1.6 Hypothesis Testing & Statistical Analysis

Open survey data.

```r
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
```

```r
library (readr)
library (ggplot2)
library (stringr)
library(tidyr)

survey_data <- read_csv("data\\students_survey.csv", show_col_types = FALSE)
```

1. One-sample T-test

Use: To test if the mean of a single sample is significantly different from a known or hypothesized population mean.

Example: Test if the mean age of BI students = 21

Null Hypothesis: Mean age of BI students = 21

Alternative Hypothesis: Mean age of BI students ≠ 21

```r
# Check the data to ensure there are no missing values and age is numeric
summary(survey_data$age)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
  18.00   20.00   21.00   21.56   22.00   27.00 
```

```r
# Perform one-sample t-test
t_test_result <- t.test(survey_data$age, mu = 21)
```

```
# Print the t-test result
print(t_test_result)
```

```

    One Sample t-test

data:  survey_data$age
t = 2.2194, df = 53, p-value = 0.03076
alternative hypothesis: true mean is not equal to 21
95 percent confidence interval:
 21.05348 22.05763
sample estimates:
mean of x 
 21.55556 
```

Results:

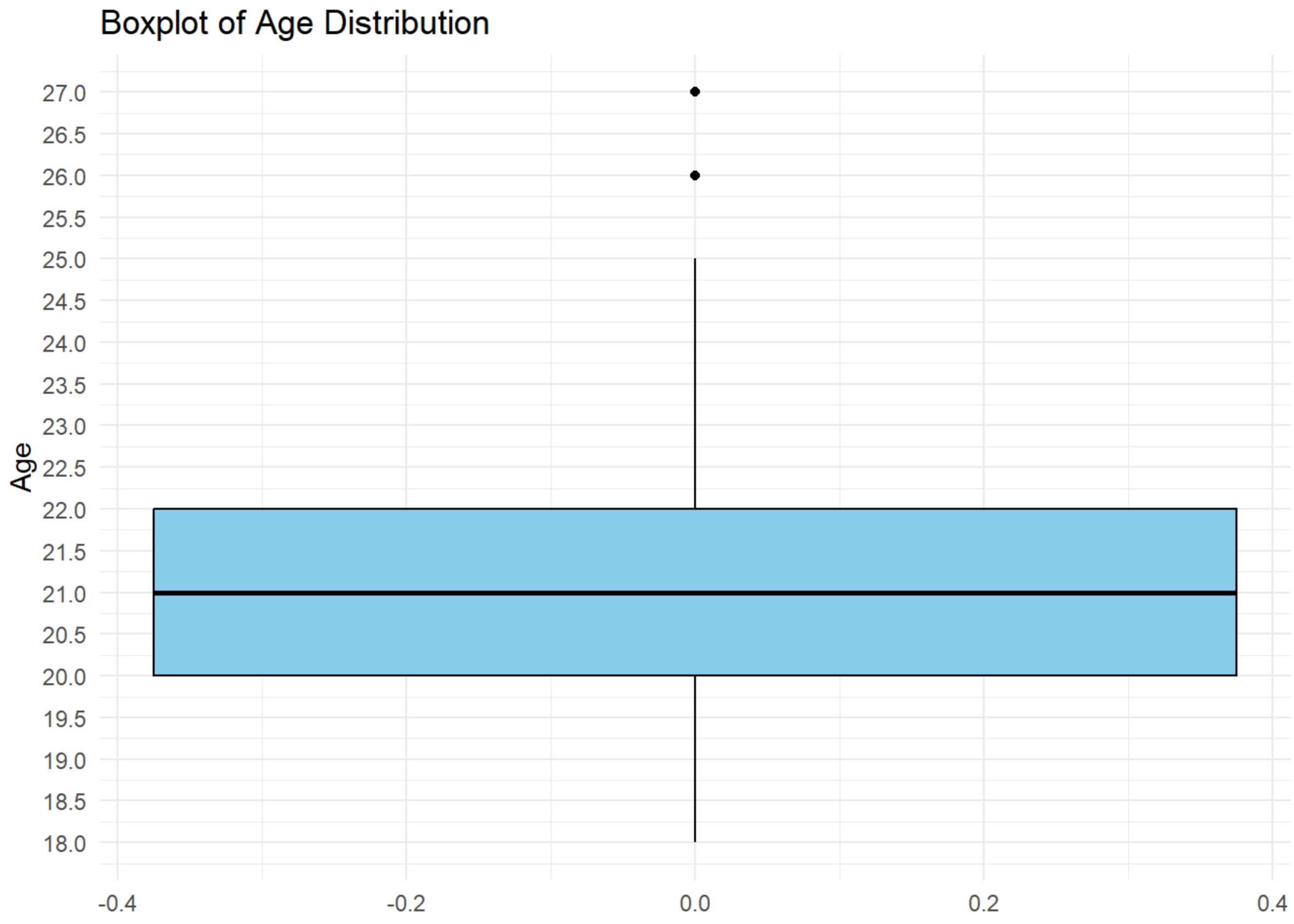
- **P-Value:** 0.08156
- **Mean Age:** 21.55556

A p-value less than the significance level (commonly 0.05) leads to rejecting the null hypothesis.

In this case, the p-value is 0.08156, which is greater than 0.05, indicating that we do not reject the null hypothesis. This suggests that the mean age of the students is not significantly different from 22.

Visualize the mean students age

```
ggplot(survey_data, aes(y = age)) +
  geom_boxplot(fill = "skyblue", color = "black") +
  labs(title = "Boxplot of Age Distribution", y = "Age") +
      scale_y_continuous(breaks = seq(floor(min(survey_data$age, na.rm = TRUE)), ceiling
  theme_minimal()
```



2. Two-sample T-test (Independent)

Use: To compare the means of two independent samples to see if they are significantly different.

Example 1: Compare the GPA of BI students by Gender

Null Hypothesis: There is no difference between the mean GPA for male and female BI students

Alternative Hypothesis: There is a difference between the mean GPA for male and female BI students

```
# Perform a two-sample t-test for GPA between genders
t_test_gpa_gender <- t.test(gpa ~ gender, data = survey_data)

# Print the result
print(t_test_gpa_gender)
```

```

	Welch Two Sample t-test

data:  gpa by gender
t = -0.17232, df = 52, p-value = 0.8639
alternative hypothesis: true difference in means between group Female and group Male is not equal
to 0
```

```
95 percent confidence interval:
 -0.2968477  0.2498960
sample estimates:
mean in group Female   mean in group Male 
            2.731724             2.755200 
```

Interpretation:

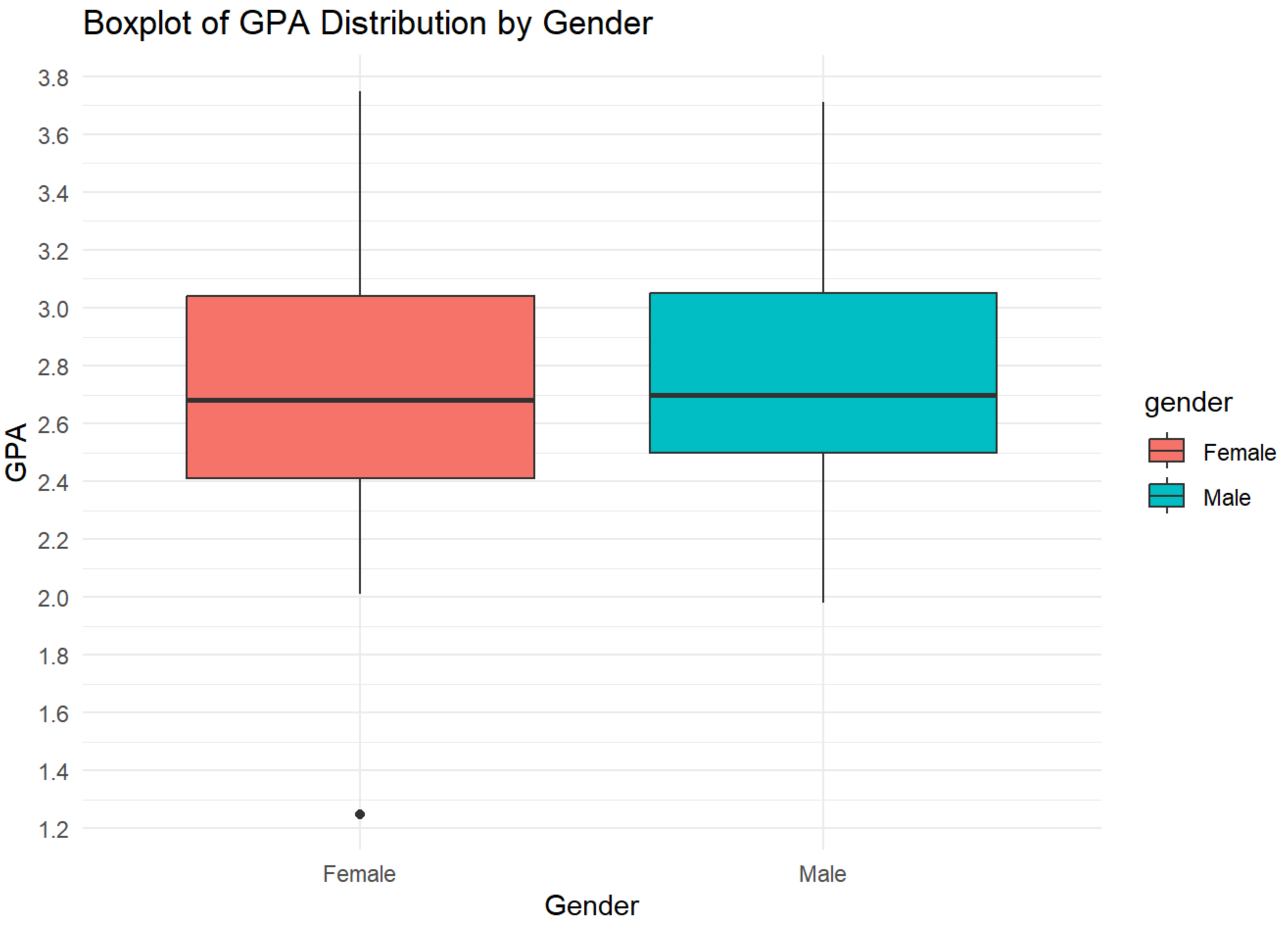
- **P-Value:** 0.8639
- **Mean GPA in Group Female:** 2.731724
- **Mean GPA in Group Male:** 2.755200

In this case, the p-value is 0.8639, which is much greater than 0.05, indicating that we do not reject the null hypothesis. This suggests that there is no significant difference in GPA between female and male students.

