

Batch: A1

Roll No.: 16010123012

Experiment No. 5

Title: Hypothesis Testing

Aim: To perform hypothesis testing using the z-test and t-test in RStudio, and draw statistical inference from the results

Course Outcome:

CO2: Gain necessary mathematical skills in probability, statistics, and basic linear algebra.

Books/ Journals/ Websites referred:

1. [The Comprehensive R Archive Network](#)
2. [Posit](#)

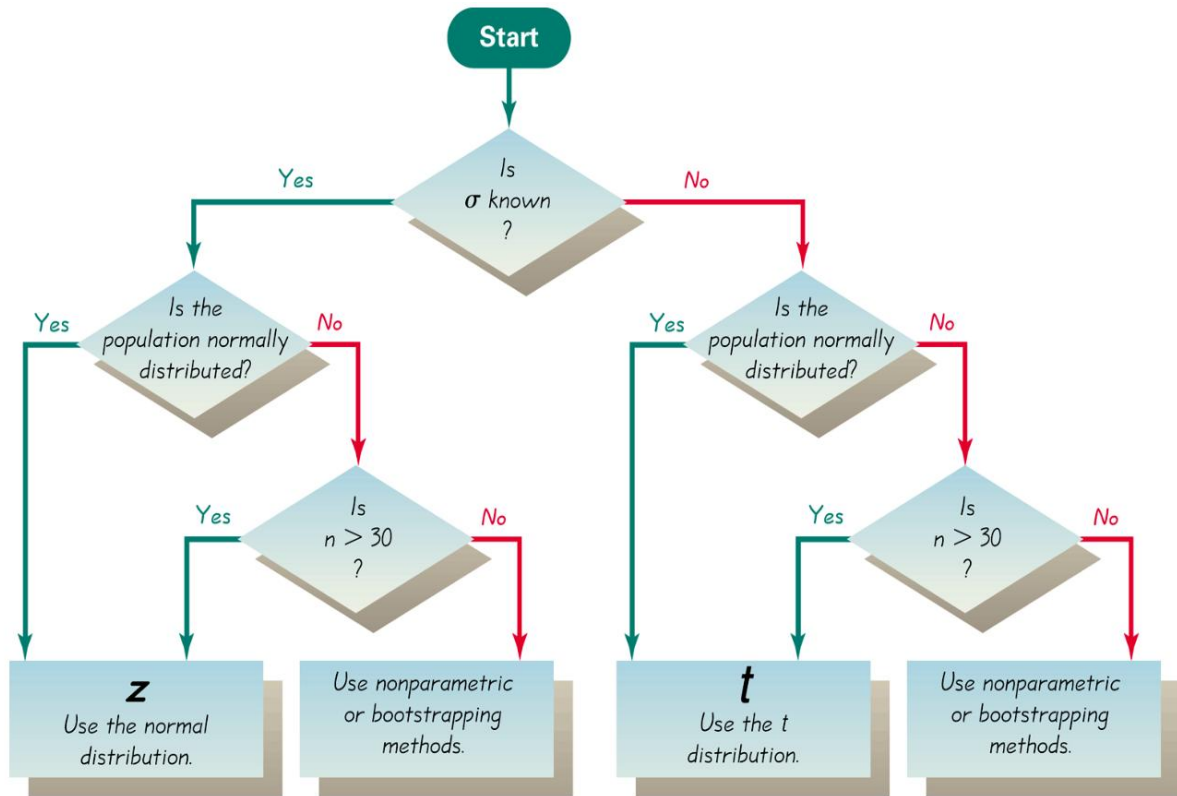
Resources used:

<https://www.rdocumentation.org/>

<https://www.w3schools.com/r/>

<https://www.geeksforgeeks.org/r-programming-language-introduction/>

Theory:



Implementation:

1. One-Sample Z-Test (One-Tailed)

The population of all verbal GRE scores are known to have a standard deviation of 8.5. The UW Psychology department hopes to receive applicants with a verbal GRE scores over 210. This year, the mean verbal GRE scores for the 42 applicants was 212.79. Using a value of $\alpha = 0.05$ is this new mean significantly greater than the desired mean of 210?

The standard error of the mean is therefore:

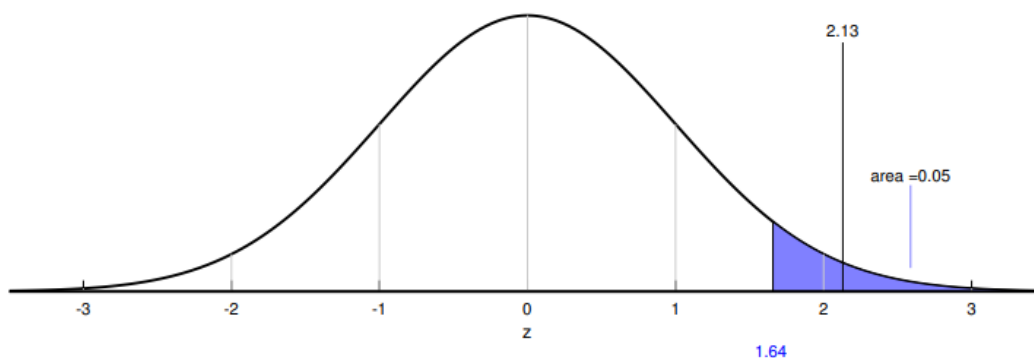
$$\sigma_{\bar{x}} = \frac{\sigma_x}{\sqrt{n}} = \frac{8.5}{\sqrt{42}} = 1.31$$

