Monday, Feb 27

Modeling Counts

Example: Consider the following data.

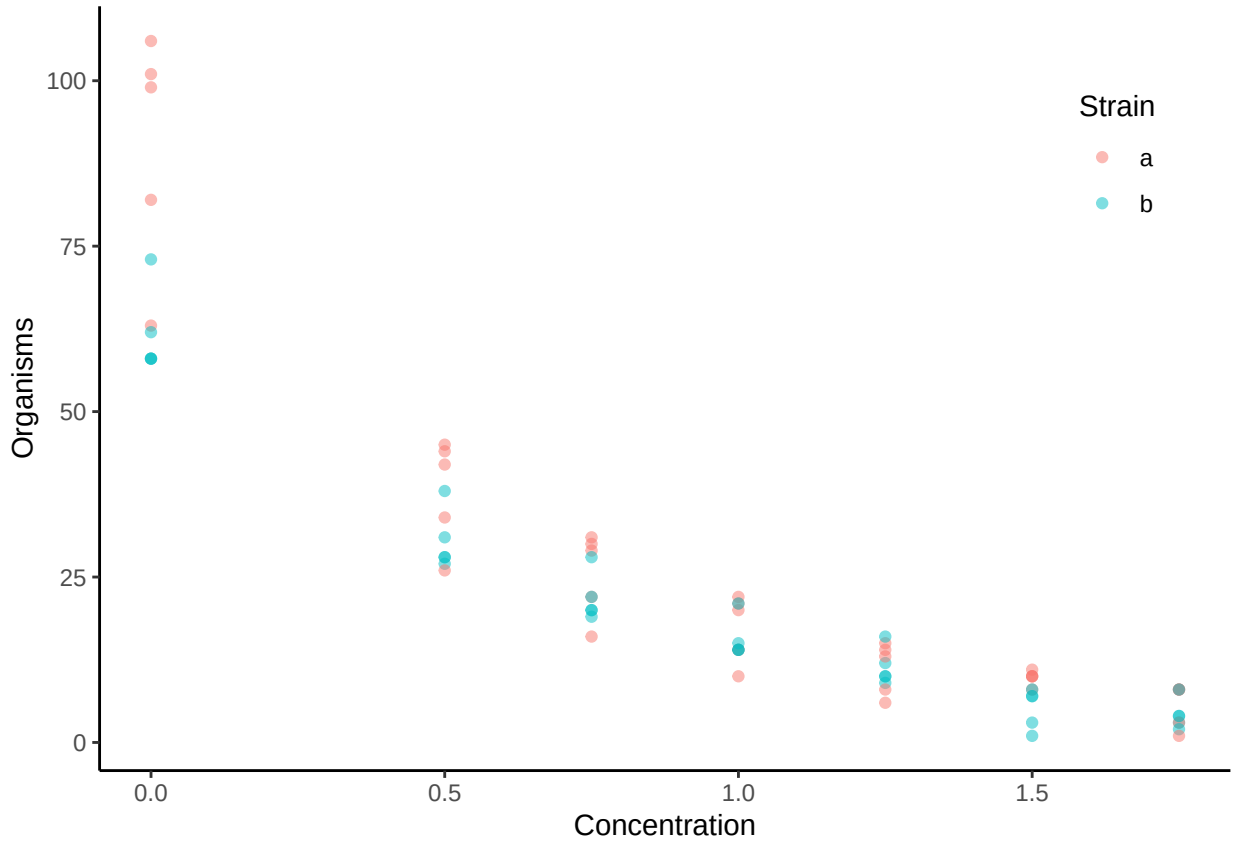
```
library(trtools) # for ceriodaphniastrain data
ceriodaphniastrain$strainf <- factor(ceriodaphniastrain$strain,
  levels = c(1,2), labels = c("a","b"))
head(ceriodaphniastrain)
```

```
  count concentration strain strainf
1    82             0      1       a
2    58             0      2       b
3   106             0      1       a
4    58             0      2       b
5    63             0      1       a
6    62             0      2       b
```

```
tail(ceriodaphniastrain)
```

```
   count concentration strain strainf
65     3          1.75      1       a
66     2          1.75      2       b
67     8          1.75      1       a
68     8          1.75      2       b
69     1          1.75      1       a
70     4          1.75      2       b
```

```
p <- ggplot(ceriodaphniastrain, aes(x = concentration, y = count, color = strainf)) +
  geom_point(alpha = 0.5) + theme_classic() +
  theme(legend.position = c(0.9, 0.8)) +
  labs(x = "Concentration", y = "Organisms", color = "Strain")
plot(p)
```



What are the complications when the response variable is a count?