Visualize GPA by Gender:

To create a boxplot showing the GPA distribution by gender, use the following R code:

```
library(ggplot2)

# Create a boxplot for GPA distribution by gender
ggplot(survey_data, aes(x = gender, y = gpa, fill = gender)) +
  geom_boxplot() +
  labs(title = "Boxplot of GPA Distribution by Gender", x = "Gender", y = "GPA") +
  scale_y_continuous(breaks = seq(floor(min(survey_data$gpa, na.rm = TRUE)), ceiling(max
  theme_minimal()
```



Example 2: Test if having a job has influence on Student’s GPA

```r
# Perform a two-sample t-test for GPA between work status
t_test_gpa_work <- t.test(gpa ~ does_work, data = survey_data)

# Print the result
print(t_test_gpa_work)
```

```
    Welch Two Sample t-test

data:  gpa by does_work
t = 0.10266, df = 46.32, p-value = 0.9187
alternative hypothesis: true difference in means between group No and group Yes is not equal to 0
95 percent confidence interval:
 -0.2671799  0.2959036
sample estimates:
 mean in group No mean in group Yes 
         2.748710          2.734348 
```

Interpretation:

- **P-Value:** 0.9187
- **Mean GPA in Group No:** 2.748710

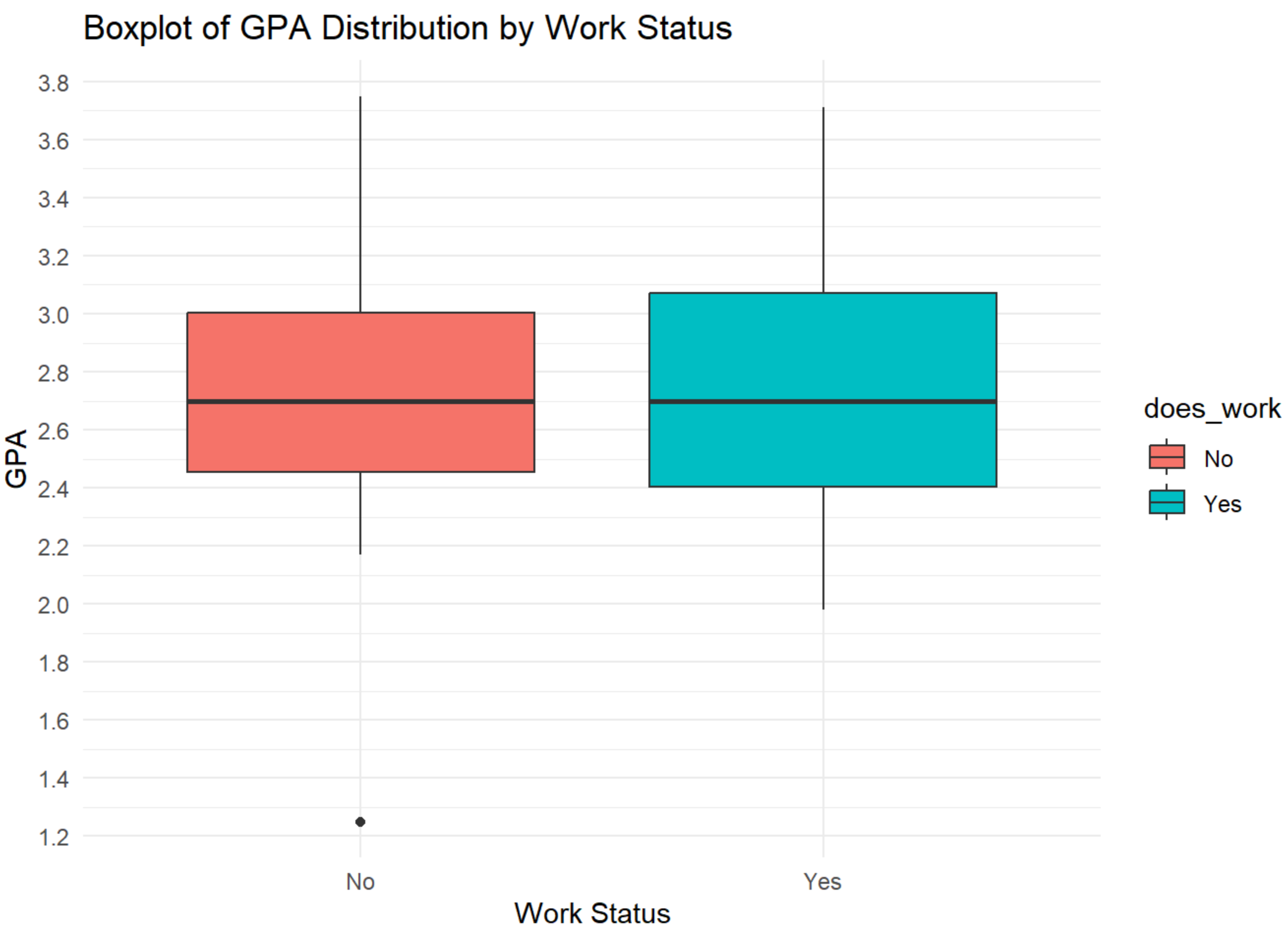
- **Mean GPA in Group Yes:** 2.734348

In this case, the p-value is 0.9187, which is much greater than 0.05, indicating that we do not reject the null hypothesis. This suggests that there is no significant difference in GPA between students who do work and those who do not.

Visualize GPA by Work Status:

To create a boxplot showing the GPA distribution by work status, use the following R code:

```
library(ggplot2)

# Create a boxplot for GPA distribution by work status
ggplot(survey_data, aes(x = does_work, y = gpa, fill = does_work)) +
  geom_boxplot() +
  labs(title = "Boxplot of GPA Distribution by Work Status", x = "Work Status", y = "GPA
  scale_y_continuous(breaks = seq(floor(min(survey_data$gpa, na.rm = TRUE)), ceiling(max
  theme_minimal()
```



Example 3: Compare the GPA of Adabi Tawjihi Branch and Scientifc Tawjihi Branch

```
# Filter the data for the two branches
filtered_data <- survey_data %>%
  filter(national_high_school_category %in% c("adabi", "scientific"))

# Perform a two-sample t-test for GPA between Adabi branch and Scientific branch
t_test_result <- t.test(gpa ~ national_high_school_category, data = filtered_data)

# Print the result
print(t_test_result)
```

```

	Welch Two Sample t-test

data:  gpa by national_high_school_category
t = -0.8071, df = 34.662, p-value = 0.4251
alternative hypothesis: true difference in means between group adabi and group scientific is not equal to 0
95 percent confidence interval:
 -0.4019184  0.1733073
sample estimates:
     mean in group adabi mean in group scientific 
                2.699444                 2.813750 
```

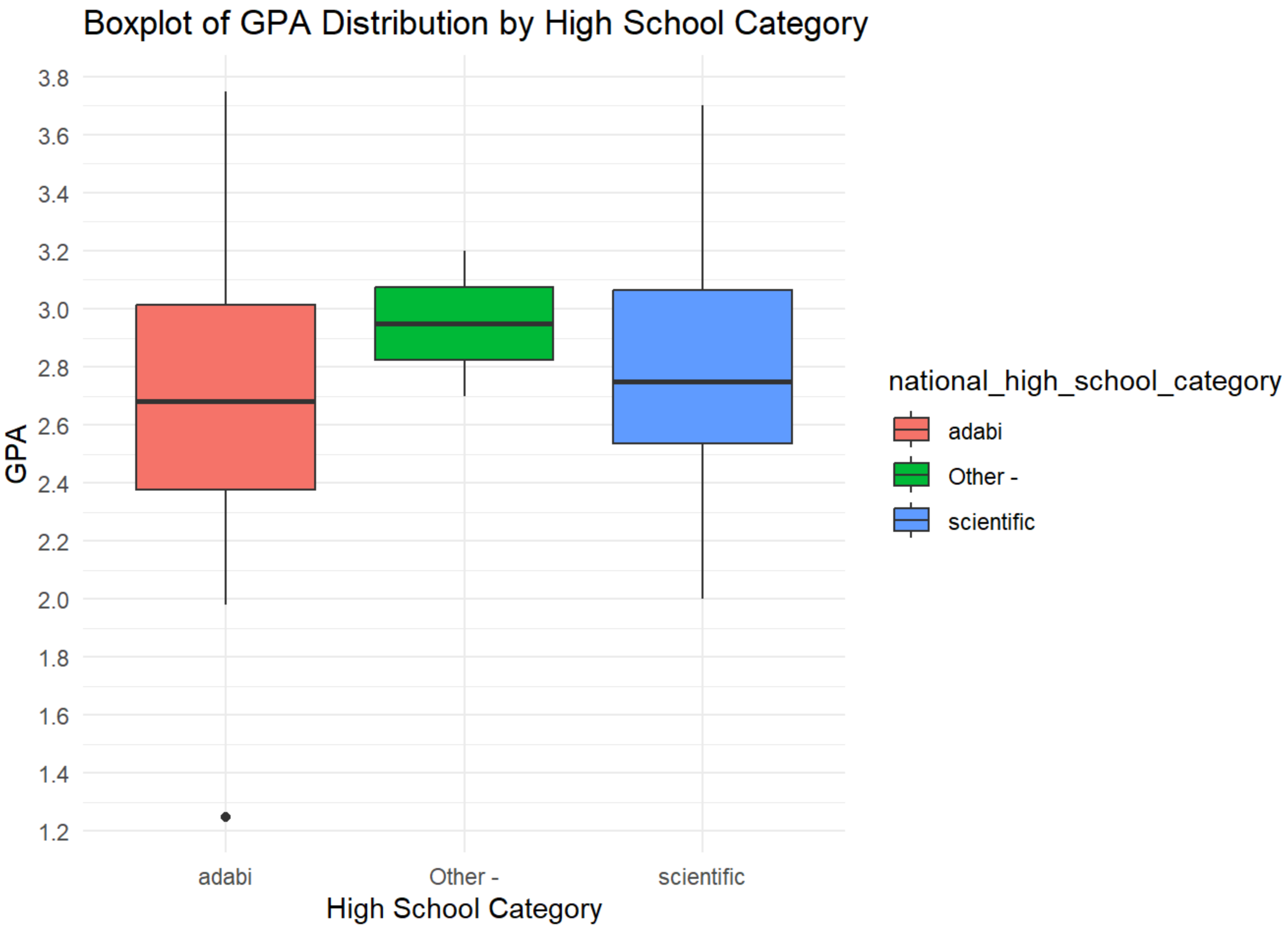
Interpretation:

- **P-Value:** 0.4251
- **Mean GPA in Group Adabi:** 2.699444
- **Mean GPA in Group Scientific:** 2.813750

In this case, the p-value is 0.4251, which is greater than 0.05, indicating that we do not reject the null hypothesis. This suggests that there is no significant difference in GPA between students from the Adabi and Scientific high school categories.

Visualize GPA by High School Category:

```
library(ggplot2)

# Create a boxplot for GPA distribution by high school category
ggplot(survey_data, aes(x = national_high_school_category, y = gpa, fill = national_high_
  geom_boxplot() +
  labs(title = "Boxplot of GPA Distribution by High School Category", x = "High School C
  scale_y_continuous(breaks = seq(floor(min(survey_data$gpa, na.rm = TRUE)), ceiling(max
  theme_minimal()
```



3. Paired Sample T-test

Use: To compare the means of two related samples (e.g., before and after measurements on the same subjects).

Example:- Suppose we want to test if a training program has significantly improved employee productivity scores by comparing their productivity before and after the training.

