Friday, Mar 22

Over-dispersion

Over-dispersion can occur for generalized linear models that assume a Poisson or binomial distribution for the response variable.

When we specify a distribution in a generalized linear model, what we are actually specifying is the *variance structure*

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

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

Over-dispersion is when

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

and *underdispersion* is when

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

Over-dispersion is fairly common in practice, but under-dispersion is relatively rare.

Over-dispersion in Poisson Regression

If Y_i has a *Poisson* distribution, then

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

so that it is implicitly assumed that $\phi = 1$ and $V(z) = z$. Over-dispersion occurs if

$$\text{Var}(Y_i) > E(Y_i).$$

Over-dispersion in Binomial Regression

If C_i has a *binomial* distribution, and $Y_i = C_i/m_i$, then

$$\text{Var}(Y_i) = E(Y_i)[1 - E(Y_i)]/m_i,$$

so that it is implicitly assumed that $\phi = 1$ and $V(z) = z(1-z)/m_i$. over-dispersion occurs if

$$\text{Var}(Y_i) > E(Y_i)[1 - E(Y_i)]/m_i.$$

In general, failing to account for over-dispersion (or a misspefication of the variance structure in general) may yield incorrect standard errors (usually too small in the case of over-dispersion), leading to incorrect test statistics and confidence intervals.

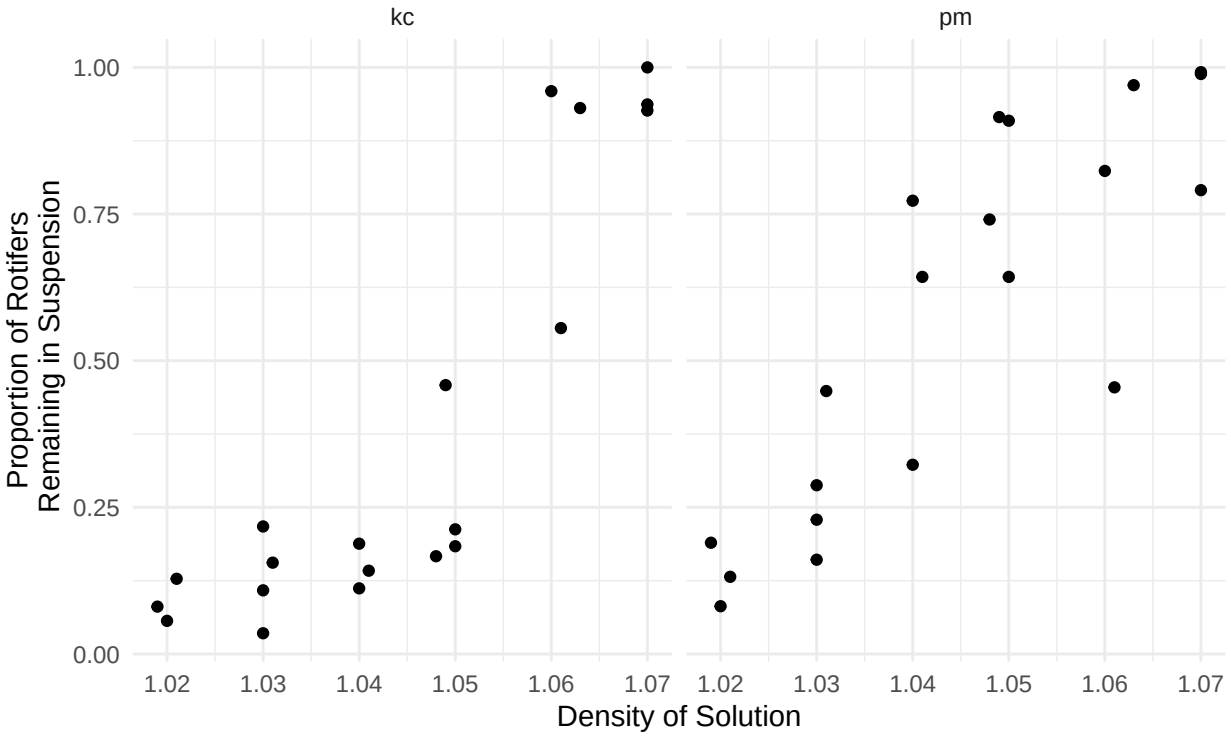
Causes of Over-dispersion

1. Wrong assumed distribution for the response variable.
2. Unobserved explanatory variables that vary over observations.

Note: A misspecified *mean structure* (e.g., failing to transform an explanatory variable or omitting a strong interaction) may appear as overdisperson.

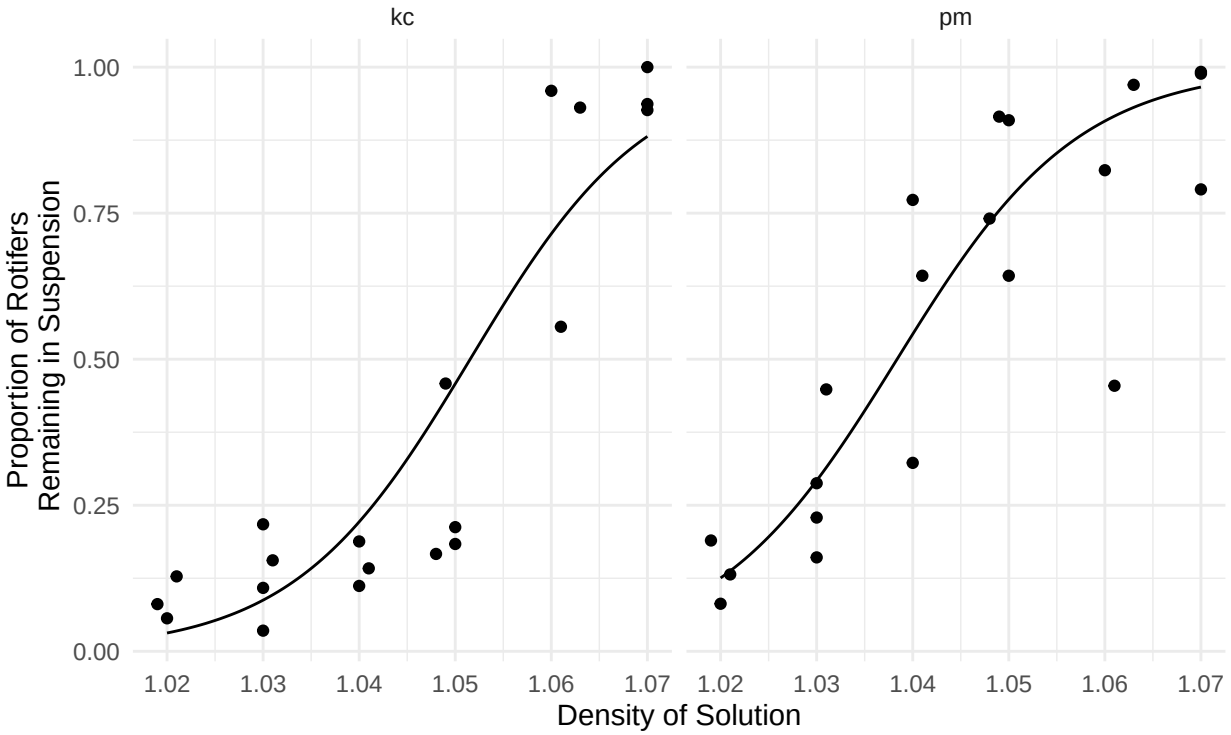
Example: Consider the following data from an experiment that investigated the proportion of rotifers of two species remaining in suspension in different solution densities after being put into a centrifuge.

```
myrotifer <- trtools::rotifer

p <- ggplot(myrotifer, aes(x = density, y = y/total)) +
  geom_point() + facet_wrap(~species) +
  labs(y = "Proportion of Rotifers\n Remaining in Suspension",
    x = "Density of Solution") + theme_minimal()
plot(p)
```



