BirdsMarsh

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Clear the console

```
rm(list = ls())
cat("\014")
```

Get data from a woodland from Data directory - Birds Marsh Wood

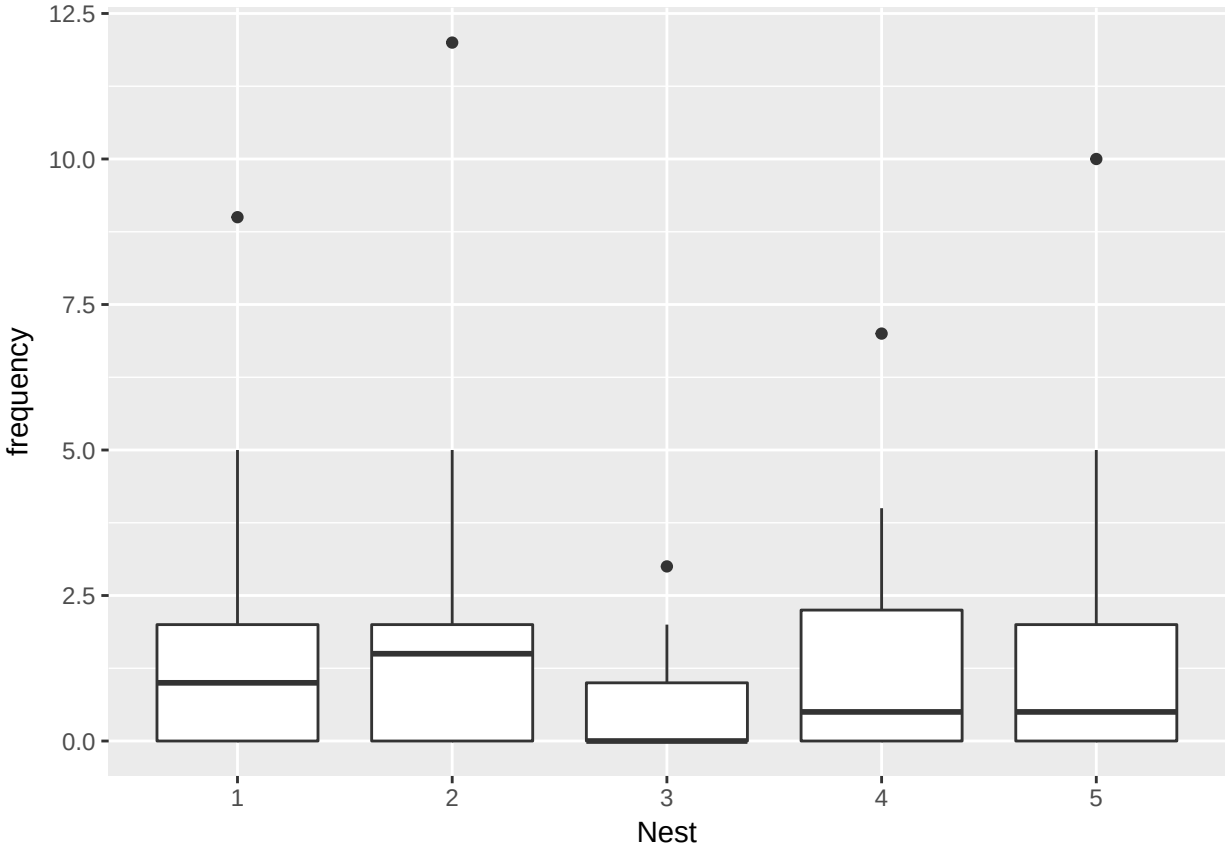
```
data = read.csv("../Data/Birds_Marsh.csv")
```

Take out the 2000 data, get a frequency table for species by plot, by nest

```
data2001_data = data[data$YR == '2000',]
species = with(data2001_data, table(data2001_data$PLOT, data2001_data$NEST))
species = as.data.frame(species)
colnames(species) = c("Plot","Nest","frequency")
```

Look at the number of species in each nest

```
library(ggplot2)
ggplot(species, (aes_string(x='Nest', y='frequency')) )+
                geom_boxplot()
```



