Count Regression Notes

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We will suppose that we have a sample of data (y_i, x_i), $i = 1, \ldots, n$ where y_i is a scalar response variable and x_i is a fixed vector of predictors taking values in $\mathbb{R}^p$.

The likelihood of the exponential family is of the form

$$l(\theta) = \langle y, \theta \rangle - c(\theta), \tag{1}$$

where y is a vector statistic having components y_i and $\theta \in \mathbb{R}^n$ is the canonical parameter vector. Without specifying a submodel, θ is unconstrained and the likelihood (1), one parameter for every observation. We will specify a canonical linear submodel of an exponential family is a submodel having parameterization

$$\theta = M\beta$$

where $\theta \in \mathbb{R}^n$ is the canonical parameter vector corresponding to the original saturated exponential family, $\beta \in \mathbb{R}^p$ is the canonical parameter vector for the submodel, and M is the model matrix with rows x_i^T. The submodel log likelihood is

$$l(\beta) = \langle M^T y, \beta \rangle - c(M\beta). \tag{2}$$

Poisson regression model with log link

The Poisson regression model is another of one of the most widely used and studied GLMs in practice. A Poisson regression model is sometimes known as a log-linear model, especially when used to model contingency tables. The Poisson regression model is used for analyzing a discrete count response variable, $y_i \in \{0, 1, 2, \ldots\}$ or a contingency table. The Poisson regression model allows for users to model the rate as a function of covariates. The log link arises as the canonical link.

For a count response variable Y and a vector of predictors X, let $\mu(x) = \mathrm{E}(Y|X = x)$. The Poisson regression model is then

$$\mu(x) = \mathrm{E}(Y|X = x) = \exp\left(x^T\beta\right). \tag{3}$$

Equivalently,

$$\log\left(\mu(x)\right) = x^T\beta.$$

In vector notation, we can express the above as

$$\boldsymbol{\mu} = \exp(M\beta) \quad \text{and} \quad \log(\boldsymbol{\mu}) = M\beta$$

where the above $\exp(\cdot)$ and $\log(\cdot)$ operations are understood as componentwise operations. To see where the log link comes from in the specification of $\mu(x)$ comes from consider the log likelihood of the Poisson distribution with rate parameter μ_i for each subject

$$\begin{aligned} l\left(\beta\right) &\propto \sum_{i=1}^{n} y_i \log(\mu_i) - \sum_{i=1}^{n} \mu_i \\ &= \sum_{i=1}^{n} y_i\theta_i - \sum_{i=1}^{n} g(\theta_i), \end{aligned}$$

where

$$\theta_i = \log(\mu_i) \qquad \text{and} \qquad \mu_i = \exp(\theta_i) = g(\theta_i).$$

We see that the Poisson regression model with log link is the same as the canonical linear submodel of an exponential family with $\theta_i = x_i^T\beta$ which in vector notation is $\theta = M\beta$. Putting this together, we have that

$$\mathrm{E}(Y|X = x) = g\left(x^T\beta\right) \qquad \text{and} \qquad g^{-1}\left(\mathrm{E}(Y|X = x)\right) = x^T\beta$$

where the link function g^{-1} is the logarithmic function, the inverse-link function (change of parameters map) is the exponential function. Hence, the name log-linear models.

Therefore, a linear function of the canonical submodel parameter vector is linked to the mean of the Poisson distribution through a change-of-parameter mapping $g(\theta)$. As stated before, this is the basis of exponential family generalized linear models with link function g^{-1}. The familiar presentation of the various model parameterizations and how they are related to each other is given in Figure 1.

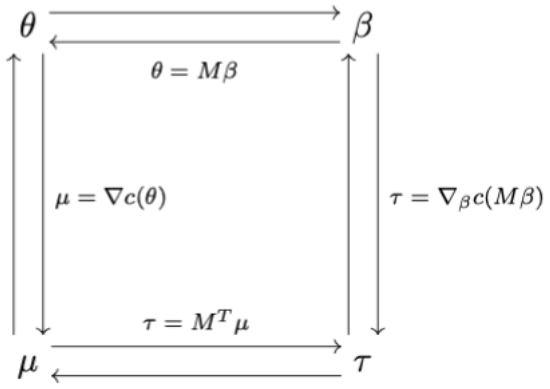


Figure 1: A depiction of the transformations necessary to change between parameterizations. Arrows going in opposite directions specify transformations and their inverses. M is a known model matrix of full column rank, and c is the cumulant function for the exponential family model.

Example: Gala data

```
rm(list = ls())
library(tidyverse)
library(faraway)
```

We will demonstrate Poisson regression modeling on the Galapagos data frame in the `faraway` package. This data frame consists of $n = 30$ observations and 7 variables in total.

For 30 Galapagos Islands, we have a count of the number of plant species found on each island and the number that are endemic to the island. We also have five geographic variables for each island. A few missing values have been filled in for simplicity. We will model the number of species using Poisson regression using the glm function in R. The Endemic variable is thrown out since it won't be used in this analysis. We create a discrete size variable based on the Area variable for demonstration purposes.

```
gala <- gala %>%
  mutate(Size = as.factor(1 + ifelse(Area > 1,1,0) + ifelse(Area > 25,1,0)))
m1 <- glm(Species ~ Elevation + Nearest + Scruz + Adjacent + Size,
          family = "poisson", data = gala, x = TRUE)
```

Now let's unpack the glm function call above. We decided that we wanted to fit an exponential family regression model with log likelihood taking the general form

$$l(\beta) = \langle M^T y, \beta \rangle - c(M\beta),$$

where y is the vector of responses β is the submodel canonical statistic vector corresponding to the model matrix M specified by the formula in the glm function call above. The first few rows of M are displayed below

```
M <- m1$x
head(M)
```

```
##              (Intercept) Elevation Nearest Scruz Adjacent Size2 Size3
## Baltra                 1       346     0.6   0.6     1.84     0     1
## Bartolome              1       109     0.6  26.3   572.33     1     0
## Caldwell               1       114     2.8  58.7     0.78     0     0
## Champion               1        46     1.9  47.4     0.18     0     0
## Coamano                1        77     1.9   1.9   903.82     0     0
## Daphne.Major           1       119     8.0   8.0     1.84     0     0
```

The specific log likelihood for the Poisson regression model can then be written as

$$l(\beta) \propto \sum_{i=1}^{n} y_i x_i^T \beta - \exp\left(x_i^T \beta\right)$$

where the x_is are the rows of the design matrix M and the y_is are the components of the response vector y (the Species variable corresponding to the number of species on each of the islands). The glm function then performs a Fisher scoring based optimization routine to maximize the above likelihood. We can view summary information for $\hat{\beta}$ and the fitting process using the summary function

```
summary(m1)
```

```
##
## Call:
## glm(formula = Species ~ Elevation + Nearest + Scruz + Adjacent +
##     Size, family = "poisson", data = gala, x = TRUE)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -10.3723   -3.5214   -0.9947    1.7193   10.6627
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.790e+00  8.108e-02  34.410  < 2e-16 ***
## Elevation    9.361e-04  5.402e-05  17.329  < 2e-16 ***
## Nearest      6.469e-03  1.748e-03   3.702 0.000214 ***
## Scruz       -6.266e-03  6.268e-04  -9.997  < 2e-16 ***
## Adjacent    -2.858e-04  2.961e-05  -9.652  < 2e-16 ***
## Size2        1.128e+00  9.535e-02  11.826  < 2e-16 ***
## Size3        2.059e+00  9.419e-02  21.856  < 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: 3510.73  on 29  degrees of freedom
## Residual deviance:  594.18  on 23  degrees of freedom
## AIC: 769.01
##
## Number of Fisher Scoring iterations: 5
```