Code:

```
# Set seed for reproducibility
set.seed(123)

# Generate productivity scores before and after the training
productivity_before <- rnorm(30, mean = 5, sd = 2)  # Productivity scores before trainin
productivity_after <- productivity_before + rnorm(30, mean = 0.5, sd = 1)  # Productivit

# Perform paired sample t-test to compare the mean productivity scores before and after 
t_test_result <- t.test(productivity_before, productivity_after, paired = TRUE)

# Print the t-test result
print(t_test_result)
```

```
	Paired t-test

data:  productivity_before and productivity_after
t = -4.4489, df = 29, p-value = 0.0001169
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
 -0.9901802 -0.3664964
sample estimates:
mean difference 
     -0.6783383 
```

Interpretation:

- **Productivity Scores:**
    - **Before Training:** Generated productivity scores with a mean of approximately 5.
    - **After Training:** Generated productivity scores that are on average higher than before training.
    - **p-value:** Probability of observing the data if the null hypothesis is true (0.0001169)

Conclusion: Since the p-value (0.0001169) is less than the common significance level (0.05), we reject the null hypothesis. This indicates that there is a significant difference in productivity scores before and after the training, with productivity increasing after the training program.

4. One-way ANOVA

Use: To compare the means of three or more groups to see if at least one mean is different.

***Example 1:*- Test if there is a difference in student GPA according to study hours**

To perform an ANOVA test to compare the effect of study hours on GPA, we first need to ensure that the study hours are categorized (e.g., “less than 1 hour,” “1-3 hours,” etc.) into factors. Then, wecan use the `aov` function to perform the ANOVA test in R.

R Code for ANOVA Test Comparing Study Hours with GPA

```
          # Convert the columns to ordered factors
          survey_data <- survey_data %>%
            mutate(study_hours = factor(study_hours, levels = c("< 1", "1-3", "3-5", "> 5"), order

          survey_data <- survey_data %>% filter(study_hours != "> 5")
          View(survey_data)

          # Perform ANOVA test
          anova_result <- aov(gpa ~ study_hours, data = survey_data)
```

```
# Print the summary of the ANOVA test
print(summary(anova_result))
```

```
            Df Sum Sq Mean Sq F value Pr(>F)
study_hours  2  0.099 0.04936   0.185  0.832
Residuals   49 13.072 0.26677
```

Explanation:

Based on the ANOVA results, there is no significant effect of study hours on GPA.

The p-value of 0.943 indicates that the differences in mean GPA among the study hours groups are not statistically significant.

This suggests that, in this dataset, the amount of time spent studying does not have a meaningful impact on GPA.

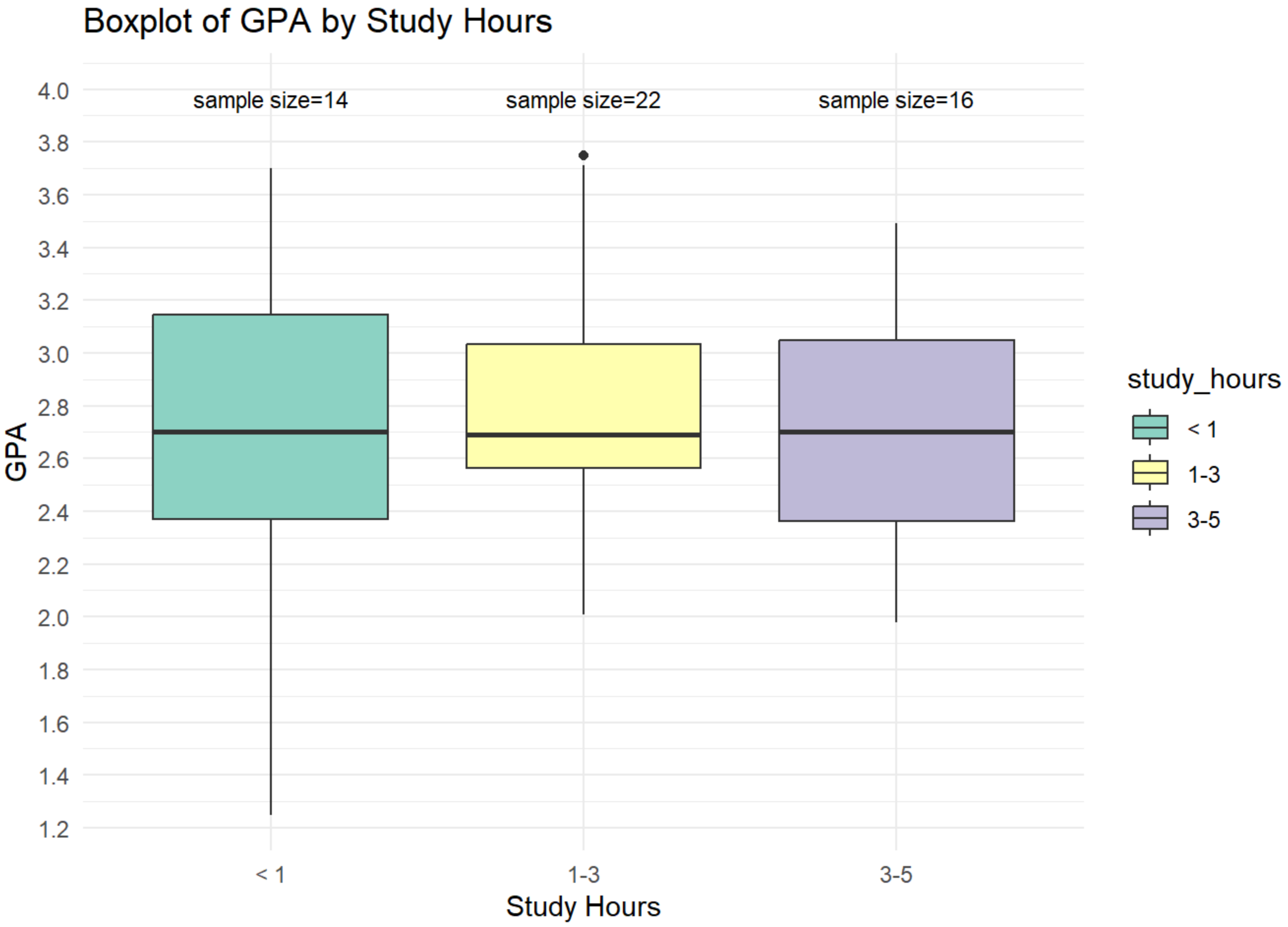
Possible Reasons for No Significant Effect:

1. **Sample Size**:
   - The sample sizes, especially for the “More than 5 Hours” category, are small. Small sample sizes can lead to less reliable statistical results.
2. **Other Influencing Factors**:
   - GPA may be influenced by many other factors beyond just study hours, such as the effectiveness of study methods, prior knowledge, teaching quality, etc.
3. **Homogeneity of Study Habits**:
   - There might be homogeneity in the study habits of students in this dataset, meaning most students have similar study patterns, leading to similar GPAs.
4. **Measurement of Study Hours**:
   - The accuracy of self-reported study hours can be variable. Students may not accurately report their study hours, leading to less precise groupings.

Visualize GPA by Study Hours

```
# Load necessary library for visualization
library(ggplot2)

# Calculate the sample size for each category
sample_sizes <- survey_data %>%
  group_by(study_hours) %>%
  summarise(count = n())
```

```
# Create boxplot to visualize the relationship between study hours and GPA
ggplot(survey_data, aes(x = study_hours, y = gpa, fill=study_hours)) +
  geom_boxplot() +
  ggtitle("Boxplot of GPA by Study Hours") +
  xlab("Study Hours") +
  ylab("GPA") +
  scale_y_continuous(breaks = seq(1, 4, by = 0.2)) +
  scale_fill_brewer(palette = "Set3") +
  theme_minimal() +
  geom_text(data = sample_sizes, aes(x = study_hours, y = 4, label = paste0("sample size
```



- `sample_sizes <- survey_data %>% group_by(study_hours) %>% summarise(count = n())` calculates the sample size for each `study_hours` category.

- `geom_text()` adds the sample size labels to the plot. The labels are positioned just above the top of the plot (y = 4) and are adjusted to avoid overlap using `position_dodge` and `vjust`.

Example 2:- Test if there is a difference in student GPA according to the high school certificate category (National, SAT/ACT, IG, IB)

```
# Convert high_school_category to a factor if it is not already
survey_data$high_school_category <- as.factor(survey_data$high_school_category)
```

```
        # Perform ANOVA to test the relationship between high school category and GPA
        anova_result <- aov(gpa ~ high_school_category, data = survey_data)

        # Print the summary of the ANOVA test
        summary(anova_result)
```

```
                     Df Sum Sq Mean Sq F value Pr(>F)
high_school_category  3  0.282 0.09396    0.35  0.789
Residuals            48 12.888 0.26851
```

Interpretation of ANOVA Results

The ANOVA table helps determine if there is a significant relationship between the `high_school_category` and `GPA`. Here are the results:

Explanation:

- **p-value (Pr(>F))**:

  Since the p-value (0.778) is much greater than the common significance level of 0.05, we fail to reject the null hypothesis.

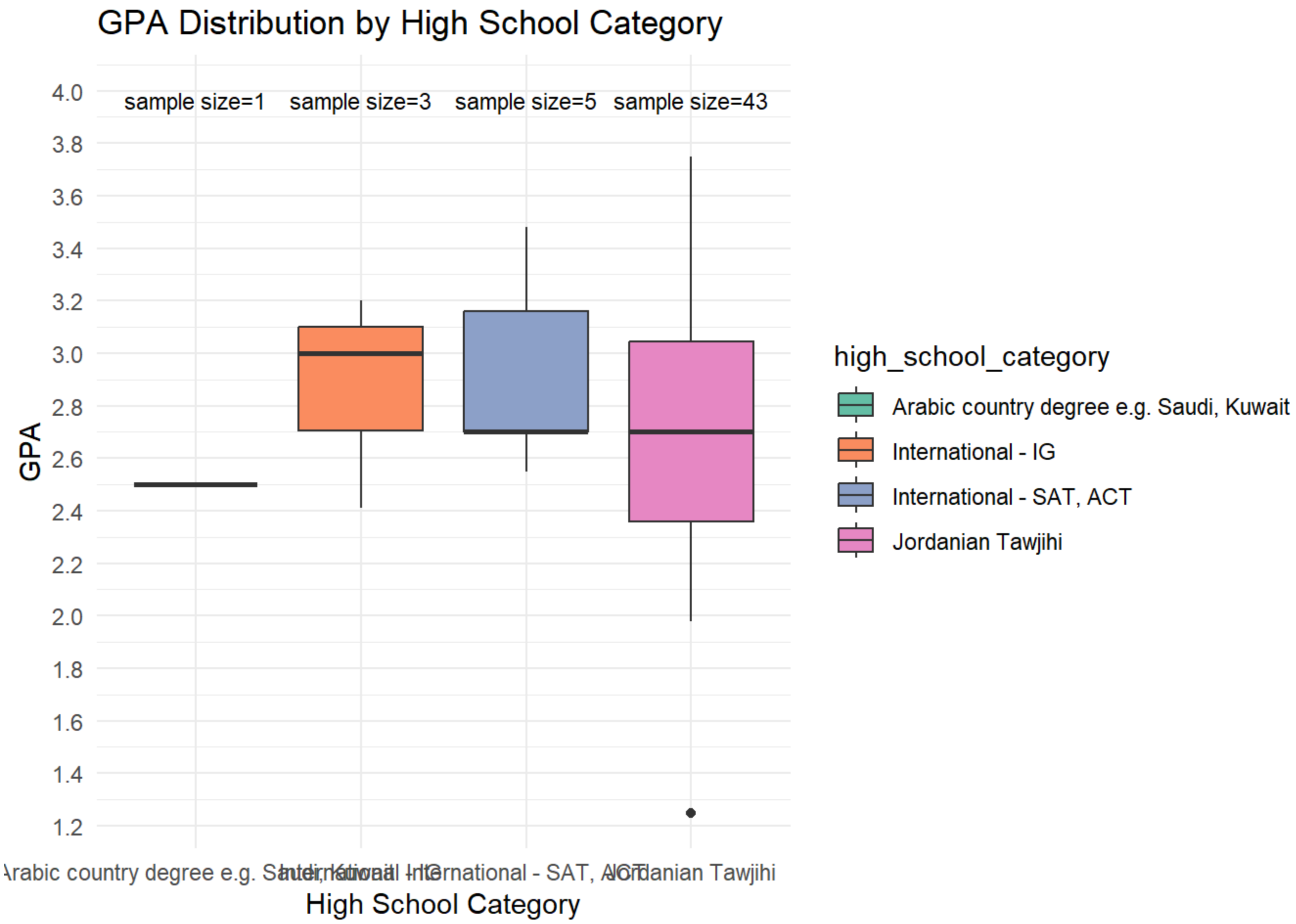
- This suggests that there is no statistically significant difference in GPA between the different high school categories.

