

# Laboratorio 4 r

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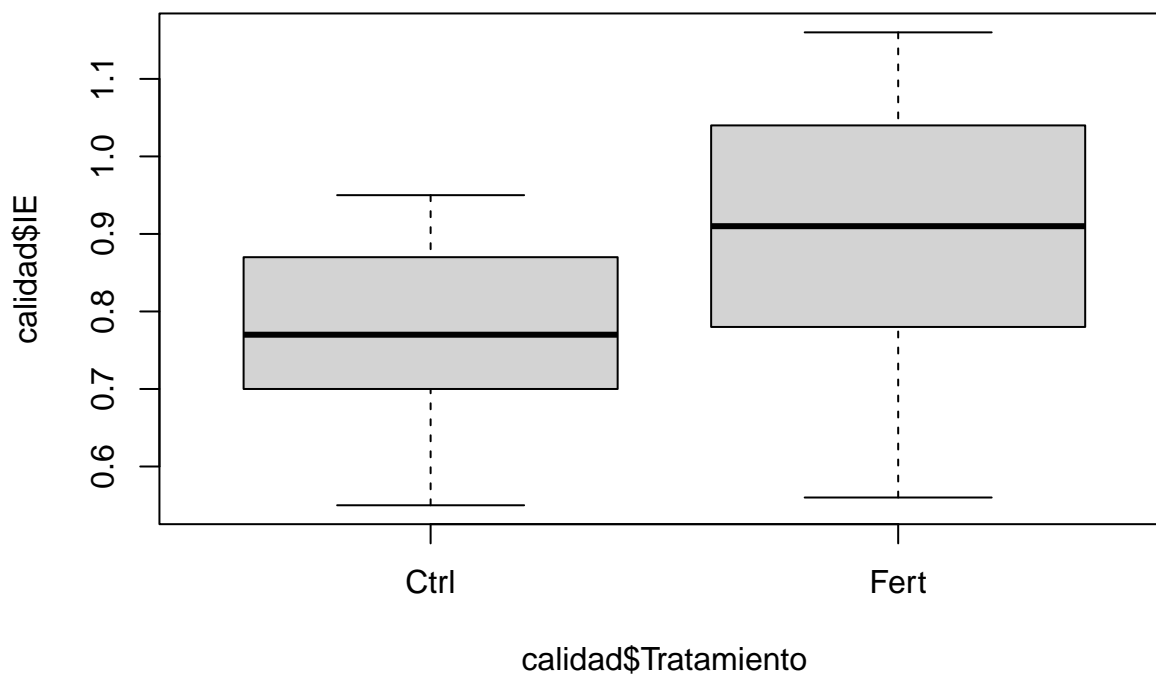
```
# Pruebas de t
# Caso de MUESTRAS
# MAGT
# 27/08/2025

# Importar datos

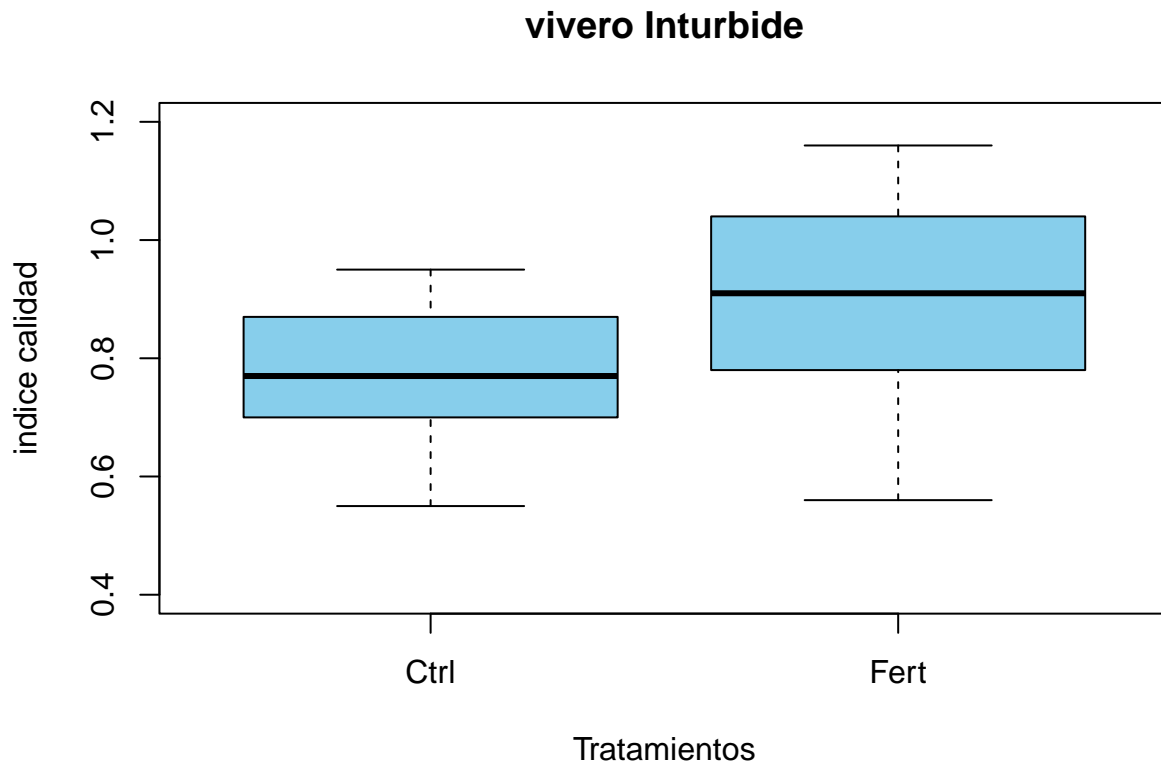
calidad <- read.csv("Calidad_de_plantass.csv", header = T)

calidad$Tratamiento <- as.factor(calidad$Tratamiento)

boxplot(calidad$IE~ calidad$Tratamiento)
```



```
boxplot(calidad$IE~calidad$Tratamiento,
        col="skyblue",
        xlab="Tratamientos",
        ylab = "indice calidad",
        ylim=c(0.4,1.2),
        main= "vivero Inturbide")
```



```
# Estadísticas descriptivas
# tapply sirve para obtener su n valor cuando contamos
# con varios grupos
```

