

Tick abundance Analysis

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Lets load our packages first

```
library(tidyverse)
library(tidyr)
library(ggplot2)
library(emmeans)
library(multcompView)
library(multcomp)
library(glmmTMB)
```

set working directory for all chunks in this file (default working directory is wherever Rmd file is)

Lets read in our data

```
ticks<-read.csv("Plot_Data.csv", header = TRUE, stringsAsFactors = TRUE)
```

Null Hypothesis: There are equal abundances of *Ixodes pacificus* in forest interiors, forest edge, and grasslands

Alternative Hypothesis: The abundances of *Ixodes pacificus* are different between forest interiors, forest edge, and grasslands

Make a boxplot & violin plot and IPACs per habitat

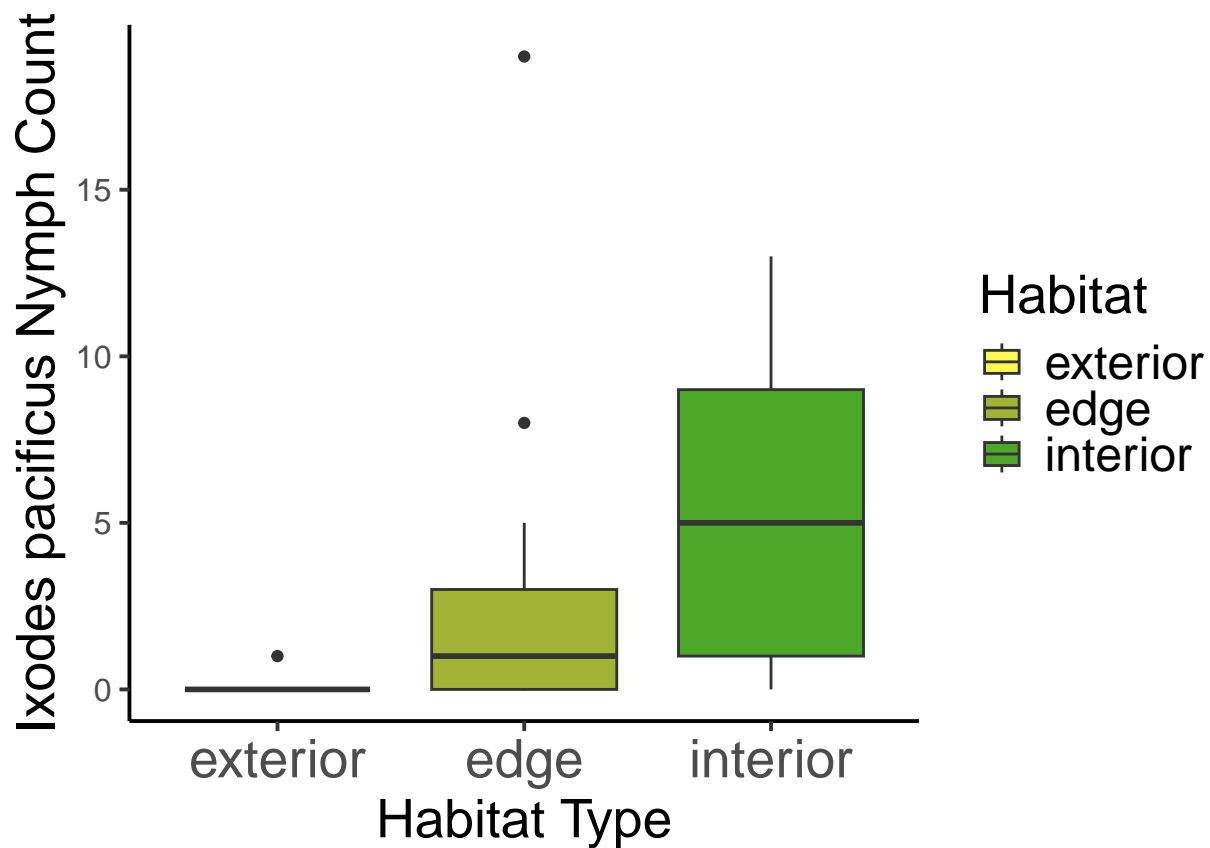
```
ticks$Habitat <- factor(ticks$Habitat, levels = c("exterior", "edge", "interior"))

p1 <- ggplot(ticks, aes(x=Habitat, y=IPAC_N, fill = Habitat)) +
  geom_boxplot() +
  theme_classic(15) +
  ylab("Ixodes pacificus Nymph Count") +
  xlab("Habitat Type") +
  scale_fill_manual(values = c("exterior" = "#FEF851", "edge" = "#A1B234", "interior" = "#4DA829")) +
```

```

theme(
  axis.title.x = element_text(size = 20),
  axis.title.y = element_text(size = 20),
  legend.title = element_text(size = 20), # Title of the legend
  axis.text.x = element_text(size = 20), # x-axis category labels
  legend.text = element_text(size = 18) # Labels inside the legend
)
p1

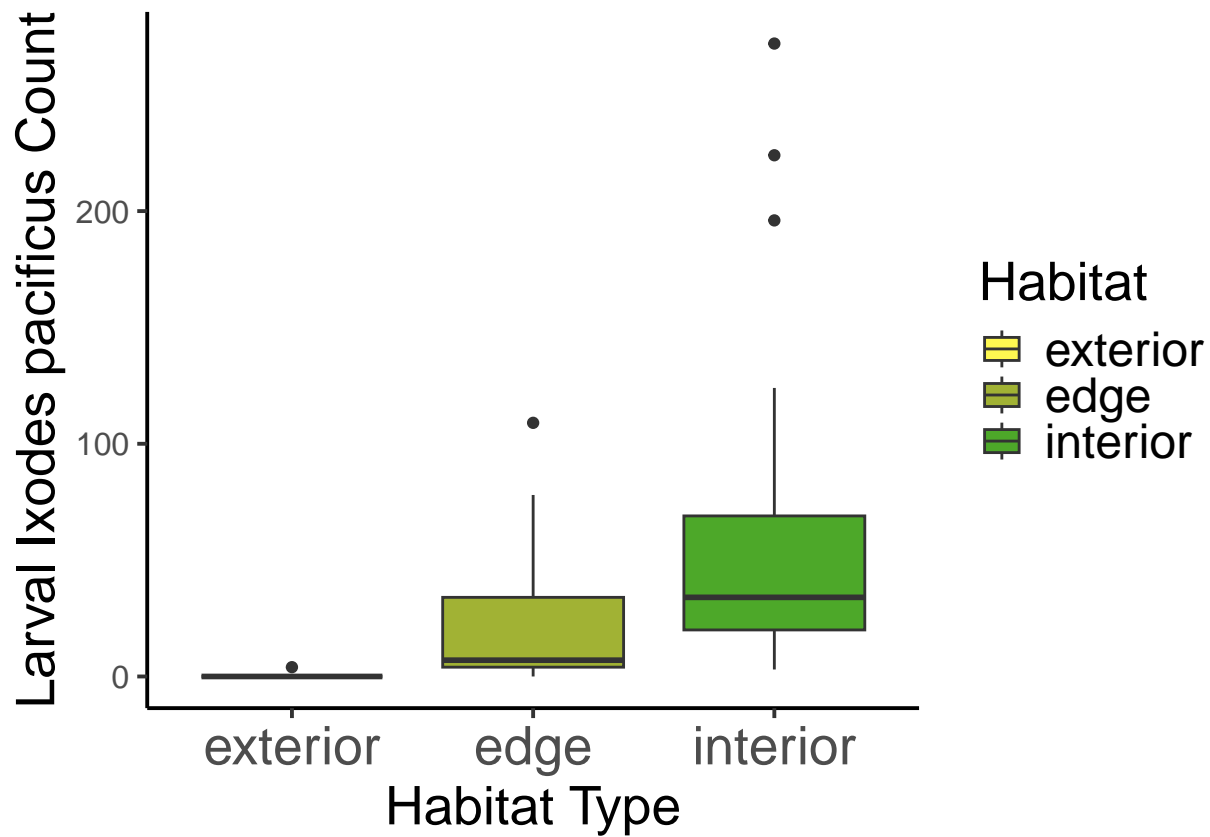
```



