07_Análisis-de-varianza.R

Usuario

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```r
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# Importar datos -------------------------------------------------------

library(repmis)
DAP <- source_data("https://www.dropbox.com/s/fbrwxypacjgeayj/Datos_Rascon_Anova.csv?dl=1")
```

```
## Downloading data from: https://www.dropbox.com/s/fbrwxypacjgeayj/Datos_Rascon_Anova.csv?dl=1
```

```
## SHA-1 hash of the downloaded data file is:
## 75a7b481bb1b844f43090d2711189c46afece8fa
```

```r
DAP$Paraje <- as.factor(DAP$Paraje)
DAP$SP <- as.factor(DAP$SP)

# Determinar estadísticas descriptivas ---------------------------------

boxplot(DAP$EDAD ~ DAP$Paraje, xlab = "Paraje", ylab = "Edad")
```
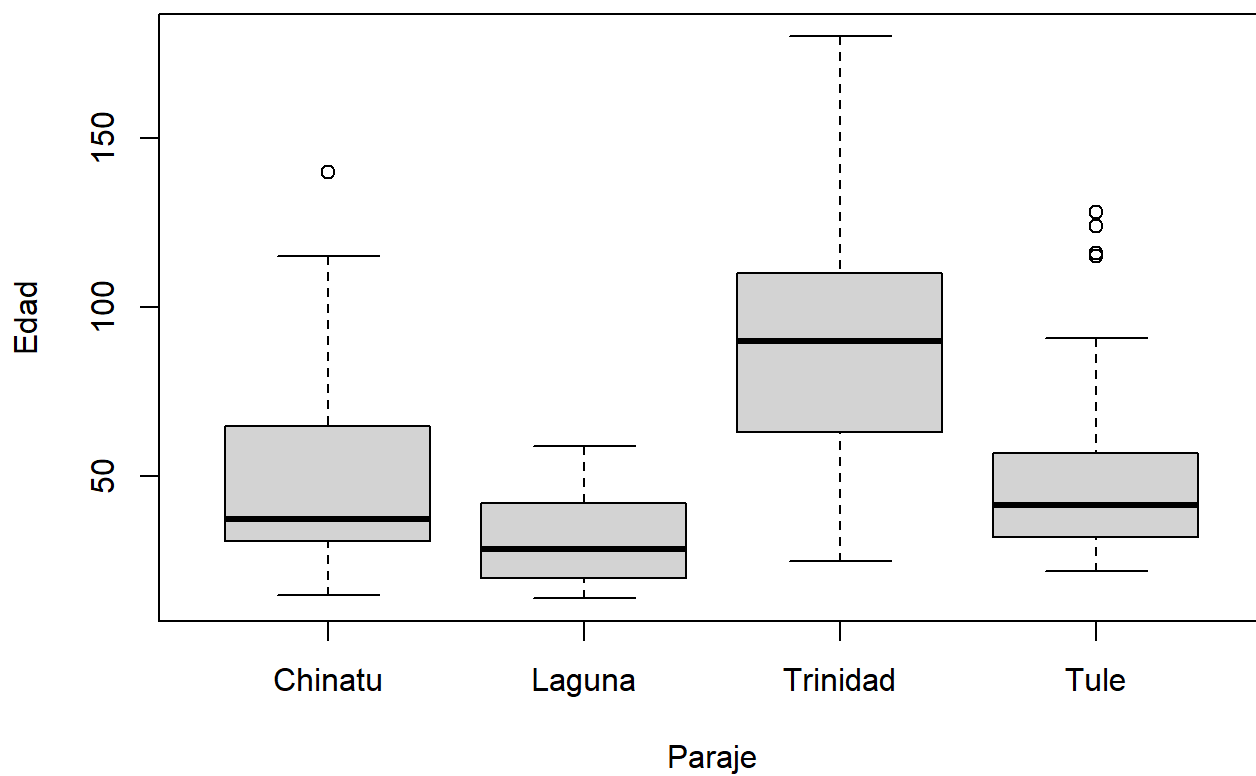
```
boxplot(DAP$DAP ~ DAP$Paraje, xlab = "Paraje", ylab = "DAP")
```
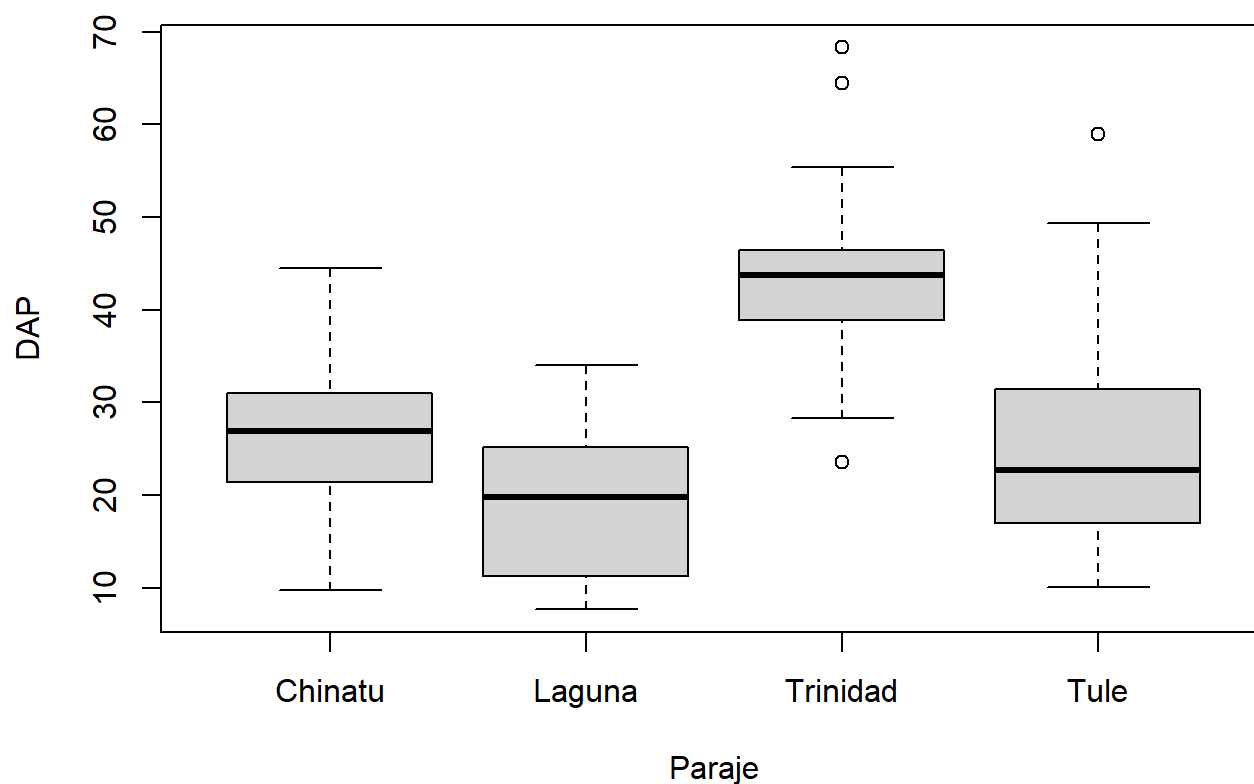
```
tapply(DAP$EDAD, DAP$Paraje, mean)
```

