Wednesday, February 26

Parameter Interpretation With Log Link Functions

A GLM with a log link function, like a Poisson regression model, has the form

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

or

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

which can also be written as a "multiplicative model" of the form

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

Recall that $e^{a+b} = e^a e^b$. For this reason the parameters $\beta_1, \beta_2, \ldots, \beta_k$ or linear functions thereof are not interpreted the same way as in the *additive* model

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

but they are still relatively easy to interpret in terms of *multiplicative* rather than *additive* changes in $E(Y)$.

Rate Ratios (Quantitative Explanatory Variable)

Consider the model

$$\log E(Y) = \beta_0 + \beta_1 x,$$

and let

$$\log E(Y_a) = \beta_0 + \beta_1(x+1) \quad \text{and} \quad \log E(Y_b) = \beta_0 + \beta_1 x$$

for an arbitrary value of x. Then the *difference* in the log of the expected values is

$$\log E(Y_a) - \log E(Y_b) = \underbrace{\beta_0 + \beta_1(x+1)}_{\log E(Y_a)} - \underbrace{(\beta_0 + \beta_1 x)}_{\log E(Y_b)} = \beta_1,$$

meaning that β_1 is the *additive* change in $\log E(Y)$ per unit increase in x.

Now consider the same model written as

$$E(Y) = e^{\beta_0} e^{\beta_1 x},$$

and let

$$E(Y_a) = e^{\beta_0} e^{\beta_1(x+1)} \quad \text{and} \quad E(Y_b) = e^{\beta_0} e^{\beta_1 x}$$

for an arbitrary value of x. Then the *ratio* of the expected values is

$$\frac{E(Y_a)}{E(Y_b)} = \frac{\overbrace{e^{\beta_0} e^{\beta_1(x+1)}}^{E(Y_a)}}{\underbrace{e^{\beta_0} e^{\beta_1 x}}_{E(Y_b)}} = \frac{e^{\beta_0} e^{\beta_1 x} e^{\beta_1}}{e^{\beta_0} e^{\beta_1 x}} = e^{\beta_1} \Rightarrow E(Y_a) = E(Y_b) e^{\beta_1},$$

so that $E(Y)$ changes by a *factor* of e^{β_1} per unit increase in x. The "exponentiated" parameter, e^{β_1}, is sometimes called a "rate ratio" because it is often the ratio of two rates when the counts are per unit space, time, or something else.

Example: Consider again the `ceriodaphniastrain` data and model.

```
library(trtools)
ceriodaphniastrain$strainf <- factor(ceriodaphniastrain$strain,
  labels = c("a","b"))
m <- glm(count ~ concentration + strainf,
  family = poisson, data = ceriodaphniastrain) # log link is default
cbind(summary(m)$coefficients, confint(m))
```

```
             Estimate Std. Error z value  Pr(>|z|) 2.5 % 97.5 %
(Intercept)     4.455     0.0391  113.82  0.00e+00  4.38   4.53
concentration  -1.543     0.0466  -33.11 2.06e-240 -1.63  -1.45
strainfb       -0.275     0.0484   -5.68  1.31e-08 -0.37  -0.18
```

```
exp(cbind(coef(m), confint(m))) # coef extracts the parameter estimates only
```

```
                    2.5 % 97.5 %
(Intercept)   86.025 79.615 92.817
concentration  0.214  0.195  0.234
strainfb       0.760  0.691  0.835
```

Note: It only makes sense to apply the exponential function to the point estimates and the endpoints of the confidence interval. A standard error of $e^{\hat{\beta}_1}$ could be obtained, but it is **not** equal to the exponentiated standard error of $\hat{\beta}_1$. A test concerning e^{β_1} can be done using either the confidence interval or by stated the hypotheses in terms of β_1 (e.g., the null hypothesis that $e^{\beta_1} = 1$ is the same as the null hypothesis that $\beta_1 = 0$).

