

07_ANOVAR.R

Usuario

2023-11-29

```
# Leobardo Estrella
# ANOVA
# 10/10/2023

# Importar datos -----

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

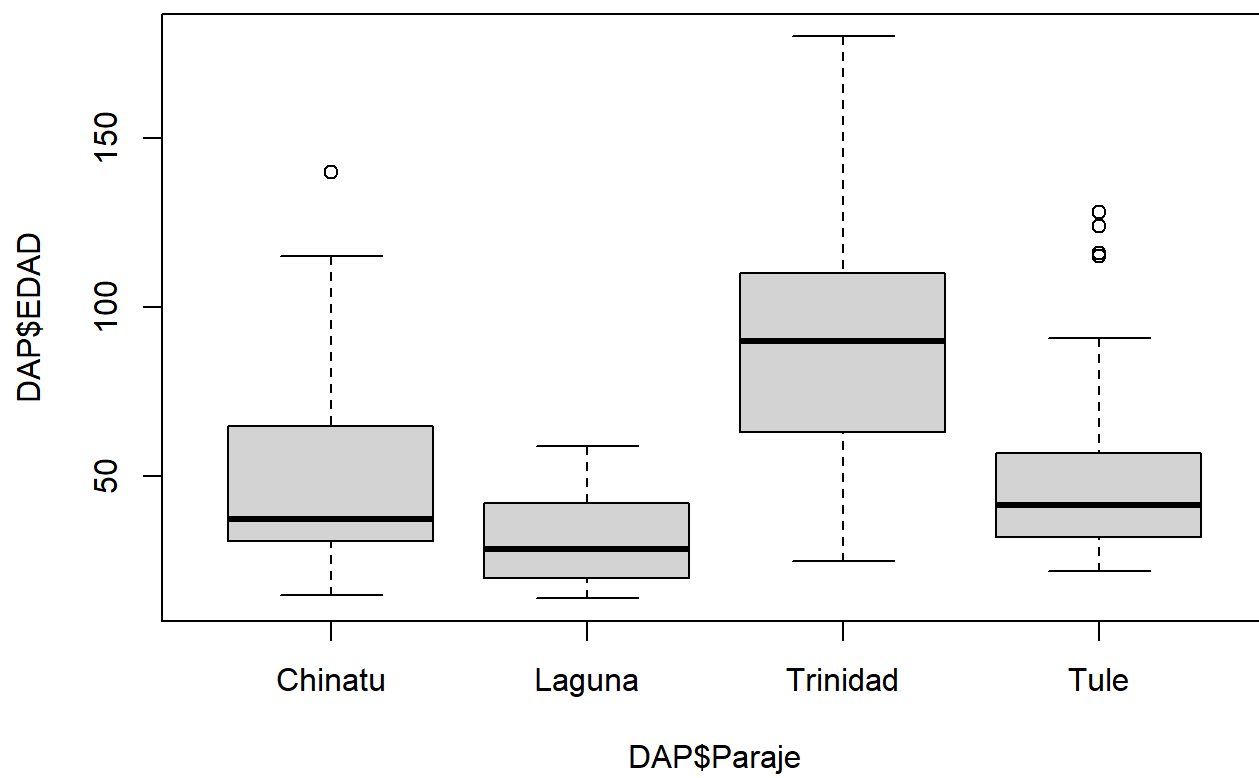
```
## Downloading data from: https://www.dropbox.com/s/fbrwxypacjgeayj/Datos_Rascon_Anova.csv?dl=1
```

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

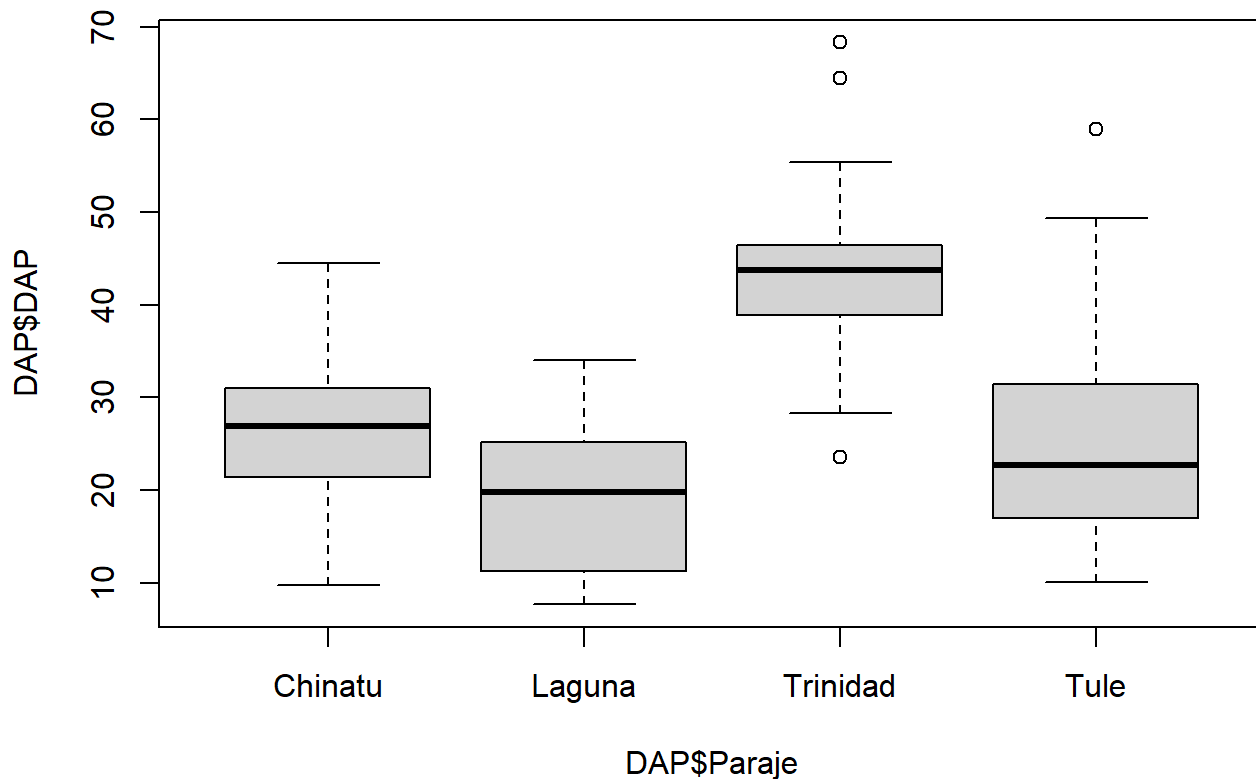
```
DAP$Paraje <- as.factor(DAP$Paraje)
DAP$SP <- as.factor (DAP$SP)

