Habitat use by Drosophilid species

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```r
library(readxl)
library(agricolae)
library(ggplot2)

dt <- read_excel("Para hablar con Sergio.xlsx",
                                   sheet = "Planilla_R-Binomial-peach")
View(dt)

dt$hab <- as.factor(dt$hab)
dt$fly_sp <- as.factor(dt$fly_sp)
dt$avb_fly_pu <- as.numeric(dt$avb_fly_pu)
```

Difference in use between drosophilid species in each habitat in peach

```r
ins_fly <- subset(dt, hab=="Inside")
out_fly <- subset(dt, hab=="Outside")
soi_fly <- subset(dt, hab=="Soil")

kruskal(ins_fly$avb_fly_pu, ins_fly$fly_sp, alpha = 0.05, p.adj = "holm", console = T)
```

```
##
## Study: ins_fly$avb_fly_pu ~ ins_fly$fly_sp
## Kruskal-Wallis test's
## Ties or no Ties
##
## Critical Value: 166.9431
## Degrees of freedom: 1
## Pvalue Chisq  : 0
##
## ins_fly$fly_sp,  means of the ranks
##
##       ins_fly.avb_fly_pu   r
## Dsp            178.275 120
## Dsuz            62.725 120
##
## Post Hoc Analysis
##
## P value adjustment method: holm
## t-Student: 1.969982
## Alpha    : 0.05
## Minimum Significant Difference: 9.693872
##
## Treatments with the same letter are not significantly different.
```

```
##
##      ins_fly$avb_fly_pu groups
## Dsp              178.275      a
## Dsuz              62.725      b
```

```r
kruskal(out_fly$avb_fly_pu, out_fly$fly_sp, alpha = 0.05, p.adj = "holm", console = T)
```

```
##
## Study: out_fly$avb_fly_pu ~ out_fly$fly_sp
## Kruskal-Wallis test's
## Ties or no Ties
##
## Critical Value: 66.78757
## Degrees of freedom: 1
## Pvalue Chisq  : 3.330669e-16
##
## out_fly$fly_sp,  means of the ranks
##
##      out_fly.avb_fly_pu   r
## Dsp            156.925 120
## Dsuz            84.075 120
##
## Post Hoc Analysis
##
## P value adjustment method: holm
## t-Student: 1.969982
## Alpha    : 0.05
## Minimum Significant Difference: 14.93783
##
## Treatments with the same letter are not significantly different.
##
##      out_fly$avb_fly_pu groups
## Dsp            156.925      a
## Dsuz            84.075      b
```

```r
kruskal(soi_fly$avb_fly_pu, soi_fly$fly_sp, alpha = 0.05, p.adj = "holm", console = T)
```

```
##
## Study: soi_fly$avb_fly_pu ~ soi_fly$fly_sp
## Kruskal-Wallis test's
## Ties or no Ties
##
## Critical Value: 122.7806
## Degrees of freedom: 1
## Pvalue Chisq  : 0
##
## soi_fly$fly_sp,  means of the ranks
##
##      soi_fly.avb_fly_pu   r
## Dsp          72.58333 120
## Dsuz        168.41667 120
##
## Post Hoc Analysis
##
## P value adjustment method: holm
```

```
## t-Student: 1.969982
## Alpha     : 0.05
## Minimum Significant Difference: 11.90597
##
## Treatments with the same letter are not significantly different.
##
##       soi_fly$avb_fly_pu groups
## Dsuz            168.41667      a
## Dsp              72.58333      b
```

Habitat use by Drosophilid species in Peach

```
sub_Dsp <- subset(dt, fly_sp == "Dsp")
sub_Dsuz <- subset(dt, fly_sp == "Dsuz")
View(sub_Dsp)

kruskal(sub_Dsp$avb_fly_pu, alpha= 0.05, sub_Dsp$hab, p.adj = ("holm"), console = T)
```