To find the probability of finding a mean above 212.79 we convert our observed mean, \bar{x} , to a z-score:

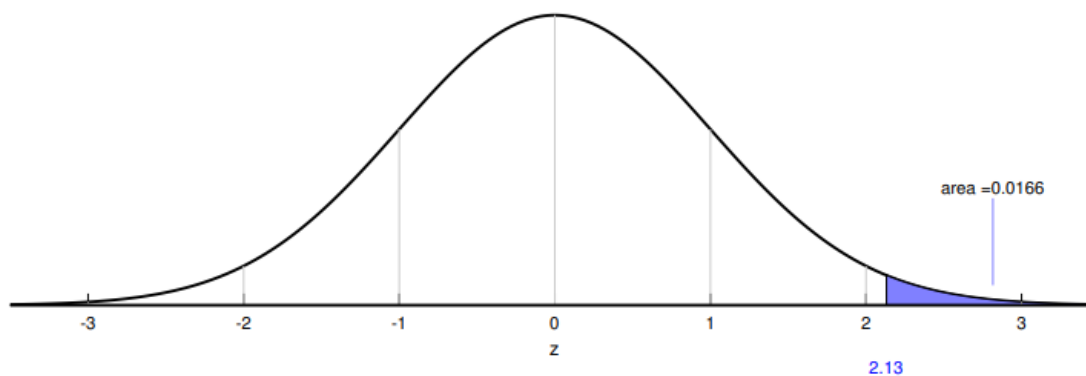
$$z = \frac{(\bar{x} - \mu_{hyp})}{\sigma_{\bar{x}}} = \frac{(212.79 - 210)}{1.31} = 2.13$$

```

> # Given data
> sigma <- 8.5
> n <- 42
> sample_mean <- 212.79
> pop_mean <- 210
> alpha <- 0.05
> # Compute Z-score
> z_score <- (sample_mean - pop_mean) / (sigma / sqrt(n))
> print(z_score)
[1] 2.127208
> # Compute p-value (one-tailed test)
> p_value <- 1 - pnorm(z_score)
> print(p_value)
[1] 0.01670141
> # Decision Rule
> if (p_value < alpha) {
+   cat("Reject H0: The new mean is significantly greater than 210.\n")
+ } else {
+   cat("Fail to Reject H0: The new mean is NOT significantly greater than 210.\n")
+ }
Reject H0: The new mean is significantly greater than 210.
  
```



Our observed value of z is 2.13 which is greater than the critical value of 1.64. We therefore reject H_0 .

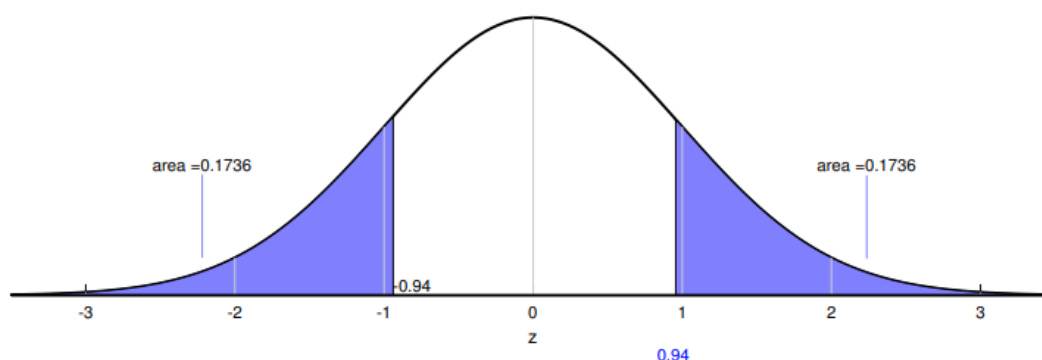


Our p-value is less than alpha (0.05). If the null hypothesis is true, then the probability of obtaining our observed mean or greater is less than 0.05. We therefore reject H_0 and state that (in APA format):

The verbal GRE scores of applicants ($M = 212.79$) is significantly greater than 210, $z=2.13$, $p = 0.0166$.

2. One-Sample Z-Test (Two-Tailed)

Suppose you start up a company that has developed a drug that is supposed to increase IQ. You know that the standard deviation of IQ in the general population is 15. You test your drug on 36 patients and obtain a mean IQ of 97.65. Using an alpha value of 0.05, is this IQ significantly different than the population mean of 100?



To solve this, we first calculate the standard error of the mean:

$$\sigma_{\bar{x}} = \frac{\sigma}{\sqrt{n}} = \frac{15}{\sqrt{36}} = 2.5$$

and then convert our observed mean to a z-score:

$$z = \frac{(\bar{x} - \mu_{hyp})}{\sigma_{\bar{x}}} = \frac{(97.65 - 100)}{2.5} = -0.94$$

The rejection region contains values of z less than -1.96 and greater than 1.96. Our observed value of z falls outside the rejection region, so we fail to reject H_0 and conclude that our drug did not have a significant effect on IQ.

```
> # Given values
> sigma <- 15
> n <- 36
> sample_mean <- 97.65
> pop_mean <- 100
> alpha <- 0.05
>
> # Calculate the Z-score
> z_score <- (sample_mean - pop_mean) / (sigma / sqrt(n))
>
> # Calculate the p-value for a two-tailed test
> p_value <- 2 * pnorm(-abs(z_score))
>
> # Print the results
> cat("Z-score:", z_score, "\n")
Z-score: -0.94
> cat("p-value:", p_value, "\n")
p-value: 0.3472176
>
> # Decision rule
> if (p_value < alpha) {
+   cat("Reject the null hypothesis: There is a significant difference.\n")
+ } else {
+   cat("Fail to reject the null hypothesis: There is no significant difference.\n")
+ }
Fail to reject the null hypothesis: There is no significant difference.
```