Logistic regression might be a reasonable model here.

```
m <- glm(cbind(y, total - y) ~ species * density,
  family = binomial, data = myrotifer)

d <- expand.grid(species = c("kc","pm"), density = seq(1.02, 1.07, length = 100))
d$yhat <- predict(m, newdata = d, type = "response")

p <- p + geom_line(aes(y = yhat), data = d)
plot(p)
```



Do these data exhibit over-dispersion for this model?

Detection of Over-dispersion

Standardized residuals can be used to detect over-dispersion. There are several types for GLMs.

1. Pearson residuals. Pearson residuals are defined as

$$\frac{y_i - \hat{y}_i}{\sqrt{\widehat{\mathrm{Var}}(Y_i)}}.$$

   Dividing a Pearson residual by another term to account for the variance $\hat{y}_i$ creates a *standardized* Pearson residual. These are obtained using `rstandard(m, type = "pearson")`.

2. Deviance residuals. The residual deviance can be decomposed into a per-observation contribution so that $D = \sum_{i=1}^{n} d_i$. Then the residual deviance is defined as

$$\mathrm{sign}(y_i - \hat{y}_i)\sqrt{d_i},$$

   where

$$\mathrm{sign}(z) = \begin{cases} 1, & \text{if } z > 0, \\ 0, & \text{if } z = 0, \\ -1, & \text{if } z < 0. \end{cases}$$

   Dividing a deviance residual by another term to account for the variance $\hat{y}_i$ creates a *standardized* deviance residual. These are obtained using `rstandard(m, type = "deviance")`. A numerical approximation to these residuals obtained when omitting the observation can be obtained using `rstudent(m)`.

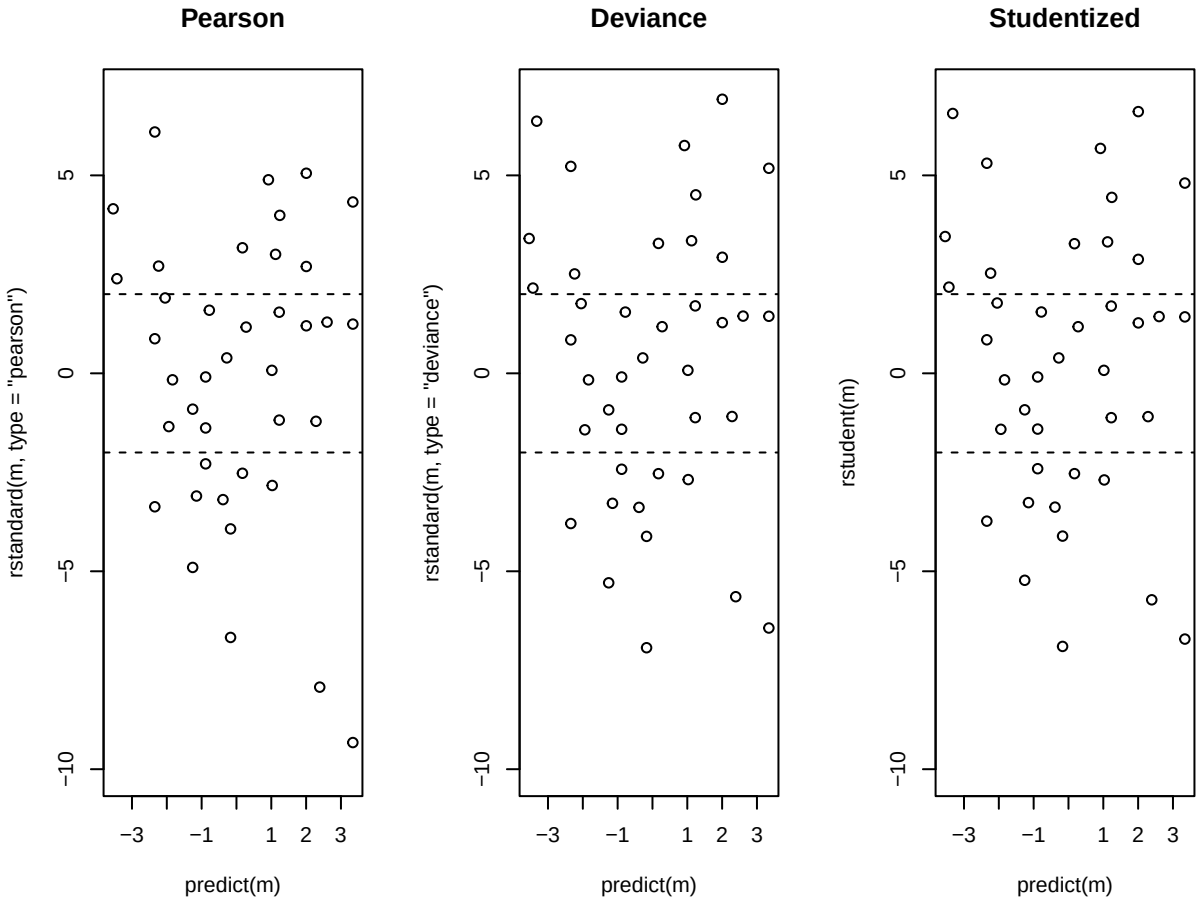
3. Studentized residuals. The function `rstudent` will produce *approximate* studentized residuals for GLMs.

Comment: If the model is correct the residuals *might* be approximately normally distributed with a mean of zero and standard deviation of one (i.e., "standard normal"), so an excess of values greater than two (in absolute value) may indicate over-dispersion or some other problem with the model. But with very *coarse*

data (e.g., very small counts in a Poisson regression model or proportions with small m_i in a logistic regression model), the distribution of these residuals is not approximately normal.