```
##
## Study: sub_Dsp$avb_fly_pu ~ sub_Dsp$hab
## Kruskal-Wallis test's
## Ties or no Ties
##
## Critical Value: 295.6566
## Degrees of freedom: 2
## Pvalue Chisq  : 0
##
## sub_Dsp$hab,  means of the ranks
##
##          sub_Dsp.avb_fly_pu    r
## Inside            290.18750  120
## Outside           190.44583  120
## Soil               60.86667  120
##
## Post Hoc Analysis
##
## P value adjustment method: holm
## t-Student: 2.405315
## Alpha     : 0.05
## Minimum Significant Difference: 13.55065
##
## Treatments with the same letter are not significantly different.
##
##          sub_Dsp$avb_fly_pu groups
## Inside            290.18750      a
## Outside           190.44583      b
## Soil               60.86667      c
```

```
kruskal(sub_Dsuz$avb_fly_pu, alpha= 0.05, sub_Dsuz$hab, p.adj = ("holm"), console = T)
```

```
##
## Study: sub_Dsuz$avb_fly_pu ~ sub_Dsuz$hab
## Kruskal-Wallis test's
## Ties or no Ties
##
## Critical Value: 40.5116
```

```
## Degrees of freedom: 2
## Pvalue Chisq  : 1.595944e-09
##
## sub_Dsuz$hab,  means of the ranks
##
##          sub_Dsuz.avb_fly_pu   r
## Inside             215.9208 120
## Outside            191.6417 120
## Soil               133.9375 120
##
## Post Hoc Analysis
##
## P value adjustment method: holm
## t-Student: 2.405315
## Alpha    : 0.05
## Minimum Significant Difference: 30.06289
##
## Treatments with the same letter are not significantly different.
##
##          sub_Dsuz$avb_fly_pu groups
## Inside             215.9208      a
## Outside            191.6417      a
## Soil               133.9375      b
```
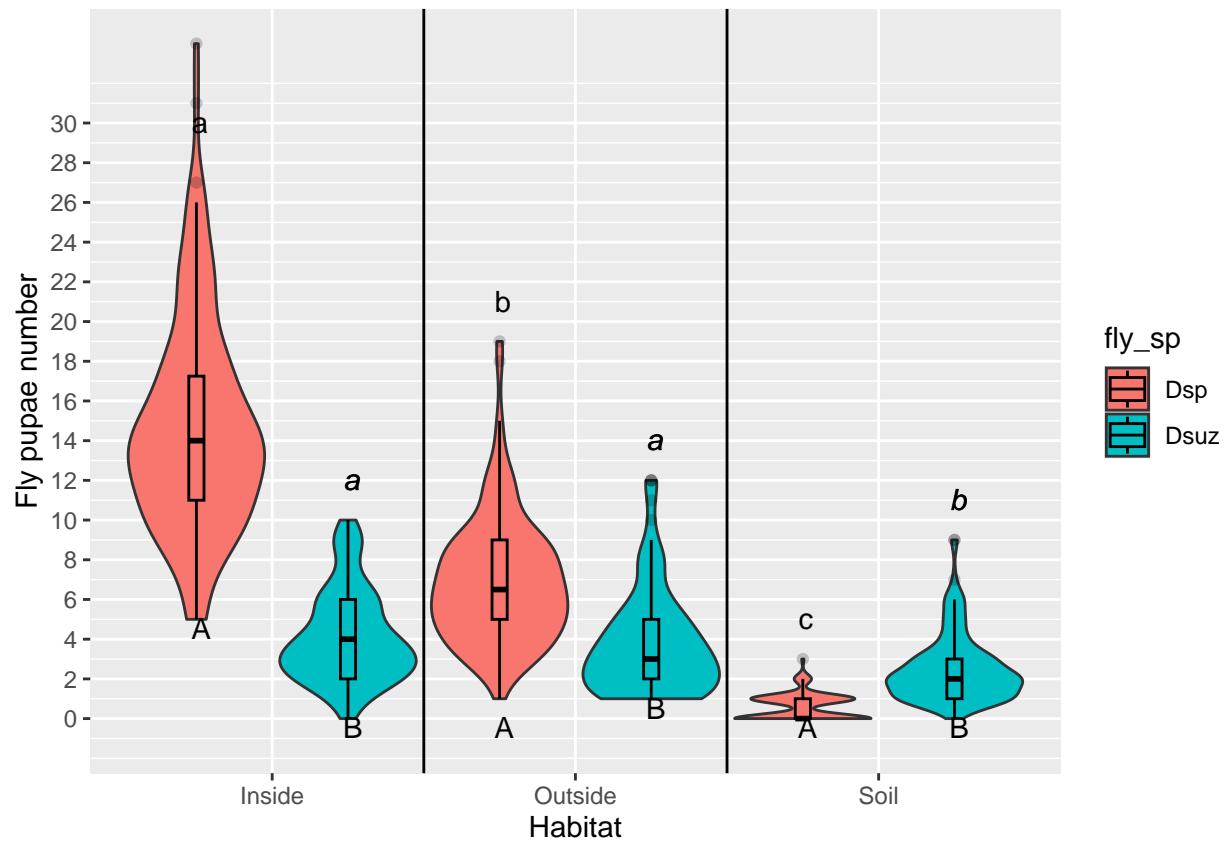
```r
ggplot(dt, aes(x = factor(hab), y = avb_fly_pu, fill = fly_sp)) +
  geom_violin(trim = T, position=position_dodge(1), scale = "width") +