# Determinar estadísticas descriptivas -----

boxplot(DAP$EDAD ~ DAP$Paraje)
```



```
boxplot(DAP$DAP ~ DAP$Paraje)
```



```
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
```

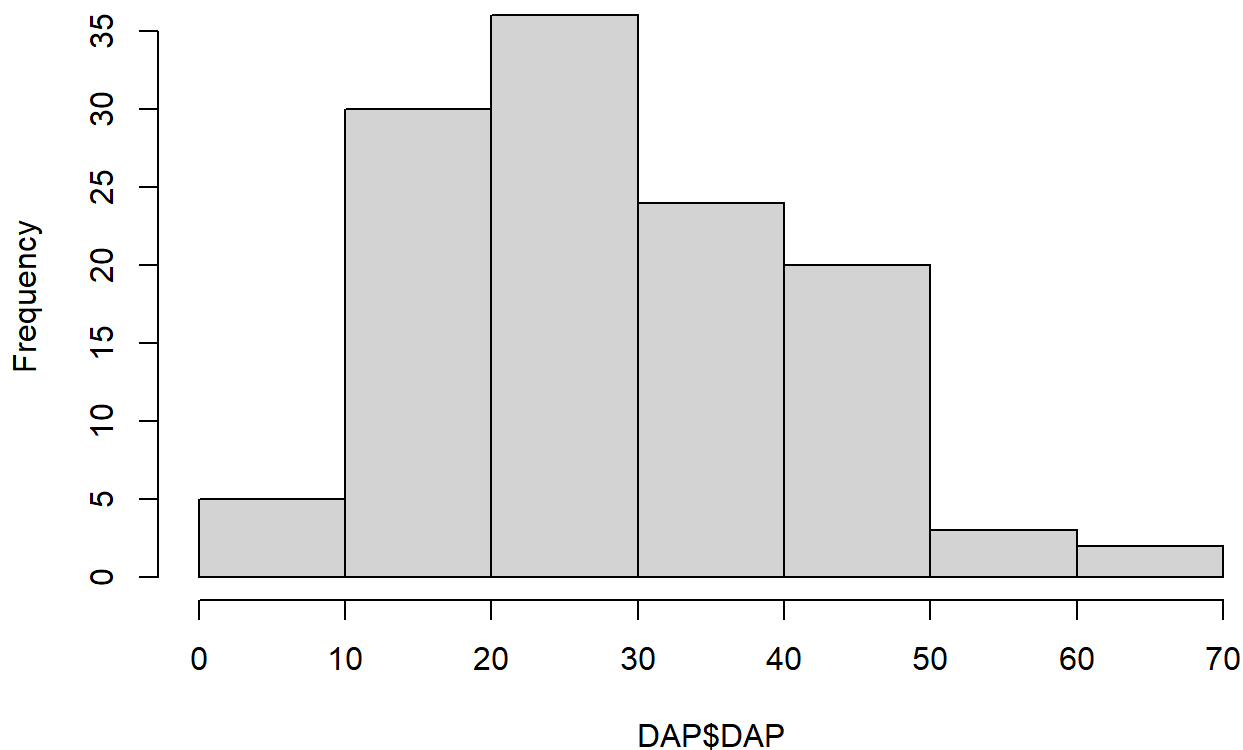
```
# Normalidad revisar -----
```

