Story_Assignment_7

2024-11-27

```
library(tidyr)
data <- read.csv("7 Guineapigdata.csv")
print(data)
```

```
##     len        supp    dose
## 1   4.2        Pill Dose0.5
## 2  11.5        Pill Dose0.5
## 3   7.3        Pill Dose0.5
## 4   5.8        Pill Dose0.5
## 5   6.4        Pill Dose0.5
## 6  10.0        Pill Dose0.5
## 7  11.2        Pill Dose0.5
## 8  11.2        Pill Dose0.5
## 9   5.2        Pill Dose0.5
## 10  7.0        Pill Dose0.5
## 11 16.5        Pill   Dose1
## 12 16.5        Pill   Dose1
## 13 15.2        Pill   Dose1
## 14 17.3        Pill   Dose1
## 15 22.5        Pill   Dose1
## 16 17.3        Pill   Dose1
## 17 13.6        Pill   Dose1
## 18 14.5        Pill   Dose1
## 19 18.8        Pill   Dose1
## 20 15.5        Pill   Dose1
## 21 23.6        Pill   Dose2
## 22 18.5        Pill   Dose2
## 23 33.9        Pill   Dose2
## 24 25.5        Pill   Dose2
## 25 26.4        Pill   Dose2
## 26 32.5        Pill   Dose2
## 27 26.7        Pill   Dose2
## 28 21.5        Pill   Dose2
## 29 23.3        Pill   Dose2
## 30 29.5        Pill   Dose2
## 31 15.2 OrangeJuice Dose0.5
## 32 21.5 OrangeJuice Dose0.5
## 33 17.6 OrangeJuice Dose0.5
## 34  9.7 OrangeJuice Dose0.5
## 35 14.5 OrangeJuice Dose0.5
## 36 10.0 OrangeJuice Dose0.5
## 37  8.2 OrangeJuice Dose0.5
## 38  9.4 OrangeJuice Dose0.5
## 39 16.5 OrangeJuice Dose0.5
## 40  9.7 OrangeJuice Dose0.5
```

```
## 41 19.7 OrangeJuice   Dose1
## 42 23.3 OrangeJuice   Dose1
## 43 23.6 OrangeJuice   Dose1
## 44 26.4 OrangeJuice   Dose1
## 45 20.0 OrangeJuice   Dose1
## 46 25.2 OrangeJuice   Dose1
## 47 25.8 OrangeJuice   Dose1
## 48 21.2 OrangeJuice   Dose1
## 49 14.5 OrangeJuice   Dose1
## 50 27.3 OrangeJuice   Dose1
## 51 25.5 OrangeJuice   Dose2
## 52 26.4 OrangeJuice   Dose2
## 53 22.4 OrangeJuice   Dose2
## 54 24.5 OrangeJuice   Dose2
## 55 24.8 OrangeJuice   Dose2
## 56 30.9 OrangeJuice   Dose2
## 57 26.4 OrangeJuice   Dose2
## 58 27.3 OrangeJuice   Dose2
## 59 29.4 OrangeJuice   Dose2
## 60 23.0 OrangeJuice   Dose2
```

```
library(car)
```

```
## Loading required package: carData
```

```
levene_test <- leveneTest(data$len ~ data$dose * data$supp, data = data)
print(levene_test)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  5  1.7086 0.1484
##       54
```

```
aov.res <- aov(formula = data$len ~ data$dose * data$supp, data=data)
print(aov.res)
```

```
## Call:
##    aov(formula = data$len ~ data$dose * data$supp, data = data)
##
## Terms:
##                  data$dose data$supp data$dose:data$supp Residuals
## Sum of Squares    2426.434   205.350             108.319   712.106
## Deg. of Freedom          2         1                   2        54
##
## Residual standard error: 3.631411
## Estimated effects may be unbalanced
```

```
summary(aov.res)
```

```
##                     Df Sum Sq Mean Sq F value   Pr(>F)
## data$dose            2 2426.4  1213.2  92.000  < 2e-16 ***
## data$supp            1  205.4   205.4  15.572 0.000231 ***
## data$dose:data$supp  2  108.3    54.2   4.107 0.021860 *
## Residuals           54  712.1    13.2
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

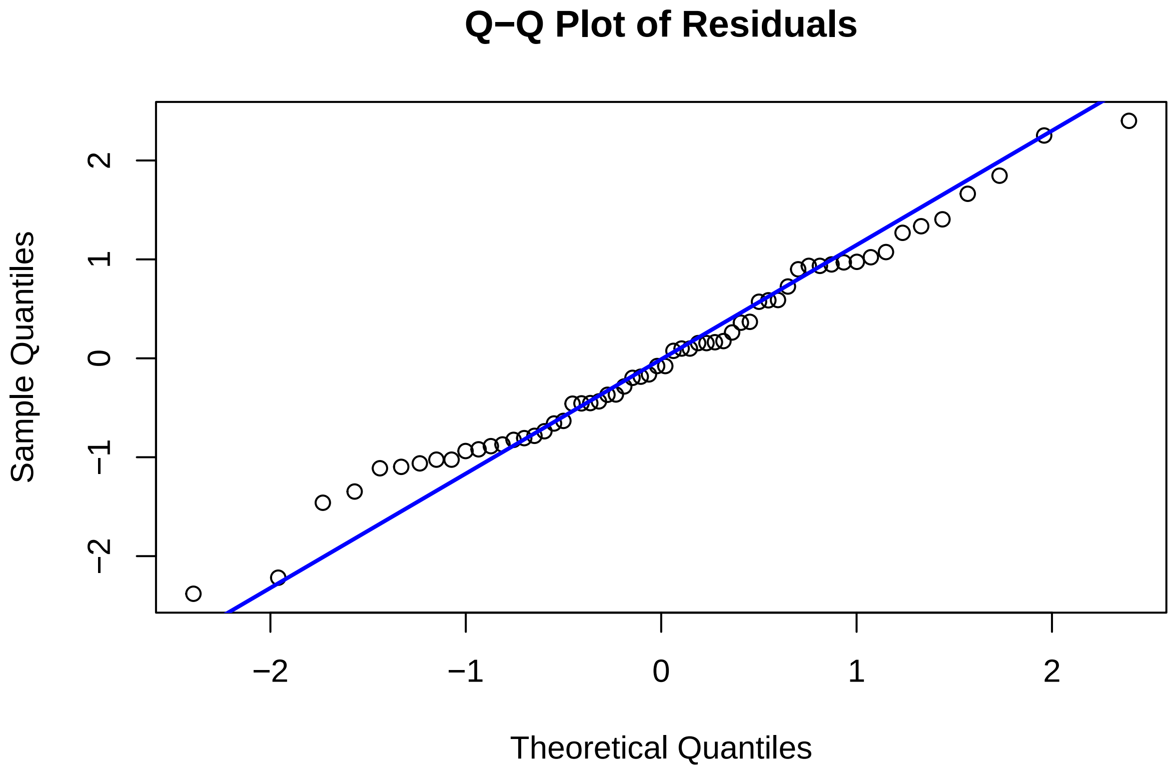
```
#Conclusions from Levene's test: Becuase the p-value is greater than .05, this means that homogeneity o

