

## Class 6: Generalised linear mixed models

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## Learning outcomes

- ▶ Understand the basics of a glmm
- ▶ See a few different examples of glmmms
- ▶ Understand how to fit basic glmms in lme4

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## Revision: generalised linear models

- ▶ Recall that the normal linear model has residuals which are normally distributed and a response variable that is conditionally normally distributed
- ▶ e.g.  $y_i = \alpha + \beta x_i + \epsilon_i$  with  $\epsilon_i \sim N(0, \sigma^2)$  and  $y_i | x_i \sim N(\alpha + \beta x_i, \sigma^2)$
- ▶ In a generalised linear model the residuals often don't exist and the response variable has a non-normal conditional distribution, e.g. Binomial, Poisson or Gamma (among many many others)
- ▶ The key to a glm is that the mean of the conditional distribution is transformed in a clever way via a *link* function, and the transformed mean is given a standard linear relationship with the covariates

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## Glm example

- ▶ Example 1: Binomial

$$y_i | x_i \sim \text{Bin}(N, p_i); \text{logit}(p_i) = \alpha + \beta x_i$$

- ▶ Example 2: Poisson

$$y_i | x_i \sim \text{Po}(\lambda_i); \log(\lambda_i) = \alpha + \beta x_i$$

- ▶ Example 3: Negative Binomial

$$y_i | x_i \sim \text{NegBin}(\phi, p_i); \text{logit}(p_i) = \alpha + \beta x_i$$

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## Some important notes about glms

- ▶ Sometimes you have the choice as to how you collect your data (e.g. collecting precise numbers as opposed to yes/no values). When you have this choice, it is almost always preferable to collect the precise values as these will give you more precise results later on. Estimating the values of  $\alpha$  and  $\beta$  in e.g. a Binomial glm is often much less precise than estimating them in a normal linear model
- ▶ There are lots of different link functions with no strong guidance as to which one you should choose. For example some people use *probit* instead of logit for Binomial models, and some people don't use any link function at all
- ▶ In the frequentist world, the fitting method becomes even more complicated when dealing with glms, often using something called Iteratively Re-weighted Least Squares (IRLS) which you might see referred to by `lme4`

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## Example: the swiss willow tit data

```
swt = read.csv('../data/swt.csv')
head(swt)
```

```
##   rep.1 rep.2 rep.3 c.2 c.3 elev forest dur.1 day.2 day.3 length alt
## 1     0     0     0  0  0  420     3    240    58    73    6.2 Low
## 2     0     0     0  0  0  450    21    160    39    62    5.1 Low
## 3     0     0     0  0  0 1050    32    120    47    74    4.3 Med
## 4     0     0     0  0  0  1110    35    180    44    71    5.4 Med
## 5     0     0     0  0  0   510     2    210    56    73    3.6 Low
## 6     0     0     0  0  0   630    60    150    56    73    6.1 Low
```

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## A first glm

- ▶ Suppose we want to fit a model on the sum  $y_i = \text{rep.1} + \text{rep.2} + \text{rep.3}$ :

$$y_i \sim \text{Bin}(N_i, p_i), \text{logit}(p_i) = \alpha + \beta(x_i - \bar{x})$$

where  $x_i$  is the percentage of forest cover

- ▶ There are no random effects in this (yet) so we currently have just a glm
- ▶ Remember that the relationship between  $x_i$  and  $p_i$  (the probability of observing a bird) is not linear. People usually use  $\exp(\beta)$  as a measure of the proportional increase in the probability associated with a unit increase in  $x$

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## Fitting the glm

```
summary(glm(cbind(y, N) ~ x, family = binomial(link = logit)))
```

```
##
## Call:
## glm(formula = cbind(y, N) ~ x, family = binomial(link = logit))
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8968  -1.0906  -0.8140   0.4749   2.1429
##
## Coefficients:
##      Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.188254   0.179000 -12.225 < 2e-16 ***
## x            0.020322   0.003289   6.178 6.49e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 332.73  on 236  degrees of freedom
## Residual deviance: 292.22  on 235  degrees of freedom
## AIC: 463.89
##
## Number of Fisher Scoring iterations: 4
```

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## Changing to a glmm

- Now extend the model to have a random intercept by altitude

$$y_{ij} \sim \text{Bin}(N_{ij}, p_{ij}), \text{logit}(p_{ij}) = \alpha_j + \beta(x_i - \bar{x})$$