3. Two-Sample Z-Test (Independent)

Example: Male vs Female Heights

A researcher wants to test whether male and female average heights are significantly different. The population standard deviations for both groups are known:

Male height: $\sigma = 7$ cm

Female height: $\sigma = 6$ cm

A random sample of 50 males and 50 females is taken:

Sample mean height for males: 175 cm

Sample mean height for females: 170 cm

Using $\alpha = 0.05$, determine whether the difference in average heights is statistically significant.

```
> # Given data
> x1 <- 175 # Sample mean of males
> x2 <- 170 # Sample mean of females
> sigma1 <- 7 # Population SD of males
> sigma2 <- 6 # Population SD of females
> n1 <- 50 # Sample size of males
> n2 <- 50 # Sample size of females
> alpha <- 0.05 # Significance level
>
> # Calculate Z-score
> z_value <- (x1 - x2) / sqrt((sigma1^2 / n1) + (sigma2^2 / n2))
>
> # Compute two-tailed p-value
> p_value <- 2 * (1 - pnorm(abs(z_value)))
>
> # Critical z-value at 95% confidence
> z_critical <- qnorm(1 - alpha/2)
>
> # Decision based on z-value
> if (abs(z_value) > z_critical) {
+   z_decision <- "Reject H0 (Significant Difference in Heights)"
+ } else {
+   z_decision <- "Fail to Reject H0 (No Significant Difference)"
+ }

> # Decision based on p-value
> if (p_value < alpha) {
+   p_decision <- "Reject H0 (Significant Difference in Heights)"
+ } else {
+   p_decision <- "Fail to Reject H0 (No Significant Difference)"
+ }
>
> # Print results
> cat("Z-value:", z_value, "\n")
Z-value: 3.834825
> cat("Critical Z-value:", z_critical, "\n")
Critical Z-value: 1.959964
> cat("P-value:", p_value, "\n")
P-value: 0.0001256538
> cat("Decision based on Z-value:", z_decision, "\n")
Decision based on Z-value: Reject H0 (Significant Difference in Heights)
> cat("Decision based on P-value:", p_decision, "\n")
Decision based on P-value: Reject H0 (Significant Difference in Heights)
```

4. Two-Sample Z-Test (Left-Tailed)

A company claims that **employees in the Marketing department** have significantly **lower** stress levels (measured on a 1-100 scale) than employees in the Sales department.

- The **population standard deviation** for stress levels in Sales is **10**.
- The **population standard deviation** for stress levels in Marketing is **8**.
- A random sample of **50 Sales employees** has a mean stress level of **70**.
- A random sample of **45 Marketing employees** has a mean stress level of **65**.
- Using $\alpha = 0.05$, test whether Marketing employees have significantly **lower** stress levels than Sales employees.

```
> # Given data
> x1 <- 70 # Sample mean of Sales employees
> x2 <- 65 # Sample mean of Marketing employees
> sigma1 <- 10 # Population SD of Sales employees
> sigma2 <- 8 # Population SD of Marketing employees
> n1 <- 50 # Sample size of Sales employees
> n2 <- 45 # Sample size of Marketing employees
> alpha <- 0.05 # Significance level
>
> # Calculate Z-score
> z_value <- (x1 - x2) / sqrt((sigma1^2 / n1) + (sigma2^2 / n2))
>
> # Compute one-tailed p-value (left-tailed test)
> p_value <- pnorm(z_value)
>
> # Critical z-value for left-tailed test
> z_critical <- qnorm(alpha)

> # Decision based on z-value
> if (z_value < z_critical) {
+   z_decision <- "Reject H0 (Marketing employees have significantly lower stress levels)"
+ } else {
+   z_decision <- "Fail to Reject H0 (No significant difference)"
+ }
>
> # Decision based on p-value
> if (p_value < alpha) {
+   p_decision <- "Reject H0 (Marketing employees have significantly lower stress levels)"
+ } else {
+   p_decision <- "Fail to Reject H0 (No significant difference)"
+ }
>
> # Print results
> cat("Z-value:", z_value, "\n")
Z-value: 2.702812
> cat("Critical Z-value:", z_critical, "\n")
Critical Z-value: -1.644854
> cat("P-value:", p_value, "\n")
P-value: 0.9965622
> cat("Decision based on Z-value:", z_decision, "\n")
Decision based on Z-value: Fail to Reject H0 (No significant difference)
> cat("Decision based on P-value:", p_decision, "\n")
Decision based on P-value: Fail to Reject H0 (No significant difference)
```

5. Paired z-test

A researcher wants to determine whether a new diet plan is effective in reducing weight. To test this, they measure the weight (in kg) of 10 participants before and after following the diet plan for 6 weeks. The data is as follows:

Participant	Before Diet	After Diet
1	70	68
2	75	74
3	80	78
4	85	83
5	90	88
6	72	70
7	78	76
8	82	80
9	88	86
10	95	92

```
> library(BSDA)
>
> # Data: Before and After weights
> before <- c(70, 75, 80, 85, 90, 72, 78, 82, 88, 95)
> after <- c(68, 74, 78, 83, 88, 70, 76, 80, 86, 92)
>
> # calculate differences
> differences <- after - before
>
> # Perform paired Z-test
> z_test_result <- z.test(x = differences,
+                         sigma.x = sd(differences),
+                         mu = 0,
+                         alternative = "two.sided")
>
> # Print results
> print(z_test_result)
```

One-sample z-Test

```
data: differences
z = -13.416, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -2.292174 -1.707826
sample estimates:
mean of x
 -2
```


t-Tests:

1. One-Sample T-Test (Two Tailed)

A normal cholesterol level is considered **less than 200 mg/dL**.