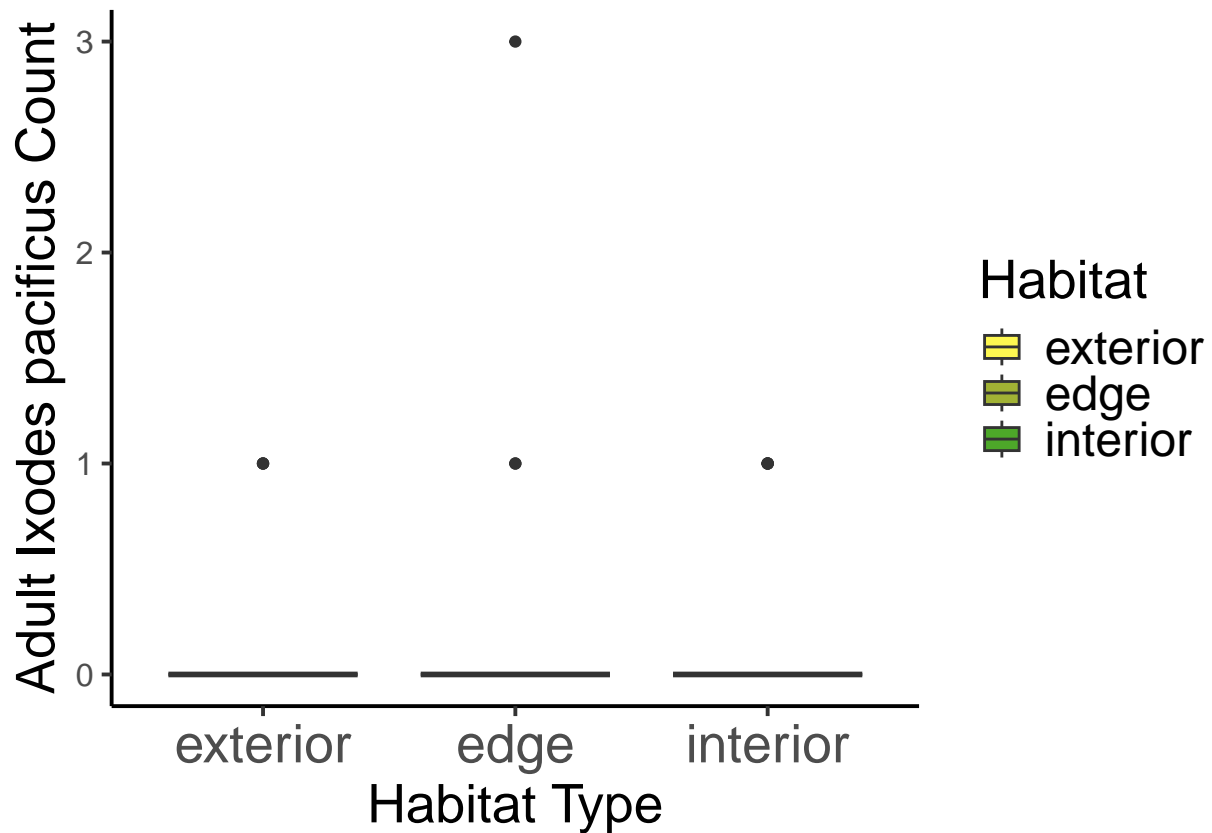
```

p2 <- ggplot(ticks,aes(x=Habitat,y=IPAC_L, fill = Habitat)) +
  geom_boxplot() +
  theme_classic(15) +
  ylab("Larval Ixodes pacificus Count") +
  xlab("Habitat Type")+
  scale_fill_manual(values = c("exterior" = "#FEF851", "edge" = "#A1B234", "interior" = "#4DA829"))+
  theme(
    axis.title.x = element_text(size = 20),
    axis.title.y = element_text(size = 20),
    legend.title = element_text(size = 20), # Title of the legend
    axis.text.x = element_text(size = 20), # x-axis category labels
    legend.text = element_text(size = 18) # Labels inside the legend
  )
p2

