Lab 6

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Count data and glmm

Up to this point, we have been working on linear models, in which the response variable has been a continuous, normally distributed variable. For today's lab we will focus on Generalized Linear Model (called so, because it generalizes the linear regression using a link function, see the slides for week 8!)

I will be borrowing from Dr. Clark Rushing https://warnell.uga.edu/directory/people/clark-rushing for this lab, taken from his **FANR 6750** course.

Dataset

Let's take a look at a data example to demonstrate this concept. The data are modified from Ver Hoef and Boveng 2007 and include 400 observed counts of harbor seals from aerial surveys conducted in coastal Alaska.

Download the harbordata.csv from the files tab in Canvas, and load it into an object called harbordata.

```
harbordata = read.csv("harbordata.csv")
#library(FANR6750)
#data("harbordata")
```

After you have downloaded it, let's explore it

```
head(harbordata)
```

```
  Survey Number substrate Reltolow      SITE
1      1    250      rock      0.0 Abbess I.
2      2    144      rock      3.2 Abbess I.
3      3      0      rock      4.9 Alava Bay
```

```
4       4     42       rock      3.6 Alava Bay
5       5     10       rock      0.0 Alava Bay
6       6      0       rock      1.6 Alava Bay
```

And finally… let's visualize it.

We will use the ggplot package. If you have never used it, let's download it:

You only need to install a package once in your computer.

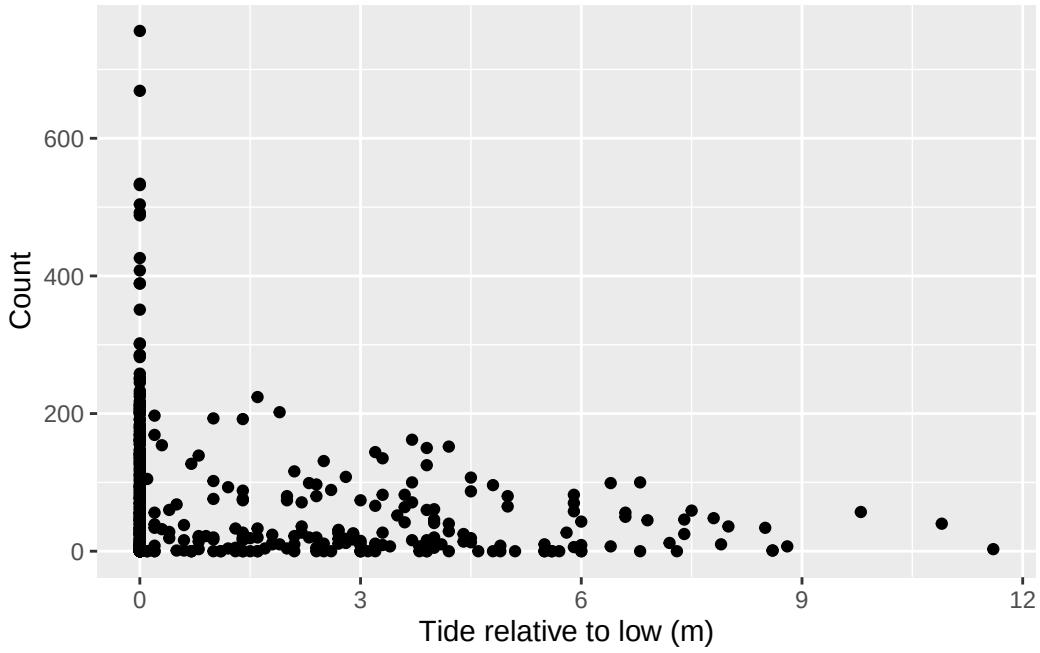
Then, let's load the package

```
library(ggplot2)
```

```
Warning: package 'ggplot2' was built under R version 4.3.3
```

And finally, let's plot the data:

```
ggplot() +
  geom_point(data = harbordata, aes(x = Reltolow, y = Number)) +
  scale_y_continuous("Count") +
  scale_x_continuous("Tide relative to low (m)")
```



Remember, this data includes aerial observations of seals

Looking at the plot, it seems like there are a ton ob observation in which 0 individuals were seen, and some in which up to 12 were seen. This might be a bit overdispersed for a Poisson distribution, but we'll worry about that later!