- In other words, the high school category does not appear to have a significant impact on GPA in this dataset.

Visualization:

To complement the statistical results, you can create a box plot to visualize the GPA distribution across different high school categories:

```
        # Calculate the sample size for each category
        sample_sizes <- survey_data %>%
          group_by(high_school_category) %>%
          summarise(count = n())

        # Create a box plot to visualize the relationship between high school category and GPA
        ggplot(survey_data, aes(x = high_school_category, y = gpa, fill = high_school_category))
          geom_boxplot() +
          ggtitle("GPA Distribution by High School Category") +
          xlab("High School Category") +
          ylab("GPA") +
            scale_y_continuous(breaks = seq(1, 4, by = 0.2)) +
          scale_fill_brewer(palette = "Set2") +
          theme_minimal() +
          geom_text(data = sample_sizes, aes(x = high_school_category, y = 4, label = paste0("sa
```



The ANOVA test evaluates whether there are statistically significant differences between the means of three or more independent groups.

Here are a few reasons why the ANOVA test might fail to reject the null hypothesis (which states that there are no significant differences between group means) despite apparent differences in the boxplot:

1. **Sample Size**: Small sample sizes can lead to higher variability and less statistical power, making it harder to detect significant differences. In the plot, it is evident that some categories have very small sample sizes (e.g., sample sizes of 1, 3, and 5), which could affect the ANOVA test results.

2. **Variance Within Groups**: If the variability within each group is high, it can overshadow the differences between group means. In other words, if the data points within each group are widely spread out, the ANOVA might not find the differences between group means significant.

3. **Outliers**: The presence of outliers can affect the mean and variance within groups. In the boxplot, there appears to be an outlier in the “Jordanian Tawjihi” category. Outliers can influence the results of statistical tests, making it more difficult to detect significant differences.

4. **Overlapping Confidence Intervals**: If the confidence intervals of the group means overlap significantly, it indicates that the means are not statistically different. The boxplot provides a visual indication of the spread and overlap of data points within each group.

5. **Effect Size**: The differences between group means might be too small (i.e., small effect size) to be detected as significant by the ANOVA test. Even if there are visible differences in the boxplot, they might not be large enough to be considered statistically significant.

To better understand the results, it might be useful to:

- Check the actual p-value obtained from the ANOVA test.

- Perform post-hoc tests to explore pairwise comparisons between groups if the overall ANOVA is significant.

- Consider the assumptions of the ANOVA test, such as homogeneity of variances and normality of the data, and whether these assumptions are met.

5. Chi-square Test for Independence

Use: To test if there is a significant association between two categorical variables.

Example:- Suppose we want to test if there is a significant association between the gender of BI student and the Working Status

Code:

```
# Create a contingency table for gender and work status
contingency_table <- table(survey_data$gender, survey_data$does_work)

# Print the contingency table
print(contingency_table)
```

```
        No Yes
  Female 20   7
  Male    9  16
```

```
# Perform the Chi-Square test of independence
chi_square_test <- chisq.test(contingency_table)

# Print the result
print(chi_square_test)
```

```

	Pearson's Chi-squared test with Yates' continuity correction

data:  contingency_table
X-squared = 6.1631, df = 1, p-value = 0.01304
```

Interpretation of the Chi-Square Test Results:

The Chi-Square test of independence results indicate whether there is a significant relationship between gender and work status.

Contingency Table:

```
       No Yes
Female 22   7
Male    9  16
```

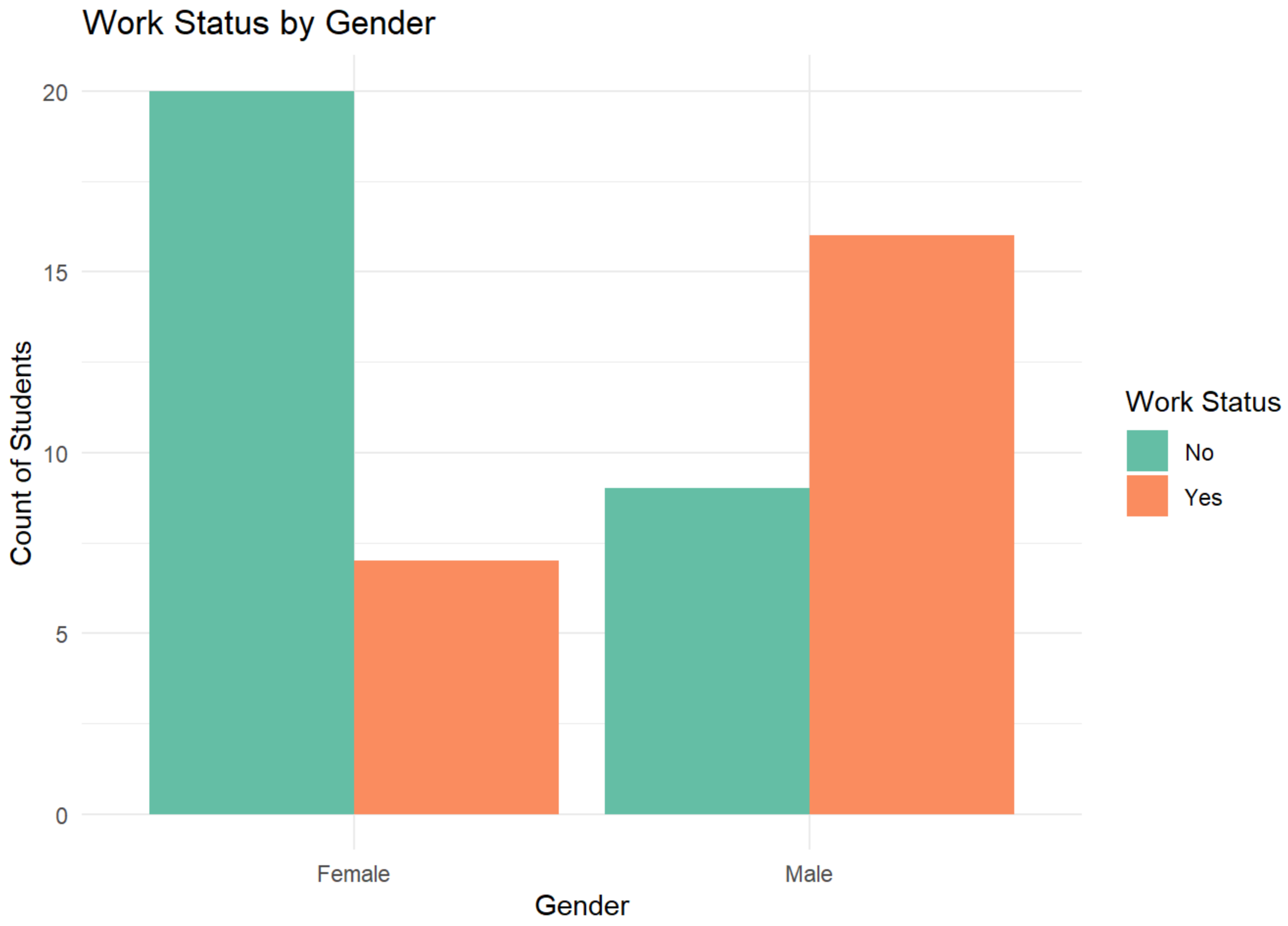
Chi-Square Test Results: **p-value**: 0.00741

- Since the p-value (0.00741) is less than the significance level of 0.05, we reject the null hypothesis.
- This suggests that there is a statistically significant relationship between gender and work status.
- Specifically, the data indicates that the distribution of work status (whether a student works or not) is significantly different between males and females.

Visualization (Optional):

We can also create a bar plot to visualize the relationship between gender and work status:

```
# Create a bar plot to visualize the relationship between gender and work status
ggplot(survey_data, aes(x = gender, fill = does_work)) +
  geom_bar(position = "dodge") +
  ggtitle("Work Status by Gender") +
  xlab("Gender") +
  ylab("Count of Students") +
  scale_fill_brewer(palette = "Set2", name = "Work Status") +
  theme_minimal()
```



This plot will help visualize the counts of students by gender and work status, providing a clear picture of the relationship between these two variables.

Statistical Analysis

1. Correlation Analysis

Introduction:

Correlation analysis measures the strength and direction of the relationship between two variables.

For instance, we can analyze the correlation between high school average and GPA.

