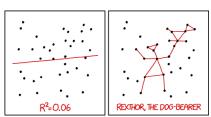
#### Generalised linear models

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## So far: linear models

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



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

$$y_i = \alpha + x_i \beta + \epsilon_i \tag{2}$$

- $y_i$  the data
- $ightharpoonup \alpha + x_i \beta$  the systematic component: "linear predictor"
- $ightharpoonup \epsilon_i$  the random component: "error"



## Key assumptions

- Linearity (straight line)
- Independence of errors
- Homoscedasticity (same variance for all errors)
- Normality (distribution of errors)

Real ecological data do not usually follow these assumptions

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

# Generalised linear models (GLMs)

GLMs as a framework were introduced by Nelder and Wedderburn (1972) uniting many different models. With a special focus on teaching statistics.

- 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 y is bounded



The basis of many statistical models in Biology

Many results are now asymptotic.

# Components of a GLM

- Systematic component:  $\eta$
- Random component: data/distribution)
- The link function: connects these components
  - This is not a data transformation
- The variance function

#### But no explicit error term

## GLM Likelihood

- We still use MLE for estimation
- But now a different likelihood function (in EF for fixed  $\phi$ )

All GLMs can be formulated as:

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

Previously:

$$\mathcal{L}(y_i; \Theta) = \frac{1}{\sigma\sqrt{2\pi}} \exp\left\{-\frac{1}{2} \frac{(y_i - \mu_i)^2}{\sigma^2}\right\} \tag{4}$$

Now:

$$\mathcal{L}(y_i; \Theta) = \exp\{\frac{y_i \eta_i - b(\eta_i)}{a(\phi)} + c(y_i, \phi)\}$$
 (5)

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

## The linear model

Writing the linear model:

$$y_i = \alpha + \mathbf{x}_i \boldsymbol{\beta} + \epsilon_i \sim \mathcal{N}(0, \sigma^2) \tag{6}$$

Is the same as:

$$\mathbb{E}(y_i|\mathbf{x}_i) = \alpha + \mathbf{x}_i\boldsymbol{\beta} \tag{7}$$

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

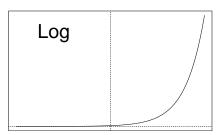
## Generalised linear model

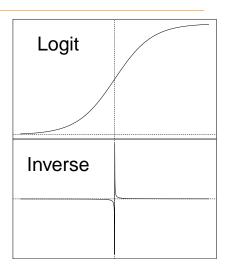
$$g\{\mathbb{E}(y_i|x_i)\} = \eta_i = \alpha + x_i\beta$$

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

 $g(\cdot)$  is the link function

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





## Variance function

Variance changes with the mean:

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

- lackbox  $\phi$ : the dispersion parameter, constant over observations
  - Fixed for some response distributions
- $lacktriangledown = a(\phi)$  is a function of the form  $\phi/w_i$  (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

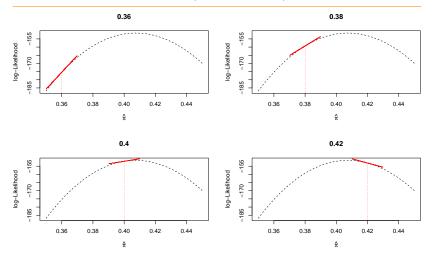
McCullagh and Nelder (1989) wrote a book that popularised the class.

# 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!

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

- (Newton-Rhapson) 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.,  $\hat{m{\eta}} = {f y} + \epsilon$ ) (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  $\mathbf{w}=a(g^{-1}(\hat{\boldsymbol{\eta}}))/\{\frac{\partial \hat{\boldsymbol{\eta}}}{\partial g^{-1}(\hat{\boldsymbol{\eta}})}^2\mathrm{var}(\mathbf{y}_i)\}$
- 4) Fit weighted LM with z as pseudodata and 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?



# Why is stuff this important?

- 1) A basic (mathematical) understanding helps apply methods correctly.
- GLMs may not always converge to the MLE. Then, you will get warnings/errors.
- 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 Im() function!
- Now the glm() function

A linear regression:

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

A glm:

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

# 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 **
             0.6554 0.1810 3.621 0.000294 ***
## X
## ---
## 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!

## Prediction

(9)

predict(model, type = "response") #Type = link alternatively

 $\hat{mu}_i = g^{-1}(\alpha + \mathbf{x}_i \boldsymbol{\beta})$ 

Newdata

predict(model, newdata = X, type = "response")#Type = link al

# 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.

$$\begin{split} & \text{Normal: } \sum_{i=1}^{n} (y_i - \hat{\mu_i})^2 \text{ Poisson: } 2 \sum_{i=1}^{n} y_i \log(y_i/\hat{\mu}_i) - y_i + \hat{\mu}_i) \\ & \text{binomial: } 2 \sum_{i=1}^{n} y_i \log(y_i/\hat{\mu}_i) + (N - y_i) \log\{(N - y_i)/(N - y_i)\} \\ & \text{gamma: } 2 \sum_{i=1}^{n} -\log\{y_i/\hat{\mu}_i\} + (y_i - \hat{\mu_i})/\hat{\mu_i} \\ & \text{and so on.} \end{split}$$

#### Deviance

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

# Asymptotic requirements

- ▶ Binomial responses:  $N\pi \ge 3$  and  $N(1-\pi) \ge 3$ 
  - $\blacktriangleright$  Deviance for N=1 has no concept of residual variability
- Poisson responses:  $\lambda \geq 3$
- $\blacktriangleright$  Gamma distribution:  $\phi \leq 3$

(Dunn and Smyth 2021)

#### Residuals

- GLMs lack an explicit error term, but it is there!
- So we can still check assumptions by residuals, though they are differently defined
- There are different types; Pearson, Deviance, Anscombe, Quantile residuals...
- We usually -hope- that they are approximately normally distributed
- Residual checking in GLMs can be difficult

(omitted details)

#### Some resources

McCullagh and Nelder Dunn and Smyth Wood  $more\ friendly\ -\ dunn\ and\ smyth\ (because\ in\ R)\ -\ free\ book\ john\ fieberg\ -\ zuur$ 

## Recap

- 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