Running a simple linear model

First off, let's look at what would happen if we ran a simple linear model. Hopefully you know how to do this by now.

Run a linear model using the "lm" function, in which Number is the response variable, and Reltolow is the explanatory variable using the harbordata dataset.

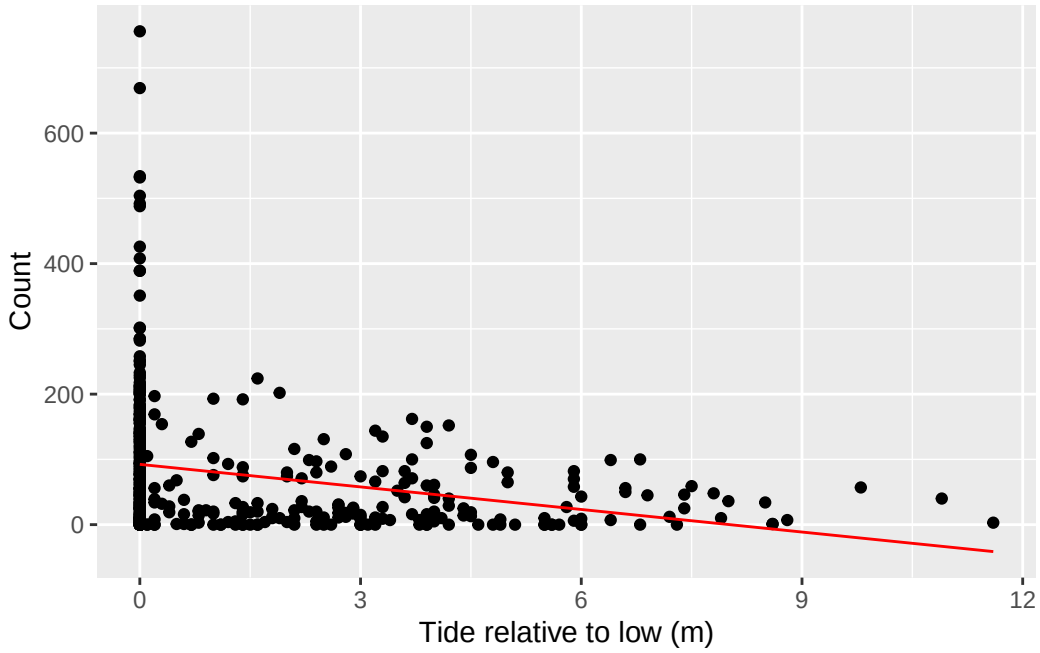
```
mod1 <- lm(Number~ Reltolow, data= harbordata)
summary(mod1)
```

```
Call:
lm(formula = Number ~ Reltolow, data = harbordata)

Residuals:
   Min     1Q Median     3Q    Max
-92.39 -63.27 -29.01  38.68 663.61

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   92.390      6.052  15.265  < 2e-16 ***
Reltolow     -11.524      2.172  -5.306 1.86e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 99.42 on 398 degrees of freedom
Multiple R-squared:  0.06607,   Adjusted R-squared:  0.06372
F-statistic: 28.16 on 1 and 398 DF,  p-value: 1.862e-07
```

While this model is significant, we know there's some stuff wrong with it (or, at least, you should know it!)

Let's add this model prediction to the plot:

```r
model_pred <- predict(mod1)

ggplot() +
  geom_point(data = harbordata, aes(x = Reltolow, y = Number)) +
  geom_line(aes(harbordata$Reltolow, model_pred), color= 'red') +
  scale_y_continuous("Count") +
  scale_x_continuous("Tide relative to low (m)")
```



Uggh, this is not good.

But remember! We can use a link function to estimate a different response. In this case:

$$log(\lambda_i) = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_p x_{ip}$$

Now, that doesn't have a random component. In this case, the random component is given by:

$$y_i \sim Poisson(\lambda_i)$$

One last problem... that random component uses λ_i, not $log(\lambda_i)$. Well, to obtain λ_i we simply use:

$$\lambda_i = e^{\beta_0} + e^{\beta_1 x_{i1}} + e^{\beta_2 x_{i2}} + \cdots + e^{\beta_z x_{zp}}$$

Fortunately, we don't have to worry about anything other than knowing which link function to use.

