Reminder Generalised linear models in R Richard B. Sherley Extensive notes, handouts of these slides, and data files for the practicals University of Exeter, Penryn Campus, UK are available at: https://exeter-data-analytics.github.io/StatModelling/ March 2020 EXETER | DOCTORAL COLLEGE Researcher Development Richard B. Sherley GLMs in R March 2020 GLMs in R March 2020 1/1Richard B. Sherley 2/1

Recap: Linear regression

Assumptions:

- 1 A linear mean function is relevant.
- Variances are equal across all predicted values of the response (homoscedatic).
- **3** Errors are **normally** distributed.
- **4** Samples collected at **random**.
- **5** Errors are **independent**.

Generalised linear models (GLMs)

- **1** A linear mean (including any explanatory variables you want to) i.e $\beta_0 + \beta_1 X_1 + \ldots + \beta_p X_p$
- **2** A link function (like an "internal" transformation).
- 3 An error structure. So far we assumed normality $\epsilon \sim \mathcal{N}(0, \sigma^2)$

Link functions

Links your mean function to the scale of the observed data e.g.

$$E(Y) = g^{-1} \left(\beta_0 + \beta_1 X\right)$$

- $\mathbb{E}(Y)$ is the **expected value** (i.e. mean of Y).
- The function $g(\cdot)$ is known as the link function, and $g^{-1}(\cdot)$ denotes the inverse of $g(\cdot)$.

GLMs in R

Simple linear regression is a special case of a GLM

- **1** A linear mean: $\beta_0 + \beta_1 X_1 + \ldots + \beta_p X_p$
- **2** An error structure: $\epsilon \sim \mathcal{N}(0, \sigma^2)$
- **3** Link function: identity $\mu = \beta_0 + \beta_1 X_1 + \ldots + \beta_p X_p$

 $Y \sim \mathcal{N}(\mu, \sigma^2)$ $\mu = \beta_0 + \beta_1 X$

GLMs in R

GLMs in R lm(height ~ weight, data=df) Is equivalent to:

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glm(height ~ weight, data=df, family=gaussian(link=identity))

family specifies the error structure **and** link function

Default link functions

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Family	Link
gaussian	identity
binomial	logit, probit or cloglog
poisson	log, identity or sqrt
Gamma	inverse, identity or log
inverse.gaussian	$1/\mu^2$
quasi	user-defined
quasibinomial	logit
quasipoisson	log

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GLM Workflow

- 1 Exploratory data analysis
- 2 Choose a suitable error term
- **3** Choose a suitable **mean function** (and **link function**)
- 4 Fit model
 - Residual checks and model fit diagnostics
 - Revise model (if necessary)
- **5** Model simplification if required
- 6 Check final model

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Poisson regression

Count data is discrete and non-negative



Poisson distribution

- **Discrete** variable, defined on the range $0, 1, \ldots, \infty$.
- A single **rate** parameter λ , where $\lambda > 0$.
- Mean = λ
- Variance = λ



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Poisson regression

$$Y \sim \mathcal{P}ois(\lambda)$$
$$\log \lambda = \beta_0 + \beta_1 X$$

Using the rules of logarithm (i.e $log(\lambda) = k$, then $\lambda = e^k$):

$$\log(\lambda) = \beta_0 + \beta_1 X$$
$$\lambda = e^{\beta_0 + \beta_1 X}$$

Thus we are effectively modelling the observed counts using an exponential distribution

glm(outcome ~ explanatory, data=df, family=poisson(link=log))

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Example: Cuckoo data

How does nestling mass affect begging rates between **reed warbler chicks** and **cuckoo chicks**?



