GLMS: Regression for Binary and Count Data

Dichotomous Predicted Variable

- This section focus on dichotomous predicted variables: such as whether a basketball player will get a hit or if a bird will be located in a spatial grid.

- Traditionally, these types of methods are generally implemented with logistic regression.

- The model can be written as:

$$y \sim Bernoulli(\mu)$$

$$\mu = logistic(\beta_0 + \beta_1 x_1 + \beta_2 x_2)$$

where the logistic function is $logistic(x) = 1/(1 + exp(-x))$.

- *Q:* What are the three components of a GLM and what are they in this specific setting? 1. Sampling Model: Bernoulli distribution for binary outcome.

2. Linear Combination of Predictors: $\beta_0 + \beta_1 x_1 + \beta_2 x_2$

3. (inverse) Link function: the logistic function is used to map the predicted variables to μ the central tendency of the data.

- *Q*: To fit this in a Bayesian framework, we need to specify priors. What parameters require priors and what distributions would be reasonable?
  - $\beta \sim N(M, S^2)$

We will explore the Swiss birds dataset for this lab to construct a logistic regression model for presence of the Willow Tit.

```
swiss.birds <- read.csv('http://www.math.montana.edu/ahoegh/teaching/stat491/data/willowtit2013.csv')
kable(head(swiss.birds))
```

siteID	elev	rlength	forest	birds	searchDuration
Q001	450	6.4	3	0	160
Q002	450	5.5	21	0	190
Q003	1050	4.3	32	1	150
Q004	950	4.5	9	0	180
Q005	1150	5.4	35	0	200
Q006	550	3.6	2	0	115

This dataset contains 242 sites and 6 variables:

```
- siteID, a unique identifier for the site, some were not sampled during this period
- elev, mean elevation of the quadrant in meters
- rlength, the length of the route walked by the birdwatcher, in kilometers
- forest, percent forest cover
- birds, binary variable for whether a bird is observed, 1 = yes
- searchDuration, time birdwatcher spent searching the site, in minutes
```

```
model.string <- 'model {
  for (i in 1:Ntotal) {
    y[i] ~ dbern(mu[i])
    mu[i] <- ilogit(beta0 + sum( beta[1:Nx] * x[i,1:Nx] ))
  }

  beta0 ~ dnorm(0,1/5^2)
  for (j in 1:Nx){
    beta[j] ~ dnorm(0, 1/5^2)
  }
}'

# Fit Model
jags.logistic <-  jags.model(textConnection(model.string),
                  data=list(y=swiss.birds$birds,
                            Ntotal=nrow(swiss.birds),
                            Nx = 4,
                            x= swiss.birds[,c('elev','rlength','forest','searchDuration')]),
                  n.chains =2, n.adapt = 10000)
```

JAGS Code

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 242
##    Unobserved stochastic nodes: 5
##    Total graph size: 2434
##
## Initializing model
```

```r
update(jags.logistic, 10000)
samples <- coda.samples(jags.logistic, variable.names = c('beta','beta0'), n.iter = 50000)

summary(samples)
```

```
##
## Iterations = 20001:70000
## Thinning interval = 1
## Number of chains = 2
## Sample size per chain = 50000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##              Mean        SD  Naive SE Time-series SE
## beta[1]  0.002217 0.0004097 1.296e-06      8.817e-06
## beta[2] -0.073980 0.1549097 4.899e-04      3.500e-03
## beta[3]  0.057270 0.0085818 2.714e-05      1.753e-04
## beta[4]  0.007535 0.0033500 1.059e-05      8.309e-05
## beta0   -7.364100 1.2681597 4.010e-03      4.522e-02
##
## 2. Quantiles for each variable:
##
##              2.5%       25%       50%       75%     97.5%
## beta[1]  0.001460  0.001935  0.002201  0.002482  0.003072
## beta[2] -0.376138 -0.178682 -0.074242  0.029972  0.230512
## beta[3]  0.041364  0.051367  0.056907  0.062860  0.074977
## beta[4]  0.001016  0.005282  0.007502  0.009754  0.014185
## beta0   -9.986206 -8.185184 -7.313870 -6.498108 -4.992411
```

