

Models for Count Data

FW8051 Statistics for Ecologists

Department of Fisheries, Wildlife and Conservation Biology



- Be able to fit regression models appropriate for count data in R and JAGS
 - Poisson regression models
 - Quasi-Poisson (R only)
 - Negative Binomial regression
- Be able to evaluate model fit
 - Residual plots
 - Goodness-of-fit tests
- Use deviances and AIC to compare models.
- Use an offset to model rates and densities, accounting for variable survey effort
- Be able to describe statistical models and their assumptions using equations and text and match parameters in these equations to estimates in computer output.

Deviance

```
fit.pois<-glm(slugs~field, data=slugs, family=poisson())
summary(fit.pois)
```

```
Call:
glm(formula = slugs ~ field, family = poisson(), data = slugs)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.1331	-1.5969	-0.9519	0.4580	4.8727

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.2429	0.1400	1.735	0.082744 .
fieldRookery	0.5790	0.1749	3.310	0.000932 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 224.86 on 79 degrees of freedom
Residual deviance: 213.44 on 78 degrees of freedom
AIC: 346.26

Number of Fisher Scoring iterations: 6

Deviance

The **deviance** is a measure of model fit when using maximum likelihood.

$$\text{Residual deviance} = 2(\log L(y|\hat{\theta}_s) - \log L(y|\hat{\theta}_0))$$

- $\log L(\hat{\theta}_s|y)$ = log-likelihood for a “saturated” model (one with a parameter for each observation).
- $\log L(\hat{\theta}_0|y)$ = log-likelihood for our model of interest evaluated at the MLEs ($\hat{\theta}_0$)

Null deviance = residual deviance for a model that only contains an intercept

It may be helpful to think of the **null deviance** and **residual deviance** as maximum likelihood equivalents to total and residual sums of squares, respectively.

Deviance

There is no R^2 for generalized linear models, but sometimes see % deviance explained (**pseudo R^2**):

$$100 \times \frac{\text{null deviance} - \text{residual deviance}}{\text{null deviance}}$$

- Null deviance \approx maximum likelihood equivalent of total sum of squares.
- Residual deviance \approx maximum likelihood equivalent of residual sum of squares

For a discussion of different pseudo- R^2 measures, see:

https://web.archive.org/web/20130701052120/http://www.ats.ucla.edu:80/stat/mult_pkg/faq/general/Pseudo_RSquareds.htm

Residuals

Deviance residuals = $\text{sign}(y_i - \mu_i) \sqrt{d_i}$, where:

- d_i is the contribution of the i^{th} observation to the residual deviance (may be useful for spotting outliers/influential points)
- $\text{sign} = 1$ if $y_i > \mu_i$ and -1 if $y_i < \mu_i$.

Pearson residuals = $\frac{Y_i - E[Y_i|X_i]}{\sqrt{\text{Var}[Y_i|X_i]}} = \frac{Y_i - \lambda_i}{\sqrt{\lambda_i}}$ for Poisson

- If the Poisson model is appropriate, these residuals should have constant variance

Often Deviance and Pearson residuals are similar.

Model comparisons

For large samples, the difference in deviances for nested models should be $\sim \chi^2$ with df = difference in number of parameters between the two models.

$$D_2 - D_1 \sim \chi^2_{df}$$

- Can use `drop1(model, test="Chi")` (equivalent to a likelihood ratio test) or `Anova` in `car` package