Another approach is to use `lincon` and the `tf` (transformation function) argument.

```
lincon(m, tf = exp)
```

```
             estimate  lower  upper
(Intercept)    86.025 79.673 92.884
concentration   0.214  0.195  0.234
strainfb        0.760  0.691  0.835
```

Note that the confidence interval endpoints are not quite the same as what we obtained using `confint`. This is because `confint` and `lincon` use different approaches to confidence intervals (more on that later).

Example: Consider a model for the expected number of matings of African elephants as a function of age.

```
library(Sleuth3)
head(case2201)
```

```
  Age Matings
1  27       0
2  28       1
3  28       1
4  28       1
5  28       3
6  29       0
```

```
m <- glm(Matings ~ Age, family = poisson, data = case2201)
cbind(summary(m)$coefficients, confint(m))
```

```
            Estimate Std. Error z value Pr(>|z|)   2.5 %  97.5 %
(Intercept)  -1.5820     0.5446    -2.9 3.68e-03 -2.6667 -0.5289
Age           0.0687     0.0137     5.0 5.81e-07  0.0417  0.0956
```

```
exp(cbind(m$coefficients, confint(m)))
```

```
                  2.5 % 97.5 %
(Intercept) 0.206 0.0695  0.589
Age         1.071 1.0426  1.100
```

Percent Change (Quantitative Explanatory Variable)

The *percent change* in the expected response is

$$100\% \times \left[\frac{E(Y_a) - E(Y_b)}{E(Y_b)}\right] = 100\% \times [E(Y_a)/E(Y_b) - 1],$$

where $E(Y_a)$ and $E(Y_b)$ are the expected responses at two different points (a and b) defined in terms of the explanatory variable(s).

1. Note that if this is *positive* then it is a percent *increase*, whereas if it is negative then it is a percent *decrease*.
2. The ratio $E(Y_a)/E(Y_b)$ is the *rate ratio*.

Example: Suppose we have the model $\log E(Y) = \beta_0 + \beta_1 x$ where x is a quantitative variable and $\beta_1 = 0.22$. Then $e^{\beta_1} \approx 1.25$. So when x increases by one unit (i.e., to $x + 1$), — i.e., from $E(Y_b) = e^{\beta_0} e^{\beta_1 x}$ to $E(Y_a) = e^{\beta_0} e^{\beta_1 (x+1)}$ then the expected response *increases* by a *factor* of

$$E(Y_a)/E(Y_b) = e^{\beta_1} \approx 1.25,$$

and because

$$100\% \times [1.25 - 1] = 25\%.$$

we can say that it *increases* by 25%.

Example: Consider again the model for the elephant mating data.

```
m <- glm(Matings ~ Age, family = poisson, data = case2201)
exp(cbind(m$coefficients, confint(m)))
```

```
                  2.5 % 97.5 %
(Intercept) 0.206 0.0695  0.589
Age         1.071 1.0426  1.100
```

The percent change in the expected count per unit (year) increase in Age is approximately 100%(1.07 - 1) = 7% (i.e., a 7% increase).

Example: Suppose we have the model $\log E(Y) = \beta_0 + \beta_1 x$ where x is a quantitative variable and $\beta_1 = -0.22$. Then $e^{\beta_1} \approx 0.8$. So when x increases by one unit (i.e., to $x + 1$), — i.e., from $E(Y_b) = e^{\beta_0} e^{\beta_1 x}$ to $E(Y_a) = e^{\beta_0} e^{\beta_1 (x+1)}$ then the expected response *decreases* by a *factor* of

$$E(Y_a)/E(Y_b) = e^{\beta_1} \approx 0.8,$$

or because

$$100\% \times [0.8 - 1] = -20\%$$

we can say that it *decreases* by 20%.

Example: Consider again the model for the `ceriodaphniastrain` data.

```
m <- glm(count ~ concentration + strainf, family = poisson, data = ceriodaphniastrain)
exp(cbind(coef(m), confint(m)))
```

```
                    2.5 % 97.5 %
(Intercept)   86.025 79.615 92.817
concentration  0.214  0.195  0.234
strainfb       0.760  0.691  0.835
```

The percent change in the expected count per unit increase in concentration is approximately 100%(0.21 - 1) = -79% (i.e., a 79% decrease or reduction).

