Binary and Binomial Models (Logistic Models)

Intended Learning Outcomes

Students will be able to:

 Fit and interpret a generalized linear model of family to binary and binomial data

Validate these models

Calculate the pseudo-R² and dispersion parameter

Recap

- Any GLM consists of three steps:
- 1. Choosing a distribution for the response variable = Binary or Binomial

Binary and Binomial Data

- Can be:
 - Binary: 0,1 encoding absence/presence, survived/died
 - Binomial: probability value → 3 out of 10 survived → 0.3

$$p = \frac{k}{n} = \frac{Number\ of\ successes}{number\ of\ trials}$$



Recap

- Any GLM consists of three steps:
- Choosing a distribution for the response variable = Binary or Binomial

2. Specifying the linear function of covariates and/or fixed factors

$$h(y_i) = \beta_0 + \beta_1 x_i + \varepsilon_i$$

Recap

- Any GLM consists of three steps:
- Choosing a distribution for the response variable = Binary or Binomial

- 2. Specifying the linear function of covariates and/or fixed factors
- Choosing a link between the predictor function and the mean of the distribution

Logit link function

Logit Link Function

The Odds Ratio

$$\ln\left(\frac{k}{n-k}\right)$$

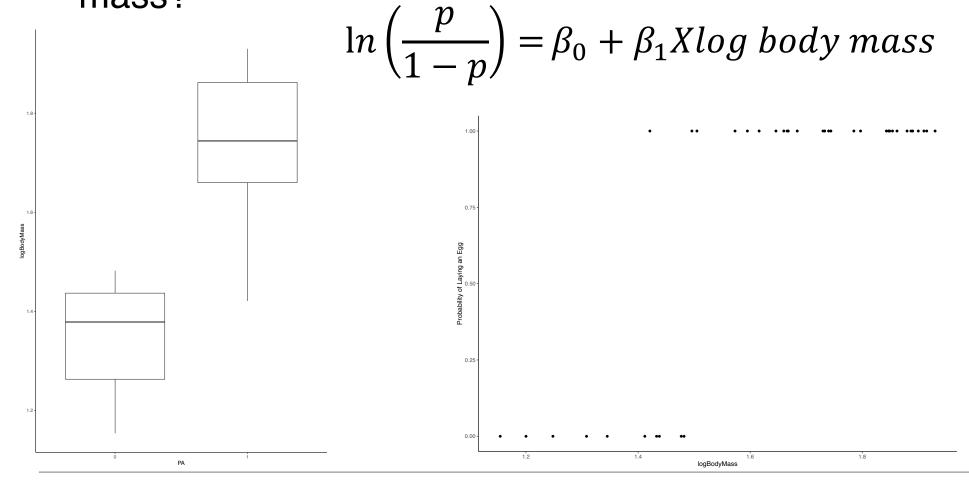
number of successes
number of failures

$$\ln\left(\frac{p}{1-p}\right)$$

Probability of successes
Probability of failures

Binary Data – Moth Eggs

Does the probability of laying an egg increase with log body mass?



Moth Eggs Example- Binary

```
Call:
glm(formula = BinaryEggs ~ logBodyMass, family = "binomial",
    data = motheggs)
Deviance Residuals:
     Min
                     Median
                10
                                    30
                                            Max
-1.25014 -0.00311
                     0.00314
                              0.05421
                                        1.99088
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
                         26.06 -1.861
(Intercept)
              -48.49
                                         0.0628
logBodyMass
              32.83
                         17.70
                                1.855
                                         0.0635
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 44.4029 on 38 degrees of freedom
Residual deviance: 9.7883 on 37 dearees of freedom
AIC: 13.788
Number of Fisher Scoring iterations: 9
                                                                             1.2
```

log Body Mass (g)

Interpreting Coefficients

The most important thing to remember with coefficients is that they are still in the log odds ratios.

$$\ln\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 X \log body \ mass$$

$$\frac{p}{1-p} = e^{\beta_0 + \beta_1 X \log body \, mass}$$

$$p = \frac{e^{\beta_0 + \beta_1 X \log body \, mass}}{1 + e^{\beta_0 + \beta_1 X \log body \, mass}}$$