We randomly sample **100 individuals** from the NHANES dataset and test:

- **H₀ (Null Hypothesis):** The mean cholesterol level in our sample is **200 mg/dL** (population mean).
- **H₁ (Alternative Hypothesis):** The mean cholesterol level **is different** from 200 mg/dL.
- We use $\alpha = 0.05$ for significance.

```
> library(NHANES)
library(ggplot2)

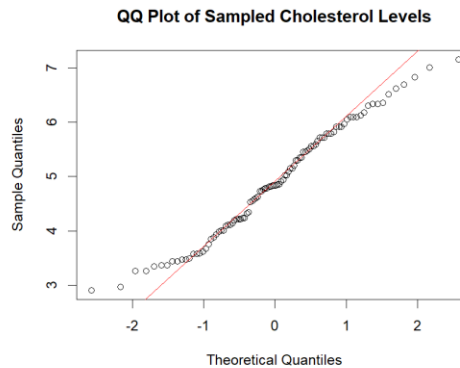
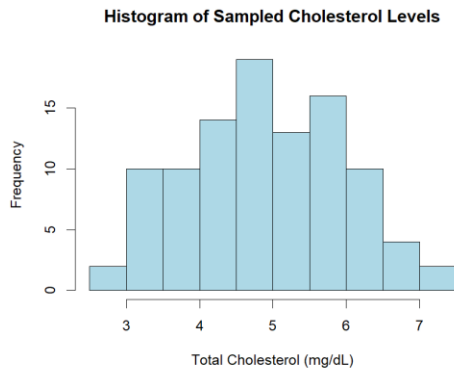
# Load and Clean Data
set.seed(123) # Ensuring reproducibility
chol_data <- na.omit(NHANES$TotChol) # Remove NA values

# Randomly select 100 Rows
sample_data <- sample(chol_data, 100, replace = FALSE)

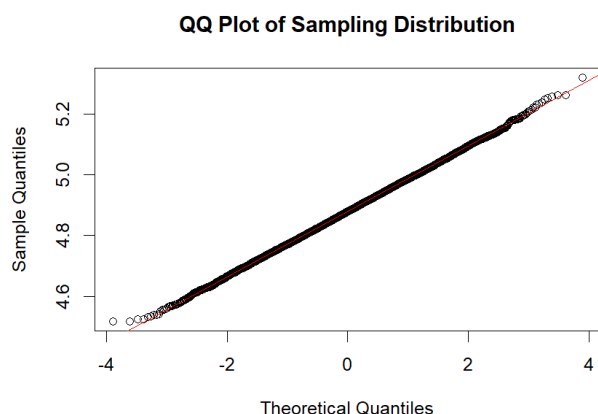
# Visualizing the Sample Distribution
hist(sample_data, breaks = 15, col="lightblue", border="black",
      main="Histogram of Sampled Cholesterol Levels",
      xlab="Total Cholesterol (mg/dL)", ylab="Frequency")

# QQ Plot to check Normality
qqnorm(sample_data, main="QQ Plot of Sampled Cholesterol Levels")
qqline(sample_data, col="red")
```

Checking the distribution of underlying data



```
> library(NHANES)
> library(ggplot2)
>
> # Remove NAs and Extract Total Cholesterol Data
> chol_data <- na.omit(NHANES$TotChol)
>
> # Set Parameters for Sampling
> sample_size <- 100 # Choose a large enough sample size
> num_samples <- 10000 # Number of samples to take
>
> # Generate Sampling Distribution
> sample_means <- replicate(num_samples, mean(sample(chol_data, sample_size, replace=TRUE)))
>
> # Plot Histogram of Sample Means
> ggplot(data.frame(sample_means), aes(x=sample_means)) +
+   geom_histogram(binwidth=1, fill="lightblue", color="black", alpha=0.7) +
+   ggtitle("Sampling Distribution of Sample Means") +
+   xlab("Sample Mean of Total cholesterol") +
+   ylab("Frequency") +
+   theme_minimal()
>
> # QQ Plot to Check Normality
> qqnorm(sample_means, main="QQ Plot of Sampling Distribution")
> qqline(sample_means, col="red")
```



```
# One-Sample T-Test
t_test_result <- t.test(sample_data, mu=200, alternative="two.sided")

# Print Test Results
print(t_test_result)

# Decision Rule
if (t_test_result$p.value < 0.05) {
  cat("Reject H0: The mean cholesterol level is significantly different from 200 mg/dL.\n")
} else {
  cat("Fail to Reject H0: No significant difference from 200 mg/dL.\n")
}





One Sample t-test

data: sample_data
t = -1891.3, df = 99, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 200
95 percent confidence interval:
 4.68681 5.09619
sample estimates:
mean of x
 4.8915

>
> # Decision Rule
> if (t_test_result$p.value < 0.05) {
+   cat("Reject H0: The mean cholesterol level is significantly different from 200 mg/dL.\n")
+ } else {
+   cat("Fail to Reject H0: No significant difference from 200 mg/dL.\n")
+ }
Reject H0: The mean cholesterol level is significantly different from 200 mg/dL.
```





Students have to explore the datasets within R libraries, Kaggle, UCI or any other freely available data repositories, frame the null and alternate hypothesis on suitable attributes and perform all the z-tests and t-tests.