Example: Let's look at the residuals for the `rotifer` model.

```
par(mfcol = c(1,3))
plot(predict(m), rstandard(m, type = "pearson"), ylim = c(-10, 7), main = "Pearson")
abline(h = c(-2,2), lty = 2)
plot(predict(m), rstandard(m, type = "deviance"), ylim = c(-10, 7), main = "Deviance")
abline(h = c(-2,2), lty = 2)
plot(predict(m), rstudent(m), ylim = c(-10, 7), main = "Studentized")
abline(h = c(-2,2), lty = 2)
```



Is there an explanation of the over-dispersion?

Another metric is to compare the residual deviance to the residual degrees of freedom in a GLM with a response variable with either a Poisson or binomial distribution. If the model is (approximately) correct then the ratio of the residual deviance to the residual degrees of freedom is approximately one.

Example: Consider the residual deviance and residual degrees of freedom for the rotifer model.

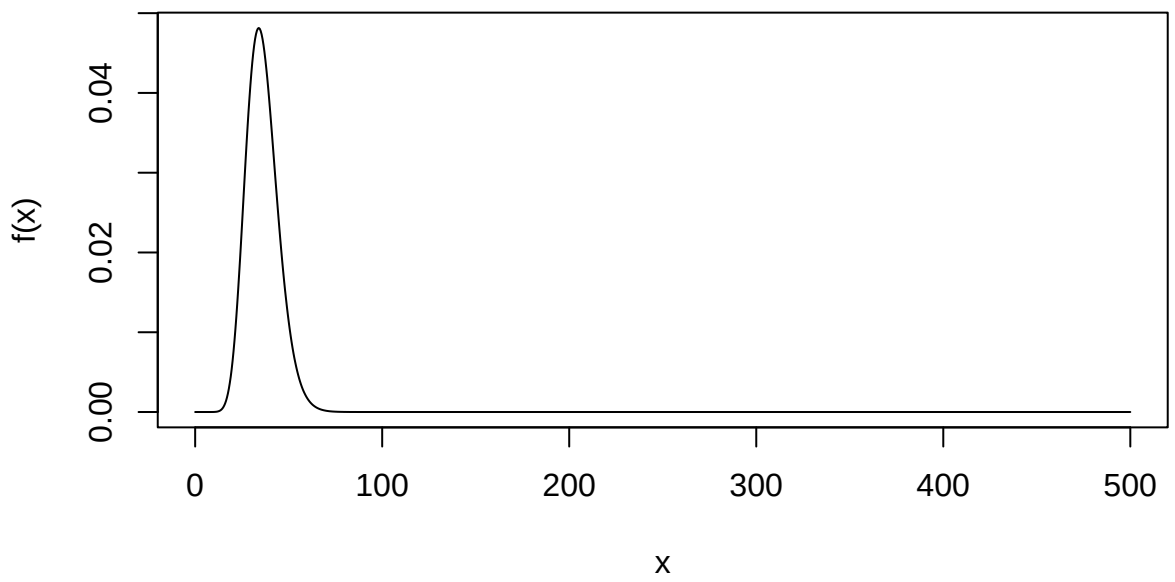
```
summary(m)
```

```
Call:
glm(formula = cbind(y, total - y) ~ species * density, family = binomial,
    data = myrotifer)
```

```
Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)       -114.35       4.03  -28.35   <2e-16 ***
speciespm            4.63       6.60    0.70     0.48
density            108.75       3.86   28.19   <2e-16 ***
speciespm:density   -3.08       6.33   -0.49     0.63
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 3180.99  on 39  degrees of freedom
Residual deviance:  434.02  on 36  degrees of freedom
AIC: 596.6

Number of Fisher Scoring iterations: 5
```

If the model is correct and there is no over-dispersion, the residual deviance has approximate a χ^2 distribution with degrees of freedom equal to the residual degrees of freedom. We can use this as an informal test for over-dispersion.

```
f <- function(x) dchisq(x, 36)
curve(f, from = 0, to = 500, n = 1000)
```




```
1 - pchisq(434.02, df = 36)
```

```
[1] 0
```

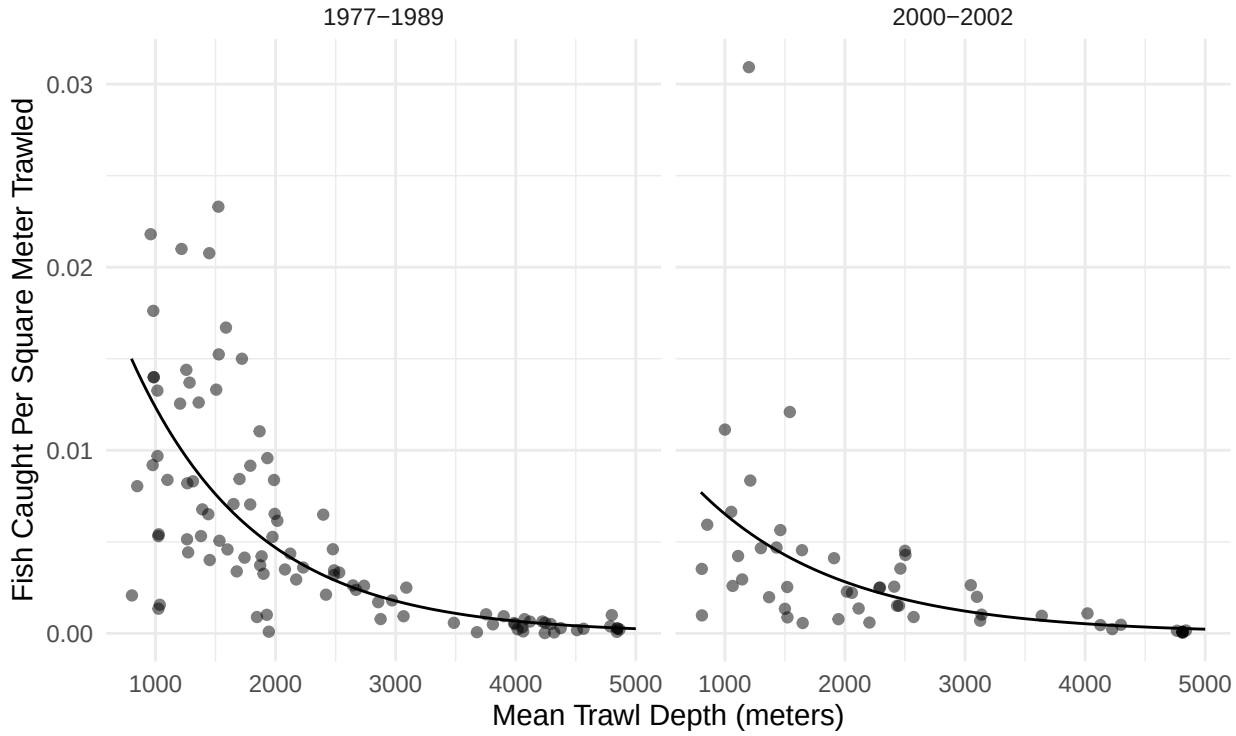
Residuals are more informative, but the residual deviance is a quick way to check to see if over-dispersion may be an issue.

