Binary and Binomial Models (Logistic Models)

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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-R^2 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:

1. 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:

1. Choosing a distribution for the response variable = Binary or Binomial

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

3. Choosing a link between the predictor function and the mean of the distribution

Logit link function

Logit Link Function

The Odds Ratio

$$\ln\left(\frac{k}{n-k}\right) \qquad \frac{number\ of\ successes}{number\ of\ failures}$$

$$\ln\left(\frac{p}{1-p}\right) \qquad \frac{Probability\ of\ successes}{Probability\ of\ failures}$$

What is the odds ratio?

$$\frac{number\ of\ successes}{number\ of\ failures} \longrightarrow \frac{12\ Alive}{3\ Dead}$$

4 times more likely to survive

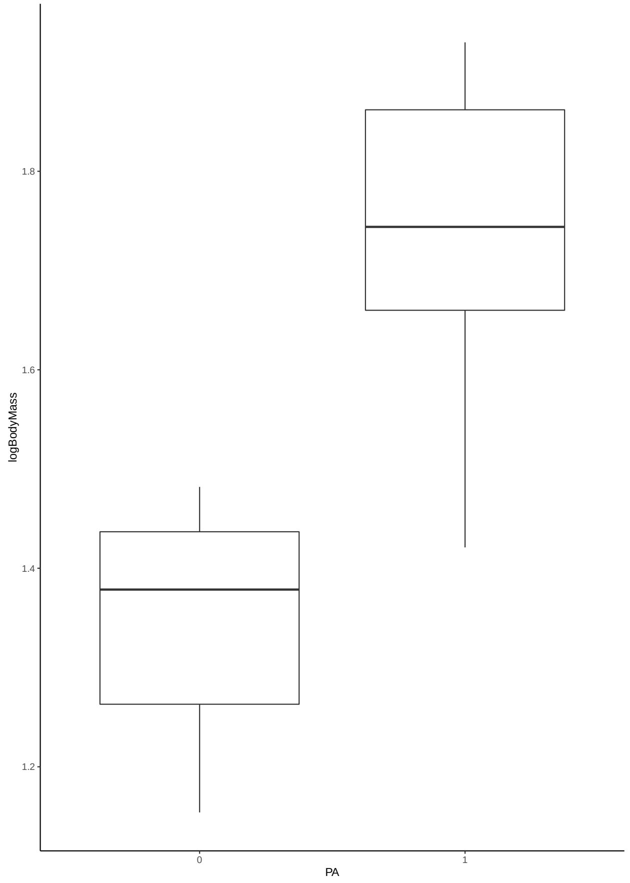
$$\frac{Probability\ of\ successes}{Probability\ of\ failures} \longrightarrow \frac{80\%\ Survival}{20\%\ Survial}$$

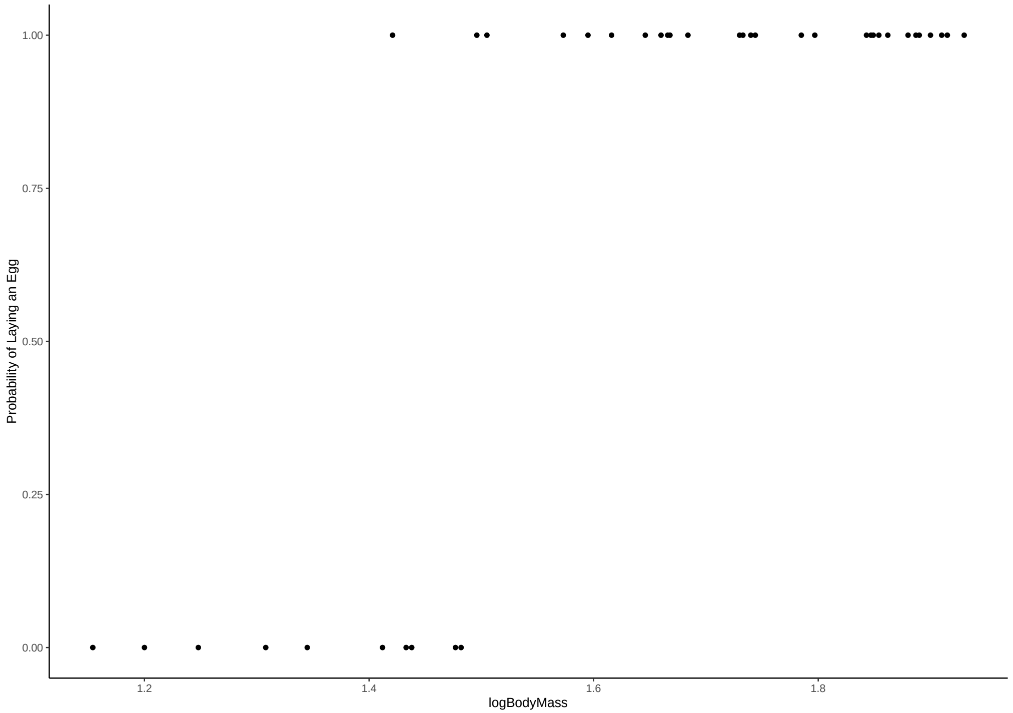
4 times more likely to survive

Binary Data – Moth Eggs

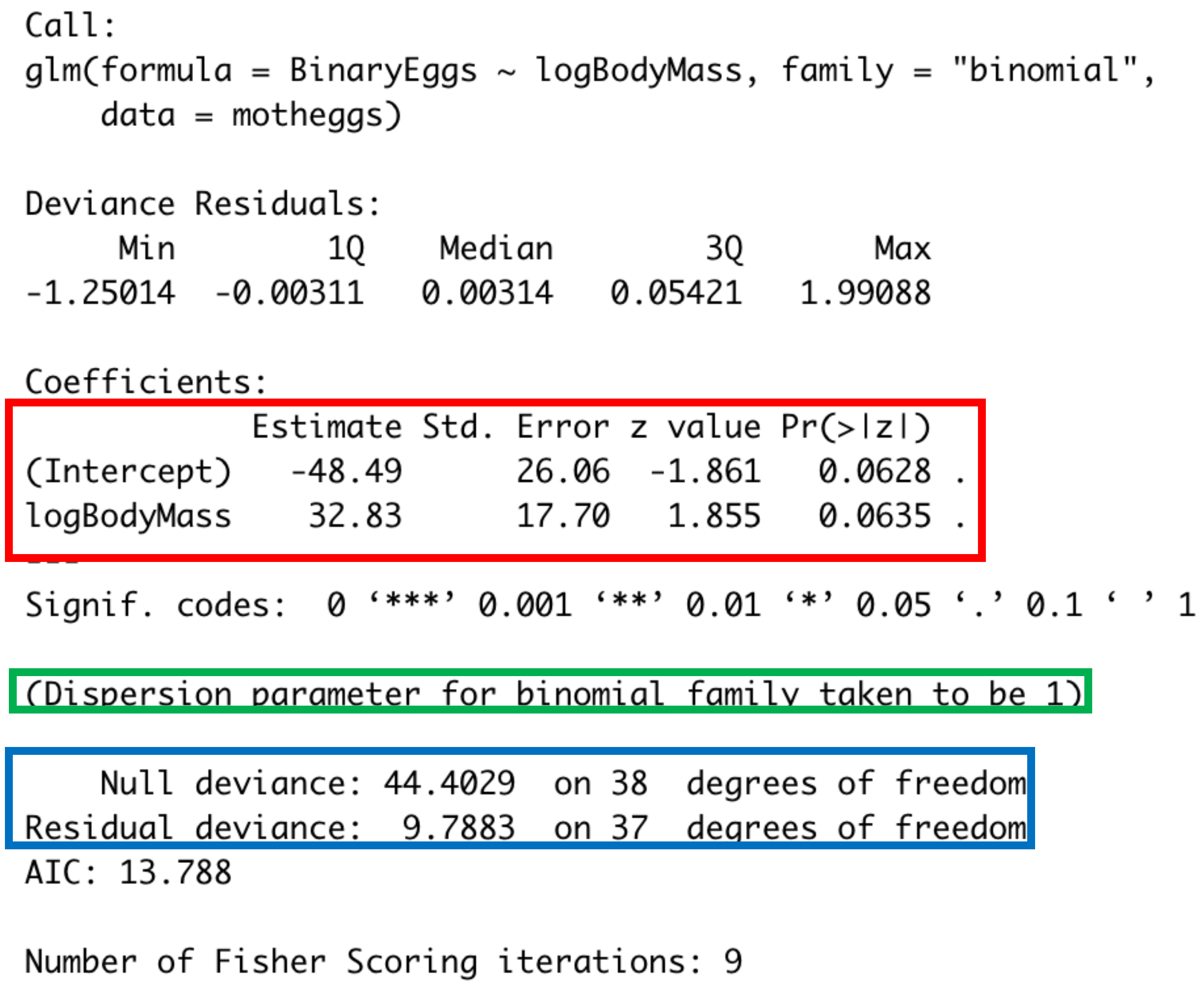
- Does the probability of laying an egg increase with log body mass?

