Logistic regression models for binary data

FW8051 Statistics for Ecologists

Department of Fisheries, Wildlife and Conservation Biology

Learning Objectives

Learning objectives

- Be able to formulate, fit, and interpret logistic regression models appropriate for binary data using R and JAGS
- Be able to compare models and evaluate model fit
- Be able to visualize models using effect plots
- Be able to describe statistical models and their assumptions using equations and text and match parameters in these equations to estimates in computer output

Logistic regression

Model for binary (0/1) data or binomial data (number of 1's out of n trials).

$$Y_i|X_i \sim \text{Bernoulli}(p_i)$$

$$logit(p_i) = log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 X_{1,i} + \ldots \beta_p X_{p,i}$$

- Random component = Bernoulli or binomial distribution
- Systematic component: logit(p_i) or log(odds) = linear combination of predictors

Remember, for binary data, $E[Y_i|X_i] = p_i$, $Var[Y_i|X_i] = p_i(1-p_i)$

$\Rightarrow p_i = \frac{\exp(\beta_0+\beta_1 X_{1,i}+\ldots\beta_p X_{p,i})}{1+\exp(\beta_0+\beta_1 X_{1,i}+\ldots\beta_p X_{p,i})}$ (can use `plogis` function in R)

Logistic regression

$$Y_i|X_i \sim \text{Bernoulli}(p_i)$$

$$logit(p_i) = log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 X_{1,i} + \ldots \beta_p X_{p,i}$$

$\frac{p}{1-p}$ is referred to as the odds.

The link function, $\log\left(\frac{p}{1-p}\right)$, is referred to as logit.

Thus, we can describe our model in the following ways:

- We are modeling $\log\left(\frac{p}{1-p}\right)$ as a linear function of $X_1, \ldots, X_p$.
- We are modeling the logit of p as a linear function of $X_1, \ldots, X_p$.
- We are modeling the log odds of p as a linear function of $X_1, \ldots, X_p$.

Odds = $\frac{p}{1-p}$

If the probability of winning a bet is = 2/3, what are the odds of winning?

odds = $\frac{p}{1-p}$ = (2/3 $\div$ 1/3) = 2 (or "2 to 1").

Table 6.1. Various probabilities, odds and log odds. The table shows how log odds are calculated from probabilities.

P_i	0.001	0.1	0.3	0.4	0.5	0.6	0.7	0.9	0.999
$1 - P_i$	0.999	0.9	0.7	0.6	0.5	0.4	0.3	0.1	0.001
O_i	0.001	0.11	0.43	0.67	1	1.5	2.33	9	999
$\mathrm{Ln}(O_i)$	−6.91	−2.20	−0.85	−0.41	0	0.41	0.85	2.20	6.91

From Zuur et al. 2007. Analyzing Ecological data

Odds can vary between 0 and ∞, so log(odds) can live on $-\infty$ to ∞.

Odds Ratios: exp(β)

Consider a regression coefficient for a categorical variable:

$$logit(p_i) = log(\frac{p_i}{1-p_i}) = \beta_0 + \beta_1 I(group = B)_i$$

$I(group = B)_i$ = 1 if observation i is from Group B and 0 if Group A

- Odds for group B = $\frac{p_B}{1-p_B}$ = exp($\beta_0 + \beta_1$)
- Odds for group A = $\frac{p_A}{1-p_A}$ = exp(β_0)

Consider the ratio of these odds:

$$\frac{\frac{p_B}{1-p_B}}{\frac{p_A}{1-p_A}} = \frac{\exp(\beta_0+\beta_1)}{\exp(\beta_0)} = \frac{e^{\beta_0}e^{\beta_1}}{e^{\beta_0}} = \exp(\beta_1)$$

So, exp(β_1) gives an odds ratio (or ratio of odds) for Group B relative to group A.

Odds Ratios: exp(β)

Consider a continuous predictor, X:

$$logit(p_i) = log(\frac{p_i}{1-p_i}) = \beta_0 + \beta_1 X_i$$

β_1 gives the change in log odds per unit change in X.