Rate Ratios (Categorical Explanatory Variable)

Consider the model

$$\log E(Y) = \beta_0 + \beta_1 x, \quad \text{or, equivalently,} \quad E(Y) = e^{\beta_0} e^{\beta_1 x},$$

where

$$x = \begin{cases} 1, & \text{if the observation is in group } a, \\ 0, & \text{if the observation is in group } b. \end{cases}$$

Then

$$E(Y) = \begin{cases} e^{\beta_0} e^{\beta_1}, & \text{if the observation is in group } a, \\ e^{\beta_0}, & \text{if the observation is in group } b. \end{cases}$$

Let

$$E(Y_a) = e^{\beta_0} e^{\beta_1} \quad \text{and} \quad E(Y_b) = e^{\beta_0}.$$

Then the *ratio* of the expected values is

$$\frac{E(Y_a)}{E(Y_b)} = \frac{e^{\beta_0} e^{\beta_1}}{e^{\beta_0}} = e^{\beta_1} \Leftrightarrow E(Y_a) = E(Y_b) e^{\beta_1}$$

so that $E(Y_a)$ is e^{β_1} times that of $E(Y_b)$. Also

$$\frac{E(Y_b)}{E(Y_a)} = \frac{e^{\beta_0}}{e^{\beta_0} e^{\beta_1}} = \frac{1}{e^{\beta_1}} = e^{-\beta_1}.$$

so that $E(Y_b)$ is $1/e^{\beta_1}$ times that of $E(Y_a)$.

Example: Consider again the `ceriodaphniastrain` data and model.

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

```
             Estimate Std. Error z value  Pr(>|z|) 2.5 % 97.5 %
(Intercept)     4.455     0.0391  113.82  0.00e+00  4.38   4.53
concentration  -1.543     0.0466  -33.11 2.06e-240 -1.63  -1.45
strainfb       -0.275     0.0484   -5.68  1.31e-08 -0.37  -0.18
```

```
exp(cbind(coef(m), confint(m)))
```

```
                    2.5 % 97.5 %
(Intercept)   86.025 79.615 92.817
concentration  0.214  0.195  0.234
strainfb       0.760  0.691  0.835
```

Alternatively we can parameterize the model.

```
ceriodaphniastrain$strainf <- relevel(ceriodaphniastrain$strainf, ref = "b")
m <- glm(count ~ concentration + strainf,
  family = poisson, data = ceriodaphniastrain)
cbind(summary(m)$coefficients, confint(m))
```

