

Monday, Mar 28

## Distributions for Overdispersion

One way to model overdispersion 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  $\zeta_i$  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  $\zeta_i$ , and  $e^{\zeta_i}$  has a *gamma* distribution such that  $E(e^{\zeta_i}) = 1$  and  $\text{Var}(e^{\zeta_i}) = \alpha > 0$ . 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  $\alpha$  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.

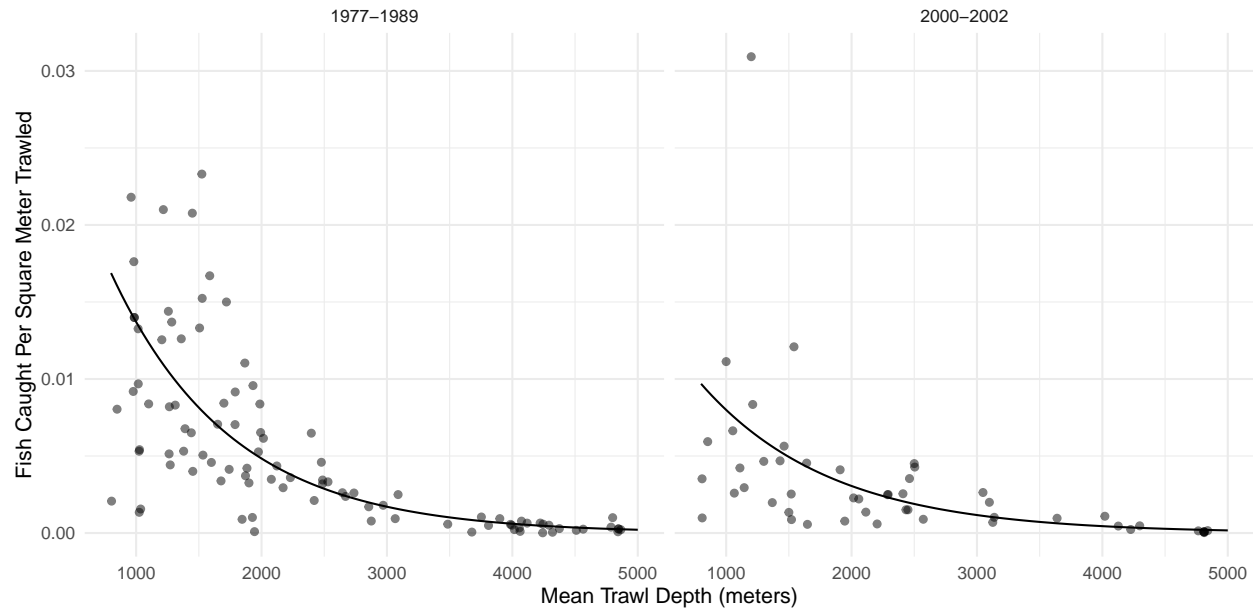
```
library(COUNT)
data(fishing)

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)

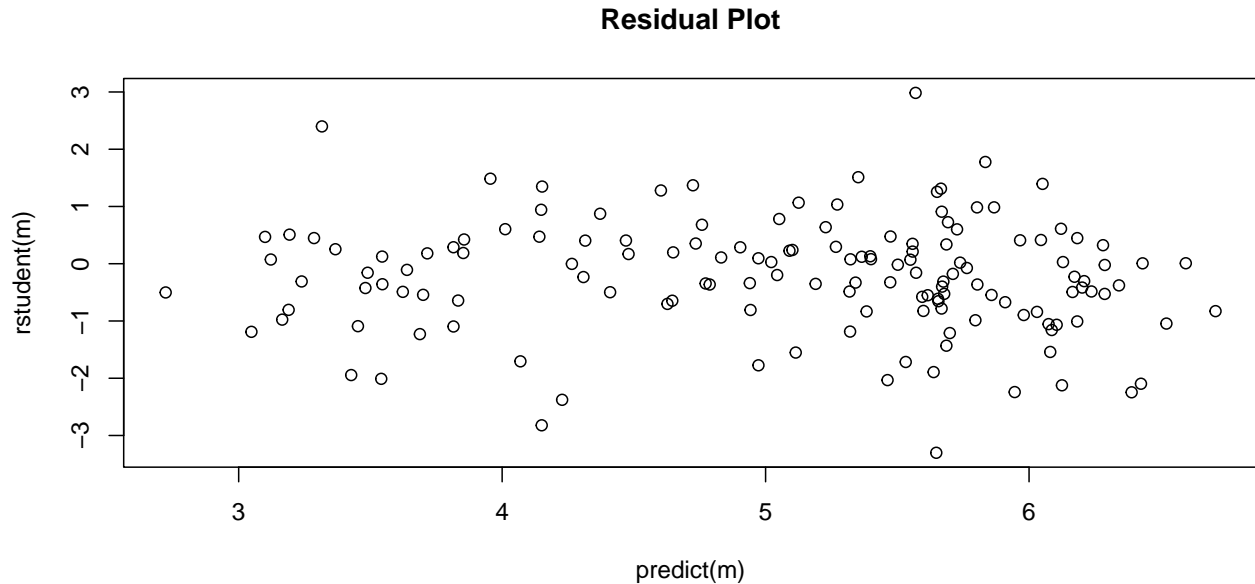
Null deviance: 471.79 on 146 degrees of freedom  
 Residual deviance: 159.31 on 143 degrees of freedom  
 AIC: 1763

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.