- Can use forward, backwards, stepwise selection (with the same dangers/caveats related to overfitting)

Alternatively, can use $\text{AIC} = -2(\log L(y|\theta)) + 2p$ for model selection

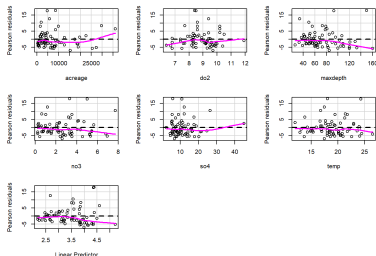
- Allows comparisons among non-nested models
- `stepAIC` in `MASS` library (for backwards selection)

Residual Plots

- Residuals versus fitted values
- Residuals versus predictors
- Residuals over time or space (to diagnose possible spatial/temporal correlation)

See `residualPlots` in `car` library for useful plots.

Residual plots



Goodness-of-fit: Is the Poisson distribution appropriate?

How can we assess overall model fit?

Think "Bayesian p-value"...

- Account for uncertainty in $\hat{\beta}$ by drawing values of β from $N(\hat{\beta}, \widehat{Cov}(\hat{\beta})^2)$
- Use the values of β above to estimate λ (`lambda.hat`)
- Simulate new data (e.g., using `rpois(n, lambda.hat)`)
- Calculate a measure of fit for both real and simulated data
- Rinse, repeat.

If the model is appropriate: "goodness-of-fit" statistics for real and simulated data should be similar

Goodness of fit test

H_0 : the data were generated by the assumed model

H_A : the data were not generated by the assumed model

- The GOF statistics for the simulated data tell us what we might expect to see if the Null hypothesis is true.
- P-value = proportion of time the GOF statistic for **our observed data** is as or more extreme than GOF statistic for the simulated data
- If p-value is small, then we have evidence that the model is not appropriate.
- If the p-value is not small, then... we do not have enough evidence to suggest the model is not appropriate

What should we use as a measure of fit?

One option (see Kery Ch 13), Pearson χ^2 statistic:

$$\chi^2_{n-p} = \sum_{i=1}^n \frac{(Y_i - \hat{E}[Y_i|X_i])^2}{\widehat{Var}[Y_i|X_i]}$$

Loop:

- Simulate a random vector of β 's using $MVN(\hat{\beta}, \widehat{Cov}(\hat{\beta})^2)$
- Use these β 's to form λ_i 's = $\exp(\beta_0 + \beta_1 X_{1,i} + \dots + \beta_p X_{p,i})$
- Simulate new data using these λ_i 's and `rpois()`.
- Calculate χ^2_{n-p} for real and simulated data (plugging in $\hat{E}[Y_i|X_i] = \widehat{Var}[Y_i|X_i] = \hat{\lambda}_i$).

p-value = proportion of times $\chi^2_{sim} \geq \chi^2_{real}$ (want large values)

Lets do this!

Overdispersion, $\text{Var}(Y|X) > E(Y|X)$

Reasons data may be overdispersed:

- Omitted variables
- Explanatory and response variables may be measured with error
- Model may be mis-specified (relationship between $\log(\mu)$ and x may be non-linear)
- Outliers
- Spatial, temporal, within-individual clustering (repeated measures)
- Response may be due to a mixture of random processes
 - Presence/absence determined by suitable habitat
 - Counts | suitable habitat may be Poisson
 - Leads to "zero-inflation" models

Consequences of Overdispersion

We may obtain reasonable estimates of β , but:

- SE may be too small
- We may select overly complex models

Before 'correcting for overdispersion', consider whether:

- You may have left out important predictors
- If you need to allow for non-linear relationships (residual plots).

Testing for Overdispersion: Residual Deviance and Pearson's χ^2

Some compare:

$$\text{Residual deviance} \quad \text{or} \quad \sum_{i=1}^n \frac{(Y_i - E[Y_i|X_i])^2}{\text{Var}[Y_i|X_i]}$$