The Estimate column in the above summary table is $\hat{\beta}$. The standard error column as estimates of the square root of the variances of the estimated submodel canonical statistic vector $\hat{\beta}$. Recall from the asymptotic theory of maximum likelihood estimation that

$$\sqrt{n}(\hat{\beta} - \beta) \xrightarrow{d} N(0, \Sigma^{-1}),$$

where Σ^{-1} is the inverse of the Fisher information matrix. We can extract these same standard errors using the vcov function

```
sqrt(diag(vcov(m1)))
```

```
##  (Intercept)    Elevation      Nearest        Scruz     Adjacent        Size2
## 8.107577e-02 5.402068e-05 1.747556e-03 6.268325e-04 2.960794e-05 9.535081e-02
##        Size3
## 9.419199e-02
```

These values are the same as those in the Std. Error column in the above summary table

```
all.equal(summary(m1)$coef[, 2], sqrt(diag(vcov(m1))))
```

```
## [1] TRUE
```

Manually write your own Fisher scoring algorithm which maximizes the Poisson regression log likelihood for this example. Report $\hat{\beta}$ and reproduce the above summary table without using the glm or summary commands.

Inference for β in Poisson regression

The Galapagos example connects the exponential family that we have developed to R-based data analysis. We motivated this connection in the logistic regression notes. In Poisson regression the link function is log, and thus $\log(\mu(x)) = x_i^T \beta$. Therefore, a unit increase in one predictor variables x_j corresponds to an increase of β_j (estimated by $\hat{\beta}_j$) in the log mean with everything else being held fixed. See the summary table below for estimates of β in our Galapagos example

```
summary(m1)
```

```
##
## Call:
## glm(formula = Species ~ Elevation + Nearest + Scruz + Adjacent +
##     Size, family = "poisson", data = gala, x = TRUE)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -10.3723   -3.5214   -0.9947    1.7193   10.6627
##
## Coefficients:
```

```
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.790e+00  8.108e-02  34.410  < 2e-16 ***
## Elevation    9.361e-04  5.402e-05  17.329  < 2e-16 ***
## Nearest      6.469e-03  1.748e-03   3.702 0.000214 ***
## Scruz       -6.266e-03  6.268e-04  -9.997  < 2e-16 ***
## Adjacent    -2.858e-04  2.961e-05  -9.652  < 2e-16 ***
## Size2        1.128e+00  9.535e-02  11.826  < 2e-16 ***
## Size3        2.059e+00  9.419e-02  21.856  < 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: 3510.73  on 29  degrees of freedom
## Residual deviance:  594.18  on 23  degrees of freedom
## AIC: 769.01
##
## Number of Fisher Scoring iterations: 5
```

Wald inference

As in linear regression we can make inferences about β_j using the Wald statistic corresponding to the hypothesis test

$$H_o : \beta_j = 0, \qquad H_a : \beta_j \neq 0,$$

which is given by

$$\frac{\hat{\beta}_j}{\text{se}(\hat{\beta}_j)} \sim N(0, 1),$$

where this distributional relationship holds under the null hypothesis $\beta_j = 0$. Similarly, we can form a confidence interval

$$\hat{\beta}_j \pm z_{\alpha/2}\text{se}(\hat{\beta}_j)$$

where $0 < \alpha < 1$ is some error threshold. The $(1 - \alpha) \times 100\%$ Wald confidence interval for the response variable $\log(\mu(x))$ at a particular x follows from the Delta method. We have that $\log(\mu(x)) = x^T\beta$ which implies that $\nabla_\beta \log(\mu(x)) = x$, and we have that

$$\sqrt{n}(\hat{\beta} - \beta) \xrightarrow{d} N(0, \Sigma^{-1})$$

Therefore,

$$\sqrt{n}\left(\log(\hat{\mu}(x)) - \log(\mu(x))\right) \xrightarrow{d} N(0, x^T\Sigma^{-1}x).$$

We can report the following $(1 - \alpha) \times 100\%$ Wald confidence interval for the log mean value

$$\log(\hat{\mu}(x)) \pm z_{\alpha/2}\sqrt{x^T\widehat{\Sigma}^{-1}x}.$$

Deviance and likelihood ratio testing

As in the logistic regression notes, let $l(\mu; y)$ denote the the log-likelihood of a GLM in the mean-value parameter μ. The deviance of a logistic or Poisson regression model is defined by

$$-2\left[l(\hat{\mu}; y) - l(y; y)\right].$$

This is the likelihood-ratio for testing the null hypothesis that the model against the general alternative (ie, the saturated model). The deviance has reference distribution

$$-2\left[l(\hat{\mu}; y) - l(y; y)\right] \approx \chi^2_{\text{df}}$$

where $\text{df} = n - p$, n is the sample size, and p is the number of model parameters. For large samples we can use the deviance statistic to test nested models. Denote $\mathcal{M}_o$ and $\mathcal{M}_a$, respectively, as the null model and the alternative model, and let $\hat{\mu}_o$ and $\hat{\mu}_a$, respectively, be the estimated mean-value parameter vectors under $\mathcal{M}_o$ and $\mathcal{M}_a$. Then the difference in deviances between the null model and the alternative model is,

$$-2\left[l(\hat{\mu}_o; y) - l(\hat{\mu}_a; y)\right] = -2\left[l(\hat{\mu}_o; y) - l(y; y)\right] - \{-2\left[l(\hat{\mu}_a; y) - l(y; y)\right]\} \approx \chi^2_{\text{df}},$$

where $\text{df} = p_a - p_o$, p_a is the number of model parameters in model $\mathcal{M}_a$, and p_o is the number of model parameters in model $\mathcal{M}_o$.

Example: Gala data (continued)

We can use the deviance and degrees of freedom objects to perform the likelihood ratio test to determine whether or not the main effects model fits the data well.

```
## test against intercept only model
pchisq(m1$null.deviance - m1$deviance, df = m1$df.null - m1$df.residual,
       lower = FALSE)
```

```
## [1] 0
```

```
m_null <- glm(Species ~ 1, family = "poisson", data = gala, x = TRUE)
anova(m_null, m1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: Species ~ 1
## Model 2: Species ~ Elevation + Nearest + Scruz + Adjacent + Size
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1        29     3510.7
## 2        23      594.2  6   2916.6 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Let's consider the smaller model that ignores the Elevation variable. A likelihood ratio test shows that the larger model is preferable at any reasonably chosen significance level α.

