08_ANOVA.R

Usuario01

2023-10-10

```
# ANOVA
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# 10/10/2023
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# Importar datos ------------------------------------------------------------

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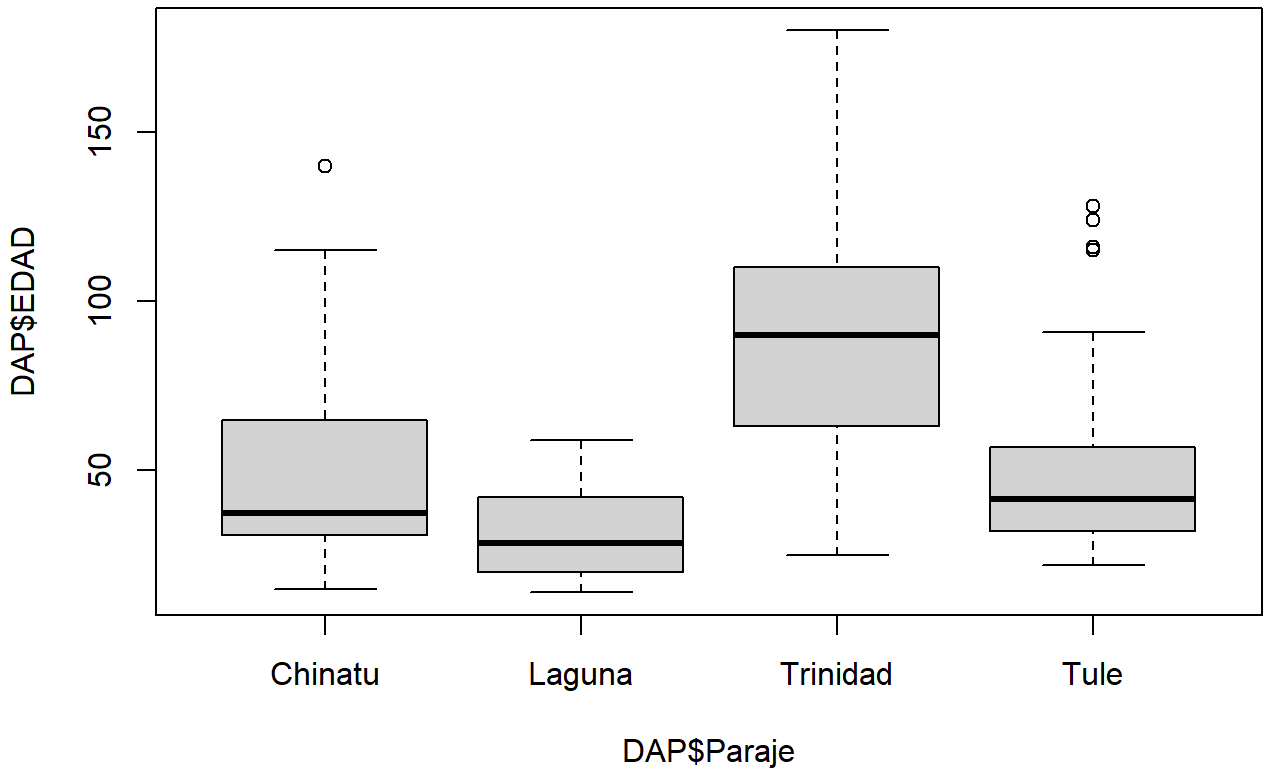
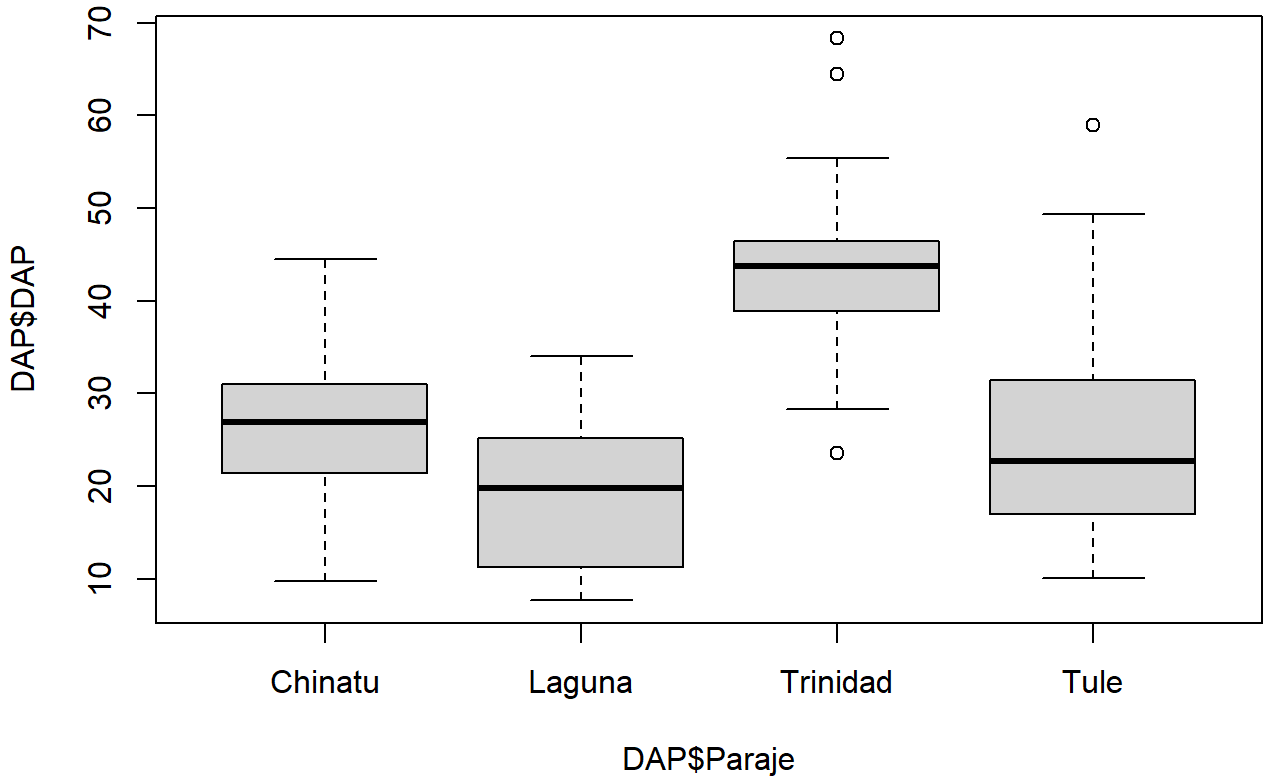