1. Nonlinear models may be necessary because $E(Y_i) > 0$.
2. Heteroscedasticity because $\text{Var}(Y_i)$ tends to increase with $E(Y_i)$.
3. Non-normal discrete distribution.

One solution would be to use a *nonlinear* regression model combined with some method to account for the heteroscedasticity, and we will revisit this approach, but for now we will consider instead a specialized model that assumes a *Poisson* rather than a normal distribution of Y_i.

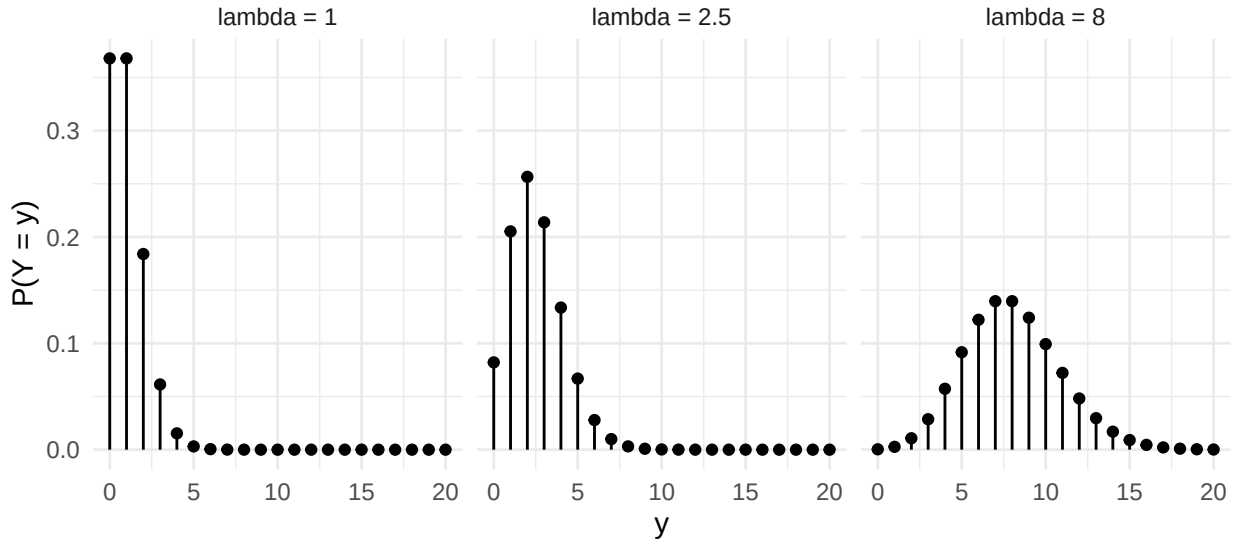
Poisson Regression

A random variable Y has a *Poisson distribution* if

$$P(Y = y) = \frac{\lambda^y e^{-\lambda}}{y!},$$

where y is a non-negative integer (i.e., $y = 0, 1, 2, \ldots$) and $\lambda > 0$ is the parameter of the distribution. Also note that $y!$ is the *factorial* of y, defined as $y! = y \times (y-1) \times (y-2) \times \cdots \times 2 \times 1$ and $0! = 1$.

It can be shown that if Y has a Poisson distribution then $E(Y) = \lambda$ and $\text{Var}(Y) = \lambda$. The parameter λ is sometimes called a "rate" parameter.



A regression model can be specified for a response variable with a Poisson distribution by assuming that

$$P(Y_i = y) = \frac{\lambda_i^y e^{-\lambda_i}}{y!}$$

where λ_i is a function of $x_{i1}, x_{i2}, \ldots, x_{ik}$. Since $\lambda_i > 0$ we might use

$$\lambda_i = \exp(\beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_k x_{ik}).$$

This implies the *nonlinear* regression model

$$E(Y_i) = \exp(\beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_k x_{ik}),$$

which can also be written as

$$\log E(Y_i) = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_k x_{ik}.$$

This kind of model is sometimes called a *log-linear* model. And because $\text{Var}(Y_i) = E(Y_i)$ the model assumes a certain pattern of heteroscedasticity. This kind of regression model is called a *Poisson regression* model.

Generalized Linear Models

Poisson regression is a member of a family of models known as *generalized linear models* (GLM). A generalized linear model has the form

$$g[E(Y_i)] = \underbrace{\beta_0 + \beta_1 x_{i1} + \beta_1 x_{i2} + \cdots + \beta_k x_{ik}}_{\eta_i}$$

where g is the *link function* and η_i is the *linear predictor* or *systematic component*. The link function is invertable so that we can also write

$$E(Y_i) = g^{-1}(\underbrace{\beta_0 + \beta_1 x_{i1} + \beta_1 x_{i2} + \cdots + \beta_k x_{ik}}_{\eta_i}) = g^{-1}(\eta_i).$$

Example: A linear regression model can be written as

$$E(Y_i) = \beta_0 + \beta_1 x_{i1} + \beta_1 x_{i2} + \cdots + \beta_k x_{ik},$$

which implies that the link function is the "identity" function $g(u) = u$, and thus so is the inverse link function $g^{-1}(v) = v$.

