

Forest and grassland habitats support pollinator diversity more than wildflowers and sunflower monoculture

Vujanović Dušanka, Losapio Gianalberto et al.

Ecological Entomology

Introduction

This Supplementary Material reports the code to reproduce the analyses and figures carried out in Vujanović, Losapio *et al.* The scope of this tutorial is to increase its reproducibility, clarity, transparency and dissemination. Data analysis was done using R version 4.1.3. This document was compiled with the ‘rmarkdown package, version 1.13. This tutorial is licensed under CC BY-NC-ND 4.0, which means you are free to share, copy and redistribute this tutorial in any medium or format under the terms of attribution of appropriate credit, non-commercial purposes and no derivatives. The citation is:

Vujanović D, Losapio G, Mészáros M, Popov S, Markov R Z, Mudri S S, Jović J, Vujić A.2022. Forest and grassland fragments support pollinator diversity more than wildflowers and sunflowers. Ecological Entomology.

Software preparation

Install R (<https://www.r-project.org>) (R Core Team 2022) if you do not have it yet.

Then, install and load the following packages.

```
# Packages
packages = c("ggplot2", "effects", "effectsize", "car", "emmeans",
             "parameters", "vegan", "readxl", "AER", "glmmTMB",
             "DHARMa")

# Install packages not yet installed
installed_packages <- packages %in% rownames(installed.packages())
if (any(installed_packages == FALSE)) {
  install.packages(packages[!installed_packages])
}
```

```
# Load packages
invisible(lapply(packages, library, character.only = TRUE))
```

Set your working directory and prepare for parallelisation.

```
setwd("/mydir")
```

Data import

Download data at the following link:

https://github.com/losapio/Forest-and-grassland-fragments-support-pollinator-diversity-more-than-wildflowers-and-sunflowers/blob/main/Data_calc.xls

Move the file in your home directory (mydir) and import it

```
data_calc <- read_excel("Data_calc.xls", sheet = "data")

# set SF as reference level
data_calc$Habitat = as.factor(data_calc$Habitat)
data_calc <- within(data_calc, Habitat <-
                    relevel(Habitat, ref = 3))
```

Data check

```
# collinearity among variables
cor(data_calc[,2:4])
```

```
##           Grassland      Forest      Water
## Grassland  1.0000000 -0.4058181  0.1796670
## Forest    -0.4058181  1.0000000  0.1688991
## Water      0.1796670  0.1688991  1.0000000
```

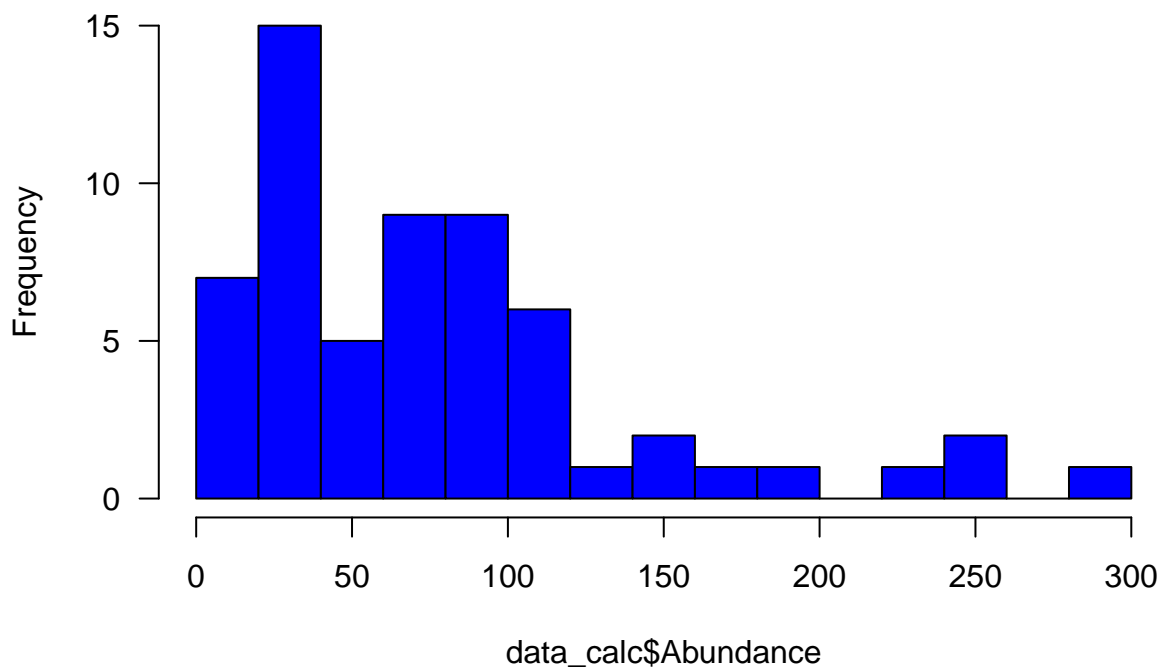
```
# summary statistics
summary(data_calc[,2:4])
```

```
##      Grassland           Forest           Water
## Min.   :0.0000  Min.   :0.0000  Min.   :0.0000
## 1st Qu.:0.0000  1st Qu.:0.0000  1st Qu.:0.0000
## Median :0.1247  Median :0.3804  Median :0.00000
## Mean   :0.3078  Mean   :0.6415  Mean   :0.07569
## 3rd Qu.:0.3862  3rd Qu.:1.0721  3rd Qu.:0.06113
## Max.   :1.3980  Max.   :2.5321  Max.   :0.62426
```

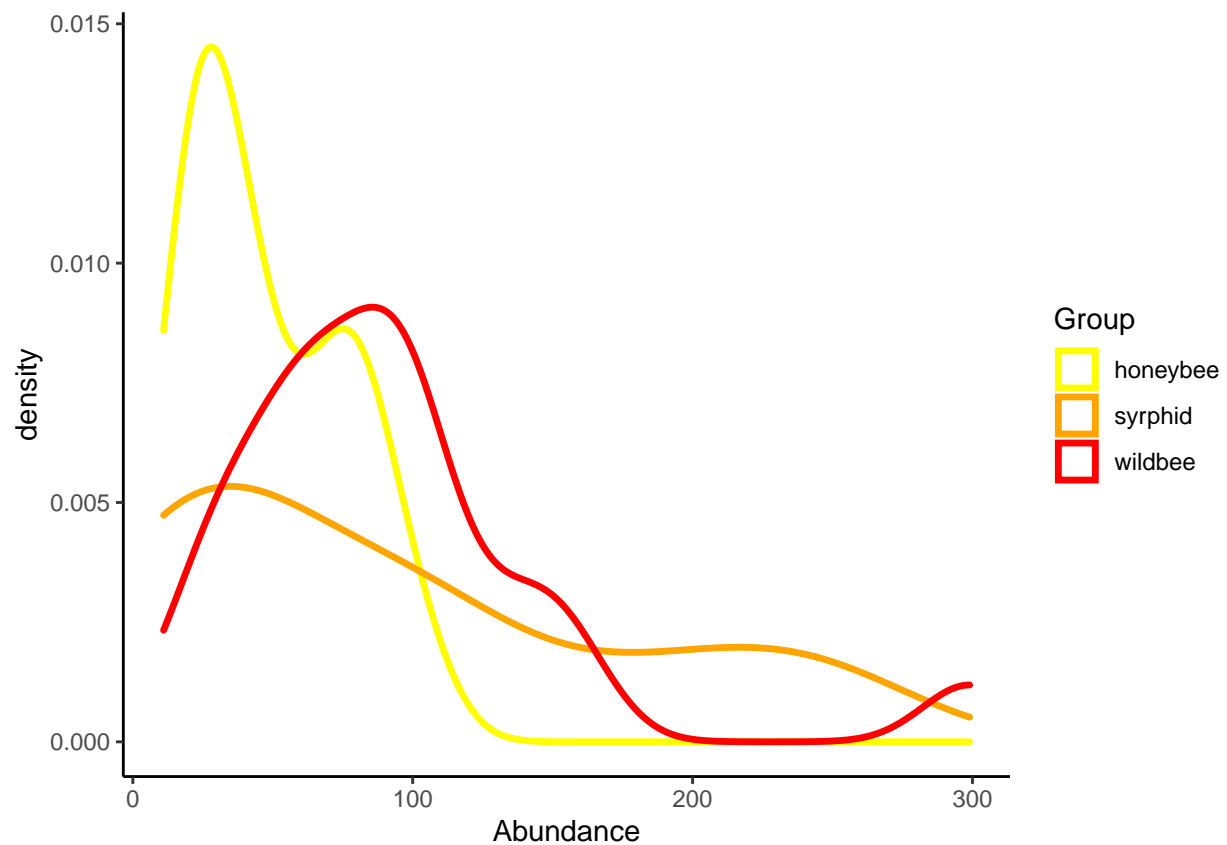
Pollinator abundance

```
data_calc$Abundance[which(data_calc$Group=="wildbee")] =  
  rowSums(wildbees[, -1])  
data_calc$Abundance[which(data_calc$Group=="syrphid")] =  
  rowSums(syrphids[, -1])  
  
data_calc$Abundance = as.numeric(data_calc$Abundance)  
  
hist(data_calc$Abundance, 20, col = 'blue', las = 1)
```

Histogram of data_calc\$Abundance



```
ggplot(data_calc, aes(x = Abundance, colour = Group)) +  
  theme_classic() +  
  geom_density(lwd = 1.2, linetype = 1) +  
  scale_color_manual(values = c("yellow", "orange", "red"))
```

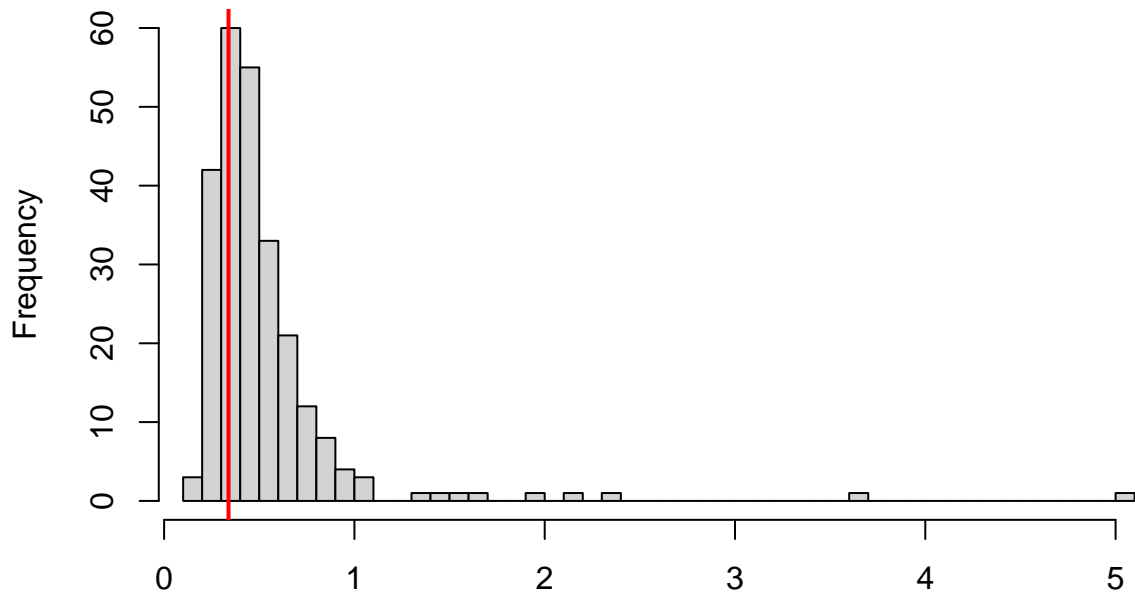


```
## model abundance
```

```
mod.ab1 = glmmTMB(Abundance ~ Group*Habitat +  
                  Group*(Grassland + Forest + Water),  
                  family = nbinom2,  
                  dispformula = ~Group,  
                  data = data_calc)
```

```
testDispersion(mod.ab1)
```

DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.552

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data:  simulationOutput
## dispersion = 0.64273, p-value = 0.552
## alternative hypothesis: two.sided
```

```
Anova(mod.ab1, type="II")
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
```

```
##
```

```
## Response: Abundance
```

	Chisq	Df	Pr(>Chisq)
## Group	36.8764	2	9.826e-09 ***
## Habitat	38.2276	3	2.530e-08 ***
## Grassland	14.7491	1	0.0001228 ***
## Forest	0.3695	1	0.5432816
## Water	0.1474	1	0.7010315
## Group:Habitat	9.4580	6	0.1494117
## Group:Grassland	0.6546	2	0.7208560
## Group:Forest	1.5229	2	0.4669858
## Group:Water	2.7237	2	0.2561823

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cohens_f(aov(mod.ab1))
```

```
## # Effect Size for ANOVA (Type I)
```

```
##
```

```
## Parameter          | Cohen's f (partial) |          95% CI
```

```
## -----
```

```
## Group              |              1.98 | [1.50, Inf]
```

```
## Habitat            |              0.72 | [0.37, Inf]
```

```
## Grassland          |              0.54 | [0.25, Inf]
```

```
## Forest             |              0.16 | [0.00, Inf]
```

```
## Water              |              0.09 | [0.00, Inf]
```

```
## Group:Habitat      |              0.35 | [0.00, Inf]
```

```
## Group:Grassland    |              0.33 | [0.00, Inf]
```

```
## Group:Forest       |              0.16 | [0.00, Inf]
```

```
## Group:Water        |              0.16 | [0.00, Inf]
```

```
##
```

```
## - One-sided CIs: upper bound fixed at [Inf].
```

```
summary(mod.ab1)
```

```
## Family: nbinom2 ( log )
```

```
## Formula:
```

```
## Abundance ~ Group * Habitat + Group * (Grassland + Forest + Water)
```

```
## Dispersion:                ~Group
```

```
## Data: data_calc
```

```
##
```

```
##      AIC      BIC  logLik deviance df.resid
```

```
##    612.8    663.1  -282.4   564.8      36
```

```
##
```

```
##
```

```
## Conditional model:
```

```
##              Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept)      3.69851    0.16079  23.002 < 2e-16 ***
```

```
## Groupsyrphid    -0.02647    0.37890  -0.070  0.94431
```

```
## Groupwildbee     0.50705    0.29333   1.729  0.08388 .
```

```
## HabitatFE        0.95262    0.29632   3.215  0.00130 **
```

```
## HabitatGR        1.24791    0.33663   3.707  0.00021 ***
```

```
## HabitatWF       -0.30774    0.20121  -1.529  0.12615
```

```
## Grassland       -1.09344    0.36518  -2.994  0.00275 **
```

```
## Forest          -0.18416    0.16474  -1.118  0.26362
```

```
## Water           0.62822    0.47091   1.334  0.18219
```

```
## Groupsyrphid:HabitatFE -0.19940    0.69529  -0.287  0.77427
```

```
## Groupwildbee:HabitatFE -0.15809    0.59899  -0.264  0.79183
```

```
## Groupsyrphid:HabitatGR  1.32121    0.84004   1.573  0.11577
```

```
## Groupwildbee:HabitatGR -0.11481    0.58896   -0.195   0.84545
## Groupsyrphid:HabitatWF  1.02183    0.47489    2.152   0.03142 *
## Groupwildbee:HabitatWF  0.67109    0.35439    1.894   0.05827 .
## Groupsyrphid:Grassland -0.56646    0.90007   -0.629   0.52912
## Groupwildbee:Grassland  0.23684    0.66586    0.356   0.72207
## Groupsyrphid:Forest    0.46663    0.38927    1.199   0.23064
## Groupwildbee:Forest    0.17426    0.31701    0.550   0.58253
## Groupsyrphid:Water     -1.07146    1.17052   -0.915   0.35999
## Groupwildbee:Water     -1.28766    0.83321   -1.545   0.12224
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Dispersion model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    2.7625     0.4307   6.413 1.42e-10 ***
## Groupsyrphid  -1.9103     0.5312  -3.596 0.000323 ***
## Groupwildbee  -1.1134     0.5418  -2.055 0.039882 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
print(model_parameters(mod.ab1))
```

```
## # Fixed Effects
```

```
##
## Parameter | Log-Mean | SE | 95% CI | z | p
## -----|-----|-----|-----|-----|-----
## (Intercept) | 3.70 | 0.16 | [ 3.38, 4.01] | 23.00 | < .001
## Group [syrphid] | -0.03 | 0.38 | [-0.77, 0.72] | -0.07 | 0.944
## Group [wildbee] | 0.51 | 0.29 | [-0.07, 1.08] | 1.73 | 0.084
## Habitat [FE] | 0.95 | 0.30 | [ 0.37, 1.53] | 3.21 | 0.001
## Habitat [GR] | 1.25 | 0.34 | [ 0.59, 1.91] | 3.71 | < .001
## Habitat [WF] | -0.31 | 0.20 | [-0.70, 0.09] | -1.53 | 0.126
## Grassland | -1.09 | 0.37 | [-1.81, -0.38] | -2.99 | 0.003
## Forest | -0.18 | 0.16 | [-0.51, 0.14] | -1.12 | 0.264
## Water | 0.63 | 0.47 | [-0.29, 1.55] | 1.33 | 0.182
## Group [syrphid] * Habitat [FE] | -0.20 | 0.70 | [-1.56, 1.16] | -0.29 | 0.774
## Group [wildbee] * Habitat [FE] | -0.16 | 0.60 | [-1.33, 1.02] | -0.26 | 0.792
## Group [syrphid] * Habitat [GR] | 1.32 | 0.84 | [-0.33, 2.97] | 1.57 | 0.116
## Group [wildbee] * Habitat [GR] | -0.11 | 0.59 | [-1.27, 1.04] | -0.19 | 0.845
## Group [syrphid] * Habitat [WF] | 1.02 | 0.47 | [ 0.09, 1.95] | 2.15 | 0.031
## Group [wildbee] * Habitat [WF] | 0.67 | 0.35 | [-0.02, 1.37] | 1.89 | 0.058
## Group [syrphid] * Grassland | -0.57 | 0.90 | [-2.33, 1.20] | -0.63 | 0.529
## Group [wildbee] * Grassland | 0.24 | 0.67 | [-1.07, 1.54] | 0.36 | 0.722
## Group [syrphid] * Forest | 0.47 | 0.39 | [-0.30, 1.23] | 1.20 | 0.231
## Group [wildbee] * Forest | 0.17 | 0.32 | [-0.45, 0.80] | 0.55 | 0.583
```

```
## Group [syrphid] * Water      |    -1.07 | 1.17 | [-3.37,  1.22] | -0.92 | 0.360
## Group [wildbee] * Water     |    -1.29 | 0.83 | [-2.92,  0.35] | -1.55 | 0.122
##
## # Dispersion
##
## Parameter      | Coefficient | SE |          95% CI |      z |      p
## -----
## (Intercept)    |          2.76 | 0.43 | [ 1.92,  3.61] |  6.41 | < .001
## Group [syrphid] |         -1.91 | 0.53 | [-2.95, -0.87] | -3.60 | < .001
## Group [wildbee] |         -1.11 | 0.54 | [-2.18, -0.05] | -2.05 | 0.040
##
## Uncertainty intervals (equal-tailed) and p-values (two-tailed) computed
## using a Wald z-distribution approximation.
```

posthoc comparison

```
contr.ab1 = emmeans(mod.ab1, pairwise ~ Group | Habitat)

print(contr.ab1)
```

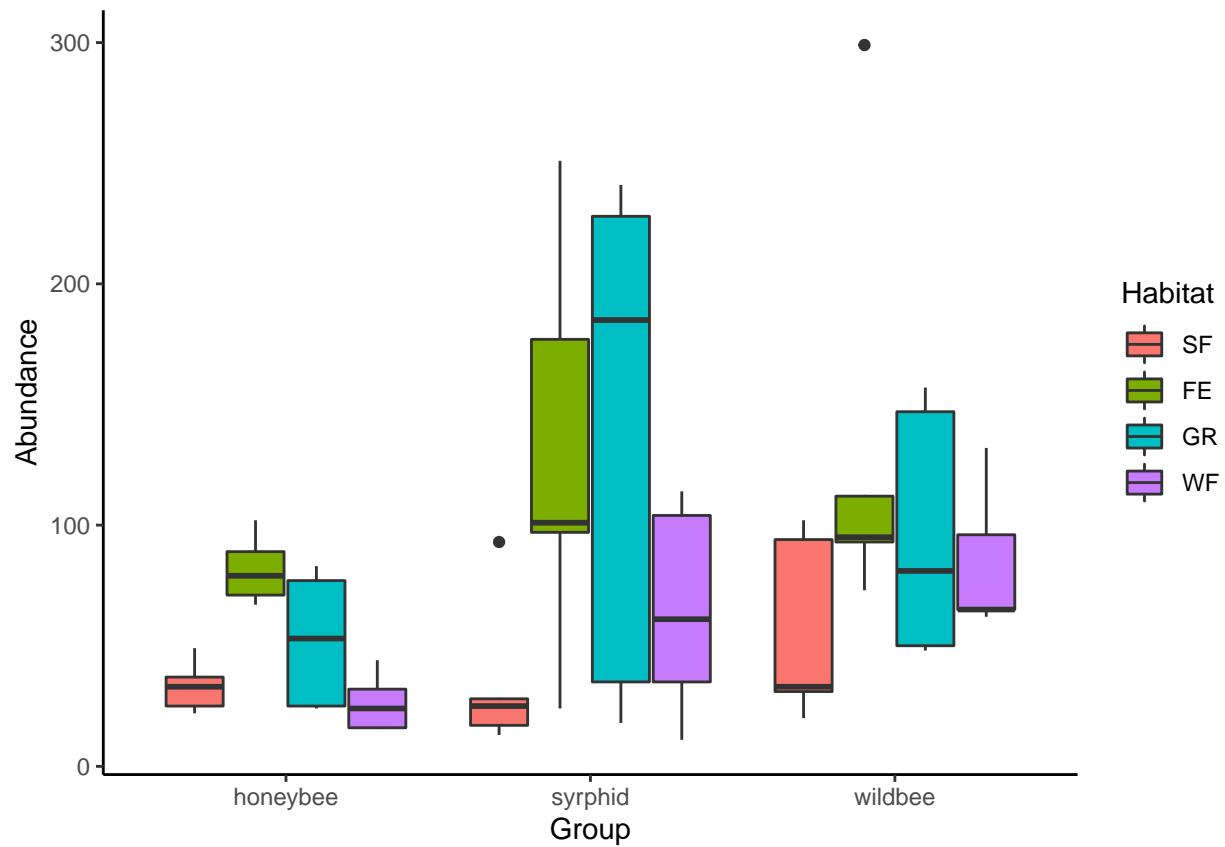
```
## $emmeans
## Habitat = SF:
##   Group    emmean    SE df lower.CL upper.CL
## honeybee   3.29 0.160 36     2.97     3.62
## syrphid    3.31 0.358 36     2.58     4.03
## wildbee    3.89 0.250 36     3.38     4.39
##
## Habitat = FE:
##   Group    emmean    SE df lower.CL upper.CL
## honeybee   4.24 0.232 36     3.77     4.71
## syrphid    4.06 0.504 36     3.04     5.08
## wildbee    4.68 0.390 36     3.89     5.47
##
## Habitat = GR:
##   Group    emmean    SE df lower.CL upper.CL
## honeybee   4.54 0.255 36     4.02     5.06
## syrphid    5.88 0.586 36     4.69     7.07
## wildbee    5.02 0.372 36     4.26     5.77
##
## Habitat = WF:
##   Group    emmean    SE df lower.CL upper.CL
## honeybee   2.98 0.185 36     2.61     3.36
## syrphid    4.02 0.347 36     3.32     4.73
## wildbee    4.25 0.270 36     3.70     4.80
##
```