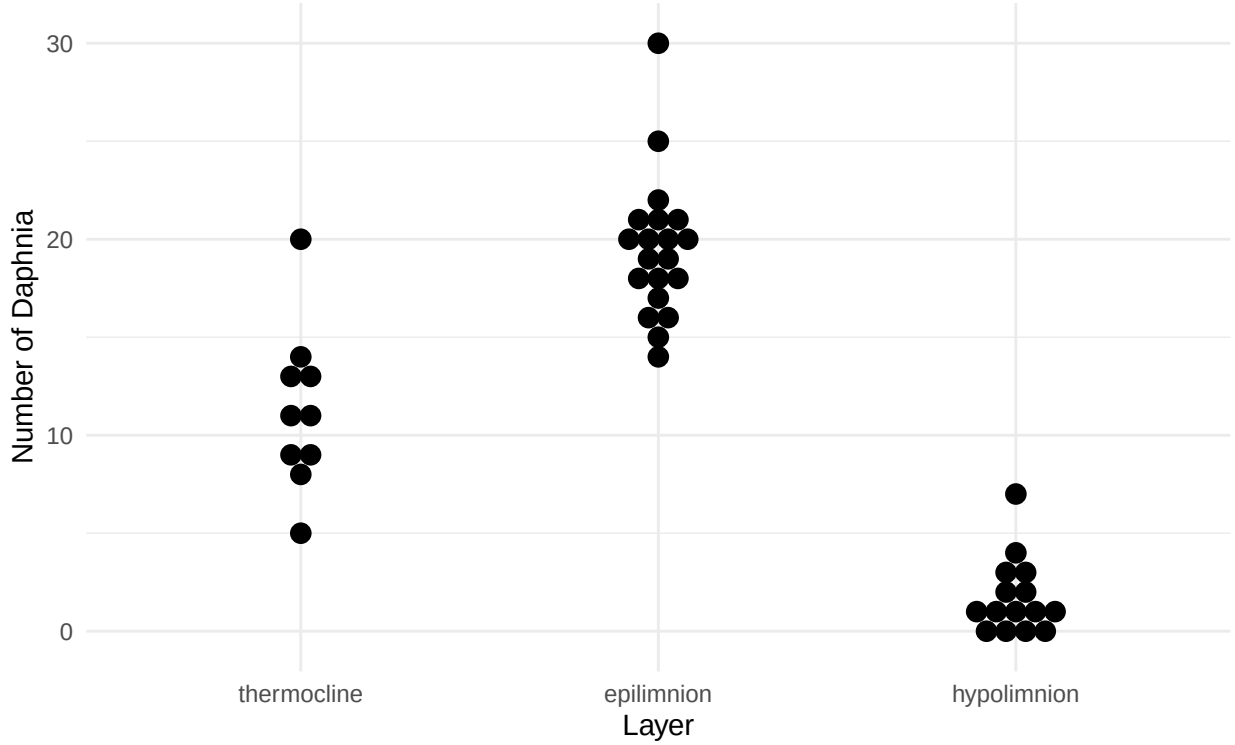
```
             Estimate Std. Error z value  Pr(>|z|) 2.5 % 97.5 %
(Intercept)     4.180     0.0430   97.14  0.00e+00  4.09   4.26
concentration  -1.543     0.0466  -33.11 2.06e-240 -1.63  -1.45
strainfa        0.275     0.0484    5.68  1.31e-08  0.18   0.37
```

```
exp(cbind(coef(m), confint(m)))
```

```
                    2.5 % 97.5 %
(Intercept)    65.344 60.008 71.034
concentration   0.214  0.195  0.234
strainfa        1.316  1.198  1.448
```

Example: Consider these data from a stratified random sampling design and a Poisson regression model.

```
library(trtools)
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)
```




```
daphniastrat$layer <- relevel(daphniastrat$layer, ref = "thermocline")
m <- glm(count ~ layer, family = poisson, data = daphniastrat)
summary(m)$coefficients
```

```
                Estimate Std. Error z value  Pr(>|z|)
(Intercept)        2.425     0.0941   25.78 1.65e-146
layerepilimnion    0.546     0.1068    5.11  3.27e-07
layerhypolimnion  -1.875     0.2175   -8.62  6.74e-18
```

```
exp(cbind(coef(m), confint(m)))
```

```
                        2.5 % 97.5 %
```

```
(Intercept)      11.300 9.3425 13.513
layerepilimnion   1.726 1.4050  2.137
layerhypolimnion  0.153 0.0981  0.231
```

Percent Larger/Smaller (Categorical Explanatory Variable)

The *percent change* in the expected response is

$$100\% \times \left[\frac{E(Y_a) - E(Y_b)}{E(Y_b)}\right] = 100\% \times [E(Y_a)/E(Y_b) - 1]\,,$$

where $E(Y_a)$ and $E(Y_b)$ are the expected responses at two different points (a and b) defined in terms of the explanatory variable(s).

1. Note that if this is *positive* then $E(Y_a)$ is that percent *larger* than $E(Y_b)$, whereas if this is *negative* then $E(Y_b)$ is that percent *smaller* than $E(Y_a)$.
2. The ratio $E(Y_a)/E(Y_b)$ is the *rate ratio*.