```

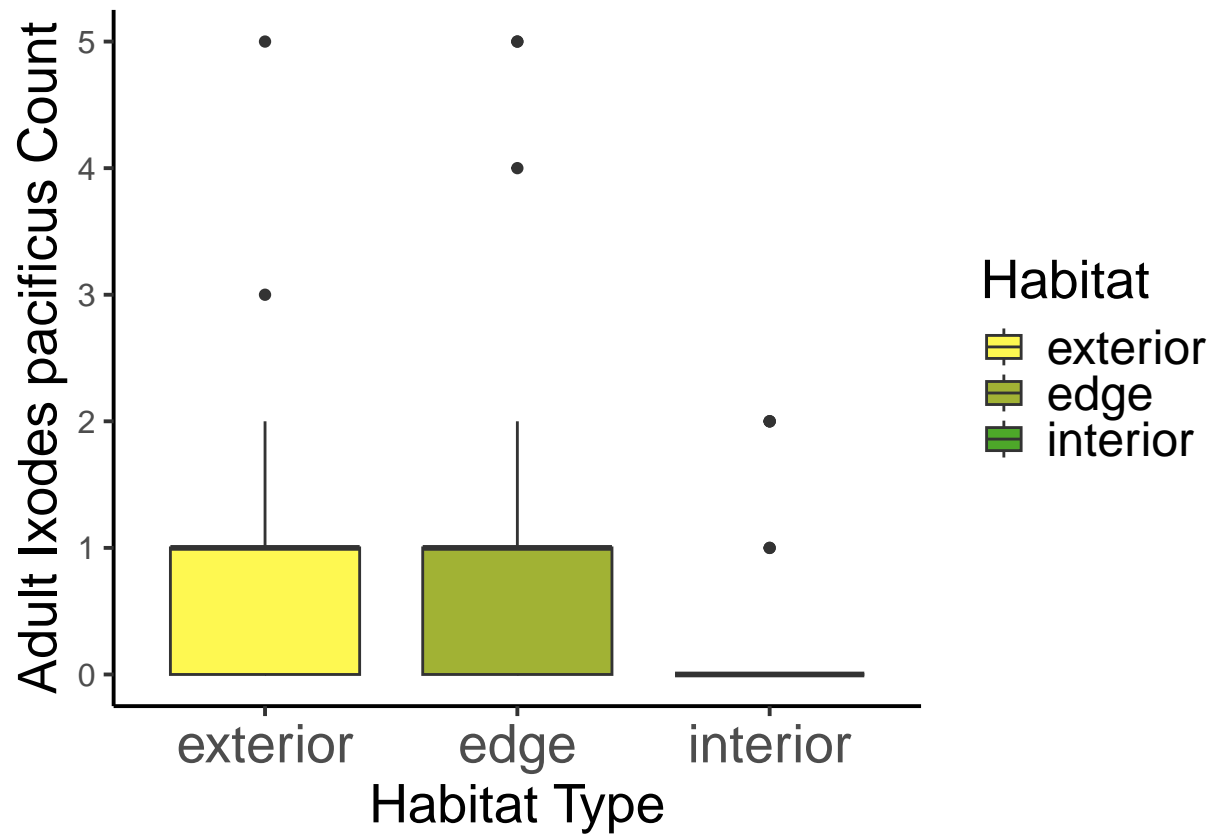


```
p3 <- ggplot(ticks,aes(x=Habitat,y=IPAC_A, fill = Habitat)) +
  geom_boxplot() +
  theme_classic(15) +
  ylab("Adult Ixodes pacificus Count") +
  xlab("Habitat Type")+
  scale_fill_manual(values = c("exterior" = "#FEF851", "edge" = "#A1B234", "interior" = "#4DA829"))+
  theme(
    axis.title.x = element_text(size = 20),
    axis.title.y = element_text(size = 20),
    legend.title = element_text(size = 20), # Title of the legend
    axis.text.x = element_text(size = 20), # x-axis category labels
    legend.text = element_text(size = 18) # Labels inside the legend
  )
p3
```