```
m_small <- glm(Species ~ Nearest + Scruz + Adjacent + Size,
          family = "poisson", data = gala, x = TRUE)

## built in likelihood ratio test using anova.glm
anova(m_small, m1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: Species ~ Nearest + Scruz + Adjacent + Size
## Model 2: Species ~ Elevation + Nearest + Scruz + Adjacent + Size
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1        24     878.14
## 2        23     594.18  1   283.96 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## perform the above directly (different machine tolerances)
pchisq(m_small$deviance - m1$deviance, df = 1, lower = FALSE)
```

```
## [1] 1.029422e-63
```

Summarize the summary table produced by a call to summary(m1).

Further testing

In this example we see that the levels of the Size variable are statistically significant at any reasonable error threshold α. Suppose instead that we wanted to test if large islands are expected to have a different number of species than medium sized islands. Informally, the summary table above suggests that large islands have mores species than medium sized islands, but this is not a formal comparison. Formally, we want to test

$$H_o : \mu_l - \mu_m = 0, \qquad H_a : \mu_l - \mu_m \neq 0,$$

where μ_l and μ_m, respectively, correspond to the mean-value parameters for large and medium-sized islands. We know that $\mu_l = \exp(\beta_l)$ and $\mu_m = \exp(\beta_m)$ where β_l and β_m, respectively, correspond to the canonical parameters for large and medium-sized islands. We can test the above hypothesis using the Delta method

$$\sqrt{n}\left[(\hat{\mu}_l - \hat{\mu}_m) - (\mu_l - \mu_m)\right] \xrightarrow{d} N\left(0, \nabla h(\beta)^T \Sigma^{-1} \nabla h(\beta)\right)$$

where $h(\beta) = \exp(\beta_l) - \exp(\beta_m) = \mu_l - \mu_m$. We obtain the estimate $\hat{\mu}_l - \hat{\mu}_m$ below

```
comp <- c(0,0,0,0,0,-1,1)
betahat <- m1$coefficients
grad <- exp(betahat) * comp
est <- sum(grad)
est
```

```
## [1] 4.747314
```

and the estimate of $\nabla h(\beta)$ is the column vector below

```
grad
```

```
## (Intercept)   Elevation     Nearest       Scruz    Adjacent       Size2
##    0.000000    0.000000    0.000000    0.000000    0.000000   -3.088284
##       Size3
##    7.835597
```

The asymptotic variance $\nabla h(\beta)^T \Sigma^{-1} \nabla h(\beta)$ and corresponding standard error are estimated below

```
InvFish <- vcov(m1)
asympVar <- as.numeric(t(grad) %*% InvFish %*% grad)
asympVar
```

```
## [1] 0.2965522
```

```
SE <- sqrt(asympVar)
SE
```

```
## [1] 0.5445661
```

The ratio $(\hat{\mu}_l - \hat{\mu}_m)/\text{se}(\hat{\mu}_l - \hat{\mu}_m)$ is given by

```
est/SE
```

```
## [1] 8.717608
```

and a corresponding 95% confidence interval is

```
est + qnorm(c(0.025,0.975)) * SE
```

```
## [1] 3.679984 5.814644
```

Keep in mind that there are three possible tests that we could have made. We can adjust for this using a Bonferroni correction

```
est + qnorm(c(0.025/3, 1-0.025/3)) * SE
```

```
## [1] 3.443633 6.050994
```

Diagnosing modeling assumptions

As with standard linear models, it is important to check the modeling assumptions of the GLM. The diagnostic methods are similar to those used for linear models with normal errors. However, some adaptions are necessary, and not all diagnostic methods will be applicable.

Residual-based diagnostics: Residuals represent the discrepancy between the model and the observed data, and are essential for exploring the adequacy of the model. In the Gaussian case, the residuals are $\hat{\epsilon} = y - \hat{\mu}$. In Faraway, these are referred to as response residuals for GLMs and they can be used directly to check the constant variance assumption in linear models with Gaussian errors. However, since the variance of the GLM is often not constant and is often a function of the canonical parameter, some modifications to the residuals are necessary.

Pearson residuals: the Pearson residual is comparable to the standardized residual used for linear models and is defined as:

$$r_P = \frac{y - \hat{\mu}}{\sqrt{\text{Var}(\hat{\mu})}}$$

where $\text{Var} = \nabla^2 c(\theta)$ is the estimated variance under the original exponential family. Notice that $\sum_{i=1}^{n} r_{P,i}^2$ is the Pearson χ^2 statistic, hence the name. Pearson residuals can be skewed for nonnormal responses.

Deviance residuals: The deviance residuals are defined by analogy to the Pearson residuals. In other words, we set the deviance residual r_D so that

$$\sum_{i=1}^{n} r_{D,i}^2 = \text{Deviance} = \sum_{i=1}^{n} d_i,$$

and

$$r_{D,i} = \text{sign}(y_i - \hat{\mu}_i)\sqrt{d_i}.$$

In Poisson regression the deviance residuals are

$$r_{D,i} = \text{sign}(y_i - \hat{\mu}_i)\left[2\left(\frac{y_i \log(y_i)}{\hat{\mu}_i} - y_i + \hat{\mu}_i\right)\right]^{1/2}.$$

We now revisit the Galapagos data to explore these residuals.

```
## Deviance residuals
head(residuals(m1))
```

```
##       Baltra    Bartolome     Caldwell     Champion      Coamano Daphne.Major
## -10.37226589  -1.51907573  -3.29219582   3.01748621  -3.92316686  -0.05066076
```