Note: For logistic regression, over-dispersion *cannot* be diagnosed in this way for *binary* data (and the residual deviance may not be reliable if the m_i are very small).

Example: Let's look again a the Poisson regression model for the trawling data.

```
library(COUNT)
data(fishing)
```

```r
m <- glm(totabund ~ period * meandepth + offset(log(sweptarea)),
  family = poisson, 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)
```



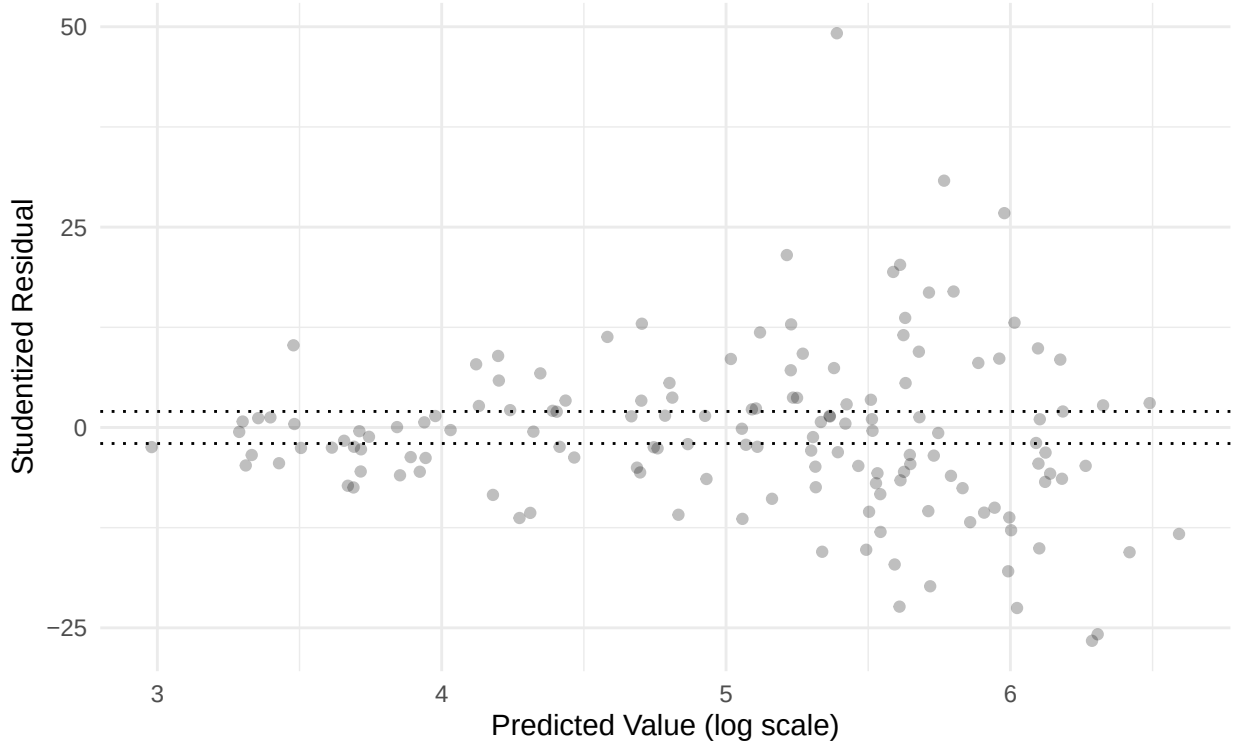
Might there be over-dispersion here?

```r
summary(m)
```

```
Call:
glm(formula = totabund ~ period * meandepth + offset(log(sweptarea)),
    family = poisson, data = fishing)

Coefficients:
                          Estimate Std. Error z value Pr(>|z|)
(Intercept)              -3.42e+00   1.49e-02 -229.67   <2e-16 ***
period2000-2002          -7.71e-01   2.97e-02  -25.94   <2e-16 ***
meandepth                -9.71e-04   7.96e-06 -121.94   <2e-16 ***
period2000-2002:meandepth  1.32e-04   1.52e-05    8.65   <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: 46176  on 146  degrees of freedom
Residual deviance: 14982  on 143  degrees of freedom
AIC: 15962

Number of Fisher Scoring iterations: 5
```

```r
fishing$eta <- predict(m)
fishing$res <- rstudent(m)

p <- ggplot(fishing, aes(x = eta, y = res)) + theme_minimal() +
  geom_point(alpha = 0.25) +
  labs(x = "Predicted Value (log scale)",
    y = "Studentized Residual") +
  geom_hline(yintercept = c(-2, 2), linetype = 3)
plot(p)
```



Over-dispersion is not the only issue here. The variance of the residuals is not constant.

Solutions to Over-dispersion

There are several potential solutions to over-dispersion.

1. Quasi-likelihood. Specify a variance structure other than the one implied by a specified distribution.
2. Specify a different distribution (possibly outside the exponential family).
3. Use a robust estimator of the standard errors (i.e., heteroscedastic consistent standard errors).

Quasi-Likelihood Solutions to Over-dispersion

The Poisson and binomial distributions assume the variance structures

$$\text{Var}(Y_i) = \phi E(Y_i) \quad \text{and} \quad \text{Var}(Y_i) = \phi E(Y_i)[1 - E(Y_i)]/m_i,$$