Students have to clearly mention the data sources, paste their code, and screenshots of output in the writeup.

Environment	History	Connections	Tutorial
 Import Dataset ▾  197 MiB ▾ 			
R ▾  Global Environment ▾			
values			
alpha	0.05		
n	42		
p_value	0.016701409454178		
pop_mean	210		
sample_mean	212.79		
sigma	8.5		
z_score	2.1272078292421		

```

> sigma <- 8.5
> n <- 42
> sample_mean <- 212.79
> pop_mean <- 210
> alpha <- 0.05
>
> z_score <- (sample_mean - pop_mean) / (sigma / sqrt(n))
> print(z_score)
[1] 2.127208
>
> p_value <- 1 - pnorm(z_score)
> print(p_value)
[1] 0.01670141
>
> if(p_value < alpha){
+   cat("Reject H0: The new mean significantly greater than 210\n")
+ }else{
+   cat("Fail to Reject H0: The new mean is NOT significantly greater than 210\n")
+ }
Reject H0: The new mean significantly greater than 210
  
```

 Import Dataset ▾  197 MiB ▾ 	
R ▾  Global Environment ▾	
values	
alpha	0.05
n	36
p_value	0.34721756067725
pop_mean	100
sample_mean	97.65
sigma	15
z_score	-0.9399999999999998

```
> sigma <- 15
> n <- 36
> sample_mean <- 97.65
> pop_mean <- 100
> alpha <- 0.05
[1] FALSE
>
> z_score <- (sample_mean - pop_mean) / (sigma / sqrt(n))
>
> p_value <- 2 * pnorm(-abs (z_score))
>
> cat("Z-score:", z_score, "\n")
Z-score: -0.94
> cat("p-value:", p_value, "\n")
p-value: 0.3472176
>
> if (p_value < alpha) {
+   cat("Reject the null hypothesis: There is a significant difference.\n")
+ } else {
+   cat("Fail to reject the null hypothesis: There is no significant difference.\n")
+ }
Fail to reject the null hypothesis: There is no significant difference.
```

R Global Environment	
values	
alpha	0.05
n	36
n1	50
n2	50
p_decision	"Reject H0 (Significant Difference in Heights)"
p_value	0.000125653754458277
pop_mean	100
sample_mean	97.65
sigma	6
sigma1	7
sigma2	6
x1	175
x2	170
z_critical	1.95996398454005
z_decision	"Reject H0 (Significant Difference in Heights)"
z_score	-0.9399999999999998
z_value	3.83482494423685

```
> x1 <- 175
> x2 <- 170
> sigma1 <- 7
> sigma2 <- 6
> n1 <- 50
> n2 <- 50
> alpha <- 0.05
>
> z_value <- (x1 - x2) / sqrt((sigma1^2 / n1) + (sigma2^2 / n2))
> p_value <- 2 * (1 - pnorm(abs(z_value)))
> z_critical <- qnorm(1 - alpha/2)
>
> if(abs(z_value) > z_critical){
+   z_decision <- "Reject H0 (Significant Difference in Heights)"
+ } else {
+   z_decision <- "Fail to reject H0(No Significant Difference)"
+ }
>
> if((p_value) < alpha){
+   p_decision <- "Reject H0 (Significant Difference in Heights)"
+ } else {
+   p_decision <- "Fail to reject H0(No Significant Difference)"
+ }
>
> cat("Z-value: ", z_value, "\n")
Z-value: 3.834825
> cat("Critical Z-value: ", z_critical, "\n")
Critical Z-value: 1.959964
> cat("Decision based on Z-value: ", z_decision, "\n")
Decision based on Z-value: Reject H0 (Significant Difference in Heights)
> cat("Decision based on P-value: ", p_decision, "\n")
Decision based on P-value: Reject H0 (Significant Difference in Heights)
```

values	
alpha	0.05
n	36
n1	50
n2	45
p_decision	"Fail to reject H0(No Significant Difference)"
p_value	0.996562222879289
pop_mean	100
sample_mean	97.65
sigma	6
sigma1	10
sigma2	8
x1	70
x2	65
z_critical	1.95996398454005
z_decision	"Fail to reject H0(No Significant Difference)"
z_score	-0.9399999999999998
z_value	2.70281238808668

```
> x1 <- 70
> x2 <- 65
> sigma1 <- 10
> sigma2 <- 8
> n1 <- 50
> n2 <- 45
> alpha <- 0.05
>
> z_value <- (x1 - x2) / sqrt((sigma1^2 / n1) + (sigma2^2 / n2))
> p_value <- pnorm(z_value)
> z_critical <- qnorm(1 - alpha/2)
>
> if(z_value < z_critical){
+   z_decision <- "Reject H0 (Significant Difference in Heights)"
+ } else {
+   z_decision <- "Fail to reject H0(No Significant Difference)"
+ }
>
> if(p_value < alpha){
+   p_decision <- "Reject H0 (Significant Difference in Heights)"
+ } else {
+   p_decision <- "Fail to reject H0(No Significant Difference)"
+ }
>
> cat("Z-value: ", z_value, "\n")
Z-value: 2.702812
> cat("Critical Z-value: ", z_critical, "\n")
Critical Z-value: 1.959964
> cat("Decision based on Z-value: ", z_decision, "\n")
Decision based on Z-value: Fail to reject H0(No Significant Difference)
> cat("Decision based on P-value: ", p_decision, "\n")
Decision based on P-value: Fail to reject H0(No Significant Difference)
```



```
> library(BSDA)
Loading required package: lattice

Attaching package: 'BSDA'

The following object is masked from 'package:datasets':

    orange

Warning message:
package 'BSDA' was built under R version 4.2.3
> before <- c(70, 75, 80, 85, 90, 72, 78, 82, 88, 95)
> after <- c(68, 74, 78, 83, 88, 70, 76, 80, 86, 92)
> differences <- after-before
> z_test_result <- z.test(x = differences,
+ sigma.x = sd(differences),
+ mu=0,
+ alternative = "two.sided")
> print(z_test_result)

One-sample z-Test

data: differences
z = -13.416, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -2.292174 -1.707826
sample estimates:
mean of x
      -2
```

