Monday, Mar 27

Distributions for Over-dispersion

One way to model over-dispersion is to assume a model of the form

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

where ζ_i is an *unobserved* unit-specific random quantity that represents one or more unobserved explanatory variables that vary over units.

The Negative Binomial Distribution

Suppose that Y_i has a Poisson distribution *conditional* on ζ_i, and e^{ζ_i} has a *gamma* distribution such that $E(e^{\gamma_i}) = 1$ and $\text{Var}(e^{\gamma_i}) = \alpha > 0$. The *marginal* distribution of Y_i is then a *negative binomial distribution*, with mean structure

$$g[E(Y_i)] = \eta_i,$$

and variance structure

$$\text{Var}(Y_i) = E(Y_i) + \alpha E(Y_i)^2 \geq E(Y_i).$$

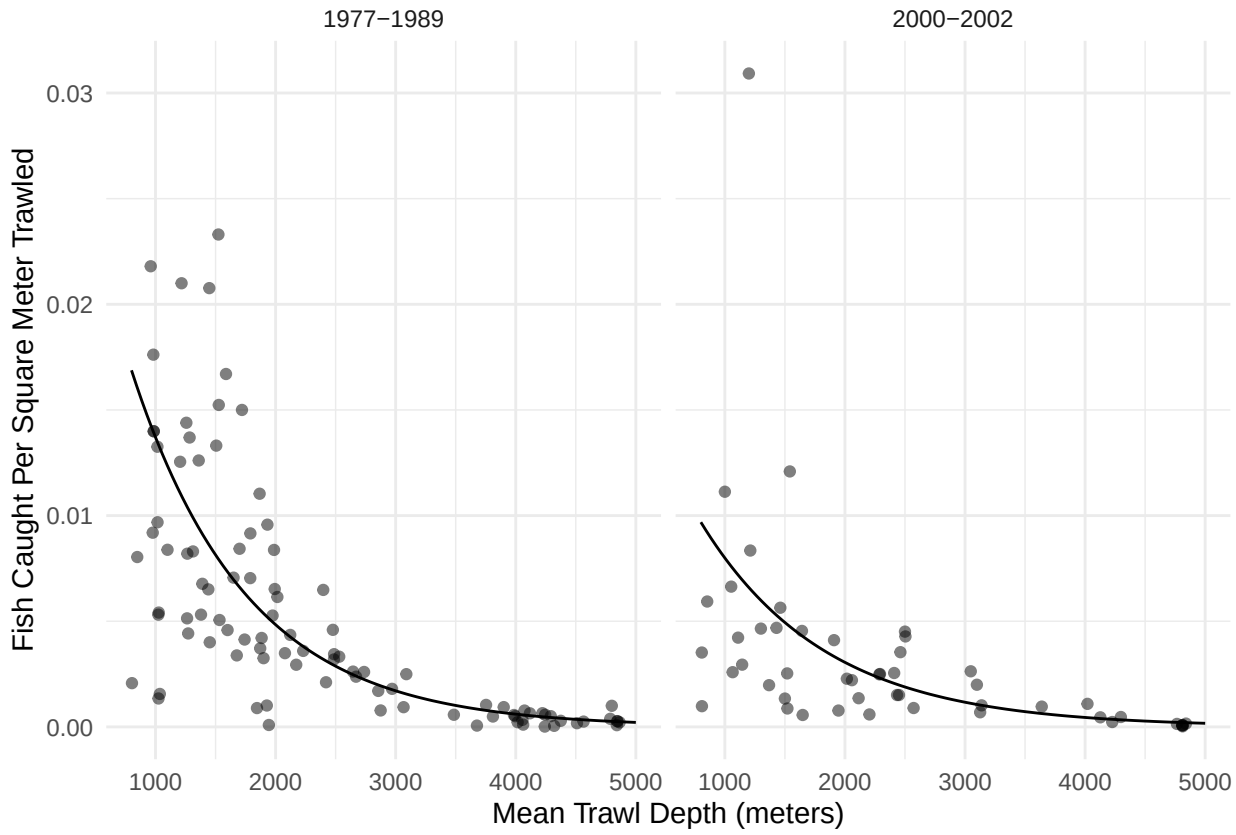
The Poisson distribution is a special case where $\alpha = 0$. This variance structure *does not* have the form

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

unless α is known (which it normally is not), so this model is not a traditional GLM. But we can make inferences using maximum likelihood.

Example: Consider our model for the trawl fishing data. Here we will consider a negative binomial regression model.

```
library(COUNT)
data(fishing)

library(MASS) # for the glm.nb function (note there is no family argument)

m <- glm.nb(totabund ~ period * meandepth + offset(log(sweptarea)),
  link = log, data = fishing)

d <- expand.grid(sweptarea = 1, period = levels(fishing$period),
  meandepth = seq(800, 5000, length = 100))
d$yhat <- predict(m, newdata = d, type = "response")

p <- ggplot(fishing, aes(x = meandepth, y = totabund/sweptarea)) +
  geom_point(alpha = 0.5) + facet_wrap(~ period) + theme_minimal() +
  labs(x = "Mean Trawl Depth (meters)",
    y = "Fish Caught Per Square Meter Trawled") +
  geom_line(aes(y = yhat), data = d)
plot(p)
```