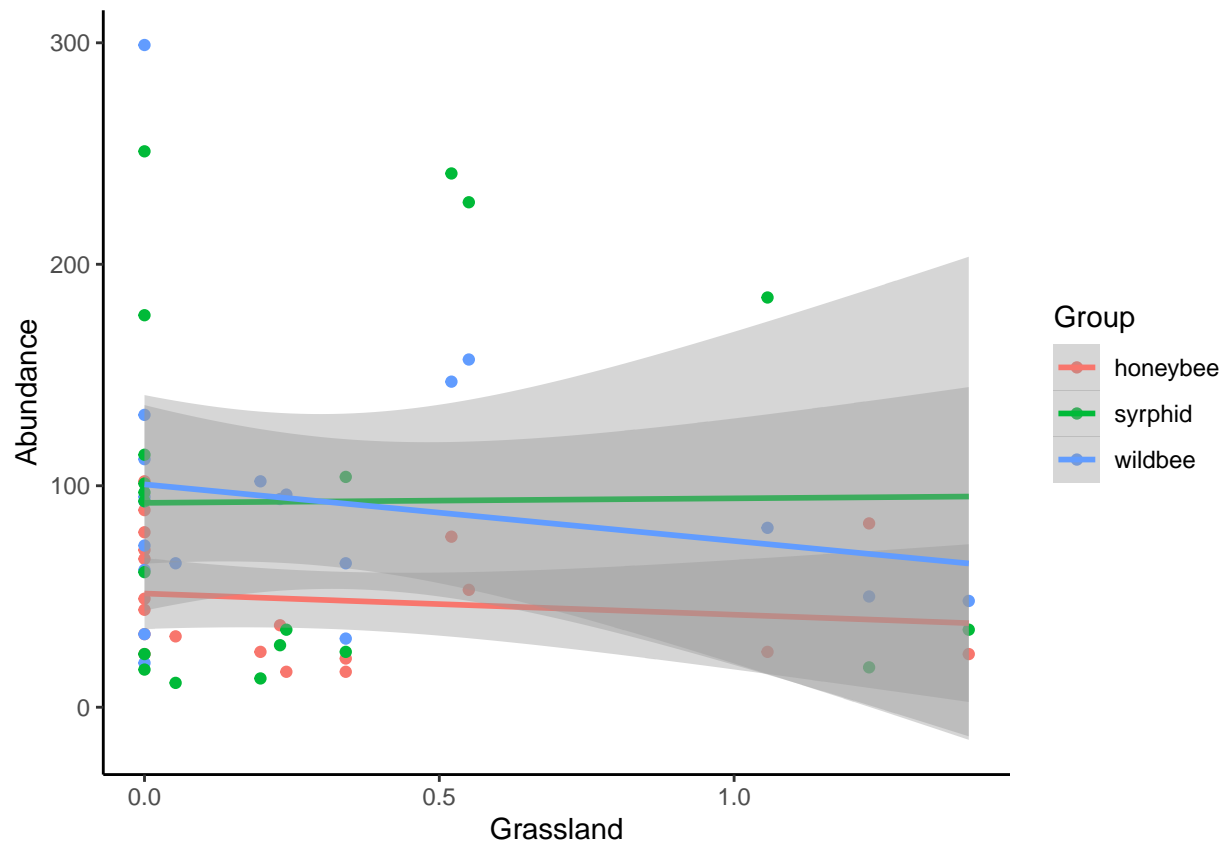
```
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
##
## $contrasts
## Habitat = SF:
## contrast      estimate      SE df t.ratio p.value
## honeybee - syrphid -0.0174 0.392 36 -0.044 0.9989
## honeybee - wildbee -0.5943 0.296 36 -2.005 0.1255
## syrphid - wildbee -0.5769 0.436 36 -1.323 0.3920
##
## Habitat = FE:
## contrast      estimate      SE df t.ratio p.value
## honeybee - syrphid  0.1820 0.554 36  0.328 0.9424
## honeybee - wildbee -0.4362 0.454 36 -0.961 0.6056
## syrphid - wildbee -0.6182 0.637 36 -0.971 0.5999
##
## Habitat = GR:
## contrast      estimate      SE df t.ratio p.value
## honeybee - syrphid -1.3386 0.639 36 -2.095 0.1051
## honeybee - wildbee -0.4795 0.451 36 -1.063 0.5426
## syrphid - wildbee  0.8591 0.694 36  1.238 0.4388
##
## Habitat = WF:
## contrast      estimate      SE df t.ratio p.value
## honeybee - syrphid -1.0392 0.394 36 -2.639 0.0320
## honeybee - wildbee -1.2654 0.327 36 -3.864 0.0013
## syrphid - wildbee -0.2262 0.440 36 -0.514 0.8651
##
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 3 estimates
```

plots

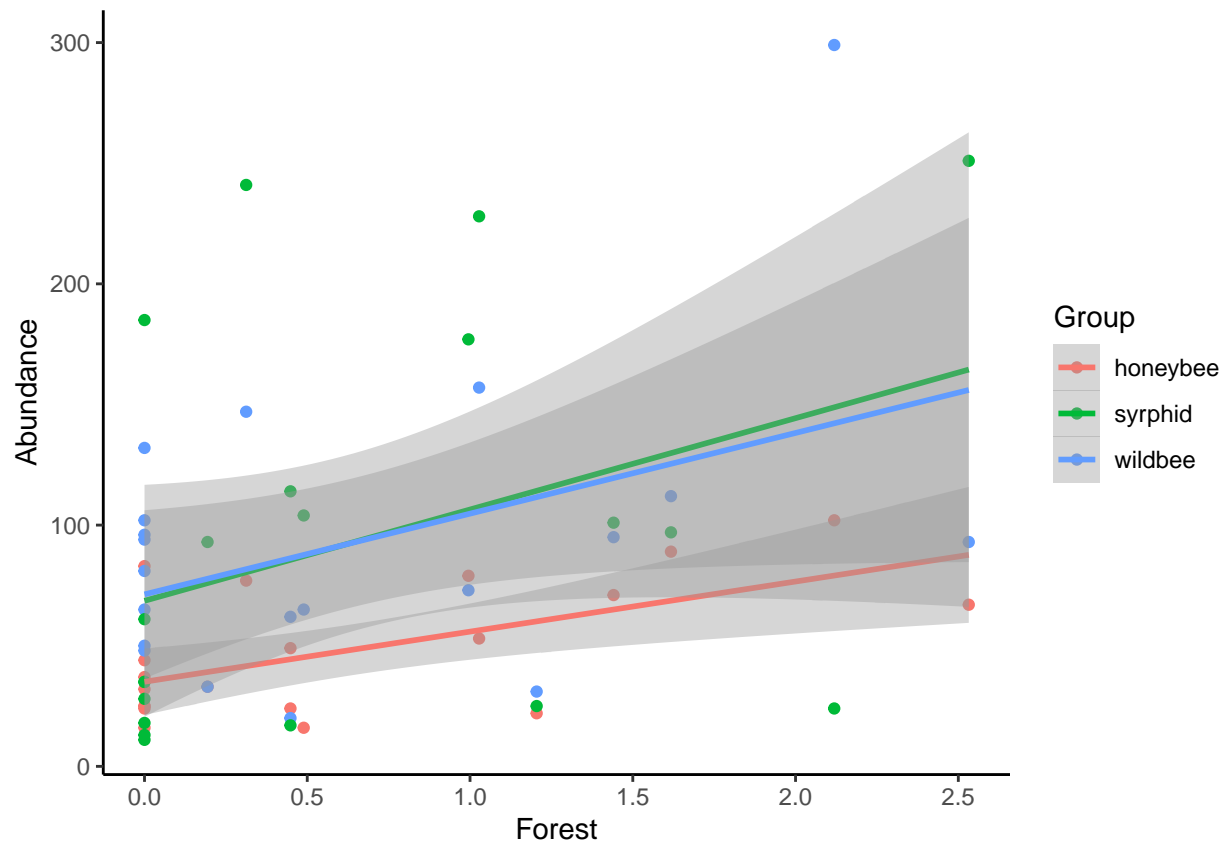
```
ggplot(data_calc, aes(x = Group,
                      y = Abundance,
                      fill = Habitat)) +
  geom_boxplot(position=position_dodge(0.8)) +
  theme_classic()
```



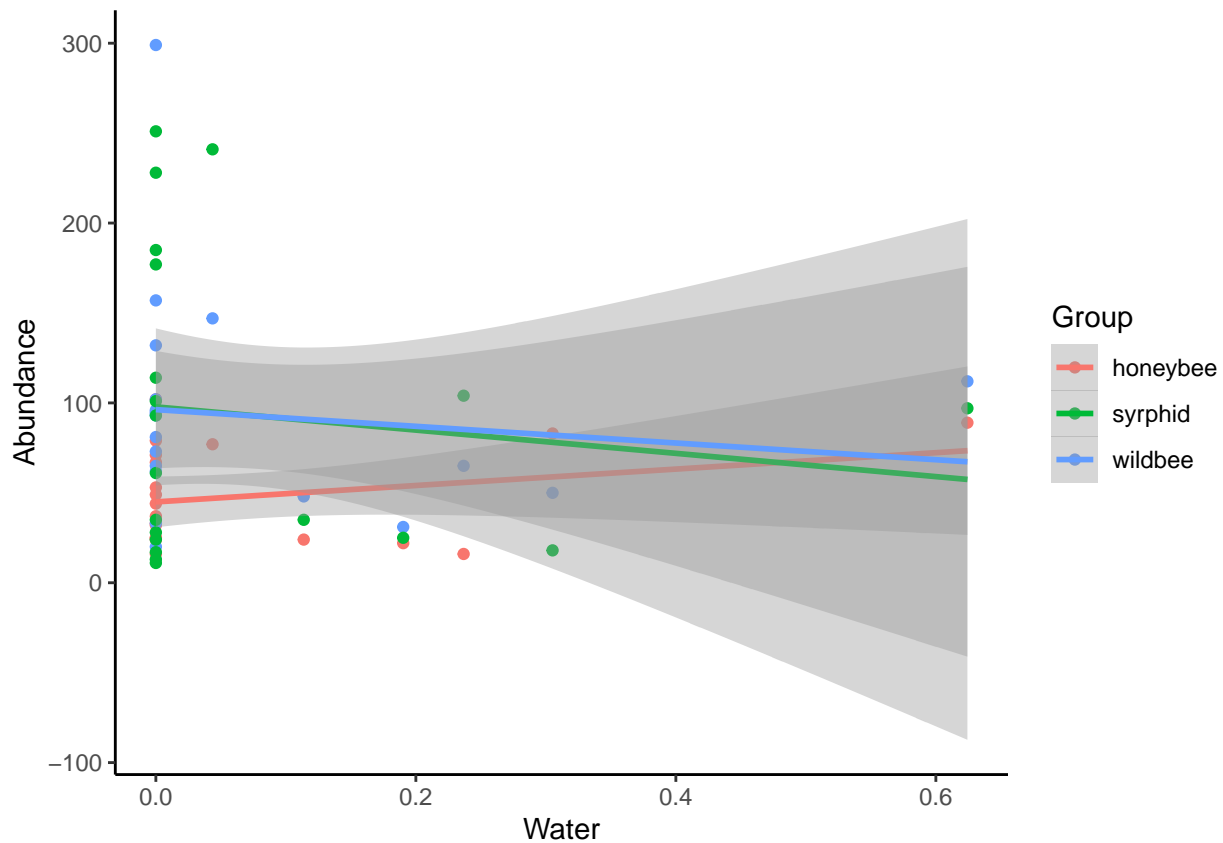
```
ggplot(data_calc, aes(x = Grassland,
                      y = Abundance,
                      colour = Group)) +
  geom_point()+
  geom_smooth(method = lm, formula = y ~ x) +
  theme_classic()
```



```
ggplot(data_calc, aes(x = Forest,
                      y = Abundance,
                      colour = Group)) +
  geom_point()+
  geom_smooth(method = lm, formula = y ~ x) +
  theme_classic()
```



```
ggplot(data_calc, aes(x = Water,
                      y = Abundance,
                      colour = Group)) +
  geom_point()+
  geom_smooth(method = lm, formula = y ~ x) +
  theme_classic()
```