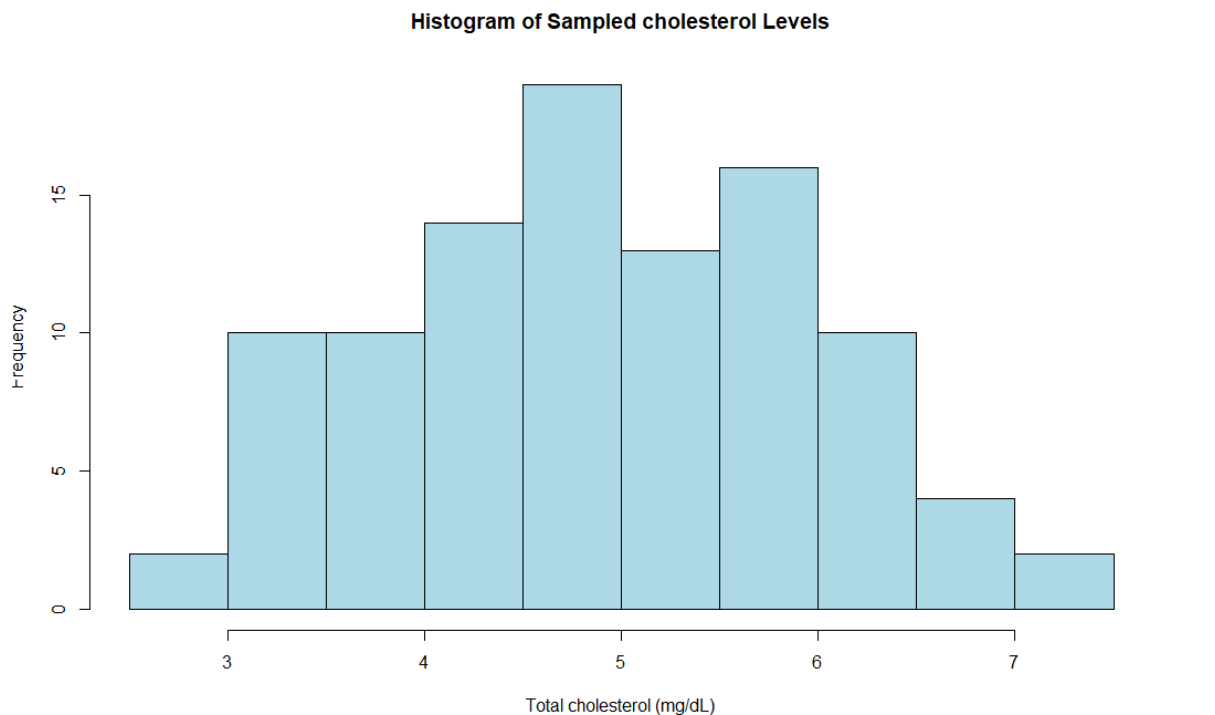
```

> library(NHANES)
Error in library(NHANES) : there is no package called 'NHANES'
> install.packages("NHANES")
WARNING: Rtools is required to build R packages but is not currently installed. Please download and
install the appropriate version of Rtools before proceeding:

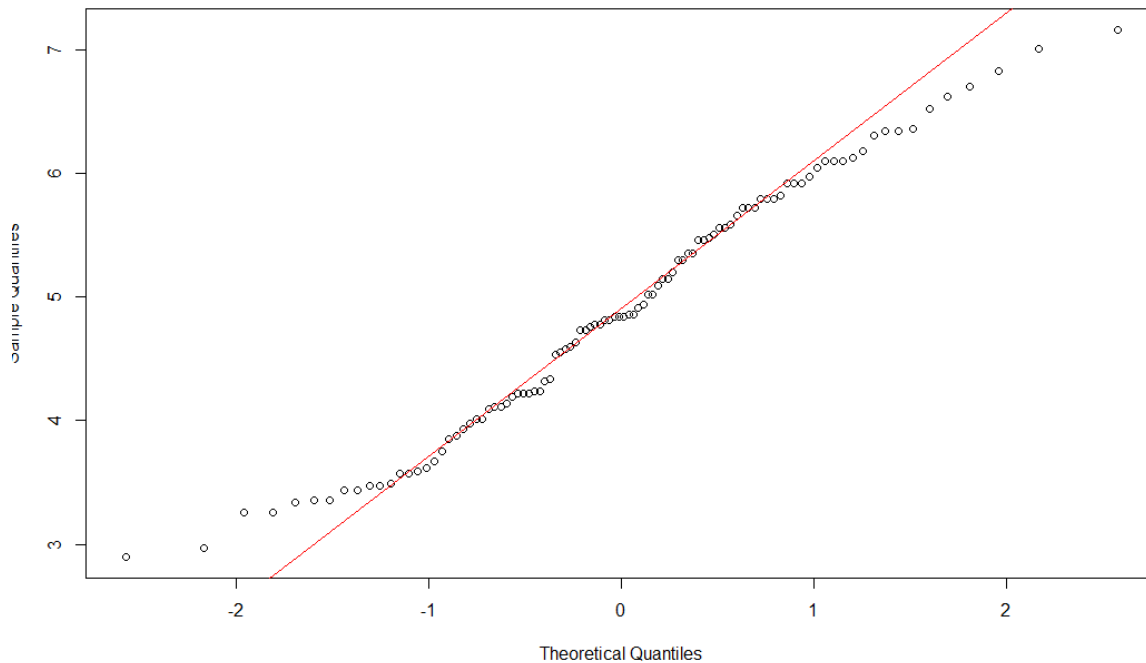
https://cran.rstudio.com/bin/windows/Rtools/
Installing package into 'C:/Users/KJSCE/AppData/Local/R/win-library/4.2'
(as 'lib' is unspecified)
trying URL 'https://cran.rstudio.com/bin/windows/contrib/4.2/NHANES_2.1.0.zip'
content type 'application/zip' length 1729661 bytes (1.6 MB)
downloaded 1.6 MB

package 'NHANES' successfully unpacked and MD5 sums checked

The downloaded binary packages are in
  C:\Users\KJSCE\AppData\Local\Temp\RtmpAHqD8n\downloaded_packages
> library (NHANES)
warning message:
package 'NHANES' was built under R version 4.2.3
> library(ggplot2)
warning message:
package 'ggplot2' was built under R version 4.2.3
> set.seed(123)
> chol_data <- na.omit(NHANES$TotChol)
> sample_data <- sample (chol_data, 100, replace = FALSE)
> hist (sample_data, breaks = 15, col="lightblue", border="black", main="Histogram of Sampled cholesterol Levels",
+       xlab="Total cholesterol (mg/dL)", ylab="Frequency")
> qqnorm(sample_data, main="QQ Plot of Sampled Cholesterol Levels")
> qqline (sample_data, col="red")
>
  