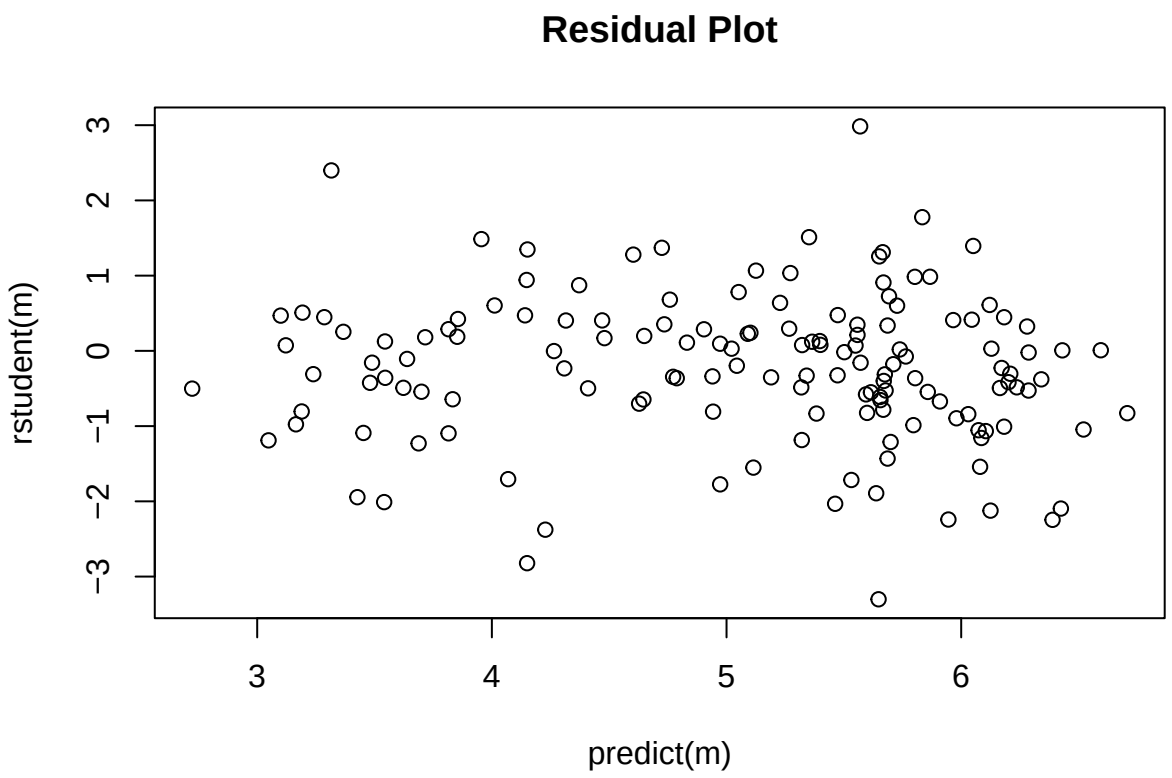



```
summary(m) # note that what glm.nb calls theta equals 1/alpha
```

```
Call:
glm.nb(formula = totabund ~ period * meandepth + offset(log(sweptarea)),
    data = fishing, link = log, init.theta = 1.961162176)

Deviance Residuals:
   Min      1Q  Median      3Q     Max
-3.366  -0.830  -0.208   0.365   2.893

Coefficients:
                          Estimate Std. Error z value Pr(>|z|)
(Intercept)              -3.25e+00   1.59e-01  -20.40   <2e-16 ***
period2000-2002          -6.19e-01   2.73e-01   -2.27    0.023 *
meandepth                -1.04e-03   5.92e-05  -17.58   <2e-16 ***
period2000-2002:meandepth  7.95e-05   1.01e-04    0.79    0.432
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(1.961) family taken to be 1)

    Null deviance: 471.79  on 146  degrees of freedom
Residual deviance: 159.31  on 143  degrees of freedom
AIC: 1763

Number of Fisher Scoring iterations: 1
```

```
          Theta:  1.961
      Std. Err.:  0.219

 2 x log-likelihood:  -1752.713
```

```
plot(predict(m), rstudent(m), main = "Residual Plot")
```



Interestingly inferences based on the negative binomial model are very similar to those obtained using quasi-likelihood assuming the variance structure $V(Y_i) = \phi E(Y_i)^2$. Here are the parameter estimates, standard errors, and confidence intervals.

```
m.negbn <- glm.nb(totabund ~ period * meandepth + offset(log(sweptarea)),
  link = log, data = fishing)
m.quasi <- glm(totabund ~ period * meandepth + offset(log(sweptarea)),
  family = quasi(link = "log", variance = "mu^2"), data = fishing)
cbind(summary(m.negbn)$coefficients, confint(m.negbn))
```

```
                            Estimate Std. Error  z value  Pr(>|z|)      2.5 %     97.5 %
(Intercept)               -3.249e+00  1.592e-01 -20.4044 1.529e-92 -3.5603979 -2.9274102
period2000-2002           -6.187e-01  2.726e-01  -2.2695 2.324e-02 -1.1815413 -0.0436165
meandepth                 -1.041e-03  5.923e-05 -17.5844 3.245e-69 -0.0011578 -0.0009213
period2000-2002:meandepth  7.955e-05  1.013e-04   0.7855 4.322e-01 -0.0001333  0.0002952
```

```
cbind(summary(m.quasi)$coefficients, confint(m.quasi))
```

```
                            Estimate Std. Error  t value  Pr(>|t|)      2.5 %     97.5 %
(Intercept)               -3.250e+00  1.592e-01 -20.4180 3.187e-44 -3.5609660 -2.9294775
period2000-2002           -6.041e-01  2.720e-01  -2.2212 2.791e-02 -1.1672726 -0.0287948
meandepth                 -1.041e-03  5.866e-05 -17.7403 5.988e-38 -0.0011552 -0.0009217
period2000-2002:meandepth  7.272e-05  9.992e-05   0.7278 4.679e-01 -0.0001381  0.0002870
```

Here are the estimates of the rate ratios for period at several different depths.

```
library(trtools)
contrast(m.negbn,
  a = list(meandepth = c(1000,2000,3000,4000,5000), period = "2000-2002", sweptarea = 1),
  b = list(meandepth = c(1000,2000,3000,4000,5000), period = "1977-1989", sweptarea = 1),
  cnames = c("1000m","2000m","3000m","4000m","5000m"), tf = exp)
```

```
      estimate  lower  upper
1000m   0.5832 0.4017 0.8468
2000m   0.6315 0.4868 0.8193
3000m   0.6838 0.5184 0.9020
4000m   0.7404 0.4928 1.1125
5000m   0.8017 0.4494 1.4301
```

```
contrast(m.quasi,
  a = list(meandepth = c(1000,2000,3000,4000,5000), period = "2000-2002", sweptarea = 1),
  b = list(meandepth = c(1000,2000,3000,4000,5000), period = "1977-1989", sweptarea = 1),
  cnames = c("1000m","2000m","3000m","4000m","5000m"), tf = exp)
```

```
      estimate  lower  upper
1000m   0.5878 0.4046 0.8540
2000m   0.6321 0.4869 0.8206
3000m   0.6798 0.5173 0.8935
4000m   0.7311 0.4905 1.0897
5000m   0.7863 0.4458 1.3867
```