Need cummulative frequency of species for each nest

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

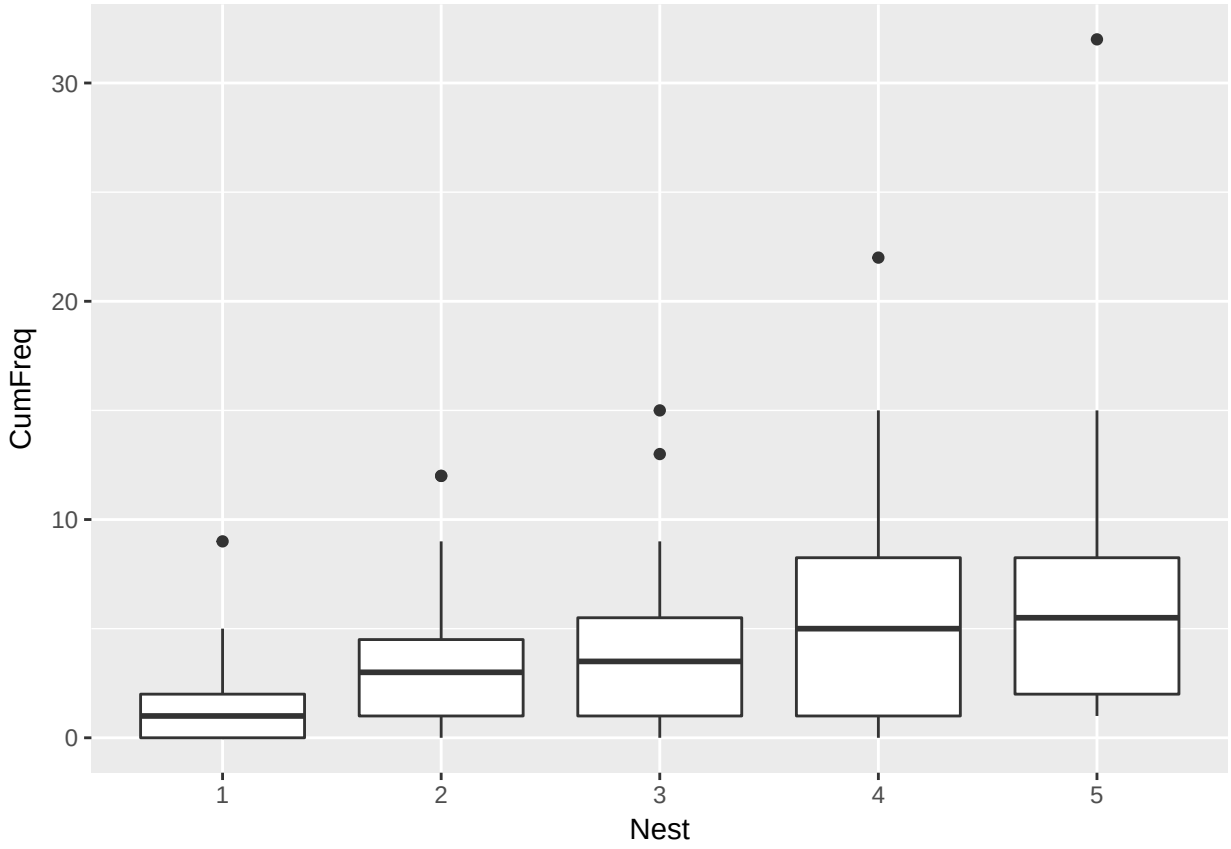
```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

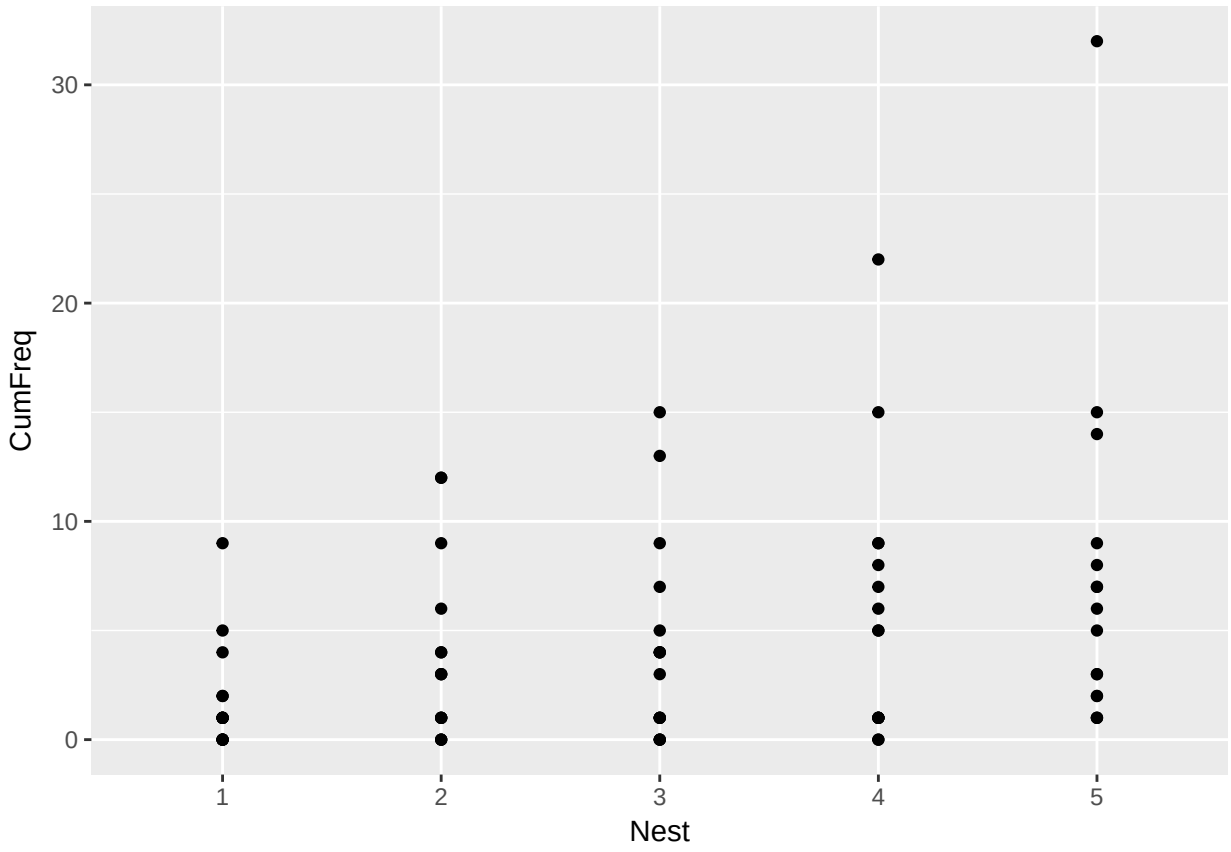
```
species = mutate(group_by(species,Plot), cumsum = cumsum(frequency))
colnames(species) = c("Plot","Nest","Freq","CumFreq")
```

Plot cumulative species per nest across all plots