  scale_y_continuous(breaks=seq(0, 30, 2)) +
  labs(x = "Habitat",
       y = "Fly pupae number") + #Título de nuestros ejes
  annotate('text', label='a',
           x= 0.74, y= 29.5, hjust=0.1, vjust=0, size=4, color='black') +
   annotate('text', label='A',
           x= 0.74, y= 4, hjust=0.1, vjust=0, size=4, color='black') +
    annotate('text', label='b',
           x= 1.74, y= 20.5, hjust=0.1, vjust=0, size=4, color='black') +
   annotate('text', label='A',
           x= 1.74, y= -1, hjust=0.1, vjust=0, size=4, color='black') +
    annotate('text', label='c',
           x= 2.74, y= 4.5, hjust=0.1, vjust=0, size=4, color='black') +
   annotate('text', label='A',
           x= 2.74, y= -1, hjust=0.1, vjust=0, size=4, color='black') +
    annotate('text', label= substitute(paste(italic("a"))),
           x= 1.24, y= 11.5, hjust=0.1, vjust=0, size=4, color='black') +
   annotate('text', label='B',
           x= 1.24, y= -1, hjust=0.1, vjust=0, size=4, color='black') +
    annotate('text', label= substitute(paste(italic("a"))),
           x= 2.24, y= 13.5, hjust=0.1, vjust=0, size=4, color='black') +
   annotate('text', label='B',
           x= 2.24, y= 0, hjust=0.1, vjust=0, size=4, color='black') +
    annotate('text', label= substitute(paste(italic("b"))),
           x= 3.24, y= 10.5, hjust=0.1, vjust=0, size=4, color='black') +
   annotate('text', label='B',
           x= 3.24, y= -1, hjust=0.1, vjust=0, size=4, color='black') +
  geom_boxplot(width=0.1, color="black", alpha=0.2, position=position_dodge(1)) +
```

```
  geom_vline(xintercept = 1.5) +
geom_vline(xintercept = 2.5)
```

```
## Warning in is.na(x): is.na() aplicado a un objeto que no es (lista o vector) de
## tipo 'language
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```