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

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

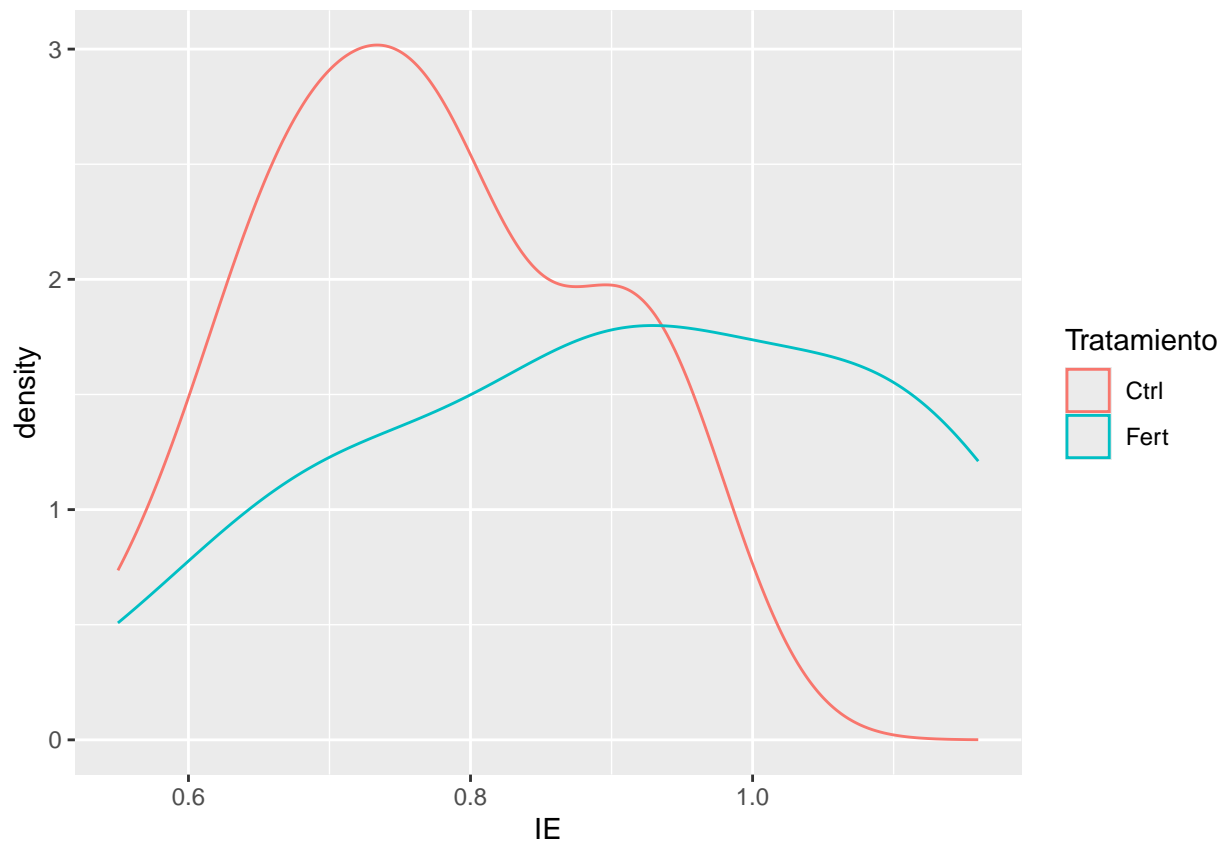
```
tapply(calidad$IE, calidad$Tratamiento, var)
```