Make a boxplot & violin plot for DEOC Adults

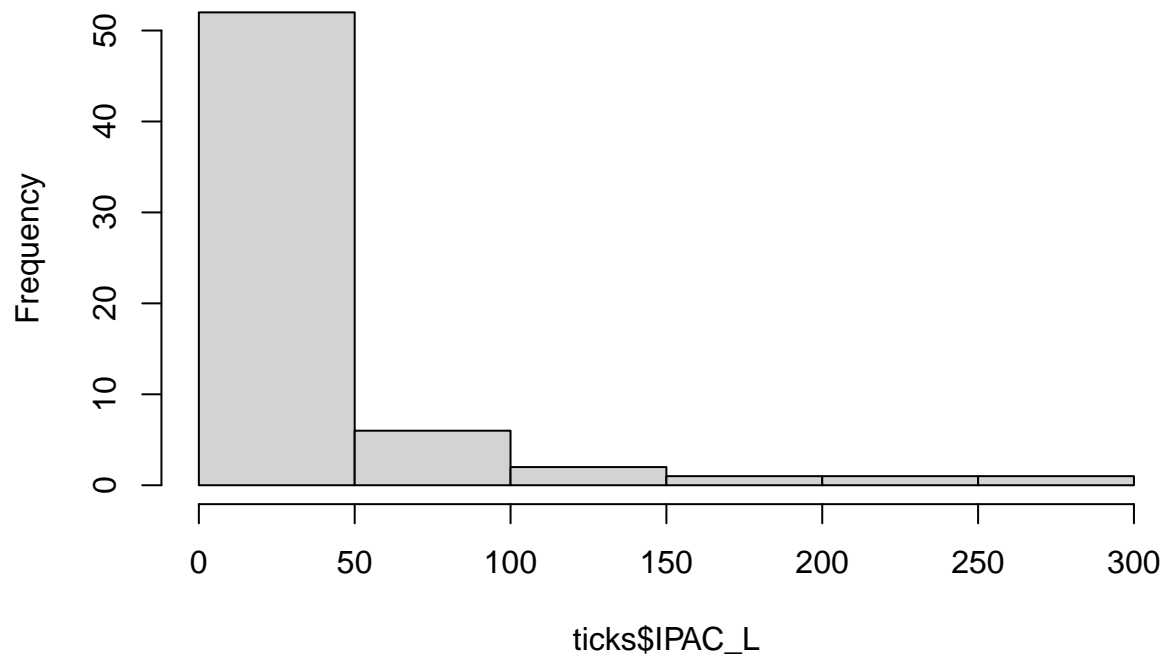
```
p4 <- ggplot(ticks,aes(x=Habitat,y=DEOC_A, fill = Habitat)) +
  geom_boxplot() +
  theme_classic(15) +
  ylab("Adult Ixodes pacificus Count") +
  xlab("Habitat Type")+
  scale_fill_manual(values = c("exterior" = "#FEF851", "edge" = "#A1B234", "interior" = "#4DA829"))+
  theme(
    axis.title.x = element_text(size = 20),
    axis.title.y = element_text(size = 20),
    legend.title = element_text(size = 20), # Title of the legend
    axis.text.x = element_text(size = 20), # x-axis category labels
    legend.text = element_text(size = 18) # Labels inside the legend
  )
p4
```



Lets look at the assumptions.