####

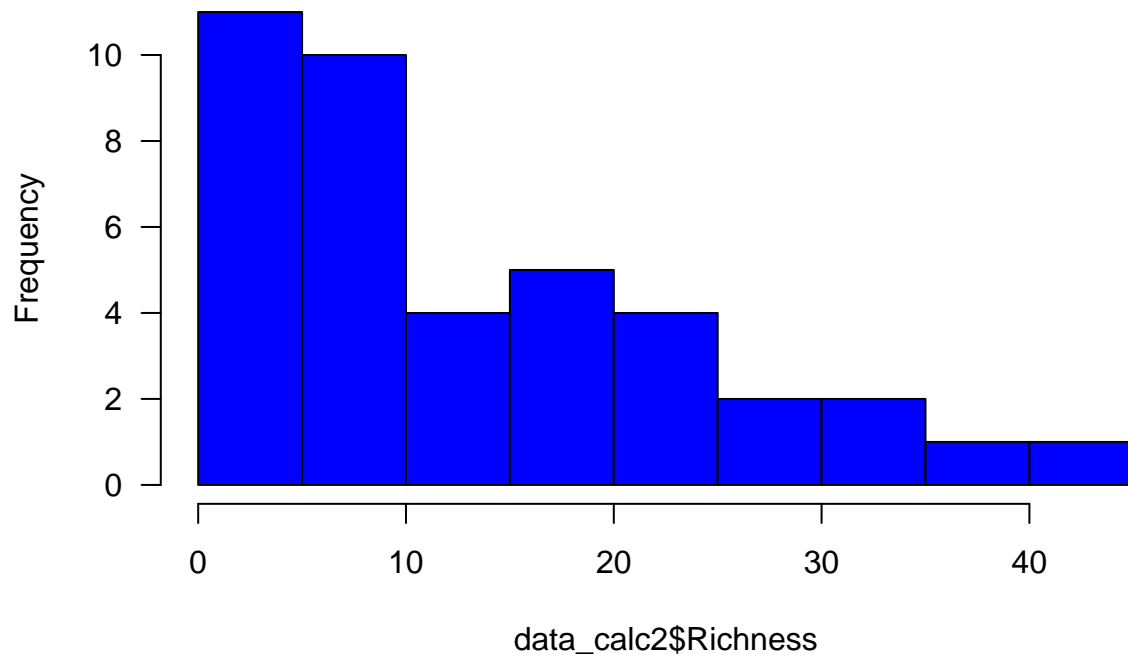
Pollinator richness

```
data_calc2 = data_calc[-(1:20),]
data_calc2$Richness = NA

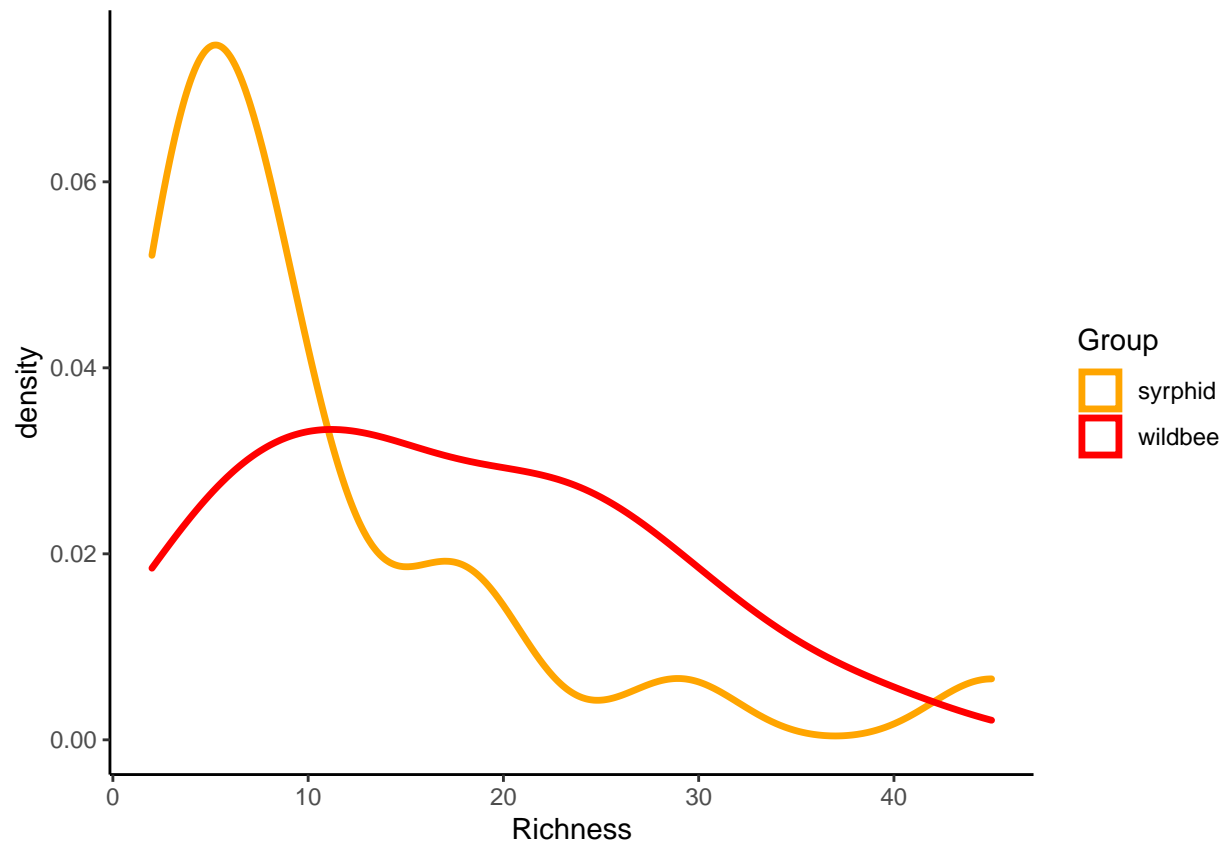
data_calc2$Richness[which(data_calc2$Group=="wildbee")] =
  specnumber(wildbees[, -1])
data_calc2$Richness[which(data_calc2$Group=="syrphid")] =
  specnumber(syrphids[, -1])

hist(data_calc2$Richness, 10, col = 'blue', las = 1)
```

Histogram of data_calc2\$Richness



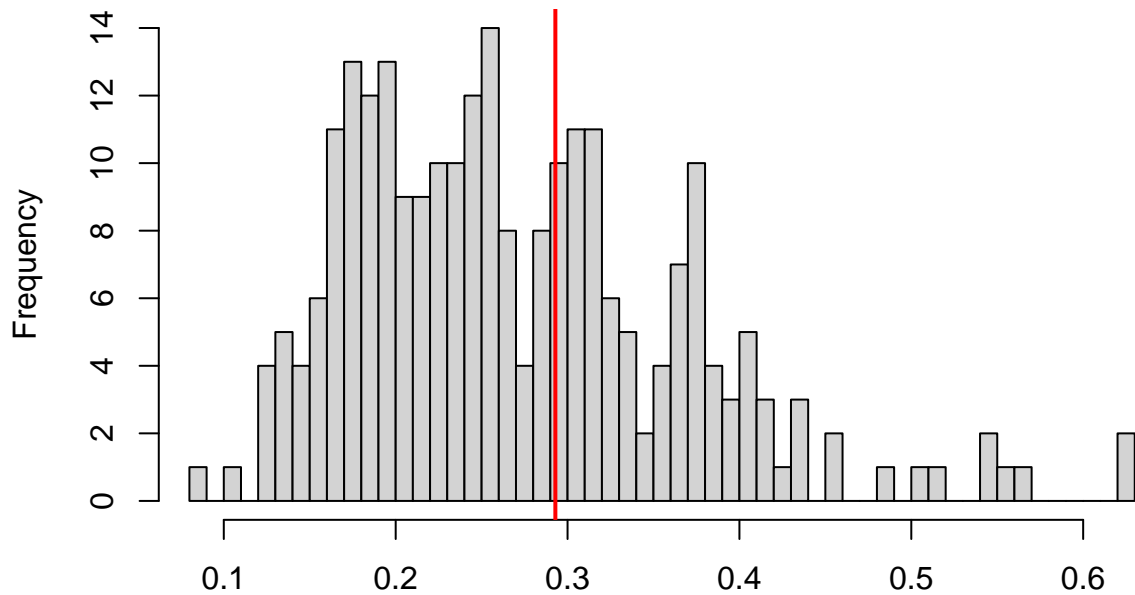
```
ggplot(data_calc2, aes(x = Richness, colour = Group)) +  
  theme_classic() +  
  geom_density(lwd = 1.2, linetype = 1) +  
  scale_color_manual(values = c("orange", "red"))
```



```
# model
mod.rich = glmmTMB(Richness ~ Group*Habitat +
                    Group* (Grassland + Forest + Water),
                    family = nbinom2,
                    dispformula = ~Group,
                    data = data_calc2)
```

```
testDispersion(mod.rich)
```

DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.744

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data:  simulationOutput
## dispersion = 1.085, p-value = 0.744
## alternative hypothesis: two.sided
```

```
Anova(mod.rich)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
```

```
##
```

```
## Response: Richness
```

	Chisq	Df	Pr(>Chisq)	
## Group	16.1729	1	5.781e-05	***
## Habitat	37.7656	3	3.169e-08	***
## Grassland	1.0217	1	0.31213	
## Forest	0.8284	1	0.36275	
## Water	0.0275	1	0.86825	
## Group:Habitat	2.9638	3	0.39723	
## Group:Grassland	0.5710	1	0.44987	
## Group:Forest	10.6687	1	0.00109	**
## Group:Water	3.7130	1	0.05399	.
## ---				


```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cohens_f(aov(mod.rich))
```