Example: Suppose we have the model $\log E(Y) = \beta_0 + \beta_1 x$ where x is an indicator variable for category a and $\beta_1 = 0.22$. Then $e^{\beta_1} \approx 1.25$, $E(Y_a) = e^{\beta_0} e^{\beta_1}$ and $E(Y_b) = e^{\beta_0}$, and $E(Y_a)$ is about 1.25 times *larger* than $E(Y_b)$ because

$$E(Y_a)/E(Y_b) = e^{\beta_1} \approx 1.25,$$

and because

$$100\% \times [1.25 - 1] = 25\%.$$

we can say that $E(Y_a)$ is about 25% *larger* than $E(Y_b)$.

Example: Suppose we have the model $\log E(Y) = \beta_0 + \beta_1 x$ where x is an indicator variable for category a and $\beta_1 = -0.22$. Then $e^{\beta_1} \approx 0.8$, $E(Y_a) = e^{\beta_0} e^{\beta_1}$ and $E(Y_b) = e^{\beta_0}$, and $E(Y_a)$ is about 0.8 times *smaller* than $E(Y_b)$ because

$$E(Y_a)/E(Y_b) = e^{\beta_1} \approx 0.8,$$

and because

$$100\% \times [0.8 - 1] = -20\%.$$

we can say that $E(Y_a)$ is about 20% *smaller* than $E(Y_b)$.

Example: Consider again the model for the daphnia data.

```
exp(cbind(coef(m), confint(m)))
```

```
                      2.5 % 97.5 %
(Intercept)      11.300 9.3425 13.513
layerepilimnion   1.726 1.4050  2.137
layerhypolimnion  0.153 0.0981  0.231
```

The expected number of daphnia per liter in the epilimnion layer is estimated to be about 100%(1.73-1) = 73% more than in the thermocline layer. And because 100%(0.15-1) = -85% we estimate that the the expected number of daphia per liter in the hypolimnion layer is 85% less than it is in the thermocline layer.

Contrasts With Log Link Functions

With a log link function a "contrast" as produced by the `contrast` function has the general form

$$\log E(Y_a) - \log E(Y_b) = \log\left[\frac{E(Y_a)}{E(Y_b)}\right],$$

where the indices a and b denote specific values of the explanatory variables. If we apply the exponential function to the contrast then it becomes

$$\exp[\log E(Y_a) - \log E(Y_b)] = \frac{E(Y_a)}{E(Y_b)},$$

So applying the exponential function to contrasts allows us to interpret them as ratios.

Example: Consider again the stratified random sampling design. Suppose we want to compare the epilimnion and thermocline layers to the hypolimnion layer. We can use `contrast` and apply the exponential function (`exp` in R) through the argument `tf` (for "transformation function"). Note that this function is only applied to the estimates and the confidence intervals.

```
trtools::contrast(m,
    a = list(layer = c("epilimnion","thermocline")),
    b = list(layer = "hypolimnion"),
    cnames = c("epil vs hypo","therm vs hypo"))
```

```
              estimate    se lower upper tvalue  df   pvalue
epil vs hypo      2.42 0.203  2.02  2.82  11.95 Inf 6.52e-33
therm vs hypo     1.87 0.218  1.45  2.30   8.62 Inf 6.74e-18
```

```
trtools::contrast(m,
    a = list(layer = c("epilimnion","thermocline")),
    b = list(layer = "hypolimnion"),
    cnames = c("epil/hypo","therm/hypo"), tf = exp)
```

```
           estimate lower upper
epil/hypo     11.25  7.56 16.73
therm/hypo     6.52  4.26  9.98
```

The following gives us inferences for the *logarithm* of the expected count for each layer.

```
trtools::contrast(m, a = list(layer = c("epilimnion","thermocline","hypolimnion")),
    cnames = c("epilimnion","thermocline","hypolimnion"))
```

```
            estimate     se lower upper tvalue  df    pvalue
epilimnion      2.97 0.0506 2.871 3.070   58.7 Inf  0.00e+00
thermocline     2.42 0.0941 2.240 2.609   25.8 Inf 1.65e-146
hypolimnion     0.55 0.1961 0.166 0.934    2.8 Inf  5.04e-03
```