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





Moth Eggs Example- Binary



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Call:
glm(formula = BinaryEggs ~ logBodyMass, family = "binomial",
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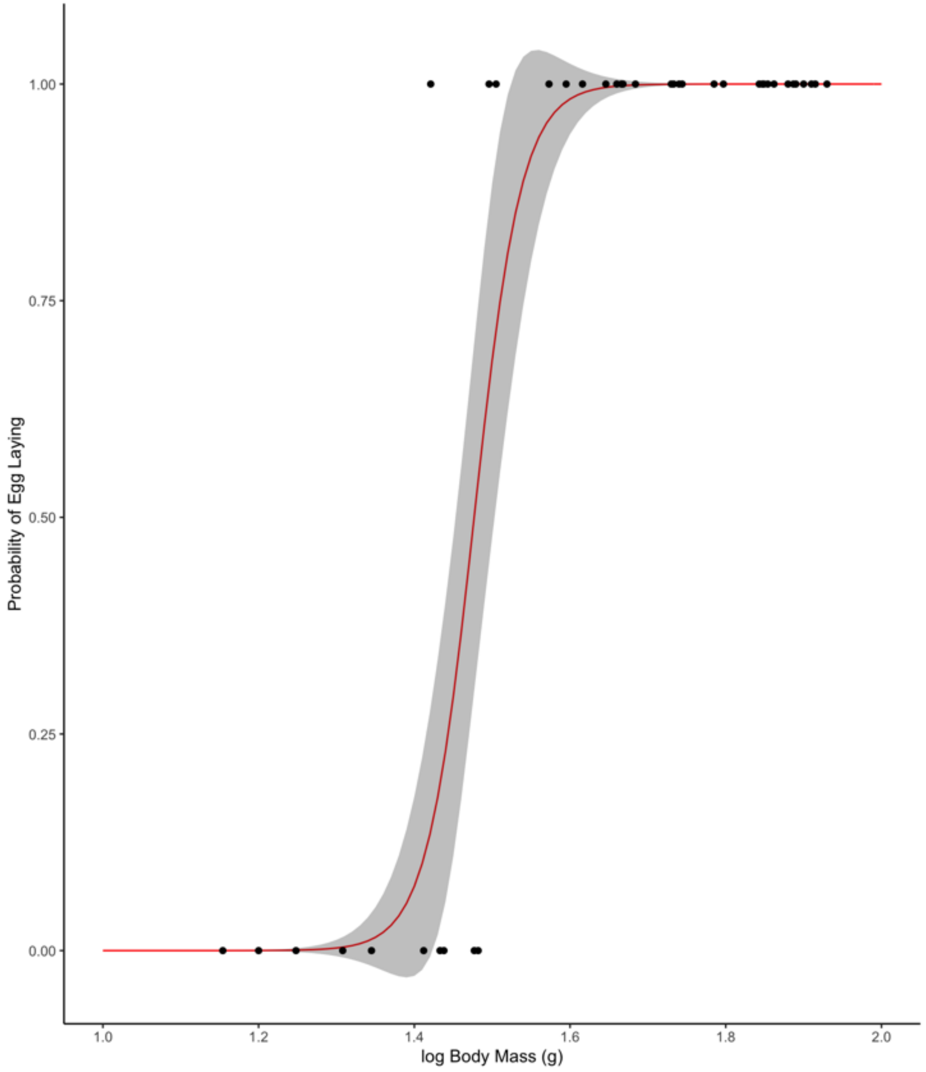
Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.25014  -0.00311   0.00314   0.05421   1.99088

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   -48.49      26.06  -1.861   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)

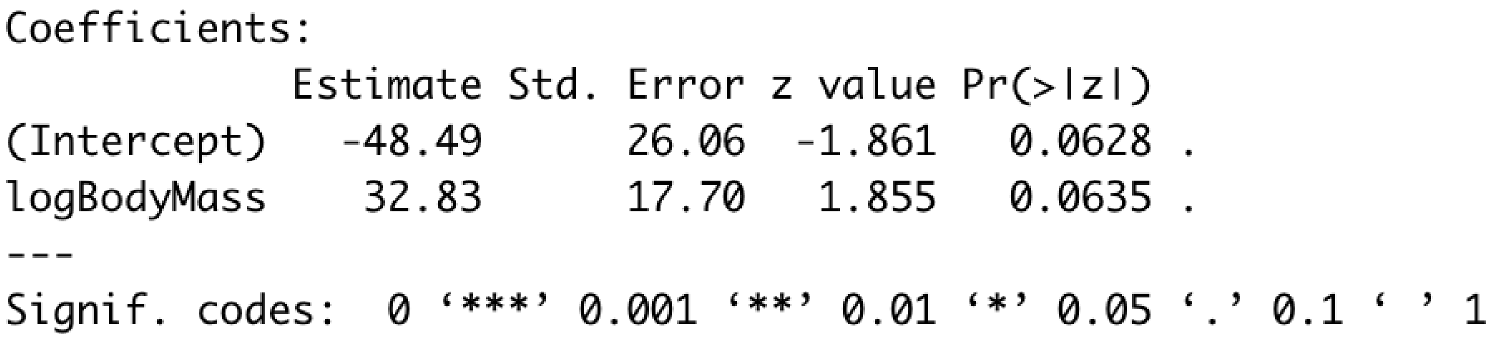
    Null deviance: 44.4029  on 38  degrees of freedom
Residual deviance:  9.7883  on 37  degrees of freedom
AIC: 13.788