```
## # Effect Size for ANOVA (Type I)
```

```
##
```

```
## Parameter          | Cohen's f (partial) |          95% CI
```

```
## -----
```

```
## Group              |              2.47 | [1.80, Inf]
```

```
## Habitat            |              1.24 | [0.76, Inf]
```

```
## Grassland          |              0.14 | [0.00, Inf]
```

```
## Forest             |             9.29e-03 | [0.00, Inf]
```

```
## Water              |              0.04 | [0.00, Inf]
```

```
## Group:Habitat      |              0.13 | [0.00, Inf]
```

```
## Group:Grassland    |              0.10 | [0.00, Inf]
```

```
## Group:Forest       |              0.53 | [0.18, Inf]
```

```
## Group:Water        |              0.45 | [0.10, Inf]
```

```
##
```

```
## - One-sided CIs: upper bound fixed at [Inf].
```

```
summary(mod.rich)
```

```
## Family: nbinom2 ( log )
```

```
## Formula:
```

```
## Richness ~ Group * Habitat + Group * (Grassland + Forest + Water)
```

```
## Dispersion:                ~Group
```

```
## Data: data_calc2
```

```
##
```

```
##      AIC      BIC  logLik deviance df.resid
```

```
##    262.7    289.7   -115.4    230.7      24
```

```
##
```

```
##
```

```
## Conditional model:
```

```
##              Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept)      1.309499   0.306480   4.273 1.93e-05 ***
```

```
## Groupwildbee      1.039258   0.360984   2.879  0.00399 **
```

```
## HabitatFE         0.786824   0.470316   1.673  0.09433 .
```

```
## HabitatGR         1.201498   0.531937   2.259  0.02390 *
```

```
## HabitatWF         0.155514   0.376927   0.413  0.67991
```

```
## Grassland         0.061074   0.570771   0.107  0.91479
```

```
## Forest            0.537164   0.251915   2.132  0.03298 *
```

```
## Water            -1.214446   0.755455  -1.608  0.10793
```

```
## Groupwildbee:HabitatFE  0.922381   0.573254   1.609  0.10761
```

```
## Groupwildbee:HabitatGR  0.017665   0.638034   0.028  0.97791
```

```
## Groupwildbee:HabitatWF -0.004573   0.444704  -0.010  0.99180
```

```
## Groupwildbee:Grassland -0.508119   0.672436  -0.756  0.44987
```

```
## Groupwildbee:Forest    -1.010241    0.309292   -3.266   0.00109 **
## Groupwildbee:Water     1.662077    0.862565    1.927   0.05399 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Dispersion model:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)    2.0963     0.5207   4.026 5.67e-05 ***
## Groupwildbee    1.3248     1.2455   1.064   0.287
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
print(model_parameters(mod.rich))
```

```
## # Fixed Effects
##
## Parameter | Log-Mean | SE | 95% CI | z | p
## -----|-----|-----|-----|-----|-----
## (Intercept) | 1.31 | 0.31 | [ 0.71, 1.91] | 4.27 | < .001
## Group [wildbee] | 1.04 | 0.36 | [ 0.33, 1.75] | 2.88 | 0.004
## Habitat [FE] | 0.79 | 0.47 | [-0.13, 1.71] | 1.67 | 0.094
## Habitat [GR] | 1.20 | 0.53 | [ 0.16, 2.24] | 2.26 | 0.024
## Habitat [WF] | 0.16 | 0.38 | [-0.58, 0.89] | 0.41 | 0.680
## Grassland | 0.06 | 0.57 | [-1.06, 1.18] | 0.11 | 0.915
## Forest | 0.54 | 0.25 | [ 0.04, 1.03] | 2.13 | 0.033
## Water | -1.21 | 0.76 | [-2.70, 0.27] | -1.61 | 0.108
## Group [wildbee] * Habitat [FE] | 0.92 | 0.57 | [-0.20, 2.05] | 1.61 | 0.108
## Group [wildbee] * Habitat [GR] | 0.02 | 0.64 | [-1.23, 1.27] | 0.03 | 0.978
## Group [wildbee] * Habitat [WF] | -4.57e-03 | 0.44 | [-0.88, 0.87] | -0.01 | 0.992
## Group [wildbee] * Grassland | -0.51 | 0.67 | [-1.83, 0.81] | -0.76 | 0.450
## Group [wildbee] * Forest | -1.01 | 0.31 | [-1.62, -0.40] | -3.27 | 0.001
## Group [wildbee] * Water | 1.66 | 0.86 | [-0.03, 3.35] | 1.93 | 0.054
##
## # Dispersion
##
## Parameter | Coefficient | SE | 95% CI | z | p
## -----|-----|-----|-----|-----|-----
## (Intercept) | 2.10 | 0.52 | [ 1.08, 3.12] | 4.03 | < .001
## Group [wildbee] | 1.32 | 1.25 | [-1.12, 3.77] | 1.06 | 0.287
##
## Uncertainty intervals (equal-tailed) and p-values (two-tailed) computed
## using a Wald z-distribution approximation.
```

```
#### posthoc comparison
```

```

contr.rich = emmeans(mod.rich, pairwise ~ Group | Habitat)

print(contr.rich$contrasts)

```

```

## Habitat = SF:
## contrast      estimate      SE df t.ratio p.value
## syrphid - wildbee  -0.361 0.350 24  -1.030  0.3135
##
## Habitat = FE:
## contrast      estimate      SE df t.ratio p.value
## syrphid - wildbee  -1.283 0.420 24  -3.052  0.0055
##
## Habitat = GR:
## contrast      estimate      SE df t.ratio p.value
## syrphid - wildbee  -0.378 0.461 24  -0.820  0.4201
##
## Habitat = WF:
## contrast      estimate      SE df t.ratio p.value
## syrphid - wildbee  -0.356 0.367 24  -0.970  0.3415
##
## Results are given on the log (not the response) scale.

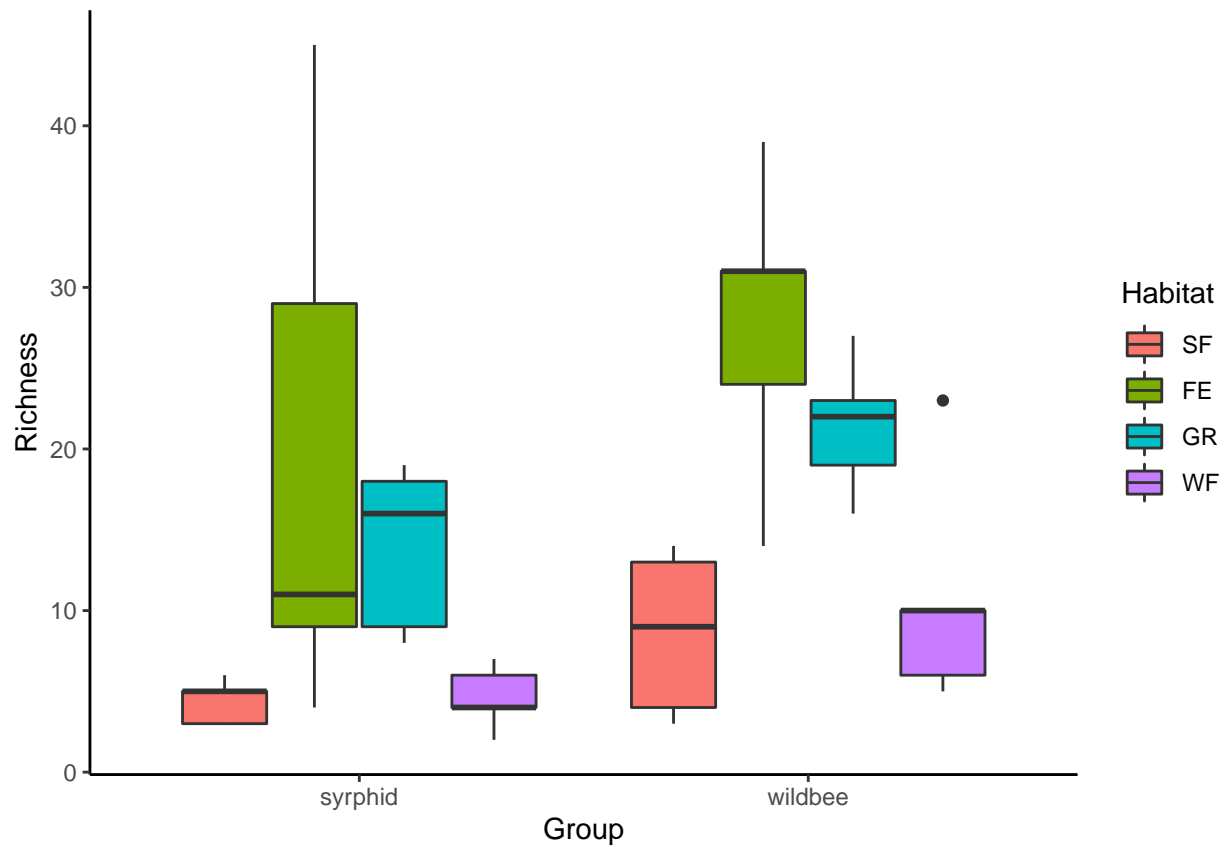
```

```

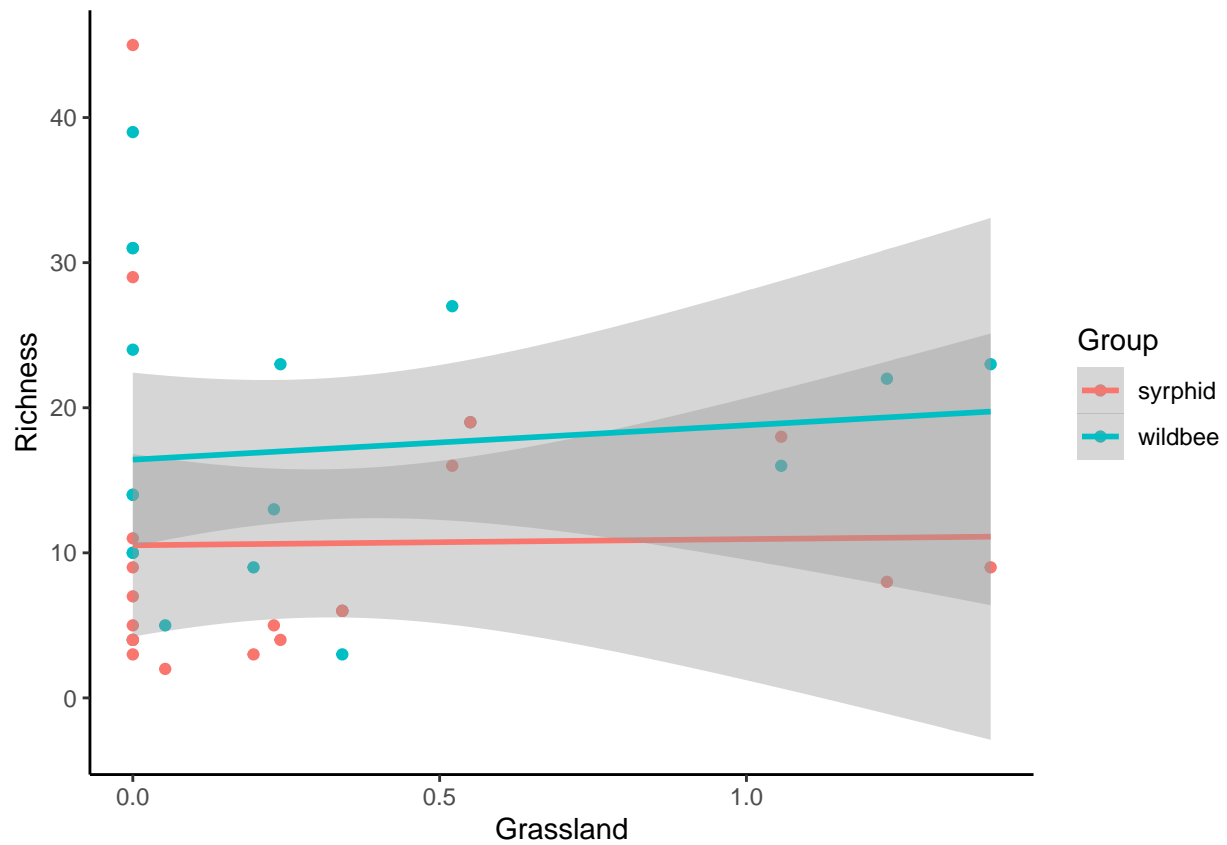
## plots

ggplot(data_calc2, aes(x = Group,
                       y = Richness,
                       fill = Habitat)) +
  geom_boxplot(position=position_dodge(0.8)) +
  theme_classic()

