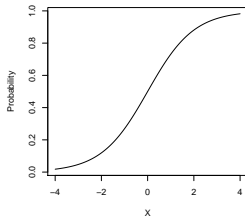


Logistic Regression

The Logistic Curve for Probabilities



The Logistic Function

$$p = \frac{e^{(a+bx)}}{1 + e^{(a+bx)}}$$

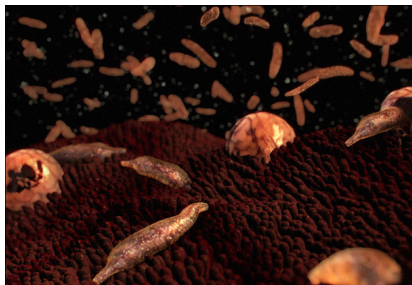
The Log Odds

$$a + bx = \text{Log} \frac{p}{1 - p}$$

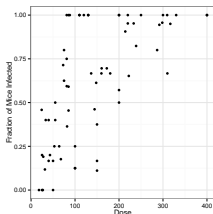
The Odds

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

Cryptosporidium



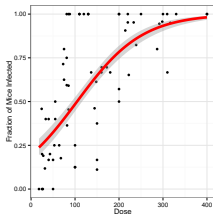
Fraction of Mice Infected = Probability of Infection



Two Different Ways of Writing the Model

```
# 1) using Heads, Tails
glm(cbind(Y, N-Y) ~ Dose, data=crypto, family=binomial)
#
#
# 2) using weights as size parameter for Binomial
glm(Y/N ~ Dose, weights=N, data=crypto, family=binomial)
```

The Fit Model



The Fit Model

```
#  
# Call:  
# glm(formula = cbind(Y, N - Y) ~ Dose, family = binomial, data = crypt  
#  
# Deviance Residuals:  
#   Min       1Q   Median       3Q      Max   
# -3.953  -1.244   0.233   1.553   3.601   
#  
# Coefficients:  
#             Estimate Std. Error z value Pr(>|z|)      
# (Intercept) -1.40777    0.14848   -9.48  <2e-16      
# Dose         0.01347    0.00105   12.87  <2e-16      
#  
# (Dispersion parameter for binomial family taken to be 1)  
#  
#   Null deviance: 434.34  on 67  degrees of freedom  
# Residual deviance: 200.51  on 66  degrees of freedom  
# AIC: 327  
#
```

The Meaning of a Logit Coefficient

Logit Coefficient: A 1 unit increase in a predictor = an increase of β increase in the log-odds ratio of the response.

$$\text{Log Odds Ratio} = \text{Log} \left(\frac{p_1}{1-p_1} / \frac{p_2}{1-p_2} \right)$$

We need to know both p_1 and β to interpret this.

The Meaning of a Logit Coefficient

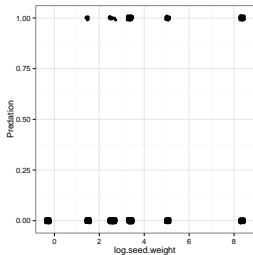
$$\text{Log Odds Ratio} = \text{Log} \left(\frac{p_1}{1-p_1} / \frac{p_2}{1-p_2} \right)$$

If $p_1 = 0.5$, Odds Ratio = 1

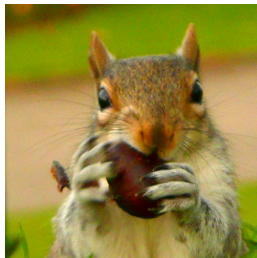
With $\beta = 0.01347$, we multiply 1 by $e^{0.01347}$.

The new odds ratio is 1.013561, which means $p=0.5033674$

What if we Only Have 1's and 0's?



Seed Predators



<http://denimandtweed.com>

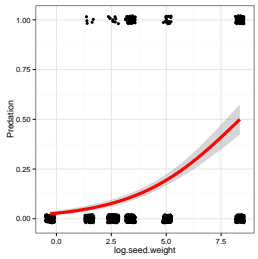
A Quick Note on Within and Transformation

```
seeds <- within(seeds, {  
  log.seed.weight <- log(seed.weight)  
})
```

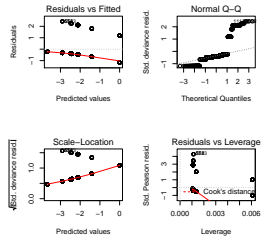
The GLM

```
seed.glm <- glm(Predation ~ log.seed.weight,  
  data=seeds, family=binomial)
```

Fitted Seed Predation Plot



Diagnostics Look Odd Due to Binned Nature of the Data



Binned Residuals Should Look Spread Out

