

Generalised Linear Models 2: Modelling Binary and Proportional Data

Michael Noonan

March 15, 2021

Biol 520C: Statistical modelling for biological data

1. Housekeeping
2. Generalised Linear Models Review
3. Logistic Regression
4. Logistic Regression on Presence-Absence Data
5. Logistic Regression on Proportion Data
6. Where to from here?

Housekeeping



- Practical 08 is up and due next Tuesday.

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- If you haven't already picked a dataset for Paper 2 I'd recommend giving it some thought.

Generalised Linear Models

Review



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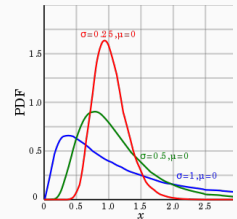
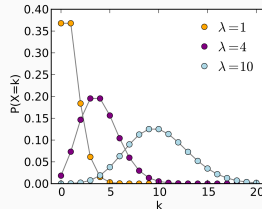
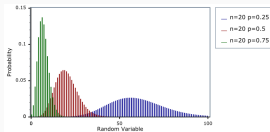
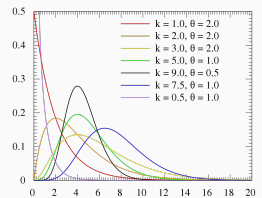
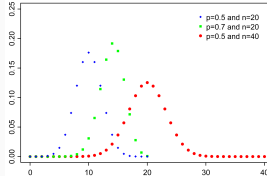
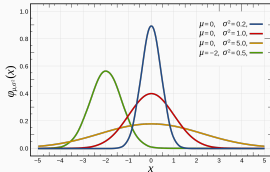
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We then saw how to fit GLMs to count data in R using the `glm()` function.



Because R functions streamline the process of fitting GLMs, the key step that's left in your hands is knowing when you will need to switch from a Gaussian model to a GLM, and identifying the correct distribution



Today's lecture



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Logistic Regression



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4. The observations are independent.
5. There is no collinearity in the independent variables.



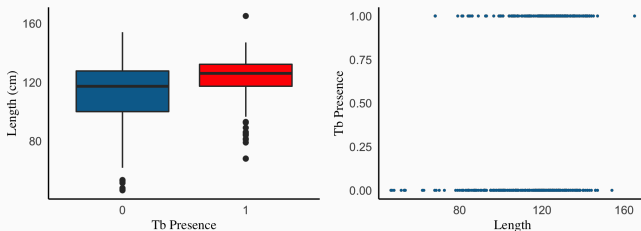
If you are going to be working with 0-1 data a lot in your career, you might consider reading a book focused entirely on this subject. A good place to start would be:

Agresti, A. (2018). An introduction to categorical data analysis. John Wiley & Sons.

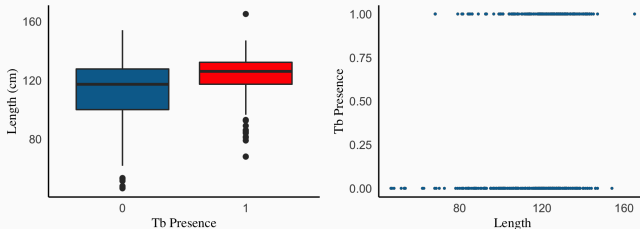
Logistic Regression on Presence-Absence Data



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With these data we're interested in knowing what whether body size related to Tb prevalence.