To produce the estimates of the expected counts we need to apply the exponential function.

```
trtools::contrast(m, a = list(layer = c("epilimnion","thermocline","hypolimnion")),
    cnames = c("epilimnion","thermocline","hypolimnion"), tf = exp)
```

```
            estimate lower upper
epilimnion     19.50 17.66 21.53
thermocline    11.30  9.40 13.59
hypolimnion     1.73  1.18  2.55
```

The **emmeans** package can also produce inferences for expected counts and rate ratios for categorical explanatory variables if we specify `type = "response"`.

```
library(emmeans)
emmeans(m, ~layer, type = "response")
```

```
 layer        rate    SE  df asymp.LCL asymp.UCL
 thermocline 11.30 1.060 Inf      9.40     13.59
 epilimnion  19.50 0.987 Inf     17.66     21.53
```

```
 hypolimnion  1.73 0.340 Inf      1.18      2.55

Confidence level used: 0.95
Intervals are back-transformed from the log scale
```

```
pairs(emmeans(m, ~layer), type = "response", adjust = "none", infer = TRUE)
```

```
 contrast                  ratio    SE  df asymp.LCL asymp.UCL null z.ratio p.value
 thermocline / epilimnion   0.58 0.062 Inf      0.47      0.71    1  -5.110  <.0001
 thermocline / hypolimnion  6.52 1.420 Inf      4.26      9.98    1   8.620  <.0001
 epilimnion / hypolimnion  11.25 2.280 Inf      7.56     16.73    1  11.950  <.0001

Confidence level used: 0.95
Intervals are back-transformed from the log scale
Tests are performed on the log scale
```

Suppose we want the rate ratios comparing the epilimnion and thermocline with the hypolimnion layer.

```
contrast(emmeans(m, ~layer, type = "response"),
  method = "trt.vs.ctrl", ref = 3, type = "response", infer = TRUE, adjust = "none")
```

```
 contrast                  ratio   SE  df asymp.LCL asymp.UCL null z.ratio p.value
 thermocline / hypolimnion  6.52 1.42 Inf      4.26      9.98    1   8.620  <.0001
 epilimnion / hypolimnion  11.25 2.28 Inf      7.56     16.73    1  11.950  <.0001

Confidence level used: 0.95
Intervals are back-transformed from the log scale
Tests are performed on the log scale
```

Another tool that you can use if you want inferences about the expected response is the `glmint` function from the **trtools** package.

```
d <- data.frame(layer = c("epilimnion","thermocline","hypolimnion"))
glmint(m, newdata = d) # syntax similar to predict and nlsint
```

```
    fit   low   upp
1 19.50 17.66 21.53
2 11.30  9.40 13.59
3  1.73  1.18  2.55
```

Example: Consider again the model for the `ceriodaphniastrain` data. Consider first the effect of increasing concentration by one percent.

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

```
             Estimate Std. Error z value  Pr(>|z|)
(Intercept)     4.180     0.0430   97.14  0.00e+00
concentration  -1.543     0.0466  -33.11 2.06e-240
strainfa        0.275     0.0484    5.68  1.31e-08
```

```
exp(cbind(coef(m), confint(m)))
```

```
                    2.5 % 97.5 %
(Intercept)   65.344 60.008 71.034
concentration  0.214  0.195  0.234
strainfa       1.316  1.198  1.448
```

We can estimate the rate ratio for a one unit increase in concentration for each strain.

```
trtools::contrast(m,
    a = list(concentration = 1, strainf = c("a","b")),
    b = list(concentration = 0, strainf = c("a","b")),
    cnames = c("a","b"), tf = exp)
```

```
  estimate lower upper
a    0.214 0.195 0.234
b    0.214 0.195 0.234
```

