Script-4.R

Usuario

2025-08-28

```
# Script 4
# 28/08/2025
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# Importar ----------------------------------------------------------------

Calidad_plantula <- read.csv("Calidad-plantula.csv", header = T)
View(Calidad_plantula)

# Creación de factor ------------------------------------------------------

Calidad_plantula$Tratamiento <- as.factor(Calidad_plantula$Tratamiento)
class(Calidad_plantula$Tratamiento)
```

```
## [1] "factor"
```

```
summary(Calidad_plantula)
```

```
##      Planta            IE         Tratamiento
##  Min.   : 1.00   Min.   :0.5500   Ctrl:21
##  1st Qu.:11.25   1st Qu.:0.7025   Fert:21
##  Median :21.50   Median :0.7950
##  Mean   :21.50   Mean   :0.8371
##  3rd Qu.:31.75   3rd Qu.:0.9375
##  Max.   :42.00   Max.   :1.1600
```

```
# Media de IE -------------------------------------------------------------
mean(Calidad_plantula$IE)
```

```
## [1] 0.8371429
```

```
# Calculo de media, desviación estándar y varianza ------------------------

tapply(Calidad_plantula$IE, Calidad_plantula$Tratamiento, mean)
```

```
##      Ctrl      Fert
## 0.7676190 0.9066667
```

```r
tapply(Calidad_plantula$IE, Calidad_plantula$Tratamiento, sd)
```

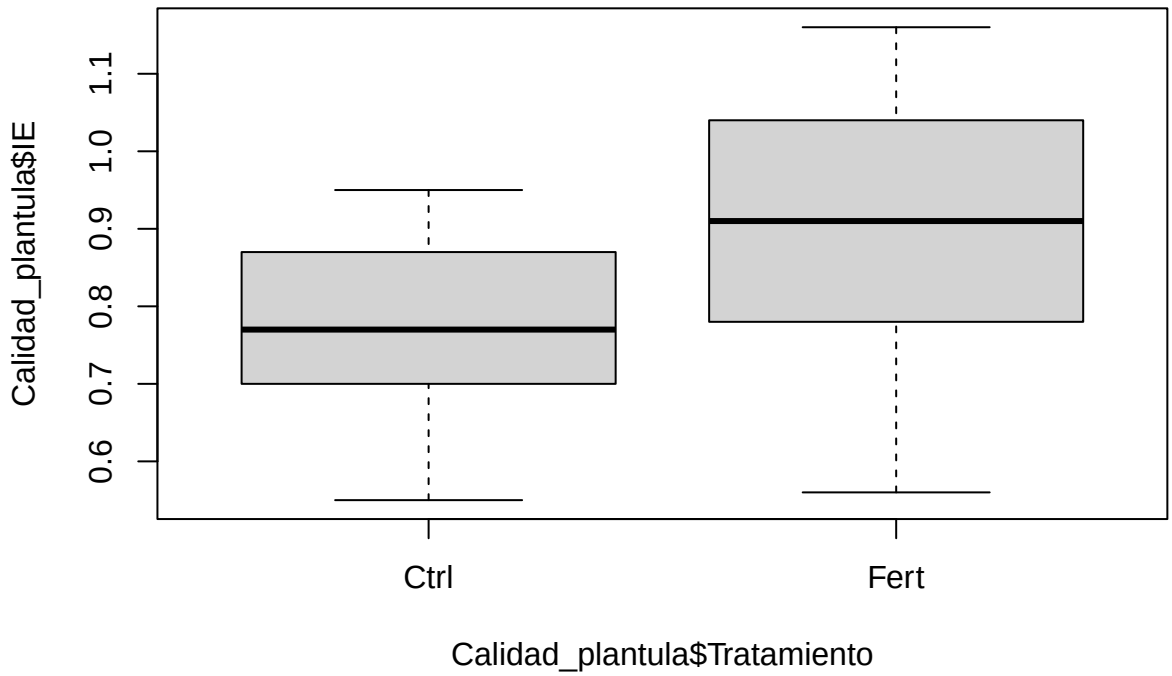
```
##      Ctrl      Fert
## 0.1153215 0.1799537
```

```r
tapply(Calidad_plantula$IE, Calidad_plantula$Tratamiento, var)
```

