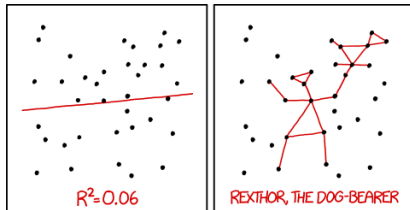


Generalised linear models

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$$y_i = \alpha + \sum_{k=1}^p x_{ik} \beta + \epsilon_i \quad (1)$$



I DON'T TRUST LINEAR REGRESSIONS WHEN IT'S HARDER TO GUESS THE DIRECTION OF THE CORRELATION FROM THE SCATTER PLOT THAN TO FIND NEW CONSTELLATIONS ON IT.

So far: linear models

$$y_i = \alpha + x_i\beta + \epsilon_i \quad (2)$$

- ▶ y_i the data
- ▶ $\alpha + x_i\beta$ the systematic component: “linear predictor”
- ▶ ϵ_i the random component: “error”



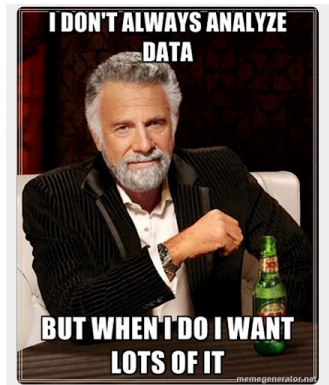
and don't range $(-\infty, \infty)$

- ▶ Linear regression
- ▶ Logistic regression
- ▶ Probit regression
- ▶ Complementary log-log regression
- ▶ Log-linear regression
- ▶ Gamma regression

Generalised linear models (2)

GLMs extend the linear model framework to address:

- ▶ Variance changes with the mean
- ▶ Range of \mathbf{y} is bounded



The basis of many statistical models in Biology

Many results are now asymptotic.

But no explicit error term

$$\mathcal{L}(y_i; \Theta) = \exp\left\{\frac{y_i \eta_i - b(\eta_i)}{a(\phi)} + c(y_i, \phi)\right\} \quad (3)$$

- ▶ for some known functions $a(\cdot)$, $b(\cdot)$ and $c(\cdot)$
- ▶ for normal distribution: $\eta_i = \mu_i$, $a(\phi) = \sigma^2$, $b(\eta_i) = -\mu^2/2$,
 $c(y_i, \phi) = -\frac{1}{2}\{y^2/\sigma^2 + \log(2\pi\sigma^2)\}$

as long as $\mathbb{E}(\epsilon_i) = 0$.

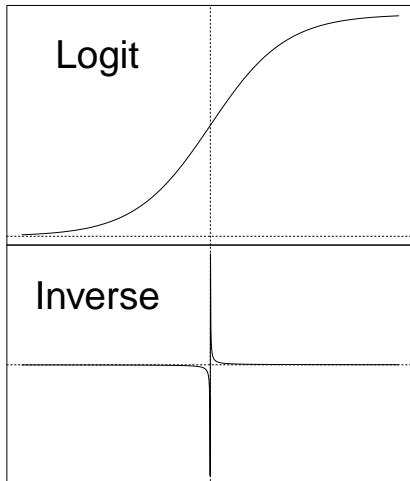
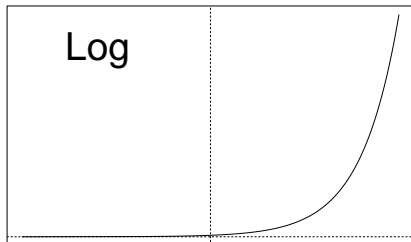
Generalised linear model

$$\begin{aligned} g\{\mathbb{E}(y_i|x_i)\} &= \eta_i = \alpha + x_i\beta \\ \mathbb{E}(y_i|x_i) &= g^{-1}(\eta_i) = g^{-1}(\alpha + x_i\beta) \end{aligned} \tag{8}$$

$g(\cdot)$ is the **link function**

The link function

- ▶ Is a smooth/monotone function
- ▶ Has an inverse $g^{-1}(\cdot)$
- ▶ Restricts the scale
- ▶ $g(\cdot)$ can be e.g.



