```
install.packages("readxl")
install.packages("stringr")
install.packages("lme4")
install.packages("nlme")
install.packages("emmeans")

library(readxl)
library(stringr)
library(lme4)
library(nlme)
library(emmeans)



#  Read the RCBD.xlsx file into R                                                    #
rcbd_data <- read_excel("rcbd.xlsx")
rcbd_data

#  Let's see what is inside this dataset by using the str() structure function                    #
str(rcbd_data)

#  The variable names are mixed case so let's use the stringr package to bring all variable names to lower case  #
```

```
colnames(rcbd_data) <- str_to_lower(names(rcbd_data), locale = "en")
colnames(rcbd_data)

#  Why would we do this again?                                          #
str(rcbd_data)

#  Using the base aov() function in base R this will conduct an ordinary least squares ANOVA          #
model <- aov(nitrogen ~ block + trmt, data=rcbd_data)
model

summary(model)



#  Let's fix our block and trmt effects                                 #
rcbd_data$block_fac = as.factor(rcbd_data$block)
rcbd_data$trmt_fac = as.factor(rcbd_data$trmt)

#  Running the aov() with block and trmt as factors                                  #
model2 <- aov(nitrogen ~ block_fac + trmt_fac, data=rcbd_data)
model2
```

```
#  Run summary on your new updated model
summary(model2)

#  What if we wanted to see Tukey means comparisons?
model3 <- aov(nitrogen ~ block_fac + factor(trmt_fac), data=rcbd_data)
TukeyHSD(model3,which='factor(trmt_fac)')
summary(model3)

#########################################################################################################
#  Calculating p-values                                                 #
1-pf(0.478,5,15)

#########################################################################################################
#  Let's do a few plots to check our residuals                          #
par(mfrow=c(2,2))
plot(model, which=5)
plot(model, which=1)
plot(model, which=2)
```

```
plot(residuals(model) ~ nitrogen, main="Residuals vs Experimental Unit", data=rcbd_data)
abline(h=0, lty=2)

shapiro.test(residuals(model))



#############################################################################################################
#  Let's rerun the ANOVA of our design, except let's use the LME4 package which handles mixed models    #
rmodel <- lmer(nitrogen ~ (1|block_fac) + trmt_fac, data=rcbd_data)
rmodel

# to see the ANOVA table from the LMER package we use the anova() function                    #
anova(rmodel)

#  Let's see what the summary() function provides us                                          #
summary(rmodel)

#  To calculate the p-value you need to add an extra piece of syntax                          #
1-pf(0.4778,5,15)
```

```
#  Residual plot and analysis                                                    #
plot(residuals(rmodel) ~ nitrogen, main="Residuals ", data=rcbd_data)
abline(h=0, lty=2)

shapiro.test(residuals(rmodel))



trmt_fac <- as.factor(rcbd_data$trmt)

#  Trying NLME
model4 <- lme(nitrogen ~ trmt_fac, random = ~1 | block_fac, data=rcbd_data)
model4

anova(model4)

summary(model4)

#  Residual plot and analysis                                                    #
plot(residuals(model4) ~ nitrogen, main="Residuals ", data=rcbd_data)
abline(h=0, lty=2)
```

```
shapiro.test(residuals(model4))

#  Means Comparisons                                                    #

model4.emm <- emmeans(model4, "trmt_fac", adjust="tukey")
pairs(model4.emm)

plot(model4.emm, comparisons = TRUE)

CLD(model4.emm)
```