#Interpretation of P-values: Factor A (Dose): The p-value shows that this factor is significant, showin
```

```
residuals_std <- rstandard(aov.res)

plot(residuals_std, main = "Standardized Residuals Plot", ylab = "Standardized Residuals", xlab = "Inde
abline(h = 0, col = "red", lty = 2)
```

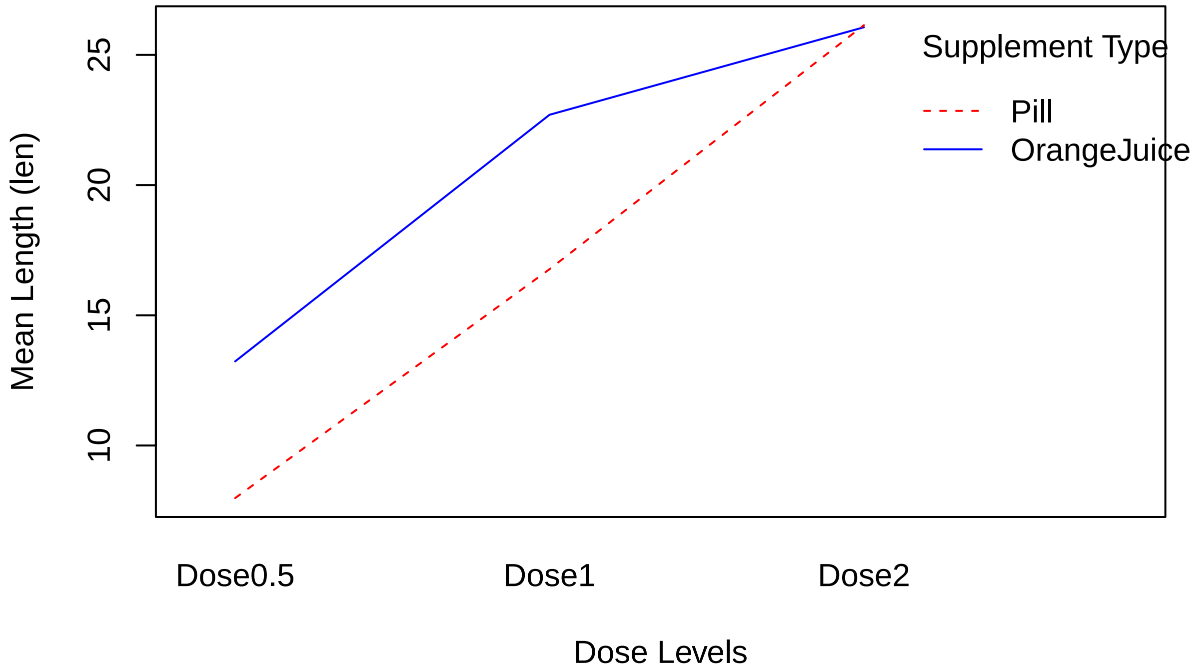
```
qqnorm(residuals_std, main = "Q-Q Plot of Residuals")
qqline(residuals_std, col = "blue", lwd = 2)
```