```
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
1		meandepth + offset(log(sweptarea))	1.832	145	-1764	
2	period * meandepth + offset(log(sweptarea))	1.961	143	-1753	1 vs 2	
	df LR stat. Pr(Chi)					
1						
2	2	11.11	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.<sup>1</sup>

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.

```
library(trtools)

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)
```

	estimate	lower	upper
kc	2.967	2.105	4.181
pm	2.877	1.836	4.507

---

<sup>1</sup>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.

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  $\eta_i$  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  $\phi$  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  $x_{i1}, x_{i2}, \dots, x_{ik}$ .

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

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

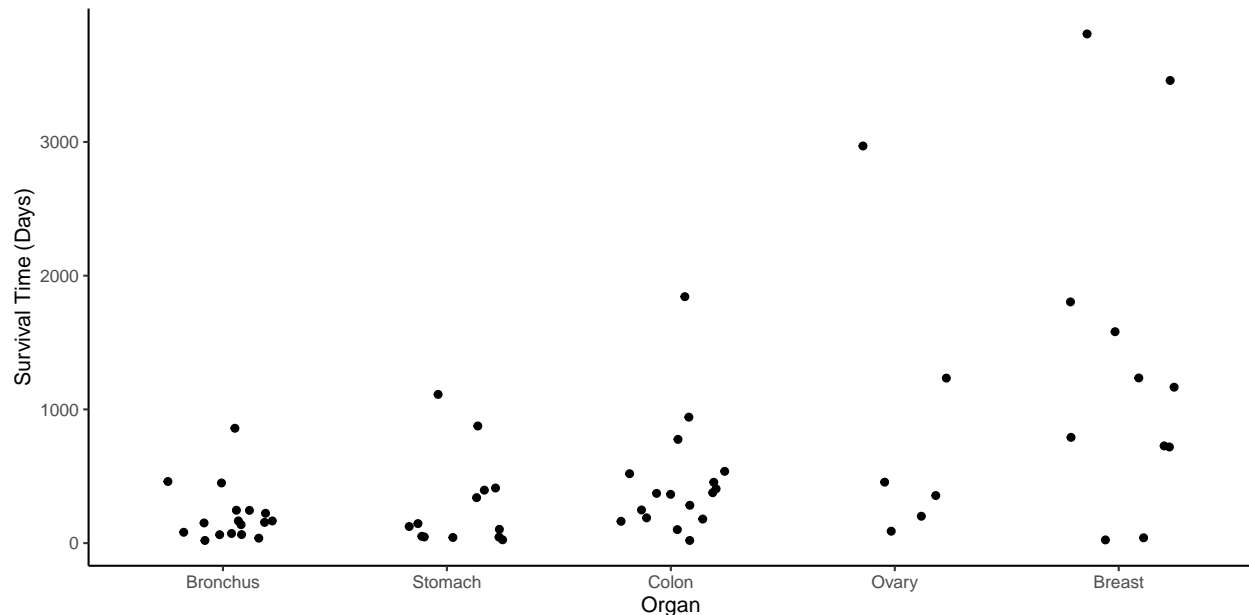
or

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

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

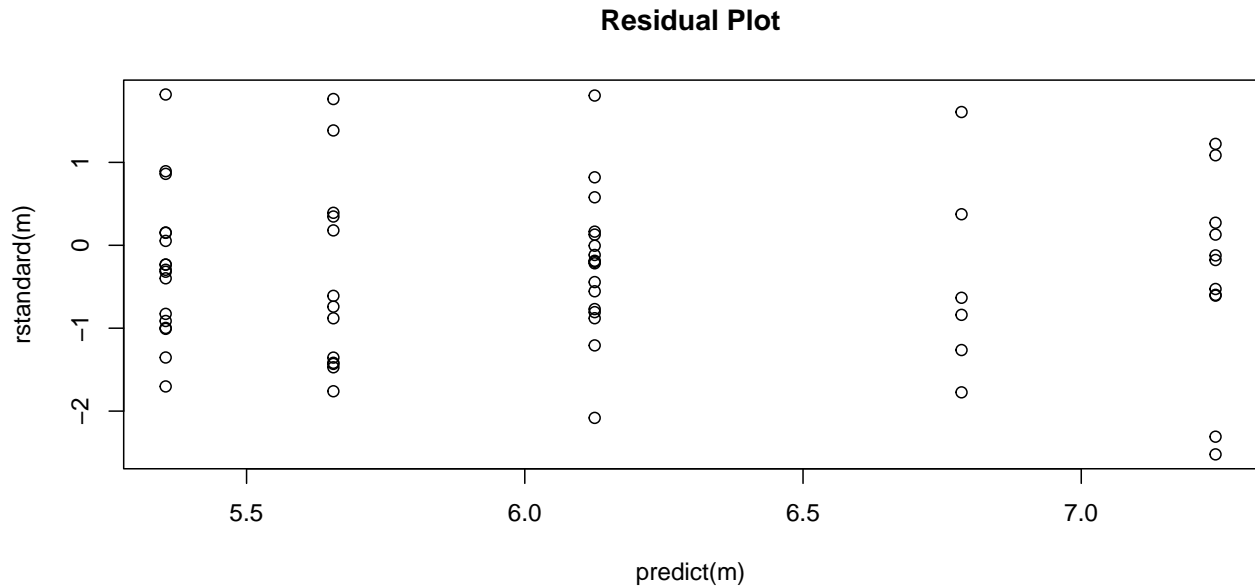
```
contrast(m, tf = exp,
  a = list(Organ = c("Stomach", "Colon", "Ovary", "Breast")),
  b = list(Organ = "Bronchus"),
  cnames = paste(c("Stomach", "Colon", "Ovary", "Breast"), "/", "Bronchus", sep = ""))
```

	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")
```



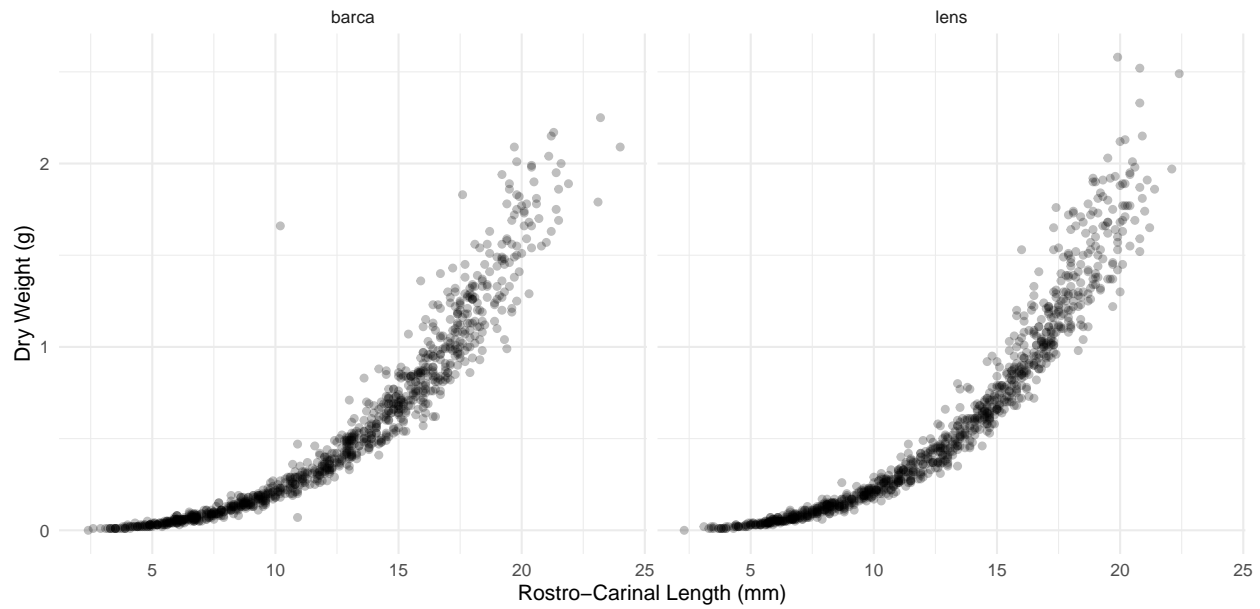


**Example:** Consider the following observations of dry weight (in grams) and rostro-carinal length (in mm) of a species of barnacles sampled from the inter-tidal zones near Punta Lens and Punta de la Barca along the Atlantic coast of Spain.