Variance function

Variance changes with the mean:

$$\text{var}(y_i; \mu_i, \phi) = \frac{\partial^2 g(\eta_i)}{\partial \eta_i^2} a(\phi)$$

- ▶ ϕ : the dispersion parameter, constant over observations
 - ▶ Fixed for some response distributions
- ▶ $a(\phi)$ is a function of the form ϕ/w_i (McCullagh and Nelder 1989)

Assumptions

- ▶ No outliers
- ▶ Independence
- ▶ Correct distribution
- ▶ Correct link function
- ▶ Correct variance function (implied by previous two)

More on checking assumptions in GLMs tomorrow.

Fitting GLMs

Unlike LMs, parameters in GLMs need to be estimated **iteratively**.

- ▶ More difficult to fit
- ▶ Requires numerical *optimisation*
- ▶ Susceptible to local convergence

Popularisation of GLMs

Nelder and Wedderburn (1972) proposed GLMs as a class to unify different forms of regression.

- ▶ Linear regression
- ▶ Probit regression
- ▶ Logistic regression
- ▶ Log-linear regression
- ▶ Gamma regression
- ▶ Inverse Gaussian regression

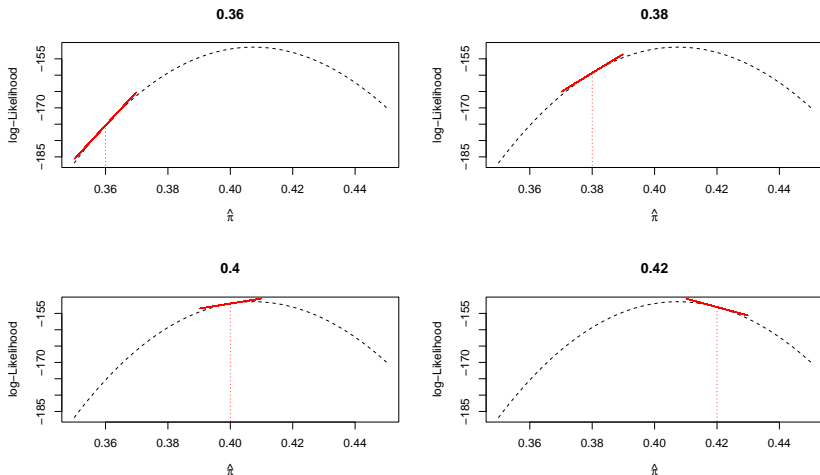
McCullagh and Nelder (1989) wrote a book that popularised the class.

Fitting GLMs

Easy and quick in R.

Mathematically more involved than LMs.

Finding the maximum (from day 1)



We need a good algorithm to find the maximum!

Finding the maximum: GLMs

$$\Theta^{t+1} = \Theta^t + \frac{\partial^2 \log\{\mathcal{L}(\mathbf{y}_i; \Theta^t)\}^{-1}}{\partial \Theta \partial \Theta^\top} \frac{\partial \mathcal{L}(\mathbf{y}_i; \Theta^t)}{\partial \Theta}$$

- ▶ (Newton-Raphson) Can get quite expensive to evaluate.
- ▶ Nelder and Wedderburn (1972) instead suggested an algorithm that fits a LM repeatedly.

Iteratively reweighted least squares (IRLs)

- 1) Start at some (decent) point (e.g., $\hat{\boldsymbol{\eta}} = \mathbf{y} + \boldsymbol{\epsilon}$) (Wood 2017)
- 2) Set $\mathbf{z}^t = \boldsymbol{\eta} + \frac{\partial \hat{\boldsymbol{\eta}}}{\partial g^{-1}(\hat{\boldsymbol{\eta}})} \{\mathbf{y} - g^{-1}(\hat{\boldsymbol{\eta}})\} / a(g^{-1}(\hat{\boldsymbol{\eta}}))$
- 3) weight with $\mathbf{w} = a(g^{-1}(\hat{\boldsymbol{\eta}})) / \{\frac{\partial \hat{\boldsymbol{\eta}}}{\partial g^{-1}(\hat{\boldsymbol{\eta}})}^2 \text{var}(\mathbf{y}_i)\}$
- 4) Fit weighted LM with \mathbf{z} as pseudodata and \mathbf{w} as weights
- 5) Repeat until convergence

(details omitted)

And that is the day researchers started liking GLMs.