Number of Fisher Scoring iterations: 9
```



Interpreting Coefficients

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



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- **Intercept:** Not biologically meaningful without standardization
- **Slope**: for every 1 log increase in body mass the log odds of laying an egg increases by 32.83 or the odds of lay an egg increases by $e^{32.83}$

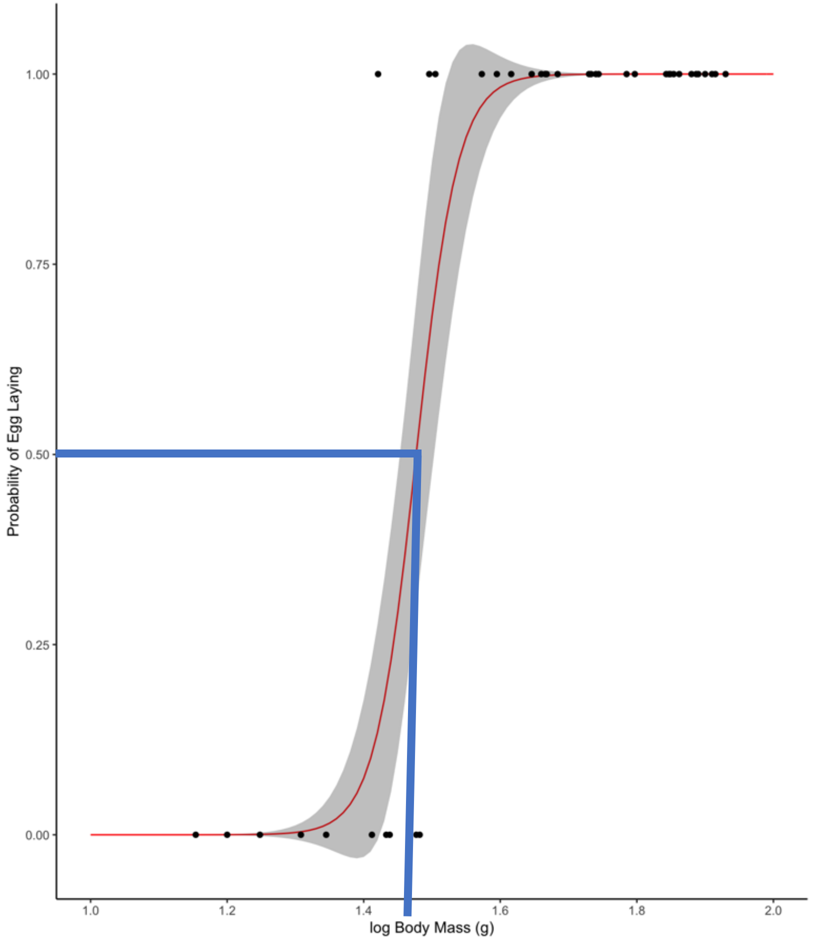
Finding the flip

- When thinking about probabilities we are interested in the point where the probability flips, i.e. an egg is more likely to be laid

- This occurs when the probability is greater than 0.5

- Solve for log body mass

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



Finding the flip – other solutions

- Where the values of β_0 and β_1 are absolute.

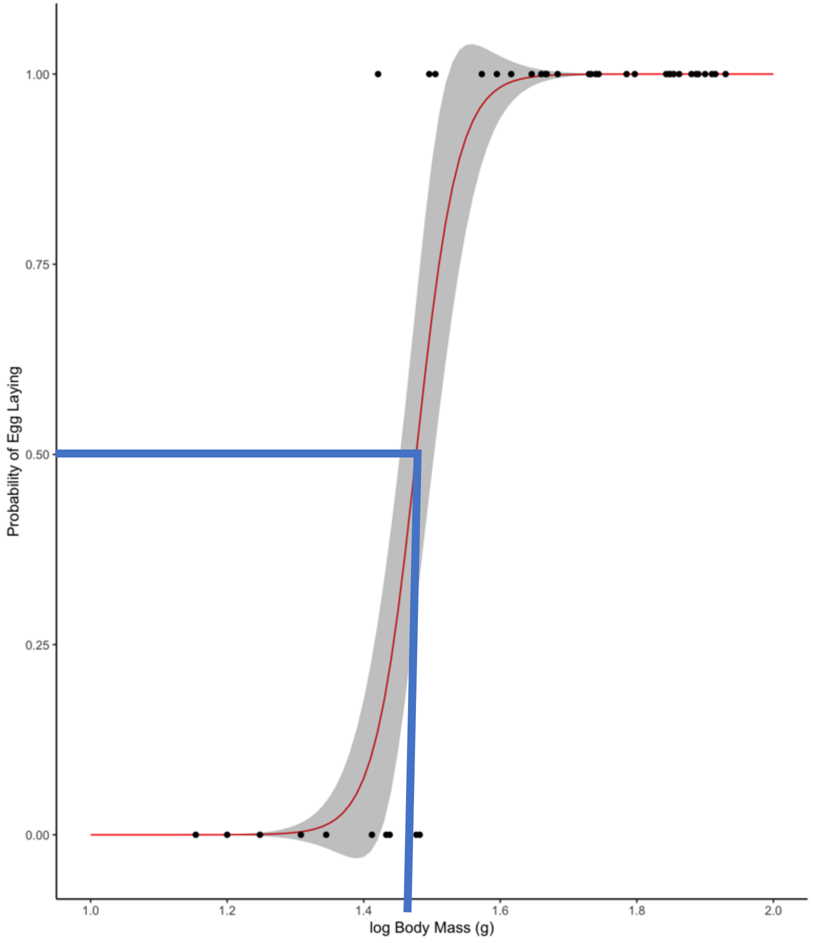
		Slope	
		Negative	Positive
Intercept	Negative	$-\left(\frac{-\beta_0}{-\beta_1}\right)$	$abs\left(\frac{-\beta_0}{\beta_1}\right)$
	Positive	$abs\left(\frac{\beta_0}{-\beta_1}\right)$	$-\left(\frac{\beta_0}{\beta_1}\right)$

Finding the flip

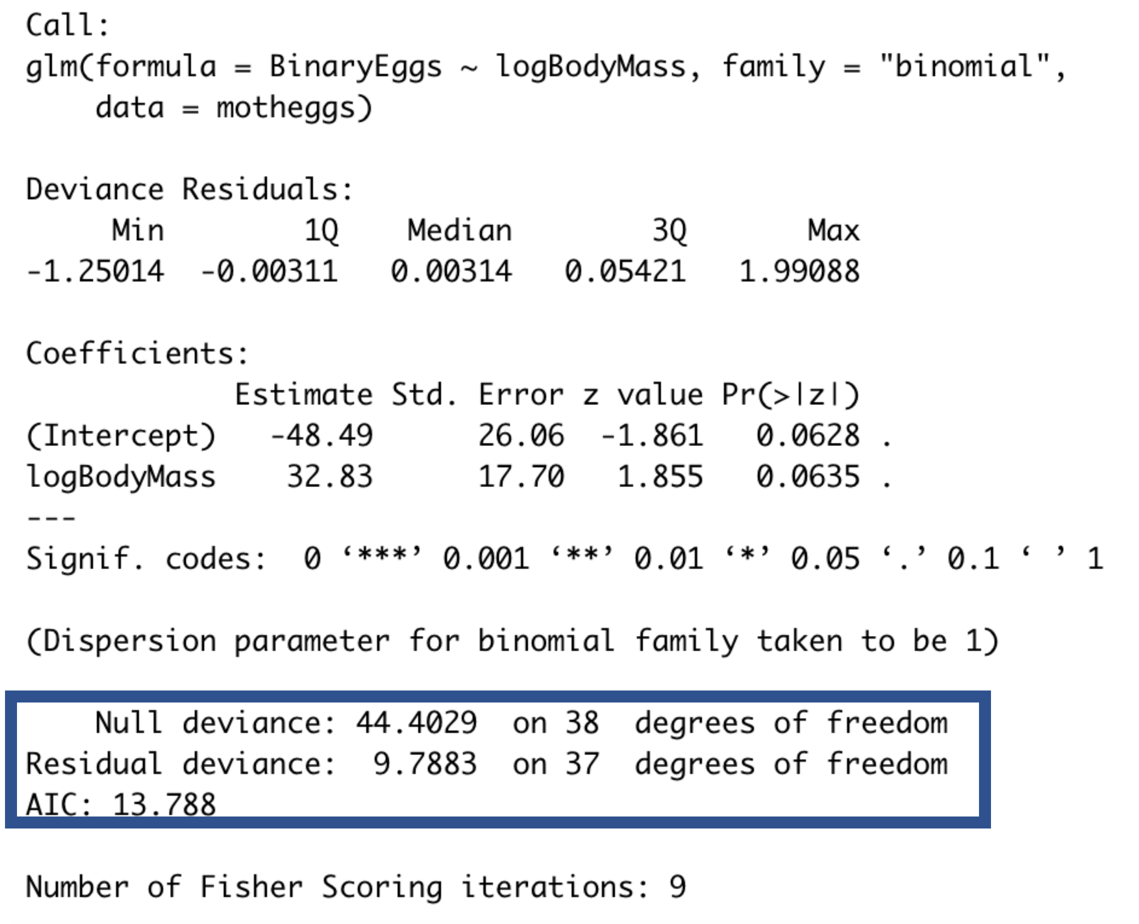
- When thinking about probabilities we are interested in the point where the probability flips, i.e. you are more likely to do something.
- The occurs when the probability is greater than 0.5
- Solve for log body mass

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

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



Pseudo-R^2 and Goodness-of-fit



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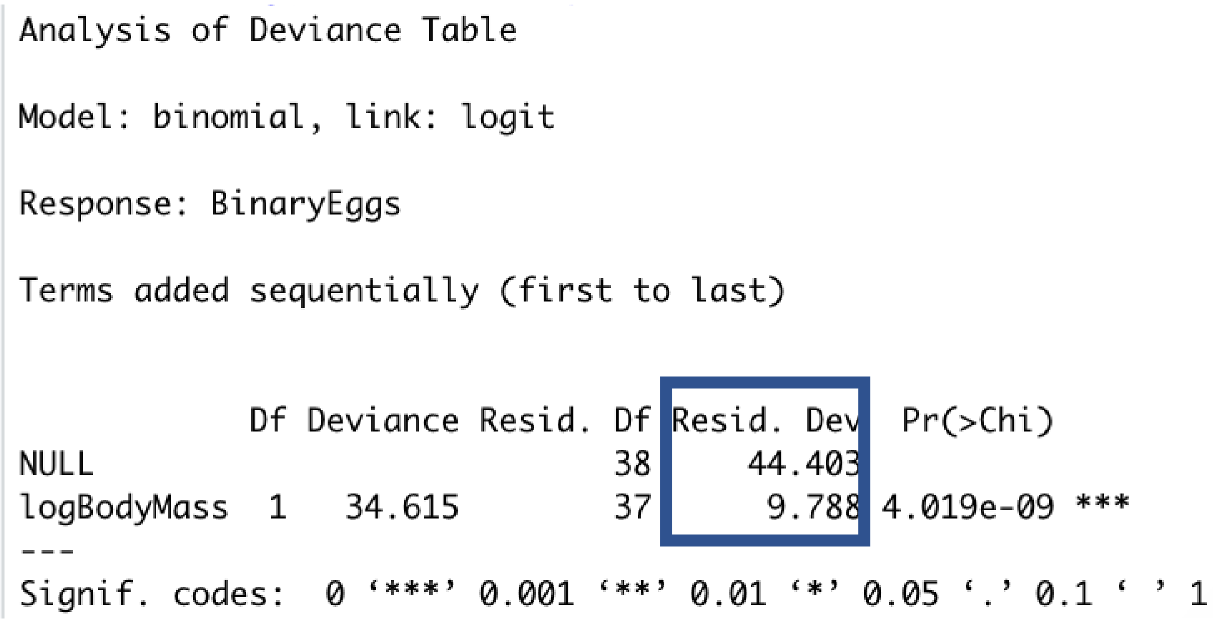