Let's run the same model, but using a GLM:

```
fm2 <- glm(Number ~ Reltolow, family = poisson(link = "log"), data = harbordata)
summary(fm2)
```

```
Call:
glm(formula = Number ~ Reltolow, family = poisson(link = "log"),
    data = harbordata)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  4.563811   0.006535  698.37   <2e-16 ***
Reltolow    -0.229939   0.003864  -59.51   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 42725  on 399  degrees of freedom
Residual deviance: 37943  on 398  degrees of freedom
AIC: 39829

Number of Fisher Scoring iterations: 5
```

New things in this function: family, and link!

This model is looking at the effect of flow, but maybe substrate type is also affecting the number of observed seals. Let's run it:

```
fm3 <- glm(Number ~ substrate + Reltolow, family = poisson(link = "log"),
           data = harbordata)
summary(fm3)
```

```
Call:
```

```
glm(formula = Number ~ substrate + Reltolow, family = poisson(link = "log"),
    data = harbordata)

Coefficients:
               Estimate Std. Error z value Pr(>|z|)
(Intercept)    5.422800   0.013433  403.69   <2e-16 ***
substraterock -1.006149   0.015286  -65.82   <2e-16 ***
substratesand -1.284207   0.035859  -35.81   <2e-16 ***
Reltolow      -0.191000   0.003858  -49.51   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 42725  on 399  degrees of freedom
Residual deviance: 34227  on 396  degrees of freedom
AIC: 36116

Number of Fisher Scoring iterations: 6
```

The GLM summary gives us an AIC value. Based on this value, which of the two models is better?

Q1. 2 pts. Which of the two models do you think explains the observed data better? Why? save the model in a new object called "smodel"

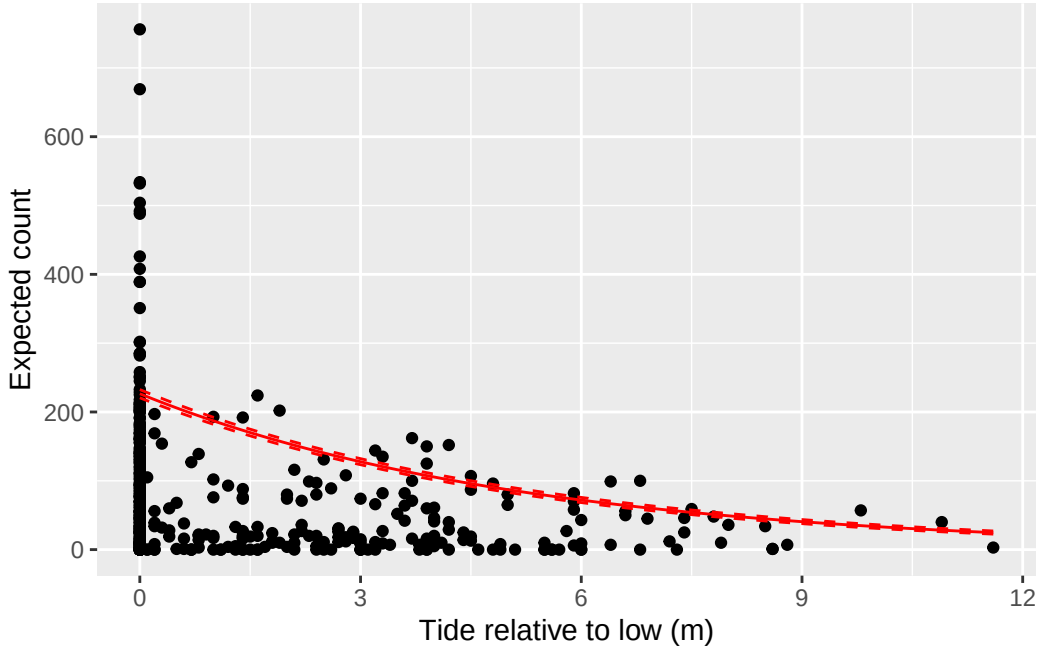
A1. The second model fm3 is better because the AIC which compares the model to the null model is lower than that of the fm2.

```
smodel<-fm3
```

