

Class 6: Hierarchical generalised linear models

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Learning outcomes:

- ▶ Understand the modelling implications of moving from linear to hierarchical generalised linear models (HGLMs)
- ▶ Know some of the different versions of Hierarchical GLMs
- ▶ Be able to fit HGLMS in JAGS
- ▶ Be able to expand and summarise fitted models

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From LMs to HGLMs

- ▶ Reminder: a hierarchical model has prior distributions on the parameters which depend on further parameters
- ▶ A generalised linear model is one in which the probability distribution is not normal, and a link function serves to match the mean of the distribution to the covariates
- ▶ Within this framework, we can borrow the ideas from the previous class to create hierarchical GLMs
- ▶ We will go through four examples: binomial-logit, Poisson, robust regression, and ordinal regression

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Example 1: binomial-logit

- ▶ In class 2, we met the Binomial-logit model for binary data:

$$y_i \sim \text{Bin}(1, p_i), \text{logit}(p_i) = \alpha + \beta(x_i - \bar{x})$$

Here $\text{logit}(p_i)$ is the link function equal to $\log\left(\frac{p_i}{1-p_i}\right)$ and transforms the bounded probabilities into an unbounded space

- ▶ If we have non-binary data we just change the likelihood:

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

- ▶ In a hierarchical version of this model, we vary the *latent parameters* α and β and give them prior distributions

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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 hierarchical model

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

$$y_i \sim \text{Bin}(N_i, p_i), \text{logit}(p_i) = \alpha_{\text{altitude}_i} + \beta_{\text{altitude}_i}(x_i - \bar{x})$$

where x_i is the percentage of forest cover

- ▶ What prior distributions should we use for α and β ?
- ▶ Useful side note: A value of 10 on the logit scale leads to a probability of about 1, and a value of -10 leads to a probability of about 0 (you can test this by typing `inv.logit(10)`) so I wouldn't expect the value of $\text{logit}(p_i)$ to ever get much bigger than 10 or smaller than -10
- ▶ I have no idea whether we are more likely to find these birds in high percentage forest or low, so I'm happy to think that β might be around zero, and be positive or negative. Forest cover ranges from 0 to 100 so that suggests that β is every likely to be bigger than 0.1 or smaller than -0.1. Perhaps $\beta \sim N(0, 0.1^2)$ is a good prior
- ▶ It looks to me like the intercept is very unlikely to be outside the range (-10, 10) so perhaps $\alpha \sim N(0, 5^2)$ is appropriate

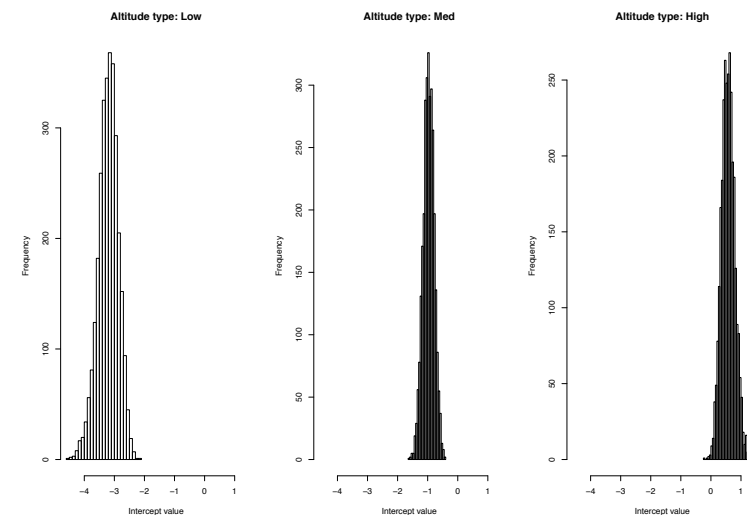
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JAGS code

```
jags_code = '
model{
  # Likelihood
  for(i in 1:N) {
    y[i] ~ dbin(p[i], N_exp[i])
    logit(p[i]) <- alpha[alt[i]] + beta[alt[i]] * (x[i] - mean(x))
  }
  # Priors
  for(j in 1:N_alt) {
    alpha[j] ~ dnorm(mu_alpha, sigma_alpha^-2)
    beta[j] ~ dnorm(mu_beta, sigma_beta^-2)
  }
  mu_alpha ~ dnorm(0, 5^-2)
  mu_beta ~ dnorm(0, 0.1^-2)
  sigma_alpha ~ dt(0,5,1)T(0,)
  sigma_beta ~ dt(0,5,1)T(0,)
}
```