```
library(ggplot2)
ggplot(species, (aes_string(x='Nest', y='CumFreq')) )+
                geom_boxplot()
```

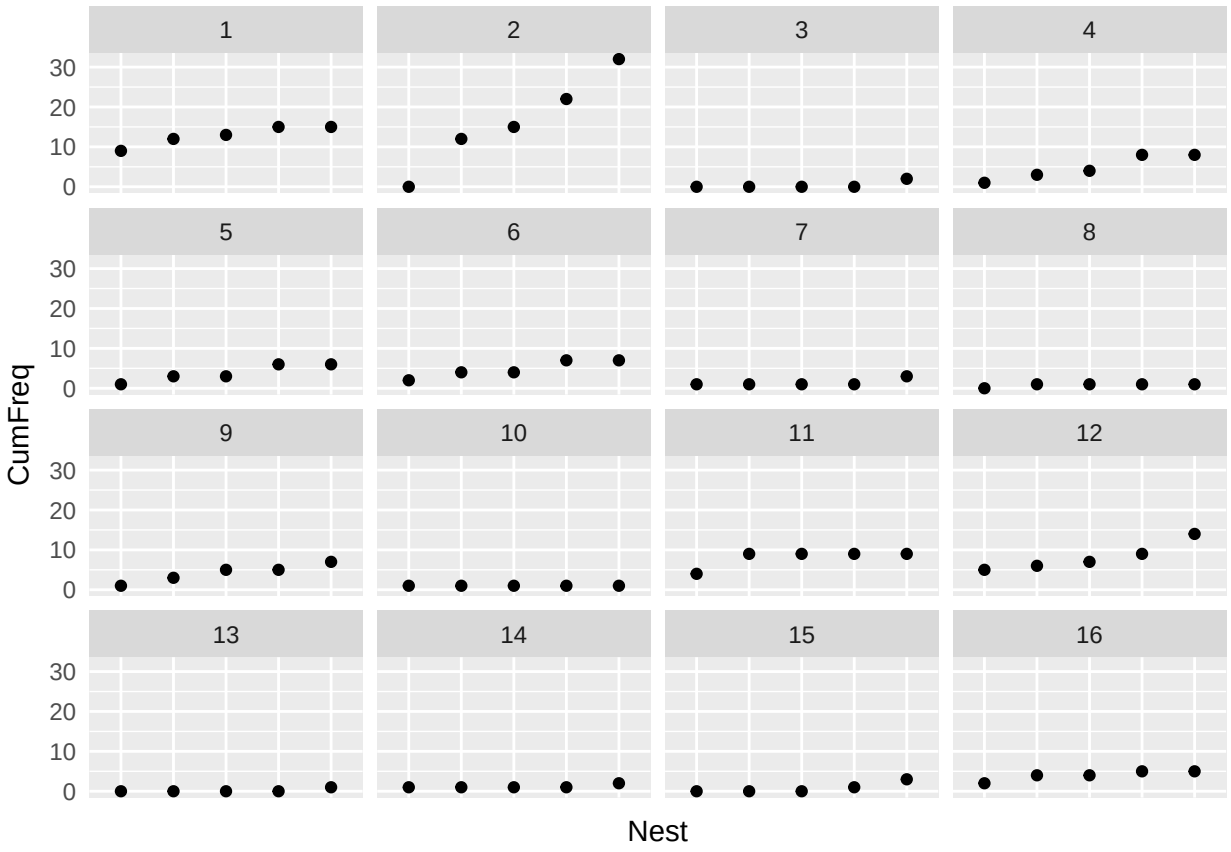



