Models for Count Data

FW8051 Statistics for Ecologists

Department of Fisheries, Wildlife and Conservation Biology

Learning Objectives

- 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.

```
glmPdace<-glm(longnosedace~acreage+do2+maxdepth+no3+so4+temp,
                        data=longnosedace, family=poisson())
summary(glmPdace)
```

```
Call:
glm(formula = longnosedace ~ acreage + do2 + maxdepth + no3 +
    so4 + temp, family = poisson(), data = longnosedace)

Deviance Residuals:
   Min      1Q  Median      3Q     Max
-9.234  -4.086  -1.662   1.771  14.362

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.564e+00  2.818e-01  -5.551 2.83e-08 ***
acreage      3.843e-05  2.079e-06  18.480  < 2e-16 ***
do2          2.259e-01  2.126e-02  10.626  < 2e-16 ***
maxdepth     1.155e-02  6.688e-04  17.270  < 2e-16 ***
no3          1.813e-01  1.068e-02  16.974  < 2e-16 ***
so4         -6.810e-03  3.622e-03  -1.880   0.0601 .
temp         7.854e-02  6.530e-03  12.028  < 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: 2766.9  on 67  degrees of freedom
```

Model

$$Dace_i \sim Poisson(\lambda_i)$$

$$\log(\lambda_i) = \beta_0 + \beta_1 Acreage_i + \beta_2 DO2_i + \beta_3 maxdepth_i +$$

$$\beta_4 NO3_i + \beta_5 SO4_i + \beta_6 temp_i$$

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$$\lambda_i = \exp(\beta_0 + \beta_1 Acreage_i + \beta_2 DO2_i + \beta_3 maxdepth_i + \beta_4 NO3_i +$$

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$$\lambda_i = e^{(\beta_0)} e^{(\beta_1 Acreage_i)} e^{(\beta_2 DO2_i)} e^{(\beta_3 maxdepth_i)} e^{(\beta_4 NO3_i)} e^{(\beta_5 SO4_i)} e^{(\beta_6 temp_i)}$$

Interpretation

$$Dace_i \sim Poisson(\lambda_i) \tag{1}$$

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- $\exp(\beta_0)$ = expected mean when all predictors are equal to 0
- β_2 = 0.226 = expected change in the log mean [i.e., $\log(\lambda)$], per unit change in D02, while holding everything else constant.

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- β_2 = 0.226 = expected change in the log mean [i.e., $\log(\lambda)$], per unit change in D02, while holding everything else constant.
- $\exp(\beta_2)$ = 1.25 = we expect the mean to increase by a factor of 1.25 for every 1 unit change in D02 (and holding everything else constant)

Inference

Rely on asymptotic Normality for Maximum Likelihood Estimators

$$\hat{\beta} \sim N(\beta, I^{-1}(\theta))$$

```
# Store coefficients and their standard errors
beta.hats <- coef(glmPdace)
ses <- sqrt(diag(vcov(glmPdace)))
round(cbind(beta.hats-1.96*ses, beta.hats+1.96*ses), 3)
```

```
##                [,1]   [,2]
## (Intercept) -2.117 -1.012
## acreage      0.000  0.000
## do2          0.184  0.268
## maxdepth     0.010  0.013
## no3          0.160  0.202
## so4         -0.014  0.000
## temp         0.066  0.091
```

Profile confidence intervals

Inverts the likelihood ratio test to form confidence intervals (see Section 10.10 of the book)

```
#' Or, can use profile likelihood intervals
confint(glmPdace)
```

```
## Waiting for profiling to be done...
```

```
##                       2.5 %        97.5 %
## (Intercept) -2.117222e+00 -1.012594e+00
## acreage      3.432623e-05  4.247872e-05
## do2          1.841122e-01  2.674327e-01
## maxdepth     1.023509e-02  1.285684e-02
## no3          1.603516e-01  2.022292e-01
## so4         -1.400207e-02  1.966821e-04
## temp         6.576200e-02  9.136105e-02
```

Confidence Intervals for exp(β)

1. Calculate a CI for β
2. Exponentiate the confidence limits

```
round(cbind(exp(beta.hats-1.96*ses), exp(beta.hats+1.96*ses)), 3)
```

```
##                [,1]  [,2]
## (Intercept) 0.120 0.363
## acreage     1.000 1.000
## do2         1.202 1.307
## maxdepth    1.010 1.013
## no3         1.174 1.224
## so4         0.986 1.000
## temp        1.068 1.096
```

Residuals

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

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

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Often Deviance and Pearson residuals are similar.

Residual Plots

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

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See also `check_model` in the `performance` package.

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

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- If the p-value is not small, then. . . .

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- If the p-value is not small, then. . . .we do not have enough evidence to suggest the model is not appropriate

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

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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 = $\exp(\beta_0 + \beta_1 X_{1,i} + \ldots \beta_p X_{p,i})$
- Simulate new data using these λ_i's and `rpois()`.
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Lets do this!

Overdispersion, $Var(Y|X) > E(Y|X)$

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- 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

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

Some compare:

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

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

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

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We may obtain reasonable estimates of β, but:

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Before 'correcting for overdispersion' , consider whether:

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

How to deal with overdispersion

Relaxing the Poisson Assumption

Poisson regression:

- $log(\lambda_i) = \log(\mu_i) = \beta_0 + \beta_1 X_{1,i} + \ldots \beta_p X_{p,i}$
- $f(y_i) \sim$ Poisson(λ_i)

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- $E[Y_| X_i] = \lambda_i = e^{\beta_0 + \beta_1 X_{1,i} + \ldots \beta_p X_{p,i}}$
- $Var[Y_i | X_i] = \lambda_i = e^{\beta_0 + \beta_1 X_{1,i} + \ldots \beta_p X_{p,i}}$

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- $E[Y_| X_i] = \lambda_i = e^{\beta_0 + \beta_1 X_{1,i} + \ldots \beta_p X_{p,i}}$
- $Var[Y_i|X_i] = \lambda_i = e^{\beta_0 + \beta_1 X_{1,i} + \ldots \beta_p X_{p,i}}$

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

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

In particular, what if $Var[Y_i|X_i] > E[Y_i|X_i]$?

Relaxing the Poisson Assumption

Poisson regression:

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

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

In particular, what if $Var[Y_i|X_i] > E[Y_i|X_i]$?

Option 1: Bootstrap!

Option 2: Variance Inflation

Another option: add a scale parameter to inflate variances.

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

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

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

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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

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

Poisson Model with Overdispersion parameter

Fit to slug data:

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Lets do this!

Option 3: Use a different distribution than Poisson

$$Dace_i \sim NegativeBinomial(\mu_i, \theta)$$

$$\log(\mu_i) = \beta_0 + \beta_1 Acreage_i + \beta_2 DO2_i + \beta_3 maxdepth_i +$$

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- $E[Y_i] = \mu_i$
- $Var[Y_i] = \mu_i + \mu_i^2/\theta$

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

Negative Binomial Models in R

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

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Lets do this and inspect goodness of fit!

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.

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- 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); see `stepAIC` in `MASS` library (for backwards selection)

AIC

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

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- $\rightarrow$ smaller AIC is better

Can use to compare nested and non-nested models.

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

Negative Binomial in JAGS

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

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

Poisson-normal model

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

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

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- $Var[Y_i|X_i] = \mu_i + (e^{\sigma^2} - 1)\mu_i^2$

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- over varying lengths of time
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$$E[Y_i|X_i]/\text{Time}_i$$

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:

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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.

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."

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/

Model comparisons

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.