Poisson Regression

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Poisson Regression

- *Poisson regression* is a form of a generalized linear model where the response variable is modeled as having a *Poisson distribution*.
- The Poisson distribution models random variables with non-negative integer values.
- For large means, the Poisson distribution is well approximated by the normal distribution.
- In biological applications, the Poisson distribution can be useful for variables that are often small integers including zero.
- The Poisson distribution is often used to model *rare events*. 
The Poisson Distribution

The Poisson distribution arises in many biological contexts. Examples of random variables for which a Poisson distribution might be reasonable include:

- the number of bacterial colonies in a Petri dish;
- the number of trees in an area of land;
- the number of offspring an individual has;
- the number of nucleotide base substitutions in a gene over a period of time;
The probability mass function of the Poisson distribution with mean $\mu$ is
\[
P \{ Y = k \mid \mu \} = \frac{e^{-\mu} \mu^k}{k!} \quad \text{for } k = 0, 1, 2, \ldots
\]

The Poisson distribution is discrete, like the binomial distribution, but has only a single parameter $\mu$ that is both the mean and the variance.
The Poisson Process arises naturally under assumptions that are often reasonable.

For the following, think of points as being exact times or locations.

The assumptions are:

- The chance of two simultaneous points is negligible;
- The expected value of the random number of points in a region is proportional to the size of the region.
- The random number of points in non-overlapping regions are independent.

Under these assumptions, the random variable that counts the number of points has a Poisson distribution.

If the expected rate of points is \( \lambda \) points per unit length (area), then the distribution of the number of points in an interval (region) of size \( t \) is \( \mu = \lambda t \).
Suppose that we assume that at a location, a particular species of plant is distributed according to a Poisson process with expected density 0.2 individuals per square meter.

In a nine square meter quadrat, what is the probability of no individuals?

**Solution:** The number of individuals has a Poisson distribution with mean \( \mu = 9 \times 0.2 = 1.8 \). The probability of this is

\[
P \{ Y = 0 \mid \mu = 1.8 \} = \frac{e^{-1.8}(1.8)^0}{0!} = 0.165299
\]

In R, we can compute this as

\[
> \text{dpois}(0, 1.8)
\]

\[
[1] 0.1652989
\]
Poisson regression is a natural choice when the response variable is a small integer.

The explanatory variables model the mean of the response variable.

Since the mean must be positive but the linear combination
\[ \eta = \beta_0 + \beta_1 x_1 + \cdots + \beta_k x_k \]
can take on any value, we need to use a link function for the parameter \( \mu \).

The standard link function is the natural logarithm.

\[ \log(\mu) = \eta = \beta_0 + \beta_1 x_1 + \cdots + \beta_k x_k \]

so that

\[ \mu = \exp(\eta) \]
**Aberrant Crypt Foci Example**

- *Aberrant crypt foci* (ACF) are abnormal collections of tube-like structures that are precursors to tumors.
- In an experiment, researchers exposed 22 rats to a carcinogen and then counted the number of ACFs in the rat colons.
- There were three treatment groups based on time since first exposure to the carcinogen, either 6, 12, or 18 weeks.
- The variables are count and endtime.
- > `acf = read.table("acf.txt", header = T)`
  > `str(acf)`

  'data.frame': 22 obs. of 2 variables:
  $ count : int 1 3 5 1 2 1 1 3 1 2 ... 
  $ endtime: int 6 6 6 6 6 6 12 12 12 ...
Plot of Data
> library(arm)
> options(digits = 7)

> acf1.glm = glm(count ~ endtime, data = acf, family = poisson)
> display(acf1.glm, digits = 3)

glm(formula = count ~ endtime, family = poisson, data = acf)

       coef.est coef.se
(Intercept) -0.322   0.400
endtime     0.119   0.026

---

n = 22, k = 2
residual deviance = 28.4, null deviance = 51.1 (difference = 22.7)
The fitted model is:

\[ E_y = \exp(-0.322 + 0.119(\text{endtime})) = 0.725 \times \exp(0.119(\text{endtime})) \]

For the three design times, 6, 12, and 18, the predicted means are:

```r
> round(exp(predict(acf1.glm, data.frame(endtime = c(6, 12, 18)))), 1)
   1   2   3
1.5 3.0 6.2
```