```
ggplot(data = species) +  geom_point(aes(x=Nest,y=CumFreq))
```



Species area for each plot.

```
library(ggplot2)
ggplot(data = species) +  geom_point(aes(x=Nest,y=CumFreq)) +   facet_wrap(~Plot) +
  theme(axis.ticks = element_blank(), axis.text.x = element_blank())
```

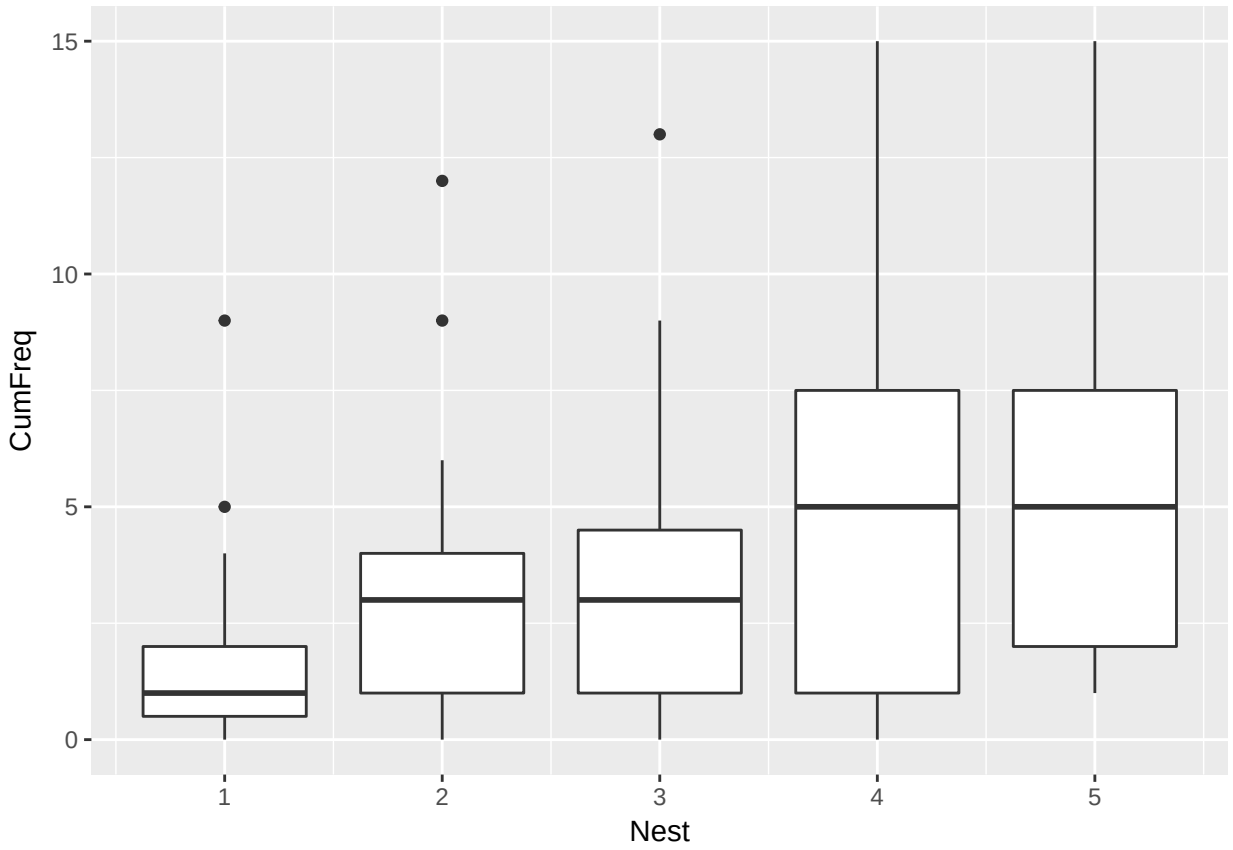