```

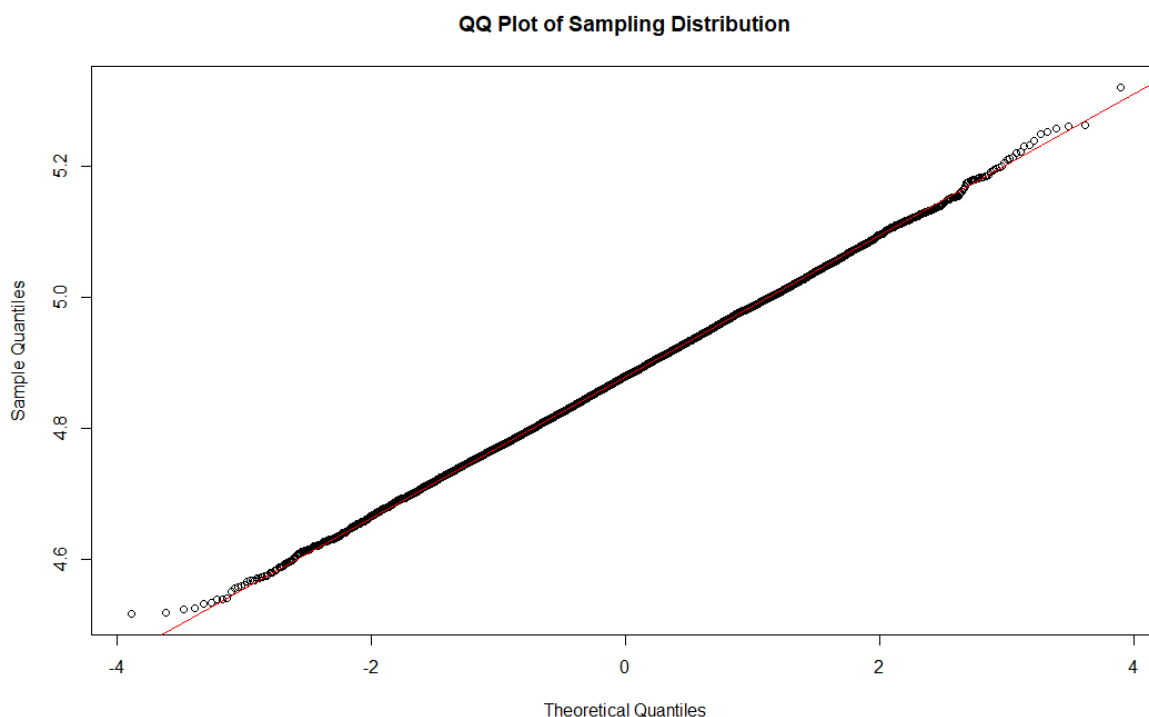


QQ Plot of Sampled Cholesterol Levels



```

> library(NHANES)
> library(ggplot2)
> chol_data <- na.omit(NHANES $TotChol)
> sample_size <- 100
> num_samples <- 10000
> sample_means <- replicate(num_samples, mean(sample(chol_data, sample_size, replace=TRUE)))
> ggplot(data.frame(sample_means), aes(x=sample_means))+
+ geom_histogram(binwidth=1, fill="lightblue", color="black", alpha=0.7) +
+ ggtitle("Sampling Distribution of Sample Means") +
+ xlab("Sample Mean of Total Cholesterol") +
+ ylab("Frequency") +
+ theme_minimal()
> qqnorm(sample_means, main="QQ Plot of Sampling Distribution")
> qqline(sample_means, col="red")
  