Let's use predict to plot the better model. We will only plot it for one type of substrate

```
predData <- data.frame(Reltolow = seq(min(harbordata$Reltolow),
                                      max(harbordata$Reltolow), length = 10000),
                       substrate= 'ice')

pred.link <- predict(smodel, newdata = predData, se.fit = TRUE)
predData$lambda <- exp(pred.link$fit) # exp is the inverse-link function
predData$lower <- exp(pred.link$fit - 1.96 * pred.link$se.fit)
```

```r
predData$upper <- exp(pred.link$fit + 1.96 * pred.link$se.fit)

ggplot() +
  geom_point(data = harbordata, aes(x = Reltolow, y = Number)) +
  geom_path(data = predData, aes(x = Reltolow, y = lambda), color= 'red') +
  geom_ribbon(data = predData, aes(x = Reltolow, ymin = lower, ymax = upper),
              fill = NA, color = "red", linetype= 'dashed') +
  scale_x_continuous("Tide relative to low (m)") +
  scale_y_continuous("Expected count")
```



Do you think this looks OK? Look at the (tiny) confident intervals compared to the great spread of the data!

Remember that I mentioned that the data looked a bit overdispersed? In Poisson, the mean and the variance are equal. That's why as λ increases, so does the spread of the data.

Q2. 4 pts. Estimate the mean and the variance of the "number" variablein the dataframe. Do you think there is overdispersion?

Q2. The mean is 74.07 and the variance is 10557.64. Because the variance is so large, I think there is overdispersion.

```r
mean(harbordata$Number)
```

```
[1] 74.07
```

```r
var(harbordata$Number)
```

```
[1] 10557.64
```

A long time ago, I talked about the use of negative binomial instead of Poisson when there is overdispersion. It allows us a lot more flexibility!

To run a glm using the negative binomial, we need a new package. Download the "MASS" package.

And now, let's run the code!

We will

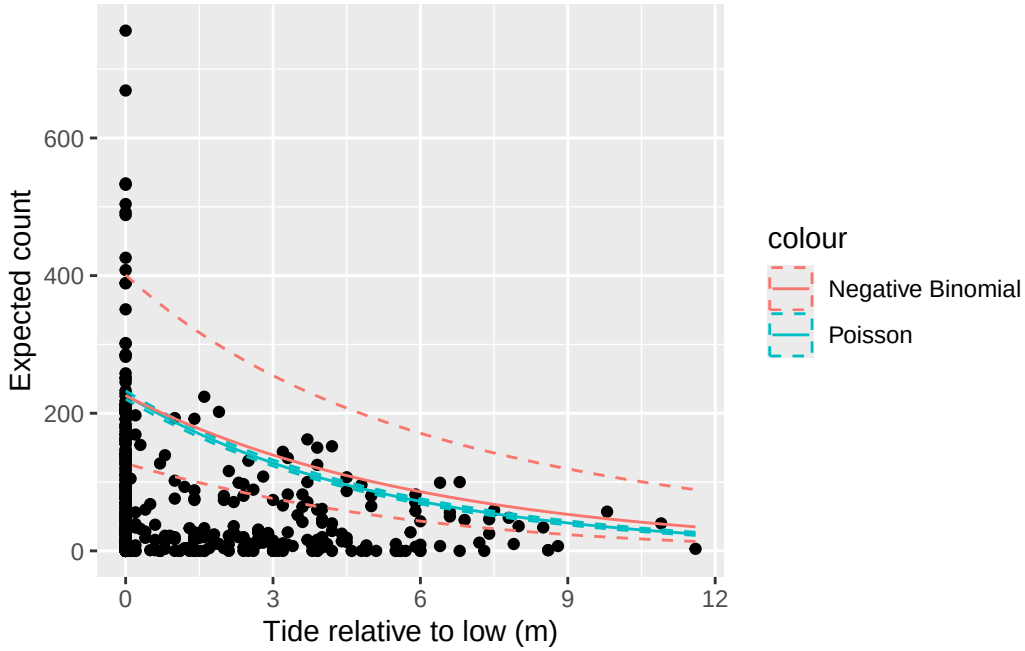
1. Run the NB model
2. Look at the summary
3. Obtain the predictors to plot
4. Plot!
5. Add the Poisson model to the plot

```r
library(MASS)
nb1 <- glm.nb(Number ~ substrate + Reltolow, data = harbordata)
summary(nb1)
```

```
Call:
glm.nb(formula = Number ~ substrate + Reltolow, data = harbordata,
    init.theta = 0.4661173743, link = log)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)     5.4190     0.2933  18.477  < 2e-16 ***
substraterock  -1.0372     0.3077  -3.371 0.000749 ***
substratesand  -1.3827     0.4500  -3.072 0.002123 **
Reltolow       -0.1608     0.0327  -4.917 8.78e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(Dispersion parameter for Negative Binomial(0.4661) family taken to be 1)

    Null deviance: 532.29  on 399  degrees of freedom
Residual deviance: 484.04  on 396  degrees of freedom
AIC: 4009.5

Number of Fisher Scoring iterations: 1

              Theta:  0.4661
          Std. Err.:  0.0319

 2 x log-likelihood:  -3999.4500
```

```
predDatanb <- data.frame(Reltolow = seq(min(harbordata$Reltolow),
                                        max(harbordata$Reltolow), length = 10000),
                         substrate= 'ice')

pred.linknb <- predict(nb1, newdata = predDatanb, se.fit = TRUE)
predDatanb$lambda <- exp(pred.linknb$fit) # exp is the inverse-link function
predDatanb$lower <- exp(pred.linknb$fit - 1.96 * pred.linknb$se.fit)
predDatanb$upper <- exp(pred.linknb$fit + 1.96 * pred.linknb$se.fit)

ggplot() +
  geom_point(data = harbordata, aes(x = Reltolow, y = Number)) +
  geom_path(data = predData, aes(x = Reltolow, y = lambda, color= 'Poisson')) +
  geom_ribbon(data = predData, aes(x = Reltolow, ymin = lower,
                                   ymax = upper, color= 'Poisson'),
              fill = NA, linetype= 'dashed') +
  geom_path(data = predDatanb, aes(x = Reltolow, y = lambda,
                                   color= 'Negative Binomial')) +
  geom_ribbon(data = predDatanb, aes(x = Reltolow, ymin = lower, ymax = upper,
              color= 'Negative Binomial'), fill = NA,
              linetype= 'dashed') +
  scale_x_continuous("Tide relative to low (m)") +
  scale_y_continuous("Expected count")
```