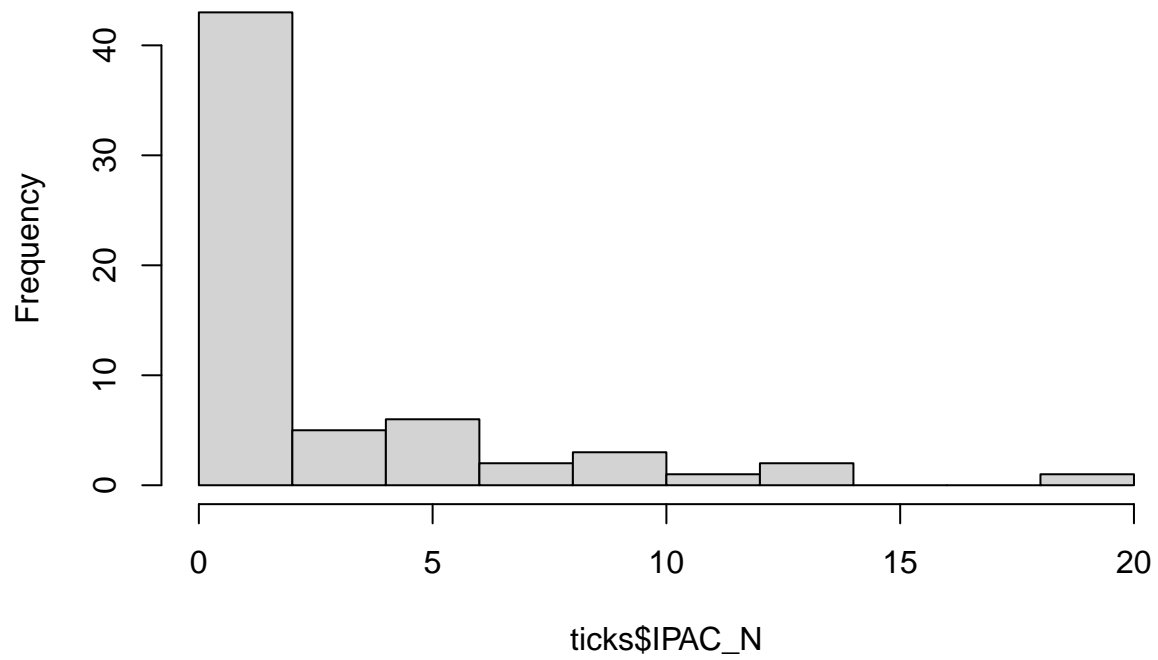
```
hist(ticks$IPAC_L)
```

Histogram of ticks\$IPAC_L



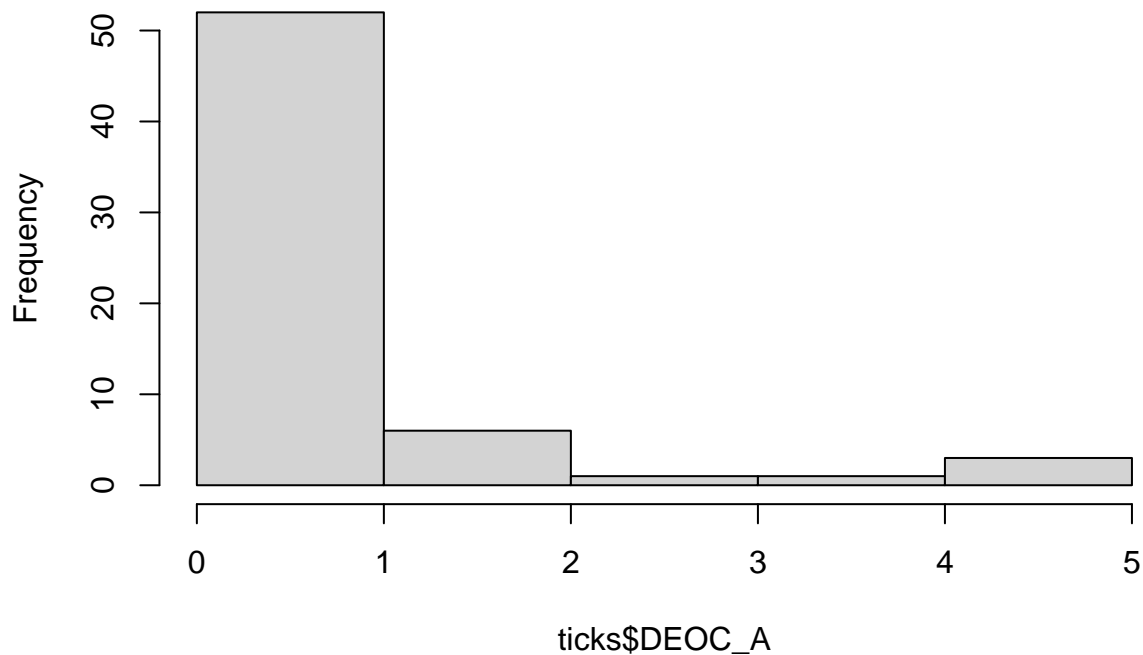
```
hist(ticks$IPAC_N)
```

Histogram of ticks\$IPAC_N



```
hist(ticks$DEOC_A)
```

Histogram of ticks\$DEOC_A



All of these are skewed to the right and are count data so that means we can use a poisson family for our GLMM. Lets start with the larvae

```
m1<- glmmTMB(IPAC_L ~ Habitat +
              (1 | Site),
              family = poisson(link = "log"),
              data = ticks)
m2<- glmmTMB(IPAC_L ~ Habitat +
              (1 | Site) + (1 | Date),
              family = poisson(link = "log"),
              data = ticks)
m3<- glmmTMB(IPAC_L ~ Habitat,
              family = poisson(link = "log"),
              data = ticks)
```

```
AIC(m1, m2, m3)
```

```
##      df      AIC
## m1  4 2104.8209
## m2  5  723.8688
## m3  3 2294.5163
```

```
summary(m2)
```

```
## Family: poisson ( log )
```



```
## Formula:          IPAC_L ~ Habitat + (1 | Site) + (1 | Date)
## Data: ticks
##
##      AIC      BIC   logLik deviance df.resid
##    723.9    734.6   -356.9    713.9      58
##
## Random effects:
##
## Conditional model:
##   Groups Name      Variance Std.Dev.
##   Site   (Intercept) 6.280e-09 7.925e-05
##   Date   (Intercept) 1.362e+00 1.167e+00
## Number of obs: 63, groups: Site, 3; Date, 24
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -2.3203     0.5554  -4.178 2.94e-05 ***
## Habitatedge      4.8101     0.5020   9.581 < 2e-16 ***
## Habitatinterior  6.2417     0.5024  12.424 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Lets do IPAC Nymphs

```
m4<- glmmTMB(IPAC_N ~ Habitat +
              (1 | Site),
              family = poisson(link = "log"),
              data = ticks)
m5<- glmmTMB(IPAC_N ~ Habitat +
              (1 | Site) + (1 | Date),
              family = poisson(link = "log"),
              data = ticks)
m6<- glmmTMB(IPAC_N ~ Habitat,
              family = poisson(link = "log"),
              data = ticks)
```

```
AIC(m4, m5, m6)
```

```