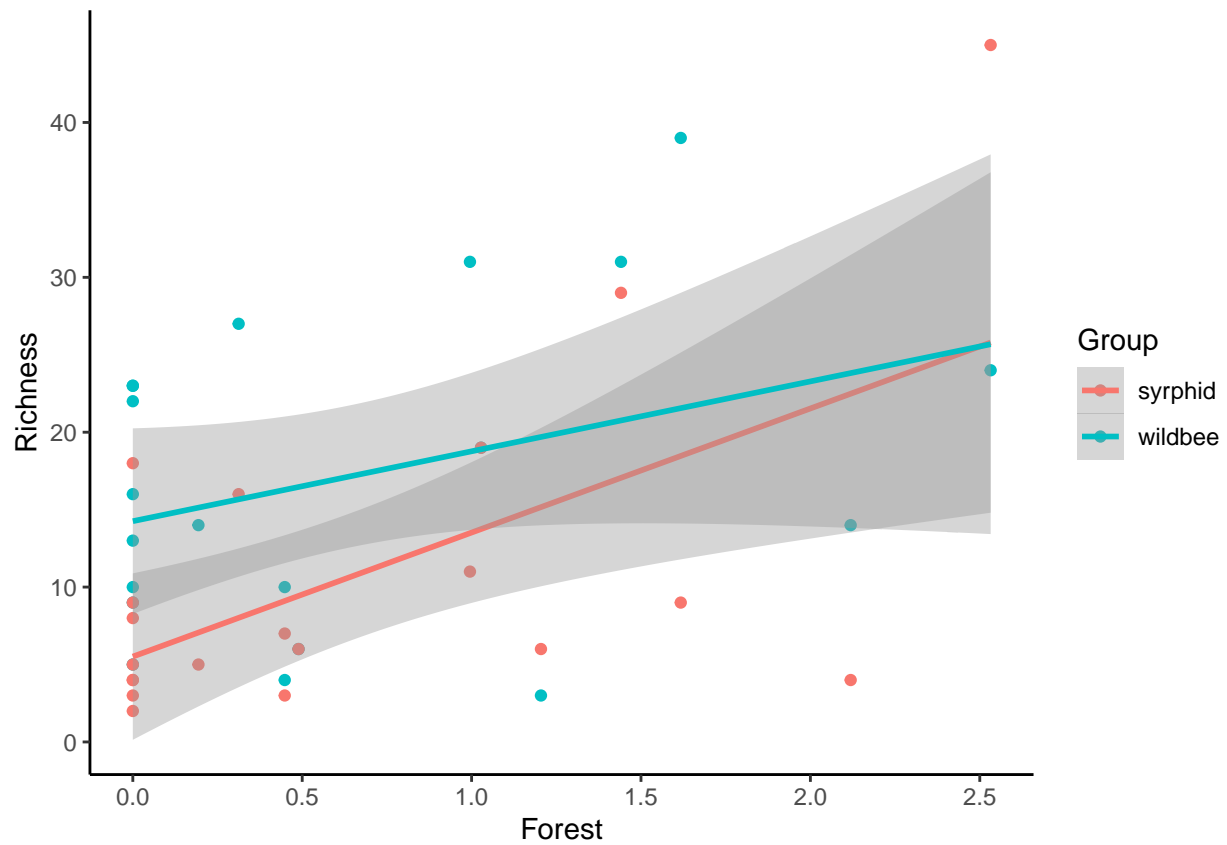
```



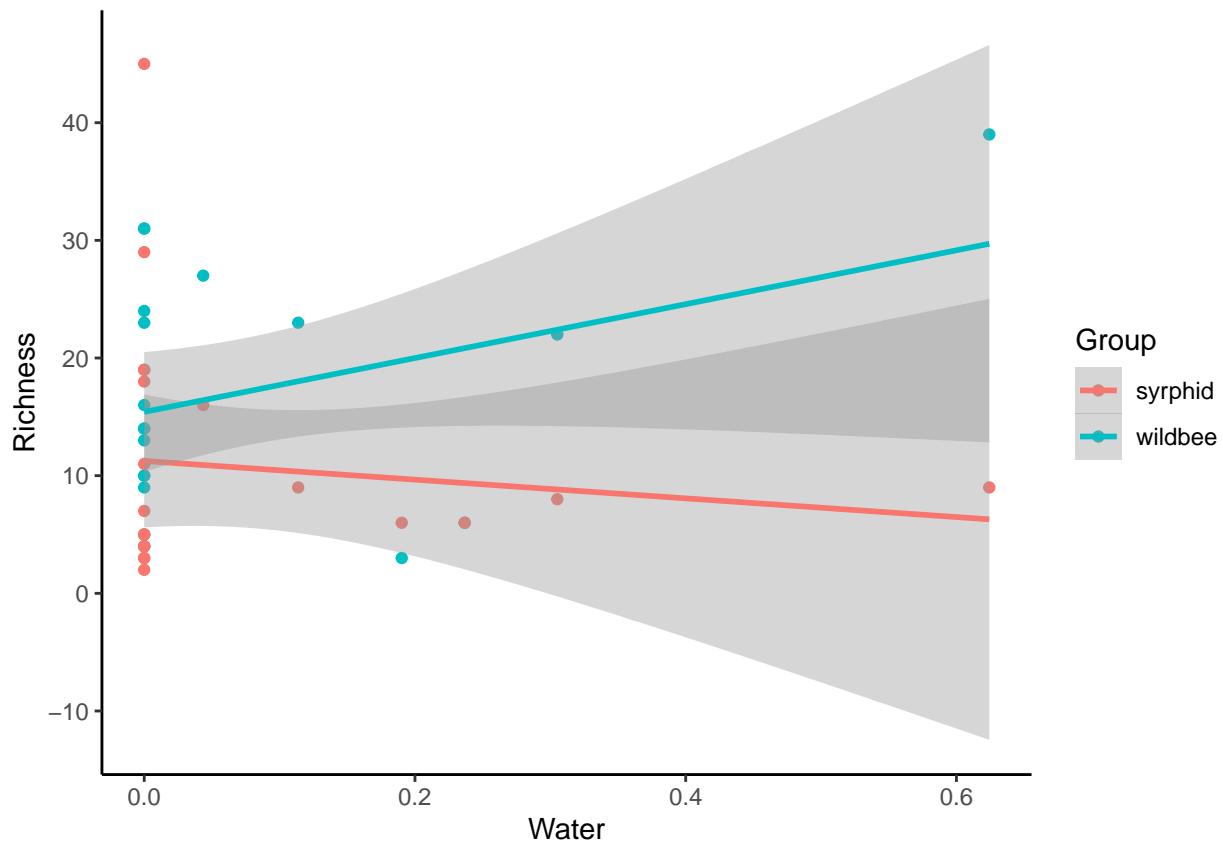
```
ggplot(data_calc2, aes(x = Grassland,
                        y = Richness,
                        colour = Group)) +
  geom_point()+
  geom_smooth(method = lm, formula = y ~ x) +
  theme_classic()
```



```
ggplot(data_calc2, aes(x = Forest,
                       y = Richness,
                       colour = Group)) +
  geom_point()+
  geom_smooth(method = lm, formula = y ~ x) +
  theme_classic()
```



```
ggplot(data_calc2, aes(x = Water,
                        y = Richness,
                        colour = Group)) +
  geom_point()+
  geom_smooth(method = lm, formula = y ~ x) +
  theme_classic()
```



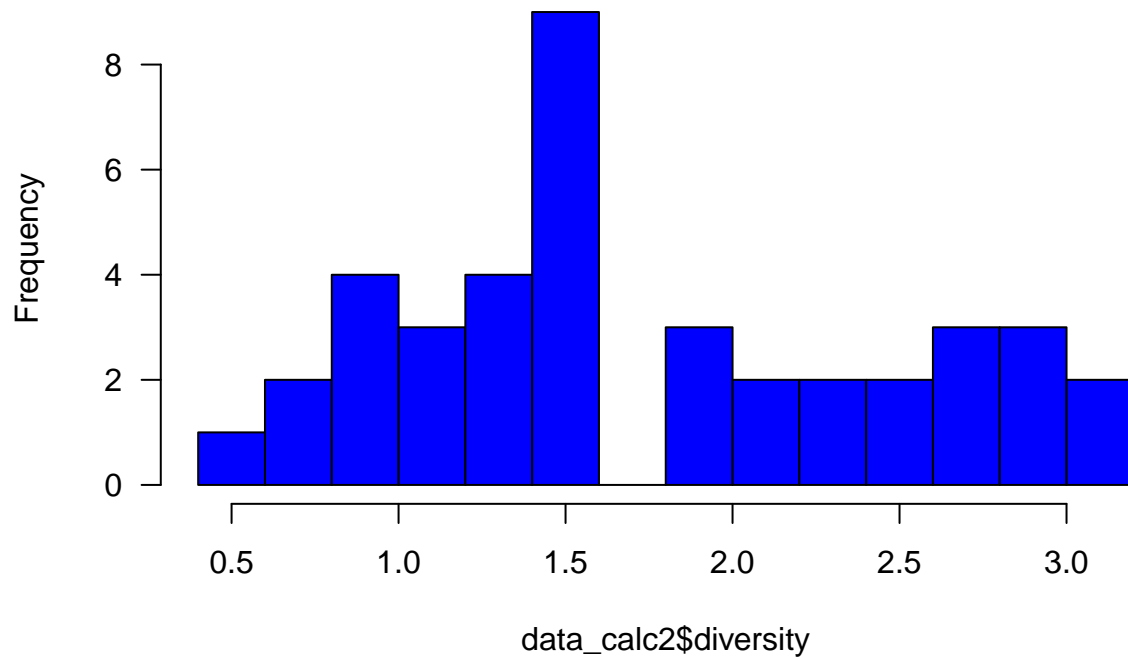
Pollinator diversity