Here are the tests (likelihood ratio and F) for the "effect" of period. The null model assumes that expected abundance per unit area trawled is the same each period at a given depth. Put another way, the null model assumes that the rate ratio for period is one for all depths.

```
m.negbn.null <- glm.nb(totabund ~ meandepth + offset(log(sweptarea)),
  link = log, data = fishing)
anova(m.negbn.null, m.negbn)
```

```
Likelihood ratio tests of Negative Binomial Models

Response: totabund
                                        Model theta Resid. df    2 x log-lik.   Test    df LR stat.
1          meandepth + offset(log(sweptarea)) 1.832       145           -1764
2 period * meandepth + offset(log(sweptarea)) 1.961       143           -1753 1 vs 2     2    11.11
   Pr(Chi)
1
2 0.003872
```

```
m.quasi.null <- glm(totabund ~ meandepth + offset(log(sweptarea)),
  family = quasi(link = "log", variance = "mu^2"), data = fishing)
anova(m.quasi.null, m.quasi, test = "F")
```

```
Analysis of Deviance Table

Model 1: totabund ~ meandepth + offset(log(sweptarea))
Model 2: totabund ~ period * meandepth + offset(log(sweptarea))
  Resid. Df Resid. Dev Df Deviance    F Pr(>F)
1       145       90.5
2       143       84.5  2     5.94 5.74  0.004 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Note: When using `anova` for a negative binomial model (estimated using the `glm.nb` function) we omit the `test = "LRT"` option which we use for generalized linear models. Somewhat confusingly, the `anova` function will do a likelihood ratio test for a `glm.nb` object, but will throw an error if we try to change the test type (even if we ask for a likelihood ratio test).

Heteroscedastic Consistent (Robust) Standard Errors

An alternative is to accept that the specified variance structure is incorrect and estimate standard errors in a way that provides *consistent* estimates despite the misspecification of the variance structure.[1]

Note: I needed to specify the data set as `trtools::rotifer` below as there is a data set of the same name in another package that was loaded earlier. It's actually the same data but in a different format from the data frame in the **trtools** package.

Example: Consider the logistic regression model for the `rotifer` data from the **trtools** package.

```
m <- glm(cbind(y, total - y) ~ species + density + species:density,
  family = binomial, data = trtools::rotifer)
```

Here are the parameter estimates and standard errors, with and without using the robust standard error estimates.

```
library(sandwich) # for the vcovHC function
library(lmtest)   # for coeftest and coefci functions
cbind(summary(m)$coefficients, confint(m))
```

```
                 Estimate Std. Error  z value   Pr(>|z|)    2.5 %   97.5 %
(Intercept)      -114.352      4.034 -28.3454 9.534e-177 -122.420 -106.598
speciespm           4.629      6.598   0.7016  4.830e-01   -8.464   17.431
density           108.746      3.857  28.1910 7.535e-175  101.332  116.460
speciespm:density  -3.077      6.329  -0.4862  6.268e-01  -15.354    9.487
```

```
cbind(coeftest(m, vcov = vcovHC), coefci(m, vcov = vcovHC))
```

```
                 Estimate Std. Error z value  Pr(>|z|)   2.5 % 97.5 %
(Intercept)      -114.352      18.31 -6.2449 4.240e-10 -150.24 -78.46
speciespm           4.629      29.91  0.1548 8.770e-01  -53.99  63.25
density           108.746      17.50  6.2137 5.175e-10   74.44 143.05
speciespm:density  -3.077      28.82 -0.1068 9.150e-01  -59.57  53.42
```

An alternative to using `coeftest` and `coefci` is `lincon(m, fcov = vcovHC)`. Now compare our inferences for the odds ratios for the effect of a 0.01 increase in density.

```
contrast(m,
  a = list(density = 0.02, species = c("kc","pm")),
  b = list(density = 0.01, species = c("kc","pm")),
  cnames = c("kc","pm"), tf = exp)
```

```
   estimate lower upper
kc    2.967 2.751 3.200
pm    2.877 2.607 3.174
```

```
contrast(m,
  a = list(density = 0.02, species = c("kc","pm")),
  b = list(density = 0.01, species = c("kc","pm")),
  cnames = c("kc","pm"), tf = exp, fcov = vcovHC)
```

[1] Consistency is a rather technical condition, but roughly speaking a *consistent estimator* is one such that its sampling distribution becomes increasingly concentrated around the value being estimated as n increases.

```
   estimate lower upper
kc    2.967 2.105 4.181
pm    2.877 1.836 4.507
```

For comparison consider also the results when using quasi-likelihood.

```
m <- glm(cbind(y, total - y) ~ species + density + species:density,
  family = quasibinomial, data = trtools::rotifer)
cbind(summary(m)$coefficients, confint(m))
```

```
                  Estimate Std. Error t value  Pr(>|t|)   2.5 % 97.5 %
(Intercept)       -114.352      14.95 -7.6472 4.736e-09 -146.02 -87.01
speciespm            4.629      24.46  0.1893 8.509e-01  -46.15  51.31
density            108.746      14.30  7.6056 5.358e-09   82.60 139.02
speciespm:density   -3.077      23.46 -0.1312 8.964e-01  -47.81  45.70
```

```
contrast(m,
  a = list(density = 0.02, species = c("kc","pm")),
  b = list(density = 0.01, species = c("kc","pm")),
  cnames = c("kc","pm"), tf = exp)
```