Example: A Poisson regression model can be written as

$$\log E(Y_i) = \beta_0 + \beta_1 x_{i1} + \beta_1 x_{i2} + \cdots + \beta_k x_{ik},$$

so the link function is $g(u) = \log(u)$, and the inverse link funtion is the exponential function $g^{-1}(v) = \exp(v)$, also written as e^v.

In a GLM the variance of Y_i is

$$\text{Var}(Y_i) = \phi V[E(Y_i)]$$

where ϕ is a *dispersion parameter* and V is the *variance function*. That is, the variance of Y_i is proportional to some function of $E(Y_i)$.

Example: Linear models typically assume homoscedasticity meaning that $\text{Var}(Y_i) = \sigma^2$ is a constant. Here the dispersion parameter is $\phi = \sigma^2$, and the variance function is just $V[E(Y_i)] = 1$.

Example: In Poisson regression we have that $\text{Var}(Y_i) = E(Y_i)$. Here the dispersion parameter is $\phi = 1$, and the variance function is the identity function $V[E(Y_i)] = E(Y_i)$.

We can write a GLM concisely as

$$E(Y_i) = g^{-1}(\eta_i), \tag{1}$$
$$\text{Var}(Y_i) = \phi V[g^{-1}(\eta_i)], \tag{2}$$

where again

$$\eta_i = \beta_0 + \beta_1 x_{i1} + \cdots + \beta_k x_{ik},$$

to define the *mean structure* and a *variance structure* for Y_i, respectively. In general, specification of a GLM involves specifying three component parts:

1. The *linear predictor* $\eta_i = \beta_0 + \beta_1 x_{i1} + \cdots + \beta_k x_{ik}$.
2. The *link function* g to relate $E(Y_i)$ to η_i as $g[E(Y_i)] = \eta_i$.
3. The *distribution* of Y_i, *or* the *variance structure* $\phi V[g^{-1}(\eta_i)]$.

The choice of distribution implies a certain variance structure when using `glm`. The distribution comes from a family of distributions known as the *exponential family* (not to be confused with what is called an *exponential distribution*).

Example: Normal linear regression is a GLM where $g(u) = u$, $g^{-1}(v) = v$, $\phi = \sigma^2$, and $V(u) = 1$ so that

$$E(Y_i) = \eta_i, \tag{3}$$
$$\text{Var}(Y_i) = \sigma^2. \tag{4}$$

Example: Poisson regression is a GLM where $g(u) = \log(u)$, $g^{-1}(v) = e^v$, $\phi = 1$, and $V(u) = u$ so that

$$\log[E(Y_i)] = \eta_i, \tag{5}$$
$$\text{Var}(Y_i) = \exp(\eta_i). \tag{6}$$

In R the function `glm` can be used to specify a generalized linear model.

Example: Recall the model for the `whiteside` data.

```
library(MASS)
m <- lm(Gas ~ Insul + Temp + Insul:Temp, data = whiteside)
summary(m)$coefficients
```

```
                Estimate Std. Error t value  Pr(>|t|)
(Intercept)       6.8538    0.13596  50.409 7.997e-46
InsulAfter       -2.1300    0.18009 -11.827 2.316e-16
Temp             -0.3932    0.02249 -17.487 1.976e-23
InsulAfter:Temp   0.1153    0.03211   3.591 7.307e-04
```

```
m <- glm(Gas ~ Insul + Temp + Insul:Temp, data = whiteside,
  family = gaussian(link = identity))
summary(m)$coefficients
```

```
               Estimate Std. Error t value  Pr(>|t|)
(Intercept)      6.8538    0.13596  50.409 7.997e-46
InsulAfter      -2.1300    0.18009 -11.827 2.316e-16
Temp            -0.3932    0.02249 -17.487 1.976e-23
InsulAfter:Temp  0.1153    0.03211   3.591 7.307e-04
```

Note that we do not explicitly state the variance structure (although we could — more on that later). Here the variance structure is implied by the choice of distribution.