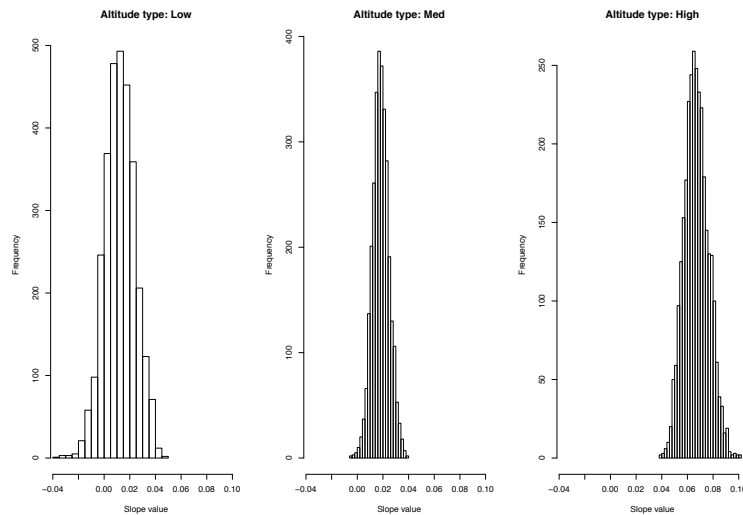
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Model fit - intercepts



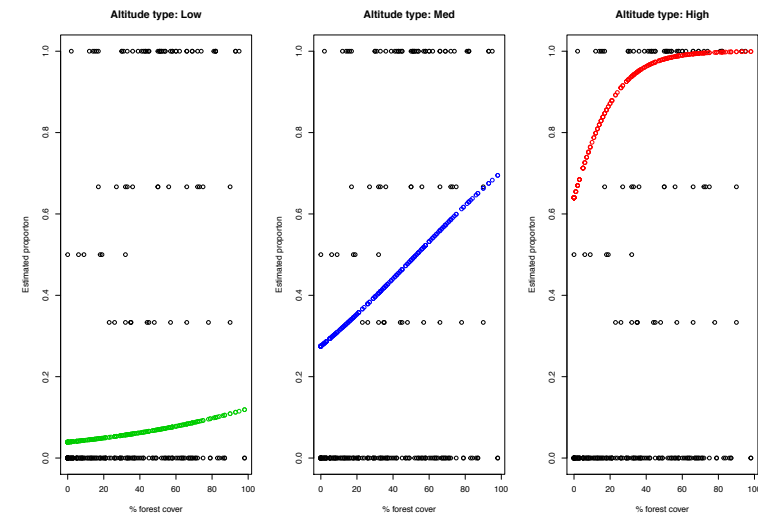
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Model fit - Slopes



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Model fit - estimated mean proportions



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Type 2: Poisson HGLMs

- For a Poisson distribution there is no upper bound on the number of counts
- We just change the likelihood (to Poisson) and the link function (to log):

$$y_i \sim Po(\lambda_i), \log(\lambda_i) = \alpha + \beta(x_i - \bar{x})$$

- We can now add our hierarchical layers into α and β , or...
- Another way we can add an extra layer is by giving $\log(\lambda_i)$ a probability distribution rather than setting it to a value
- This is a way of introducing *over-dispersion*, i.e. saying that the data are more variable than that expected by a standard Poisson distribution with our existing covariates

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An over-dispersed model

- The over-dispersed model looks like:

$$y_i \sim Po(\lambda_i), \log(\lambda_i) \sim N(\alpha + \beta(x_i - \bar{x}), \sigma^2)$$

where σ is the over-dispersion parameter

- We now need to estimate prior distributions for α , β , and σ
- We will use the SWT data again, but pretend that we didn't know that they had gone out N times looking for the birds

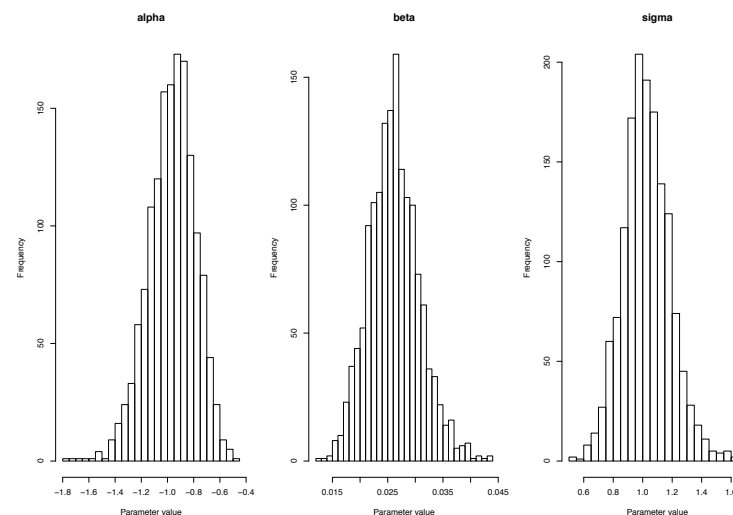
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JAGS code for OD Poisson

```
jags_code = '  
model{  
  # Likelihood  
  for(i in 1:N) {  
    y[i] ~ dpois(exp(log_lambda[i]))  
    log_lambda[i] ~ dnorm(alpha + beta * (x[i] - mean(x)),  
  }  
  alpha ~ dnorm(0, 5^-2)  
  beta ~ dnorm(0, 0.1^-2)  
  sigma ~ dt(0,5,1)T(0,)  
}
```