Even though the CI is larger, this better represents the real world observations!

Download the alligatordata.csv file.

Q3. 12 pts. Estimate clutch size as a function of lenght, habitat, and length + habitat using both methods (Poisson and NB)

```
alligator=read.csv("alligatordata.csv")
head(alligator)
```

```
  Nest Eggs Length            Habitat
1    1   62   13.8     Brackish marsh
2    2   22    8.1     Brackish marsh
3    3   41   10.7 Intermediate marsh
4    4   37   11.1     Brackish marsh
5    5   23    7.0 Intermediate marsh
6    6   29    7.3              Swamp
```

```
alligator$Habitat = as.factor(alligator$Habitat)
summary(alligator)
```

```
      Nest             Eggs           Length                    Habitat
```

```
 Min.   :  1.00   Min.   :20.00   Min.   : 6.00   Brackish marsh    :150
 1st Qu.: 88.25   1st Qu.:31.00   1st Qu.: 8.10   Intermediate marsh: 78
 Median :175.50   Median :39.00   Median :10.60   Swamp             :122
 Mean   :175.50   Mean   :40.91   Mean   :10.53
 3rd Qu.:262.75   3rd Qu.:48.75   3rd Qu.:12.90
 Max.   :350.00   Max.   :82.00   Max.   :14.90
```

```
am_pois <- glm(Eggs ~ Length + Habitat + Length:Habitat, family = poisson(link = "log"),  dat
summary(am_pois)
```

```

Call:
glm(formula = Eggs ~ Length + Habitat + Length:Habitat, family = poisson(link = "log"),
    data = alligator)

Coefficients:
                                  Estimate Std. Error z value Pr(>|z|)
(Intercept)                       2.855675   0.058373  48.921   <2e-16 ***
Length                            0.076246   0.005266  14.478   <2e-16 ***
HabitatIntermediate marsh         0.059500   0.097301   0.612    0.541
HabitatSwamp                     -0.053845   0.082606  -0.652    0.515
Length:HabitatIntermediate marsh  0.004644   0.008254   0.563    0.574
Length:HabitatSwamp               0.005720   0.007405   0.772    0.440
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 1342.39  on 349  degrees of freedom
Residual deviance:  608.48  on 344  degrees of freedom
AIC: 2547.6

Number of Fisher Scoring iterations: 4
```

```
am_nb <- glm.nb(Eggs ~ Length + Habitat + Length:Habitat, data = alligator)
summary(am_nb)
```

```

Call:
glm.nb(formula = Eggs ~ Length + Habitat + Length:Habitat, data = alligator,
    init.theta = 55.03075957, link = log)
```

```
Coefficients:
                                 Estimate Std. Error z value Pr(>|z|)
(Intercept)                      2.862381   0.075015  38.157   <2e-16 ***
Length                           0.075611   0.006887  10.980   <2e-16 ***
HabitatIntermediate marsh        0.053040   0.126509   0.419    0.675
HabitatSwamp                    -0.053845   0.105997  -0.508    0.611
Length:HabitatIntermediate marsh 0.005259   0.010920   0.482    0.630
Length:HabitatSwamp              0.005721   0.009696   0.590    0.555
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(55.0308) family taken to be 1)

    Null deviance: 766.96  on 349  degrees of freedom
Residual deviance: 349.10  on 344  degrees of freedom
AIC: 2482.3

Number of Fisher Scoring iterations: 1

              Theta:  55.03
          Std. Err.:  9.79

 2 x log-likelihood:  -2468.269
```

