2 -0.3832060 -2.06995421 Male

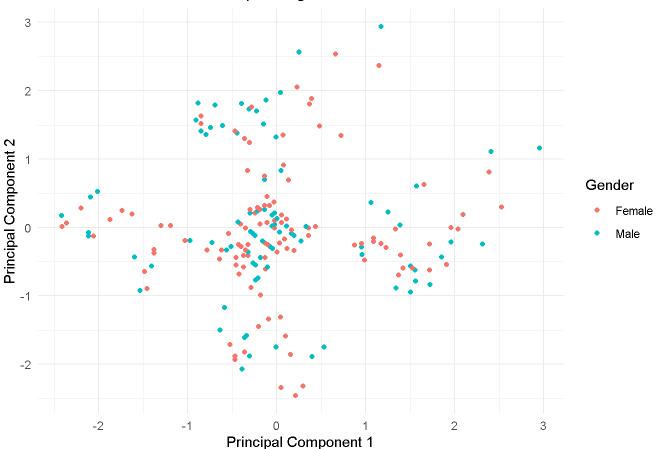
## 3 -2.4099544 0.01063875 Female

## 4 -0.4658128 -1.93350280 Female

## 5 -1.4520347 -0.89343631 Female

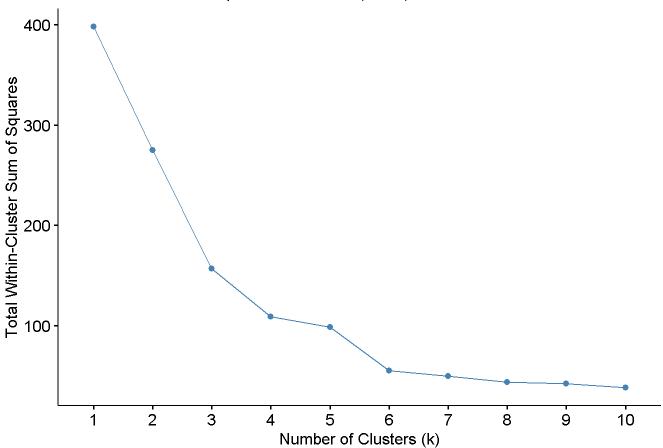
## 6 -0.4662728 -1.87919822 Female
```

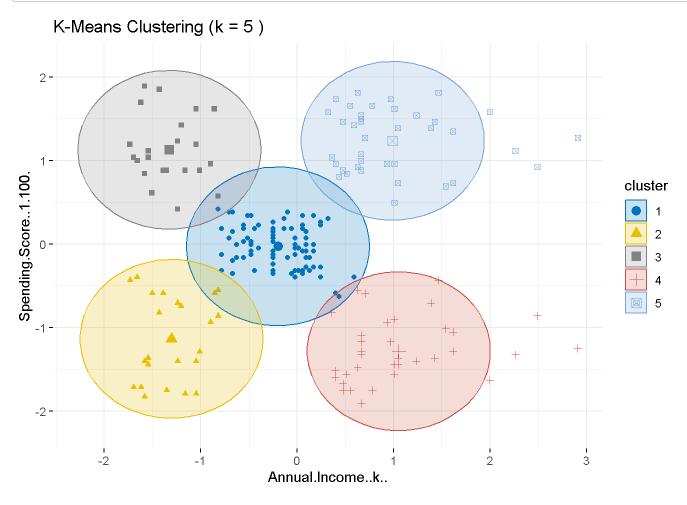
PCA: Annual Income and Spending Score



```
# Load required libraries
library(factoextra)
library(dplyr)
# Select the relevant features
clustering_data <- mall_customers %>%
  select(Annual.Income..k.., Spending.Score..1.100.)
# Scale the data
scaled_data <- scale(clustering_data)</pre>
# Perform PCA
pca <- prcomp(scaled_data, center = TRUE, scale. = TRUE)</pre>
# Create PCA data (scores for the first two principal components)
pca_data <- as.data.frame(pca$x)</pre>
# Elbow method to determine optimal number of clusters on PCA data
fviz_nbclust(pca_data, kmeans, method = "wss") +
  labs(title = "Elbow Method for Optimal Clusters (PCA)",
       x = "Number of Clusters (k)",
       y = "Total Within-Cluster Sum of Squares")
```

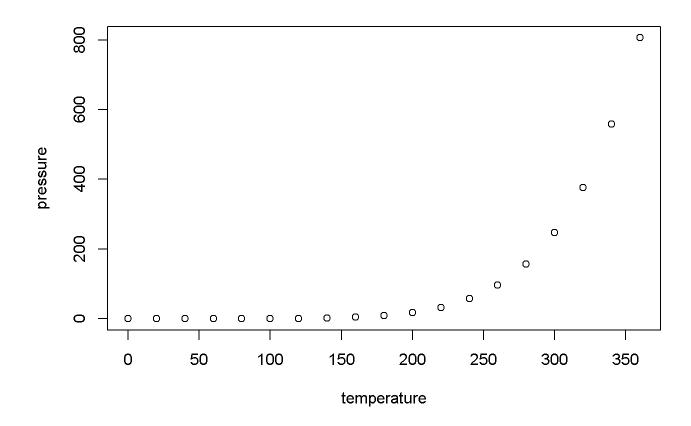
Elbow Method for Optimal Clusters (PCA)





Including Plots

You can also embed plots, for example:



Note that the echo = FALSE parameter was added to the code chunk to prevent printing of the R code that generated the plot.