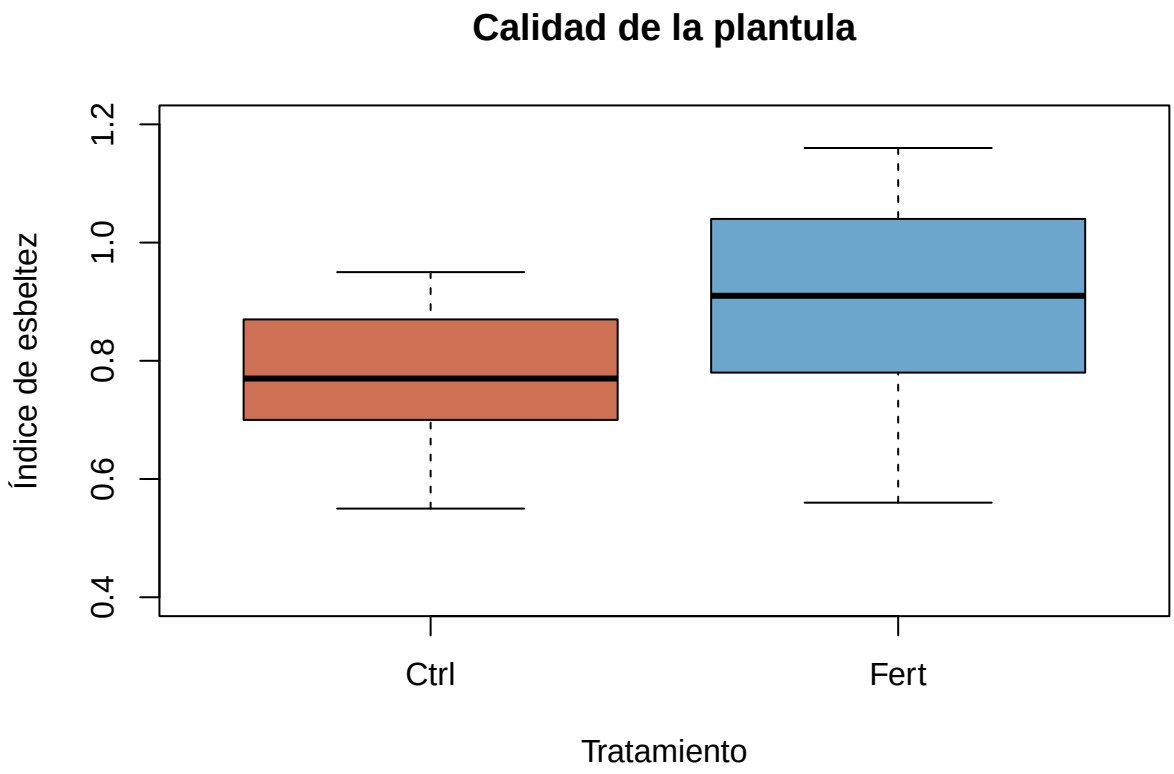
```
##       Ctrl       Fert
## 0.01329905 0.03238333
```

```r
# Crear objeto colores ----------------------------------------------------
colores <- c("salmon3", "skyblue3")

# Boxplot con índice de esbeltez y tratamiento ----------------------------
boxplot(Calidad_plantula$IE~ Calidad_plantula$Tratamiento)
```




```r
# Boxplot de datos de vivero (IE-Tratamiento) ----------------------------
boxplot(Calidad_plantula$IE~ Calidad_plantula$Tratamiento,
        col =colores, main = "Calidad de la plantula", xlab = "Tratamiento",
        ylab = "Índice de esbeltez", ylim = c(0.4,1.2) )
```