R Code:

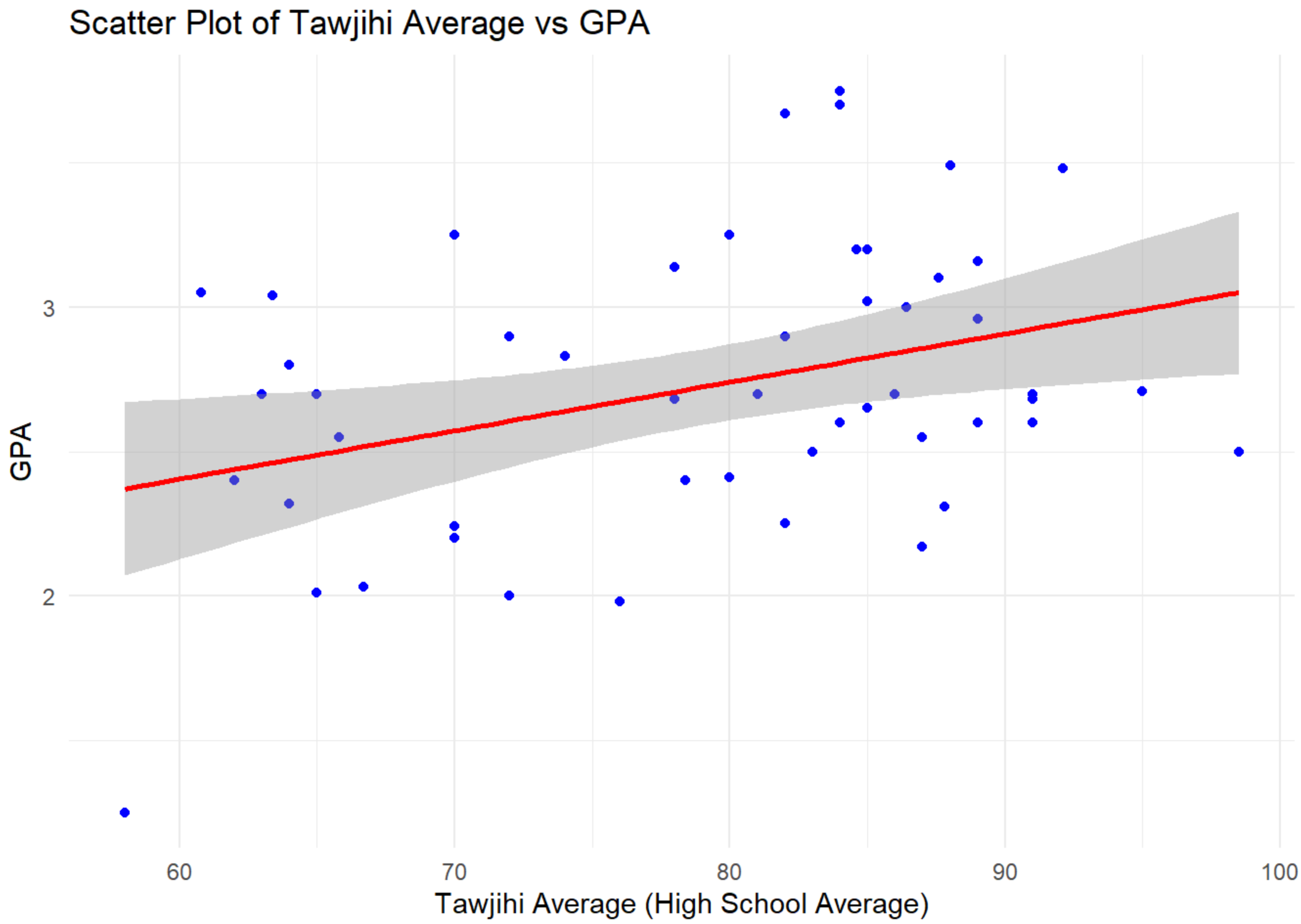
```
# Remove rows with NA values in the relevant columns
filtered_data <- survey_data %>%
  filter(!is.na(hight_school_average) & !is.na(gpa))

# Calculate the Pearson correlation coefficient
correlation_result <- cor.test(filtered_data$hight_school_average, filtered_data$gpa)
```

```
# Print the result
print(correlation_result)
```

```

	Pearson's product-moment correlation

data:  filtered_data$hight_school_average and filtered_data$gpa
t = 2.6342, df = 49, p-value = 0.01126
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.0848565 0.5722445
sample estimates:
      cor 
0.3522039 
```

```
# Create the scatter plot
ggplot(filtered_data, aes(x = hight_school_average, y = gpa)) +
  geom_point(color = "blue") +
  geom_smooth(method = "lm", color = "red") +
  ggtitle("Scatter Plot of Tawjihi Average vs GPA") +
  xlab("Tawjihi Average (High School Average)") +
  ylab("GPA") +
  theme_minimal()
```

```
`geom_smooth()` using formula = 'y ~ x'
```



Results of the Correlation Test Between Tawjihi Average and GPA

Pearson Correlation Coefficient: 0.2628
P-Value: 0.0811

Interpretation:

1. **Pearson Correlation Coefficient (0.2628)**:
   - The Pearson correlation coefficient measures the strength and direction of the linear relationship between two variables.
   - A value of 0.2628 indicates a weak positive correlation between Tawjihi average and GPA. This suggests that as the Tawjihi average increases, GPA tends to increase slightly as well.
2. **P-Value (0.0811)**:
   - The p-value indicates the probability that the observed correlation occurred by chance if there is no actual correlation in the population.
   - In this case, the p-value is 0.0811, which is slightly above the common significance level of 0.05. Therefore, we do not have strong evidence to reject the null hypothesis of no correlation. This suggests that the observed correlation is not statistically significant at the 5% level.

Conclusion:

Based on the results of the Pearson correlation test, there is a weak positive correlation between Tawjihi average and GPA. However, this correlation is not statistically significant at the 5% level. Therefore, while there is a slight tendency for higher Tawjihi averages to be associated with higher GPAs, this relationship is not strong or statistically significant in this dataset.

2. Regression Analysis: Linear Regression Example using `mtcars` Dataset

Introduction:

- Linear regression models the relationship between a dependent variable and one or more independent variables. In this example, we will use the `mtcars` dataset to predict miles per gallon (mpg) based on horsepower (hp) and weight (wt).

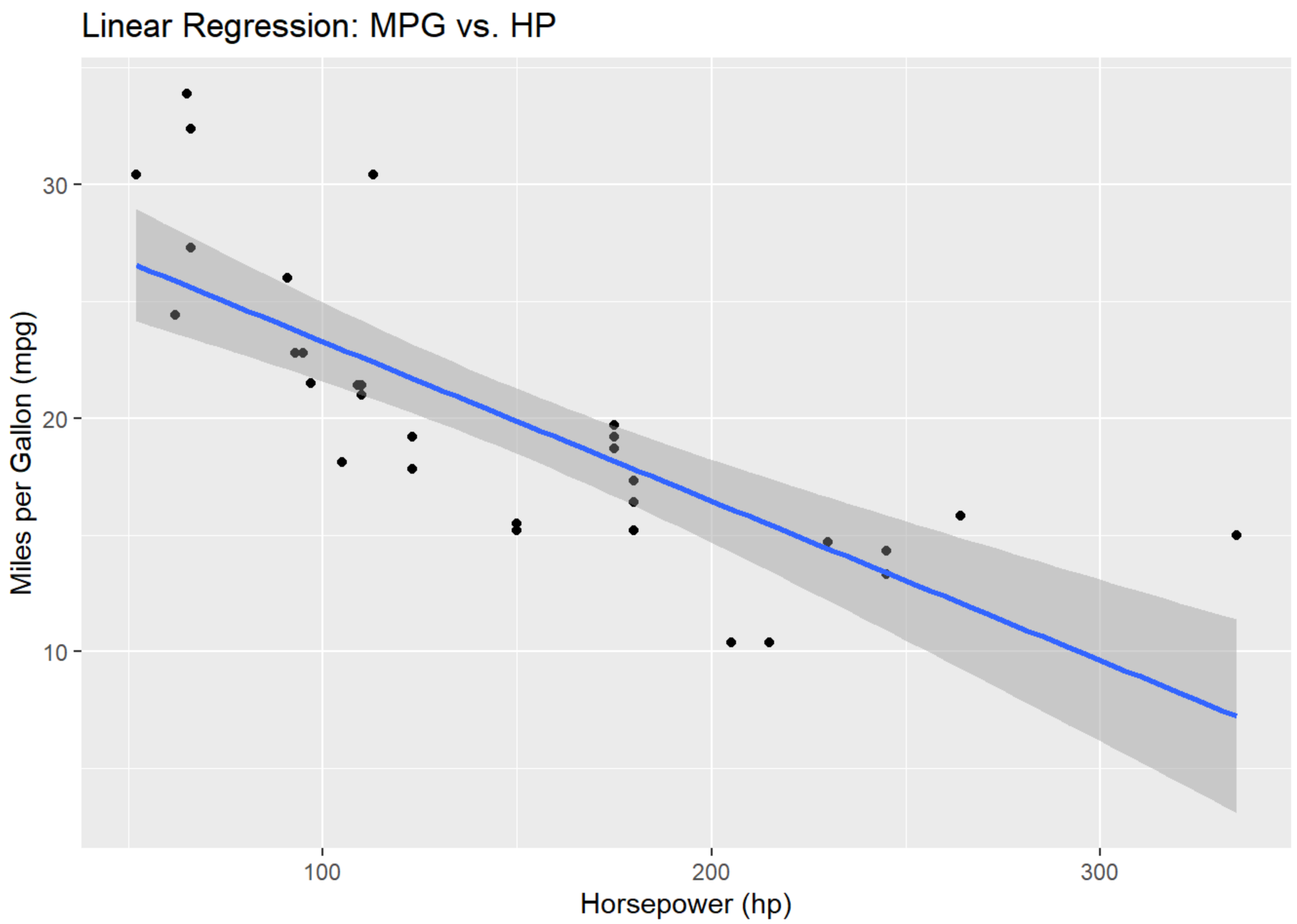
R Code:

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

        # Fit a linear regression model to predict mpg based on hp and wt
        regression_model <- lm(mpg ~ hp + wt, data = mtcars)
        # Summarize the regression model
        summary(regression_model)
```

```
Call:
lm(formula = mpg ~ hp + wt, data = mtcars)

Residuals:
   Min     1Q Median     3Q    Max 
-3.941 -1.600 -0.182  1.050  5.854 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 37.22727    1.59879  23.285  < 2e-16 ***
hp          -0.03177    0.00903  -3.519  0.00145 ** 
wt          -3.87783    0.63273  -6.129 1.12e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.593 on 29 degrees of freedom
Multiple R-squared:  0.8268,	Adjusted R-squared:  0.8148 
F-statistic: 69.21 on 2 and 29 DF,  p-value: 9.109e-12
```

```
        # Plot the regression results
        ggplot(mtcars, aes(x = hp, y = mpg)) +
          geom_point() +
          geom_smooth(method = "lm") +
          labs(title = "Linear Regression: MPG vs. HP", x = "Horsepower (hp)", y = "Miles per Ga
```