```
Analysis of Deviance Table

Model: binomial, link: logit

Response: BinaryEggs

Terms added sequentially (first to last)


            Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
NULL                           38     44.403
logBodyMass  1   34.615        37      9.788 4.019e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

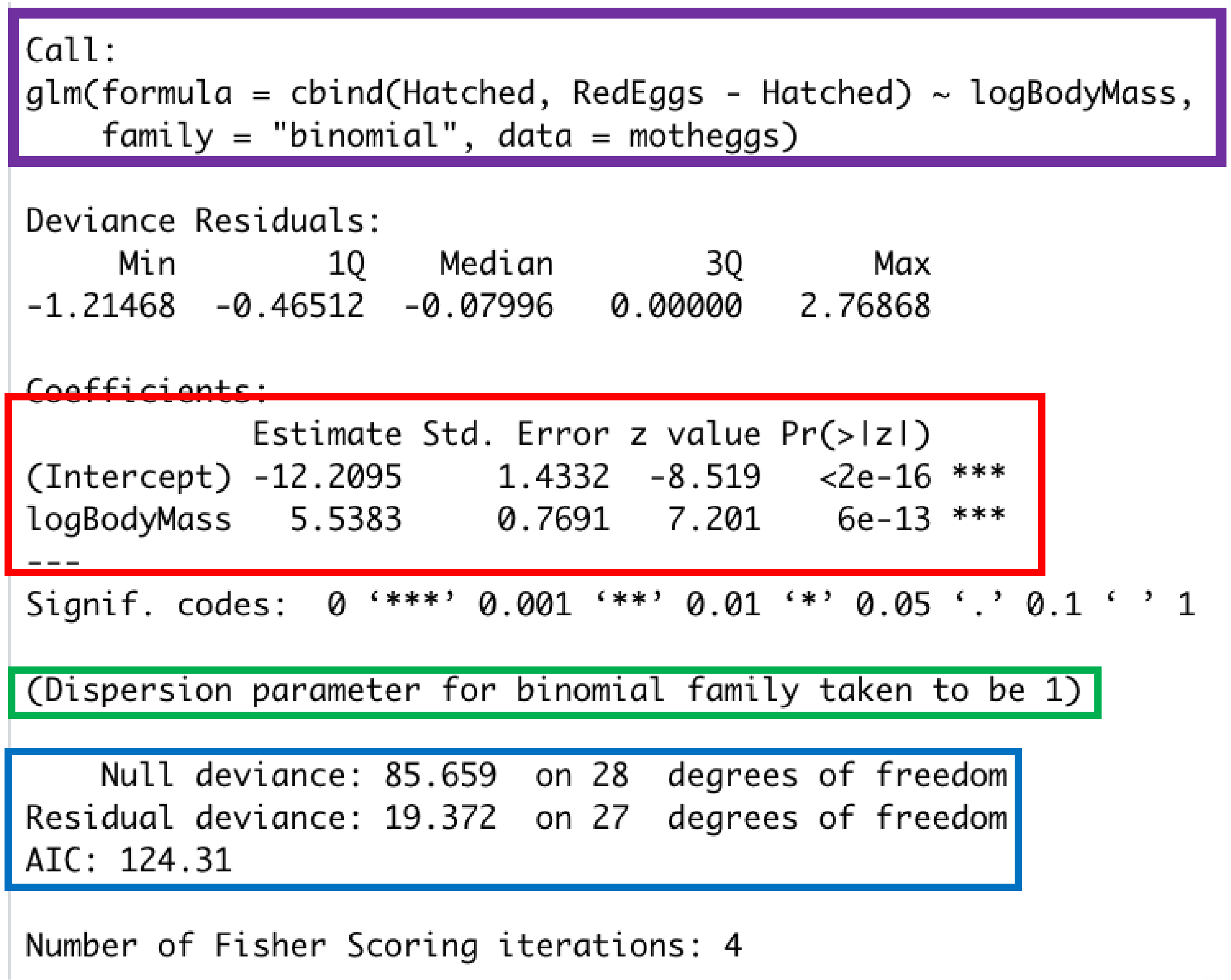
- Pseudo-R^2:
  - 1-(9.89/44.40) = 0.78

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)

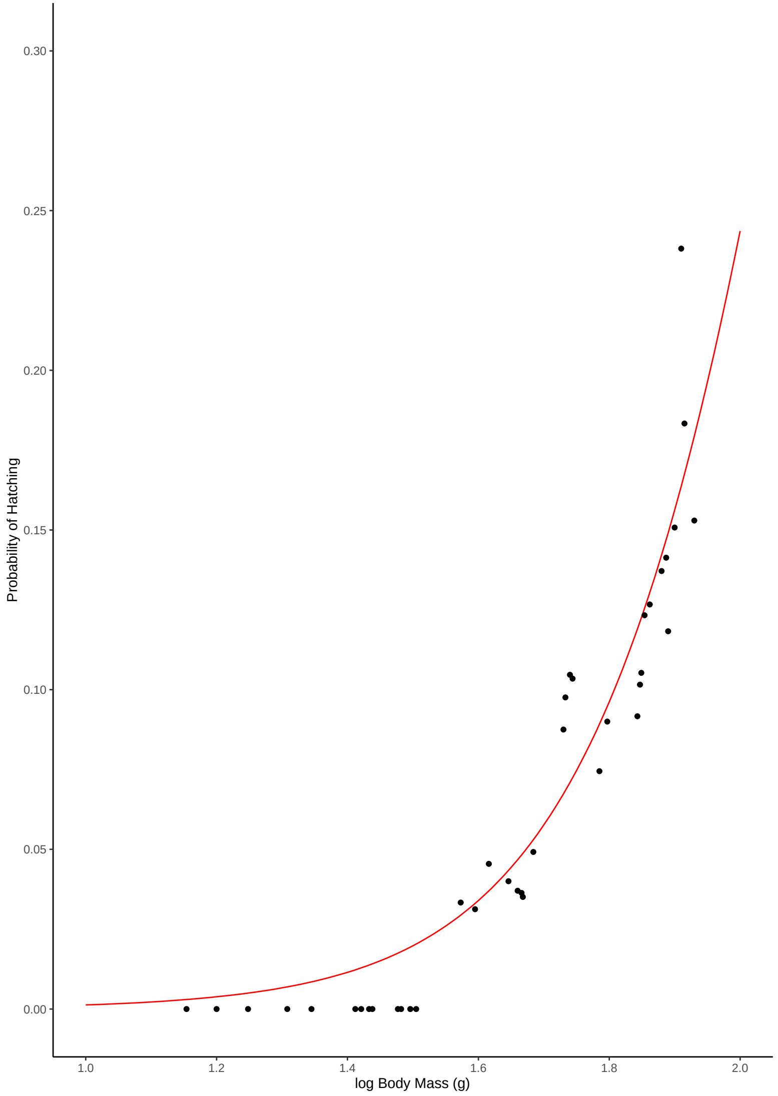
Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.21468  -0.46512  -0.07996   0.00000   2.76868

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 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

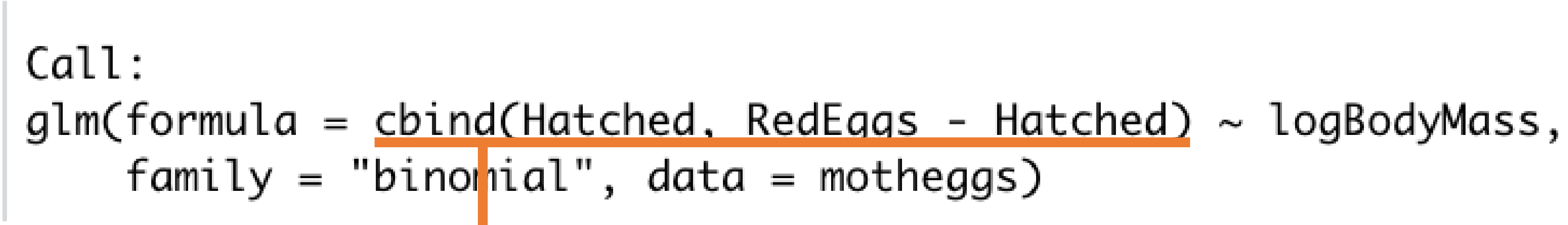
    Null deviance: 85.659  on 28  degrees of freedom
Residual deviance: 19.372  on 27  degrees of freedom
AIC: 124.31