to a χ^2 distribution with $n - p$ degrees of freedom.

Large values can be caused by:

- Mis-specified model (missing predictors)
- Mis-specified distribution
- Outliers
- Small numbers of observations for any set of unique covariate values

So, best to test using (predictive) simulation techniques discussed earlier (e.g., using the Pearson χ^2 statistic).

Relaxing the Poisson Assumption

Poisson regression:

- $\log(\lambda_i) = \log(\mu_i) = \beta_0 + \beta_1 X_{1,i} + \dots + \beta_p X_{p,i}$
- $f(y_i) \sim \text{Poisson}(\lambda_i)$
- $E[Y_i|X_i] = \lambda_i = e^{\beta_0 + \beta_1 X_{1,i} + \dots + \beta_p X_{p,i}}$
- $\text{Var}[Y_i|X_i] = \lambda_i = e^{\beta_0 + \beta_1 X_{1,i} + \dots + \beta_p X_{p,i}}$

What if $E[Y_i|X_i] = \exp(\beta_0 + \beta_1 X_{1,i} + \dots + \beta_p X_{p,i})$ is appropriate, but the Poisson distribution is not?

In particular, what if $\text{Var}[Y_i|X_i] > E[Y_i|X_i]$?

Option 1: Bootstrap!

Option 2: Variance Inflation

Another option: add a scale parameter to inflate variances.

- $E[Y_i|X_i] = \mu = e^{\beta_0 + \beta_1 X_{i,1} + \dots + \beta_p X_{i,p}}$
- $\text{Var}[Y_i|X_i] = \phi \mu = \phi e^{\beta_0 + \beta_1 X_{i,1} + \dots + \beta_p X_{i,p}}$

Estimate of overdispersion, $\hat{\phi}$ by either:

- $\hat{\phi} = \frac{\text{Residual deviance}}{(n-p)}$
- $\hat{\phi} = \frac{1}{n-p} \sum_{i=1}^n \frac{(Y_i - E[Y_i|X_i])^2}{\text{Var}[Y_i|X_i]}$ (what R does, probably better)

Zuur et al. recommend:

- If $\phi > 1.5$ should adjust for overdispersion
- If greater than 15 or 20, consider alternative methods (Negative Binomial, zero-inflation models, Poisson-Normal model)

Variance Inflation: Quasilikelihood

In R, can use `glm` with `family = quasipoisson()`

Will estimate an inflation factor using:

$$\hat{\phi} = \frac{1}{n-p} \sum_{i=1}^n \frac{(Y_i - E[Y_i|X_i])^2}{\text{Var}[Y_i|X_i]}$$

- $\hat{\beta}$ will be unchanged, but SE will be larger by a factor of $\sqrt{\hat{\phi}}$.
- No longer “maximum likelihood”
- **quasilikelihood** (more on this later)
- Modeling the first two moments of Y ($E[Y|X]$, $\text{Var}[Y|X]$)

Poisson Model with Overdispersion parameter

Fit to slug data:

- $\hat{\beta}$ does not change
- SE's inflated by $\sqrt{\hat{\phi}}$

Lets do this!

Option 3: Use a different distribution than Poisson

Negative Binomial: $X \sim \text{NegBin}(\mu, \theta)$

$$P(Y = y) = \binom{y+\theta-1}{y} \left(\frac{\theta}{\mu+\theta} \right)^\theta \left(\frac{\mu}{\mu+\theta} \right)^y$$

- $E[Y] = \mu$
- $\text{Var}(Y) = \mu + \frac{\mu^2}{\theta}$
- In R: ***nbinom**, with parameters (`prob = p`, `size = n`) or (`mu = \mu`, `size = \theta`)
- JAGS: **dnegbin** with parameters (p, θ)

Overdispersed relative to Poisson ($\text{Var}(x)/E[x] = 1 + \frac{\mu}{\theta}$) versus 1 for Poisson

Poisson is a limiting case (when $\theta \rightarrow \infty$)

Negative Binomial Models in R

Can fit negative binomial models in R using the `glm.nb` function in the MASS library

- $\log(E[Y_i|X_i]) = \log(\mu_i) = \beta_0 + \beta_1 X_{1,i} + \dots + \beta_p X_{p,i}$
- $Y_i|X_i \sim \text{NegBin}(\mu_i, \theta)$

`glm.nb(y ~ x, data=)`

Lets do this!

Negative Binomial in JAGS

JAGS: **dnegbin** specified in terms of parameters (p, θ)

We will specify the model in terms of μ and θ , then solve for p :