```
   estimate lower upper
kc    2.967 2.220 3.965
pm    2.877 1.973 4.195
```

Recall that heteroscedastic consistent standard errors are best used with generous sample sizes. For modest sample sizes (such as this experiment) quasi-likelihood is probably better.

Generalized Linear Models Revisited

Recall that a generalized linear model (GLM) 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*. This is the *mean structure* of the model.

The *variance structure* of a GLM is

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

where ϕ is a *dispersion parameter* and V is the *variance function*.

If we define $h = g^{-1}$ so that $E(Y_i) = h(\eta_i)$ we can write a GLM concisely as

$$E(Y_i) = h(\eta_i) \tag{1}$$
$$\text{Var}(Y_i) = \phi V[h(\eta_i)] \tag{2}$$

to define the *mean structure* and a *variance structure* for Y_i, respectively, by specifying the mean and variance of Y_i to be functions of $x_{i1}, x_{i2}, \ldots, x_{ik}$.

The specification of a generalized linear model therefore requires three components.

1. The *systematic component* $\eta_i = \beta_0 + \beta_1 x_{i1} + \beta_1 x_{i2} + \cdots + \beta_k x_{ik}$.
2. The *link function* g for the mean structure $g[E(Y_i)] = \eta_i$.
3. The *distribution* of the response variable Y_i, which implies the variance structure $\text{Var}(Y_i) = \phi V[E(Y_i)]$, or we can specify the variance structure *directly*.

Four common distributions from the exponential family of distributions (normal/Gaussian, Poisson, gamma, and inverse-Gaussian) imply variance structures of the form

$$\text{Var}(Y_i) = \phi E(Y_i)^p$$

The values of p are $p = 0$ (normal/Gaussian), $p = 1$ (Poisson if $\phi = 1$), $p = 2$ (gamma), and $p = 3$ (inverse-Gaussian). Also note that when using quasi-likelihood we can use other values of p via the `tweedie` function from the **statmod** package.

GLMs for Gamma-Distributed Response Variables

If Y_i has a *gamma* distribution then Y_i is a positive and continuous random variable, and $\text{Var}(Y_i) = \phi E(Y_i)^2$. Such models are sometimes suitable for response variables that are bounded below by zero and right-skewed. Common link functions include the *log* and *inverse* functions. With a log link function we have a mean structure like that for Poisson regression where

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

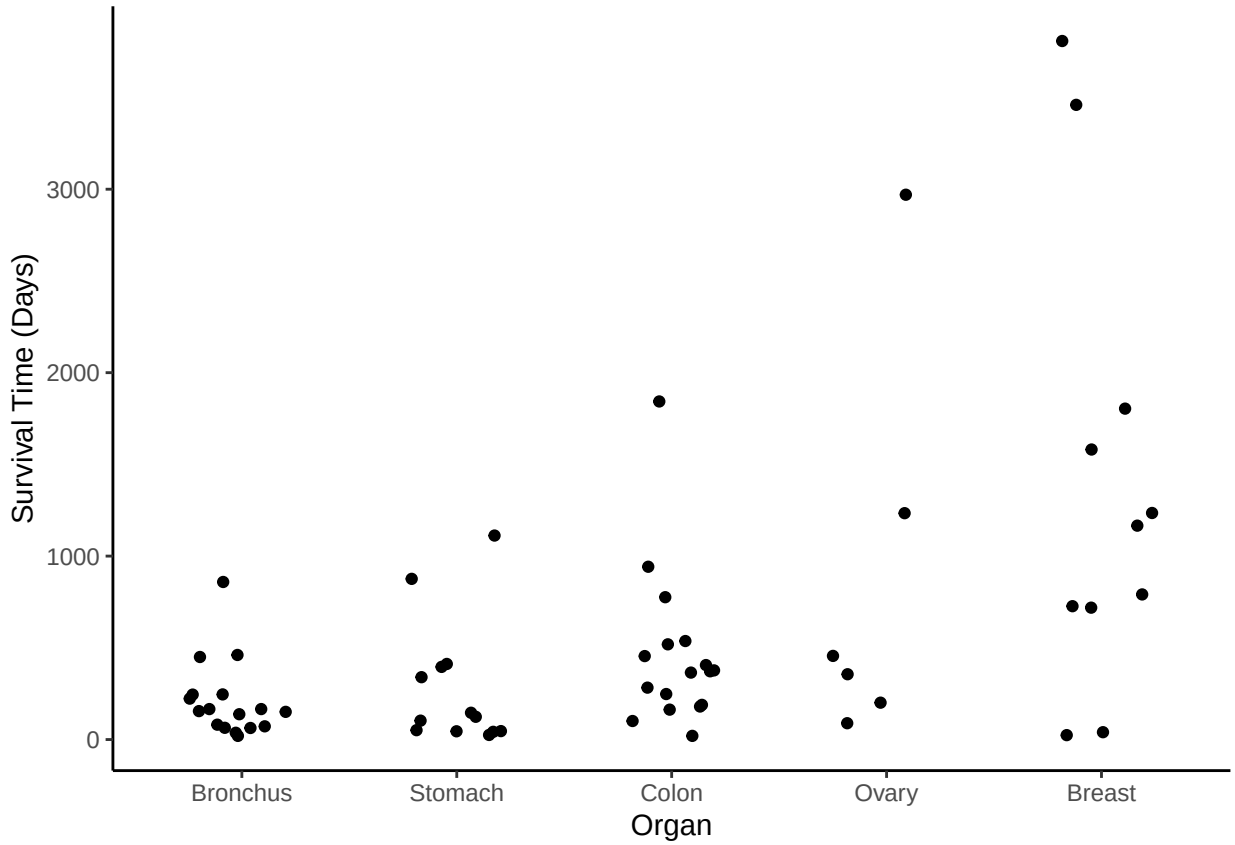
or

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

so the effects of explanatory variables and contrasts can be interpreted by applying the exponential function e^x and interpreting the effects as multiplicative factors or percent increase/decrease or percent larger/smaller.

Example: Consider again the cancer survival time data.

```
library(Stat2Data)
data(CancerSurvival)
CancerSurvival$Organ <- with(CancerSurvival, reorder(Organ, Survival, mean))
p <- ggplot(CancerSurvival, aes(x = Organ, y = Survival)) +
  geom_jitter(height = 0, width = 0.25) +
  labs(y = "Survival Time (Days)") + theme_classic()
plot(p)
```



A gamma model might be appropriate here. First consider a model with a log link function.