Example: Now consider the following Poisson regression model for the `ceriodaphniastrain` data.

```
m <- glm(count ~ concentration + strainf, data = ceriodaphniastrain,
  family = poisson(link = log))
summary(m)$coefficients
```

```
             Estimate Std. Error z value   Pr(>|z|)
(Intercept)     4.455    0.03914 113.819  0.000e+00
concentration  -1.543    0.04660 -33.111 2.057e-240
strainfb       -0.275    0.04837  -5.684  1.313e-08
```

This model can be written as

$$E(Y_i) = \exp(\beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2}),$$

or

$$\log E(Y_i) = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2}$$

where x_{i1} is the concentration for the i-th observation, and x_{i2} is an indicator variable for strain such that

$$x_{i2} = \begin{cases} 1, & \text{if the strain is b,} \\ 0, & \text{otherwise,} \end{cases}$$

so that the model can be written case-wise as

$$\log E(Y_i) = \begin{cases} \beta_0 + \beta_1 c_i, & \text{if the strain is a,} \\ \beta_0 + \beta_2 + \beta_1 c_i, & \text{if the strain is b,} \end{cases}$$

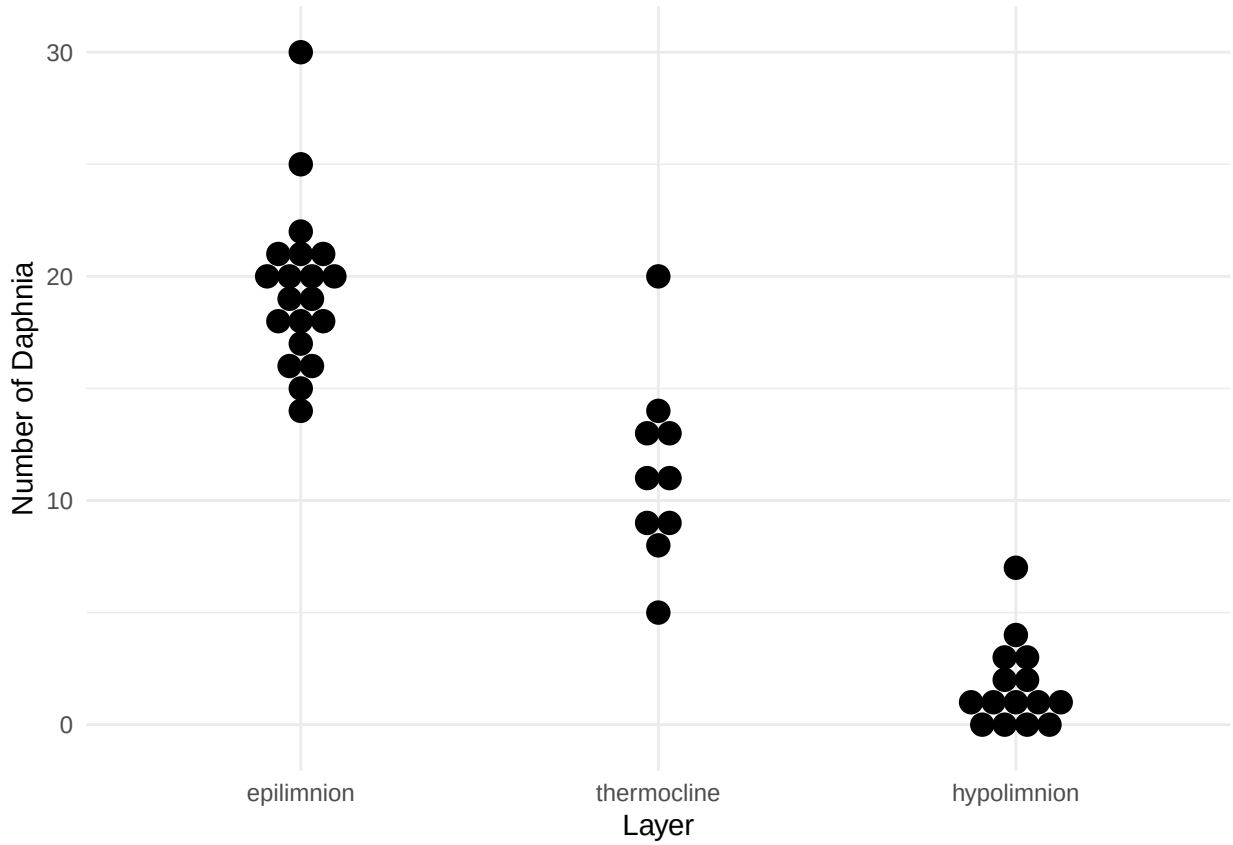
or

$$E(Y_i) = \begin{cases} \exp(\beta_0 + \beta_1 c_i), & \text{if the strain is a,} \\ \exp(\beta_0 + \beta_2 + \beta_1 c_i), & \text{if the strain is b,} \end{cases}$$

if we let $c_i = x_{i1}$ denote the concentration for the i-th observation. Also note that because Y_i is assumed to have a Poisson distribution, $\text{Var}(Y_i) = E(Y_i)$.