```
data_calc2$diversity = NA
```

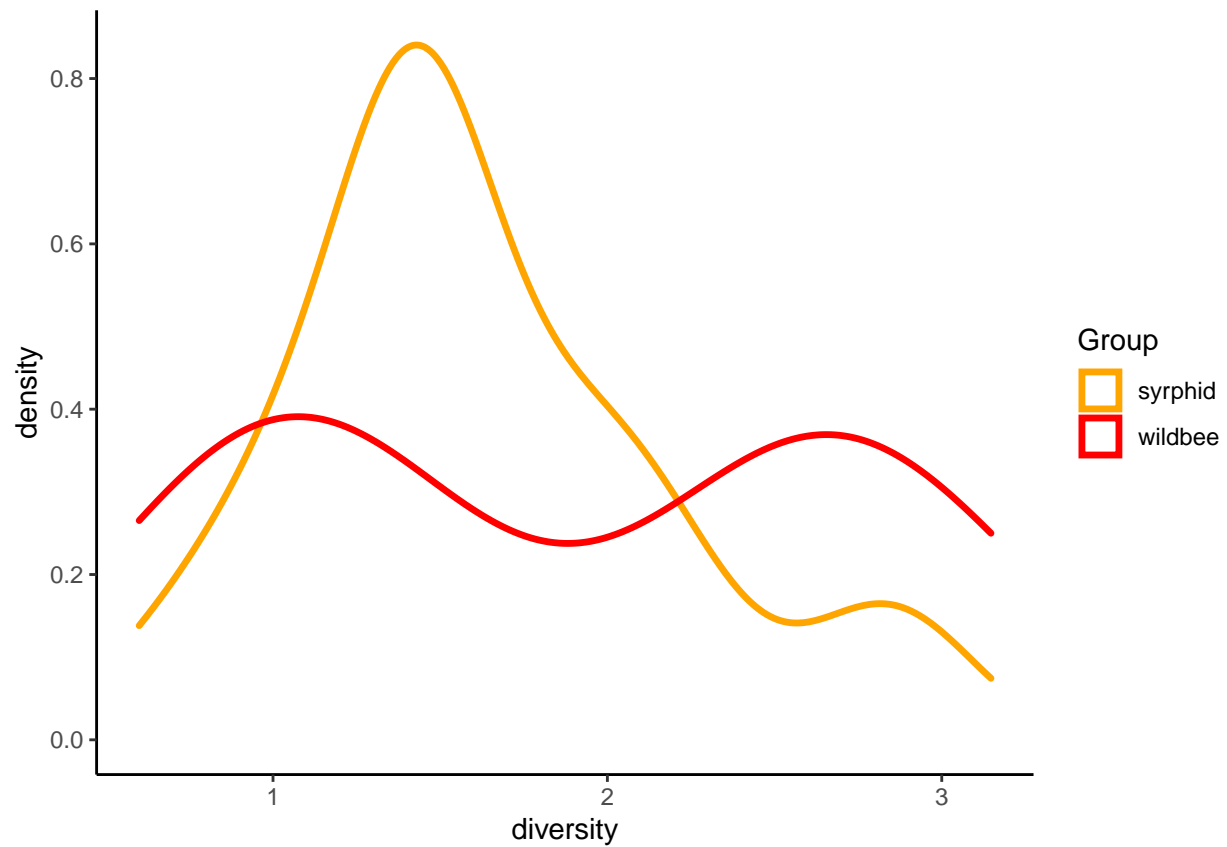
```
data_calc2$diversity[which(data_calc2$Group=="wildbee")] =  
  diversity(wildbees[, -1], "shannon")  
data_calc2$diversity[which(data_calc2$Group=="syrphid")] =  
  diversity(syrphids[, -1], "shannon")
```

```
hist(data_calc2$diversity, 10, col = 'blue', las = 1)
```

Histogram of data_calc2\$diversity



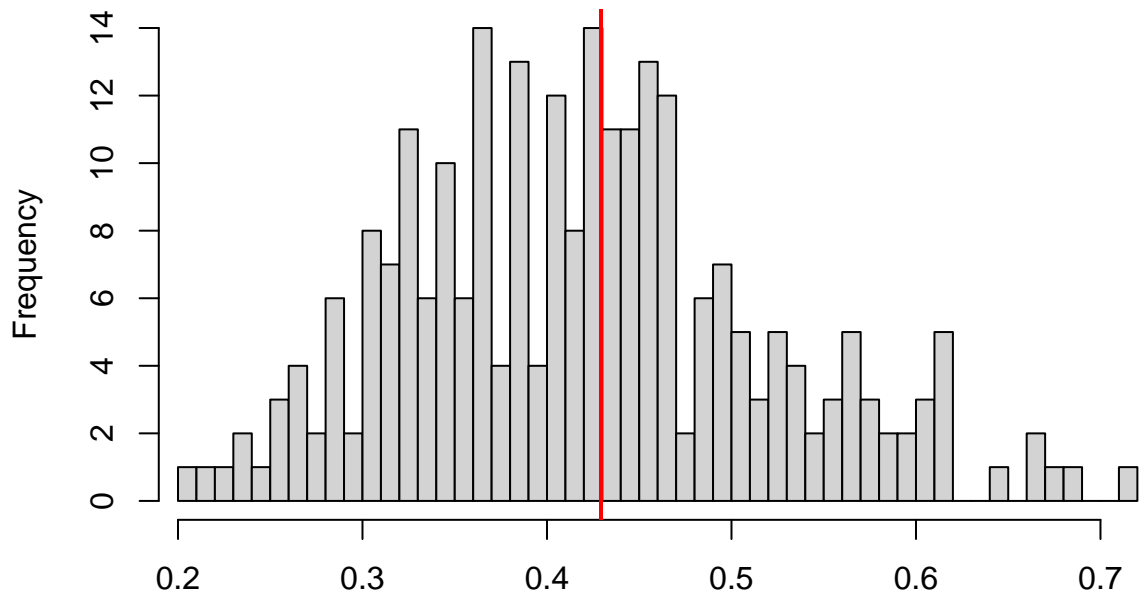
```
ggplot(data_calc2, aes(x = diversity, colour = Group)) +  
  theme_classic() +  
  geom_density(lwd = 1.2, linetype = 1) +  
  scale_color_manual(values = c("orange", "red"))
```

```
# model
mod.div = glmmTMB(diversity ~ Group*Habitat +
  Group* (Grassland + Forest + Water),
  family = gaussian,
  dispformula = ~Group,
  data = data_calc2)
```

```
testDispersion(mod.div)
```

DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



Simulated values, red line = fitted model. p-value (two.sided) = 0.888

```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data:  simulationOutput
## dispersion = 1.021, p-value = 0.888
## alternative hypothesis: two.sided
```

```
Anova(mod.div)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
```

```
##
```

```
## Response: diversity
```

	Chisq	Df	Pr(>Chisq)
## Group	2.3930	1	0.121881
## Habitat	12.8661	3	0.004935 **
## Grassland	0.1061	1	0.744572
## Forest	0.0763	1	0.782326
## Water	0.1855	1	0.666702
## Group:Habitat	8.3679	3	0.038991 *
## Group:Grassland	0.9019	1	0.342265
## Group:Forest	7.8241	1	0.005155 **
## Group:Water	2.5268	1	0.111930

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cohens_f(aov(mod.div))
```

```
## # Effect Size for ANOVA (Type I)
```

```
##
```

```
## Parameter          | Cohen's f (partial) |          95% CI
```

```
## -----
```

```
## Group              |              3.66 | [2.74, Inf]
```

```
## Habitat            |              1.00 | [0.54, Inf]
```

```
## Grassland          |              0.03 | [0.00, Inf]
```

```
## Forest             |              0.13 | [0.00, Inf]
```

```
## Water              |              0.03 | [0.00, Inf]
```

```
## Group:Habitat      |              0.23 | [0.00, Inf]
```

```
## Group:Grassland    |              0.03 | [0.00, Inf]
```

```
## Group:Forest       |              0.42 | [0.05, Inf]
```

```
## Group:Water        |              0.25 | [0.00, Inf]
```

```
##
```

```
## - One-sided CIs: upper bound fixed at [Inf].
```

```
summary(mod.div)
```

```
## Family: gaussian ( identity )
```

```
## Formula:
```

```
## diversity ~ Group * Habitat + Group * (Grassland + Forest + Water)
```

```
## Dispersion:                ~Group
```

```
## Data: data_calc2
```

```
##
```

```
##      AIC      BIC  logLik deviance df.resid
```

```
##      83.1     110.1   -25.6     51.1      24
```

```
##
```

```
##
```

```
## Conditional model:
```

```
##              Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept)      1.08755    0.20099   5.411 6.27e-08 ***
```

```
## Groupwildbee      0.39403    0.36136   1.090  0.27553
```

```
## HabitatFE         0.34253    0.36567   0.937  0.34891
```

```
## HabitatGR         0.55730    0.41990   1.327  0.18443
```

```
## HabitatWF         0.07344    0.24113   0.305  0.76069
```

```
## Grassland         0.36182    0.45285   0.799  0.42430
```

```
## Forest            0.36937    0.20688   1.785  0.07420 .
```

```
## Water            -0.74112    0.59670  -1.242  0.21422
```

```
## Groupwildbee:HabitatFE 1.74700    0.65744   2.657  0.00788 **
```

```
## Groupwildbee:HabitatGR 0.77644    0.75493   1.028  0.30372
```

```
## Groupwildbee:HabitatWF -0.06140    0.43353  -0.142  0.88737
```

```
## Groupwildbee:Grassland -0.77323    0.81418  -0.950  0.34226
```

```
## Groupwildbee:Forest    -1.04043    0.37196  -2.797  0.00516 **
## Groupwildbee:Water     1.70531     1.07281   1.590  0.11193
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Dispersion model:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.9619     0.3162  -6.204  5.5e-10 ***
## Groupwildbee   0.8031     0.4472   1.796  0.0725 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
print(model_parameters(mod.div))
```

```
## # Fixed Effects
```

```
##
## Parameter | Coefficient | SE | 95% CI | z | p
## -----|-----|-----|-----|-----|-----
## (Intercept) | 1.09 | 0.20 | [ 0.69, 1.48] | 5.41 | < .001
## Group [wildbee] | 0.39 | 0.36 | [-0.31, 1.10] | 1.09 | 0.276
## Habitat [FE] | 0.34 | 0.37 | [-0.37, 1.06] | 0.94 | 0.349
## Habitat [GR] | 0.56 | 0.42 | [-0.27, 1.38] | 1.33 | 0.184
## Habitat [WF] | 0.07 | 0.24 | [-0.40, 0.55] | 0.30 | 0.761
## Grassland | 0.36 | 0.45 | [-0.53, 1.25] | 0.80 | 0.424
## Forest | 0.37 | 0.21 | [-0.04, 0.77] | 1.79 | 0.074
## Water | -0.74 | 0.60 | [-1.91, 0.43] | -1.24 | 0.214
## Group [wildbee] * Habitat [FE] | 1.75 | 0.66 | [ 0.46, 3.04] | 2.66 | 0.008
## Group [wildbee] * Habitat [GR] | 0.78 | 0.75 | [-0.70, 2.26] | 1.03 | 0.304
## Group [wildbee] * Habitat [WF] | -0.06 | 0.43 | [-0.91, 0.79] | -0.14 | 0.887
## Group [wildbee] * Grassland | -0.77 | 0.81 | [-2.37, 0.82] | -0.95 | 0.342
## Group [wildbee] * Forest | -1.04 | 0.37 | [-1.77, -0.31] | -2.80 | 0.005
## Group [wildbee] * Water | 1.71 | 1.07 | [-0.40, 3.81] | 1.59 | 0.112
##
```

```
## # Dispersion
```

```
##
## Parameter | Coefficient | SE | 95% CI | z | p
## -----|-----|-----|-----|-----|-----
## (Intercept) | -1.96 | 0.32 | [-2.58, -1.34] | -6.20 | < .001
## Group [wildbee] | 0.80 | 0.45 | [-0.07, 1.68] | 1.80 | 0.073
##
```

```
## Uncertainty intervals (equal-tailed) and p-values (two-tailed) computed
## using a Wald z-distribution approximation.
```

```
## contrasts
```