Probability Change

•Intercept: Not biologically meaningful without standardisation Coefficients:

Slope:

Log Odds Ratio Probability

$$\log\left(\frac{p_s}{1-p_s}\right) \longrightarrow p_s$$

$$\frac{e^{\beta_1}}{1 + e^{\beta_1}} = \frac{e^{32.83}}{1 + e^{32.82}} = 1 \text{ or } 100\%$$

Probability Change

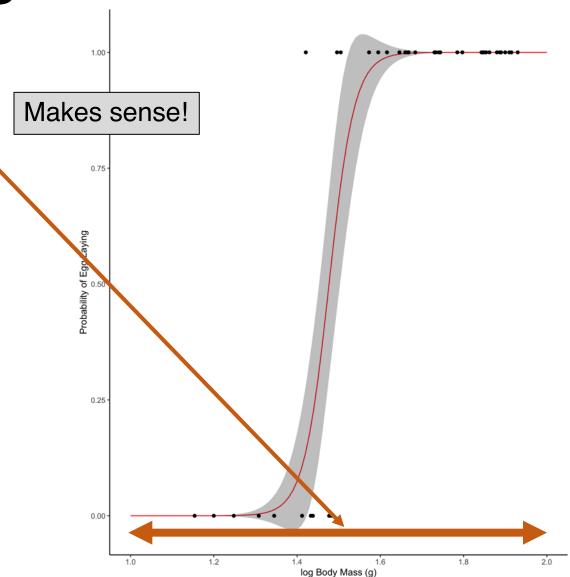
Coefficients:

For every 1 log increase in body mass, the probability of a vapourer moth laying an egg increases by 100%.

$$\frac{e^{\beta_1}}{1 + e^{\beta_1}} = \frac{e^{32.83}}{1 + e^{32.82}} = 1 \text{ or } 100\%$$

Probability Change

For every 1 log increase in body mass, the probability of a vapourer moth laying an egg increases by 100%.

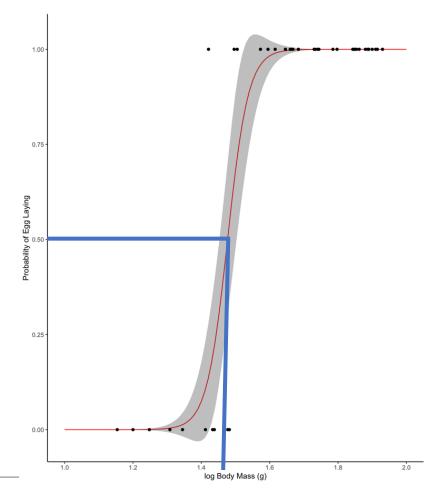


Finding the flip

- When thinking about probabilities we are interested in the point where the probability flips, i.e. you are more likely to do something.
- The occurs when the probability is greater than
 0.5
- Solve for log body mass

$$0.5 = \frac{e^{-48.49 + 32.83X log body mass}}{1 + e^{-48.49 + 32.83X log body mass}}$$

■ Value of
$$\frac{\beta_0}{\beta_1} = \frac{48.49}{32.83} = 1.48$$



Finding the flip – other solutions

■ Where the values of β_0 and β_1 are absolute.

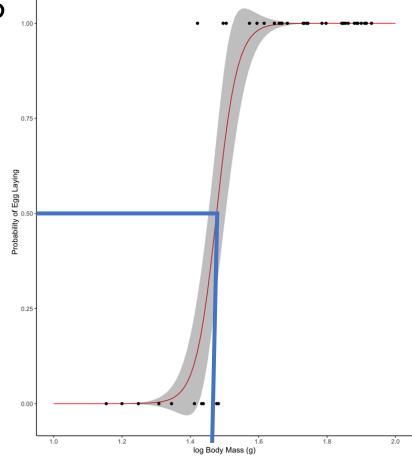
		Slope	
		Negative	Positive
Intercept	Negative	$-rac{eta_0}{eta_1}$	$\frac{eta_0}{eta_1}$
	Positive	$rac{eta_0}{eta_1}$	$-rac{eta_0}{eta_1}$

Finding the flip

- When thinking about probabilities we are interested in the point where the probability flips, i.e. you are more likely to do something.
- The occurs when the probability is greater than 0.5
- Solve for log body mass

$$0.5 = \frac{e^{-48.49 + 32.83X log body mass}}{1 + e^{-48.49 + 32.83X log body mass}}$$

- Value of $\frac{\beta_0}{\beta_1} = \frac{48.49}{32.83} = 1.48$
- We can infer then that vapourer moths weighing over 1.48 logs of body mass are more likely to lay an egg.