Example: Recall the daphnia survey.

```
library(trtools) # for daphniastrat
library(ggplot2)
p <- ggplot(daphniastrat, aes(x = layer, y = count)) +
  geom_dotplot(binaxis = "y", binwidth = 1, stackdir = "center") +
  labs(x = "Layer", y = "Number of Daphnia") + theme_minimal()
plot(p)
```



A Poisson regression model for these data might be specified as follows.

```
m <- glm(count ~ layer, family = poisson(link = log), data = daphniastrat)
summary(m)$coefficients
```

```
                 Estimate Std. Error z value  Pr(>|z|)
(Intercept)        2.9704    0.05064  58.661 0.000e+00
layerthermocline  -0.5456    0.10683  -5.107 3.272e-07
layerhypolimnion  -2.4204    0.20255 -11.950 6.519e-33
```

So the model is $\log E(Y_i) = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2}$, where Y_i is the i-th count, and x_{i1} and x_{i2} are defined as

$$x_{i1} = \begin{cases} 1, & \text{if the } i\text{-th observation is from the thermocline layer,} \\ 0, & \text{otherwise,} \end{cases}$$

and

$$x_{i2} = \begin{cases} 1, & \text{if the } i\text{-th observation is from the hypolimnion layer,} \\ 0, & \text{otherwise.} \end{cases}$$

So the model can be written case-wise as

$$\log E(Y_i) = \begin{cases} \beta_0, & \text{if the } i\text{-th observation is from the epilimnion layer,} \\ \beta_0 + \beta_1, & \text{if the } i\text{-th observation is from the thermocline layer,} \\ \beta_0 + \beta_2, & \text{if the } i\text{-th observation is from the hypolimnion layer,} \end{cases}$$

or

$$E(Y_i) = \begin{cases} \exp(\beta_0), & \text{if the } i\text{-th observation is from the epilimnion layer,} \\ \exp(\beta_0 + \beta_1), & \text{if the } i\text{-th observation is from the thermocline layer,} \\ \exp(\beta_0 + \beta_2), & \text{if the } i\text{-th observation is from the hypolimnion layer.} \end{cases}$$

And of course we have that $\text{Var}(Y_i) = E(Y_i)$.

