

STATISTICAL ANALYSIS OF DALLY RECRUITMENT

R version 3.5.2 (2018-12-20) -- "Eggshell Igloo"
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Platform: i386-w64-mingw32/i386 (32-bit)

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```
> library(readxl)
> DallyR <- read_excel("C:/Users/USUARIO/Desktop/FOTOS NUEVAS/CUANTIFI
CACIÓN GLIPICANOS/DallyR.xlsx")
> View(DallyR)
> attach(DallyR)
> Trat=split(DallyR$D11,DallyR$Tratamiento,drop=FALSE)
> shapiro.test(Trat$Ihog)
```

Shapiro-wilk normality test

data: Trat\$Ihog
W = 0.91208, p-value = 0.4105

```
> shapiro.test(Trat$DFN)
```

Shapiro-wilk normality test

data: Trat\$DFN
W = 0.96125, p-value = 0.8294

```
> shapiro.test(Trat$DFN1)
```

Shapiro-wilk normality test

data: Trat\$DFN1
W = 0.97862, p-value = 0.9526

```
> shapiro.test(Trat$DFN2)
```

Shapiro-wilk normality test

data: Trat\$DFN2
W = 0.98548, p-value = 0.9818

```
> shapiro.test(Trat$DIg)
```

Shapiro-wilk normality test

data: Trat\$DIg
W = 0.92607, p-value = 0.518

```
pairwise.t.test(D11,Tratamiento, paired = FALSE)
```

Pairwise comparisons using t tests with pooled SD

data: D11 and Tratamiento

	DFN	DFN1	DFN2	DIg	FN1+++
DFN1	0.027	-	-	-	-
DFN2	0.023	1.000	-	-	-
DIg	4.7e-10	6.1e-07	8.1e-07	-	-
FN1+++	1.0e-09	1.0e-06	1.3e-06	1.000	-
Ihog	9.9e-11	1.1e-07	1.5e-07	1.000	1.000

P value adjustment method: holm

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```
> library(readxl)
> Dallyliker <- read_excel("C:/Users/USUARIO/Desktop/FOTOS NUEVAS/CUAN
TIFICACIÓN GLIPICANOS/Dallyliker.xlsx")
> View(Dallyliker)
> attach(Dallyliker)
> Trat=split(Dallyliker$DLP,Dallyliker$Tratamiento,drop=FALSE)
> shapiro.test(Trat$Ihog)
```

Shapiro-wilk normality test

data: Trat\$Ihog
W = 0.86281, p-value = 0.1604

```
> shapiro.test(Trat$DFN)
```

Shapiro-wilk normality test

data: Trat\$DFN
W = 0.87104, p-value = 0.1896

```
> shapiro.test(Trat$DFN1)
```

Shapiro-wilk normality test

data: Trat\$DFN1
W = 0.90397, p-value = 0.3557

```
> shapiro.test(Trat$DFN2)
```

Shapiro-wilk normality test

data: Trat\$DFN2
W = 0.91788, p-value = 0.4531

```
> shapiro.test(Trat$`FN1+++`)
```

Shapiro-wilk normality test

data: Trat\$`FN1+++`
W = 0.97769, p-value = 0.9219
> shapiro.test(Trat\$Dig)

Shapiro-wilk normality test

data: Trat\$Dig
W = 0.90305, p-value = 0.3498

```
> pairwise.t.test(DLP,Tratamiento)
```

Pairwise comparisons using t tests with pooled SD

data: DLP and Tratamiento

	DFN	DFN1	DFN2	Dig	FN1+++
DFN1	0.0324	-	-	-	-
DFN2	6.4e-06	0.0288	-	-	-
Dig	6.4e-07	0.0037	1.0000	-	-
FN1+++	1.3e-06	0.0037	1.0000	1.0000	-
Ihog	1.8e-06	0.0094	1.0000	1.0000	1.0000

P value adjustment method:holm

STATISTICAL ANALYSIS OF HH RECRUITMENT

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Type 'q()' to quit R.

```
> library(readxl)
> HhR <- read_excel("C:/Users/USUARIO/Desktop/FOTOS NUEVAS/CUANTIFICAC
IÓN HH/HhR.xlsx")
> View(HhR)
> attach(HhR)
> Trat=split(HhR$Hh,HhR$Tratamiento,drop=FALSE)
> shapiro.test(Trat$Ihog)
```

Shapiro-wilk normality test

```
data:  Trat$Ihog
W = 0.91411, p-value = 0.464
```

```
> shapiro.test(Trat$DFN)
```

Shapiro-wilk normality test

```
data:  Trat$DFN
W = 0.94515, p-value = 0.6855
```

```
> shapiro.test(Trat$DFN1)
```

Shapiro-wilk normality test

```
data:  Trat$DFN1
W = 0.83649, p-value = 0.09214
```

```
> shapiro.test(Trat$DFN2)
```

Shapiro-wilk normality test

```
data:  Trat$DFN2
W = 0.94824, p-value = 0.726
```

```
> shapiro.test(Trat$`FN1 Cherry`)
```

Shapiro-wilk normality test

```
data:  Trat$`FN1 Cherry`
W = 0.87792, p-value = 0.2174
```

```
> shapiro.test(Trat$`FN1+++`)
```

Shapiro-wilk normality test

```
data:  Trat$`FN1+++`
W = 0.97907, p-value = 0.9549
```

```
> pairwise.t.test(Hh,Tratamiento)
```

Pairwise comparisons using t tests with pooled SD

data: Hh and Tratamiento

	DFN	DFN1	DFN2	FN1 Cherry	FN1+++
DFN1	1.000	-	-	-	-
DFN2	3.3e-06	9.6e-06	-	-	-
FN1 Cherry	0.012	0.027	0.027	-	-
FN1+++	1.000	1.000	9.6e-06	0.027	-
Ihog	< 2e-16	< 2e-16	< 2e-16	< 2e-16	< 2e-16

P value adjustment method: holm

```
> pairwise.t.test(Hh,Tratamiento, paired = FALSE)
```

Pairwise comparisons using t tests with pooled SD

data: Hh and Tratamiento

	DFN	DFN1	DFN2	FN1 Cherry	FN1+++
DFN1	1.000	-	-	-	-
DFN2	3.3e-06	9.6e-06	-	-	-
FN1 Cherry	0.012	0.027	0.027	-	-
FN1+++	1.000	1.000	9.6e-06	0.027	-
Ihog	< 2e-16	< 2e-16	< 2e-16	< 2e-16	< 2e-16

P value adjustment method:holm