```
## Downloading data from: https://www.dropbox.com/s/fbrwxypacjgeayj/Datos_Rascon_Anova.csv?dl=1
```

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

```
DAP$Paraje <- as.factor(DAP$Paraje)
DAP$SP <- as.factor(DAP$SP)
#Convertir características a factor


# Determinar estadística descriptiva ----------------------------------------

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
```

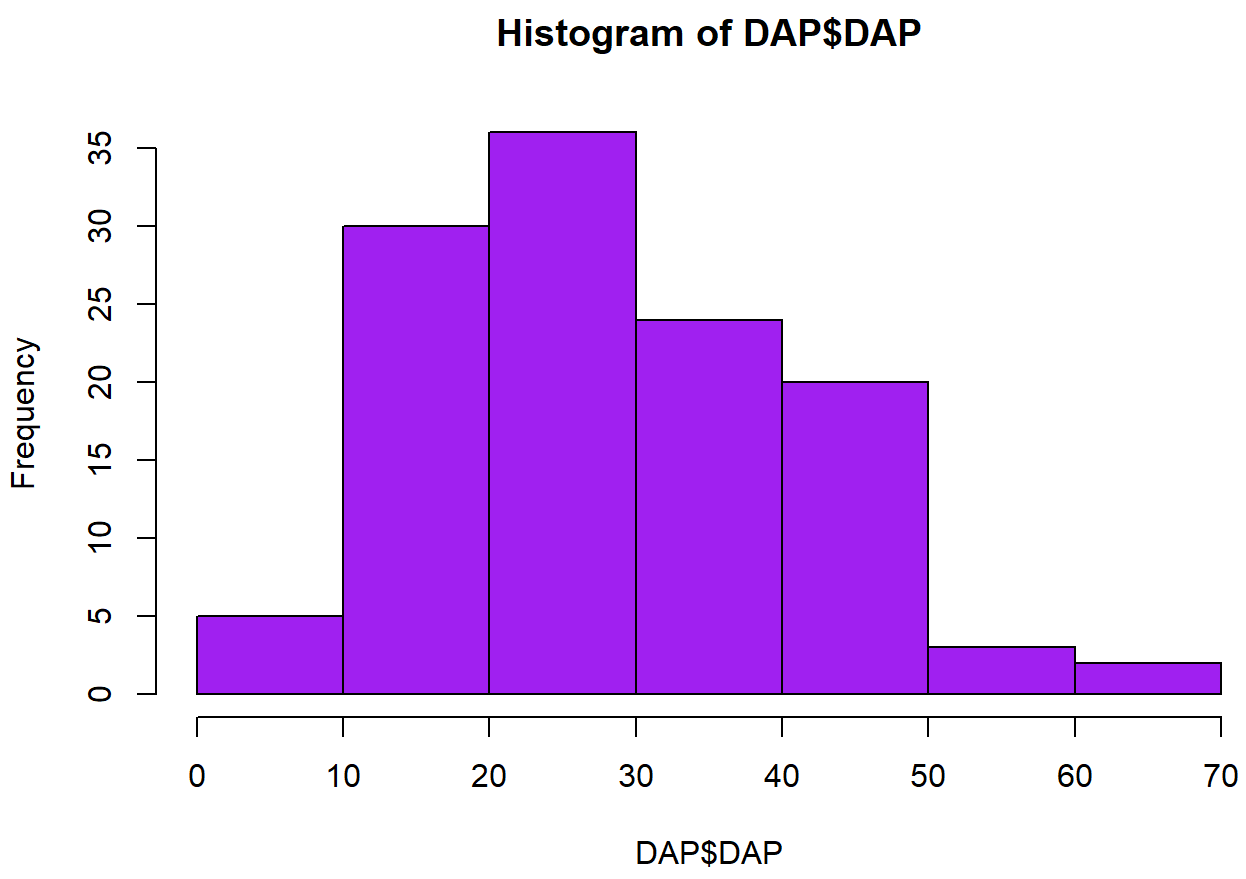
```