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library(nlme)

Fit_Linear <- gls(Tb ~ Length,
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summary(Fit_Linear)
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Generalized least squares fit by maximum likelihood

Model: Tb ~ Length

Data: data

	AIC	BIC	logLik
	680.8635	693.4711	-337.4317

Coefficients:

	Value	Std.Error	t-value	p-value
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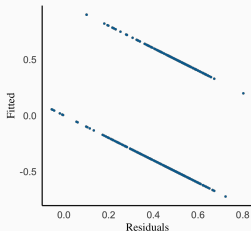
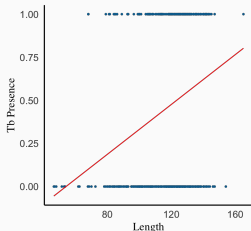
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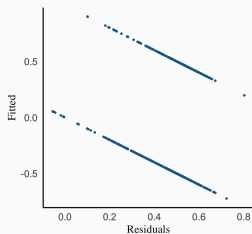
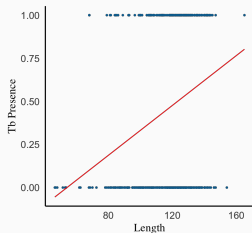
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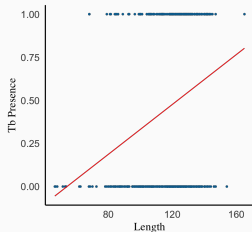
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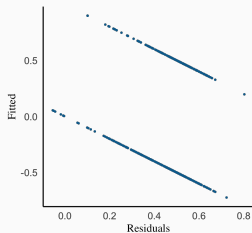


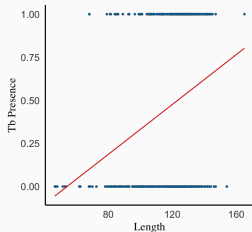
Linear regression on 0-1 data



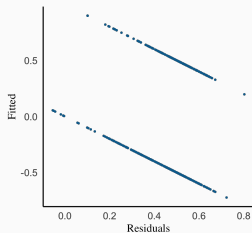


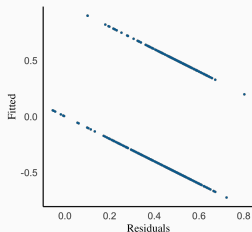
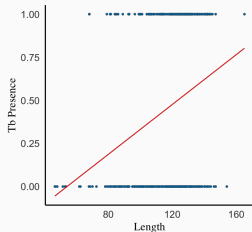
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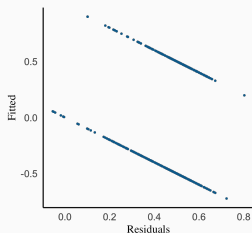
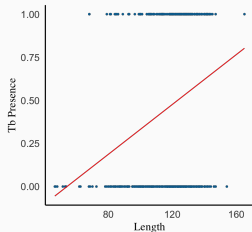


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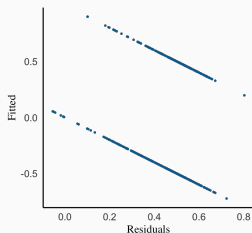
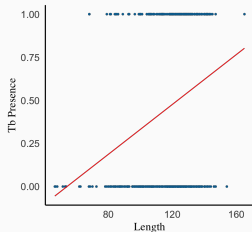
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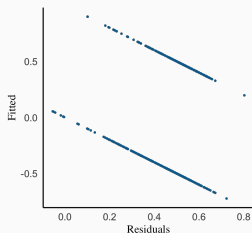
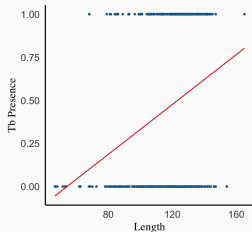


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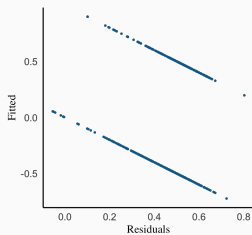
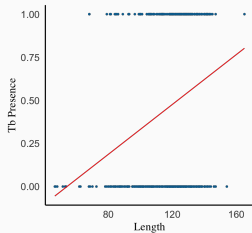
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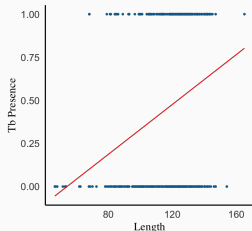
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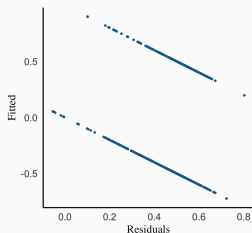
Can a boar have 0.45 Tb?