##      df      AIC
## m4  4 301.7075
## m5  5 227.4870
## m6  3 299.9437
```

```
summary(m5)
```

```
## Family: poisson ( log )
## Formula:          IPAC_N ~ Habitat + (1 | Site) + (1 | Date)
## Data: ticks
##
##      AIC      BIC   logLik deviance df.resid
```

```
##      227.5      238.2     -108.7      217.5          58
##
## Random effects:
##
## Conditional model:
## Groups Name      Variance Std.Dev.
## Site (Intercept) 1.502e-09 3.875e-05
## Date (Intercept) 1.135e+00 1.066e+00
## Number of obs: 63, groups: Site, 3; Date, 24
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -3.639      1.033  -3.521  0.00043 ***
## Habitatedge      3.970      1.009   3.933  8.38e-05 ***
## Habitatinterior  5.088      1.013   5.025  5.04e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Lets do IPAC DEOC

```
m7<- glmmTMB(DEOC_A ~ Habitat +
             (1 | Site),
             family = poisson(link = "log"),
             data = ticks)
m8<- glmmTMB(DEOC_A ~ Habitat +
             (1 | Site) + (1 | Date),
             family = poisson(link = "log"),
             data = ticks)
m9<- glmmTMB(DEOC_A ~ Habitat,
             family = poisson(link = "log"),
             data = ticks)
```

```
AIC(m7, m8, m9)
```

```
##      df      AIC
## m7  4 163.8057
## m8  5 163.7918
## m9  3 167.5636
```

```
summary(m8)
```

```
## Family: poisson ( log )
## Formula:      DEOC_A ~ Habitat + (1 | Site) + (1 | Date)
## Data: ticks
##
##      AIC      BIC  logLik deviance df.resid
##    163.8    174.5   -76.9    153.8      58
##
## Random effects:
##
```

```
## Conditional model:
## Groups Name      Variance Std.Dev.
## Site (Intercept) 0.2259   0.4753
## Date (Intercept) 0.2192   0.4681
## Number of obs: 63, groups: Site, 3; Date, 24
##
## Conditional model:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.4008    0.3998  -1.002   0.3161
## Habitatedge     0.2877    0.3118   0.923   0.3562
## Habitatinterior -0.8094    0.4334  -1.868   0.0618 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Now lets run the emmeans for the models that we picked.

Lets start with IPAC larvae