```



```
> t_test_result <- t.test(sample_data, mu=200, alternative="two.sided")
> print(t_test_result)
```

One Sample t-test

```
data: sample_data
t = -1891.3, df = 99, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 200
95 percent confidence interval:
 4.68681 5.09619
sample estimates:
mean of x
 4.8915
```

```
> if (t_test_result$p.value < 0.05) {
+ cat("Reject Ho: The mean cholesterol level is significantly different from 200 mg/dL.\n")
+ } else {
+ cat("Fail to Reject Ho: No significant difference from 200 mg/dL.\n")
+ }
Reject Ho: The mean cholesterol level is significantly different from 200 mg/dL.
```

Conclusion:

I successfully performed hypothesis testing using the Z-test and T-test in RStudio, gaining a deeper understanding of statistical inference. By applying these tests to real-world datasets, I was able to compare means, evaluate statistical significance, and determine whether observed differences were due to chance. The Z-test proved useful for large samples with known population variance, while the T-test was essential for smaller samples where variance was unknown. This experiment reinforced the importance of selecting the appropriate statistical test based on sample size and data characteristics, ensuring accurate and meaningful

conclusions in data analysis.

Post Lab questions:

1. A university requires applicants to have a **minimum GRE score of 320**. You sample **36 applicants**, and their **mean GRE score is 322.5**, with a known **population standard deviation of 8**. At $\alpha = 0.05$, can we conclude that the average GRE score of applicants is significantly greater than 320?

```
> sample_mean <- 322.5
> pop_mean <- 320
> sigma <- 8
> n <- 36
> alpha <- 0.05
>
> z_value <- (sample_mean - pop_mean) / (sigma / sqrt(n))
> z_critical <- qnorm(1 - alpha)
>
> if (z_value > z_critical) {
+   decision <- "Reject H0 (The average GRE score is significantly greater than 320)"
+ } else {
+   decision <- "Fail to Reject H0 (No significant difference in GRE scores)"
+ }
>
> cat("Z-value:", z_value, "\n")
Z-value: 1.875
> cat("Critical Z-value:", z_critical, "\n")
Critical Z-value: 1.644854
> cat("Decision:", decision, "\n")
Decision: Reject H0 (The average GRE score is significantly greater than 320)
```

2. The average SAT Math score in a country is **500**, with a known standard deviation of **100**. You collect a **random sample of 50 students**, and their **mean score is 520**. At $\alpha = 0.05$, can we conclude that the sample mean significantly differs from 500?

```
> sample_mean <- 520
> pop_mean <- 500
> sigma <- 100
> n <- 50
> alpha <- 0.05
>
> z_value <- (sample_mean - pop_mean) / (sigma / sqrt(n))
> z_critical <- qnorm(1 - alpha / 2)
>
> if (abs(z_value) > z_critical) {
+   decision <- "Reject H0 (The sample mean significantly differs from 500)"
+ } else {
+   decision <- "Fail to Reject H0 (No significant difference in SAT Math scores)"
+ }
>
> cat("Z-value:", z_value, "\n")
Z-value: 1.414214
> cat("Critical Z-value:", z_critical, "\n")
Critical Z-value: 1.959964
> cat("Decision:", decision, "\n")
Decision: Fail to Reject H0 (No significant difference in SAT Math scores)
```

3. A weight-loss program was tested on **20 individuals** by measuring their weights **before and after** the program. The **mean weight before** the program was **80 kg** (SD = 5). The **mean weight after** the program was **78 kg** (SD = 4.5). The **differences** are assumed to be normally distributed. At $\alpha = 0.05$, is the weight loss significant?

```
> before_mean <- 80
> after_mean <- 78
> before_sd <- 5
> after_sd <- 4.5
> n <- 20
> alpha <- 0.05
>
> mean_diff <- before_mean - after_mean
> sd_diff <- sqrt((before_sd^2 + after_sd^2) / 2)
> se_diff <- sd_diff / sqrt(n)
>
> t_value <- mean_diff / se_diff
> t_critical <- qt(1 - alpha / 2, df = n - 1)
>
> if (abs(t_value) > t_critical) {
+   decision <- "Reject H0 (The weight loss is significant)"
+ } else {
+   decision <- "Fail to Reject H0 (No significant weight loss)"
+ }
>
> cat("T-value:", t_value, "\n")
T-value: 1.880402
> cat("Critical T-value:", t_critical, "\n")
Critical T-value: 2.093024
> cat("Decision:", decision, "\n")
Decision: Fail to Reject H0 (No significant weight loss)
```

4. When should you use a Z-test instead of a T-test? Explain with examples and discuss the role of sample size in determining which test to use.

When choosing between a Z-test and a T-test, the decision primarily depends on sample size and whether the population variance is known. A Z-test is appropriate when the sample size is large ($n \geq 30$) and the population variance is known, as the Central Limit Theorem assures that the sampling distribution approximates normality. For example, if a university measures the heights of 50 students and the standard deviation is known, a Z-test would be suitable. On the other hand, a T-test is used for smaller samples ($n < 30$) or when the population variance is unknown, because the T-distribution accounts for additional variability. For instance, if a company assesses the impact of a training program on 20 employees without knowing the population standard deviation, a T-test is the better choice.