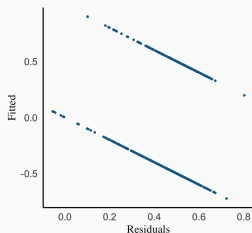
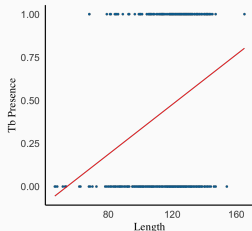
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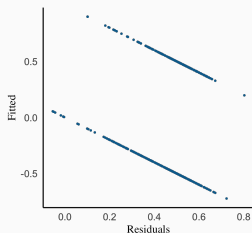
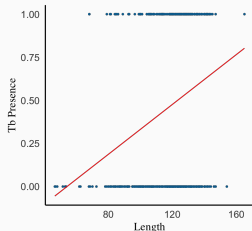
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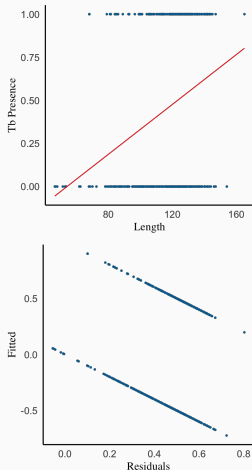
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We need a deterministic function that maps the values between 0 and 1, and a dist. that makes more sense.

Step 1: Distributional assumption



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Can you think of a good candidate for 0,1 data?

The binomial distribution describes the probability of obtaining k yes/no successes in a sample of size n , or in other words, the distribution of the number of successful trials among a defined number of trials.

Parameters: n and p

Type: Discrete

Biological scenarios: Mark recapture data, live vs dead survival data, killed by a predator or not, yes/no behavioural outcomes, anything with a discrete yes/no outcome.

PMF: $\binom{n}{k} p^k (1-p)^{n-k}$

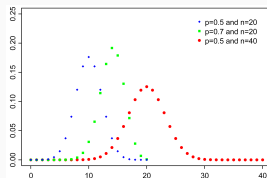
where

$$\binom{n}{k} = \frac{n!}{k!(n-k)!}$$

Range: discrete ($0 \leq x \leq n$)

Mean: np

Variance: $np(1-p)$



Step 2: Specify the deterministic model



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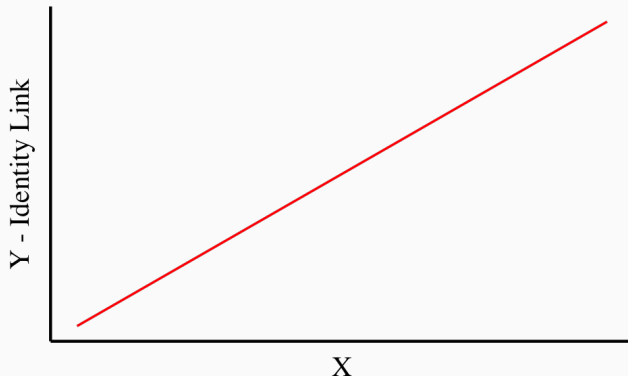
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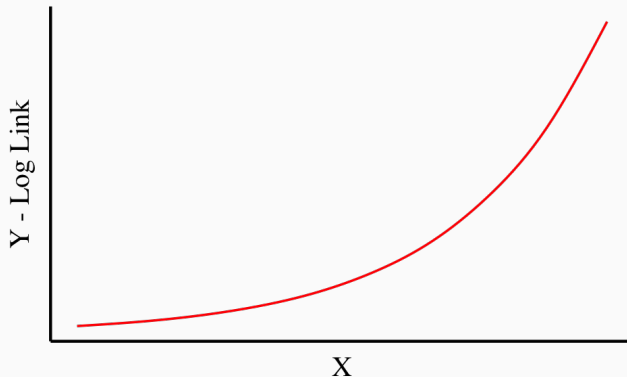
Standard linear regr. with an 'identity link' maps values between $-\infty, \infty$.