```
## Pearson residuals
head(residuals(m1, "pearson"))
```

```
##       Baltra    Bartolome     Caldwell     Champion      Coamano Daphne.Major
##  -8.90760179  -1.45715550  -2.73281460   3.41729331  -3.13259915  -0.05056044
```

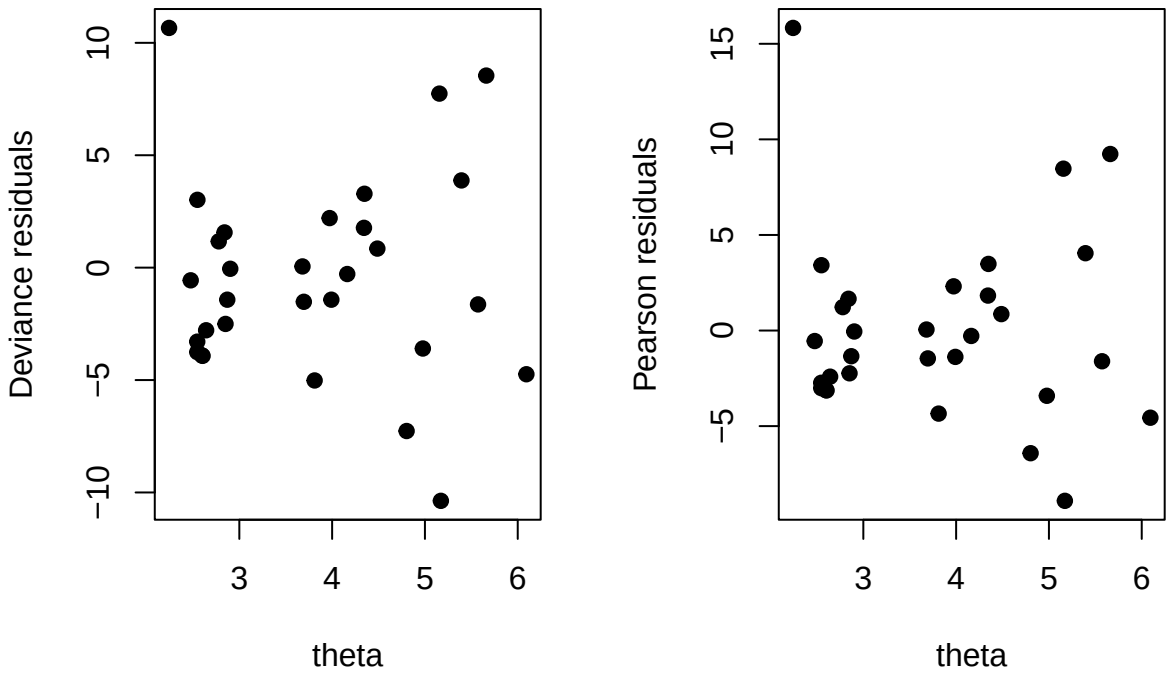
For linear models, the residuals vs. fitted values plot is probably the single most valuable graphic. For GLMs, we must decide on the appropriate scale for the fitted values. Usually, it is better to plot on the scale of the linear predictors (θ) than on the fitted responses (μ).

We are looking for features in these residuals vs. fitted values plots. First of all, is there any nonlinear relationship between the residuals and the fitted values? If so, this would be an indication of a lack of fit that might be rectified by a change in the model. For a linear model, we may transform the response variable but this is likely impractical for a GLM since it would change the assumed distribution of the response variable. We might also consider changing the link function, but often this undesirable since the canonical link functions faciliate desirable theoretical properties and yield models which are relatively easy to interpret.

It is best to make a change in the choice of predictors or transformations to these predictors since this involves the least disruption to the GLM theoretical foundations.

The plots below show the residuals as a function of $\hat{\theta}_i = x_i^T \hat{\beta}$.

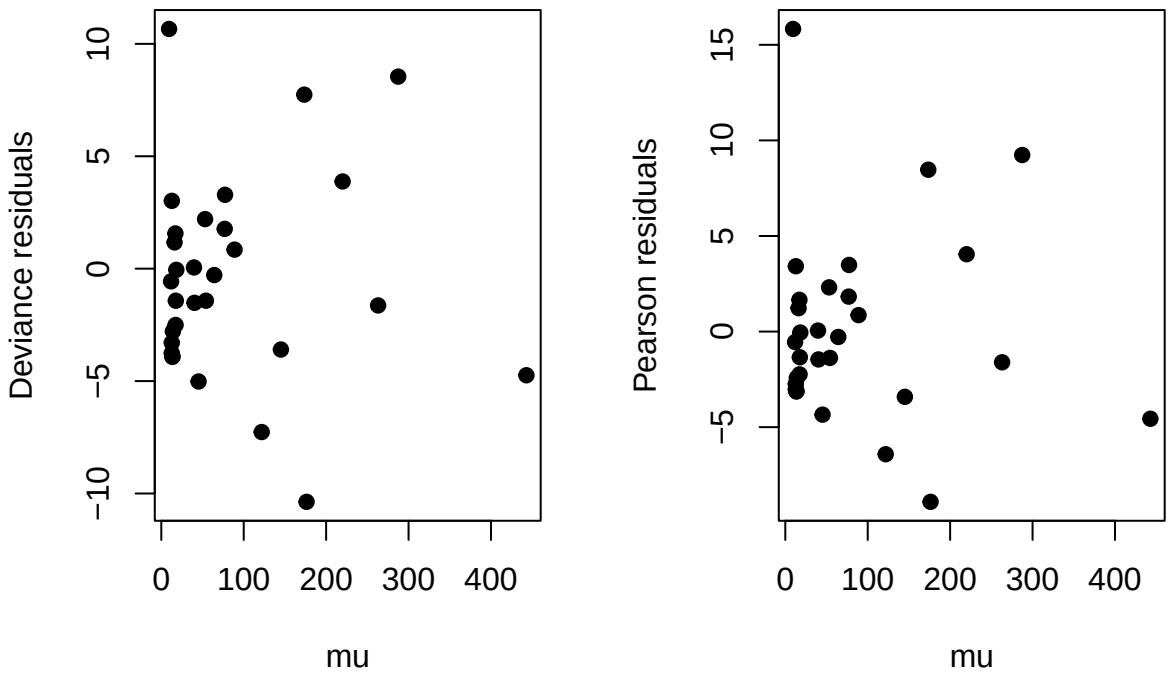
```
theta <- as.numeric(M %*% betahat)
par(mfrow = c(1,2))
plot(theta, residuals(m1), xlab = "theta", ylab = "Deviance residuals", pch = 19)
plot(theta, residuals(m1, "pearson"), pch = 19,
     xlab = "theta", ylab = "Pearson residuals")
```



The plots below show the residuals as a function of $\hat{\mu}$.

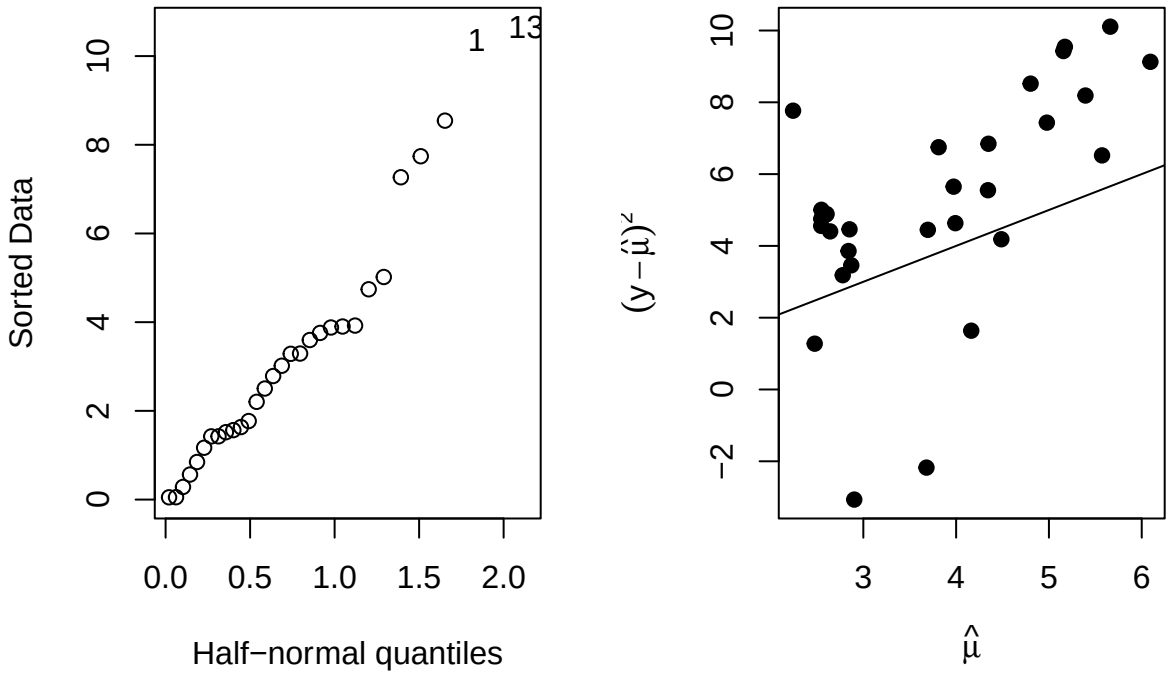
```
par(mfrow = c(1,2))
plot(predict(m1, type = "response"), residuals(m1),
```

```
     xlab = "mu", ylab = "Deviance residuals", pch = 19)
plot(predict(m1, type = "response"), residuals(m1, "pearson"),
     xlab = "mu", ylab = "Pearson residuals", pch = 19)
```



A half-normal plot of the residuals of the Poisson model is shown on the left and the relationship between the mean and the variance is shown on the right. A line showing that the variance increases linearly in the mean (not a perfect slope of 1) is also shown.