Cuckoo model

Count data are **discrete** and **positive**

So, we will try a **Poisson model** with a **log** link function:

$$\log(\lambda) = \beta_0 + \beta_1 M_i + \beta_2 S_i + \beta_3 M_i S_i$$

Where M_i is nestling mass and S_i a **dummy** variable

 $S_i = \begin{cases} 1 & \text{if } i \text{ is warbler,} \\ 0 & \text{otherwise} \end{cases}$

And $M_i S_i$ is an ${\rm interaction}$ term allowing ${\rm different}$ slopes for the two species

Cuckoo data



Cuckoo model

The mean regression lines for the two species look like this:

• Cuckoo $(S_i = 0)$:

$$\log(\lambda) = \beta_0 + \beta_1 M_i + (\beta_2 \times 0) + (\beta_3 \times M_i \times 0)$$
$$\log(\lambda) = \beta_0 + \beta_1 M_i$$

- Intercept = β_0 , Gradient = β_1
- Warbler $(S_i = 1)$:

$$\log(\lambda) = \beta_0 + \beta_1 M_i + (\beta_2 x 1) + (\beta_3 \times M_i \times 1)$$
$$\log(\lambda) = \beta_0 + \beta_1 M_i + \beta_2 + \beta_3 M_i$$
$$\log(\lambda) = (\beta_0 + \beta_2) + (\beta_1 + \beta_3) M_i$$

• Intercept =
$$(\beta_0 + \beta_2)$$
, Gradient = $(\beta_1 + \beta_3)$

Cuckoo model



Logistic regression

Consider a **categorical** response variable with two levels (e.g pass/fail). These type of **binary** data are assumed to be **Bernoulli** distributed:

 $Y \sim \mathcal{B}ern(p)$

- A probability parameter p, where 0 .
- Mean = p

Logistic regression

• Variance = p(1-p)



Logistic regression

$$Y \sim \mathcal{N}(\mu, \sigma^2) \qquad Y \sim \mathcal{P}ois(\lambda) \qquad Y \sim \mathcal{B}ern(p)$$
$$\mu = \beta_0 + \beta_1 X \qquad \log(\lambda) = \beta_0 + \beta_1 X \qquad ?? = \beta_0 + \beta_1 X$$

$$Y \sim \mathcal{B}ern(p)$$
$$\log\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 X$$
$$\operatorname{logit}(p) = \beta_0 + \beta_1 X$$

 $\log\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 X$ $p = \frac{e^{\beta_0 + \beta_1 X}}{1 + e^{\beta_0 + \beta_1 X}}$ 9 0.8 ю 0.6 logit(p) 0 ٩ 0.4 Ϋ́ 0.2 -10 0.0 -10 10 10 -5 0 5 -10 -5 5 0 х х explanatory, data=df, family=binomial(link=logit)) glm(response ~ Richard B. Sherley GLMs in R

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1992 US election survey

Voters were asked if they preferred George Bush (Republican) or Bill Clinton (Democrat).

- Income was characterised on a 5-point scale (1 poor to 5 rich).
- Question: Do voters with higher incomes prefer conservative candidates?



1992 US election survey



1992 US election survey

fit <- glm(Vote ~ Income, data=USA, family=binomial(link=logit)) summary(fit)</pre>



1992 US election survey

$$Y \sim \mathcal{B}ern(p)$$
$$\log\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 X$$

- '(Intercept)' = $\beta_0 = -1.3$
- 'Income' = $\beta_1 = 0.303$

It is common to interpret variables according to some **central tendency** e.g at the central income category (i.e X = 3)

$$\begin{split} P(\mathsf{Republican vote at } X = 3) &= \mathsf{logit}^{-1} \left(-1.3 + 0.3 \times 3 \right) \\ &= \frac{e^{-1.3 + 0.3 \times 3}}{1 + e^{-1.3 + 0.3 \times 3}} \\ &= 0.40. \end{split}$$

Summary

- GLMs are powerful and flexible
- They can be used to fit a wide variety of data types
- Model checking becomes trickier
- Extensions include: mixed models; survival models; generalised additive models (GAMs).

GLMs in R

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