Compare this to the sample means:

```r
> with(acf, round(sapply(split(count, factor(endtime)), + mean), 1))
  6  12  18
 2.0 2.1 6.7
```
Interpreting the Parameter

- The estimated parameter for endtime is 0.119.
- \( \exp(0.119) = 1.126. \)
- An increase of one hour corresponds to an estimated increase of the count by about 12.6%.
Residual Plot

![Residual Plot](image)

- **Residuals**
- **Fitted Values**

Poisson Regression Example
Standardized Residuals

- The mean and standard deviation of the Poisson distribution are $\mu$ and $\sqrt{\mu}$.
- We can standardize residuals by subtracting the fitted values and dividing by the square root of the fitted values.

$$z_i = \frac{y_i - \hat{y}_i}{\sqrt{\hat{y}_i}}$$

- We can estimate the overdispersion by dividing the sum of squared standardized residuals by the degrees of freedom.

$$\hat{\sigma}^2 = \frac{\sum_{i=1}^{n} z_i^2}{n - k}$$
Numerical Example

```r
> z = with(acf, (count - fitted(acf1(glm)))/sqrt(fitted(acf1(glm))))
> sum(z^2)/(22 - 2)

[1] 1.292732
```
The Poisson distribution assumes that the variance is equal to the mean.

In real situations, this can fail when either:
- There is a “random effect” for the individuals; or
- There is a tendency for observations to cluster.

We can examine this using a *quasipoisson* model.
Quasi-Poisson Model

```r
> acf1q.glm = glm(count ~ endtime, data = acf, family = quasipoisson)
> display(acf1q.glm, digits = 3)

glm(formula = count ~ endtime, family = quasipoisson, data = acf)
         coef.est  coef.se
(Intercept) -0.322   0.455
endtime       0.119   0.030

---

n = 22, k = 2
residual deviance = 28.4, null deviance = 51.1 (difference = 22.7)
overdispersion parameter = 1.3
```
The dispersion parameter is estimated to be 1.3, more than 1.0. We can test this with a *simulation*. 
> mu = fitted(acf1(glm))
> disp = rep(NA, 1000)
> for (i in 1:1000) {
+   x = rpois(22, mu)
+   z = (x - mu)/sqrt(mu)
+   disp[i] = sum(z^2)/(22 - 2)
+ }
> summary(disp)

       Min. 1st Qu.  Median    Mean 3rd Qu.   Max.
0.3838   0.8359   1.0440   1.0930  1.2930  3.2120
Density Plot
We can also try a model with a quadratic predictor.
Quadratic Predictor

\[ \text{acf2.glm} = \text{glm}(\text{count} \sim \text{endtime} + I(\text{endtime}^2), \text{data} = \text{acf}, + \text{family} = \text{poisson}) \]

\[ \text{display(acf2.glm, digits = 3)} \]

\[
\text{glm(formula} = \text{count} \sim \text{endtime} + I(\text{endtime}^2), \text{family} = \text{poisson,} \\
\text{data = acf)} \\
\]

<table>
<thead>
<tr>
<th>coef.est</th>
<th>coef.se</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>1.722</td>
</tr>
<tr>
<td>endtime</td>
<td>-0.262</td>
</tr>
<tr>
<td>I(endtime^2)</td>
<td>0.015</td>
</tr>
</tbody>
</table>

---

n = 22, k = 3
residual deviance = 24.5, null deviance = 51.1 (difference = 26.6)
Plots of Fitted Models

Poisson Regression Example
Notice that the fitted quadratic model goes through the estimated means.

Three points define a parabola.

An ANOVA of the models shows the quadratic term does help a little.

\[
\begin{align*}
\text{Model 1: } & \text{count} \sim \text{endtime} \\
\text{Model 2: } & \text{count} \sim \text{endtime} + \text{I}(\text{endtime}^2)
\end{align*}
\]

<table>
<thead>
<tr>
<th>Resid. Df</th>
<th>Resid. Dev</th>
<th>Df</th>
<th>Deviance</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>28.3694</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>24.5146</td>
<td>1</td>
<td>3.8548</td>
</tr>
</tbody>
</table>

\[
1 - pchisq(3.85, 1)
\]

[1] 0.04974599
Residual Plot