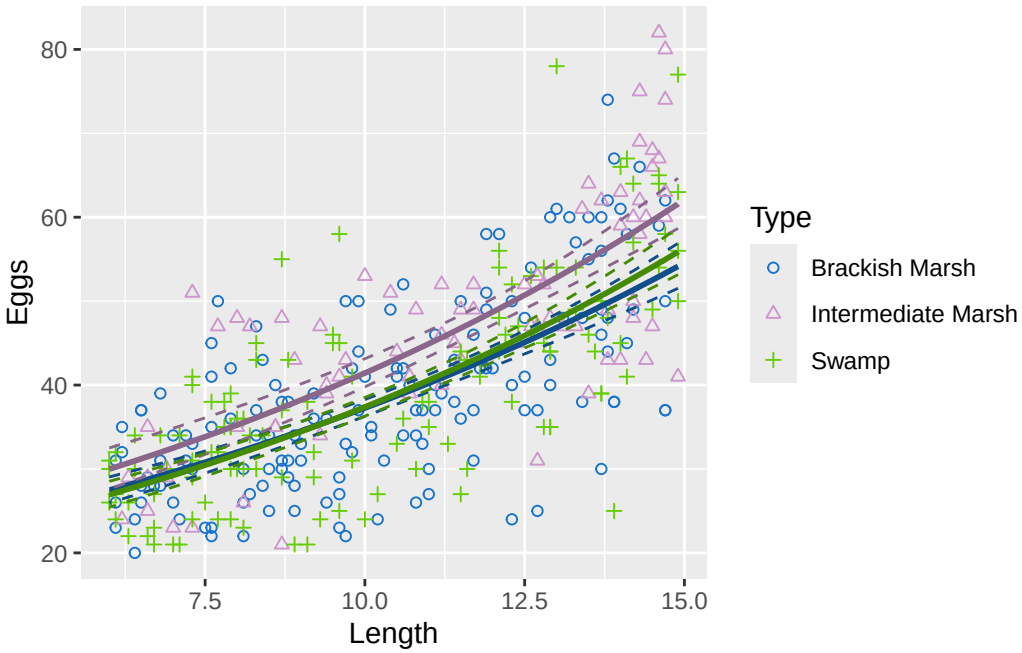
Q4. 4 pts. Choose the best model from Q3 and describe it

A4. Since the negative binomial model's AIC is lower than that of the poisson model.