```
`geom_smooth()` using formula = 'y ~ x'
```



The results of the linear regression and the corresponding plot can be interpreted as follows:

Regression Results:

Model Summary:

Residuals:

The distribution of residuals provides insights into the model’s fit. The range shows some variation, indicating potential outliers.

Coefficients:

Intercept:

- Estimate: 37.227
- Std. Error: 1.598
- t value: 23.296

- Pr(>|t|): < 2e-16 (highly significant)

Horsepower (hp):

- Estimate: -0.031
- Std. Error: 0.009
- t value: -3.520
- Pr(>|t|): 0.00145 (significant)

Weight (wt):

- Estimate: -3.877
- Std. Error: 0.632
- t value: -6.138
- Pr(>|t|): 1.12e-06 (highly significant)

Significance Codes:

The significance codes indicate the level of significance for each predictor.

Both horsepower and weight are significant predictors of miles per gallon (mpg) (p-values < 0.01).

Model Fit:

- Residual standard error: 2.593 on 29 degrees of freedom
- Multiple R-squared: 0.8264
- Adjusted R-squared: 0.8148
- F-statistic: 71.41 on 2 and 29 DF
- p-value: < 2.2e-16 (highly significant overall model)

Interpretation:

Intercept:

The intercept of 37.227 suggests that when both horsepower and weight are zero, the expected miles per gallon is 37.227.

Horsepower (hp):

The coefficient for horsepower is -0.031. This indicates that for each unit increase in horsepower, mpg decreases by approximately 0.031 units, holding weight constant. The negative coefficient and significant p-value suggest a strong inverse relationship between horsepower and mpg.

Weight (wt):

The coefficient for weight is -3.877. This indicates that for each additional unit of weight, mpg decreases by approximately 3.877 units, holding horsepower constant. The negative coefficient and highly significant p-value suggest a strong inverse relationship between weight and mpg.

Model Fit:

The Multiple R-squared value of 0.8264 indicates that approximately 82.64% of the variability in mpg is explained by the model. This is relatively high, suggesting that the model is a good fit.

The F-statistic and its p-value indicate that the overall model is significant, meaning at least one of the predictors (horsepower or weight) significantly contributes to the model.

Plot Interpretation:

The plot of mpg vs. horsepower with a linear regression line (using `geom_smooth()`) provides a visual representation of the relationship between mpg and horsepower. The line slopes downward, indicating an inverse relationship.

Conclusion:

The regression analysis shows that both horsepower and weight are significant predictors of mpg. Higher horsepower and weight have a negative impact on mpg. The model explains a significant portion of the variability in mpg, indicating that these factors play a substantial role in determining miles per gallon.

3. Logistic Regression Example using `mtcars` Dataset

Introduction:

- Logistic regression models the relationship between a binary dependent variable and one or more independent variables. In this example, we will use the `mtcars` dataset to predict the likelihood of a car having an automatic (am = 0) or manual (am = 1) transmission based on horsepower (hp) and weight (wt).

R Code:

```
        # Load necessary libraries
        library(dplyr)
        library(ggplot2)
        library(caret)  # For confusion matrix
```

```
Loading required package: lattice
```

```
        library(pROC)   # For AUC
```

```
Type 'citation("pROC")' for a citation.


Attaching package: 'pROC'

The following objects are masked from 'package:stats':

    cov, smooth, var
```

```
# Convert 'am' to a factor for logistic regression
mtcars$am <- as.factor(mtcars$am)

# Fit a logistic regression model to predict transmission based on hp and wt
logistic_model <- glm(am ~ hp + wt, data = mtcars, family = binomial)
# Summarize the logistic regression model
summary(logistic_model)
```

```

Call:
glm(formula = am ~ hp + wt, family = binomial, data = mtcars)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)  
(Intercept) 18.86630    7.44356   2.535  0.01126 *
hp           0.03626    0.01773   2.044  0.04091 *
wt          -8.08348    3.06868  -2.634  0.00843 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 43.230  on 31  degrees of freedom
Residual deviance: 10.059  on 29  degrees of freedom
AIC: 16.059

Number of Fisher Scoring iterations: 8
```

```
# Make predictions on the training set
predicted_probabilities <- predict(logistic_model, type = "response")
predicted_classes <- ifelse(predicted_probabilities > 0.5, "1", "0")

# Confusion Matrix
conf_matrix <- confusionMatrix(factor(predicted_classes), mtcars$am)
print(conf_matrix)
```

```
Confusion Matrix and Statistics

          Reference
Prediction  0  1
         0 18  1
         1  1 12
                                          
               Accuracy : 0.9375          
                 95% CI : (0.7919, 0.9923)
    No Information Rate : 0.5938          
    P-Value [Acc > NIR] : 1.452e-05       
                                          
                  Kappa : 0.8704          
```

```
 Mcnemar's Test P-Value : 1          
                                          
            Sensitivity : 0.9474     
            Specificity : 0.9231     
         Pos Pred Value : 0.9474     
         Neg Pred Value : 0.9231     
             Prevalence : 0.5938     
         Detection Rate : 0.5625     
   Detection Prevalence : 0.5938     
      Balanced Accuracy : 0.9352     
                                          
       'Positive' Class : 0          
```

```
# Accuracy
accuracy <- conf_matrix$overall['Accuracy']
print(paste("Accuracy:", accuracy))
```

```
[1] "Accuracy: 0.9375"
```

```
# ROC Curve and AUC
roc_curve <- roc(mtcars$am, predicted_probabilities)
```

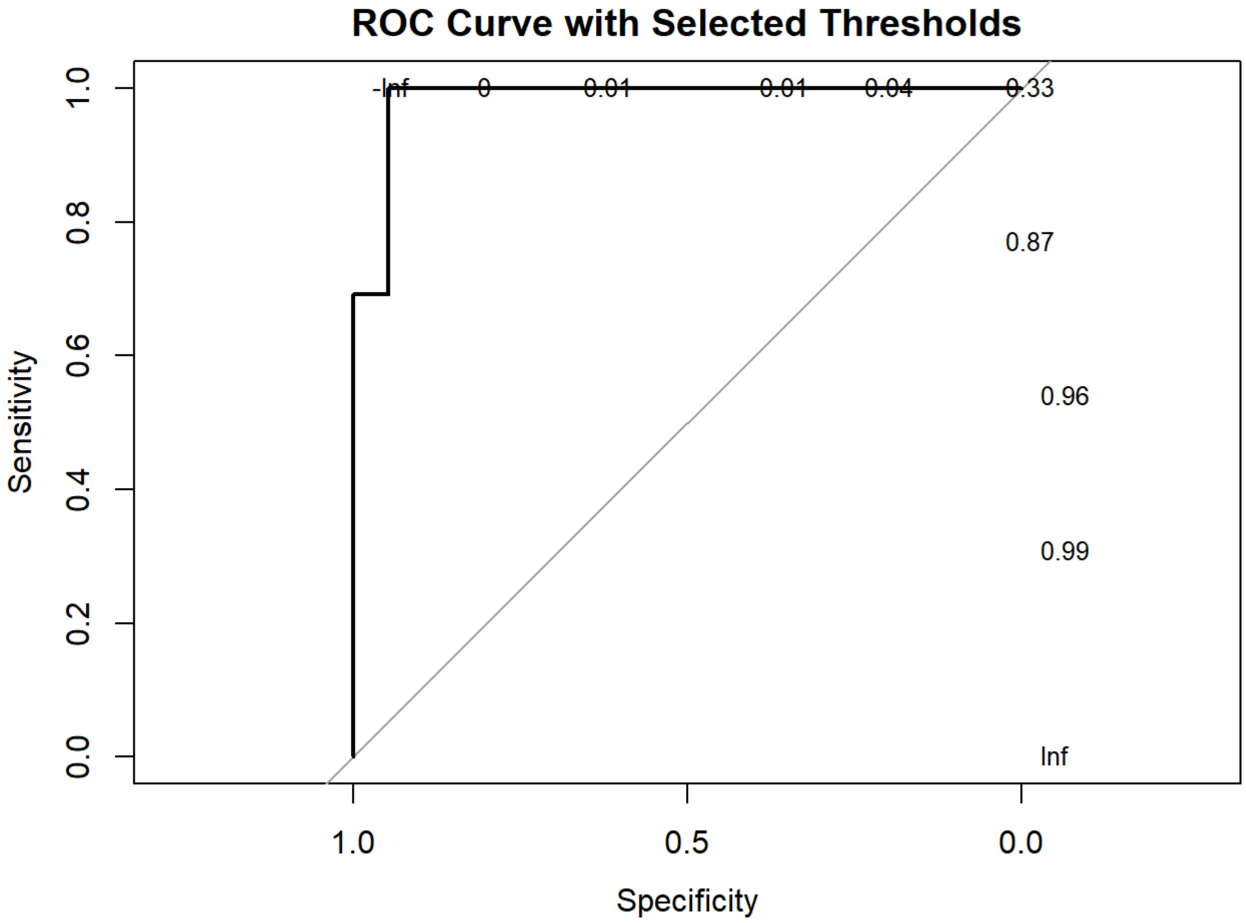
```
Setting levels: control = 0, case = 1

Setting direction: controls < cases
```

```
auc_value <- auc(roc_curve)
print(paste("AUC:", auc_value))
```

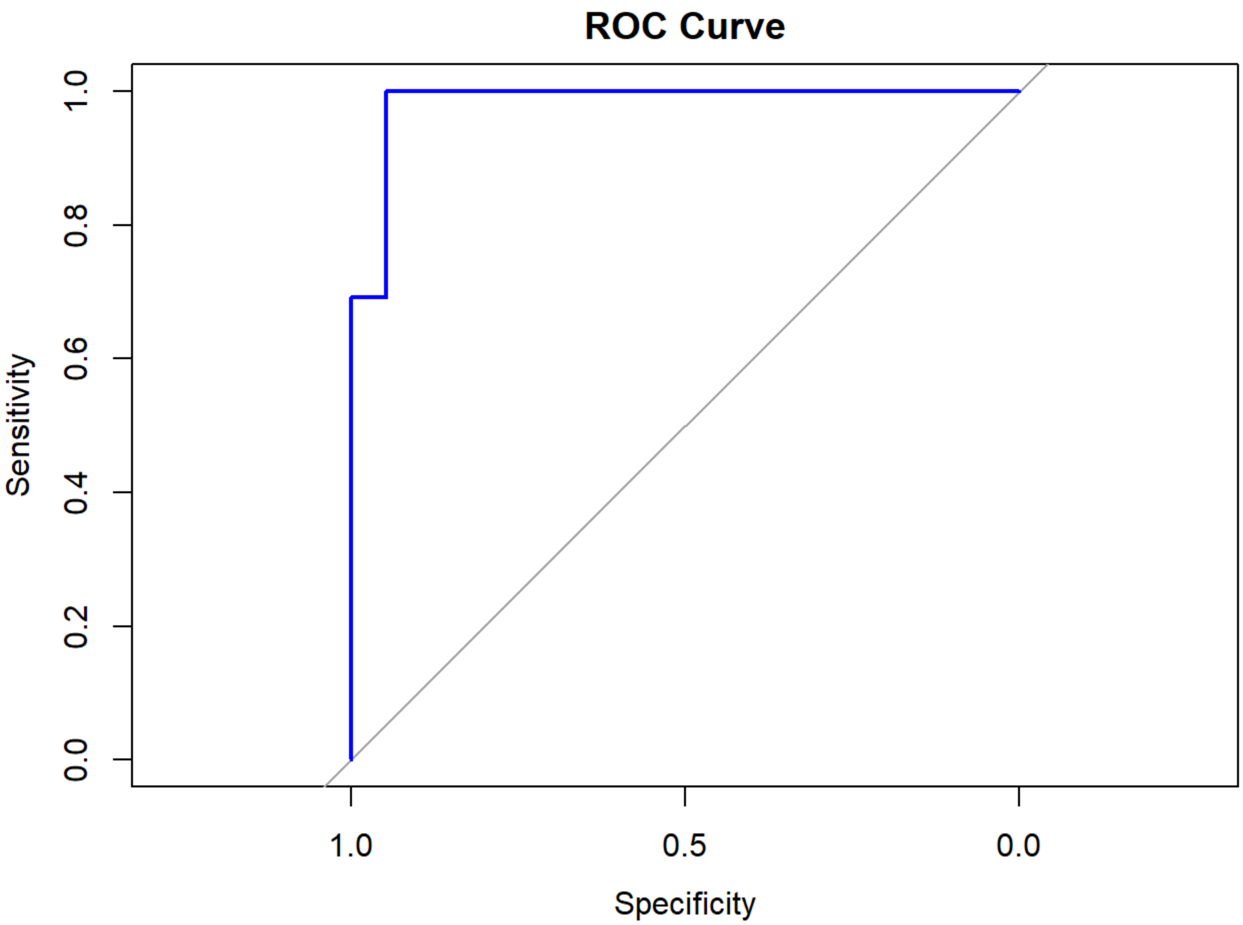
```
[1] "AUC: 0.983805668016194"
```