- Odds when $X_i = a$ is given by $\frac{p_i}{1-p_i}$ = exp($\beta_0 + \beta_1 a$)
- Odds when $X_j = a + 1$ is given by $\frac{p_j}{1-p_j}$ = exp($\beta_0 + \beta_1(a+1)$)

Consider the ratio of these odds:

$$\frac{\frac{p_j}{1-p_j}}{\frac{p_i}{1-p_i}} = \frac{\exp(\beta_0+\beta_1(a+1))}{\exp(\beta_0+\beta_1 a)} = \frac{e^{\beta_0}e^{\beta_1 a}e^{\beta_1}}{e^{\beta_0}e^{\beta_1 a}} = \exp(\beta_1)$$

So, exp(β_1), gives the odds ratio for two observation that differ by 1 unit of X.

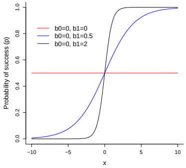
Multiple predictors

For multiple predictor models,

exp(β_i) gives the odds ratio for observations where X_i differs by 1 unit, <u>while holding everything else constant</u>!

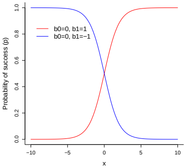
The odds is expected to increase by a factor of exp(β_i) when X_i increases by 1 unit, <u>and everything else is held constant</u>!

$$logit(p_i) = log(\frac{p_i}{1-p_i}) = \beta_0 + \beta_1 X_i$$



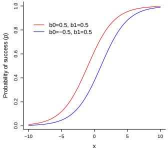
The slope coefficient β_1 controls how quickly we transition from 0 to 1.

$$logit(p_i) = log(\frac{p_i}{1-p_i}) = \beta_0 + \beta_1 x_i$$



The sign of β_1 determines if p increases or decreases as we increase X.

$$logit(p_i) = log(\frac{p_i}{1-p_i}) = \beta_0 + \beta_1 X_i$$



β_0:

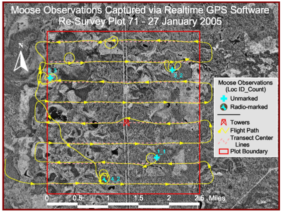
- Controls the height of the curve when $X = 0$.
- Gives the log odds of detection when all predictor variables = 0
- $E[Y_i|X_i = 0] = \frac{exp(\beta_0)}{1+exp(\beta_0)}$ (equals 1/2 if $\beta_0 = 0$).

Sightability Surveys: Minnesota Moose

124 'trials', 2005-2007

n_0 = 65 missed groups

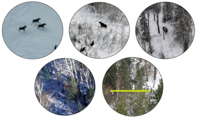
n_1 = 59 observed groups



- Binary observations, $Y_i = 0$ (missed) or 1 (seen).
- Covariates thought to influence detection.

Covariates

- Visual obstruction
- Survey year (may be due to different observers)



$$Y_i|X_i \sim Bernoulli(p_i)$$

$$logit(p_i) = \log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 voc_i$$

Assumptions:

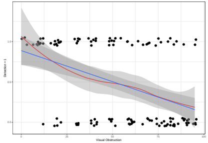
- observations are independent
- log odds is a linear function of *voc*
- mean and variance depend on *voc*

$E[Y_i|X_i] = p_i$; $Var[Y_i|X_i] = p_i(1-p_i)$ with:

$p_i = \frac{\exp(\beta_0+\beta_1 voc_i)}{1+\exp(\beta_0+\beta_1 voc_i)}$

Visual Obstruction

```
ggplot(exp.m, aes(voc,observed))+theme_bw()+
   geom_point(position = position_jitter(w = 2, h = 0.05), size=3) +
   geom_smooth(colour="red")  +geom_smooth(method="lm")+
 xlab("Visual Obstruction") +
  ylab("Detection = 1")
```



- `lm` would eventually predict $p_i \geq 1$ and $p_i \leq 0$
- `lm` assumes constant variance rather than $var(p_i) = p_i(1-p_i)$

```
mod1<-glm(observed~voc, data=exp.m, family=binomial())
summary(mod1)
```

```
Call:
glm(formula = observed ~ voc, family = binomial(), data = exp.m)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.759933   0.460137   3.825 0.000131 ***
voc         -0.034792   0.007753  -4.487 7.21e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 171.61  on 123  degrees of freedom
Residual deviance: 147.38  on 122  degrees of freedom
AIC: 151.38

Number of Fisher Scoring iterations: 4
```

```r
mod1$coef
```

```
(Intercept)         voc
 1.75993309 -0.03479153
```

Regression coefficient for voc (visual obstruction) = -0.039.