```
shapiro_test <- shapiro.test(residuals_std)
print(shapiro_test)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals_std
## W = 0.98499, p-value = 0.6694
```

```
interaction.plot(
  x.factor = data$dose,
  trace.factor = data$supp,
  response = data$len,
  xlab = "Dose Levels",
  ylab = "Mean Length (len)",
  trace.label = "Supplement Type",
  col = c("blue", "red"),
  lty = 1:2
)
```



```
#Interpretations of standardized residuals, QQ-plot and Shapiro-Wilks: In the standarized residuals plo

#Interpetation of interaction plot: Becuase the lines are not straight accross and are in fact are slop
```

```
grandmean <- mean(data$len)

Ameans <- c(
  mean(data[data$dose == "Dose0.5", "len"]),
  mean(data[data$dose == "Dose1", "len"]),
  mean(data[data$dose == "Dose2", "len"])
)

Bmeans <- c(
  mean(data[data$supp == "Pill", "len"]),
  mean(data[data$supp == "OrangeJuice", "len"])
)

ABmeans <- c(
  mean(data[data$dose == "Dose0.5" & data$supp == "Pill", "len"]),
  mean(data[data$dose == "Dose1" & data$supp == "Pill", "len"]),
  mean(data[data$dose == "Dose2" & data$supp == "Pill", "len"]),
  mean(data[data$dose == "Dose0.5" & data$supp == "OrangeJuice", "len"]),
  mean(data[data$dose == "Dose1" & data$supp == "OrangeJuice", "len"]),
  mean(data[data$dose == "Dose2" & data$supp == "OrangeJuice", "len"])
)

totalss <- sum((data$len - grandmean)^2)

cellss <- (nrow(data) / length(ABmeans)) * sum((ABmeans - grandmean)^2)

errorss <- totalss - cellss
```

```
Afactorss <- (nrow(data) / length(Ameans)) * sum((Ameans - grandmean)^2)

Bfactorss <- (nrow(data) / length(Bmeans)) * sum((Bmeans - grandmean)^2)

interactions <- cellss - Afactorss - Bfactorss

totaldf <- nrow(data) - 1
celldf <- length(ABmeans) - 1
Adf <- length(Ameans) - 1
Bdf <- length(Bmeans) - 1
interactiondf <- Adf * Bdf
errordf <- totaldf - celldf

AMS <- Afactorss / Adf
BMS <- Bfactorss / Bdf
interactionMS <- interactions / interactiondf
errorMS <- errorss / errordf

FA <- AMS / errorMS
FB <- BMS / errorMS
Finteraction <- interactionMS / errorMS

p_value_A <- pf(FA, Adf, errordf, lower.tail = FALSE)
p_value_B <- pf(FB, Bdf, errordf, lower.tail = FALSE)
p_value_interaction <- pf(Finteraction, interactiondf, errordf, lower.tail = FALSE)

list(
  FA = FA,
  FB = FB,
  Finteraction = Finteraction,
  p_value_A = p_value_A,
  p_value_B = p_value_B,
  p_value_interaction = p_value_interaction
)
```

```
## $FA
## [1] 91.99996
##
## $FB
## [1] 15.57198
##
## $Finteraction
## [1] 4.106991
##
## $p_value_A
## [1] 4.046291e-18
##
## $p_value_B
## [1] 0.0002311828
##
## $p_value_interaction
## [1] 0.02186027
```

```r
anova_table <- data.frame(
  Source = c("Factor A (Dose)", "Factor B (Supplement)", "Interaction (Dose × Supplement)", "Error", "To
  SS = c(Afactorss, Bfactorss, interactions, errorss, totalss),
  DF = c(Adf, Bdf, interactiondf, errordf, totaldf),
  MS = c(AMS, BMS, interactionMS, errorMS, NA),
  F = c(FA, FB, Finteraction, NA, NA),
  p_value = c(p_value_A, p_value_B, p_value_interaction, NA, NA)
)

print(anova_table)
```

```
##                            Source       SS DF         MS         F      p_value
## 1                 Factor A (Dose) 2426.434  2 1213.21717 91.999965 4.046291e-18
## 2           Factor B (Supplement)  205.350  1  205.35000 15.571979 2.311828e-04
## 3 Interaction (Dose × Supplement)  108.319  2   54.15950  4.106991 2.186027e-02
## 4                           Error  712.106 54   13.18715        NA           NA
## 5                           Total 3452.209 59         NA        NA           NA
```