ANOVA-PRE_GERM.R

Usuario

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```
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##code insert section

# importar datos --------------------------------------------------------


setwd("C:/REPOSITORIO GIT/D_experimental/Scripts/")

germ <- read.csv("pregerminacion.csv", header = TRUE)

germ$TRATAMIENTO <- as.factor(germ$TRATAMIENTO)


# grafica ---------------------------------------------------------------

boxplot(germ$PG ~ germ$TRATAMIENTO,
        col="pink",
        xlab="TRATAMIENTO GERMINATIVO",
        ylab=" % GERMINACION")
```
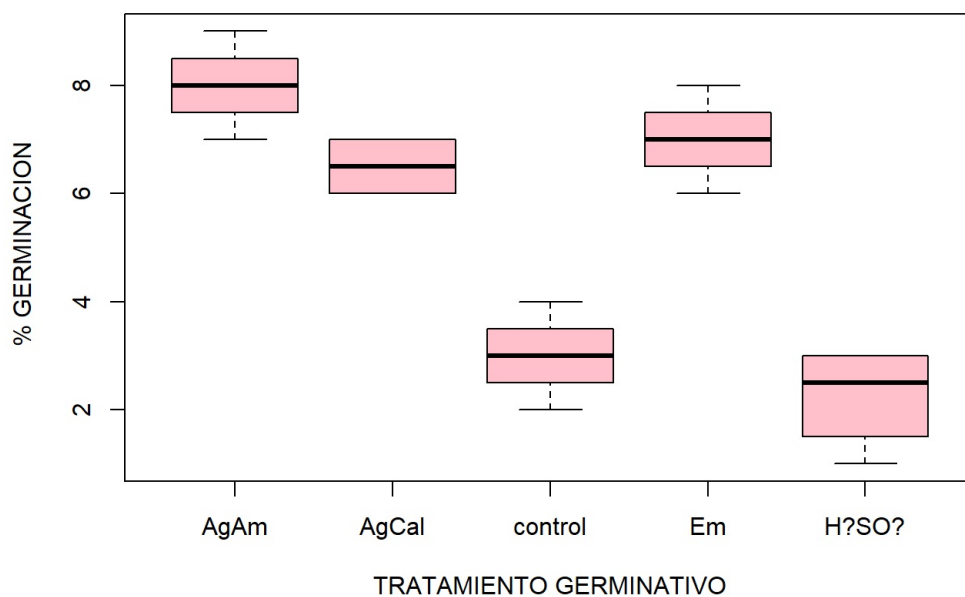


```
# ordenar los tratamientos ----------------------------------------------

levels(germ$TRATAMIENTO)
```

```
## [1] "AgAm"    "AgCal"   "control" "Em"      "H?SO?"
```

```
germ$TRATAMIENTO <- factor(germ$TRATAMIENTO, levels =c("control", "Em", "AgAm", "AgCal", "H?SO?"))
levels(germ$TRATAMIENTO)
```

```
## [1] "control" "Em"      "AgAm"    "AgCal"   "H?SO?"
```

```
tapply(germ$PG, germ$TRATAMIENTO, mean)
```

```
## control      Em    AgAm   AgCal   H?SO?
##    3.00    7.00    8.00    6.50    2.25
```

```
tapply(germ$PG, germ$TRATAMIENTO, var)
```

```
##    control        Em      AgAm      AgCal      H?SO?
## 0.6666667 0.6666667 0.6666667 0.3333333 0.9166667
```

```
# ANOVA -------------------------------------------------------------

germ.aov <- aov(germ$PG ~ germ$TRATAMIENTO)
summary(germ.aov)
```

```
##                   Df Sum Sq Mean Sq F value   Pr(>F)
## germ$TRATAMIENTO   4 104.80   26.20   40.31 7.42e-08 ***
## Residuals         15   9.75    0.65
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# PRUEBA DE TUCKEY -------------------------------------------------------

