**Biostatistics Project Output File**

**LNG IUS User study data:**

**R output Code:**

> lnguser\_data <- read.csv("/Users/mamoon/Desktop/Documents/Biostatistics\_Project/2024Dec21\_Contraceptive\_Data/Dec\_Contraceptive\_Data.csv")

> # Calculate group-wise statistics

> group\_stats <- lnguser\_data %>%

+ group\_by(Contra\_type) %>%

+ summarise(

+ Mean\_BP = mean(Mean\_BP, na.rm = TRUE),

+ SD\_BP = sd(Mean\_BP, na.rm = TRUE)

+ )

> # Print the results

> print(group\_stats)

# A tibble: 2 × 3

Contra\_type Mean\_BP SD\_BP

<int> <dbl> <dbl>

1 0 88.9 5.23

2 1 88.7 6.53

> lnguser\_data <- read.csv("/Users/mamoon/Desktop/Documents/Biostatistics\_Project/2024Dec21\_Contraceptive\_Data/Dec\_Contraceptive\_Data.csv")

> View(lnguser\_data)

> library(tidyverse)

── Attaching core tidyverse packages ──────────────────────────── tidyverse 2.0.0 ──

✔ forcats 1.0.0 ✔ stringr 1.5.1

✔ lubridate 1.9.3 ✔ tibble 3.2.1

✔ purrr 1.0.2 ✔ tidyr 1.3.1

✔ readr 2.1.5

── Conflicts ────────────────────────────────────────────── tidyverse\_conflicts() ──

✖ dplyr::filter() masks stats::filter()

✖ dplyr::lag() masks stats::lag()

✖ car::recode() masks dplyr::recode()

✖ purrr::some() masks car::some()

ℹ Use the conflicted package to force all conflicts to become errors

> summary(lnguser\_data)

v1\_IDNO v6\_FaciName v7\_InsertionDate v11\_ClientName

Length:170 Length:170 Length:170 Length:170

Class :character Class :character Class :character Class :character

Mode :character Mode :character Mode :character Mode :character

v12\_ClientAge Age\_CompletedClient v19\_ClientsDist v20\_ClientsUpaz

Min. :16.00 Min. :18.00 Length:170 Length:170

1st Qu.:24.00 1st Qu.:25.00 Class :character Class :character

Median :28.50 Median :30.00 Mode :character Mode :character

Mean :29.38 Mean :30.21

3rd Qu.:34.00 3rd Qu.:35.00

Max. :49.00 Max. :46.00

NA's :86

v22\_UsingFPmethod v23\_IfYesMethod v24\_ReasonsForLNGmethod Contra\_type

Length:170 Length:170 Min. :1.000 Min. :0.0

Class :character Class :character 1st Qu.:1.000 1st Qu.:0.0

Mode :character Mode :character Median :1.000 Median :1.0

Mean :1.568 Mean :0.6

3rd Qu.:2.000 3rd Qu.:1.0

Max. :7.000 Max. :1.0

NA's :1

v51\_Weight v52\_Temperature v53\_Pulse v54\_Bloodpressure v55\_Anaemia

Min. : 35.0 Min. :96.00 Min. :65.00 Length:170 Min. :1.00

1st Qu.: 51.0 1st Qu.:98.00 1st Qu.:72.00 Class :character 1st Qu.:2.00

Median : 56.0 Median :98.00 Median :74.00 Mode :character Median :4.00

Mean : 58.5 Mean :97.95 Mean :74.99 Mean :3.26

3rd Qu.: 64.0 3rd Qu.:98.00 3rd Qu.:76.75 3rd Qu.:4.00

Max. :151.0 Max. :99.00 Max. :92.00 Max. :4.00

NA's :1

v56\_BreastExam Mean\_BP

Min. :1 Min. : 70.00

1st Qu.:1 1st Qu.: 83.33

Median :1 Median : 90.00

Mean :1 Mean : 88.77

3rd Qu.:1 3rd Qu.: 93.33

Max. :1 Max. :103.33

NA's :1

> mean(lnguser\_data$v12\_ClientAge)

[1] 29.38235

> sd(agebirthwgt$v12\_ClientAge)