```
shapiro.test(DAP$DAP) ##NORMAVILIDAD
```

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

```
hist(DAP$DAP) ## HISTOGRAMA
```

Histogram of DAP\$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
```

```
# La varianza de los tratamientos son iguales
```

```
# Transformar DAP para cumplir normalidad
```

```
DAP$raiz <- sqrt(DAP$DAP)
```

```
# Probar normalidad a los datos transformados (raiz cuadrada)
```

```
shapiro.test(DAP$raiz)
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: DAP$raiz
```

```
## W = 0.98341, p-value = 0.1473
```

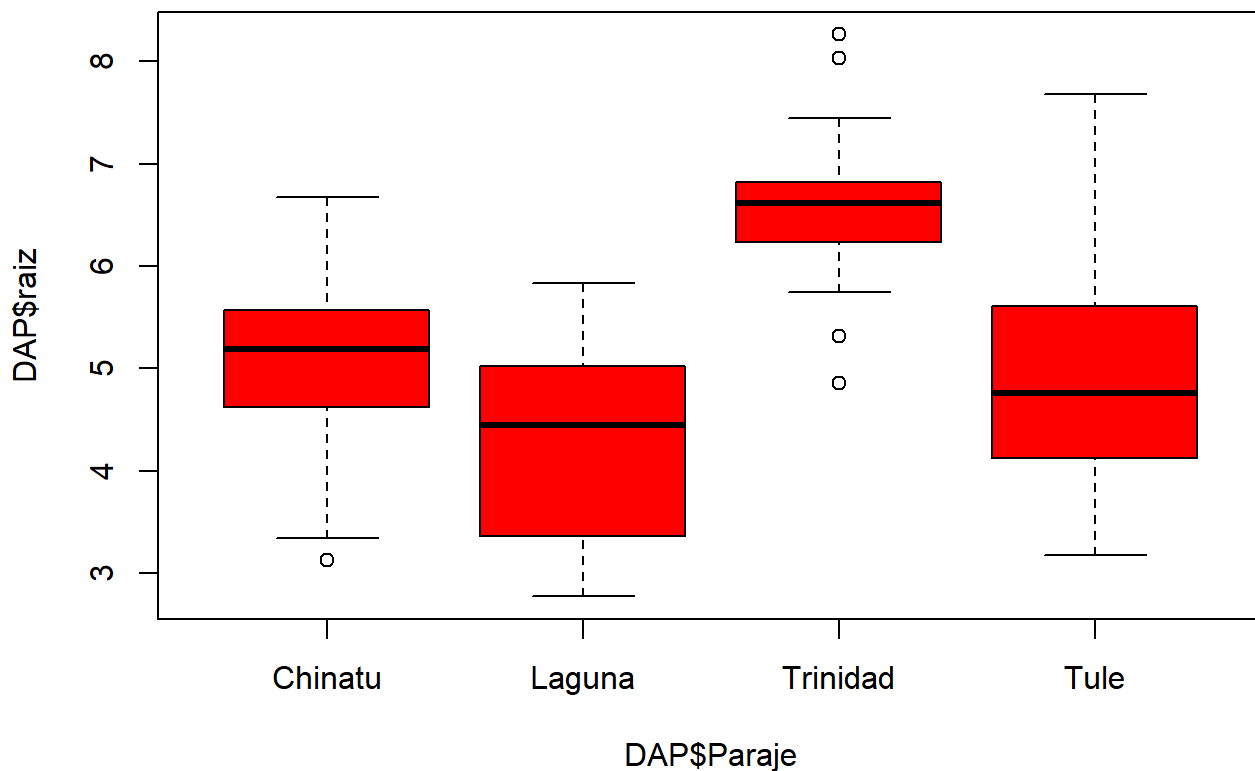
```
# Probar homogeneidad de varianzas de Los datos transformados
bartlett.test(DAP$raiz ~ DAP$Paraje)
```

```
##
## 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,
         col = "red")
```



```
# encontrar las diferencias significativas
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
```

```
# graficar diferencias significativas
plot(TukeyHSD(dap.aov))
```

95% family-wise confidence level