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Model run



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Notes about OD Poisson model

- ▶ The way to think about OD models is via the data generating process. Draw a DAG and think about how these processes might arise
- ▶ We could compare this model to one without over dispersion via DIC (or if time, cross validation). We should also compute a posterior predictive distribution for full comparison
- ▶ In general, the parameter values (i.e. alpha and beta) tend to be more uncertain when you add in over dispersion
- ▶ Also in the data set is a variable called dur which represents how long they spent looking for the birds. This could be added in as an offset via the likelihood:

```
y[i] ~ dpois(dur[i] * exp(log_lambda[i]))
```

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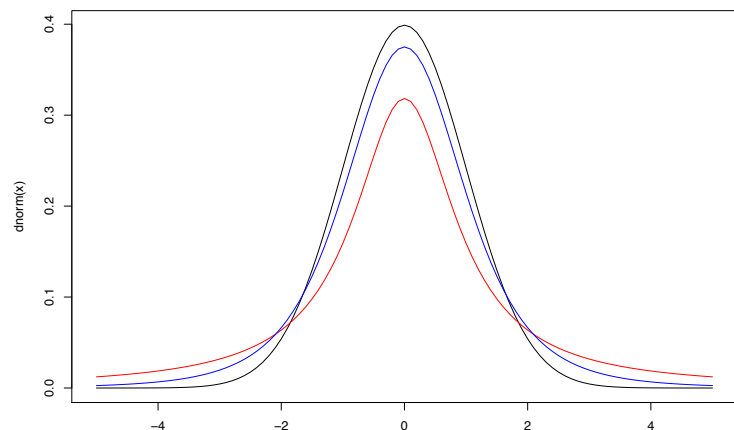
Type 3: *t*-distributed HGLMs

- ▶ How do Bayesians deal with outliers?
- ▶ A common view is that we should delete these observations before we run the model, but what if we can't find a reason for doing so
- ▶ A good Bayesian will include outliers as part of the model.
- ▶ One way of doing this is by switching from a normal distribution to a *t*-distribution

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Normal vs t

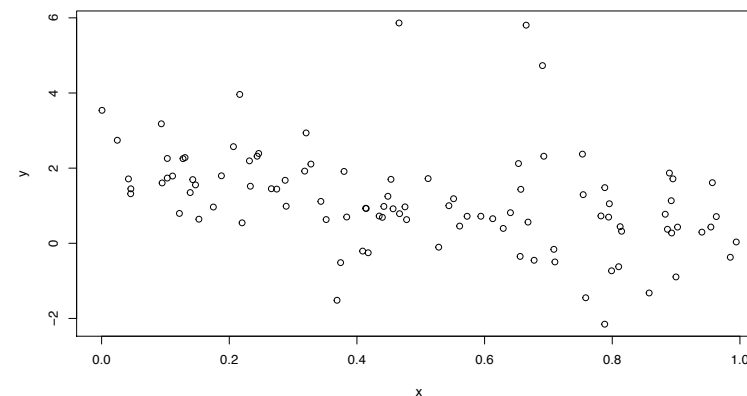
```
curve(dnorm, from = -5, to = 5)
curve(dt(x, df = 1), add = TRUE, col = 'red')
curve(dt(x, df = 4), add = TRUE, col = 'blue')
```



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Polluted data

► Suppose we had some data which looked like this:



There are a few observations here which look a bit odd

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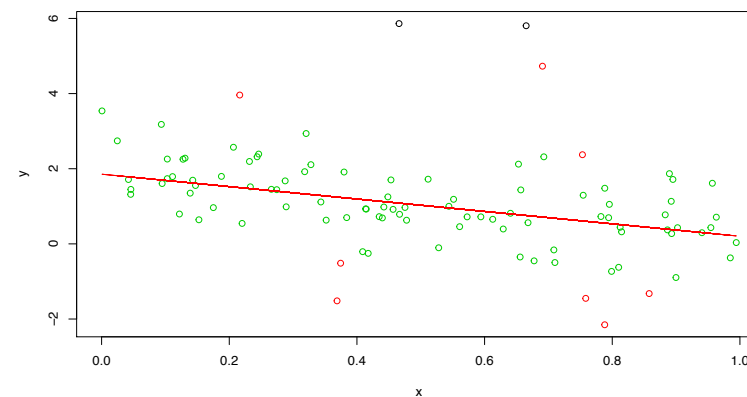
JAGS code for a t -model

```
jags_code = '
model{
  # Likelihood
  for(i in 1:N) {
    y[i] ~ dt(alpha + beta * (x[i] - mean(x)),
              sigma, df[i] + 1)
    df[i] ~ dbin(p, 10)
  }
  p ~ dunif(0, 1)
  alpha ~ dnorm(0, 1^-2)
  beta ~ dnorm(0, 1^-2)
  sigma ~ dt(0,1,1)T(0,)
}
```