tapply(DAP$EDAD, DAP$Paraje, var)
```

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

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

shapiro.test(DAP$DAP)
```

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

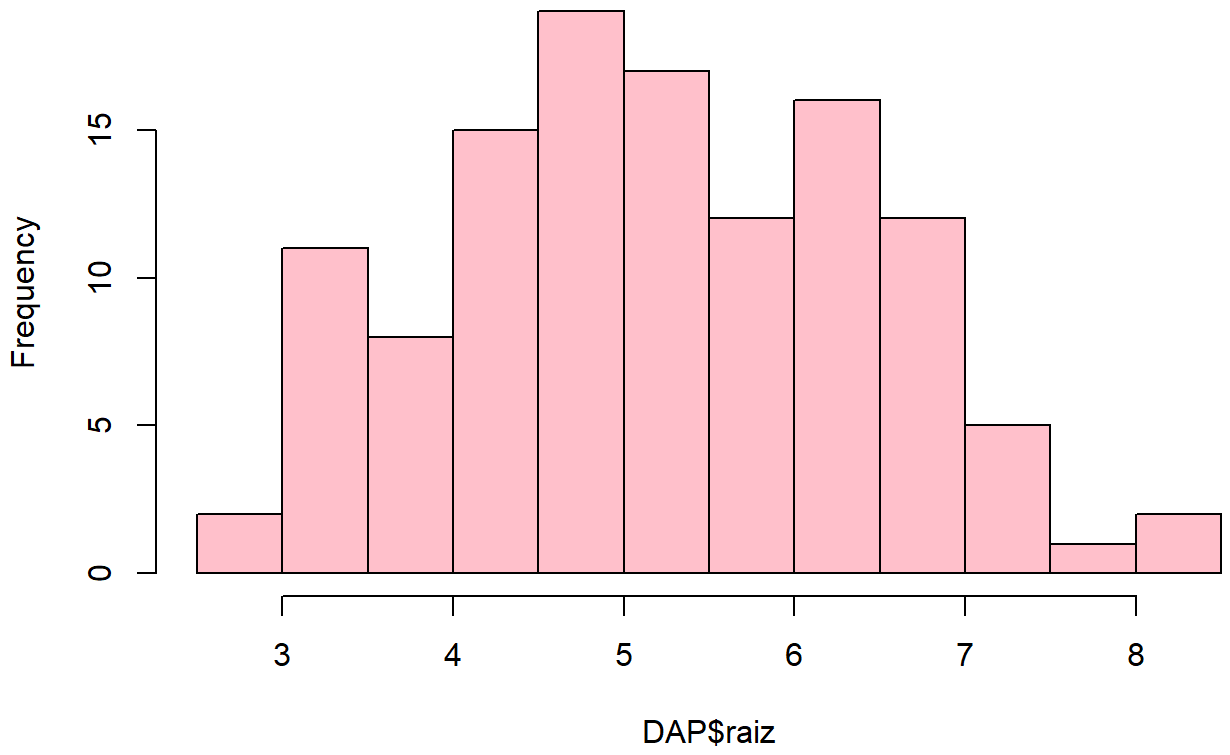
```
hist(DAP$DAP,
     col = "purple")
```




```
# 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,
     col = "pink")
```




```
# 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
```