```
par(mfrow = c(1,2))
halfnorm(residuals(m1), pch = 19)
plot(log(fitted(m1)),log((gala$Species-fitted(m1))^2),
     xlab= expression(hat(mu)),ylab=expression((y-hat(mu))^2),
     pch = 19)
abline(0,1)
```



We see that the variance is proportional to, but larger than, the mean. When the variance assumption of the Poisson regression model is broken but the link function and choice of predictors are correct, the estimates of β are consistent, but the standard errors will be wrong.

Overdispersion

The Poisson distribution has only one parameter (mean equals variance) and is therefore not very flexible for empirical fitting purposes. We can generalize by allowing ourselves a dispersion parameter to allow for increased flexibility in various Poisson models. For example, suppose the Poisson response Y has rate λ which is itself a random variable. The tendency to fail for a machine may vary from unit to unit even though they are the same model. We can model this by letting λ be gamma distributed with $E(\lambda) = \mu$ and $\text{Var}(\lambda) = \mu/\phi$. Now Y is negative binomial with mean $\text{E}(Y) = \mu$. The mean is the same as the Poisson, but the variance $\text{Var}(Y) = \mu(1+\phi)/\phi$ which is not equal to μ.

If we know the specific data generating process, as in the above example, we could model the response as a negative binomial or some other more flexible distribution. However, when the mechanism is not known, we can introduce a dispersion parameter ϕ such that $\text{Var}(Y) = \phi\text{E}(Y) = \phi\mu$. The case $\phi = 1$ is the regular Poisson regression case, while $\phi > 1$ is overdispersion and $\phi < 1$ is underdispersion.

A common explanation for large deviance (or poor fit) is the presence of a few outliers. When large number of points are identified as outliers, they become unexceptional, and it may be the case that the error distribution is misspecified. In the presence of overdispersion, the exponential family takes on a different functional form

$$f(y|\theta,\phi) = \exp\left(\frac{\langle y,\theta\rangle - c(\theta)}{a(\phi)} - b(y,\phi)\right), \tag{4}$$

where y, θ, and $c(\theta)$ are as before, ϕ is a dispersion parameter, and $b(y,\phi)$ is a function of the data y and the dispersion parameter ϕ. From the perspective of the canonical exponential families that we have motivated throughout, the function $b(y,\phi)$ is similar to the base measure h that was dropped from consideration in log likelihood based arguments that focused on the parameters. Notice that the density (4) is a generalization of the exponential family density which specifies that $a(\phi) = 1$ and $b(y,\phi) = \log(h(y))$. Note that the dispersion parameter can be estimated using

$$\hat{\phi} = \frac{\sum_{i=1}^{n}(y-\hat{\mu}_i)^2/\hat{\mu}_i}{n-p}$$

Notice that the estimation of the dispersion and the regression parameters is independent, so choosing a dispersion other than one has no effect on the regression parameter estimates.

We investigate the overdispersed Poisson regression model with respect to the Galapogas data.

```
n <- nrow(gala)
p <- length(betahat)
y <- gala$Species

## estimate dispersion directly
fits <- predict(m1, type = "response")
dp <- sum((y - fits)^2/fits) / (n - p)
summary(m1, dispersion = dp)
```

```
##
## Call:
## glm(formula = Species ~ Elevation + Nearest + Scruz + Adjacent +
##     Size, family = "poisson", data = gala, x = TRUE)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -10.3723   -3.5214   -0.9947    1.7193   10.6627
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.7897965  0.4437393   6.287 3.24e-10 ***
## Elevation    0.0009361  0.0002957   3.166  0.00154 **
## Nearest      0.0064693  0.0095646   0.676  0.49880
## Scruz       -0.0062665  0.0034307  -1.827  0.06776 .
## Adjacent    -0.0002858  0.0001620  -1.764  0.07781 .
## Size2        1.1276155  0.5218686   2.161  0.03072 *
## Size3        2.0586771  0.5155262   3.993 6.51e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 29.9553)
##
##     Null deviance: 3510.73  on 29  degrees of freedom
## Residual deviance:  594.18  on 23  degrees of freedom
## AIC: 769.01
##
## Number of Fisher Scoring iterations: 5
```

```
## fit the model with dispersion
m2 <- glm(Species ~ Elevation + Nearest + Scruz + Adjacent + Size,
          family = "quasipoisson", data = gala, x = TRUE)
summary(m2)
```

```
##
## Call:
## glm(formula = Species ~ Elevation + Nearest + Scruz + Adjacent +
##     Size, family = "quasipoisson", data = gala, x = TRUE)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -10.3723   -3.5214   -0.9947    1.7193   10.6627
```

```
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.7897965  0.4437452   6.287 2.05e-06 ***
## Elevation    0.0009361  0.0002957   3.166 0.004314 **
## Nearest      0.0064693  0.0095648   0.676 0.505552
## Scruz       -0.0062665  0.0034308  -1.827 0.080777 .
## Adjacent    -0.0002858  0.0001621  -1.764 0.091094 .
## Size2        1.1276155  0.5218755   2.161 0.041376 *
## Size3        2.0586771  0.5155330   3.993 0.000572 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 29.95609)
##
##     Null deviance: 3510.73  on 29  degrees of freedom
## Residual deviance:  594.18  on 23  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 5
```

In this case the dispersion is quite large leading to an increase in standard errors of over a factor of 5

```
## dispersion and sqrt(dispersion)
c(dp, sqrt(dp))
```

```
## [1] 29.955296  5.473143
```

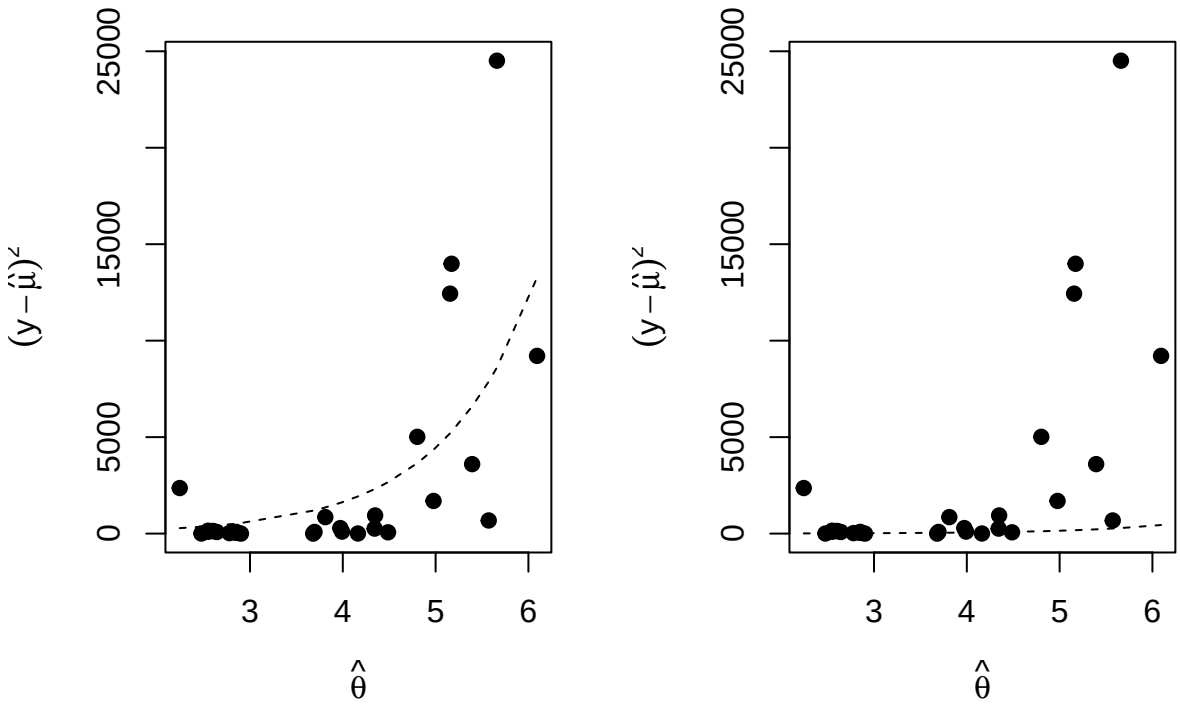
```
se <- function(model) sqrt(diag(vcov(model)))
round(data.frame(coef.m1=coef(m1), coef.m2=coef(m2), se.m1=se(m1), se.m2=se(m2),
                 ratio=se(m2)/se(m1)), 4)
```