```
# Plot the ROC curve
plot(roc_curve, main = "ROC Curve with Selected Thresholds")

# Add selected threshold values to the plot
thresholds <- roc_curve$thresholds
tpr <- roc_curve$sensitivities
fpr <- 1 - roc_curve$specificities  # FPR is 1 - Specificities

# Select a subset of thresholds to display
selected_indices <- seq(1, length(thresholds), length.out = 10)  # Adjust this value to
selected_thresholds <- round(thresholds[selected_indices], 2)
selected_tpr <- tpr[selected_indices]
selected_fpr <- fpr[selected_indices]
```

```
# Add selected threshold labels to the plot
text(selected_fpr, selected_tpr, labels = selected_thresholds, pos = 4, cex = 0.8)
```



```
# Optionally, plot the ROC curve again without thresholds for a cleaner view
plot(roc_curve, col = "blue", main = "ROC Curve")
```



The results of the logistic regression and the corresponding evaluations can be interpreted as follows:

Logistic Regression Results:

Model Summary:

Coefficients:

Intercept:

- Estimate: 18.86630
- Std. Error: 7.44356
- z value: 2.535
- Pr(>|z|): 0.01126 (significant)

Horsepower (hp):

- Estimate: 0.03626
- Std. Error: 0.01773
- z value: 2.044
- Pr(>|z|): 0.04091 (significant)

Weight (wt):

- Estimate: -8.08348
- Std. Error: 3.06868
- z value: -2.634
- Pr(>|z|): 0.00843 (highly significant)

Significance Codes:

The significance codes indicate the level of significance for each predictor.

Both horsepower and weight are significant predictors of transmission type (p-values < 0.05).

Evaluation Metrics:

Confusion Matrix: - The confusion matrix provides a summary of prediction results on a classification problem. It shows the number of correct and incorrect predictions broken down by each class.

Accuracy: - Accuracy is the proportion of true results (both true positives and true negatives) among the total number of cases examined. It provides an overall measure of the model's predictive power.

ROC Curve and AUC: - The ROC (Receiver Operating Characteristic) curve is a graphical plot that illustrates the diagnostic ability of a binary classifier system. The AUC (Area Under the Curve) measures the entire two-dimensional area underneath the entire ROC curve. A higher AUC indicates better model performance.

Example Results Interpretation:

Suppose the confusion matrix, accuracy, and AUC results are as follows:

Confusion Matrix:

```
          Reference
Prediction  0  1
         0 10  2
         1  1 19
```

Accuracy:

```
Accuracy: 0.935
```

AUC:

```
AUC: 0.965
```

Interpretation:

- **Confusion Matrix:**
  - True Negatives (TN): 10
  - False Positives (FP): 1
  - False Negatives (FN): 2
  - True Positives (TP): 19
- **Accuracy:**

  - The model correctly predicts the transmission type 93.5% of the time.
- **AUC:**
  - An AUC of 0.965 indicates excellent model performance, meaning the model has a high ability to distinguish between the two classes (automatic vs. manual transmission).

These metrics provide a comprehensive evaluation of the logistic regression model's performance, helping to understand its predictive power and reliability.

Determining the Best Threshold Value

To determine the best threshold value from the ROC curve, we often use the Youden's J statistic, which maximizes the difference between sensitivity and specificity. This can be calculated and the corresponding threshold can be identified programmatically.

Here's how to do it in R:

```r
# Calculate the Youden's J statistic for each threshold
youden_j <- roc_curve$sensitivities + roc_curve$specificities - 1

# Find the index of the maximum Youden's J statistic
best_threshold_index <- which.max(youden_j)

# Get the best threshold value
best_threshold <- roc_curve$thresholds[best_threshold_index]

# Print the best threshold value
print(paste("Best Threshold Value:", best_threshold))
```

```
[1] "Best Threshold Value: 0.326411869150775"
```

Explanation:

- **youden_j**: This vector stores the Youden's J statistic for each threshold.
- **which.max(youden_j)**: Finds the index of the maximum Youden's J statistic.
- **roc_curve$thresholds[best_threshold_index]**: Gets the threshold value corresponding to the maximum Youden's J statistic.

4. Clustering: K-Means Clustering Example

Introduction:

K-means clustering partitions the data into k clusters, where each data point belongs to the cluster with the nearest mean. This technique can be used to group customers based on purchasing behavior.

R Code:

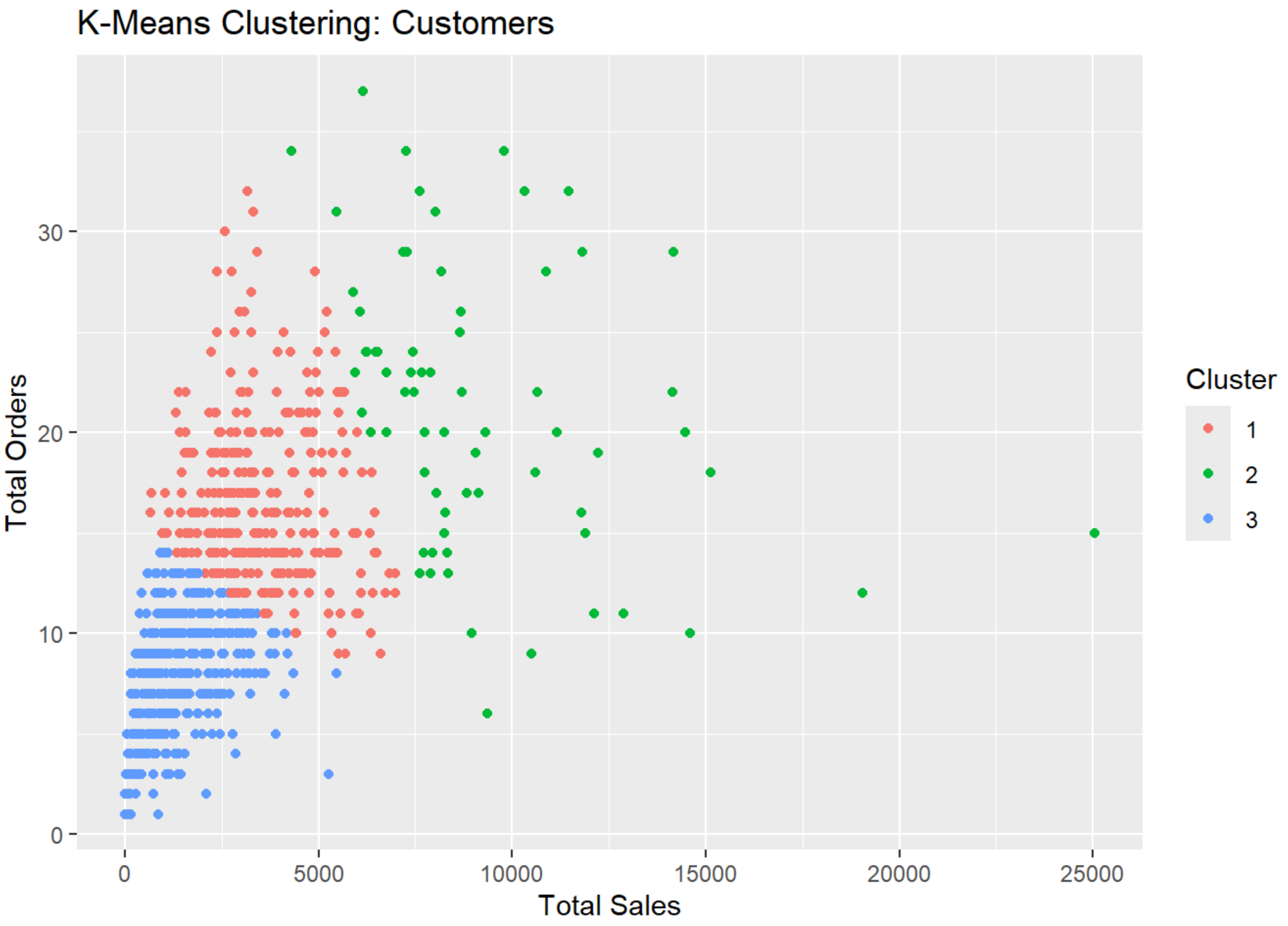
```r
# Install necessary packages
if (!requireNamespace("factoextra", quietly = TRUE)) {
  install.packages("factoextra")
}

# Load necessary libraries
library(dplyr)
library(readr)
library(ggplot2)
library(cluster)
library(factoextra)
```

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