```
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

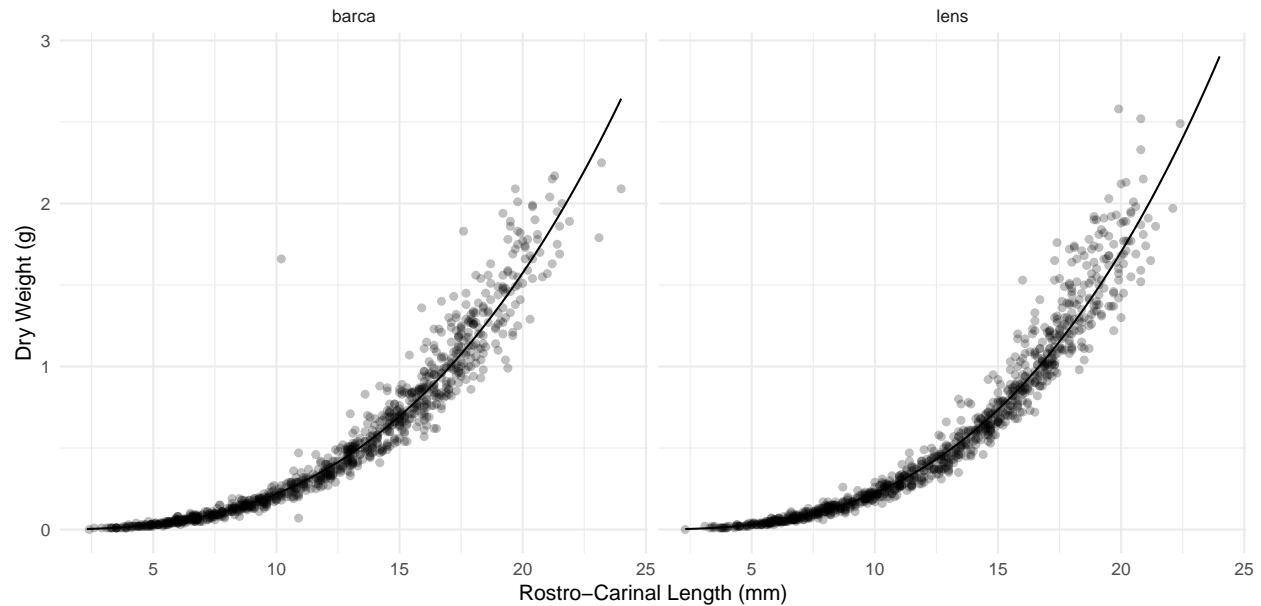
$$\log E(Y_i) = \beta_0 + \beta_1 \log x_i.$$