Number of Fisher Scoring iterations: 4
```



Model Formula

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



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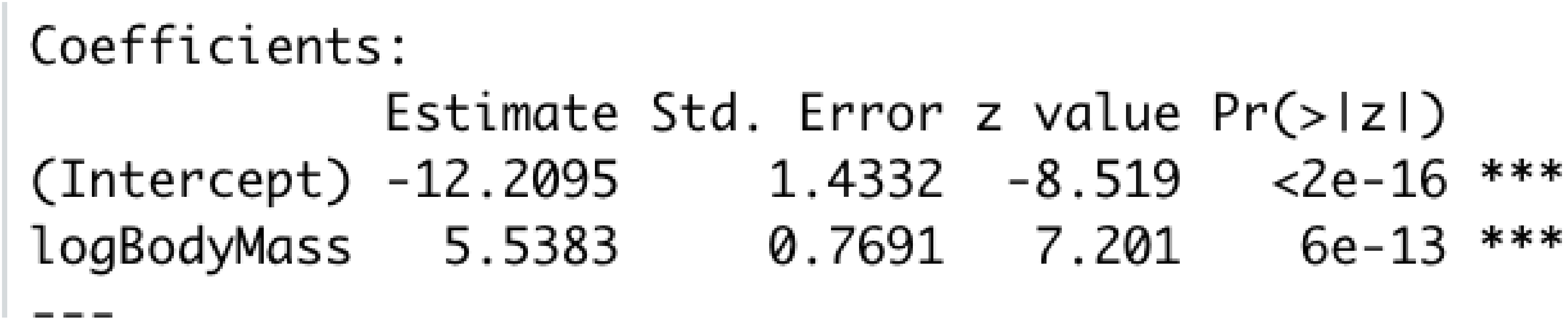
```

$$\frac{number\ of\ eggs\ hatched}{number\ of\ eggs\ not\ hatched} \longrightarrow \ln\left(\frac{k}{n-k}\right)$$

Interpreting Coefficients



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---
```

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

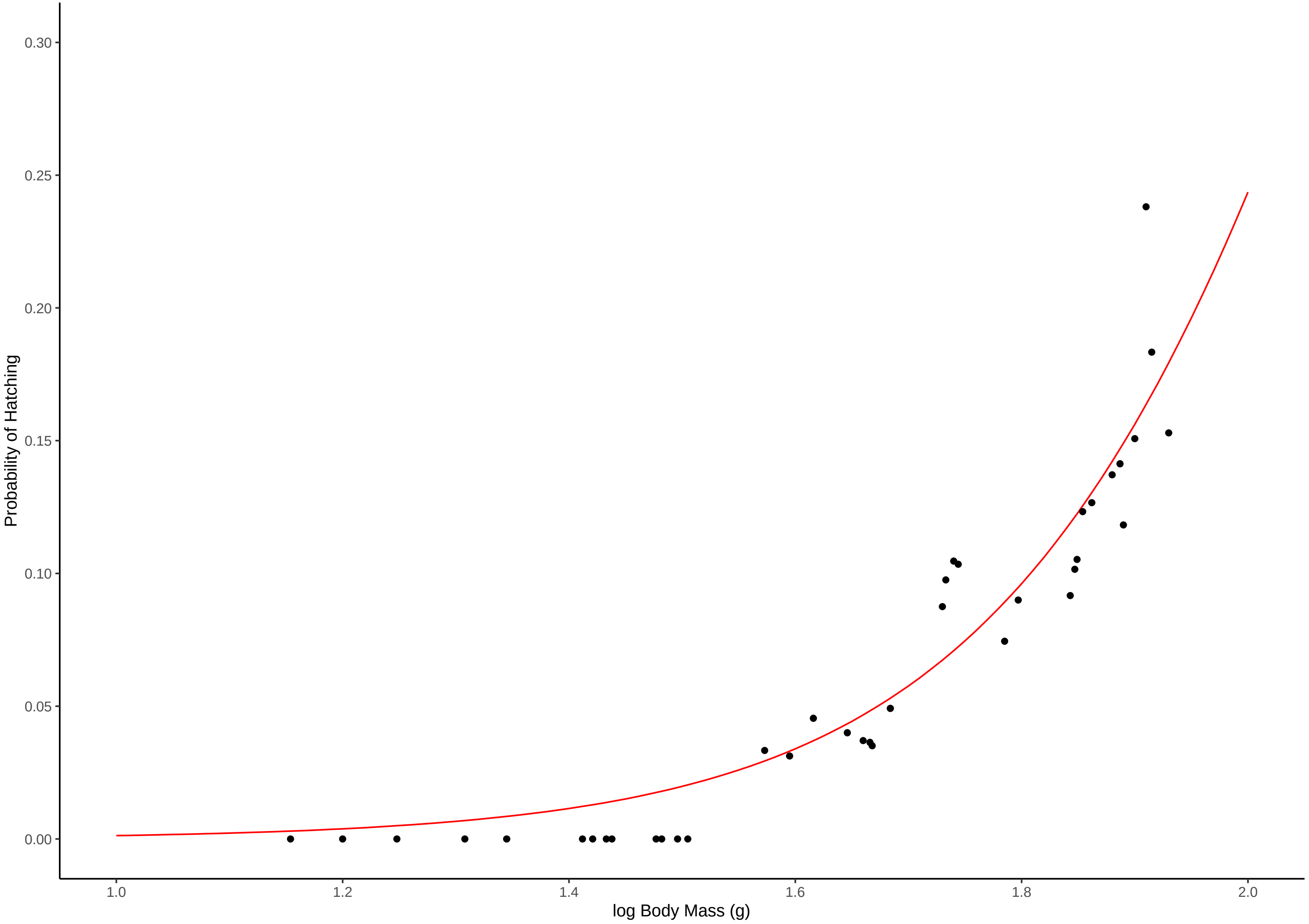
OR

- For a one log increase in body mass the odds of a moth egg hatching is 254.68 more likely

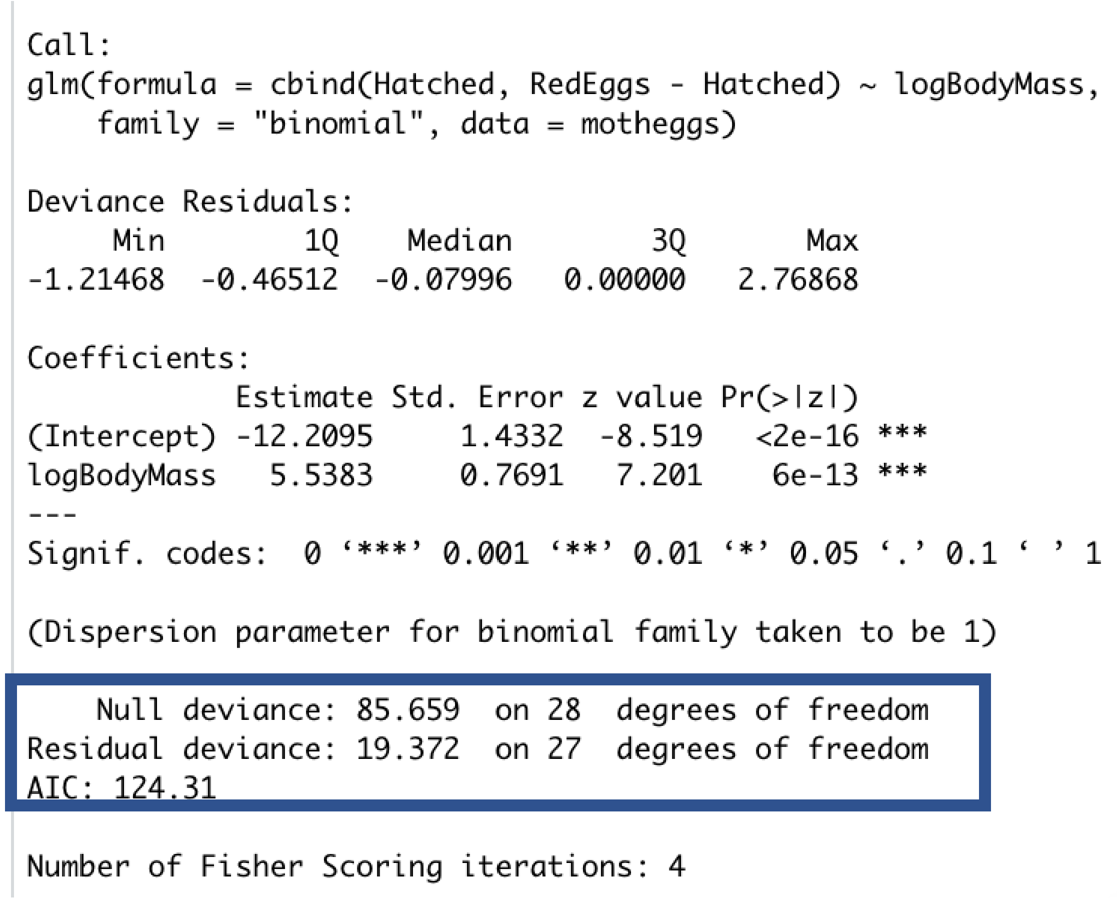
We could find the flip

$$abs\left(\frac{-\beta_0}{\beta_1}\right) = \frac{-12.2095}{5.5383} = -2.20 = 2.20$$

- This is problematic as we extrapolating beyond our data, i.e. no moth weighed more that 2.20 logs and 0.5 probability is outside of the y-axis range



Pseudo R^2 and Goodness-of-Fit



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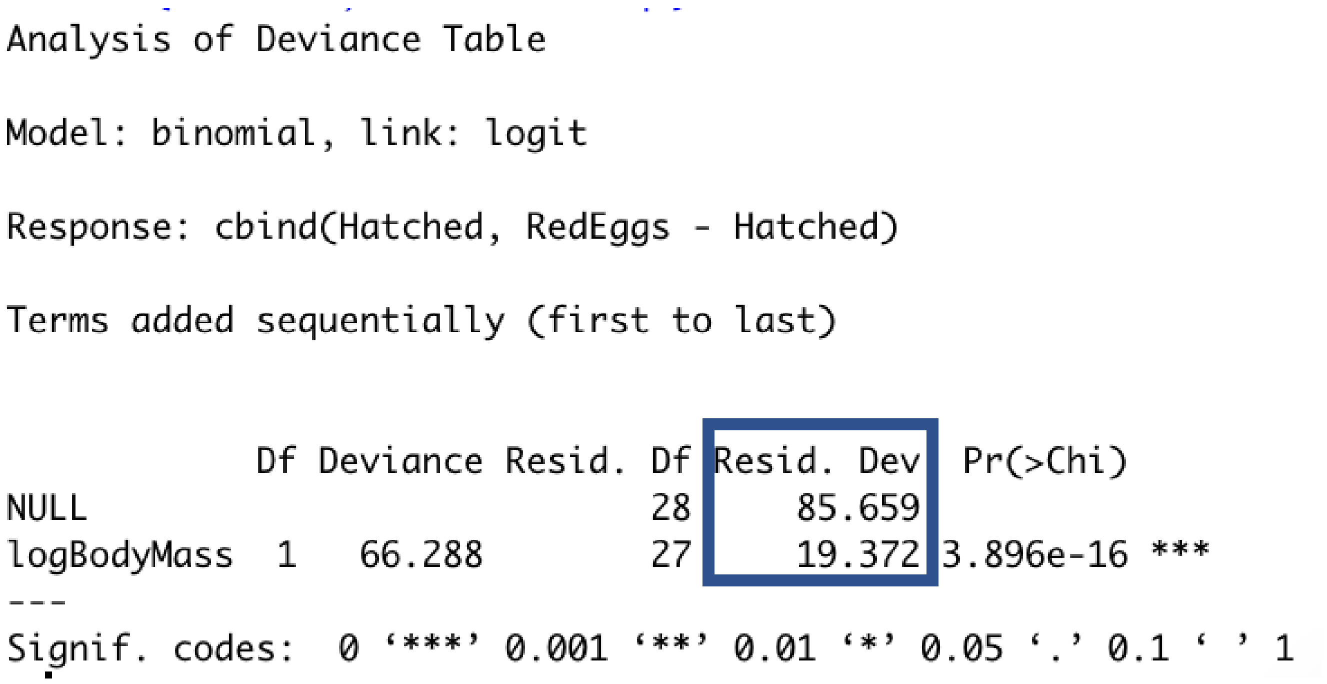