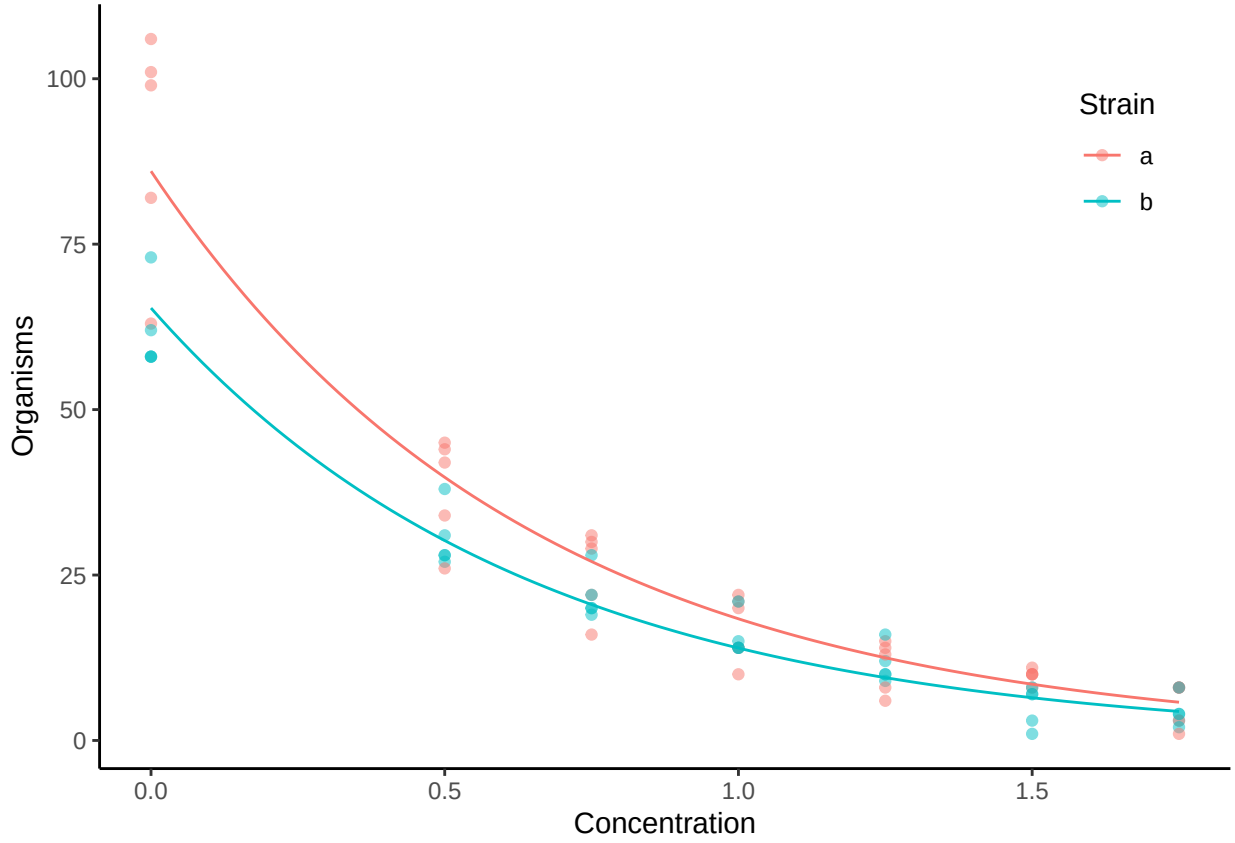
Visualization of a GLM

Visualization of a GLM be done in the usual way provided we use the `type = response` option when using `predict`. The default, which is `type = link`, returns $\hat{\eta}_i = \hat{\beta}_0 + \hat{\beta}_1 x_{i1} + \cdots + \hat{\beta}_k x_{ik}$ which is the estimate of $\log E(Y_i)$.

```
m <- glm(count ~ concentration + strainf, data = ceriodaphniastrain,
  family = poisson(link = log))

d <- expand.grid(concentration = seq(0, 1.75, length = 100), strainf = c("a","b"))
d$yhat <- predict(m, newdata = d, type = "response") # note type = "response" argument

p <- ggplot(ceriodaphniastrain, aes(x = concentration, y = count, color = strainf)) +
  geom_point(alpha = 0.5) + theme_classic() + geom_line(aes(y = yhat), data = d) +
  theme(legend.position = c(0.9, 0.8)) +
  labs(x = "Concentration", y = "Organisms", color = "Strain")
plot(p)
```



To compute confidence intervals for the expected response you can use the `glmint` function from the **trtools** package.

```
d <- expand.grid(concentration = seq(0, 1.75, length = 100), strainf = c("a","b"))
d <- cbind(d, glmint(m, newdata = d))
head(d)
```