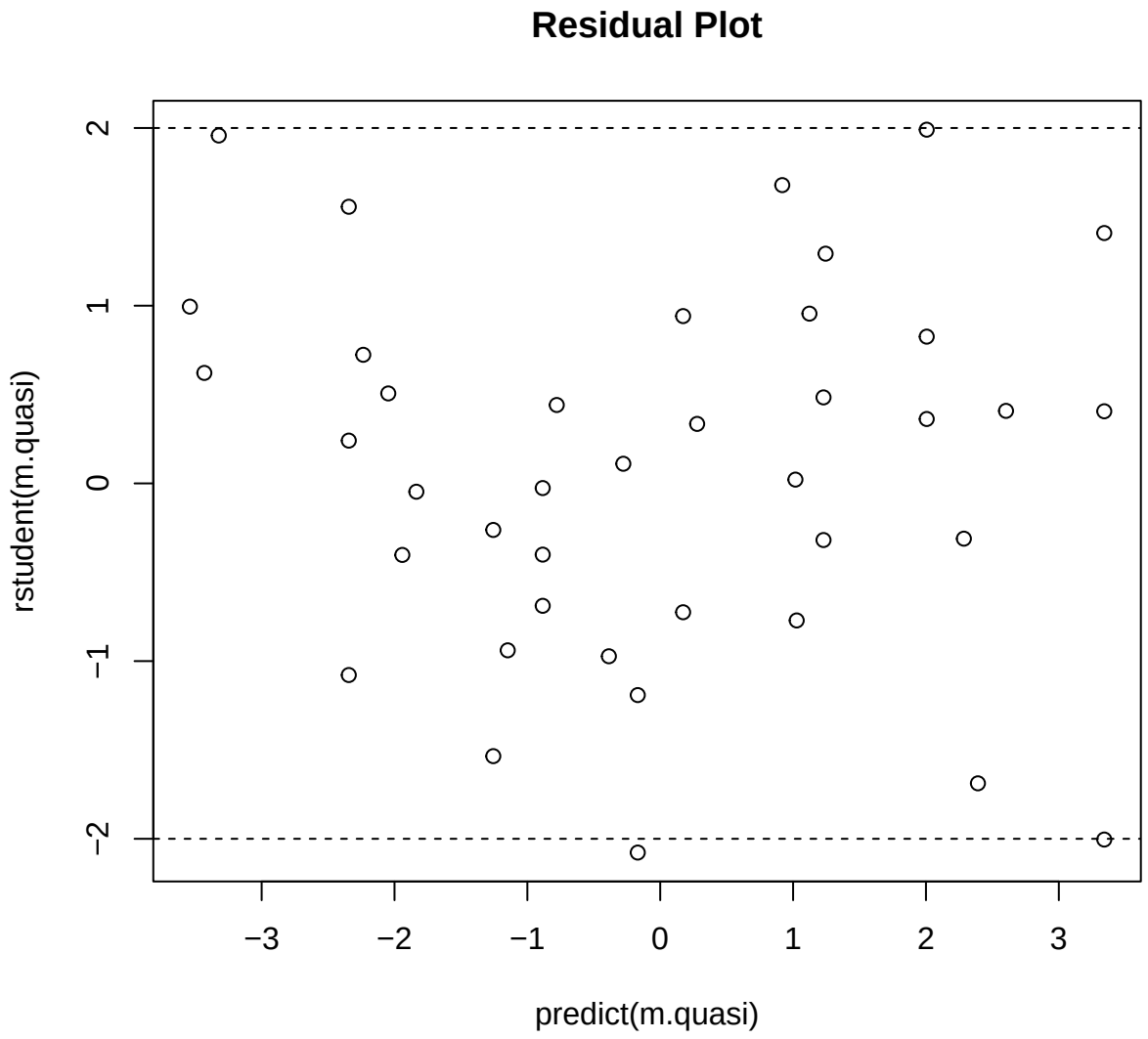
respectively, where the *dispersion parameter* is *fixed* at $\phi = 1$. One solution is to allow ϕ to be an unknown parameter to "relax" the variance structure and allow the variance to be larger than it would be for a Poisson or binomial distribution. The dispersion parameter can be estimated. R uses

$$\hat{\phi} = \frac{1}{n-p} \sum_{i=1}^{n} \frac{(y_i - \hat{y}_i)^2}{\text{V}(\hat{y}_i)},$$

which is analogous to the estimate of σ^2 in a normal linear model. This is a quasi-likelihood approach because the variance structures with $\phi \neq 1$ do not correspond to a binomial or Poisson distribution. This kind of quasi-likelihood can be done with `glm` by using `quasipoisson` or `quasibinomial` instead of `poisson` or `binomial`, respectively, when specifying the `family` argument.

Example: Consider again the rotifer model.

```
m.quasi <- glm(cbind(y, total - y) ~ species + density + species:density,
  family = quasibinomial, data = myrotifer)
plot(predict(m.quasi), rstudent(m.quasi), main = "Residual Plot")
abline(h = c(-2,2), lty = 2)
```



Note: You **cannot** compare the residual deviance to the residual degrees of freedom as a diagnostic to determine if using quasi-likelihood was successful, but standardized residuals are still appropriate.

How does this impact our inferences?

```
m.binom <- glm(cbind(y, total - y) ~ species + density + species:density,
  family = binomial, data = myrotifer)
cbind(summary(m.binom)$coefficients, confint(m.binom))
```

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

```
                  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
```

```
# odds ratios for effect of a 0.01 unit increase in density
trtools::contrast(m.binom,
  a = list(species = c("kc","pm"), density = 0.02),
  b = list(species = c("kc","pm"), density = 0.01),
  cnames = c("kc","pm"), tf = exp)
```

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

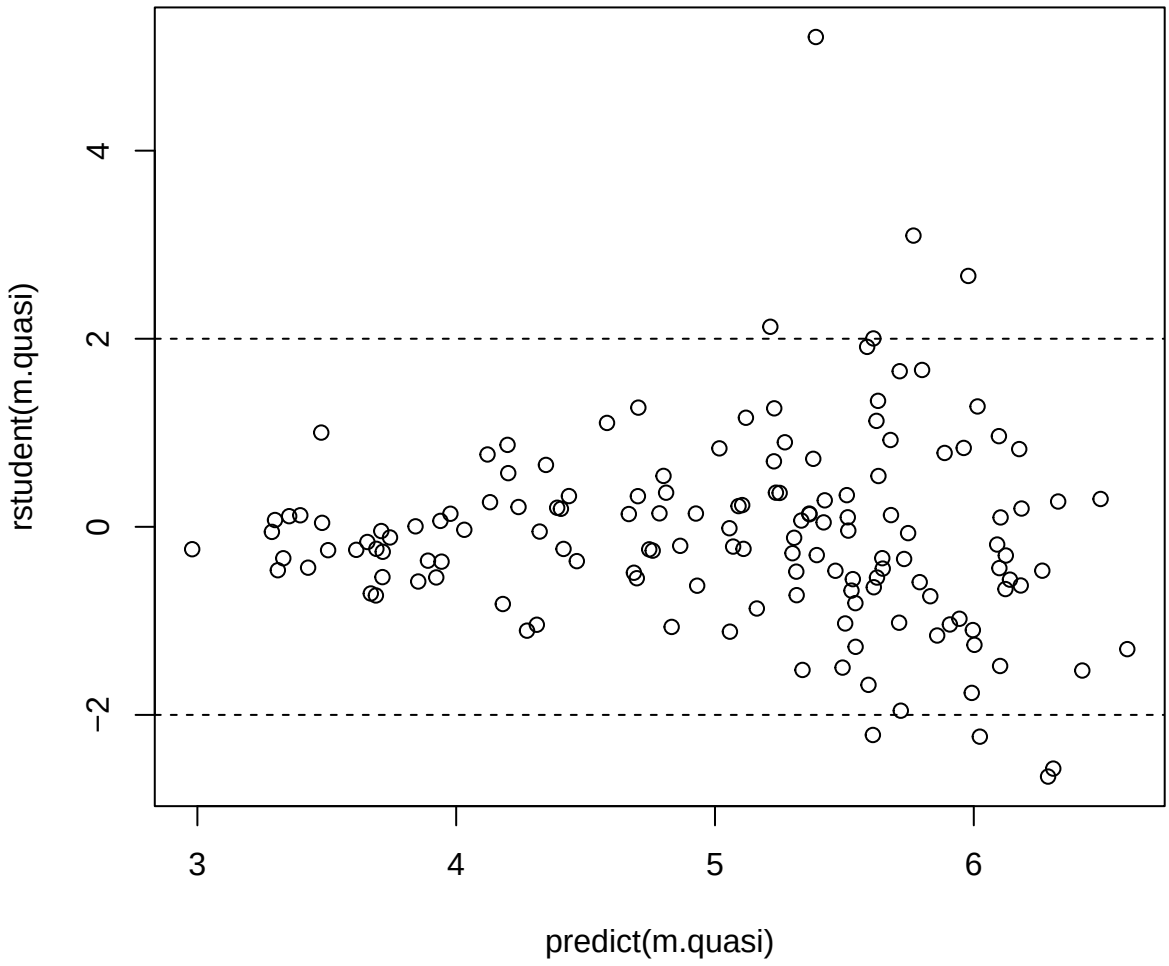
```
# odds ratios for effect of a 0.01 unit increase in density
trtools::contrast(m.quasi,
  a = list(species = c("kc","pm"), density = 0.02),
  b = list(species = c("kc","pm"), density = 0.01),
  cnames = c("kc","pm"), tf = exp)
```