$$\mu = \beta_0 + \beta_1 X$$



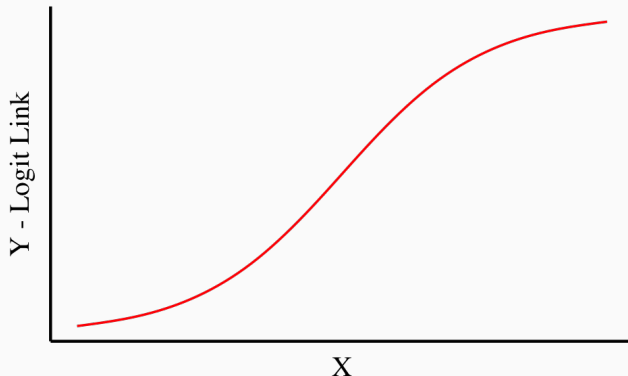
Last lecture we saw how a 'log link' maps values between $0, \infty$.

$$\mu = e^{\beta_0 + \beta_1 X}$$



The 'logit link' is a link function that maps values between 0, 1. (How?)

$$\mu = \frac{e^{\beta_0 + \beta_1 X}}{1 + e^{\beta_0 + \beta_1 X}}$$





Now we have all the pieces we need for fitting our GLM:

$$Y_i \sim \text{Binomial}(1, \pi_i) \quad E(Y_i) = \pi_i \quad \text{and} \quad \text{Var}(Y_i) = \pi_i \times (1 - \pi_i)$$

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summary(Fit_Logistic)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.137107    0.695381  -5.949 2.69e-09
Length       0.033531    0.005767   5.814 6.09e-09
---

(Dispersion parameter for binomial family taken to be
1)

Null deviance: 681.25  on 493  degrees of freedom
Residual deviance: 641.23  on 492  degrees of freedom
AIC: 645.23
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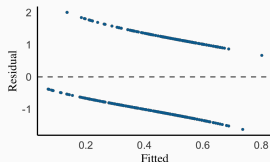
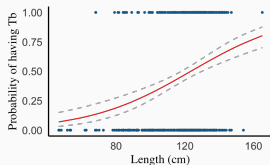
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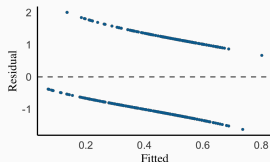
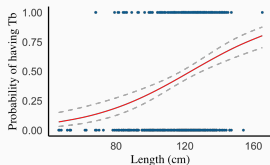
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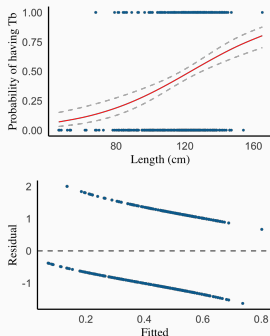
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In logistic regression Pseudo- R^2 are almost always going to be low. Not very informative!





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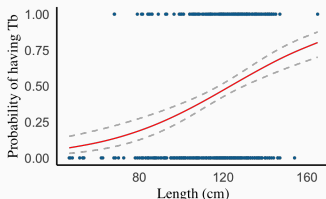
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```
library(DAAG)
```