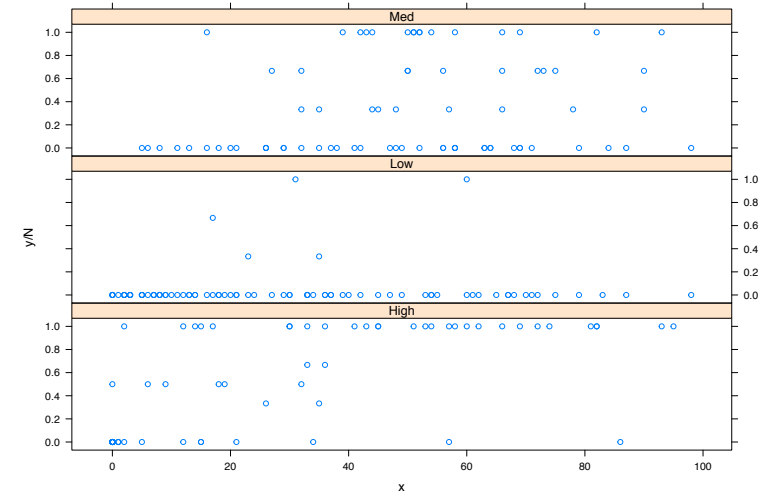
with  $\alpha_j \sim N(\mu_\alpha, \sigma_\alpha^2)$ .

- Now  $y_{ij}$  is the count for observation  $i$  at altitude  $j$ . Other parameters defined similarly
- This means that there will be three different  $\alpha_j$  values for altitude low, medium and high

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## Plot of the data

```
xyplot(y/N ~ x|alt, swt, type='p',
       layout=c(1,3), index.cond = function(x,y)max(y))
```



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## Fitting the glmm

```
glmm_1 = glmer(cbind(y, N) ~ x + (1 | alt),
               family = binomial, data = swt)
summary(glmm_1)
```

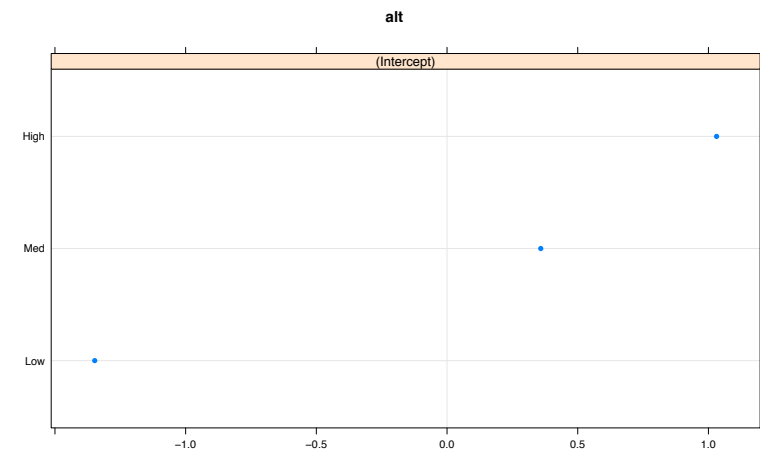
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: cbind(y, N) ~ x + (1 | alt)
## Data: swt
##
##      AIC      BIC    logLik deviance df.resid
## 397.1    407.5   -195.5    391.1     234
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.8988 -0.7074 -0.3283  0.2221  5.8152
##
## Random effects:
## Groups Name         Variance Std.Dev.
## alt    (Intercept)  1.072    1.036
## Number of obs: 237, groups: alt, 3
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.416608   0.631343  -3.828 0.000129 ***
## x             0.018246   0.003536   5.160 2.47e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## x -0.257
```

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## Look at the random effects

```
library(lattice)
dotplot(ranef(glmm_1))
```

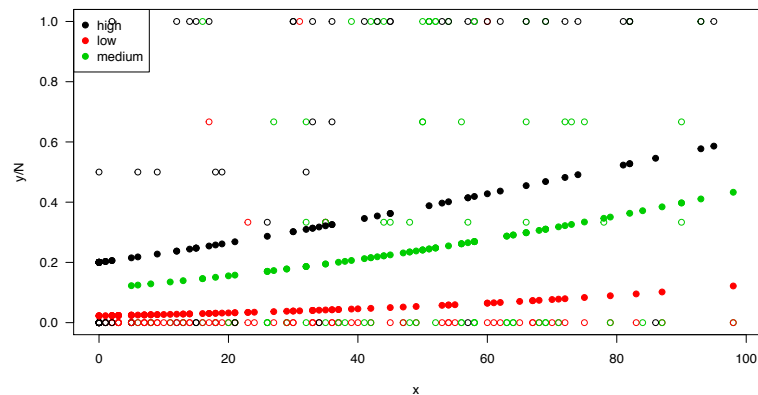
```
## $alt
```



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## Plot the probabilities