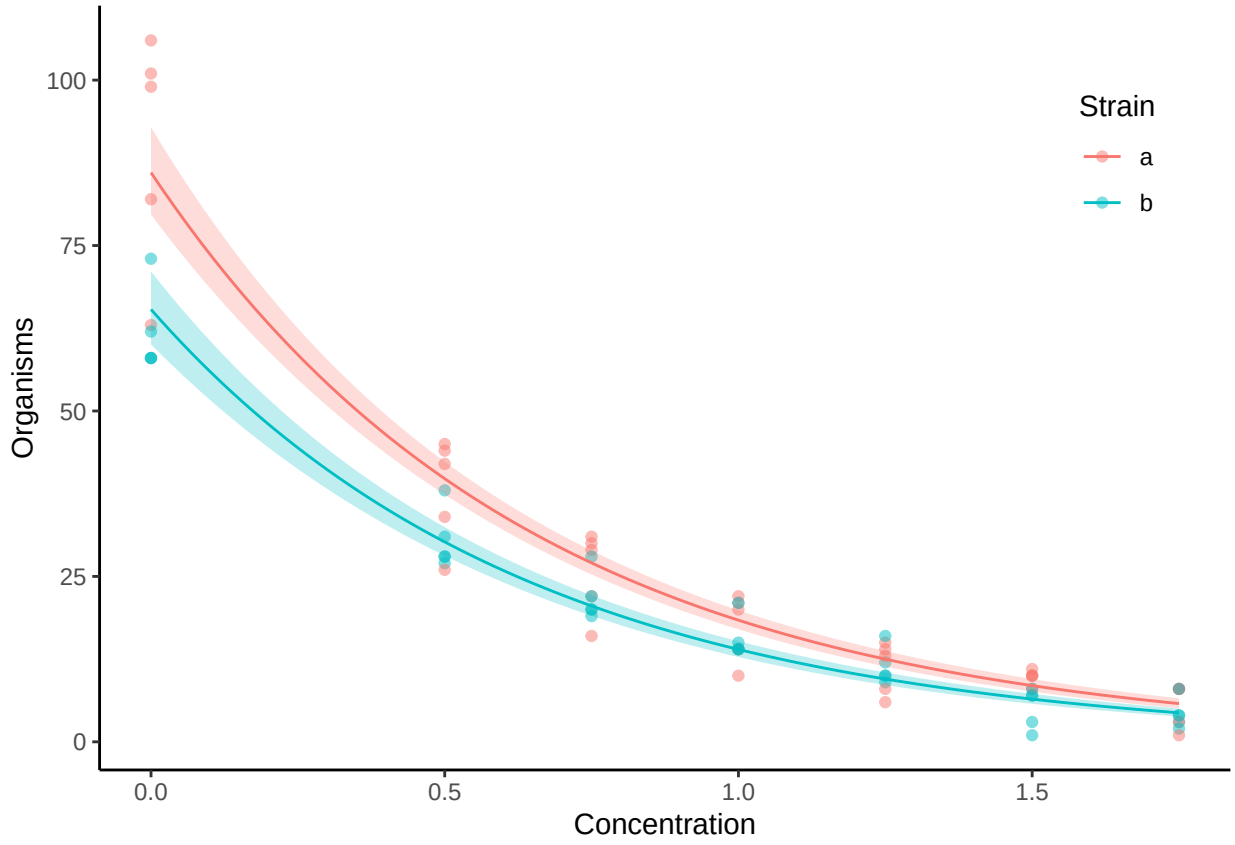
```
  concentration strainf   fit   low   upp
1       0.00000       a 86.03 79.67 92.88
2       0.01768       a 83.71 77.60 90.30
3       0.03535       a 81.46 75.58 87.79
```

```
4       0.05303       a 79.27 73.61 85.35
5       0.07071       a 77.13 71.69 82.99
6       0.08838       a 75.06 69.82 80.68
```

```
p <- ggplot(ceriodaphniastrain, aes(x = concentration, y = count, color = strainf)) +
  geom_point(alpha = 0.5) + theme_classic() +
  geom_line(aes(y = fit), data = d) +
  geom_ribbon(aes(ymin = low, ymax = upp, y = NULL, fill = strainf),
    color = NA, alpha = 0.25, data = d) +
  theme(legend.position = c(0.9, 0.8)) + guides(fill = FALSE) +
  labs(x = "Concentration", y = "Organisms", color = "Strain")
```

```
Warning: The `<scale>` argument of `guides()` cannot be `FALSE`. Use
"none" instead as of ggplot2 3.3.4.
```

```
plot(p)
```