- The log odds of being detected decreases by 0.039 per unit increase in visual obstruction
- The odds of being detected decreases by a factor of exp(0.039) = 0.96 per unit increase in visual obstruction

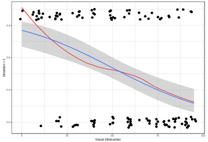
Intercept = 2.12 = log(odds) of detection when VOC = 0.

```r
# p(Y=1|voc=0) = exp(coef(mod1)[1])/(1+exp(coef(mod1)[1]))
plogis(coef(mod1)[1])
```

```
(Intercept)
  0.8532013
```

We see roughly 85% of moose if there is no visual obstruction.

```r
ggplot(exp.m, aes(voc,observed))+ theme_bw() +
    geom_point(position = position_jitter(w = 2, h = 0.05), size=3) +
    xlab("Visual Obstruction") +  geom_smooth(se=F, colour="red") +
    stat_smooth(method="glm", method.args = list(family = "binomial"))+
    ylab("Detection = 1")
```



```r
exp.m$year<-as.factor(exp.m$year)
mod2<-glm(observed~voc+year, data=exp.m, family=binomial())
summary(mod2)
```

```
Call:
glm(formula = observed ~ voc + year, family = binomial(), data = exp.m)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.453203   0.622248   3.942 8.06e-05 ***
voc         -0.037391   0.008199  -4.560 5.11e-06 ***
year2006    -0.453862   0.516567  -0.879   0.3796
year2007    -1.111884   0.508269  -2.188   0.0287 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 171.61  on 123  degrees of freedom
Residual deviance: 142.23  on 120  degrees of freedom
AIC: 150.23

Number of Fisher Scoring iterations: 4
```

```r
coef(mod2)
```

```
(Intercept)         voc    year2006    year2007
 2.45320264 -0.03739118 -0.45386154 -1.11188432
```

Year 2005: $log(p_i/(1-p_i)) = 2.45 - 0.037VOC$

Year 2006: $log(p_i/(1-p_i)) = 2.45 - 0.037VOC - 0.45$

So,-0.45 gives the difference in log odds between years 2005 and 2004 (if we hold VOC constant).

exp(-0.45) = 0.63 = odds ratio (year 2006 to year 2005)

odds ratio = $\frac{p_{2006}/(1-p_{2006})}{p_{2005}/(1-p_{2005})} = 0.63$

Supporting Theory

The estimates of β are maximum likelihood estimates, found by maximizing:

$$L(\beta; y, x) = \prod_{i=1}^{n} p_i^{y_i}(1-p_i)^{1-y_i}, \text{ with}$$
$$p_i = \frac{e^{\beta_0+\beta_1 x_1+\ldots\beta_k x_k}}{1+e^{\beta_0+\beta_1 x_1+\ldots\beta_k x_k}}$$

Remember, for large samples, $\hat{\beta} \sim N(\beta, \Sigma)$.

We can use this theory to conduct tests (z-statistics and p-values in output by the `summary` function) and to get confidence intervals.

- $\text{logit}(p) = \beta_0 + \beta_1 x_1 + \ldots \beta_k x_k$ is more "Normal" than p
- Generate confidence intervals for logit(p), then back-transform to get confidence intervals for p
- Ensures the confidence intervals will live on the (0,1) scale
- Intervals will not be symmetric

Confint

```
(ci.prof<-confint(mod2))
```

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

```
                  2.5 %     97.5 %
(Intercept)  1.30341777  3.7586692
voc         -0.05448153 -0.0221268
year2006    -1.48479529  0.5516852
year2007    -2.14380706 -0.1382692
```

These are profile-likelihood based confidence intervals based on "inverting" the likelihood ratio test (see Maximum Likelihood notes).

```
exp(ci.prof[3,])
```

```
    2.5 %    97.5 %
0.2265487 1.7361764
```

Profile-likelihood based intervals should have better statistical properties with small data sets (better coverage rates).