```
CVbinary(Fit_Logistic)
```

```
Fold: 3 8 4 5 9 10 2 6 7 1
```

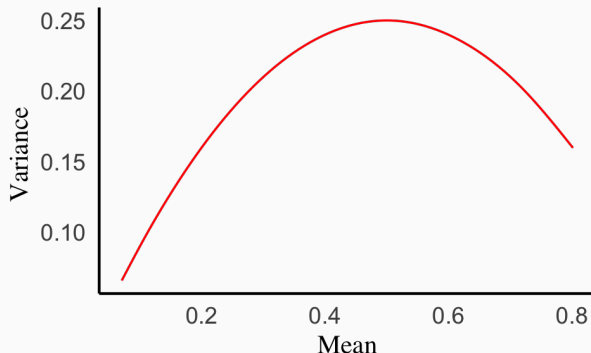
```
Internal estimate of accuracy = 0.615
```

```
Cross-validation estimate of accuracy = 0.615
```



For our model the mean and variance are given by:

$$E(Y_i) = \pi_i \quad \text{and} \quad \text{Var}(Y_i) = \pi_i \times (1 - \pi_i)$$



Variance is largest for intermediate values of π_i .

Logistic Regression on Proportion Data



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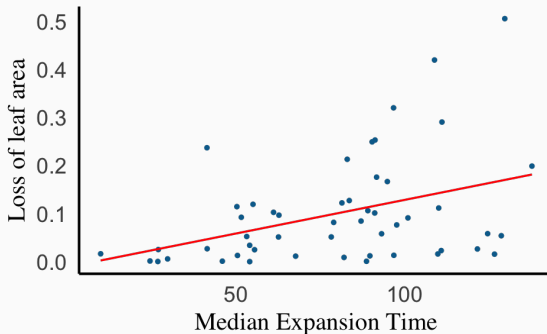
Proportions scale between 0-1, but can take any value between these limits.

Most of the time, ecologists model proportion data using an $\arcsin(\sqrt{p})$ transformation, but this is not an ideal solution:

Warton, D. I., & Hui, F. K. (2011). The arcsine is asinine: the analysis of proportions in ecology. *Ecology*, 92(1), 3-10.



This example forms part of a paper asking whether plant species with small leaves have shorter expansion times than large leaved counterparts (Moles & Westoby 2000). The data we're going to work with are the percentage loss of leaf area in relation to median expansion time.



Note A linear regression shows a significant relationship



All the pieces we need for our GLM:

Leaf Loss_{*i*} $\sim \text{Binomial}(1, \pi_i)$ $E(Y_i) = \pi_i$ and $\text{Var}(Y_i) = \pi_i \times (1 - \pi_i)$

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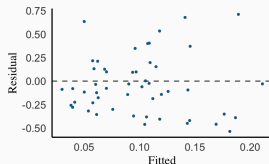
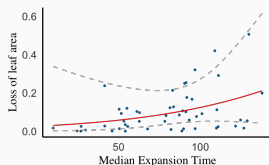
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What to write in a paper



THE UNIVERSITY OF BRITISH COLUMBIA
Okanagan Campus

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For example, for our boar data we would say that we assumed our data were binomially distributed and that we modelled them using a logit link:

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Present all of your model outputs in a table, put diagnostic plots in supp. material, if you performed model selection make it clear how you got from A to B.

Where to from here?



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We covered log links and logit links, but there are a number of different link functions that you can use when fitting GLMs. The General idea stays the same, use the one that maps the response variable onto the right scale (e.g., don't use a log-link for a binomial GLM).



We also saw how if our models are of the form:

$$Y_i = \beta_0 + \beta_1 X_i + \varepsilon_i, \quad \varepsilon_i \sim \mathcal{N}(0, \sigma_i^2)$$

modifying the off-diagonals of the correlation matrix can correct for various forms of autocorrelation.

$$V = \sigma^2 \underbrace{\begin{bmatrix} 1 & 0 & \cdots & 0 \\ 0 & 1 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & 1 \end{bmatrix}}_{\text{correlation matrix}}$$

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... but because we're working with different distributions now those approaches don't translate cleanly.



If you find yourself with zero-inflated data you might need to use mixture models that are comprised of combinations of different distributions. See Zuur et al. (2009) Ch. 11.