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

```
# Observamos que la varianza del grupo fert es 3 veces
# más grande que el grupo control (Ctrl)
```

```
# Revisar el comportamiento de los datos
library("ggplot2")

ggplot(calidad, aes(x = IE, color = Tratamiento))+geom_density()
```



```
tapply(calidad$IE, calidad$Tratamiento, sd)
```

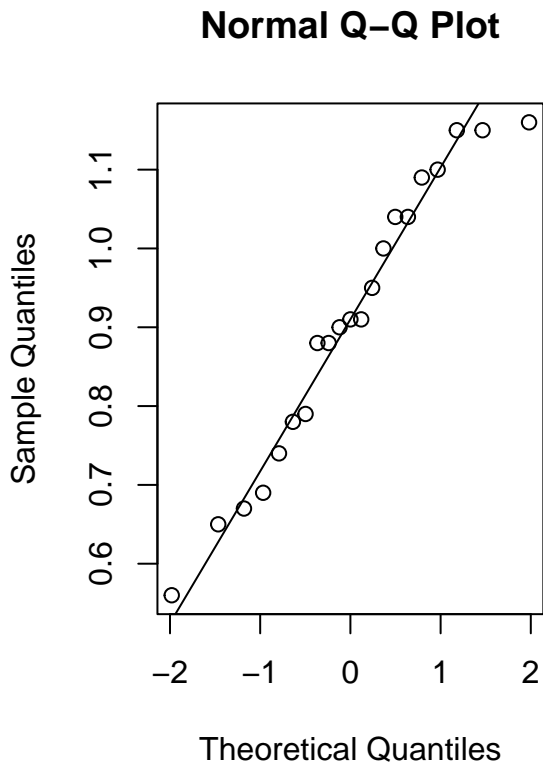
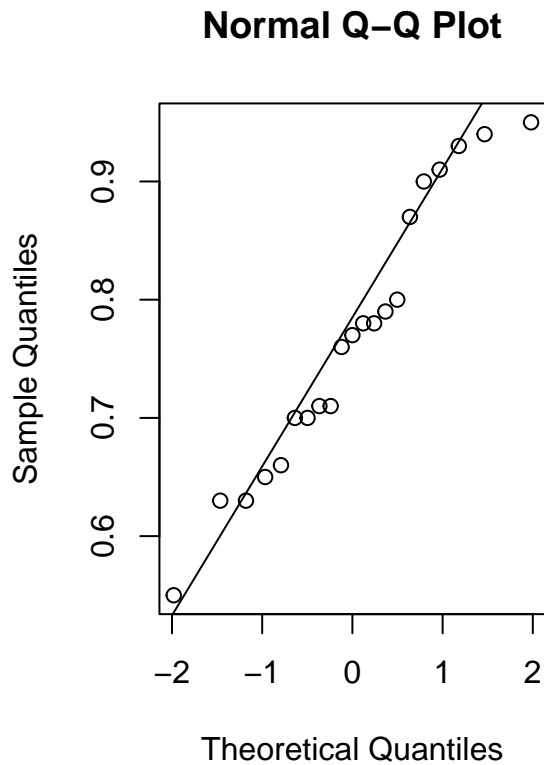
```
##      Ctrl      Fert
## 0.1153215 0.1799537
```

```
# Separar los datos por tratamiento usando subset
```

```
df_ctlr <- subset(calidad, Tratamiento == "Ctrl")
df_fert <- subset(calidad, Tratamiento != "Ctrl")
```

```
# qqnorm revisar normalidad
```

```
par(mfrow = c(1, 2))
qqnorm(df_ctlr$IE); qqline(df_ctlr$IE)
qqnorm(df_fert$IE); qqline(df_fert$IE)
```



```
par(mfrow = c(1, 1))
```

```
# prueba de normalidad
```

```
shapiro.test(df_ctrlr$IE)
```

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

```
shapiro.test(df_fert$IE)
```

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

```
# Revisar homogenidad de varianzas
var.test(df_ctrlr$IE, df_fert$IE)
```

```
##
## F test to compare two variances
##
## data:  df_ctlr$IE and df_fert$IE
## 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
```

```
var.test(calidad$IE ~ calidad$Tratamiento)
```

```
##
## F test to compare two variances
##
## data:  calidad$IE by calidad$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
```

```
# Aplicar la prueba de t, varianzas iguales
# dos colas = two.sided
```

```
t.test(calidad$IE ~ calidad$Tratamiento,
       var.equal = T,
       alternative = "two.sided")
```

```
##
## Two Sample t-test
##
## data:  calidad$IE by calidad$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
```

```
# Medir el efecto
```

```
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
}
```

```
d_cal <- cohens_efecto(df_ctrl$IE, df_fert$IE)
```