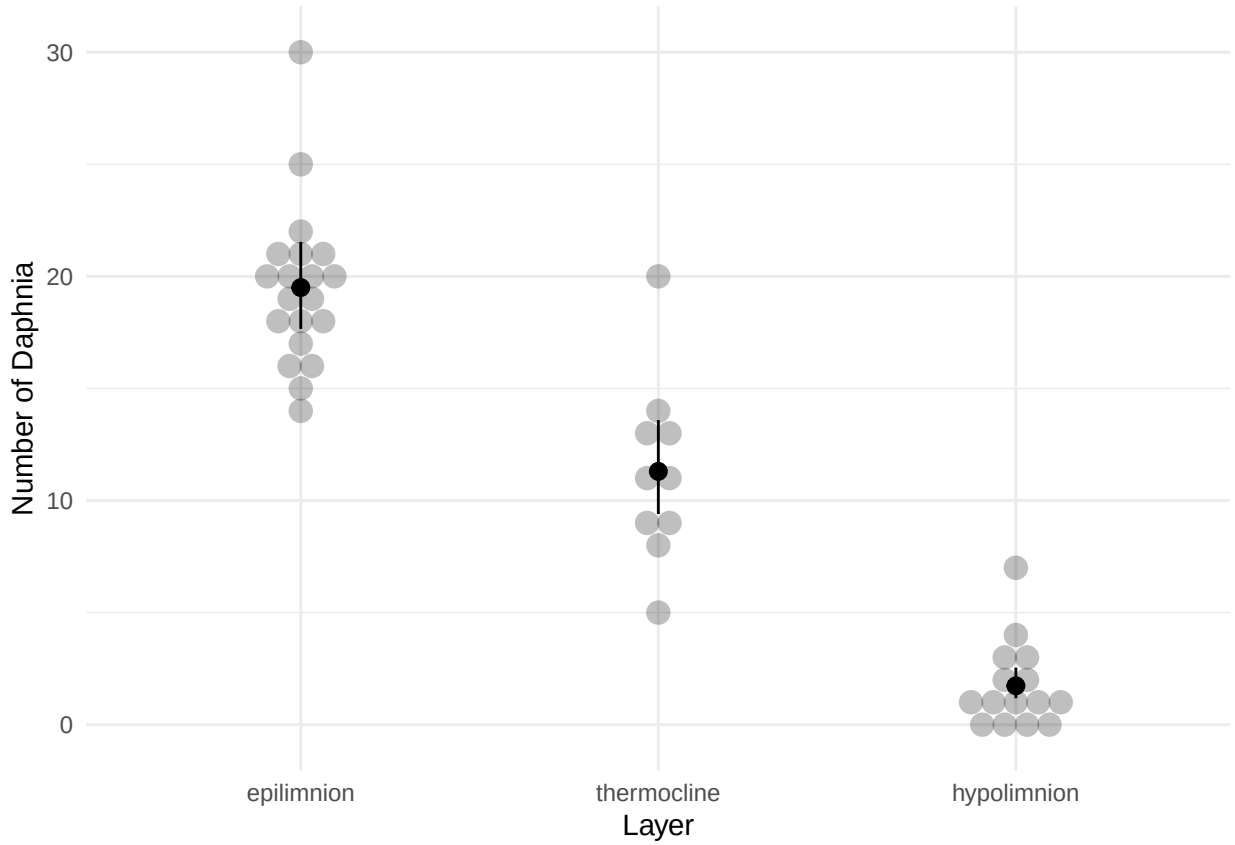


We might visualize the model for the `daphniastrat` data as follows.

```
m <- glm(count ~ layer, family = poisson(link = log), data = daphniastrat)

d <- data.frame(layer = unique(daphniastrat$layer))
d <- cbind(d, glmint(m, newdata = d))

p <- ggplot(daphniastrat, aes(x = layer, y = count)) +
  geom_dotplot(binaxis = "y", binwidth = 1, stackdir = "center", alpha = 0.25) +
  labs(x = "Layer", y = "Number of Daphnia") +
  theme_minimal() + geom_pointrange(aes(y = fit, ymin = low, ymax = upp), data = d)
plot(p)
```



GLMs Versus Nonlinear Regression

There is a very close relationship between a GLM and a nonlinear regression model. We can try to estimate the model above using `nlm` as follows, using the estimates as starting values for convenience.

```
m <- nls(count ~ exp(b0 + b1 * concentration + b2 * (strainf == "b")),
  data = ceriodaphniastrain, start = list(b0 = 7, b1 = -2, b2 = 0.12))
summary(m)$coefficients
```

```
   Estimate Std. Error t value  Pr(>|t|)
b0   4.4821    0.02894  154.86 2.486e-87
b1  -1.5679    0.06232  -25.16 7.441e-36
b2  -0.3267    0.04506   -7.25 5.402e-10
```

The estimates are not the same. But consider that the GLM assumes that

$$\text{Var}(Y_i) = E(Y_i),$$

so our weights should be $w_i = 1/E(Y_i)$. Consider then an iteratively weighted least squares algorithm with $w_i = 1/\hat{y}_i$.

```
ceriodaphniastrain$w <- 1
for (i in 1:10) {
  m <- nls(count ~ exp(b0 + b1 * concentration + b2 * (strainf == "b")),
    data = ceriodaphniastrain, start = list(b0 = 7, b1 = -2, b2 = 0.12),
    weights = w)
  ceriodaphniastrain$w <- 1 / predict(m, type = "response")
}
summary(m)$coefficients
```

```
   Estimate Std. Error t value  Pr(>|t|)
b0    4.455    0.04272 104.273 7.167e-76
b1   -1.543    0.05087 -30.334 7.309e-41
b2   -0.275    0.05280  -5.208 1.988e-06
```

Compare that with what we obtained using `glm`.

```
m <- glm(count ~ concentration + strainf, data = ceriodaphniastrain,
  family = poisson(link = log))
summary(m)$coefficients
```

```
             Estimate Std. Error z value   Pr(>|z|)
(Intercept)     4.455    0.03914 113.819  0.000e+00
concentration  -1.543    0.04660 -33.111 2.057e-240
strainfb       -0.275    0.04837  -5.684  1.313e-08
```

The parameter estimates are the same, but the standard errors are not. Why? The GLM assumes $\text{Var}(Y_i) = E(Y_i)$ whereas the iteratively weighted least squares approach assumes $\text{Var}(Y_i) \propto E(Y_i)$.

GLMs Versus Response Variable Transformations

It is important to note that, for example, the GLM

$$\log E(Y_i) = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_k x_{ik}.$$

is *not* equivalent to a linear model with a transformed response,

$$E[\log(Y_i)] = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_k x_{ik},$$

because $\log[E(Y_i)] \neq E[\log(Y_i)]$ (although in practice they can produce similar results).