Pseudo-R² and Goodness-of-fit

```
Call:
alm(formula = BinaryEggs ~ logBodyMass, family = "binomial",
   data = mothegas)
Deviance Residuals:
    Min
                     Median
                                            Max
-1.25014 -0.00311 0.00314
                              0.05421
                                       1.99088
Coefficients:
           Estimate Std. Error z value Pr(>|z|)
             -48.49
                         26.06 -1.861
                                        0.0628 .
(Intercept)
logBodyMass
              32.83
                         17.70 1.855
                                         0.0635 .
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 44.4029 on 38 degrees of freedom
```

```
Residual deviance: 9.7883 on 37 degrees of freedom
AIC: 13.788
```

Number of Fisher Scoring iterations: 9

```
Analysis of Deviance Table
Model: binomial, link: logit
Response: BinaryEggs
Terms added sequentially (first to last)
           Df Deviance Resid. Df Resid. Dev
                                             Pr(>Chi)
NULL
                                     44.403
logBodyMass 1 34.615
                              37
                                      9.788 4.019e-09 ***
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' '1
```

Pseudo-R²:

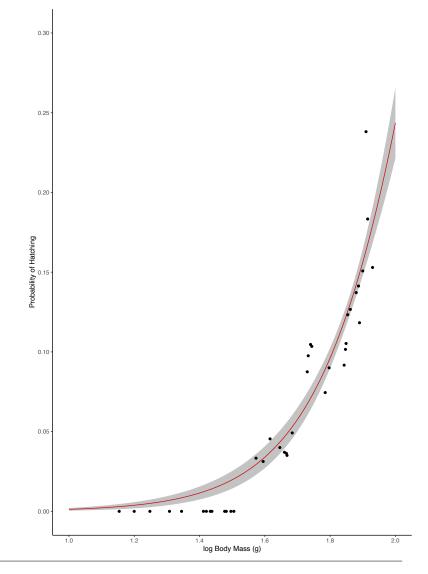
-1-(9.89/44.40) = 0.78

Model Validation

- Validation is difficult as the response variable consists only of 0's and 1's and so the diagnostic plots aren't reliable.
- ■There is still debate regarding the use of quasi-likelihood approaches for binary data quasi-binomial but these are regarded as controversial they are supported by the glm function in R however.

Moth Eggs Example- Binomial

```
Call:
glm(formula = cbind(Hatched, RedEggs - Hatched) ~ logBodyMass,
   family = "binomial", data = motheggs)
Deviance Residuals:
    Min
               10
                     Median
                                           Max
-1.21468 -0.46512 -0.07996 0.00000
                                       2.76868
Coofficients
           Estimate Std. Error z value Pr(>|z|)
(Intercept) -12.2095
                        1.4332 -8.519
                                        <2e-16 ***
                        0.7691 7.201
logBodyMass 5.5383
                                         6e-13 ***
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 85.659 on 28 degrees of freedom
Residual deviance: 19.372 on 27 degrees of freedom
AIC: 124.31
Number of Fisher Scoring iterations: 4
```



Model Formula

•Does maternal body weight affect the probability of eggs hatching?

```
Call: glm(formula = cbind(Hatched, RedEggs - Hatched) \sim logBodyMass, family = "binomial", data = motheggs)
\frac{number\ of\ eggs\ hatched}{number\ of\ eggs\ not\ hatched} \longrightarrow ln\left(\frac{k}{n-k}\right)
```