Iteratively reweighted least squares (IRLs)

Prevents having to do numerical optimisation.

The end?



AND THEY
LIVED HAPPILY
EVER AFTER

Why is stuff this important?

- 1) A basic (mathematical) understanding helps apply methods correctly.
- 2) GLMs may not always converge to the MLE. Then, you will get warnings/errors.
- 3) If you understand them, you might know what to do! Similar problems in a lot of more complex models (e.g., GLMMs).

Often used GLMs in ecology

- ▶ Binomial: occurrence/counts. Presence of species, number of germinated seeds out of a total
- ▶ Poisson: counts. Number of fish caught
- ▶ Negative binomial (fixed dispersion): counts. Overdispersed fish.
- ▶ Gamma: (positive) continuous. Body size
- ▶ Ordinal (cumulative link). Plant cover classes

Binomial:

in R

- ▶ Similar to the `lm()` function!
- ▶ Now the `glm()` function

A linear regression:

```
model <- glm(y ~ x, family = gaussian(link = identity), data = data)
```

A glm:

```
model <- glm(y ~ x, family = poisson(link = log), data = data)
```

Output

```
##
## Call:
## glm(formula = y ~ X, family = "poisson")
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.5965      0.1820   3.278 0.001045 **
## X            0.6554      0.1810   3.621 0.000294 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 45.250  on 19  degrees of freedom
## Residual deviance: 31.486  on 18  degrees of freedom
## AIC: 78.867
##
## Number of Fisher Scoring iterations: 5
```

Back-transformation

- ▶ Confidence intervals can be back-transformed to the response scale
 - ▶ as long as we have “monotonicity” of the link function
- ▶ Standard errors cannot be back-transformed!

Intervals for $\hat{\mu}_i$

- ▶ Confidence intervals
- ▶ Prediction intervals

More on predicting tomorrow in the practical

Deviance

- ▶ LMs used RSS to quantify fit
- ▶ GLMs use deviance to quantify **lack of fit**
- ▶ Deviance $D(\mathbf{y}; \hat{\boldsymbol{\mu}})$ is different for every GLM.

Normal: $\sum_{i=1}^n (y_i - \hat{\mu}_i)^2$ Poisson: $2 \sum_{i=1}^n y_i \log(y_i / \hat{\mu}_i) - y_i + \hat{\mu}_i$

binomial: $2 \sum_{i=1}^n y_i \log(y_i / \hat{\mu}_i) + (N - y_i) \log\{(N - y_i) / (N - \hat{\mu}_i)\}$

gamma: $2 \sum_{i=1}^n -\log\{y_i / \hat{\mu}_i\} + (y_i - \hat{\mu}_i) / \hat{\mu}_i$

and so on.

- ▶ Measures (twice) difference to a model that perfectly fits the data (“saturated model”)
 - ▶ equal to RSS for linear regression
- ▶ Can be used for hypothesis testing, calculate $R^2_{deviance}$, and “deviance residuals”

(Dunn and Smyth 2021)

(omitted details)

Some resources

McCullagh and Nelder Dunn and Smyth Wood

more friendly - dunn and smyth (because in R) - free book john
fieberg - zuur

- ▶ Remember to bring all components together
- ▶ Parameter estimates, uncertainty, multiple predictors, interaction, model selection
- ▶ GLMs for when assumptions of LMs fail (which is very often)
- ▶ We covered components of GLMs here
- ▶ And how they are fitted in R
- ▶ Deviance and residuals