```
##             coef.m1 coef.m2  se.m1  se.m2  ratio
## (Intercept)  2.7898  2.7898 0.0811 0.4437 5.4732
## Elevation    0.0009  0.0009 0.0001 0.0003 5.4732
## Nearest      0.0065  0.0065 0.0017 0.0096 5.4732
## Scruz       -0.0063 -0.0063 0.0006 0.0034 5.4732
## Adjacent    -0.0003 -0.0003 0.0000 0.0002 5.4732
## Size2        1.1276  1.1276 0.0954 0.5219 5.4732
## Size3        2.0587  2.0587 0.0942 0.5155 5.4732
```

The overdispersed Poisson model clearly offers improvements to the residuals vs fitted values plot

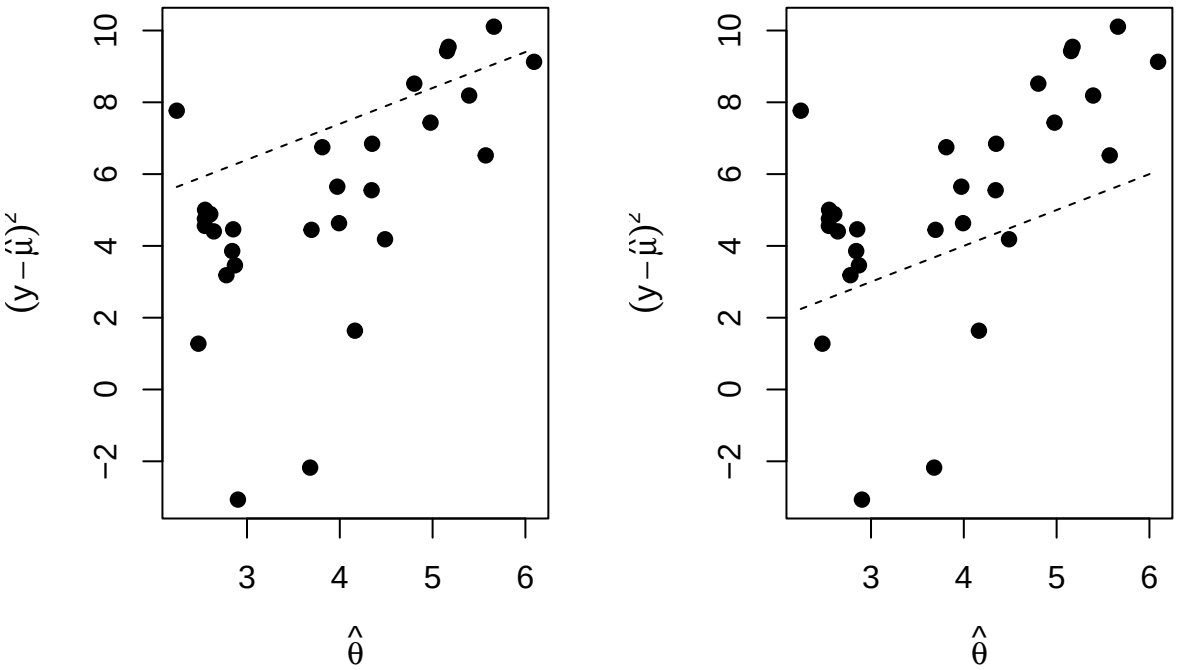
```
# dispersion
par(mfrow = c(1,2))
plot(predict(m1), (gala$Species - fitted(m1))^2,
     xlab= expression(hat(theta)),ylab=expression((y-hat(mu))^2),
     pch = 19)
lines(sort(predict(m1)), dp*sort(fitted(m1)), lty="dashed")

# no dispersion
plot(predict(m1), (gala$Species - fitted(m1))^2,
     xlab= expression(hat(theta)),ylab=expression((y-hat(mu))^2),
     pch = 19)
lines(sort(predict(m1)), sort(fitted(m1)), lty="dashed")
```




```
# log mean-value scale with dispersion (this distorts the success)
par(mfrow = c(1,2))
plot(log(fitted(m1)), log((gala$Species - fitted(m1))^2),
     xlab= expression(hat(theta)),ylab=expression((y-hat(mu))^2),
     pch = 19)
lines(log(sort(fitted(m1))), log(dp*sort(fitted(m1))), lty="dashed")

# log mean-value scale with no dispersion
plot(log(fitted(m1)), log((gala$Species - fitted(m1))^2),
     xlab= expression(hat(theta)),ylab=expression((y-hat(mu))^2),
     pch = 19)
lines(log(sort(fitted(m1))), log(sort(fitted(m1))), lty="dashed")
```



The `AER` package includes a function that allows for one to test whether or not dispersion is present. We can see that dispersion is present at most reasonable significance testing levels.

```
library(AER)
dispersiontest(m1, trafo=1)
```

```
##
##  Overdispersion test
##
## data:  m1
## z = 2.5007, p-value = 0.006198
## alternative hypothesis: true alpha is greater than 0
## sample estimates:
##    alpha
## 21.92009
```

Note that the `AER` package defines dispersion differently than the `glm` function.

Negative Binomial regression

Given a series of independent trials, each trial with probability of success p, let Z be the number of trials until the kth success. This is the basis for the negative binomial distribution. The mass function for the negative binomial distribution is:

$$\mathbb{P}(Z = z) = \binom{z-1}{k-1} p^k (1-p)^{z-k}, \qquad z = k, k+1, \ldots$$

The negative binomial distribution can arise naturally in several ways. One can envision a system that can withstand k hits before failure. The probability of a hit in a given time period is p. The negative binomial also arises from the generalization of the Poisson where the rate parameter is gamma distributed. The negative binomial also comes up as a limiting distribution for urn schemes that can be used to model contagion.

We get a more convenient parameterization if we let $Y = Z - k$ and $p = (1+\alpha)^{-1}$ so that:

$$\mathbb{P}(Y = y) = \binom{y+k-1}{k-1} \frac{\alpha^y}{(1+\alpha)^{y+k}}, \qquad y = 0, 1, 2, \ldots$$

then $\mathrm{E}(Y) = \mu = k\alpha$ and $\mathrm{Var}(Y) = k\alpha + k\alpha^2 = \mu + \mu^2/k$. The log-likelihood is then

$$\sum_{i=1}^{n} \left(y_i \log\left(\frac{\alpha}{1+\alpha}\right) - k\log(1+\alpha) + \sum_{j=0}^{y_i-1} \log(j+k) - \log(y_i!) \right).$$

The most convenient way to link the mean response μ to a linear combination of the the predictors X in typical GLM fashion is through

$$\log\left(\frac{\mu}{\mu+k}\right) = \log\left(\frac{\alpha}{1+\alpha}\right) = \theta = x^T\beta.$$

We can specify the change of parameters map $g : \theta \to \mu$ and the link function as $g^{-1} : \mu \to \theta$ as

$$g(\theta) = \frac{ke^\theta}{1-e^\theta} = \mu, \qquad g^{-1}(\mu) = \log\left(\frac{\mu}{\mu+k}\right) = x^T\beta.$$

We can regard k as fixed and determined by the application or as an additional parameter to be estimated.

Example: Solder data

Consider this example. ATT ran an experiment varying five factors relevant to a wave-soldering procedure for mounting components on printed circuit boards. The response variable, skips, is a count of how many solder skips appeared in a visual inspection. The data comes from Comizzoli et al. (1990) (See the source material on the help page for the solder dataset in the faraway package). We start with a Poisson regression:

```
library(faraway)
modp <- glm(skips ~ . , family=poisson, data=solder)
c(deviance(modp), df.residual(modp))
```

```
## [1] 1796.973  881.000
```

We see that the full model has a residual deviance of 1797 on 881 degrees of freedom. This is not a good fit (as a rule of thumb, deviance should be less than degrees of freedom for a well-fitting submodel). Perhaps including interaction terms will improve the fit:

```
modp2 <- glm(skips ~ (Opening +Solder + Mask + PadType + Panel)^2,
             family=poisson, data=solder)
c(deviance(modp2), df.residual(modp2))
```

```
## [1] 1007.736  773.000
```

```
pchisq(deviance(modp2), df.residual(modp2), lower=FALSE)
```

```
## [1] 2.238499e-08
```

The fit is improved but not enough to conclude that the model fits. We could try adding more interactions but that would make interpretation increasingly difficult. A check for outliers reveals no problem. An alternative model for counts is the negative binomial. The functions for fitting come from the `MASS` package. We can specify the link parameter k. Here we choose $k = 1$ to demonstrate the method, although there is no substantive motivation from this application to use this value. Note that the $k = 1$ case corresponds to an assumption of a geometric distribution for the response.