```r
#summary(glm(birds ~ elev + rlength +forest + searchDuration, family='binomial', data=swiss.birds))
```

Interpretation of Logistic Regression Coefficients

Recall this model can be written as: $logit(\mu) = \beta_0 + \beta_1 x_1 + \ldots \beta_p x_p$.

- When x_i increases or decreases by 1 unit, then logit(μ) increases or decreases by β_i.

- The logit function for μ can be expressed as $logit(\mu) = \log(\frac{\mu}{1-\mu})$.

- In this setting, μ is the probability of y = 1, so

$$logit(\mu) = \log(\frac{Pr[y=1]}{1-Pr[y=1]}) = \log(\frac{Pr[y=1]}{Pr[y=0]})$$

- This ratio: $\frac{Pr[y=1]}{Pr[y=0]}$ is known as the odds, so $logit(\mu)$ is the log-odds of an outcome in favor of 1 rather than 0.

- Suppose the logistic regression for the Swiss birds had the following coefficients: $\beta_0 = -6$, $\beta_{elev} = .002$, and $\beta_{forest} = .06$.

  - Compute the probability for observing a bird in a quadrant with: elevation = 1500 meters and forest cover of 60 %. $1/(1 + exp(-(-6 + .002 * 1500 + .06 * 60))) = 0.6456563$

  - How do we interpret the meaning for the coefficent β_{forest}? Each unit increases the log-odds by .06. So for instance, if the forest cover was 70% rather than the 60% above the log-odds of observing a bird would increase by 0.6.
  - The log-odds are different than a probability as in this case (conditional on the elevation) the probability increases to: $1/(1 + exp(-(-6 + .002 * 1500 + .06 * 70))) = 0.7685248$

- Note that an unit increase in the log-odds does not have a unit increase in the probability.

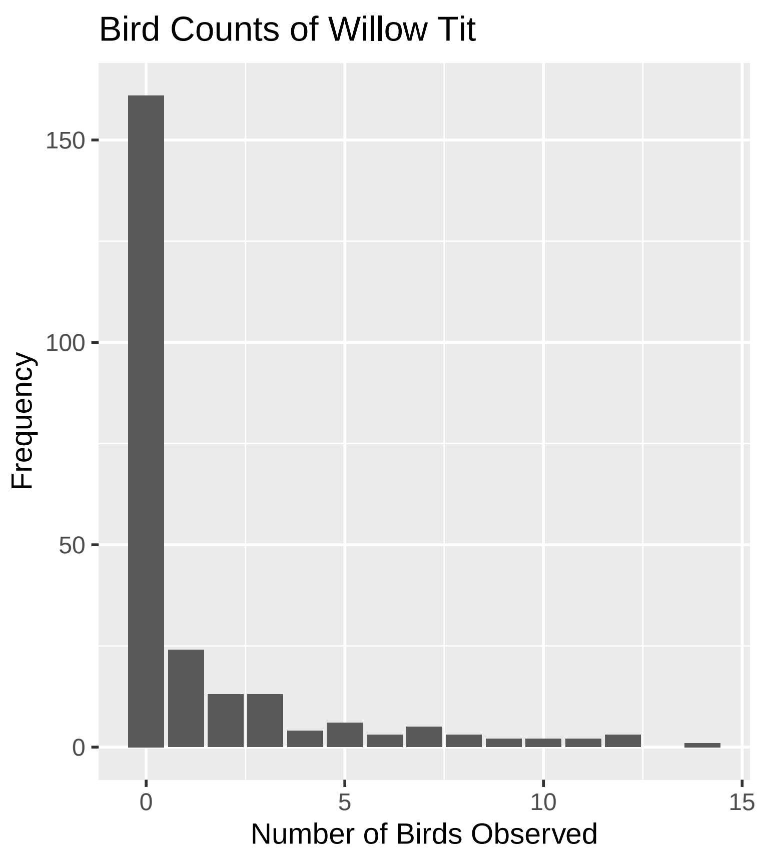
Count Predicted Variable

- Now reconsider the willow tit dataset and consider modeling not just the presence / absence of birds, but directly modeling the number of birds observed in each spatial region.

```
birds <- read.csv('http://math.montana.edu/ahoegh/teaching/stat491/data/willowtit2013_count.csv')
head(birds)
```

```
##   siteID elev rlength forest bird.count searchDuration
## 1   Q001  450     6.4      3          0            160
## 2   Q002  450     5.5     21          0            190
## 3   Q003 1050     4.3     32          3            150
## 4   Q004  950     4.5      9          0            180
## 5   Q005 1150     5.4     35          0            200
## 6   Q006  550     3.6      2          0            115
```

```
ggplot(aes(bird.count), data=birds) + geom_bar() + ylab('Frequency') + xlab('Number of Birds Observed')
  ggtitle('Bird Counts of Willow Tit')
```



1. Sampling Model: In general the Poisson model will be used as a sampling model for count data: -$y|\mu \sim Poisson(\mu) = \mu^y \exp(-\mu)/y!$.
   - the mean and variance of the Poisson distribution are both μ
   - if this is not a reasonable assumption, the negative binomial distribution can be used
2. Linear Combination of Predictors: The same principles apply here as the other GLM settings.
3. Link Function: The support for count data is values greater than or equal to zero. -$X\beta = \log(\mu)$, so the inverse-link function is the exponential function.
   - $\mu = \exp(X\beta)$.