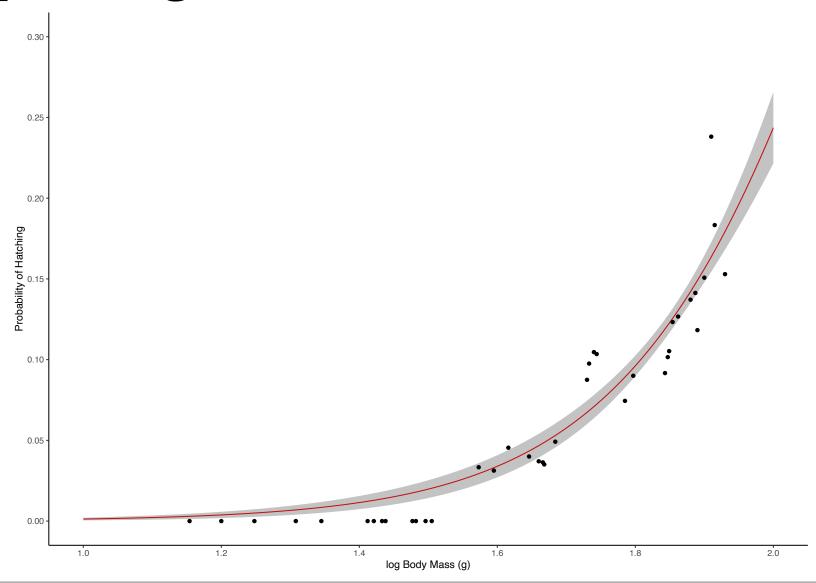
Interpreting Coefficients

For a milligram increase in body mass increases the log odds of a moth egg hatching by 5.54

Probability of egg hatching =
$$\frac{e^{-12.21+5.54X\log body \ mass}}{1+e^{-12.21+5.54X\log body \ mass}}$$

Because the relationship between logit and probability is not linear we can't just back transform the slope coefficient to get a probability change instead it is more common to plot to model and infer from that.

Interpreting Coefficients



Pseudo R² and Goodness-of-Fit

Number of Fisher Scoring iterations: 4

```
Call:
                                                             Analysis of Deviance Table
glm(formula = cbind(Hatched, RedEggs - Hatched) ~ logBodyMass,
   family = "binomial", data = motheggs)
                                                             Model: binomial, link: logit
Deviance Residuals:
                    Median
    Min
                                         Max
                                                             Response: cbind(Hatched, RedEgas - Hatched)
-1.21468 -0.46512 -0.07996
                            0.00000
                                     2.76868
                                                             Terms added sequentially (first to last)
Coefficients:
           Estimate Std. Error z value Pr(>|z|)
(Intercept) -12.2095
                   1.4332 -8.519
                                      <2e-16 ***
logBodyMass 5.5383
                      0.7691 7.201
                                       6e-13 ***
                                                                          Df Deviance Resid. Df Resid. Dev Pr(>Chi)
                                                             NULL
                                                                                                       85.659
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
                                                                                                       19.372 3.896e-16 ***
                                                             logBodyMass 1 66.288
(Dispersion parameter for binomial family taken to be 1)
                                                             Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
   Null deviance: 85.659 on 28 degrees of freedom
Residual deviance: 19.372 on 27 degrees of freedom
AIC: 124.31
```

Goodness-of-fit:

■ pseudo-R²: $1 - (^{19.37}/_{85.66}) = 0.77$

Model Validation

```
Null deviance: 85.659 on 28 degrees of freedom
Residual deviance: 19.372 on 27 degrees of freedom
AIC: 124.31
```

- $-(^{19.372}/_{27}) = 0.71 \rightarrow \text{underdispersed}$
- Underdispersion methods are less developed
- If overdispersed can fit a quasi-binomial approach and investigate the following factors:
 - Too simplistic (missing explanatory variables and/or interaction terms)
 - Explanatory variables measured on different scales
 - A covariate has a non-linear effect
 - One or more outliers
 - Zero inflation
 - Inherent dependency in the data i.e. pseudoreplication

Summary

 Logistic models can handle binary outcomes (0,1) and binomials via the log odds ratio

 The logit function abstracts the interpretation of the coefficients and instead plotting is preferable

 Logistic models fitted to binary data are hard to validate and quasi-likelihood approaches are generally avoided, however, these can be implemented with binomial data