```
m <- glm(Survival ~ Organ, family = Gamma(link = log), data = CancerSurvival)
cbind(summary(m)$coefficients, confint(m))
```

```
             Estimate Std. Error t value  Pr(>|t|)    2.5 % 97.5 %
(Intercept)    5.3546     0.2504 21.3854 1.773e-29  4.90101  5.889
OrganStomach   0.3013     0.3804  0.7923 4.314e-01 -0.44036  1.068
OrganColon     0.7709     0.3541  2.1772 3.348e-02  0.06991  1.472
OrganOvary     1.4302     0.4902  2.9174 4.987e-03  0.52462  2.486
OrganBreast    1.8867     0.3995  4.7228 1.479e-05  1.11572  2.702
```

We might compare the survival times to the type of cancer with lowest expected survival time.

```
contrast(m, tf = exp,
  a = list(Organ = c("Stomach","Colon","Ovary","Breast")),
  b = list(Organ = "Bronchus"),
  cnames = paste(c("Stomach","Colon","Ovary","Breast"), "/", "Bronchus", sep = ""))
```

```
                estimate  lower  upper
Stomach/Bronchus    1.352 0.6314  2.893
Colon/Bronchus      2.162 1.0644  4.391
Ovary/Bronchus      4.180 1.5671 11.147
Breast/Bronchus     6.597 2.9663 14.673
```

Now suppose we specify the same variance structure directly. Note that the results are *identical*.

```
m <- glm(Survival ~ Organ, family = quasi(link = log, variance = "mu^2"), data = CancerSurvival)
cbind(summary(m)$coefficients, confint(m))
```

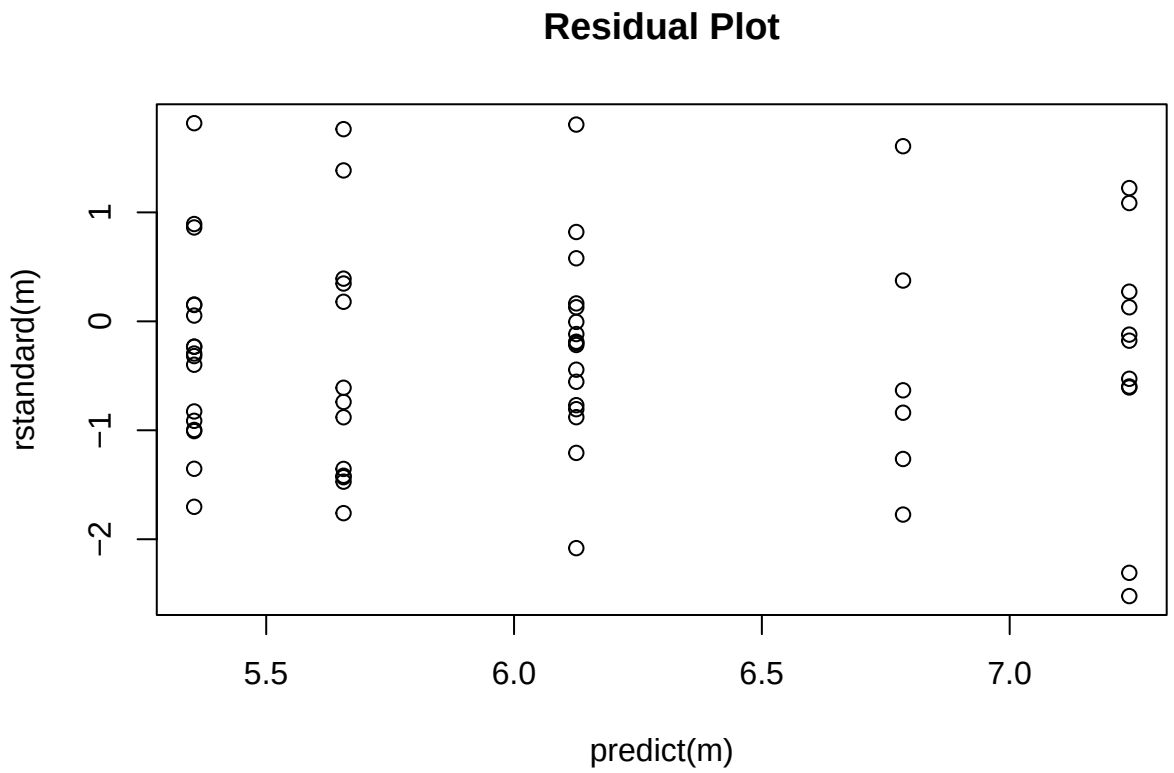
```
             Estimate Std. Error t value  Pr(>|t|)    2.5 % 97.5 %
(Intercept)    5.3546     0.2504 21.3854 1.773e-29  4.90101  5.889
OrganStomach   0.3013     0.3804  0.7923 4.314e-01 -0.44036  1.068
OrganColon     0.7709     0.3541  2.1772 3.348e-02  0.06991  1.472
OrganOvary     1.4302     0.4902  2.9174 4.987e-03  0.52462  2.486
OrganBreast    1.8867     0.3995  4.7228 1.479e-05  1.11572  2.702
```

```
contrast(m, tf = exp,
  a = list(Organ = c("Stomach","Colon","Ovary","Breast")),
  b = list(Organ = "Bronchus"),
  cnames = paste(c("Stomach","Colon","Ovary","Breast"), "/", "Bronchus", sep = ""))
```

```
                estimate  lower  upper
Stomach/Bronchus    1.352 0.6314  2.893
Colon/Bronchus      2.162 1.0644  4.391
Ovary/Bronchus      4.180 1.5671 11.147
Breast/Bronchus     6.597 2.9663 14.673
```

Naturally we should check the residuals to see if the variance structure is reasonable.