```
##  Chinatu   Laguna Trinidad     Tule
## 48.70000 30.70000 93.40000 53.13333
```
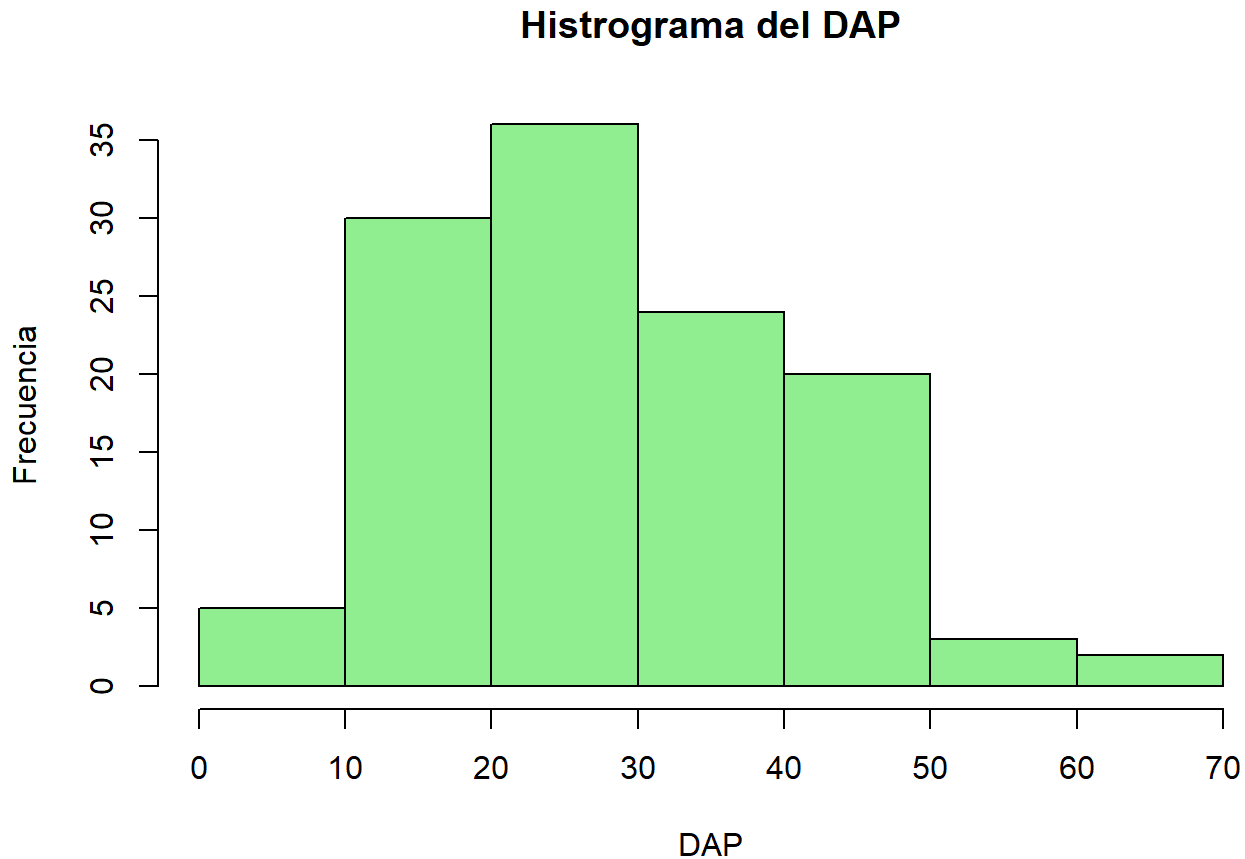
```
tapply(DAP$EDAD, DAP$Paraje, var)
```