[1] NA

> mean(lnguser\_data$Mean\_BP)

[1] 88.77059

> sd(lnguser\_data$Mean\_BP)

[1] 6.03075

> mean(lnguser\_data$v51\_Weight)

[1] 58.5

> sd(lnguser\_data$v51\_Weight)

[1] 12.01244

> hormon.counts <- table(lnguser\_data$Contra\_type)

> proportions <- prop.table(table(lnguser\_data$Contra\_type)) \*100

> library(dplyr)

> library(broom)

> qqnorm(lnguser\_data$v51\_Weight)

> qqline(lnguser\_data$v51\_Weight)

A graph of a normal q-q plot

Description automatically generated

> qqnorm(lnguser\_data$Mean\_BP)

> qqline(lnguser\_data$Mean\_BP)

A graph of a normal q-q plot

Description automatically generated

> plot(lnguser\_data$v51\_Weight, lnguser\_data$Mean\_BP, main="Scatterplot")

> cor\_result <- cor.test(lnguser\_data$v51\_Weight, lnguser\_data$Mean\_BP)

A diagram of a scatterplot

Description automatically generated

> print(cor\_result)

Pearson's product-moment correlation

data: lnguser\_data$v51\_Weight and lnguser\_data$Mean\_BP

t = 0.62557, df = 168, p-value = 0.5324

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

-0.1030542 0.1972905

sample estimates:

cor

0.04820778

> var.test(lnguser\_data$Mean\_BP ~ lnguser\_data$Contra\_type)

F test to compare two variances

data: lnguser\_data$Mean\_BP by lnguser\_data$Contra\_type

F = 0.63186, num df = 67, denom df = 101, p-value = 0.04554

alternative hypothesis: true ratio of variances is not equal to 1

95 percent confidence interval:

0.4110192 0.9907977

sample estimates:

ratio of variances

0.6318631

> t.test(lnguser\_data$Mean\_BP ~ lnguser\_data$Contra\_type, var.equal=TRUE)

Two Sample t-test

data: lnguser\_data$Mean\_BP by lnguser\_data$Contra\_type

t = 0.21759, df = 168, p-value = 0.828

alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0

95 percent confidence interval:

-1.662069 2.073834

sample estimates:

mean in group 0 mean in group 1

88.58824 88.38235

> lnguser\_data$Contra\_typeCate <- factor(lnguser\_data$Contra\_type)

> lm(lnguser\_data$v51\_Weight ~ lnguser\_data$Mean\_BP + lnguser\_data$Contra\_typeCate)

Call:

lm(formula = lnguser\_data$v51\_Weight ~ lnguser\_data$Mean\_BP +

lnguser\_data$Contra\_typeCate)

Coefficients:

(Intercept) lnguser\_data$Mean\_BP

49.99516 0.09036

lnguser\_data$Contra\_typeCate1

0.85194

> regresult <- lm(lnguser\_data$Mean\_BP ~ lnguser\_data$v51\_Weight + lnguser\_data$Contra\_typeCate)

> summary(regresult)

Call:

lm(formula = lnguser\_data$Mean\_BP ~ lnguser\_data$v51\_Weight +

lnguser\_data$Contra\_typeCate)

Residuals:

Min 1Q Median 3Q Max

-18.725 -5.363 1.762 4.591 15.046

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 87.26790 2.36720 36.865 <2e-16 \*\*\*

lnguser\_data$v51\_Weight 0.02276 0.03880 0.587 0.558

lnguser\_data$Contra\_typeCate1 -0.22485 0.94859 -0.237 0.813

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 6.056 on 167 degrees of freedom

Multiple R-squared: 0.002338, Adjusted R-squared: -0.00961

F-statistic: 0.1957 on 2 and 167 DF, p-value: 0.8225

> model1.anova <- model.matrix(regresult)

> anova(update(regresult, .

+ ~ model1.anova))

Analysis of Variance Table

Response: lnguser\_data$Mean\_BP

Df Sum Sq Mean Sq F value Pr(>F)

model1.anova 2 14.4 7.176 0.1957 0.8225

Residuals 167 6123.9 36.670

> plot(regresult, which=1)

A graph of a number of values

Description automatically generated with medium confidence