```
plot(predict(m), rstandard(m), main = "Residual Plot")
```



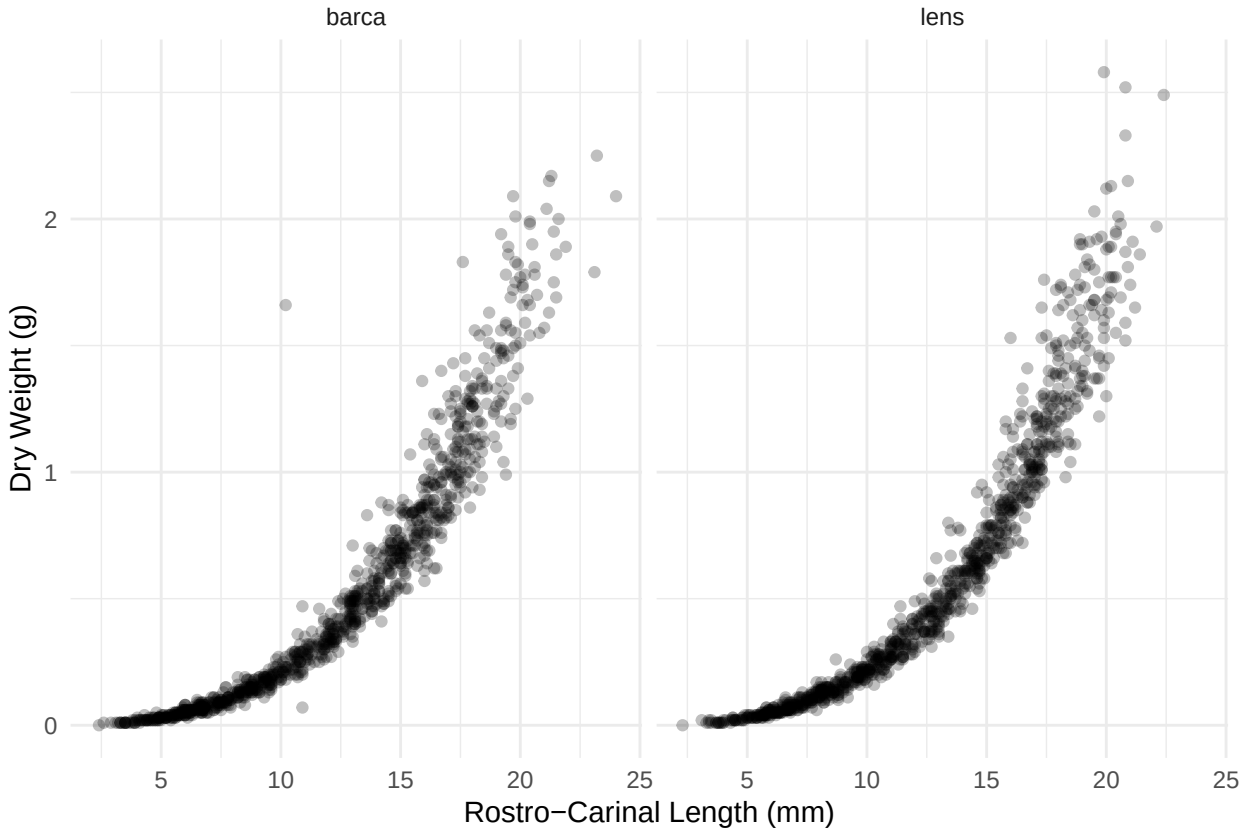
Example: Consider the following observations of dry weight (in grams) and rostro-carinal length (in mm) of a species of barnacles sampled from the inter-tidal zones near Punta Lens and Punta de la Barca along the Atlantic coast of Spain.

```
library(npregfast)
head(barnacle)
```

```
    DW   RC     F
1 0.14  9.5 barca
2 0.00  2.4 barca
```

```
3 0.42 13.1 barca
4 0.01  3.7 barca
5 0.03  5.6 barca
6 1.56 18.6 barca
```

```
p <- ggplot(barnacle, aes(x = RC, y = DW))
p <- p + geom_point(alpha = 0.25) + facet_wrap(~ F) + theme_minimal()
p <- p + labs(x = "Rostro-Carinal Length (mm)", y = "Dry Weight (g)")
plot(p)
```



A common allometric regression model would have the form

$$E(Y_i) = ax_i^b$$

where Y_i is the dry weight for the i-th observation, and x_i is the rostro-carinal length for the i-th observation. We can also write this as

$$\log E(Y_i) = \log a + b \log x_i$$

or, equivalently,

$$E(Y_i) = \exp(\log a + b \log x_i)$$

or

$$E(Y_i) = \exp(\beta_0 + \beta_1 \log x_i)$$

where $\beta_0 = \log a$ and $\beta_1 = b$. This is basically a log-linear model since we can write

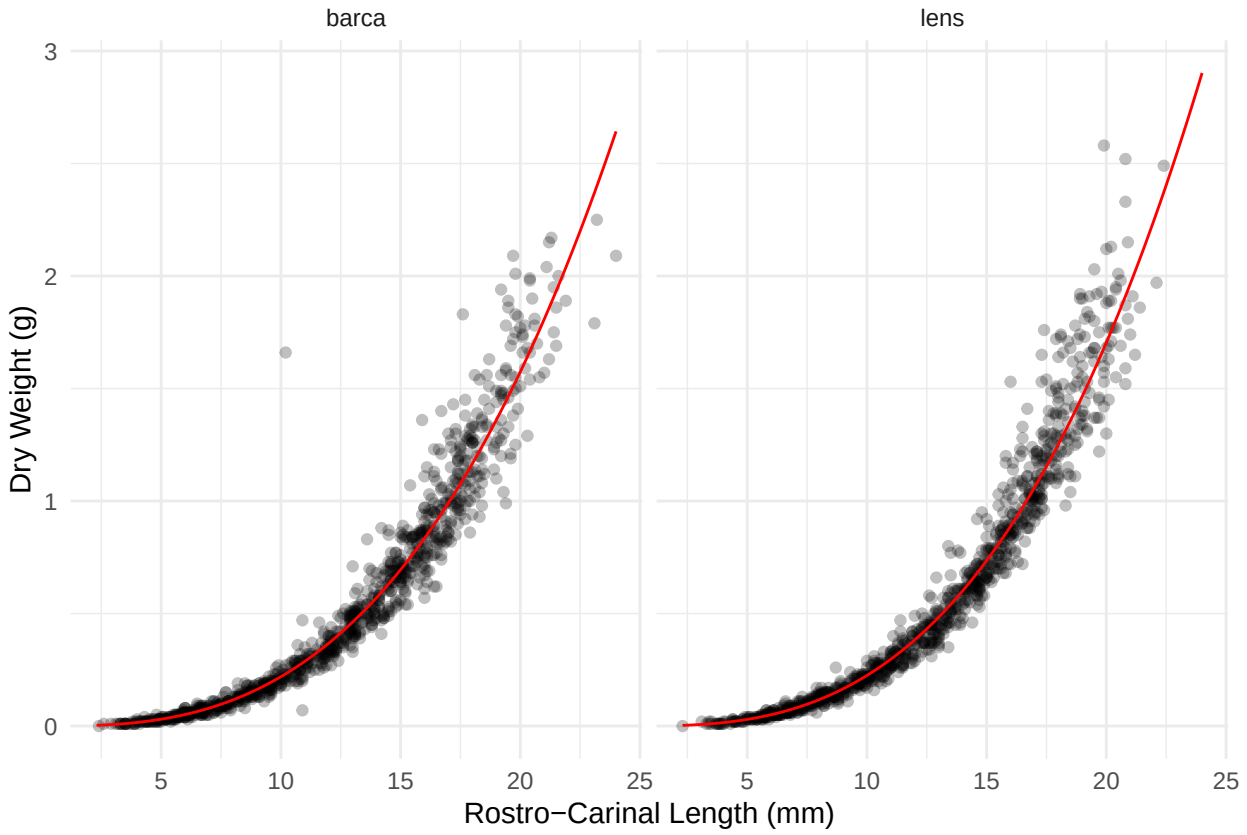
$$\log E(Y_i) = \beta_0 + \beta_1 \log x_i.$$

Because dry weight is continuous and positive, with the variability appearing to increase with the expected dry weight, we might specify a gamma distribution for dry weight.