```
p_est = predict(glmm_1, type = 'response')
plot(x, y/N, col = swt$alt, las = 1)
points(x, p_est, col = swt$alt, pch = 19)
legend('topleft', c('high', 'low', 'medium'), pch = 19, col =
```



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## A model with varying intercepts and slopes

```
glmm_2 = glmer(cbind(y, N) ~ (x | alt),
               family = binomial, data = swt)
summary(glmm_2)
```

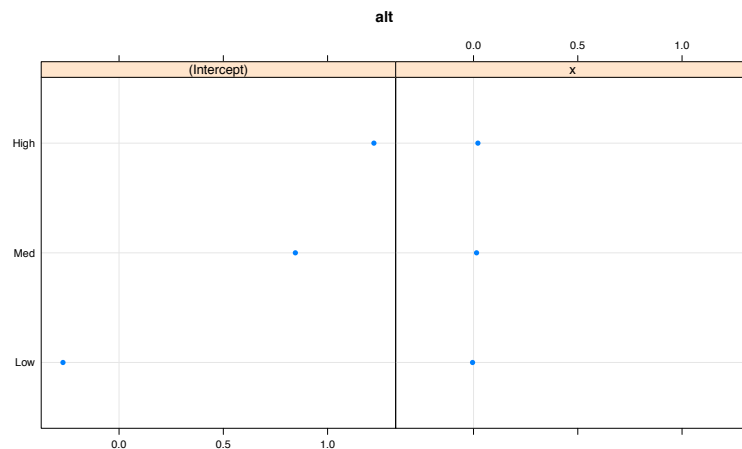
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: cbind(y, N) ~ (x | alt)
## Data: swt
##
## AIC      BIC    logLik deviance df.resid
##  401.2    415.1   -196.6   393.2     233
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0280 -0.6716 -0.3727  0.1687  6.0027
##
## Random effects:
## Groups Name      Variance Std.Dev. Corr
## alt      (Intercept) 0.7797798 0.88305
##          x          0.0002299 0.01516  1.00
## Number of obs: 237, groups: alt, 3
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.7114      0.5904  -4.593 4.38e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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## Plot the new random effects

```
dotplot(ranef(glmm_2))
```

```
## $alt
```



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## Compare the two binomial models

```
anova(glmm_1, glmm_2)
```

```
## Data: swt
## Models:
## glmm_1: cbind(y, N) ~ x + (1 | alt)
## glmm_2: cbind(y, N) ~ (x | alt)
##           Df    AIC    BIC logLik deviance Chisq Chi Df P
## glmm_1    3 397.07 407.48 -195.54   391.07
## glmm_2    4 401.22 415.09 -196.61   393.22      0    1
```

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## A Poisson model - glm set-up

- If we wanted a Poisson glm we would set it up as:

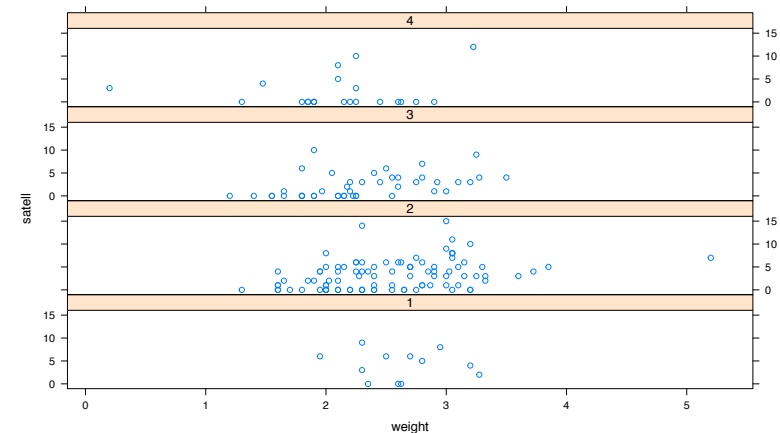
$$y_i \sim \text{Po}(\lambda_i); \log(\lambda_i) = \alpha + \beta x_i$$

- log is the link function here. Again people often use  $\exp(\beta)$  as an estimate of how the rate parameter  $\lambda$  is affected by  $x$
- The Poisson is a really un-realistic model. Remember it assumes that the mean and the variance of  $y$  are the same. This almost never occurs in real data

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## Poisson glm - example data