If plot 2 is removed from the data, is there any difference between nest 1 and cumulative total in nest 5? PS, converting nest and plot to numeric for linear model

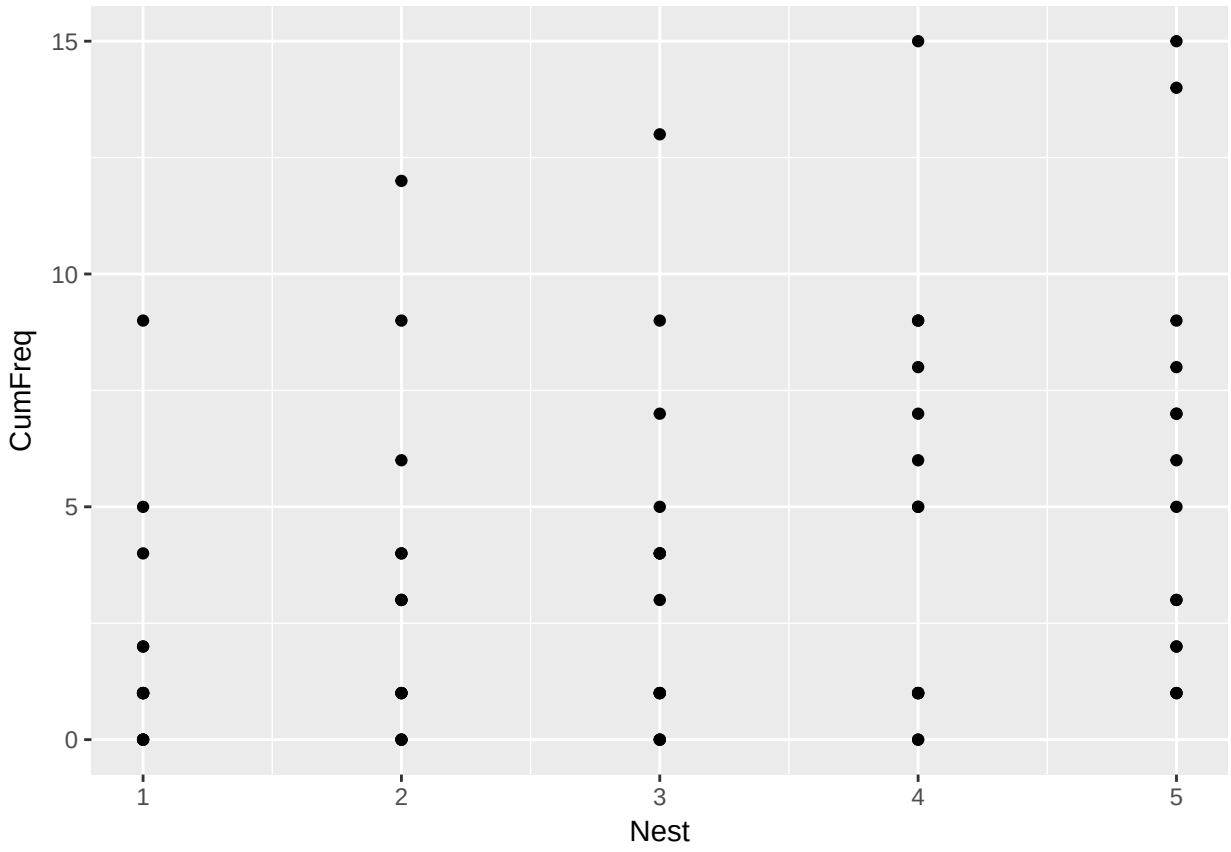
```
reduced_species = species[species$Plot != 2,]
reduced_species$Plot = as.numeric(reduced_species$Plot)
reduced_species$Nest = as.numeric(reduced_species$Nest)
```

Replot this reduced dataset