Q5. 6 pts. Use the poisson regression model to plot the relationship between number of eggs and female length, for all three habitat types, on the same graph. The graph should include points color-coded by habitat, a legend and confidence intervals

```r
#Set up data frame for predictor data for each habitat type
predData2_brack = data.frame(Length = seq(min(alligator$Length),
                                          max(alligator$Length),length = 10000),
                             Habitat = as.factor('Brackish marsh'),
                             show.legend = TRUE)

predData2_int = data.frame(Length = seq(min(alligator$Length),
                                        max(alligator$Length), length = 10000),
                           Habitat = as.factor('Intermediate marsh'))

predData2_swamp = data.frame(Length = seq(min(alligator$Length),
                                          max(alligator$Length), length = 10000),
                             Habitat = as.factor('Swamp'))

#Implement prediction for Brackish Marsh
pred.link2_brack <- predict(am_pois, newdata = predData2_brack, se.fit = TRUE)
predData2_brack$lambda <- exp(pred.link2_brack$fit) # exp is the inverse-link function
predData2_brack$lower <- exp(pred.link2_brack$fit - 1.96*pred.link2_brack$se.fit)
predData2_brack$upper <- exp(pred.link2_brack$fit + 1.96*pred.link2_brack$se.fit)

#Implement prediction for Intermediate Swamp
pred.link2_int <- predict(am_pois, newdata = predData2_int, se.fit = TRUE)
predData2_int$lambda <- exp(pred.link2_int$fit)
predData2_int$lower <- exp(pred.link2_int$fit - 1.96*pred.link2_int$se.fit)
predData2_int$upper <- exp(pred.link2_int$fit + 1.96*pred.link2_int$se.fit)

#Implement prediction for Swamp
pred.link2_swamp <- predict(am_pois, newdata = predData2_swamp, se.fit = TRUE)
predData2_swamp$lambda <- exp(pred.link2_swamp$fit)
predData2_swamp$lower <- exp(pred.link2_swamp$fit - 1.96*pred.link2_swamp$se.fit)
predData2_swamp$upper <- exp(pred.link2_swamp$fit + 1.96*pred.link2_swamp$se.fit)

#Extract all data points into separate data points for each habitat type
brack_df = data.frame(alligator[which(alligator$Habitat == "Brackish marsh"), ])
int_df = data.frame(alligator[which(alligator$Habitat == "Intermediate marsh"), ])
swamp_df = data.frame(alligator[which(alligator$Habitat == "Swamp"), ])

## Begin plot
ggplot() +
#plot all data points by color
geom_point(data = brack_df, aes(x = Length, y = Eggs, color='Brackish Marsh'),
           shape=1) +
```

```
geom_point(data = int_df, aes(x = Length, y = Eggs, color='Intermediate Marsh'),
           shape=2) +
geom_point(data = swamp_df, aes(x = Length, y = Eggs, color='Swamp'),
           shape=3) +

#plot poisson regression model and confidence intervals for Brackish Marsh
geom_path(data = predData2_brack, aes(x = Length, y = lambda),
          linewidth=1, color= 'dodgerblue4') +
geom_ribbon(data = predData2_brack, aes(x = Length,
                                        ymin = lower,
                                        ymax = upper),
            fill = NA, linewidth=0.5, color = "dodgerblue4", linetype= 'dashed') +

#plot poisson regression model and confidence intervals for Intermediate Marsh
geom_path(data = predData2_int, aes(x = Length, y = lambda),
          linewidth = 1, color= 'plum4') +
geom_ribbon(data = predData2_int, aes(x = Length,
                                      ymin = lower,
                                      ymax = upper),
            linewidth=0.5, fill = NA, color = "plum4", linetype= 'dashed') +

#plot poisson regression model and confidence intervals for Swamp
geom_path(data = predData2_swamp, aes(x = Length, y = lambda),
          linewidth = 1, color= 'chartreuse4') +
geom_ribbon(data = predData2_swamp, aes(x = Length,
                                        ymin = lower,
                                        ymax = upper),
            linewidth=0.5, fill = NA, color = "chartreuse4", linetype= 'dashed') +

#Change color of standard data for person preference and visibility
scale_color_manual(name = 'Type', values = c('Brackish Marsh' = 'dodgerblue3','Intermediate
```



EXTRA CREDIT: up to 4 pts. Question 5 might be a bit hard for some of you. If you figure out a good way to plot it, start a new discussion in Canvas and share your plot/code. There are many ways to plot this, so, if you have an alternative way of plotting it, you can upload it even if someone else has done it already. You can also modify previous responses if you have suggestions on how to do it. In order to get the extra credit, you need to post by end of day Friday 29th. This is so we have a chance to help students working on this Question.

Total points: 28