```
horseshoe = read.csv('../data/horseshoe.csv')
xyplot(satell ~ weight | as.factor(color), horseshoe,
       type='p', layout=c(1,4))
```



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## Fit Poisson glm

```
summary(glm(satell ~ weight, data = horseshoe, family = poisson(link = log)))
```

```
##
## Call:
## glm(formula = satell ~ weight, family = poisson(link = log),
##      data = horseshoe)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.9182  -2.0169  -0.5926   1.0290   4.9755
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.36997    0.17811  -2.077   0.0378 *
## weight       0.56837    0.06496   8.750  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 632.79  on 172  degrees of freedom
## Residual deviance: 564.35  on 171  degrees of freedom
## AIC: 923.65
##
## Number of Fisher Scoring iterations: 5
```

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## A Poisson glmm

```
glmm_3 = glmer(satell ~ weight + (1 | color),
               family = poisson, data = horseshoe)
summary(glmm_3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: satell ~ weight + (1 | color)
## Data: horseshoe
##
##      AIC      BIC    logLik deviance df.resid
##    924.6    934.1   -459.3    918.6     170
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0931  -1.4290  -0.4841   1.0286   6.9111
##
## Random effects:
## Groups Name          Variance Std.Dev.
## color (Intercept) 0.01212  0.1101
## Number of obs: 173, groups: color, 4
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.3249    0.1920  -1.692   0.0907 .
## weight       0.5453    0.0683   7.983 1.42e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## weight -0.917
```

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## A different type of Poisson model

- ▶ As previously stated the Poisson is a bit unrealistic (because of mean = variance assumption)
- ▶ Random effects can be added in to model overdispersion:

$$y_i \sim \text{Po}(\lambda_i), \log(\lambda_i) = \alpha + \beta x_i + \epsilon_i$$

with  $\epsilon_i \sim N(0, \sigma^2)$

- ▶ This is just adding an *individual-level* random effect (or a residual term) and is the same as:

$$\log(\lambda_i) \sim N(\alpha + \beta x_i, \sigma^2)$$

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## Poisson over-dispersion model

```
horseshoe$obs <- 1:nrow(horseshoe)
glmm_4 = glmer(satell ~ weight + (1 | obs),
               family = poisson, data = horseshoe,
               control = glmerControl(optimizer = "Nelder_Mead"))
summary(glmm_4)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: satell ~ weight + (1 | obs)
## Data: horseshoe
## Control: glmerControl(optimizer = "Nelder_Mead")
##
##      AIC      BIC    logLik deviance df.resid
## 769.5    778.9   -381.7    763.5      170
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.05174 -0.78335 -0.00272  0.34225  1.39463
##
## Random effects:
## Groups Name      Variance Std.Dev.
## obs    (Intercept) 0.9822   0.9911
## Number of obs: 173, groups:  obs, 173
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.4538     0.4352  -3.340 0.000837 ***
## weight       0.8254     0.1624   5.083 3.71e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
##              -0.000
```

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## Model results

```
anova(glmm_3, glmm_4)
```

```
## Data: horseshoe
## Models:
## glmm_3: satell ~ weight + (1 | color)
## glmm_4: satell ~ weight + (1 | obs)
##      Df    AIC    BIC logLik deviance Chisq Chi Df I
## glmm_3  3 924.60 934.06 -459.30   918.60
## glmm_4  3 769.48 778.94 -381.74   763.48 155.12    0
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Poisson OD model a far better fit

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## Some notes on glmm

- ▶ Really just scratching the surface. Many many options for distributions and link functions
- ▶ Basic idea (and computational approach) is exactly the same as for lmer
- ▶ Individual level random effects are often useful in glmms as they can represent over-dispersion. They essentially just add a residual effect into the linked mean

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## Summary

- ▶ We have seen a Binomial and a Poisson generalised linear mixed model (glmm)
- ▶ Very simple to fit in `lme4` using the `glmer` function. Exactly the same formula approach
- ▶ Over-dispersion a useful trick for getting good-fitting models