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

Note that point estimates are unchanged, but standard errors, tests, and confidence intervals are affected.

Example: Now let's try the same approach with trawling data.

```
m.quasi <- glm(totabund ~ period * meandepth + offset(log(sweptarea)),
  family = quasipoisson, data = fishing)
plot(predict(m.quasi), rstudent(m.quasi), main = "Residual Plot")
abline(h = c(-2,2), lty = 2)
```



That was maybe somewhat less successful. Note the "megaphone" pattern. The assumed variance structure is

$$\mathrm{Var}(Y_i) = \phi E(Y_i).$$

We could relax this by assuming instead

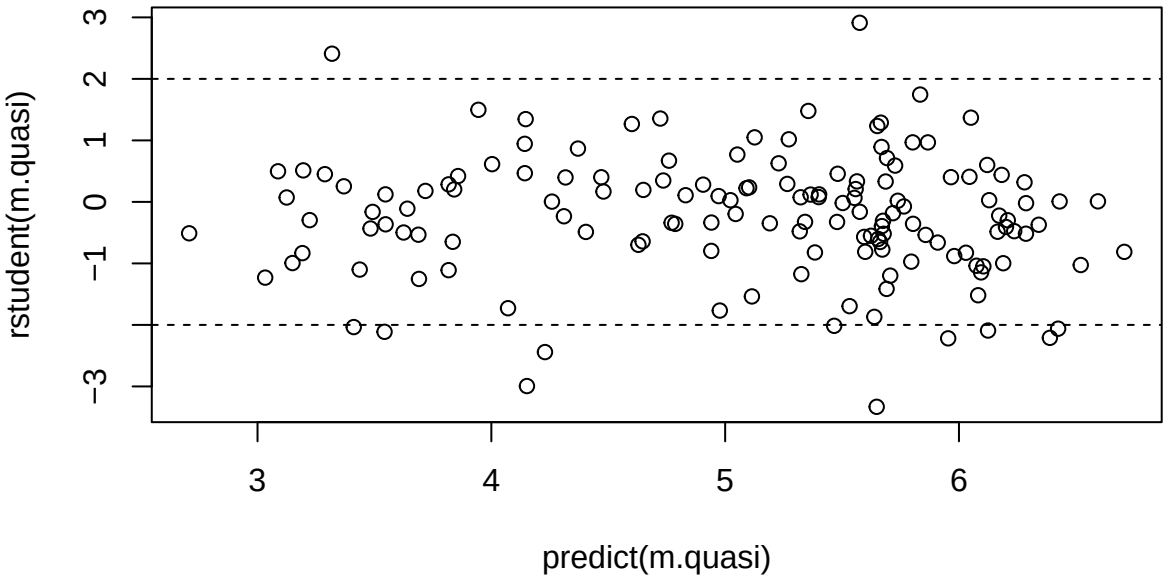
$$\mathrm{Var}(Y_i) = \phi E(Y_i)^p.$$

for some $p > 1$. If $p = 1$, 2, or 3 then we can use `quasi`. Here we are using it for $p = 2$.

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

```
                           Estimate Std. Error  t value  Pr(>|t|)
(Intercept)              -3.250e+00  1.592e-01 -20.4180 3.187e-44
period2000-2002          -6.041e-01  2.720e-01  -2.2212 2.791e-02
meandepth                -1.041e-03  5.866e-05 -17.7403 5.988e-38
period2000-2002:meandepth  7.272e-05  9.992e-05   0.7278 4.679e-01
```

```
plot(predict(m.quasi), rstudent(m.quasi), main = "Residual Plot")
abline(h = c(-2,2), lty = 2)
```



Note that `quasi(link = "log", variance = "mu")` is the same as `quasipoisson`. For more options consider `family = tweedie`. The `tweedie` family defines power functions for link and variance functions of the form

$$E(Y_i)^q = \eta_i \quad \text{and} \quad \text{Var}(Y_i) = \phi E(Y_i)^p,$$

where $E(Y_i)^0 \equiv \log E(Y_i)$ when using `tweedie` (not mathematically of course — this is just for interface purposes). For example, to replicate the quasi-likelihood model above we can use the following.

```
library(statmod) # for tweedie "family"
m.tweedie <- glm(totabund ~ period * meandepth + offset(log(sweptarea)),
  family = tweedie(link.power = 0, var.power = 2), data = fishing)
summary(m.tweedie)$coefficients
```

```
                            Estimate Std. Error  t value  Pr(>|t|)
(Intercept)               -3.250e+00  1.592e-01 -20.4180 3.187e-44
period2000-2002           -6.041e-01  2.720e-01  -2.2212 2.791e-02
meandepth                 -1.041e-03  5.866e-05 -17.7403 5.988e-38
period2000-2002:meandepth  7.272e-05  9.992e-05   0.7278 4.679e-01
```

The powers p and q are not required to be integers when using `tweedie`.

Whether or not we use quasi-likelihood will affect the standard errors, as well as tests and confidence intervals. Failing to account for substantial over-dispersion can result in biased standard errors, and thus incorrect tests and confidence intervals. Estimates of parameters (of functions thereof such as what we get from `contrast`) may or may not change, depending on the variance structure.

```
m.poisson <- glm(totabund ~ period * meandepth + offset(log(sweptarea)),
  family = poisson, data = fishing)
# rate ratios for year
trtools::contrast(m.poisson,
  a = list(sweptarea = 1, meandepth = c(1000,2000,3000,4000,5000), period = "2000-2002"),
  b = list(sweptarea = 1, meandepth = c(1000,2000,3000,4000,5000), period = "1977-1989"),
  cnames = c("1000m","2000m","3000m","4000m","5000m"), tf = exp)
```

```
      estimate  lower  upper
1000m   0.5277 0.5100 0.5460
```

```
2000m   0.6020 0.5861 0.6183
3000m   0.6869 0.6565 0.7187
4000m   0.7837 0.7293 0.8421
5000m   0.8941 0.8087 0.9885
```

```
trtools::contrast(m.tweedie,
  a = list(sweptarea = 1, meandepth = c(1000,2000,3000,4000,5000), period = "2000-2002"),
  b = list(sweptarea = 1, meandepth = c(1000,2000,3000,4000,5000), period = "1977-1989"),
  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
```

Inferences With Quasi-Likelihood

Using quasi-likelihood instead of maximum likelihood changes how inferences are made in several ways.