Difference in use between drosophilid species in each habitat in guava

```
library(readxl)
library(agricolae)

dt2 <- read_excel("guava_data.xlsx",
                  sheet = "Hoja1")
View(dt2)

dt2$hab <- as.factor(dt2$hab)
dt2$fly_sp <- as.factor(dt2$fly_sp)
dt2$tric_suc <- as.numeric(dt2$tric_suc)
dt2$pach_suc <- as.numeric(dt2$pach_suc)

attach(dt2)
```

```r
ins_fly <- subset(dt2, hab=="Inside")
out_fly <- subset(dt2, hab=="Outside")
soi_fly <- subset(dt2, hab=="Soil")

kruskal(ins_fly$avb_fly_pu, ins_fly$fly_sp, alpha = 0.05, p.adj = "holm", console = T)
```

```
##
## Study: ins_fly$avb_fly_pu ~ ins_fly$fly_sp
## Kruskal-Wallis test's
## Ties or no Ties
##
## Critical Value: 173.9573
## Degrees of freedom: 1
## Pvalue Chisq  : 0
##
## ins_fly$fly_sp,  means of the ranks
##
##       ins_fly.avb_fly_pu   r
## Dsp           178.99583 120
## Dsuz           62.00417 120
##
## Post Hoc Analysis
##
## P value adjustment method: holm
## t-Student: 1.969982
## Alpha     : 0.05
## Minimum Significant Difference: 9.134957
##
## Treatments with the same letter are not significantly different.
##
##       ins_fly$avb_fly_pu groups
## Dsp           178.99583      a
## Dsuz           62.00417      b
```

```r
kruskal(out_fly$avb_fly_pu, out_fly$fly_sp, alpha = 0.05, p.adj = "holm", console = T)
```

```
##
## Study: out_fly$avb_fly_pu ~ out_fly$fly_sp
## Kruskal-Wallis test's
## Ties or no Ties
##
## Critical Value: 108.9104
## Degrees of freedom: 1
## Pvalue Chisq  : 0
##
## out_fly$fly_sp,  means of the ranks
##
##       out_fly.avb_fly_pu   r
## Dsp               166.7 120
## Dsuz               74.3 120
##
## Post Hoc Analysis
##
```

```
## P value adjustment method: holm
## t-Student: 1.969982
## Alpha     : 0.05
## Minimum Significant Difference: 12.89532
##
## Treatments with the same letter are not significantly different.
##
##      out_fly$avb_fly_pu groups
## Dsp             166.7      a
## Dsuz             74.3      b
```

```r
kruskal(soi_fly$avb_fly_pu, soi_fly$fly_sp, alpha = 0.05, p.adj = "holm", console = T)
```

```
##
## Study: soi_fly$avb_fly_pu ~ soi_fly$fly_sp
## Kruskal-Wallis test's
## Ties or no Ties
##
## Critical Value: 4.912938
## Degrees of freedom: 1
## Pvalue Chisq  : 0.02665627
##
## soi_fly$fly_sp,  means of the ranks
##
##      soi_fly.avb_fly_pu   r
## Dsp          111.7792 120
## Dsuz         129.2208 120
##
## Post Hoc Analysis
##
## P value adjustment method: holm
## t-Student: 1.969982
## Alpha     : 0.05
## Minimum Significant Difference: 15.37375
##
## Treatments with the same letter are not significantly different.
##
##      soi_fly$avb_fly_pu groups
## Dsuz         129.2208      a
## Dsp          111.7792      b
```