```
Analysis of Deviance Table

Model: binomial, link: logit

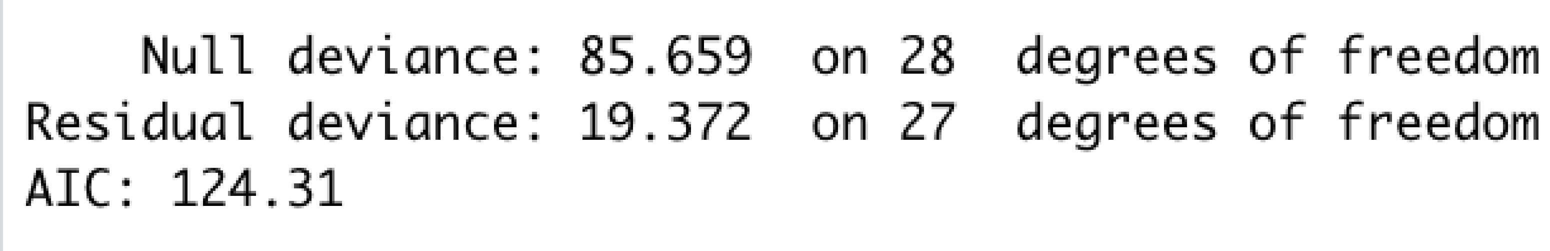
Response: cbind(Hatched, RedEggs - Hatched)

Terms added sequentially (first to last)


            Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
NULL                           28     85.659
logBodyMass  1   66.288        27     19.372 3.896e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

- Goodness-of-fit:
  - pseudo-R^2: $1 - \left({}^{19.37}/_{85.66}\right) = 0.77$

Model Validation



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

- $\left({}^{19.372}/_{27}\right) = 0.71$ → **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 [mixed models]

Another Example – Deer Data

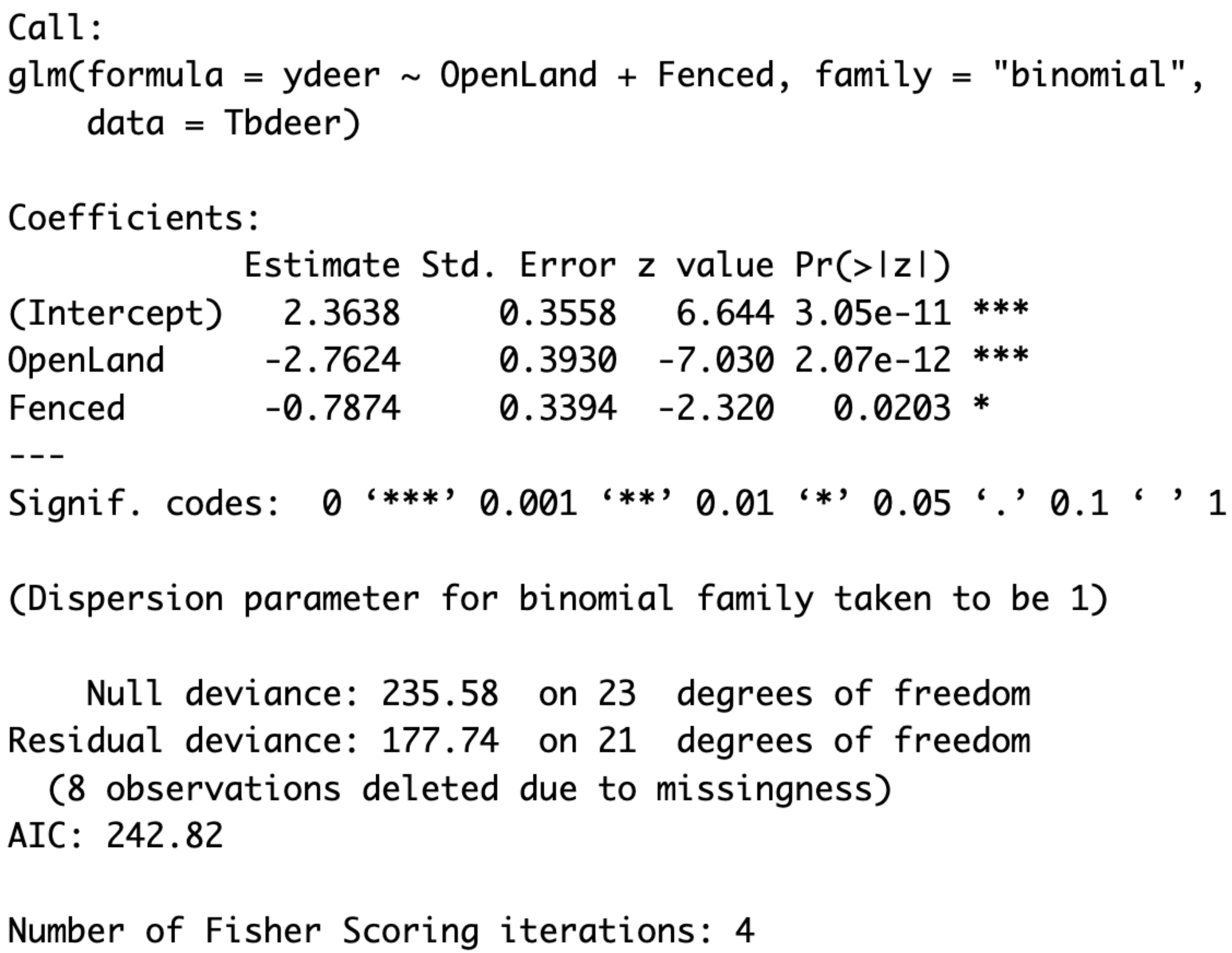
- Parasite infection *Elaphostrongylus cervi* of red deer