```
library(MASS)
```

```
##
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':
##
##     select
```

```
modn <- glm(skips ~ ., negative.binomial(1), solder)
modn
```

```
##
## Call:  glm(formula = skips ~ ., family = negative.binomial(1), data = solder)
##
## Coefficients:
## (Intercept)     OpeningM     OpeningS   SolderThin       MaskA3       MaskA6
##    -1.57251      0.50852      2.00093      1.04754      0.65065      2.52776
##      MaskB3       MaskB6    PadTypeD6    PadTypeD7    PadTypeL4    PadTypeL6
##     1.26631      2.07062     -0.45434      0.01979      0.46751     -0.46812
##   PadTypeL7    PadTypeL8    PadTypeL9    PadTypeW4    PadTypeW9       Panel2
##    -0.28999     -0.08057     -0.51864     -0.13917     -1.48133      0.29536
##      Panel3
##     0.34262
##
## Degrees of Freedom: 899 Total (i.e. Null);  881 Residual
## Null Deviance:       1743
## Residual Deviance: 556.7     AIC: 3884
```

```
## LRT test
pchisq(deviance(modn), df.residual(modn), lower=FALSE)
```

```
## [1] 1
```

We could experiment with different values of k, but there is a more direct way of achieving this by allowing the parameter k to vary and be estimated using maximum likelihood in:

```
modn <- glm.nb(skips ~ ., solder)
summary(modn)
```

```
##
## Call:
## glm.nb(formula = skips ~ ., data = solder, init.theta = 4.52811339,
##     link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.7047  -1.0109  -0.3921   0.4480   2.8869
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.29859    0.13202  -9.837  < 2e-16 ***
## OpeningM     0.50353    0.07932   6.348 2.18e-10 ***
## OpeningS     1.91104    0.07111  26.876  < 2e-16 ***
## SolderThin   0.93513    0.05323  17.567  < 2e-16 ***
## MaskA3       0.58383    0.09592   6.087 1.15e-09 ***
## MaskA6       2.26096    0.10101  22.384  < 2e-16 ***
## MaskB3       1.20651    0.09572  12.605  < 2e-16 ***
## MaskB6       1.98172    0.09158  21.638  < 2e-16 ***
## PadTypeD6   -0.46189    0.11145  -4.144 3.41e-05 ***
## PadTypeD7   -0.03182    0.10584  -0.301 0.763655
## PadTypeL4    0.38119    0.10177   3.745 0.000180 ***
## PadTypeL6   -0.57860    0.11327  -5.108 3.25e-07 ***
## PadTypeL7   -0.36569    0.11006  -3.323 0.000891 ***
## PadTypeL8   -0.15882    0.10734  -1.480 0.138953
```

```
## PadTypeL9   -0.56554    0.11306  -5.002 5.67e-07 ***
## PadTypeW4   -0.19851    0.10783  -1.841 0.065630 .
## PadTypeW9   -1.56332    0.13538 -11.547  < 2e-16 ***
## Panel2       0.29574    0.06322   4.678 2.90e-06 ***
## Panel3       0.33380    0.06298   5.300 1.16e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(4.5281) family taken to be 1)
##
##     Null deviance: 4097.6  on 899  degrees of freedom
## Residual deviance: 1012.1  on 881  degrees of freedom
## AIC: 3679.5
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  4.528
##           Std. Err.:  0.518
##
##  2 x log-likelihood:  -3639.514
```

We see that $\hat{k} = 4.528$ with a standard error of 0.518. We can compare negative binomial models using the usual inferential techniques. For instance, we see that the overall fit is much improved.

```
## LRT test
pchisq(deviance(modn), df.residual(modn), lower=FALSE)
```

```
## [1] 0.001367546
```

Zero Inflated Count Models

Sometimes we see count response data where the number of zeroes appearing is significantly greater than the Poisson or negative binomial models would predict. This commonly arises in life history analyses of plants and animals where many subjects die before they reproduce, arrest and bookings data where many people are either not arrested or receive zero day sentences, and insurance claims data. Modifying the Poisson by adding a dispersion parameter does not adequately model this divergence from the standard count distributions.

We consider a sample of 915 biochemistry graduate students. The response variable is the number of articles produced during the last three years of the PhD. We are interested in how this is influenced by the gender, marital status, number of children, prestige of the department and productivity of the advisor of the student. The dataset may be found in the `pscl` package. We start by fitting a Poisson regression model:

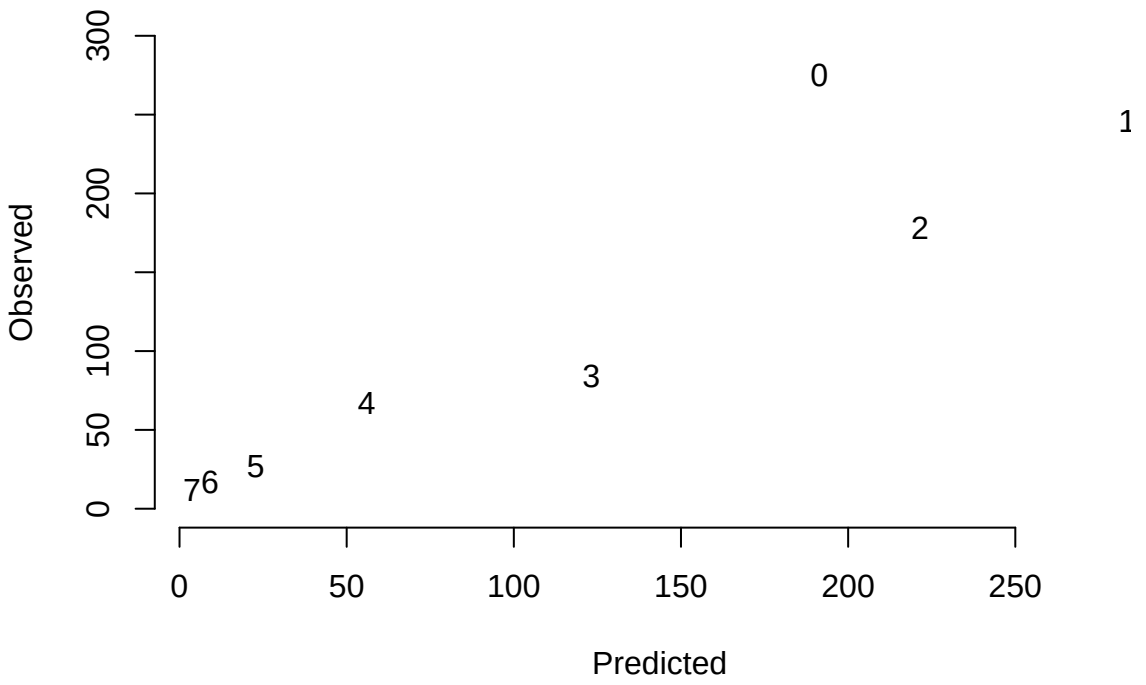
```
library(pscl)
modp <- glm(art ~ ., data=bioChemists, family=poisson)
sumary(modp)
```