```
library(emmeans)
em2 <- emmeans(m2, ~ Habitat)

# Pairwise comparisons between habitat types
pairs(em2, adjust = "tukey")

## contrast      estimate      SE df z.ratio p.value
## exterior - edge      -4.81 0.5020 Inf  -9.581 <.0001
## exterior - interior  -6.24 0.5020 Inf -12.424 <.0001
## edge - interior     -1.43 0.0666 Inf -21.497 <.0001
##
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Lets start with IPAC Nymphs

```
library(emmeans)
em5 <- emmeans(m5, ~ Habitat)

# Pairwise comparisons between habitat types
pairs(em5, adjust = "tukey")

## contrast      estimate      SE df z.ratio p.value
## exterior - edge      -3.97 1.010 Inf  -3.933 0.0002
## exterior - interior  -5.09 1.010 Inf  -5.025 <.0001
## edge - interior     -1.12 0.211 Inf  -5.309 <.0001
##
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Lets start with DEOC Adults

```
library(emmeans)
em8 <- emmeans(m8, ~ Habitat)

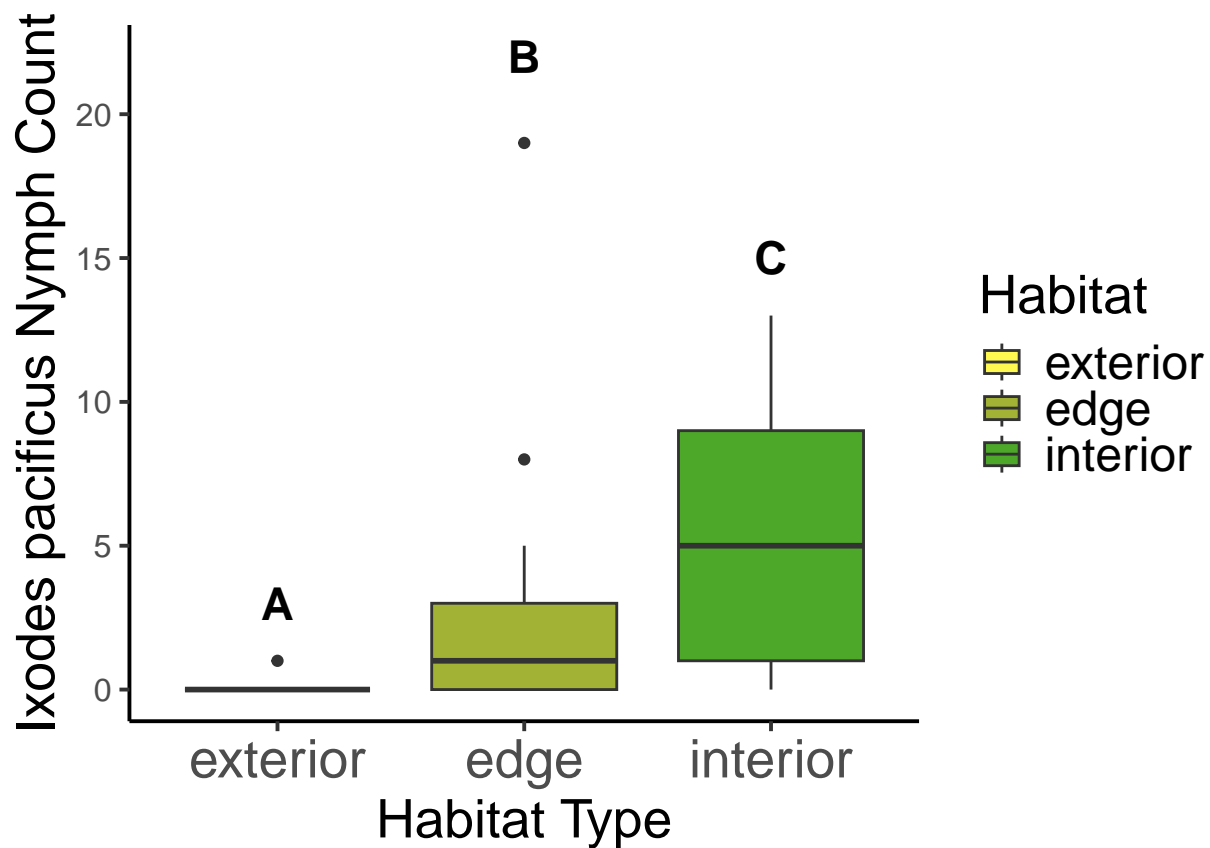
# Pairwise comparisons between habitat types
pairs(em8, adjust = "tukey")
```

contrast	estimate	SE	df	z.ratio	p.value