1. The standard errors are multiplied by $\sqrt{\hat{\phi}}$. If $\hat{\phi} > 1$ (which it probably is if over-dispersion is present) then the standard errors will be larger (and thus failing to account for over-dispersion leads us to usually underestimate them). Note that this adjustment is made automatically when using quasi-likelihood.
2. Wald confidence intervals and tests for a single parameter or function of parameters are based on the t distribution rather than the standard normal distribution. The t distribution is believed to provide more accurate results, although it is still an approximation.
3. Using `confint` or `anova` use the F distribution rather than the χ^2 distribution. The underlying test statistic is similar to the F test statistic used in normal linear models. When using `anova` you should use `test = "F"` rather than `test = "LRT"` if you are using quasi-likelihood.
4. Function in **emmeans** do not adjust the degrees of freedom for estimating the dispersion parameter when using quasi-likelihood. This does not make much difference unless n is small. But you can specify the it manually via the `df` argument (use the degrees of freedom for the residual deviance from `summary` or extract it with `modelname$df.residual`). But `contrast` and `lincon` do not require manual specification, although you can via the `df` argument for those functions.

```
library(emmeans)
m.quasi <- glm(cbind(y, total - y) ~ species + density + species:density,
  family = quasibinomial, data = myrotifer)
trtools::contrast(m.quasi,
  a = list(species = c("kc","pm"), density = 0.02),
  b = list(species = c("kc","pm"), density = 0.01),
  cnames = c("kc","pm"), tf = exp)
```

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

```
pairs(emmeans(m.quasi, ~density|species, at = list(density = c(0.02, 0.01)),
  type = "response"), infer = TRUE) # wrong df
```

```
species = kc:
 contrast                 odds.ratio    SE  df asymp.LCL asymp.UCL null z.ratio p.value
 density0.02 / density0.01       2.97 0.424 Inf      2.24      3.93    1   7.606  <.0001
```

```
species = pm:
 contrast                  odds.ratio    SE  df asymp.LCL asymp.UCL null z.ratio p.value
 density0.02 / density0.01       2.88 0.535 Inf      2.00      4.14    1   5.681  <.0001

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

```
pairs(emmeans(m.quasi, ~density|species, at = list(density = c(0.02, 0.01)),
  type = "response"), infer = TRUE, df = m.quasi$df.residual) # correct df
```

```
species = kc:
 contrast                  odds.ratio    SE df lower.CL upper.CL null t.ratio p.value
 density0.02 / density0.01       2.97 0.424 36     2.22     3.96    1   7.606  <.0001

species = pm:
 contrast                  odds.ratio    SE df lower.CL upper.CL null t.ratio p.value
 density0.02 / density0.01       2.88 0.535 36     1.97     4.20    1   5.681  <.0001

Degrees-of-freedom method: user-specified
Confidence level used: 0.95
Intervals are back-transformed from the log odds ratio scale
Tests are performed on the log odds ratio scale
```

Admittedly it does not make much difference here.

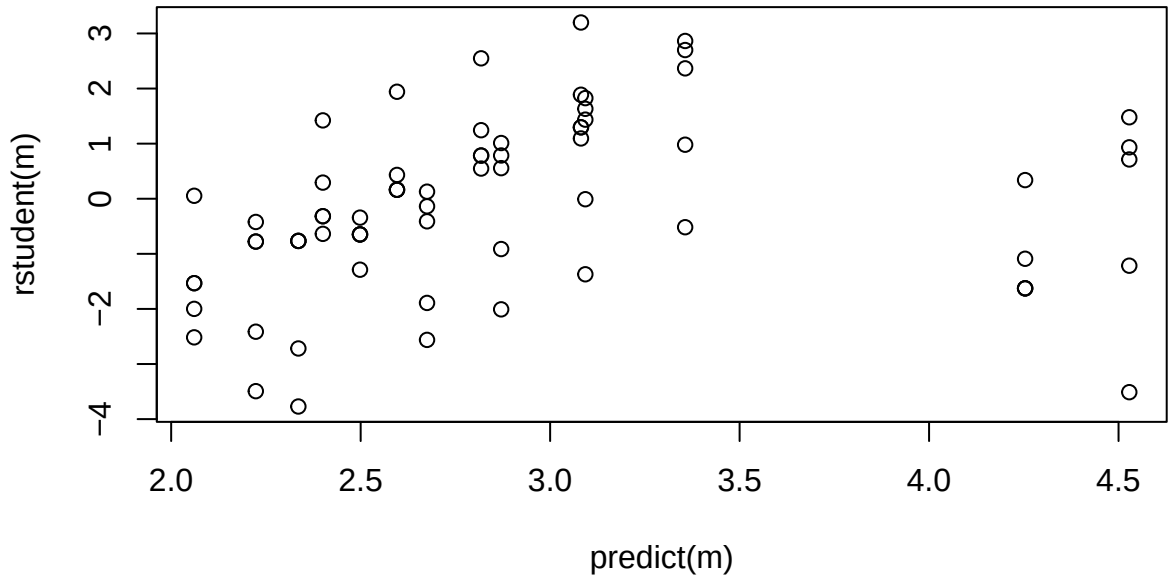
Misspecified Mean Structures and over-dispersion

A poorly specified *mean structure* may be mistaken for over-dispersion.