```
##               Estimate Std. Error z value  Pr(>|z|)
## (Intercept)  0.3046168  0.1029814  2.9580  0.003097
## femWomen    -0.2245942  0.0546135 -4.1124 3.915e-05
## marMarried   0.1552434  0.0613744  2.5294  0.011424
## kid5        -0.1848827  0.0401269 -4.6075 4.076e-06
## phd          0.0128226  0.0263970  0.4858  0.627139
## ment         0.0255427  0.0020061 12.7327 < 2.2e-16
##
## n = 915 p = 6
## Deviance = 1634.37098 Null Deviance = 1817.40530 (Difference = 183.03432)
```

We can see that deviance is significantly larger than the degrees of freedom (a rule of thumb indicated poor fit). Some experimentation reveals that this cannot be solved by using a richer linear predictor or by eliminating some outliers [Faraway, 2016]. We might consider a dispersed Poisson model or negative binomial but some thought suggests that there are good reasons why a disproportionate number of students might produce no articles at all.

We count and predict how many students produce between zero and seven articles. Very few students produce more than seven articles so we ignore these. The `predprob` function produces the predicted probabilities for each case. By summing these, we get the expected number for each article count.

```
ocount <- table(bioChemists$art)[1:8]
pcount <- colSums(predprob(modp)[,1:8])
plot(pcount, ocount, type="n", xlab="Predicted", ylab="Observed",
     ylim = c(0, 300), axes = FALSE)
axis(side = 1)
axis(side = 2)
text(pcount,ocount, 0:7)
```



We see that there are many more students with zero articles than would be predicted by the Poisson model. In contrast, the relationship between observed and predicted is linear for the students who produce at least one article.

We now consider a zero-inflated Poisson model. First, some motivation. Suppose we ask the general public how many games of chess they have played in the last month. Some people will say zero because they do not play chess but some zero responses will be from chess players who have not managed a game in the last month. Circumstances such as these require a *mixture* model. A general specification of this model takes the form:

$$\begin{aligned}\mathbb{P}(Y=0) &= \phi + (1-\phi)f(0)\\ \mathbb{P}(Y=j) &= (1-\phi)f(j), \qquad j>0.\end{aligned}$$

The parameter ϕ represents the proportion of subjects who will always respond zero (the non-chess players in the motivating example). One can model the proportion ϕ using the binary response model. The distribution f models the counts of those individuals that can have a positive response. Note that it is possible that some

of these individuals will have zero response which combine with the always-zero individuals. We can use a Poisson model for f in which case this is called zero-inflated Poisson model.

```
modz <- zeroinfl(art ~ ., data=bioChemists)
summary(modz)
```

```
##
## Call:
## zeroinfl(formula = art ~ ., data = bioChemists)
##
## Pearson residuals:
##     Min      1Q  Median      3Q     Max
## -2.3253 -0.8652 -0.2826  0.5404  7.2976
##
## Count model coefficients (poisson with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.640839   0.121307   5.283 1.27e-07 ***
## femWomen    -0.209144   0.063405  -3.299 0.000972 ***
## marMarried   0.103750   0.071111   1.459 0.144567
## kid5        -0.143320   0.047429  -3.022 0.002513 **
## phd         -0.006166   0.031008  -0.199 0.842376
## ment         0.018098   0.002294   7.888 3.07e-15 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.577060   0.509386  -1.133  0.25728
## femWomen     0.109752   0.280082   0.392  0.69517
## marMarried  -0.354018   0.317611  -1.115  0.26501
## kid5         0.217095   0.196483   1.105  0.26920
## phd          0.001275   0.145263   0.009  0.99300
## ment        -0.134114   0.045243  -2.964  0.00303 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of iterations in BFGS optimization: 19
## Log-likelihood: -1605 on 12 Df
```

We notice that the `ment` variable which counts the number of articles produced by the mentor is the most significant predictor in both the Poisson and binary regressions. This is because the zero-inflated approach models the probability of a zero count (not the probability of a successful 1 count). Hence there is no contradiction.

We can use the standard likelihood testing theory to compare nested models. For example, suppose we consider a simplified version of the zero-inflated Poisson model where we now have different predictors for the two components of the model. The count part of the model is specified before the | and the binary response model after.

```
# smaller model
modz2 <- zeroinfl(art ~ fem+kid5+ment | ment, data=bioChemists)

# summary table for smaller model
summary(modz2)
```

```
##
## Call:
## zeroinfl(formula = art ~ fem + kid5 + ment | ment, data = bioChemists)
```

```
##
## Pearson residuals:
##     Min      1Q  Median      3Q     Max
## -2.2802 -0.8807 -0.2718  0.5131  7.4788
##
## Count model coefficients (poisson with log link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.694517   0.053025  13.098  < 2e-16 ***
## femWomen    -0.233857   0.058400  -4.004 6.22e-05 ***
## kid5        -0.126516   0.039668  -3.189  0.00143 **
## ment         0.018004   0.002224   8.096 5.67e-16 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.68488    0.20529  -3.336 0.000849 ***
## ment        -0.12680    0.03981  -3.185 0.001448 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of iterations in BFGS optimization: 22
## Log-likelihood: -1608 on 6 Df
```

```
# test of nested models
pchisq(2*(modz$loglik-modz2$loglik), 6, lower = FALSE)
```

```
## [1] 0.4041153
```

Given the large p-value of 0.4, we conclude that our simplification of the model is justifiable. For interpretation, the exponentiated coefficients are more useful:

```
exp(coef(modz2))
```

```
## count_(Intercept)    count_femWomen        count_kid5        count_ment
##         2.0027411         0.7914748         0.8811604         1.0181669
##  zero_(Intercept)         zero_ment
##         0.5041522         0.8809081
```

We can also use the model to make predictions. Consider a single male with no children whose mentor produced six articles:

```
newman <- data.frame(fem="Men",mar="Single",kid5=0,ment=6)
predict(modz2, newdata=newman, type="prob")[1:6]
```

```
## [1] 0.27758792 0.19394034 0.21635997 0.16091421 0.08975799 0.04005363
```

We see that most likely outcome for this student is that no articles will be produced with a probability of 0.278. We can query the probability of no production from the zero part of the model:

```
predict(modz2, newdata=newman, type="zero")
```

```
##        1
## 0.190666
```

So the additional probability to make this up to 0.278 comes from the Poisson count part of the model. This difference might be attributed to students who had the potential to write an article.

We note that the zero-inflated Poisson distribution also arises as a special case of an aster model used in life history analyses for populations of plants or animals. The aster model can be thought of as a generalized generalized linear regression model and it models individuals through stages of their lifecycle. One can think

of a simple lifecycle:

$$1 \to Y_1 \to Y_2,$$

where Y_1 encodes subjects either reaching or not reaching a reproductive stage (modeled as a binary random variable) and then, conditional on reproduction, Y_2 encodes how many offspring produced by the subjects in the reproductive stage (modeled as a 0-truncated Poisson random variable).

Acknowledgments

These notes borrow materials from Faraway [2016] and Charles Geyer's notes on exponential families and other topics.

References

J. J. Faraway. *Extending the linear model with R: generalized linear, mixed effects and nonparametric regression models*. CRC press, 2016.