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)

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
Residual deviance: 1590.0  on 61  degrees of freedom
AIC: 1936.9

Number of Fisher Scoring iterations: 5
```

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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- β_2 = 0.226 =

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- $\exp(\beta_0)$ = expected mean when all predictors are equal to 0
- $\beta_2 = 0.226$ = expected change in the log mean [i.e., $\log(\lambda)$], per unit change in D02, while holding everything else constant.

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- $\exp(\beta_2) = 1.25$

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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.
- $\exp(\beta_2)$ = 1.25 = we expect the mean to increase <u>by a factor</u> 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)

```r
#' 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
```

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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

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

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- 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/Psuedo_RSquareds.htm

Residuals

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

- d_i is the contribution of the ith 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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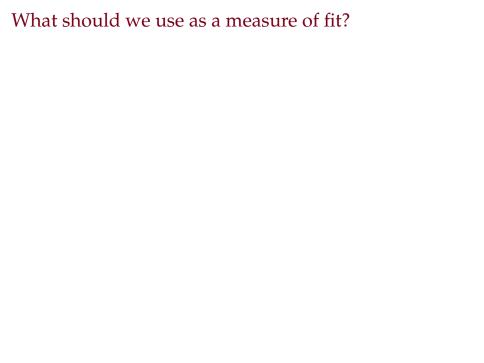H_A: the data were not generated by the assumed model

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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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- 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:

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

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

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Option 1: Bootstrap!

Option 2: Variance Inflation

Another option: add a scale parameter to inflate variances.

- $E[Y_i|X_i] = \mu = e^{\beta_0 + \beta_1 X_{1,i} + ... \beta_p X_{p,i}}$
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Estimate of overdispersion, $\hat{\phi}$ by either:

- $\hat{\phi} = \dfrac{\text{Residual deviance}}{(n-p)}$
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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)

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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

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

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

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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 $logL(\hat{\theta}|y)$ + 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

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

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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

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

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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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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:

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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.