Habitat use by Drosophilid species in Peach

```r
sub_Dsp <- subset(dt2, fly_sp == "Dsp")
sub_Dsuz <- subset(dt2, fly_sp == "Dsuz")

kruskal(sub_Dsp$avb_fly_pu, alpha= 0.05, sub_Dsp$hab, p.adj = ("holm"), console = T)
```

```
##
## Study: sub_Dsp$avb_fly_pu ~ sub_Dsp$hab
## Kruskal-Wallis test's
## Ties or no Ties
##
## Critical Value: 295.6091
## Degrees of freedom: 2
## Pvalue Chisq  : 0
```

```
##
## sub_Dsp$hab,  means of the ranks
##
##          sub_Dsp.avb_fly_pu   r
## Inside           290.10000 120
## Outside          190.28333 120
## Soil              61.11667 120
##
## Post Hoc Analysis
##
## P value adjustment method: holm
## t-Student: 2.405315
## Alpha     : 0.05
## Minimum Significant Difference: 13.53574
##
## Treatments with the same letter are not significantly different.
##
##          sub_Dsp$avb_fly_pu groups
## Inside          290.10000      a
## Outside         190.28333      b
## Soil             61.11667      c
```

```r
kruskal(sub_Dsuz$avb_fly_pu, alpha= 0.05, sub_Dsuz$hab, p.adj = ("holm"), console = T)
```

```
##
## Study: sub_Dsuz$avb_fly_pu ~ sub_Dsuz$hab
## Kruskal-Wallis test's
## Ties or no Ties
##
## Critical Value: 5.114484
## Degrees of freedom: 2
## Pvalue Chisq  : 0.07751823
##
## sub_Dsuz$hab,  means of the ranks
##
##          sub_Dsuz.avb_fly_pu   r
## Inside            190.575 120
## Outside           186.275 120
## Soil              164.650 120
##
## Post Hoc Analysis
##
## P value adjustment method: holm
## t-Student: 2.405315
## Alpha     : 0.05
## Minimum Significant Difference: 29.42533
##
## Treatments with the same letter are not significantly different.
##
##          sub_Dsuz$avb_fly_pu groups
## Inside            190.575      a
## Outside           186.275      a
## Soil              164.650      a
```

```r
library(ggplot2)

ggplot(dt2, aes(x = factor(hab), y = avb_fly_pu, fill = fly_sp)) +
  geom_violin(trim = T, position=position_dodge(1), scale = "width") +
  scale_y_continuous(breaks=seq(0, 33, 2)) +
  labs(x = "Habitat",
       y = "Fly pupae number in guavas") + #Título de nuestros ejes
  annotate('text', label='a',
           x= 0.74, y= 32.5, hjust=0.1, vjust=0, size=4, color='black') +
  annotate('text', label='A',
           x= 0.74, y= 3.5, hjust=0.1, vjust=0, size=4, color='black') +

  annotate('text', label='b',
           x= 1.74, y= 18.5, hjust=0.1, vjust=0, size=4, color='black') +
   annotate('text', label='A',
           x= 1.74, y= 0, hjust=0.1, vjust=0, size=4, color='black') +
    annotate('text', label='c',
           x= 2.74, y= 5.5, hjust=0.1, vjust=0, size=4, color='black') +
   annotate('text', label='A',
           x= 2.74, y= -2, hjust=0.1, vjust=0, size=4, color='black') +
    annotate('text', label= substitute(paste(italic("a"))),
           x= 1.24, y= 12.5, hjust=0.1, vjust=0, size=4, color='black') +
   annotate('text', label= substitute(paste(italic("B"))),
           x= 1.24, y= -2, hjust=0.1, vjust=0, size=4, color='black') +
    annotate('text', label= substitute(paste(italic("a"))),
           x= 2.24, y= 11.5, hjust=0.1, vjust=0, size=4, color='black') +
   annotate('text', label= substitute(paste(italic("B"))),
           x= 2.24, y= -2, hjust=0.1, vjust=0, size=4, color='black') +
    annotate('text', label= substitute(paste(italic("a"))),
           x= 3.24, y= 8.5, hjust=0.1, vjust=0, size=4, color='black') +
   annotate('text', label= substitute(paste(italic("B"))),
           x= 3.24, y= -2, hjust=0.1, vjust=0, size=4, color='black') +
    geom_boxplot(width=0.1, color="black", alpha=0.2, position=position_dodge(1)) +
geom_vline(xintercept = 1.5) +
geom_vline(xintercept = 2.5)
```

```
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```