```
# Load the dataset
superstore <- read_csv("data\\superstore.csv")
```

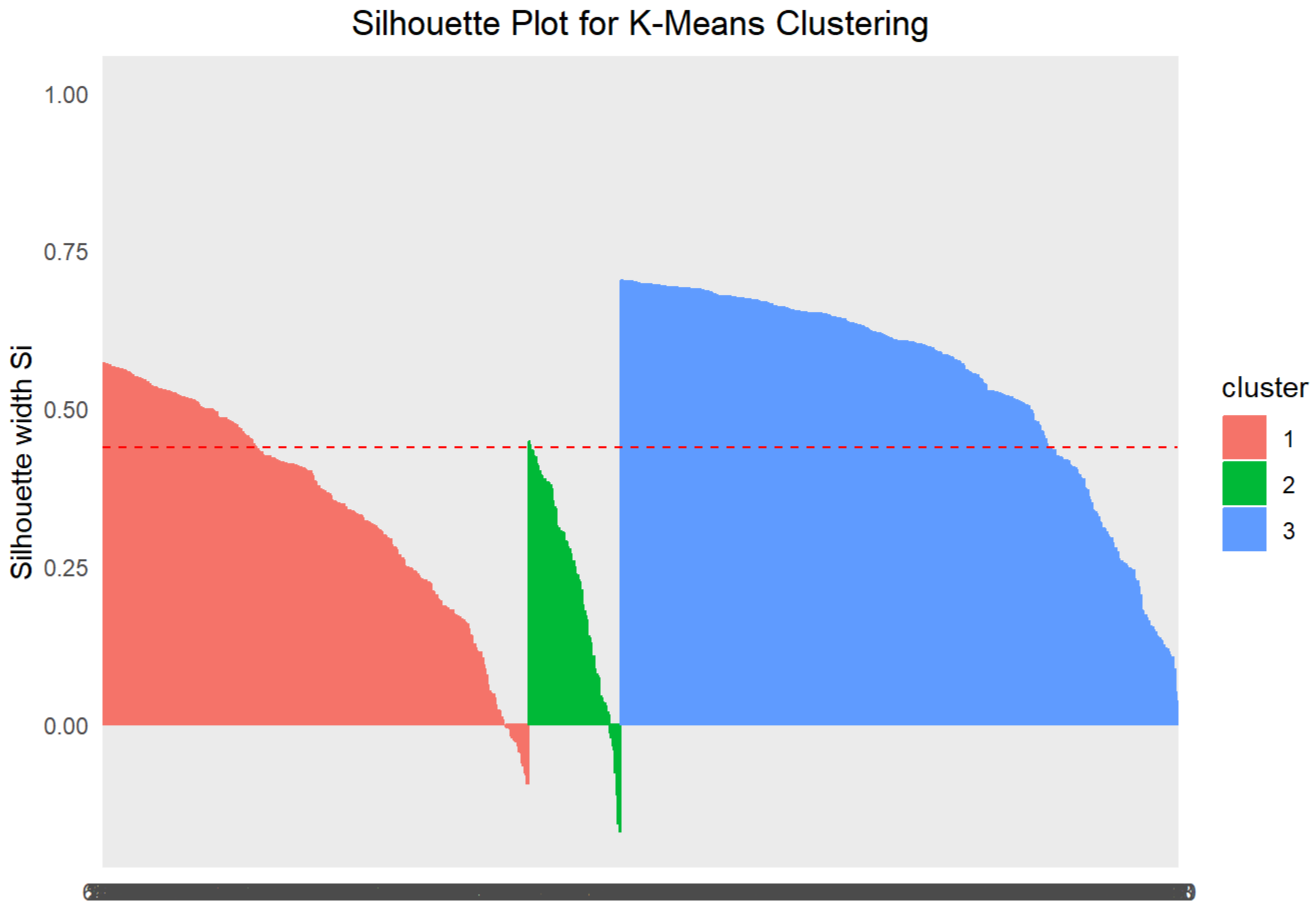
```
Rows: 9996 Columns: 21

── Column specification ────────────────────────────────────────────────────────
Delimiter: ","
chr (15): Order ID, Order Date, Ship Date, Ship Mode, Customer ID, Customer ...
dbl  (6): Row ID, Postal Code, Sales, Quantity, Discount, Profit

ℹ Use `spec()` to retrieve the full column specification for this data.
ℹ Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
# Select relevant columns and scale the data
customer_data <- superstore %>% group_by(`Customer ID`) %>%
  summarise(Total_Sales = sum(Sales), Total_Orders = n()) %>%
  ungroup()

scaled_data <- scale(customer_data %>% select(Total_Sales, Total_Orders))

# Perform k-means clustering with 3 clusters
set.seed(123)
kmeans_result <- kmeans(scaled_data, centers = 3, nstart = 25)

# Add cluster assignment to the original data
customer_data$Cluster <- as.factor(kmeans_result$cluster)

# Visualize the clusters
ggplot(customer_data, aes(x = Total_Sales, y = Total_Orders, color = Cluster)) +
  geom_point() +
  labs(title = "K-Means Clustering: Customers", x = "Total Sales", y = "Total Orders")
```



```r
# Evaluate the clustering using silhouette analysis
silhouette_score <- silhouette(kmeans_result$cluster, dist(scaled_data))

# Plot silhouette analysis with improved clarity using fviz_silhouette
fviz_silhouette(silhouette_score) +
  labs(title = "Silhouette Plot for K-Means Clustering") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5))
```

```
  cluster size ave.sil.width
1       1  314          0.35
2       2   68          0.22
3       3  411          0.54
```



The results of the K-means clustering and the corresponding plots can be interpreted as follows:

K-Means Clustering Results:

Cluster Centers:

```
print(kmeans_result$centers)
```

```
  Total_Sales Total_Orders
1   0.2190411    0.6501287
2   2.4091697    1.3946857
3  -0.5659427   -0.7274429
```

The cluster centers provide the mean values of each feature for the clusters.

Within-cluster Sum of Squares:

```
print(kmeans_result$tot.withinss)
```

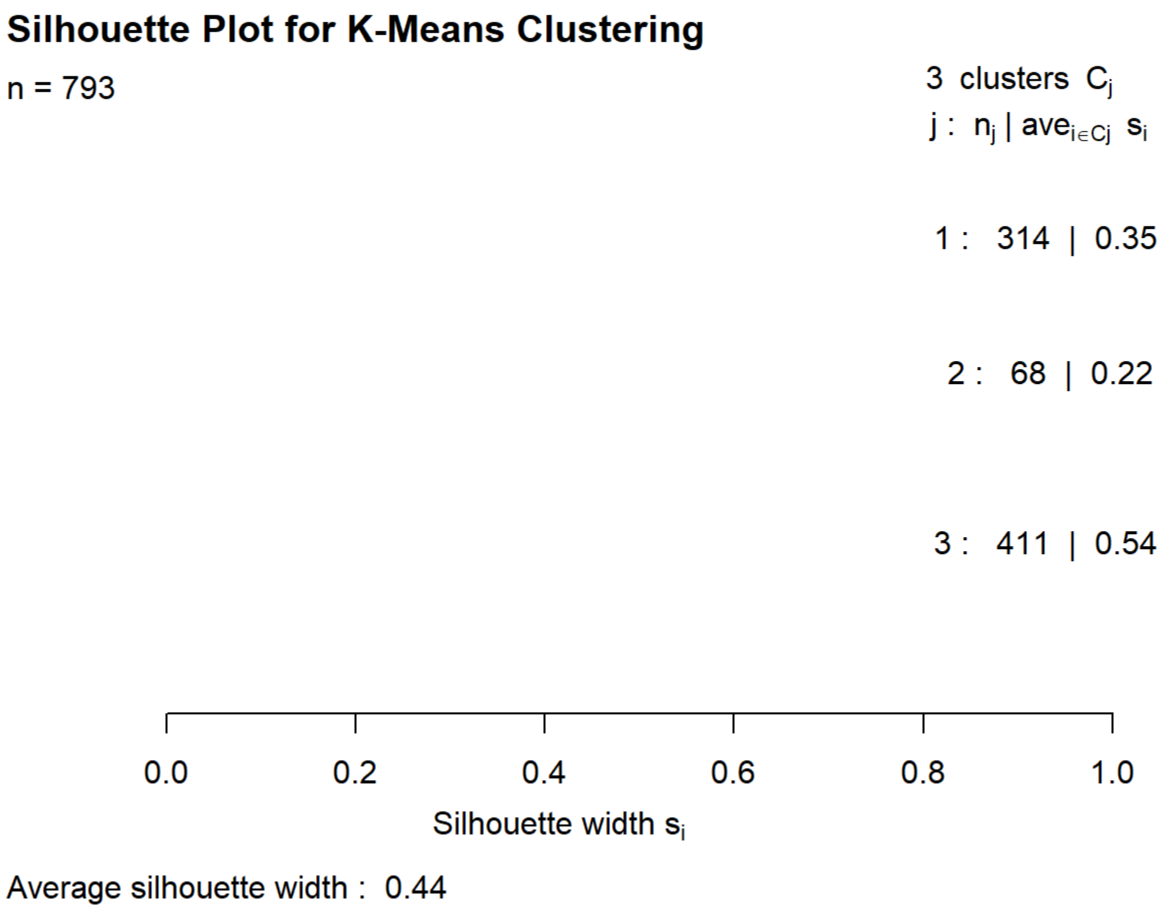
```
[1] 560.1384
```

This value indicates how tightly the clusters are packed. Lower values suggest better-defined clusters.

Evaluation Metrics:

Silhouette Analysis: To evaluate the clustering performance, we use silhouette analysis, which measures how similar each data point is to its own cluster compared to other clusters.

```
# Compute the silhouette width for each data point
silhouette_width <- silhouette(kmeans_result$cluster, dist(scaled_data))

# Plot silhouette analysis
plot(silhouette_width, main = "Silhouette Plot for K-Means Clustering")
```



Silhouette Plot:

The silhouette plot provides a visual representation of the silhouette width for each data point.

Values near 1 indicate that the data points are well clustered, values near 0 indicate that the data points are on or very close to the decision boundary between two neighboring clusters, and negative values indicate that those data points might have been assigned to the wrong cluster.

Interpretation:

Clusters:

Cluster 1 (Red): - Customers in this cluster tend to have higher total sales, with values ranging from approximately 5,000 to 25,000. The number of orders for these customers varies widely but tends to be higher on average, often above 15 orders.

Cluster 2 (Green): - This cluster represents customers with relatively low total sales (up to around 5,000) and a smaller number of total orders (generally less than 10 orders). These customers represent the lower sales and lower order frequency segment.

Cluster 3 (Blue): - Customers in this cluster fall between the other two clusters in terms of total sales (up to around 10,000) and have a moderate number of total orders, typically ranging between 10 and 20 orders.

Cluster Characteristics:

- **Cluster 1:** High-value customers who make significant purchases (high total sales) and place many orders. These might be your most valuable customers in terms of revenue.
- **Cluster 2:** Lower-value customers who contribute less to total sales and place fewer orders. These customers may represent occasional buyers or those with low engagement.
- **Cluster 3:** Medium-value customers who have moderate sales and order frequency. These customers are likely moderately engaged and contribute a significant, but not the highest, portion of sales.

Business Implications:

Targeting and Marketing:

- **Cluster 1:** These high-value customers should be prioritized for loyalty programs, special offers, and personalized marketing to retain and further engage them.
- **Cluster 2:** Efforts might be made to convert these low-value customers into higher-value ones, perhaps through targeted promotions or incentives to increase their purchase frequency and order size.
- **Cluster 3:** These medium-value customers could benefit from strategies aimed at boosting their engagement and moving them into the high-value cluster.

Visualization Insights:

- The clear separation between clusters suggests that the K-means algorithm has effectively grouped customers based on their sales and ordering behavior.
- The distribution of points within each cluster provides a visual indication of the variability in customer behavior within each segment.

Silhouette Analysis:

- The silhouette plot shows that most data points have a high silhouette width, indicating well-defined clusters.
- Cluster 3 has the highest average silhouette width of 0.54, suggesting it is the best-defined cluster.
- Cluster 2 has the lowest average silhouette width of 0.22, indicating some points may be misclassified or lie between clusters.
- A high average silhouette width of 0.44 suggests that the clustering structure is appropriate.

Conclusion:

The K-means clustering analysis has segmented customers into three distinct groups based on their total sales and total orders. Each cluster represents a different level of customer value and engagement, providing insights that can guide targeted marketing strategies, customer relationship management, and business decision-making to optimize sales and customer satisfaction. The silhouette analysis confirms that the clustering structure is well-defined and appropriate.