```
library(trtools)
ceriodaphniastrain$strain <- factor(ceriodaphniastrain$strain, labels = c("a","b"))
m <- glm(count ~ strain + sqrt(concentration), family = poisson, data = ceriodaphniastrain)
summary(m)
```

```
Call:
glm(formula = count ~ strain + sqrt(concentration), family = poisson,
    data = ceriodaphniastrain)

Coefficients:
                   Estimate Std. Error z value Pr(>|z|)
(Intercept)          4.5284     0.0400  113.08  < 2e-16 ***
strainb             -0.2750     0.0484   -5.68  1.3e-08 ***
sqrt(concentration) -1.6576     0.0474  -34.99  < 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: 1359.38  on 69  degrees of freedom
Residual deviance:  164.28  on 67  degrees of freedom
AIC: 493.9

Number of Fisher Scoring iterations: 4
```

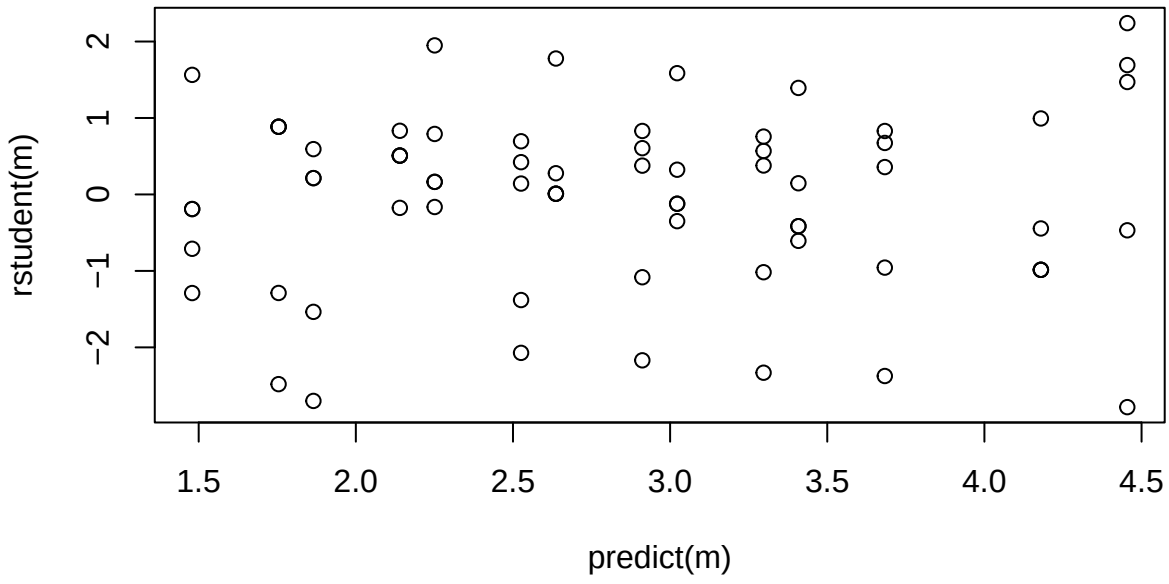
```r
plot(predict(m), rstudent(m))
```




```r
m <- glm(count ~ strain + concentration, family = poisson, data = ceriodaphniastrain)
summary(m)
```

```
Call:
glm(formula = count ~ strain + concentration, family = poisson,
    data = ceriodaphniastrain)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)     4.4546     0.0391  113.82  < 2e-16 ***
strainb        -0.2750     0.0484   -5.68  1.3e-08 ***
concentration  -1.5431     0.0466  -33.11  < 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: 1359.381  on 69  degrees of freedom
Residual deviance:   86.376  on 67  degrees of freedom
AIC: 416

Number of Fisher Scoring iterations: 4
```

```r
plot(predict(m), rstudent(m))
```



Quasi-Likelihood and Nonlinear Regression

Quasi-likelihood for a GLM is essentially the same as using (nonlinear) regression with iteratively weighted least squares to account for heteroscedasticity. The weights are

$$w_i = \frac{1}{V(\hat{y}_i)},$$

where V is the variance function.

Example: Consider the model for the trawling data where the variance is proportional to $E(Y_i)^2$. To estimate this model using iteratively weighted least squares we use weights of $w_i = 1/E(Y_i)^2$.

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

```
                            Estimate Std. Error  t value  Pr(>|t|)
(Intercept)               -3.250e+00  1.592e-01 -20.4180 3.187e-44
period2000-2002           -6.041e-01  2.720e-01  -2.2212 2.791e-02
meandepth                 -1.041e-03  5.866e-05 -17.7403 5.988e-38
period2000-2002:meandepth  7.272e-05  9.992e-05   0.7278 4.679e-01
```

```
fishing$w <- 1
for (i in 1:10) {
  m.iwls <- nls(totabund ~ exp(b0 + b1*(period == "2000-2002") + b2*meandepth +
    b3*(period == "2000-2002")*meandepth + log(sweptarea)), data = fishing,
    start = list(b0 = -3, b1 = -0.6, b2 = 0, b3 = 0), weights = w)
  fishing$w <- 1 / predict(m.iwls)^2
}
summary(m.iwls)$coefficients
```

```
     Estimate Std. Error  t value  Pr(>|t|)
b0 -3.250e+00  1.592e-01 -20.4179 3.189e-44
b1 -6.041e-01  2.720e-01  -2.2213 2.790e-02
b2 -1.041e-03  5.866e-05 -17.7402 5.991e-38
b3  7.273e-05  9.992e-05   0.7279 4.679e-01
```

Example: Consider the model for the rotifer data. Here the variance is proportional to $E(Y_i)[1-E(Y_i)_i]/m_i$ (recall that m_i is the "total possible" for the counts). To estimate this model using iteratively weighted least squares we use weights of

$$w_i = \frac{m_i}{E(Y_i)[1-E(Y_i)]}.$$

```
m.binomial <- glm(cbind(y, total - y) ~ species * density,
  family = quasibinomial, data = myrotifer)
summary(m.binomial)$coefficients
```

```
                 Estimate Std. Error t value  Pr(>|t|)
(Intercept)      -114.352      14.95 -7.6472 4.736e-09
speciespm           4.629      24.46  0.1893 8.509e-01
density           108.746      14.30  7.6056 5.358e-09
speciespm:density  -3.077      23.46 -0.1312 8.964e-01
```

```
myrotifer$w <- 1
for (i in 1:20) {
    m <- nls(y/total ~ plogis(b0 + b1*(species == "pm") + b2*density +
      b3*(species == "pm")*density), data = myrotifer, weights = w,
      start = list(b0 = -114, b1 = 4.6, b2 = 109, b3 = -3))
    myrotifer$yhat <- predict(m)
    myrotifer$w <- myrotifer$total / (myrotifer$yhat * (1 - myrotifer$yhat))
}
summary(m)$coefficients
```

```
   Estimate Std. Error t value  Pr(>|t|)
b0 -114.338      14.95 -7.6485 4.718e-09
b1    4.614      24.46  0.1887 8.514e-01
b2  108.732      14.29  7.6069 5.338e-09
b3   -3.063      23.46 -0.1306 8.968e-01
```

Note that `plogis` is the function $e^x/(1+e^x)$. The model can be written as

$$E(Y_i) = \frac{e^{\eta_i}}{1+e^{\eta_i}}$$

where Y_i is the observed *proportion*, and

$$\eta_i = \beta_0 + \beta_1 s_i + \beta_2 d_i + \beta_3 s_i d_i,$$

where s_i is an indicator variable for the `pm` species, and d_i is the density.

Using iteratively weighted least squares is not necessary if we can use `quasi` or `tweedie`, but it is a useful option for cases where the variance structure is outside what can be done with `quasi` or `tweedie` (although one can *program* new variance structures).