- Measured as number of individuals infected by the parasite

- Explanatory variables:
  - Fenced (yes or no)
  - % open land, scrubs and pine plantation
  - Number of *Quercus* plants per area

- Hypothesis:
  - % open land has a negative impact on parasite burden
  - Fencing decreases parasite infection

Another Example – Deer Data



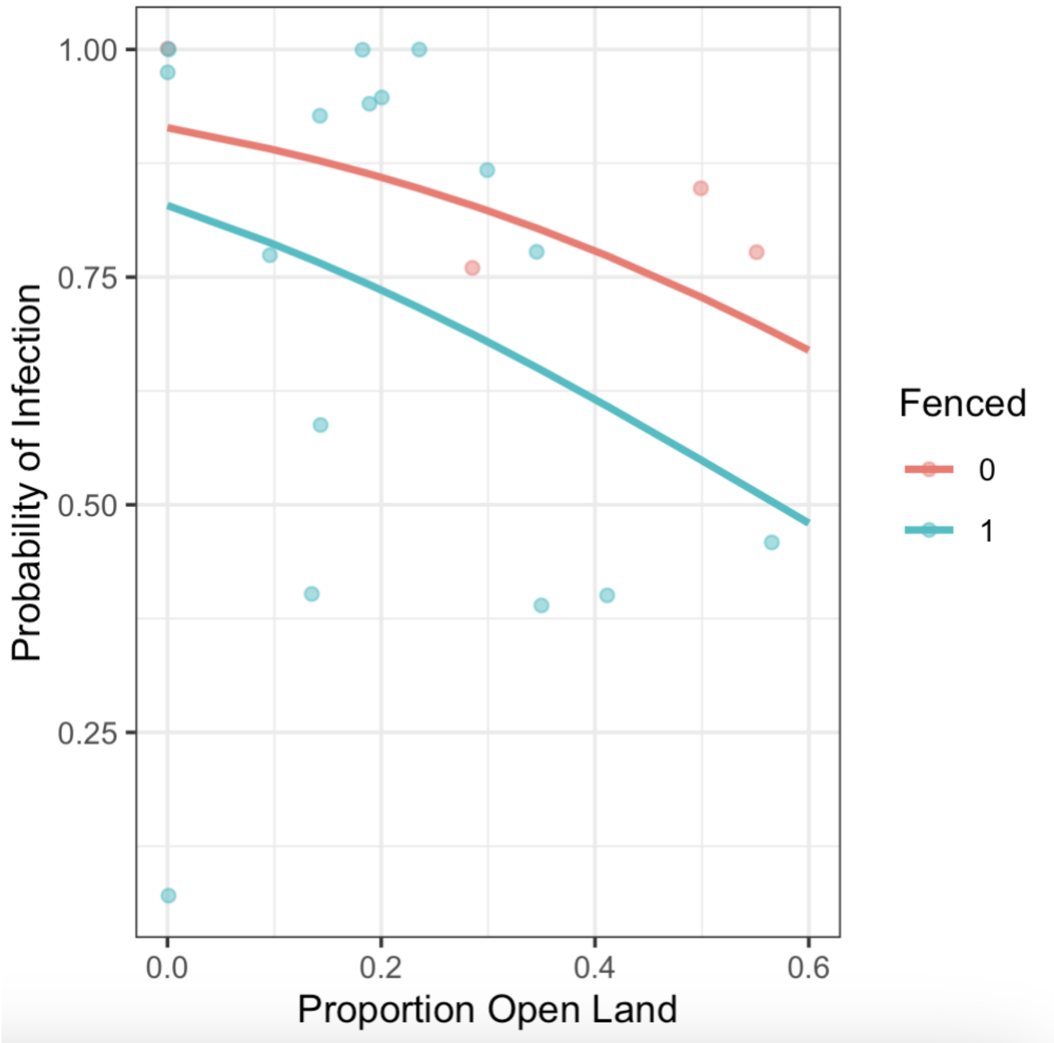
```
Call:
glm(formula = ydeer ~ OpenLand + Fenced, family = "binomial", 
    data = Tbdeer)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)    
(Intercept)   2.3638     0.3558   6.644 3.05e-11 ***
OpenLand     -2.7624     0.3930  -7.030 2.07e-12 ***
Fenced       -0.7874     0.3394  -2.320   0.0203 *  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 235.58  on 23  degrees of freedom
Residual deviance: 177.74  on 21  degrees of freedom
  (8 observations deleted due to missingness)
AIC: 242.82

Number of Fisher Scoring iterations: 4
```



Another Example – Deer Data

- What are the model equations for:

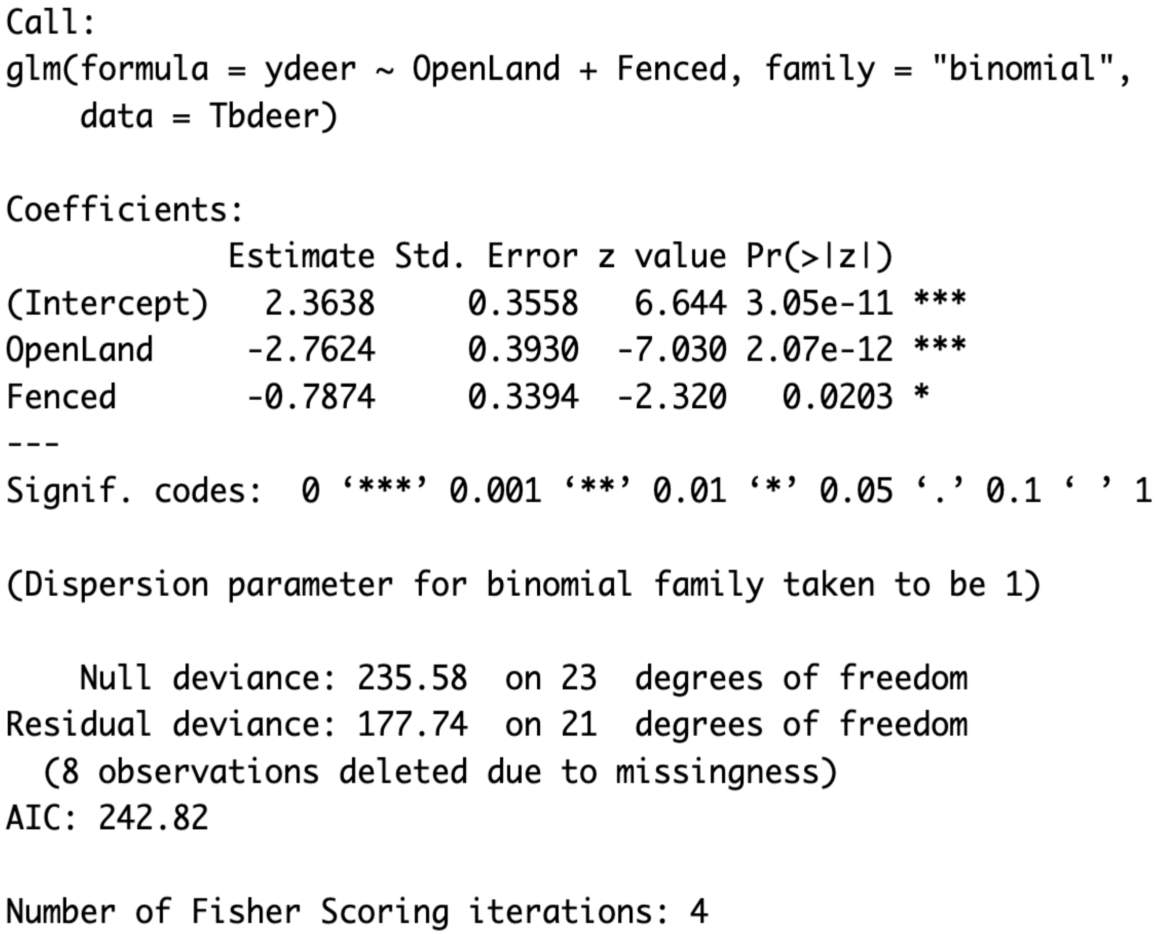
- Unfenced:

$$\ln\left(\frac{p}{1-p}\right) = 2.37 - 2.76\ * OpenLand$$

- Fenced:

$$\ln\left(\frac{p}{1-p}\right) = 2.37 - 2.76\ * OpenLand - 0.79$$

$$\ln\left(\frac{p}{1-p}\right) = 1.58 - 2.76\ * OpenLand$$



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Another Example – Deer Data

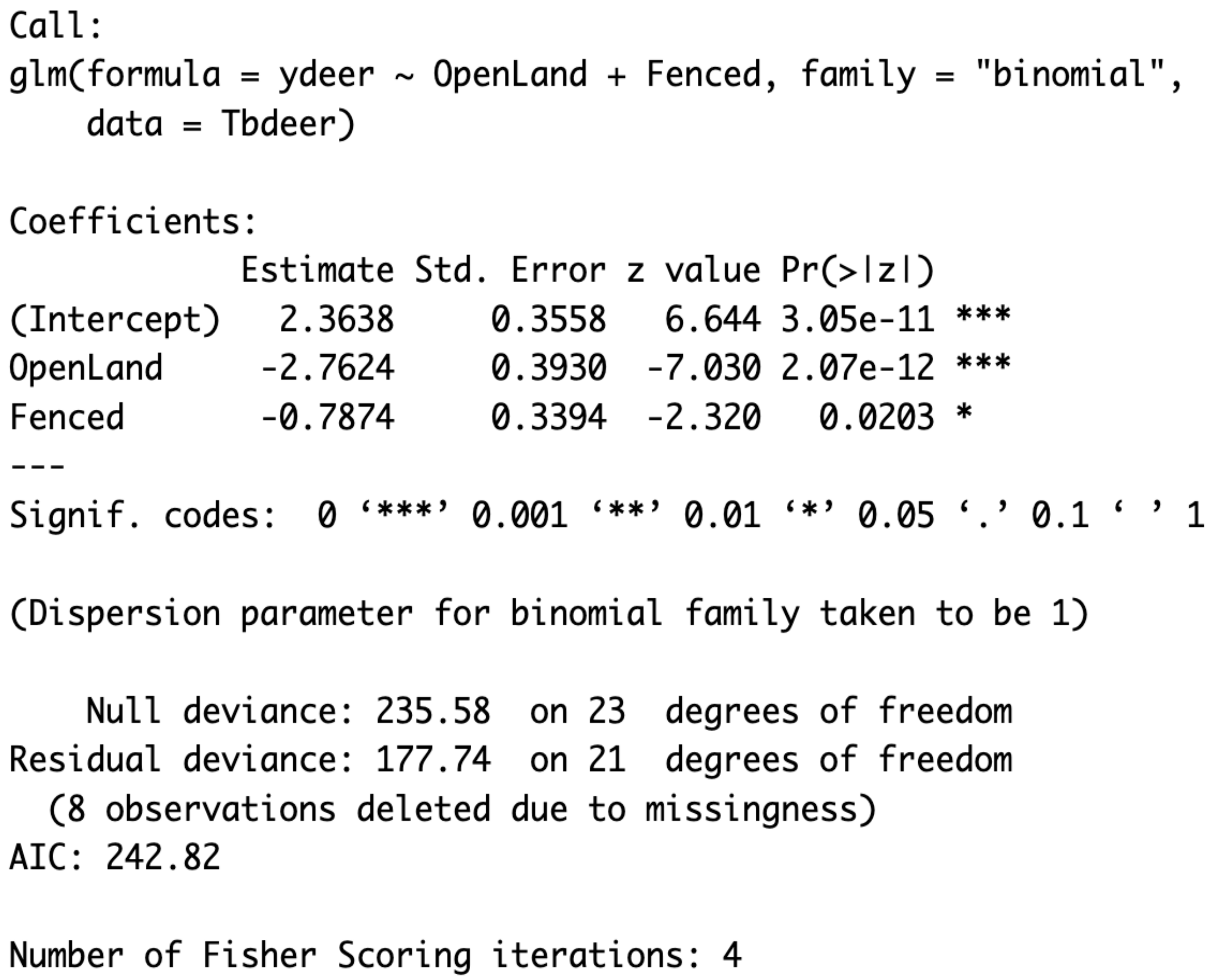
- What are the flip points for:

- Unfenced:

$$abs\left(\frac{2.37}{-2.76}\right) = 0.86$$

- Fenced:

$$abs\left(\frac{1.58}{-2.76}\right) = 0.57$$



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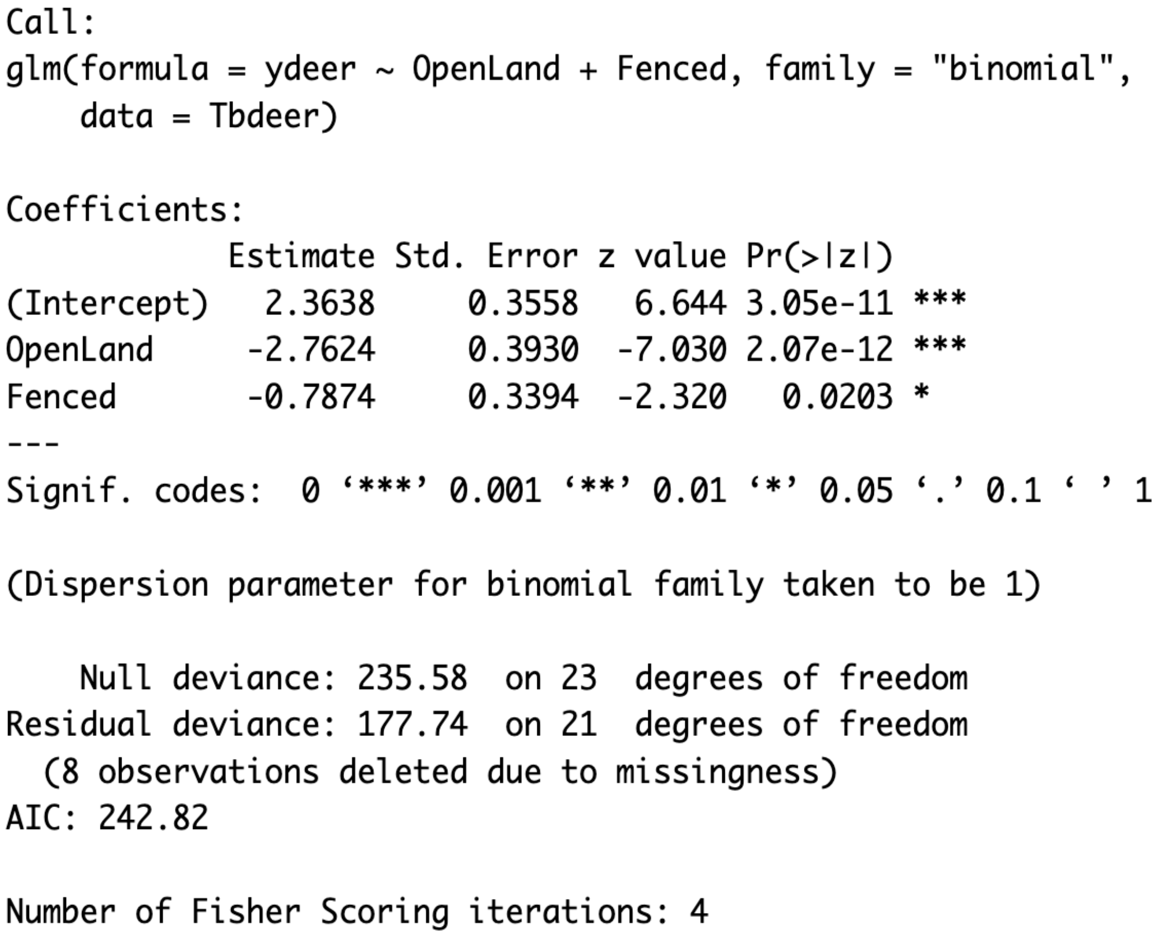
$$\ln\left(\frac{p}{1-p}\right) = 1.58 - 2.76\ * OpenLand$$

- R-squared: $1 - \left(\frac{177.74}{235.58}\right) = 0.25$
- Dispersion parameter: $177.74/21 = 8.46$



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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
- All generalized linear models can include random effects to address to non-independence and/or correct for overdispersion