```
barnacle <- subset(barnacle, DW > 0) # remove observations of zero weight to avoid errors
m <- glm(DW ~ F + log(RC) + F:log(RC), family = Gamma(link = log), data = barnacle)
summary(m)$coefficients
```

```
             Estimate Std. Error  t value  Pr(>|t|)
(Intercept)  -8.06129    0.03898 -206.786 0.0000000
Flens        -0.15688    0.05724   -2.741 0.0061837
log(RC)       2.84234    0.01585  179.296 0.0000000
Flens:log(RC) 0.07884    0.02315    3.405 0.0006744
```

```
d <- expand.grid(F = c("barca","lens"), RC = seq(2.3, 24, length = 100))
d$yhat <- predict(m, newdata = d, type = "response")
p <- p + geom_line(aes(y = yhat), color = "red", data = d)
plot(p)
```




```
# effect of a 20% increase in RC
contrast(m, tf = exp,
    a = list(F = c("barca","lens"), RC = 6),
    b = list(F = c("barca","lens"), RC = 5),
    cnames = c("barca","lens"))
```

```
      estimate lower upper
barca    1.679 1.670 1.689
lens     1.703 1.693 1.714
```

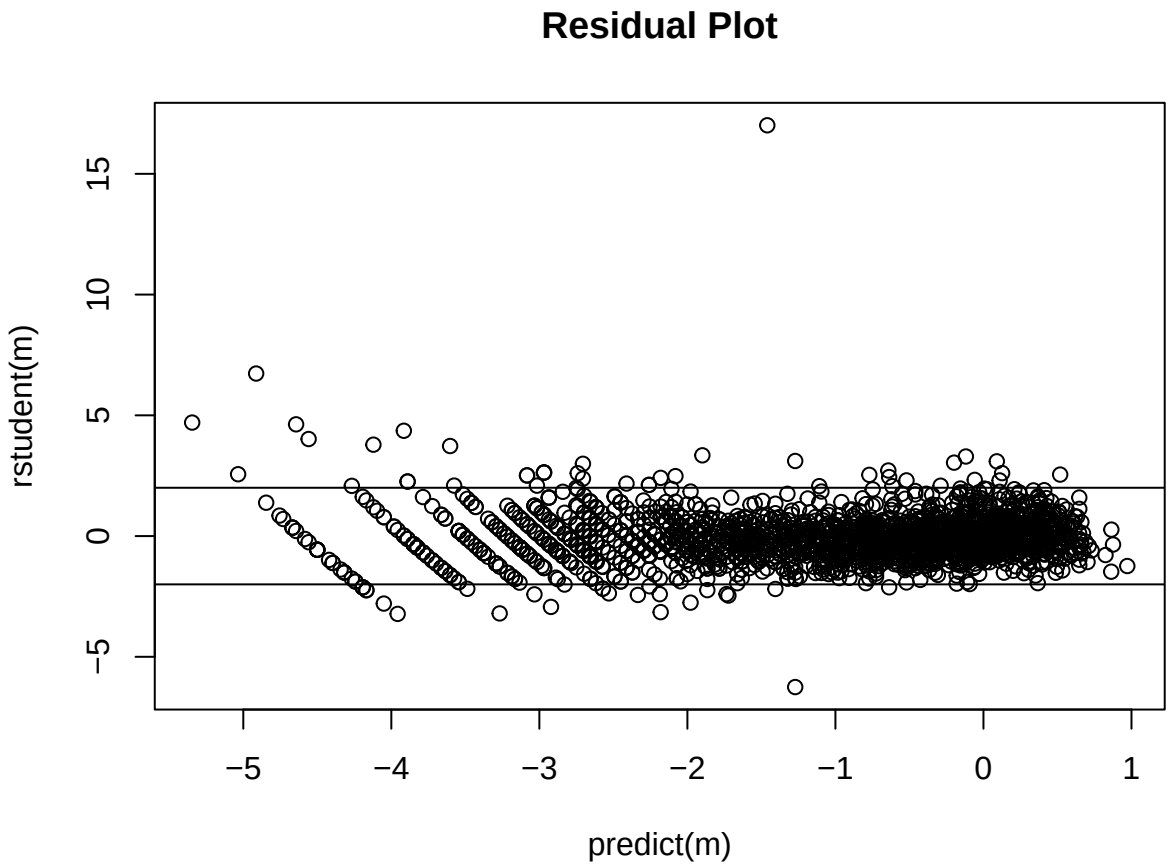
```
# comparing the two locations at different values of RC
contrast(m, tf = exp,
    a = list(F = "lens", RC = c(10,15,20)),
    b = list(F = "barca", RC = c(10,15,20)),
```

```
    cnames = c("10mm","15mm","20mm"))
```

```
     estimate lower upper
10mm    1.025 1.004 1.046
15mm    1.058 1.034 1.083
20mm    1.083 1.048 1.118
```

Checking the residuals.