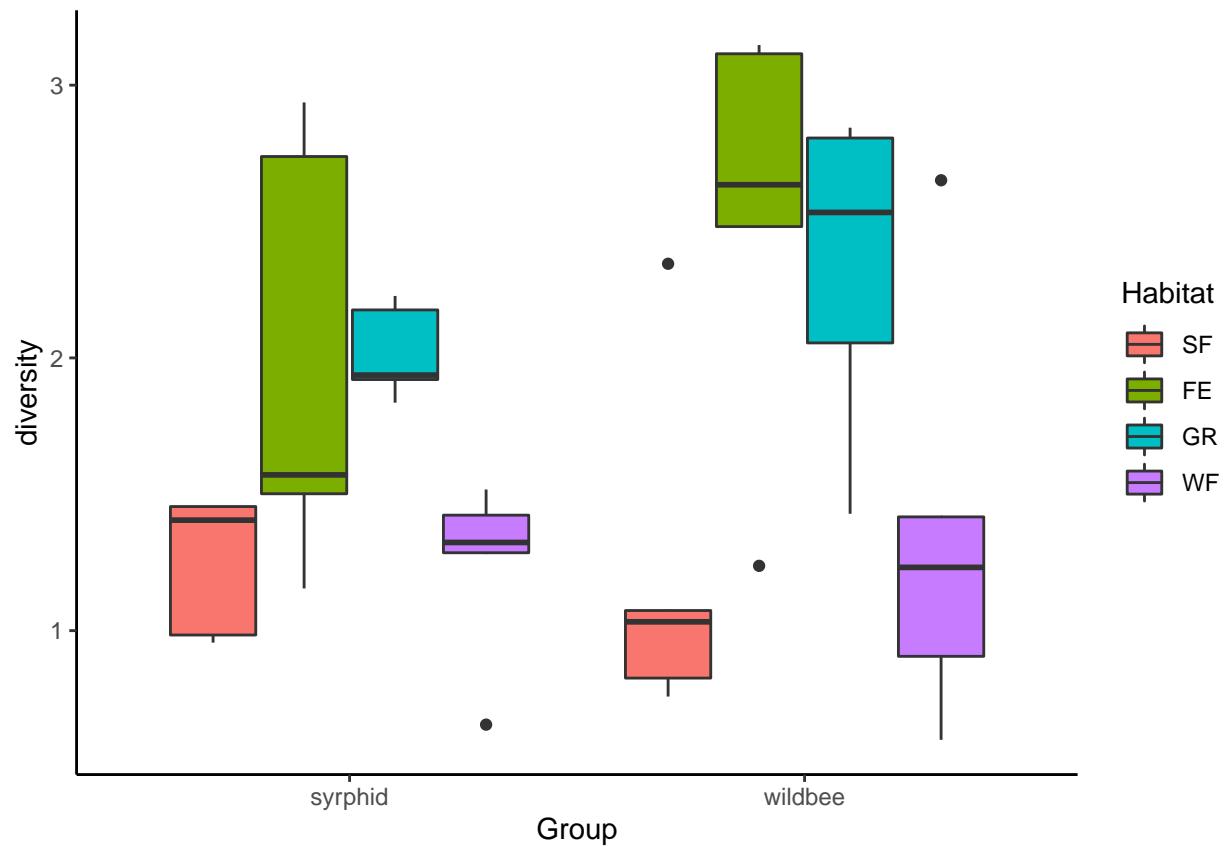
```
contr.div = emmeans(mod.div, pairwise ~ Group | Habitat)

print(contr.div$contrasts)
```

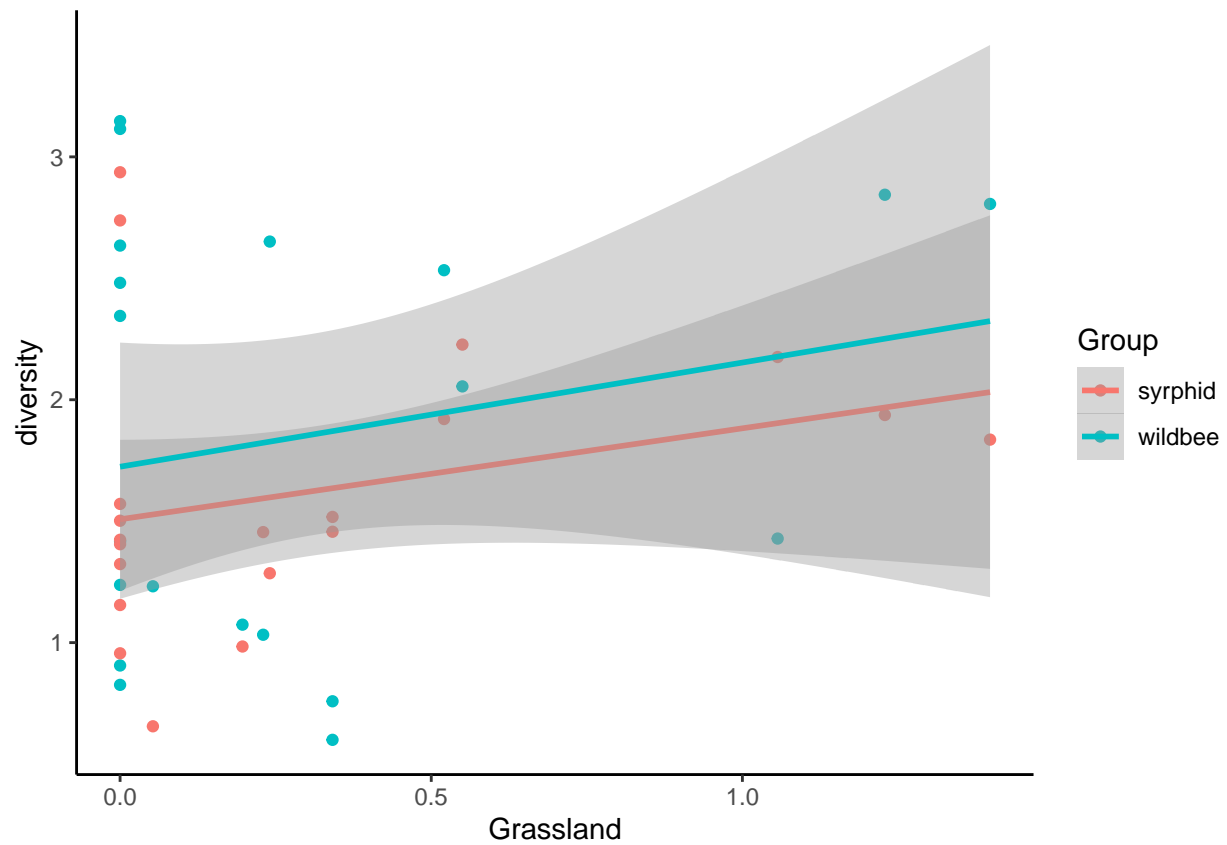
```
## Habitat = SF:
## contrast      estimate      SE df t.ratio p.value
## syrphid - wildbee    0.382 0.347 24   1.103  0.2811
##
## Habitat = FE:
## contrast      estimate      SE df t.ratio p.value
## syrphid - wildbee   -1.365 0.527 24  -2.589  0.0161
##
## Habitat = GR:
## contrast      estimate      SE df t.ratio p.value
## syrphid - wildbee   -0.394 0.586 24  -0.673  0.5074
##
## Habitat = WF:
## contrast      estimate      SE df t.ratio p.value
## syrphid - wildbee    0.444 0.387 24   1.146  0.2630
```

plots

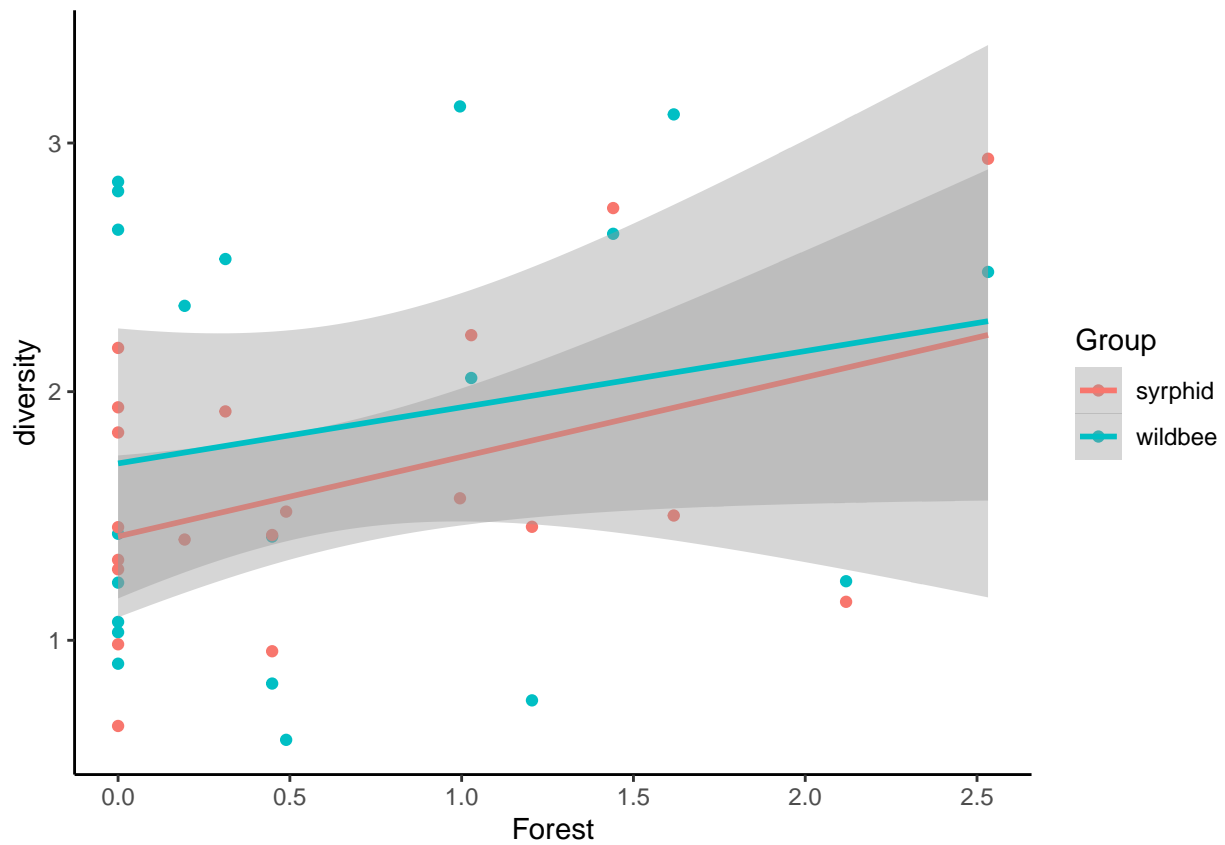
```
ggplot(data_calc2, aes(x = Group,
                       y = diversity,
                       fill = Habitat)) +
  geom_boxplot(position=position_dodge(0.8)) +
  theme_classic()
```



```
ggplot(data_calc2, aes(x = Grassland,
                        y = diversity,
                        colour = Group)) +
  geom_point()+
  geom_smooth(method = lm, formula = y ~ x) +
  theme_classic()
```



```
ggplot(data_calc2, aes(x = Forest,
                       y = diversity,
                       colour = Group)) +
  geom_point()+
  geom_smooth(method = lm, formula = y ~ x) +
  theme_classic()
```



```
ggplot(data_calc2, aes(x = Water,
                        y = diversity,
                        colour = Group)) +
  geom_point()+
  geom_smooth(method = lm, formula = y ~ x) +
  theme_classic()
```