```
##   Chinatu    Laguna  Trinidad      Tule
##  837.3207  150.4931 1427.4897  998.2575
```

```
# Normalidad reviasr -------------------------------------------------------

shapiro.test(DAP$DAP)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  DAP$DAP
## W = 0.96548, p-value = 0.003575
```

```
hist(DAP$DAP, xlab = "DAP", ylab = "Frecuencia", main = "Histrograma del DAP", col = "lightgree
n")
```

Histrograma del DAP


```
# Los datos del DAP no son normales

bartlett.test(DAP$DAP ~ DAP$Paraje)
```
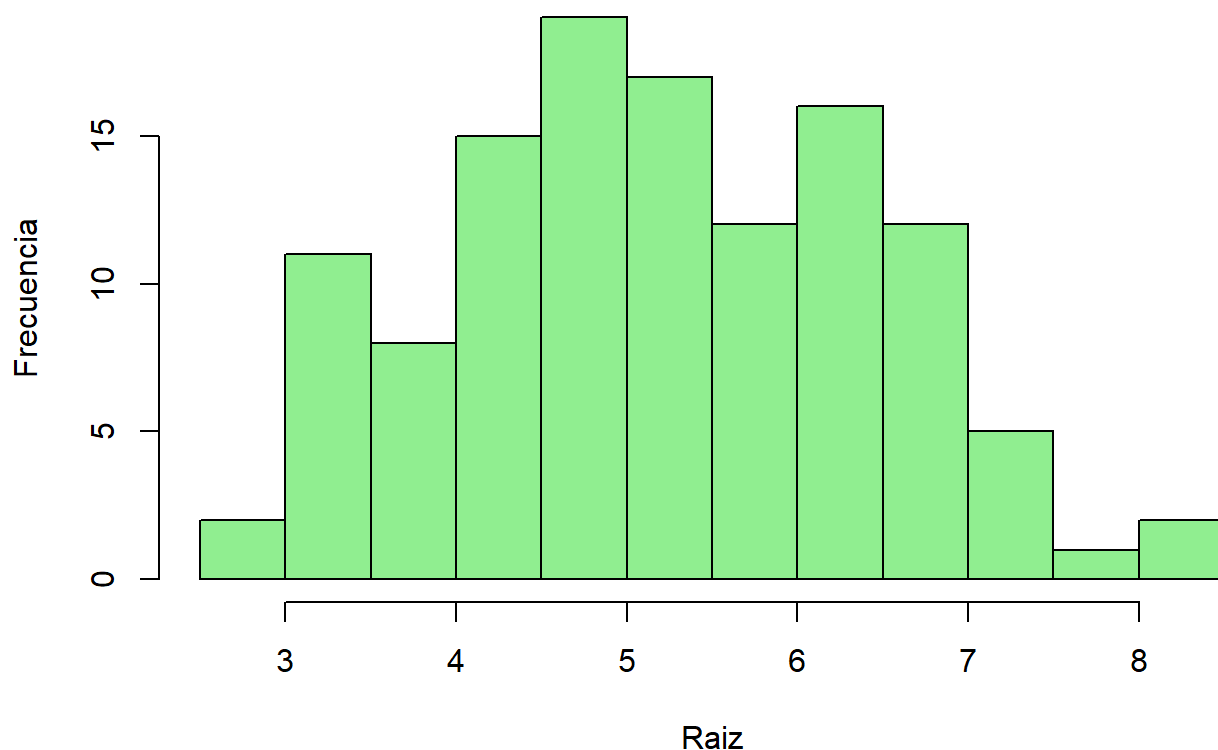
```
##
##  Bartlett test of homogeneity of variances
##
## data:  DAP$DAP by DAP$Paraje
## Bartlett's K-squared = 6.6622, df = 3, p-value = 0.08348
```

```
# Las varianzas de los tratamientos son iguales

# Transformar DAP para cumplir normalidad --------------------------------

DAP$raiz <- sqrt(DAP$DAP)
hist(DAP$raiz, xlab = "Raiz", ylab = "Frecuencia", main = "Histrograma de la raiz del DAP", col
= "lightgreen")
```

Histrograma de la raiz del DAP


```
# Probar normalidad a los datos transformados (raíz cuadrada) -------------

shapiro.test(DAP$raiz)
```

```
##
##   Shapiro-Wilk normality test
##
## data:  DAP$raiz
## W = 0.98341, p-value = 0.1473
```