exterior - edge	-0.288	0.312	Inf	-0.923	0.6259
exterior - interior	0.809	0.433	Inf	1.868	0.1481
edge - interior	1.097	0.417	Inf	2.631	0.0232

Results are given on the log (not the response) scale.
P value adjustment: tukey method for comparing a family of 3 estimates

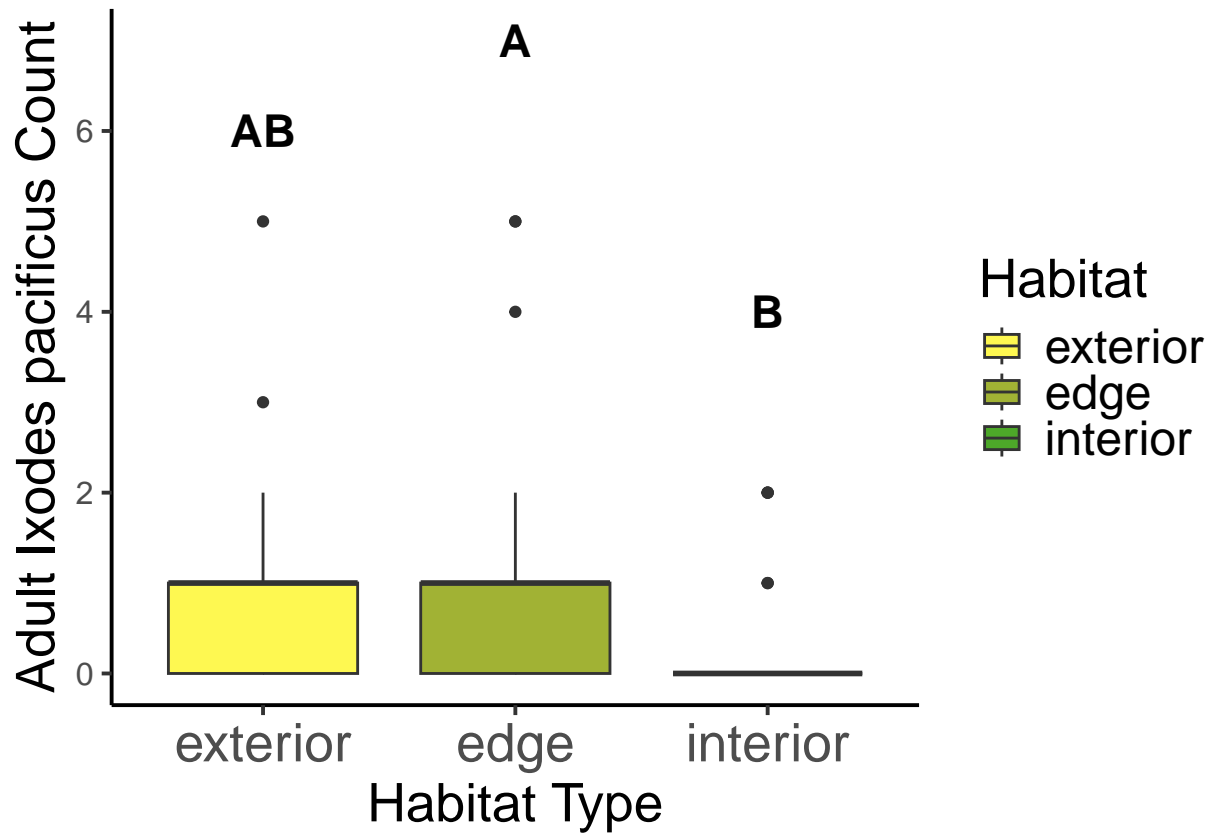
Finalize Figures for IPAC N

```
p1+ annotate("text", x = 1, y = 3, label = "A", size = 6, fontface = "bold") + annotate("text", x = 2, y = 20, label = "B", size = 6, fontface = "bold") + annotate("text", x = 3, y = 15, label = "C", size = 6, fontface = "bold")
```



Finalize Figures for DEOC adults

```
p4+ annotate("text", x = 1, y = 6, label = "AB", size = 6, fontface = "bold") + annotate("text", x = 2,
```



Results

For nymphal *Ixodes pacificus* we observed that their populations increase as you move along a gradient from grassland to oakwoodlands. Each habitat surveyed had a significantly different abundance of ticks. For our *Dermocentor occidentalis* adults we observed the most abundances in grasslands (exterior) forest edge, while interior experienced the lowest abundances.