Here is how we can do that with the **emmeans** package. This statement will give us the expected response for concentrations one unit apart for each strain.

```
emmeans(m, ~concentration|strainf,
  at = list(concentration = c(1,0)), type = "response")
```

```
strainf = b:
 concentration rate   SE  df asymp.LCL asymp.UCL
             1 14.0 0.61 Inf      12.8      15.2
             0 65.3 2.81 Inf      60.1      71.1

strainf = a:
 concentration rate   SE  df asymp.LCL asymp.UCL
             1 18.4 0.73 Inf      17.0      19.9
             0 86.0 3.37 Inf      79.7      92.9

Confidence level used: 0.95
Intervals are back-transformed from the log scale
```

Now we can compare them.

```
pairs(emmeans(m, ~concentration|strainf, at = list(concentration = c(1,0)),
  type = "response"), infer = TRUE)
```

```
strainf = b:
 contrast                       ratio      SE  df asymp.LCL asymp.UCL null z.ratio p.value
 concentration1 / concentration0 0.214 0.00996 Inf     0.195     0.234    1 -33.100  <.0001

strainf = a:
 contrast                       ratio      SE  df asymp.LCL asymp.UCL null z.ratio p.value
 concentration1 / concentration0 0.214 0.00996 Inf     0.195     0.234    1 -33.100  <.0001

Confidence level used: 0.95
Intervals are back-transformed from the log scale
Tests are performed on the log scale
```

We can estimate the rate ratio comparing the strains at difference concentrations.

```
trtools::contrast(m,
    a = list(concentration = c(0, 1, 2), strainf = "a"),
    b = list(concentration = c(0, 1, 2), strainf = "b"),
    cnames = c("0%", "1%", "2%"), tf = exp)
```

```
   estimate lower upper
0%     1.32   1.2  1.45
1%     1.32   1.2  1.45
2%     1.32   1.2  1.45
```

We can also use `contrast` to estimate the expected count for, say, strain `a` at different concentration values.

```
trtools::contrast(m, a = list(concentration = c(0, 1, 2), strainf = "a"),
  cnames = c("0%", "1%", "2%"), tf = exp)
```

```
   estimate lower upper
0%    86.03 79.67 92.88
1%    18.39 17.01 19.87
2%     3.93  3.38  4.57
```

We can also use the **emmeans** package for inferences about expected counts and rate ratios for categorical explanatory variables.

```
library(emmeans)
emmeans(m, ~ strainf, type = "response",
  at = list(concentration = 0))
```

```
 strainf rate   SE  df asymp.LCL asymp.UCL
 b       65.3 2.81 Inf      60.1      71.1
 a       86.0 3.37 Inf      79.7      92.9

Confidence level used: 0.95
Intervals are back-transformed from the log scale
```

```
pairs(emmeans(m, ~ strainf, type = "response",
  at = list(concentration = 0)), reverse = TRUE)
```

```
 contrast ratio     SE  df null z.ratio p.value
 a / b     1.32 0.0637 Inf    1   5.680  <.0001

Tests are performed on the log scale
```

Now suppose we add an interaction between concentration and strain.

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

```
                      Estimate Std. Error z value Pr(>|z|)
(Intercept)              4.144     0.0510   81.25 0.00e+00
concentration           -1.473     0.0701  -21.01 4.80e-98
strainfa                 0.337     0.0670    5.02 5.11e-07
concentration:strainfa  -0.125     0.0939   -1.34 1.82e-01
```

```
trtools::contrast(m,
    a = list(concentration = 1, strainf = c("a","b")),
    b = list(concentration = 0, strainf = c("a","b")),
    cnames = c("a","b"), tf = exp)
```

```
  estimate lower upper
a    0.202 0.179 0.229
b    0.229 0.200 0.263
```

```
trtools::contrast(m,
    a = list(concentration = c(0, 1, 2), strainf = "a"),
    b = list(concentration = c(0, 1, 2), strainf = "b"),
    cnames = c("0%", "1%", "2%"), tf = exp)
```

```
   estimate lower upper
0%     1.40 1.228  1.60
```

```
1%      1.24 1.082  1.41
2%      1.09 0.813  1.46
```

Now the rate ratio for concentration depends on strain and the rate ratio for strain depends on concentration when there is an interaction term.