```
plot(predict(m), rstudent(m), main = "Residual Plot")
abline(-2,0)
abline(2,0)
```



Note: Eliminating a couple of observations due to having a zero dry weight is not of much consequence here since there are so many observations. But if there were fewer observations this would not be a good idea. A better approach would be to just specify the same model using `quasi`. Note that using `quasi` with `variance = "mu^2"` is effectively equivalent to using `family = gamma`.

```
m <- glm(DW ~ F + log(RC) + F:log(RC), data = barnacle,
  family = quasi(link = "log", variance = "mu^2"))
summary(m)$coefficients
```

```
             Estimate Std. Error  t value  Pr(>|t|)
(Intercept)  -8.06129    0.03898 -206.786 0.0000000
Flens        -0.15688    0.05724   -2.741 0.0061837
log(RC)       2.84234    0.01585  179.296 0.0000000
Flens:log(RC) 0.07884    0.02315    3.405 0.0006744
```

```
# effect of a 20% increase in RC
contrast(m, tf = exp,
    a = list(F = c("barca","lens"), RC = 6),
    b = list(F = c("barca","lens"), RC = 5),
    cnames = c("barca","lens"))
```

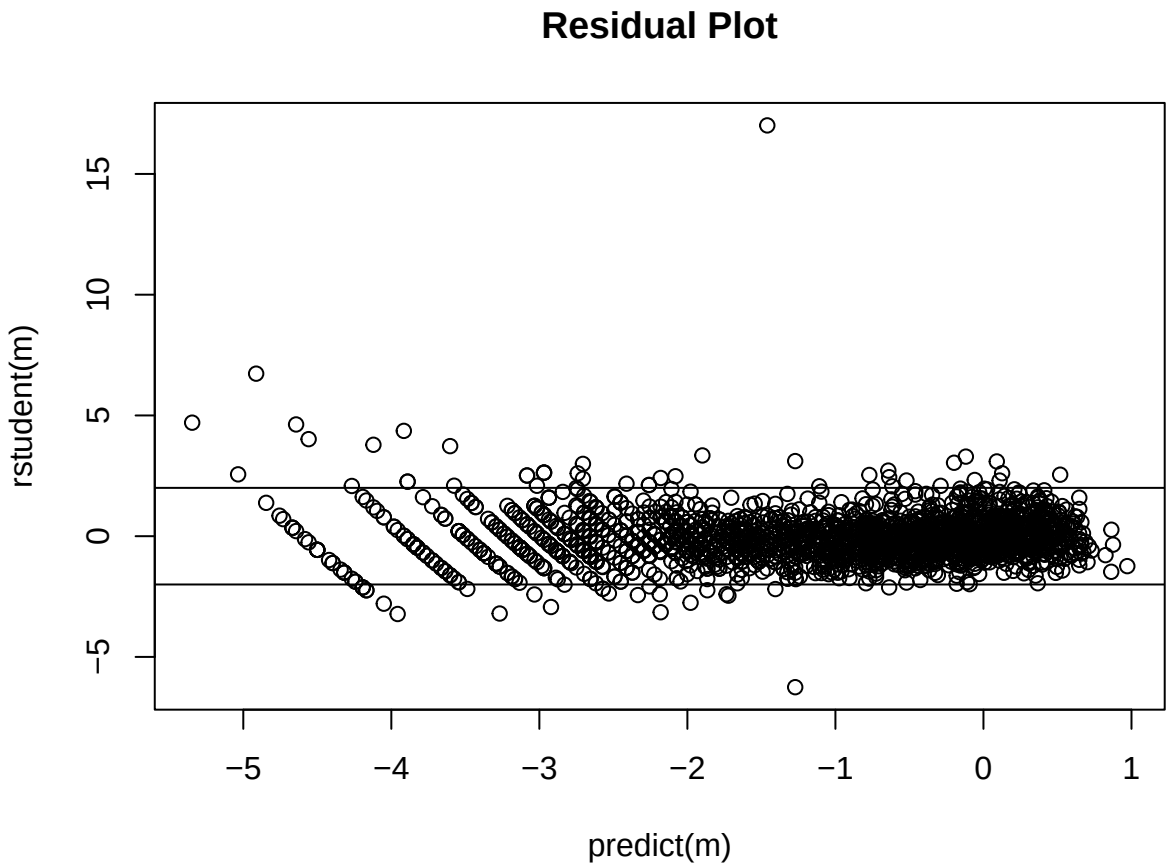
```
      estimate lower upper
barca    1.679 1.670 1.689
lens     1.703 1.693 1.714
```

```
# comparing the two locations at different values of RC
contrast(m, tf = exp,
    a = list(F = "lens", RC = c(10,15,20)),
    b = list(F = "barca", RC = c(10,15,20)),
    cnames = c("10mm","15mm","20mm"))
```

```
     estimate lower upper
10mm    1.025 1.004 1.046
15mm    1.058 1.034 1.083
20mm    1.083 1.048 1.118
```

Checking the residuals.

```
plot(predict(m), rstudent(m), main = "Residual Plot")
abline(-2,0)
abline(2,0)
```



Inverse-gaussian GLMs are similar. There the variance increases a bit faster with the expected response. To estimate such a model use `family = inverse.gaussian`. An equivalent model is to use `quasi` with

variance = mu^3.