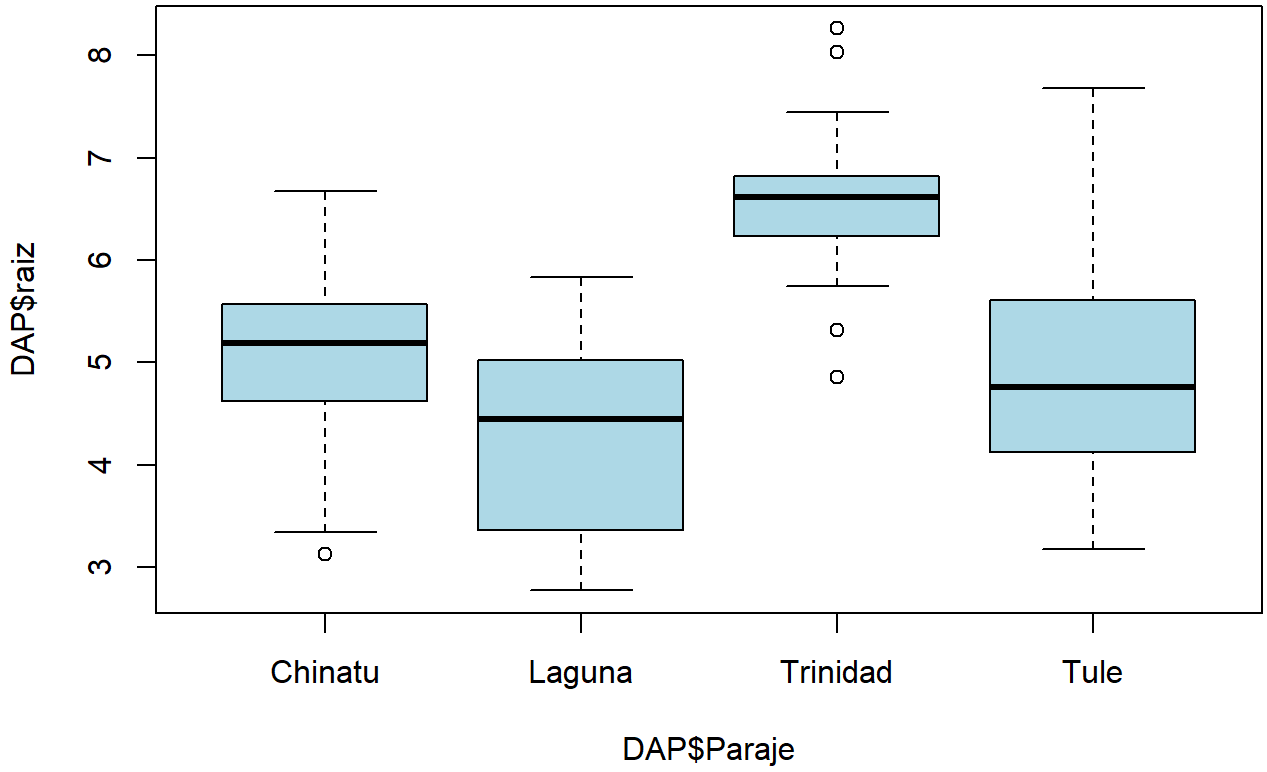
```
# Los datos son normales

# 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
```

```
# Análisis de varianza ----------------------------------------------------

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 = "lightblue")
```




```
# NOTAS:
# Sí hay diferencias significativas entre la variable
# La localidad hace cambios significativos entre el DAP de los árboles


# Prueba de Tukey ---------------------------------------------------------

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
```

```
# Ayuda a determinar diferencias significativas entre los factores (parajes)

# Gráfica para observar diferencias significativas entre factores
plot(TukeyHSD(dap.aov))
```