If confidence limits for β include 0 or confidence limits for $exp(\beta)$ include 1, then we do not have enough evidence to say that years differ in their detection probabilities.

```
mod2$coef
```

```
(Intercept)         voc    year2006    year2007
 2.45320264 -0.03739118 -0.45386154 -1.11188432
```

```
sqrt(diag(vcov(mod2)))
```

```
(Intercept)         voc    year2006    year2007
0.622247867 0.008199483 0.516567443 0.508269279
```

```
exp(rep(0.006879, 2)+c(-1.96, 1.96)*0.53664) # exp(beta +/-1.96SE)
```

```
[1] 0.3517145 2.8826021
```

95% Confidence interval for odds ratio = (0.35, 2.88) includes 1 (not statistically significant)

Goodness-of-fit

Can adapt our general approach for testing goodness-of-fit using Pearson residuals (r_i)

$$r_i = \frac{Y_i - E[Y_i|X_i]}{\sqrt{Var[Y_i|X_i]}}$$

- $E[Y_i|X_i] = p_i = \frac{exp(\beta_0+\beta_1 x_1+\ldots\beta_k x_k)}{1+exp(\beta_0+\beta_1 x_1+\ldots\beta_k x_k)}$
- $Var[Y_i|X_i] = p_i(1-p_i)$

See textbook for an implementation of this test...

Hosmer-Lemeshow test (similar test)

Group Observations by deciles of their predicted values to form groups, then calculate the expected and observed number of successes and failures for each group:

Model Results

	$G_1=[0,\hat{\pi}_1]$	$G_2=(\hat{\pi}_1,\hat{\pi}_2]$	...	$G_{10}=(\hat{\pi}_9,1]$
Successes	$\sum_{x_i\in G_1}\hat{\pi}_i$	$\sum_{x_i\in G_2}\hat{\pi}_i$	...	$\sum_{x_i\in G_{10}}\hat{\pi}_i$
Failures	$n_1-\sum_{x_i\in G_1}\hat{\pi}_i$	$n_2-\sum_{x_i\in G_2}\hat{\pi}_i$	...	$n_{10}-\sum_{x_i\in G_{10}}\hat{\pi}_i$

Observed Results

	$G_1=[0,\hat{\pi}_1]$	$G_2=(\hat{\pi}_1,\hat{\pi}_2]$	...	$G_{10}=(\hat{\pi}_9,1]$
Successes	$\sum_{x_i\in G_1}y_i$	$\sum_{x_i\in G_2}y_i$	...	$\sum_{x_i\in G_{10}}y_i$
Failures	$n_1-\sum_{x_i\in G_1}y_i$	$n_2-\sum_{x_i\in G_2}y_i$	...	$n_{10}-\sum_{x_i\in G_{10}}y_i$

See: **Goodness of fit with binary data** here: http://www.unc.edu/courses/2010fall/ecol/563/001/docs/lectures/lecture21.htm

Hosmer-Lemeshow Test

$$\chi^2 = \sum_{i=1}^{n_g} \frac{(O_i - E_i)^2}{E_i} \sim \chi^2_{g-2}$$

where g = number of groups.

Hosmer-Lemeshow test

```
library(ResourceSelection)
hoslem.test(exp.m$observed, fitted(mod1), g=8)
```

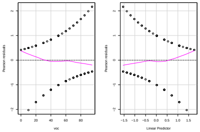
```

    Hosmer and Lemeshow goodness of fit (GOF) test

data:  exp.m$observed, fitted(mod1)
X-squared = 3.2505, df = 6, p-value = 0.7768
```

Residual plots

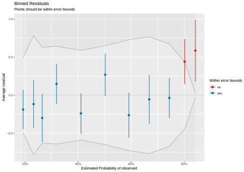
```
car::residualPlots(mod1)
```




```
    Test stat Pr(>|Test stat|)
voc    0.6873           0.4071
```

Binned residual plot

```
binplot<-performance::binned_residuals(mod1)
plot(binplot)
```