```
log(mu[i]) <- alpha + beta*IBook[i]
p[i] <- theta/(theta+mu[i])
slugs[i] ~ dnegbin(p[i],theta)
```

- $E[Y_i|X_i] = \mu_i = e^{\beta_0 + \beta_1 X_{1,i} + \dots + \beta_p X_{p,i}}$
- $\text{Var}[Y_i|X_i] = \mu_i + \frac{\mu_i^2}{\theta}$

Practice Opportunity: Fit this model to slug data (and use the above mean/variance equations) to fill in the code needed to calculate the Bayesian p-value.

Poisson-normal model

$$\log(\lambda_i) = \log(\mu_i) = \beta_0 + \beta_1 X_{1,i} + \dots + \beta_p X_{p,i} + \epsilon_i$$

$$\epsilon_i \sim N(0, \sigma^2)$$

- $E[Y_i|X_i, \epsilon_i = 0] = \mu_i = \exp^{\beta_0 + \beta_1 X_{1,i} + \dots + \beta_p X_{p,i}} \neq E[Y_i|X_i]$
- $E[Y_i|X_i] = e^{\beta_0 + \beta_1 X_{1,i} + \dots + \beta_p X_{p,i} + \frac{1}{2}\sigma^2}$
- $\text{Var}[Y_i|X_i] = \mu_i + (e^{\sigma^2} - 1)\mu_i^2$

Poisson-normal model

Practice Opportunity:

- Fit this model in JAGS, by adapting your old code
- Add appropriate code for the goodness of fit test

Or, have a look at Rglms.html file with solutions.

AIC

AIC = $-2 \times \log L(\hat{\theta}|y) + 2 \times \text{number of parameters}$

- measure of “fit” with “penalty” for model complexity
- the larger log-likelihood, the smaller AIC
- for similar likelihoods, AIC will be smaller for simpler models
- → smaller AIC is better

DIC

Not without its problems:

- Not always appropriate for certain types of models (problematic if you have latent variables, e.g., mixture models)

Model Comparisons

DIC = **Deviance Information Criterion** = is often used to compare models.

Deviance: $D = -2\log L(\theta|y)$ (has a posterior distribution)

DIC is calculated from:

- \bar{D} = the mean of the posterior deviance
- \hat{D} = the deviance calculated using the posterior means of the model parameters

Estimated effective number of parameters in a model, $p_D = \bar{D} - \hat{D}$, and DIC as $\hat{D} + 2p_D$:

$$\text{DIC} = \hat{D} + 2p_D = (\bar{D} - p_D) + 2p_D = \bar{D} + p_D$$

DIC

Martyn Plummer (creator of JAGS):

DIC [like AIC] is (an approximation to) a theoretical out-of-sample predictive error.

“The deviance information criterion (DIC) is widely used for Bayesian model comparison, despite the lack of a clear theoretical foundation... valid only when the effective number of parameters in the model is much smaller than the number of independent observations. In disease mapping, a typical application of DIC, this assumption does not hold and DIC under-penalizes more complex models. Another deviance-based loss function, derived from the same decision-theoretic framework, is applied to mixture models, which have previously been considered an unsuitable application for DIC.”

Andrew Gelman: “I don’t really ever know what to make of DIC. On one hand, it seems sensible. . . On the other hand, I don’t really have any idea what I would do with DIC in any real example. In our book we included an example of DIC—people use it and we don’t have any great alternatives—but I had to be pretty careful that the example made sense. Unlike the usual setting where we use a method and that gives us insight into a problem, here we used our insight into the problem to make sure that in this particular case the method gave a reasonable answer.”

http://andrewgelman.com/2011/06/22/deviance_dic_ai/

There are other potential options out there (e.g., WIC, cross-validation estimates of predictive error, etc)

Hooten, Mevin B, and N Thompson Hobbs. 2015. “A Guide to Bayesian Model Selection for Ecologists.” Ecological Monographs 85 (1): 3–28.

Offsets

Count data, Y , are often collected:

- over varying lengths of time
- in sample units that have different areas

We may be interested in modeling rates:

$$E[Y_i|X_i]/\text{Time}_i$$

Or densities:

$$E[Y_i|X_i]/\text{Area}_i$$

We may want to account for variable survey effort (varying times or areas)!

Offsets

Poisson and negative binomial models for rate data:

$$\log(E[Y_i|X_i]/\text{Time}_i) = \beta_0 + \beta_1 X_{1,i} + \dots + \beta_p X_{p,i}$$

$$\Rightarrow \log(E[Y_i|X_i]) - \log(\text{Time}_i) = \beta_0 + \beta_1 X_{1,i} + \dots + \beta_p X_{p,i}$$

$$\Rightarrow \log(E[Y_i|X_i]) = \log(\text{Time}_i) + \beta_0 + \beta_1 X_{1,i} + \dots + \beta_p X_{p,i}$$

$\log(\text{Time}_i)$ is called an **offset** and can be modeled using:

```
glm(y~x + offset(log(time)), data= , family = poisson())
```

An **offset** is an explanatory variable with a regression coefficient fixed at 1.

See [PoissonOffsetTemplate.R](#) and [PoissonOffset.R](#) (in the Generalized linear models folder) for an exercise fitting a Poisson model with an offset.