##en ANOVA - TUCKEY comparar trat y dice quien es diferente de quien

TukeyHSD(germ.aov, conf.level = 0.95)
```
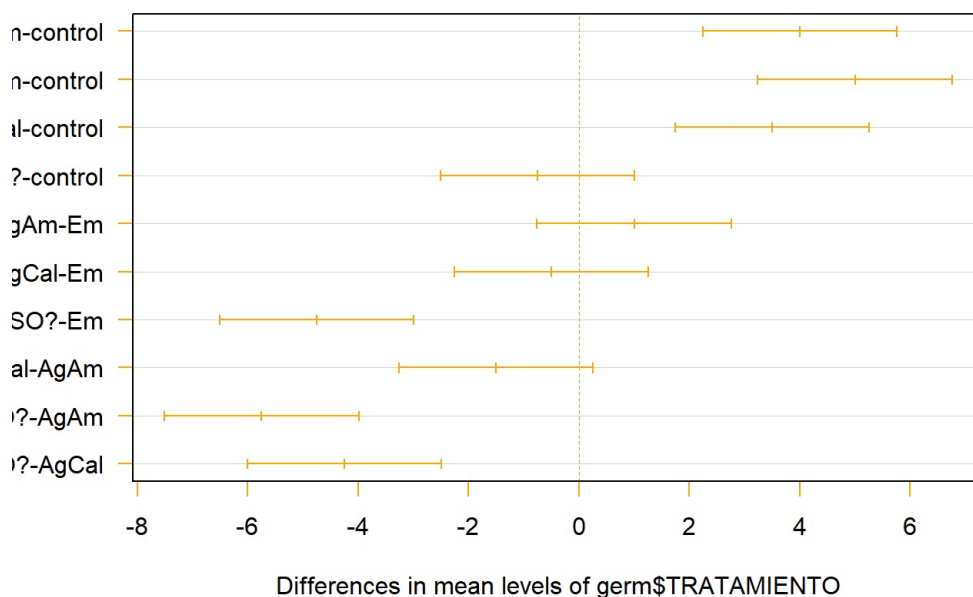
```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = germ$PG ~ germ$TRATAMIENTO)
##
## $`germ$TRATAMIENTO`
##              diff       lwr        upr     p adj
## Em-control   4.00  2.2396122  5.7603878 0.0000356
## AgAm-control 5.00  3.2396122  6.7603878 0.0000024
## AgCal-control 3.50 1.7396122  5.2603878 0.0001587
## H?SO?-control -0.75 -2.5103878  1.0103878 0.6862491
## AgAm-Em      1.00 -0.7603878  2.7603878 0.4332120
## AgCal-Em    -0.50 -2.2603878  1.2603878 0.9009428
## H?SO?-Em    -4.75 -6.5103878 -2.9896122 0.0000045
## AgCal-AgAm  -1.50 -3.2603878  0.2603878 0.1140897
## H?SO?-AgAm  -5.75 -7.5103878 -3.9896122 0.0000004
## H?SO?-AgCal -4.25 -6.0103878 -2.4896122 0.0000175
```

```
##entre Em- ctrl diferencia de 4% y SI hay dif
##entre Agam- ctrl diferencia de 5% y SI hay dif
##entre AgCal- ctrl diferencia de 3.5% y SI hay dif

plot(TukeyHSD(germ.aov), las =1, col="orange")
```

95% family-wise confidence level

Differences in mean levels of germ$TRATAMIENTO

```
# agregar letras de diferencias ------------------------------------------


boxplot(germ$PG ~ germ$TRATAMIENTO,
        col="pink",
        xlab="TRATAMIENTO GERMINATIVO",
        ylab=" % GERMINACION",
        ylim=c(0,10))
text(1,4.2, "a", col="red")
text(2,8.3,"b", col="blue")
text(3,9.4,"b", col="blue")
text(4,7.4,"b", col="blue")
text(5,3.3,"a", col="red")
```