```
library(ggplot2)
ggplot(reduced_species, (aes_string(x='Nest', y='CumFreq', group = 'Nest')) )+  geom_boxplot()
```




```
ggplot(data = reduced_species) +  geom_point(aes(x=Nest,y=CumFreq))
```



Anova on reduced species

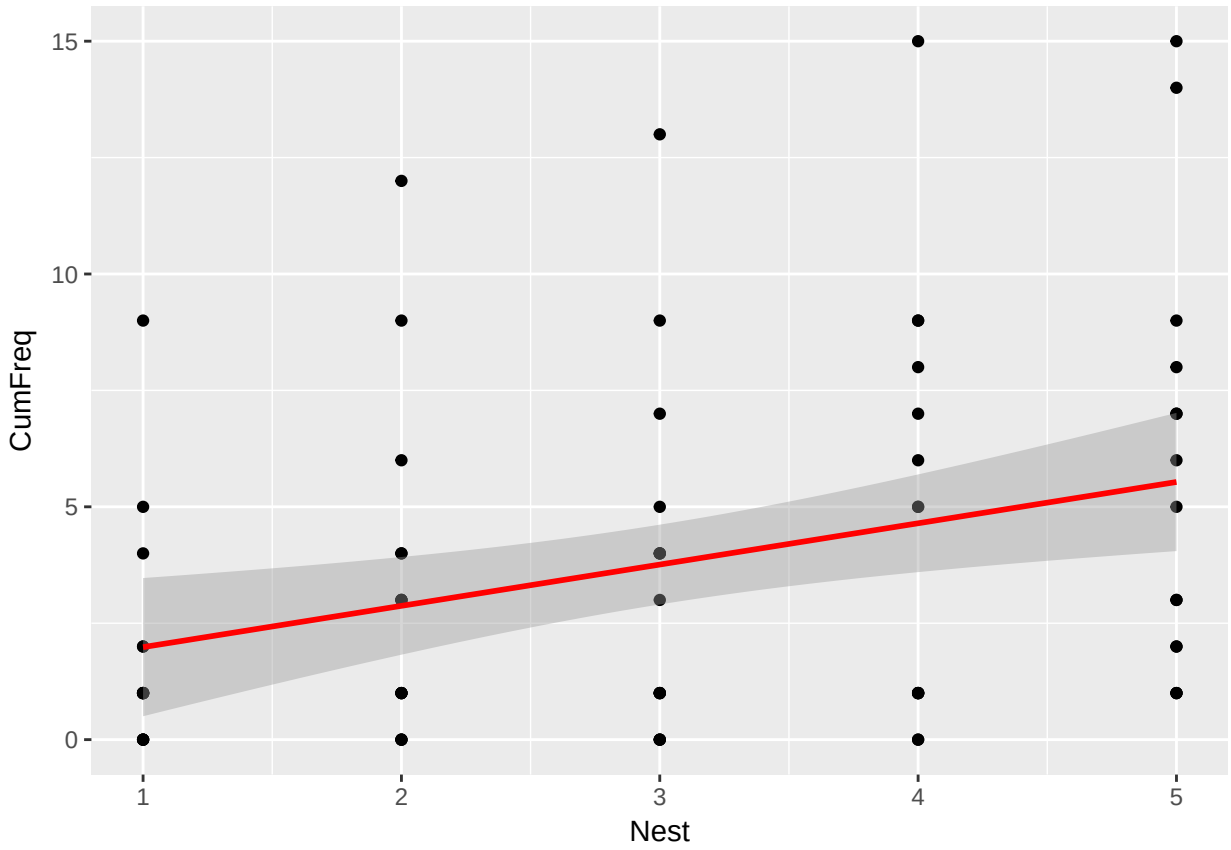
```
model = lm(CumFreq ~ Nest, data =  reduced_species)
 ANOVA <- anova(model)
 print(ANOVA)
```

```
## Analysis of Variance Table
##
## Response: CumFreq
##           Df  Sum Sq Mean Sq F value   Pr(>F)
## Nest       1  117.93  117.93  8.5086 0.004694 **
## Residuals 73 1011.75   13.86
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
 print(model$coefficients)
```

```
## (Intercept)        Nest
##   1.1000000   0.8866667
```

```
ggplot(reduced_species, aes(x=Nest, y = CumFreq)) + geom_point() + stat_smooth(method = "lm", col = 'red
```



the next bit i will do