library(readxl)

library(ggplot2)

library(dplyr)

data <- read\_excel("MWHC.xlsx")

# Factor as categorical

data$Treatment <- as.factor(data$Treatment)

#Mean,sd,se

treatment\_means <- data %>%

group\_by(Treatment) %>%

summarize(Mean\_MWHC = mean(MWHC, na.rm = TRUE))

regression\_model <- lm(MWHC ~ as.numeric(Treatment), data = data)

separate\_means\_model <- lm(MWHC ~ Treatment, data = data)

#ANOVA lack of fit

lack\_of\_fit\_table <- anova(regression\_model, separate\_means\_model)

print("ANOVA Lack-of-Fit Table:")

print(lack\_of\_fit\_table)

p\_value <- summary(regression\_model)$coefficients[2, 4]

#Plot

ggplot(data, aes(x = as.numeric(Treatment), y = MWHC)) +

geom\_point(aes(color = Treatment), size = 3) +

geom\_smooth(method = "lm", se = TRUE, color = "blue", fill = "lightblue") +

geom\_point(data = treatment\_means, aes(x = as.numeric(Treatment), y = Mean\_MWHC),

color = "red", size = 4, shape = 17) +

labs(

title = "Maximum Water Holding Capacity of Digestate",

x = "Treatment (w/w)",

y = "MWHC (%)"

) +

theme\_minimal() +

scale\_x\_continuous(

breaks = 1:length(levels(data$Treatment)),

labels = levels(data$Treatment)

) +

theme(legend.position = "none") +

annotate("text", x = max(as.numeric(data$Treatment)) - 0.5, y = max(data$MWHC),

label = paste("p-value =", round(p\_value, 4)), size = 5, color = "black")