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), 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
```

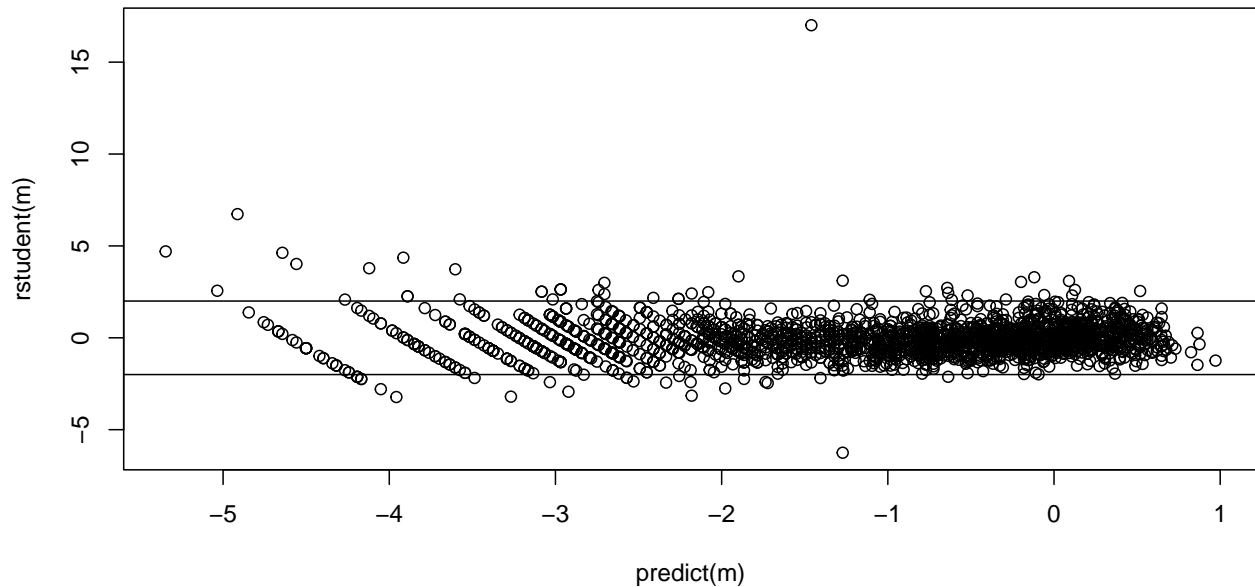
```
contrast(m, tf = exp,
  a = list(F = "lens", RC = c(10, 15, 20)),
  b = list(F = "barca", RC = c(10, 15, 20)),
  cnames = c("10mm", "15mm", "20mm"))
```

	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)
```

## Residual Plot



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

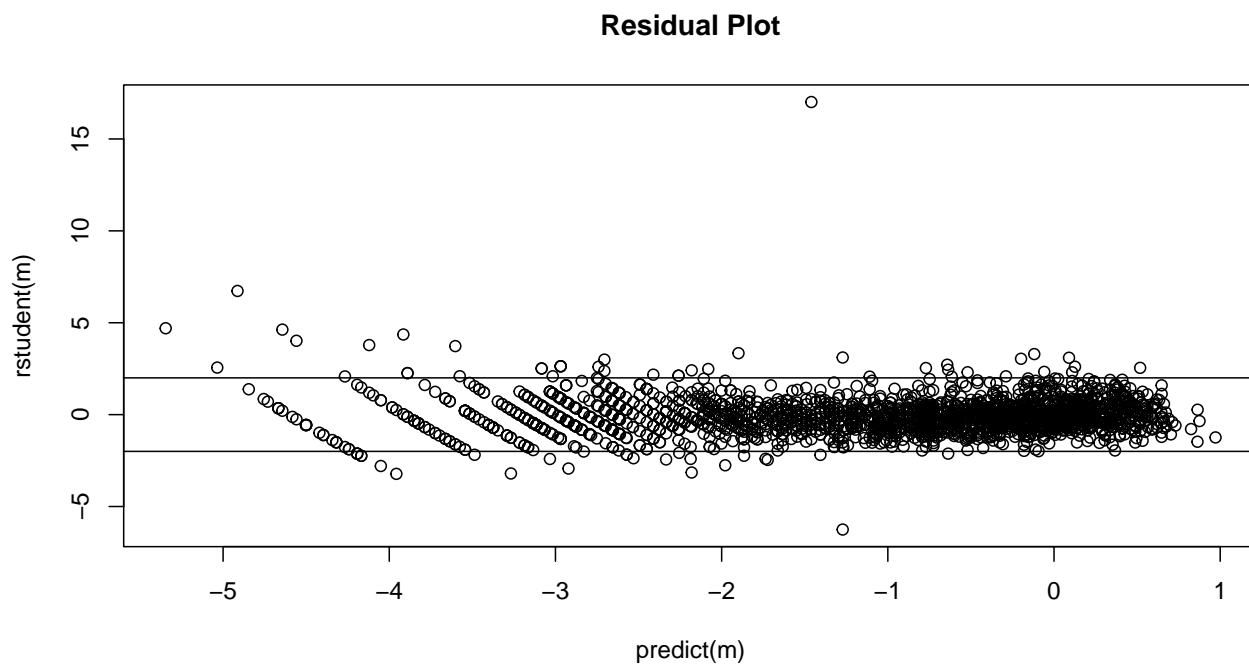
*# comparing the two locations at different values of RC*

```
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`.