Likelihood ratio tests

We can again use difference in deviences (equivalent to likelihood ratio tests) to compare full and reduced models.

```
drop1(mod2, test="Chisq")
```

```
Single term deletions

Model:
observed ~ voc + year
       Df Deviance    AIC     LRT  Pr(>Chi)
<none>      142.23 150.23
voc     1   168.20 174.20 25.9720 3.464e-07 ***
year    2   147.38 151.38  5.1558   0.07593 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

voc is an important predictor, the importance of `year` is less clear.

ANOVA function (car package)

Or use Anova in car package

```
library(car)
```

```
Anova(mod2)
```

```
Analysis of Deviance Table (Type II tests)

Response: observed
     LR Chisq Df Pr(>Chisq)
voc   25.9720  1  3.464e-07 ***
year   5.1558  2    0.07593 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

AIC

We can compare nested or non-nested models using the AIC function

```
AIC(mod1, mod2)
```

```
     df      AIC
mod1  2 151.3824
mod2  4 150.2266
```

Probability Scale

We can also summarize models by getting predicted values: $P(\text{detect animal}|\text{voc})$:

- $logit(p_i) = \beta_0 + \beta_1 x_1 + \ldots \beta_k x_k$
- $P(Y_i = 1|X = x) = p_i = \frac{e^{\beta_0+\beta_1 x_1+\ldots\beta_k x_k}}{1+e^{\beta_0+\beta_1 x_1+\ldots\beta_k x_k}}$ (inverse logit)

We can use `predict(model, newdata=, type="link", se=TRUE)` to get predictions on logit scale.

Then use `plogis(p.hat$fit +/- 1.95*p.hat$se.fit)` to transform the limits back to the probability scale.

A note on model visualization

Model 2: observed $\sim$ voc + year is additive on the logit scale

- Differences in logit(p) among years will not depend on voc
- Differences in p, will however, depend on voc!

See: Section 16.6.3 in the book

- Can always create your own "effect" plots by calculating predicted values for different combinations of your predicted values
- Can use the `effects` package or `ggeffects` to do something similar

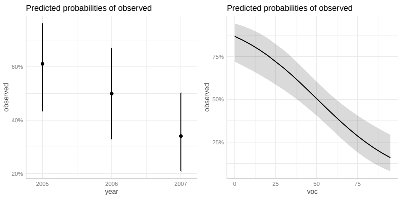
Effect plots on probability scale

Use `effects` or `ggeffects` package:

- Fixes all continuous covariates (other than the one of interest) at their mean values
- Categorical predictors: averages predictions on link scale, weighted by proportion of data in each category, then back transforms to probability scale
- These are refereed to as <u>marginal predictions</u> by `ggeffects`

Effect plots

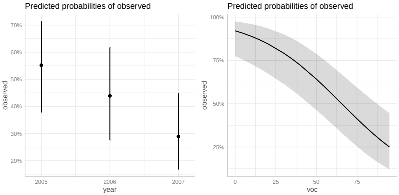
```r
library(ggeffects); library(patchwork)
p1 <- plot(ggeffect(mod2, "year"))
p2 <- plot(ggeffect(mod2, "voc"))
p1 + p2
```



Adjusted plots

Instead of averaging predictions across years, we could set year to a specific value. This leads to adjusted plots.

```r
library(ggeffects); library(patchwork)
p1 <- plot(ggpredict(mod2, "year"))
p2 <- plot(ggpredict(mod2, "voc"))
p1 + p2
```



JAGS

Will use a similar structure as we used for count models:

- A linear predictor, $\eta = \beta_0 + \beta_1 x_1$ (x_1 = voc)
- $p_i = g^{-1}(\eta) = \frac{e^{\eta_i}}{1+e^{\eta_i}}$
- $Y[i] \sim$ dbin(p[i],1)
- Require priors for β_0 and β_1, e.g., N(0, 0.01)

Gelman's recommendations (see arxiv.org/pdf/0901.4011.pdf):

- scale continuous predictors so they have mean 0 and sd = 0.5
- using a non-informative Cauchy prior dt(0, pow(2.5,-2), 1)

In class exercise: adapt the JAGS code for fitting mod1 (voc only) to allow fitting of mod2 (voc + year).