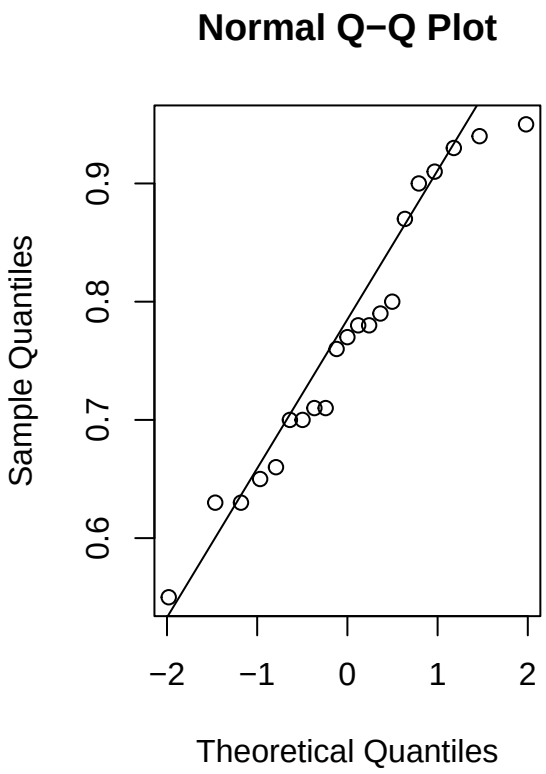


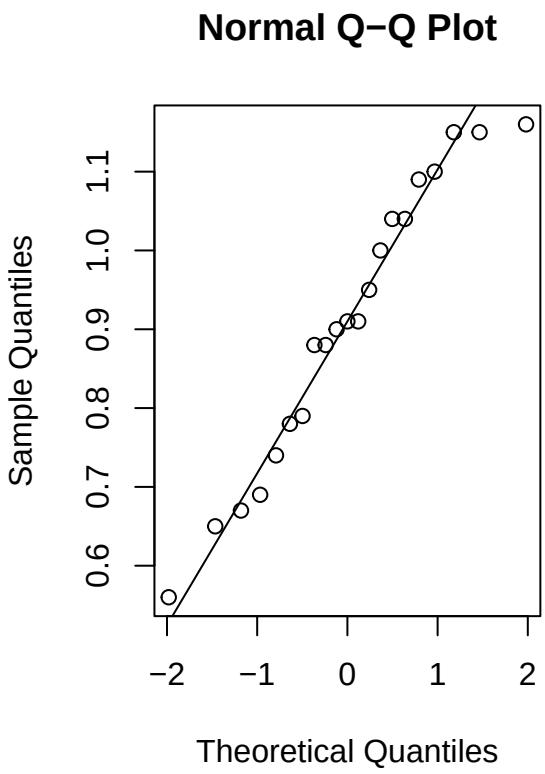

```
# Aplicar un subconjunto para cada tratamiento ----------------------------

df_Ctrl <- subset(Calidad_plantula$IE, Calidad_plantula$Tratamiento == "Ctrl")
df_Ctrl <- subset(Calidad_plantula, Tratamiento == "Ctrl")
df_Fert <- subset(Calidad_plantula, Tratamiento == "Fert")

# Graficos de normalidad ---------------------------------------------------

par(mfrow=c(1,2)) # Ver graficos juntos
qqnorm(df_Ctrl$IE); qqline(df_Ctrl$IE)
qqnorm(df_Fert$IE); qqline(df_Fert$IE)
```






```r
par(mfrow=c(1,1)) # Volver a ver un solo grafico

# Prueba de normalidad ----------------------------------------------------
shapiro.test(df_Ctrl$IE)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  df_Ctrl$IE
## W = 0.9532, p-value = 0.3908
```

```r
shapiro.test(df_Fert$IE)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  df_Fert$IE
## W = 0.95339, p-value = 0.3941
```

```r
# Revisar Homogeneidad (Varianza) -----------------------------------------
var.test(Calidad_plantula$IE ~ Calidad_plantula$Tratamiento)
```

```
##
##  F test to compare two variances
```

```
##
## data:  Calidad_plantula$IE by Calidad_plantula$Tratamiento
## F = 0.41068, num df = 20, denom df = 20, p-value = 0.05304
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.1666376 1.0121038
## sample estimates:
## ratio of variances
##          0.4106757
```

```
# Prueba de t ------------------------------------------------------------
t.test(Calidad_plantula$IE ~ Calidad_plantula$Tratamiento,
       alternative = "two.sided", var.equal = T) # Prueba con dos colas
```

```
##
##  Two Sample t-test
##
## data:  Calidad_plantula$IE by Calidad_plantula$Tratamiento
## t = -2.9813, df = 40, p-value = 0.004868
## alternative hypothesis: true difference in means between group Ctrl and group Fert is not equal to 0
## 95 percent confidence interval:
##  -0.23331192 -0.04478332
## sample estimates:
## mean in group Ctrl mean in group Fert
##          0.7676190          0.9066667
```

```
t.test(Calidad_plantula$IE ~ Calidad_plantula$Tratamiento,
       alternative = "two.sided", var.equal = F) # Prueba de Welch
```

```
##
##  Welch Two Sample t-test
##
## data:  Calidad_plantula$IE by Calidad_plantula$Tratamiento
## t = -2.9813, df = 34.056, p-value = 0.00527
## alternative hypothesis: true difference in means between group Ctrl and group Fert is not equal to 0
## 95 percent confidence interval:
##  -0.23382707 -0.04426816
## sample estimates:
## mean in group Ctrl mean in group Fert
##          0.7676190          0.9066667
```

```
t.test(Calidad_plantula$IE ~ Calidad_plantula$Tratamiento,
       alternative = "greater", var.equal = T) # Prueba con greater
```

```
##
##  Two Sample t-test
##
## data:  Calidad_plantula$IE by Calidad_plantula$Tratamiento
## t = -2.9813, df = 40, p-value = 0.9976
## alternative hypothesis: true difference in means between group Ctrl and group Fert is greater than 0
## 95 percent confidence interval:
##  -0.2175835        Inf
```

```
## sample estimates:
## mean in group Ctrl mean in group Fert
##          0.7676190          0.9066667
```

```r
# Crear funcion para medir efecto de cohens ---------------------------------
cohens_efecto <- function(x, y) {
  n1 <- length(x); n2 <- length(y)
  s1 <- sd(x); s2 <- sd(y)
  sp <- sqrt(((n1 - 1) * s1^2 + (n2 - 1) * s2^2) / (n1 + n2 - 2))
  (mean(x) - mean(y)) / sp
  }

# Efecto ------------------------------------------------------------------
d1_cal <- cohens_efecto(df_Ctrl$IE, df_Fert$IE)
d1_cal
```

```
## [1] -0.9200347
```

```r
round(d1_cal,2) # Redondear resultado
```

```
## [1] -0.92
```