```
# Los datos de ahora son normales

# Probar homogeneidad de varianzas de los datos transformados -------------

bartlett.test(DAP$raiz ~ DAP$Paraje)
```
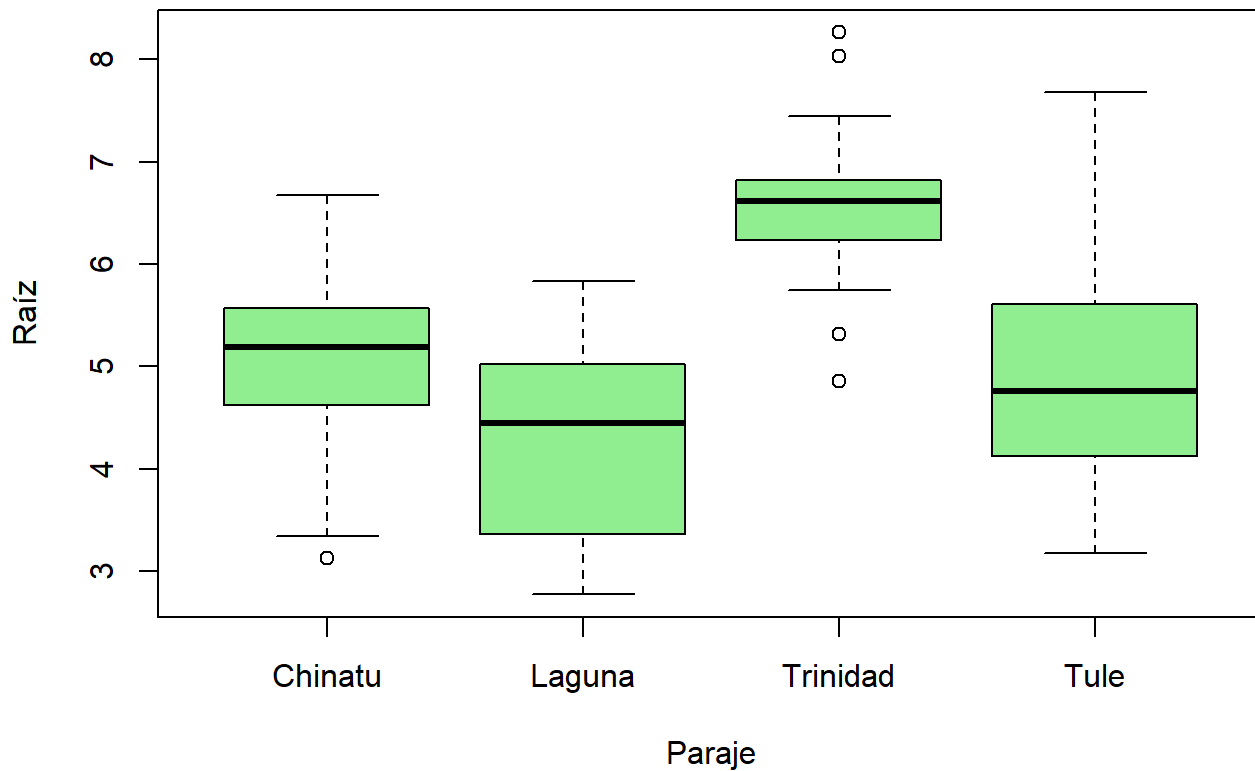
```
##
##   Bartlett test of homogeneity of variances
##
## data:  DAP$raiz by DAP$Paraje
## Bartlett's K-squared = 7.6911, df = 3, p-value = 0.05285
```

```
dap.aov <- aov(DAP$raiz ~ DAP$Paraje)
summary(dap.aov)
```

```
##                 Df Sum Sq Mean Sq F value    Pr(>F)
## DAP$Paraje    3  84.09   28.029    33.2 1.45e-15 ***
## Residuals   116  97.94    0.844
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
boxplot(DAP$raiz ~ DAP$Paraje, ylab = "Raíz", xlab = "Paraje", main = "Boxplot", col = "lightgre
en")
```

Boxplot


```
TukeyHSD(dap.aov)
```

```
##     Tukey multiple comparisons of means
##       95% family-wise confidence level
##
## Fit: aov(formula = DAP$raiz ~ DAP$Paraje)
##
## $`DAP$Paraje`
##                       diff          lwr          upr       p adj
## Laguna-Chinatu   -0.7331899 -1.351610796 -0.1147691 0.0131794
## Trinidad-Chinatu  1.5391985  0.920777631  2.1576194 0.0000000
## Tule-Chinatu     -0.1190328 -0.737453617  0.4993881 0.9585122
## Trinidad-Laguna   2.2723884  1.653967564  2.8908093 0.0000000
## Tule-Laguna       0.6141572 -0.004263685  1.2325780 0.0523230
## Tule-Trinidad    -1.6582312 -2.276652111 -1.0398104 0.0000000
```

```
plot(TukeyHSD(dap.aov))
```

95% family-wise confidence level

Differences in mean levels of DAP$Paraje