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Output from the model

```
dfs = jags_run$BUGSoutput$median$df
pars = jags_run$BUGSoutput$mean
plot(x, y, col = as.factor(dfs))
lines(x, as.numeric(pars$alpha) +
      as.numeric(pars$beta)*(x - mean(x)),
      col = 'red')
```



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Prior distributions on the degrees of freedom

- ▶ Here I've set a prior distribution on the degrees of freedom parameter to be Binomial with the maximum value to be $10+1 = 11$
- ▶ The probability of each observation being an outlier is p , set to be uniform between 0 and 1
- ▶ We thus also create a posterior distribution for the probability that each observation is an outlier
- ▶ The Binomial distribution we use has a peak at the degrees of freedom being 6 or 7, we might instead use a discrete uniform prior though this is harder to code in JAGS/Stan

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Type 4: Ordinal data HGLMs

- ▶ Often we have a response variable which is ordinal, e.g. disagree, neutral, agree, etc
- ▶ There are lots of different (and complicated) ways to model such data
- ▶ Perhaps the easiest is to think of it as a hierarchical model with 'cut-points' on a latent linear regression

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An ordinal model example

- ▶ Suppose $y_i = \{\text{disagree, neutral, agree}\}$ and we make it dependent on a latent continuous variable z_i , so that :

$$y_i = \begin{cases} \text{agree} & \text{if } z_i > 0.5 \\ \text{neutral} & \text{if } -0.5 < z_i \leq 0.5 \\ \text{disagree} & \text{if } z_i \leq -0.5 \end{cases}$$

- ▶ We then give z_i a prior distribution, e.g. $N(\beta_0 + \beta_1 x_i, \sigma^2)$

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Fitting ordinal models in JAGS

```
jags_code = '
model{
  # Likelihood
  for(i in 1:N) {
    z[i] ~ dnorm(alpha + beta * (x[i] - mean(x)),
                sigma^-2)
    y[i] ~ dinterval(z[i], cuts)
  }
  alpha ~ dnorm(0, 100^-2)
  beta ~ dnorm(0, 100^-2)
  sigma ~ dt(0, 10, 1)T(0, )
}
```

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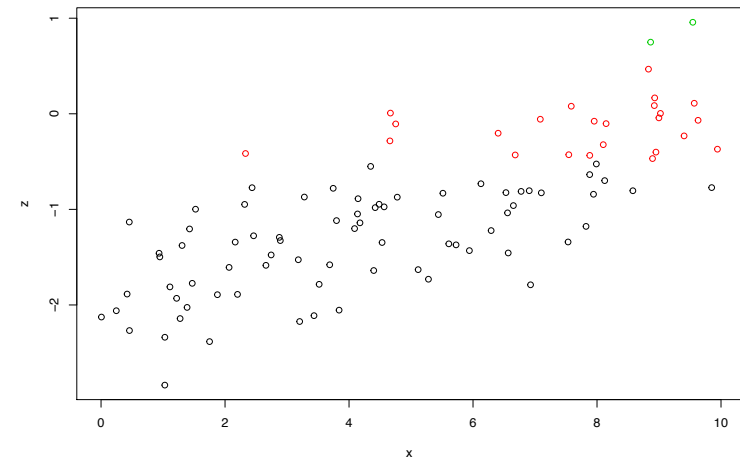
Simulating some example data

```
N = 100
alpha = -1
beta = 0.2
sigma = 0.51
set.seed(123)
x = runif(N, 0, 10)
cuts = c(-0.5, 0.5)
z = rnorm(N, alpha + beta * (x - mean(x)), sigma)
y = findInterval(z, cuts)
```

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Simulated data - plot

```
plot(x, z, col = y + 1)
```



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Fitting in JAGS - needs initial values

```
jags_inits = function() {
  z = runif(N, -0.5, 0.5)
  z[y==0] = runif(sum(y==0), -1, -0.5)
  z[y==2] = runif(sum(y==2), 0.5, 1)
  return(list(z = z))
}
jags_run = jags(data = list(N = N,
                           y = y,
                           x = x,
                           cuts = cuts),
               inits = jags_inits,
               parameters.to.save = c('alpha',
                                     'beta',
                                     'sigma'),
               model.file = textConnection(jags_code))
```

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Output

```
print(jags_run)
```

```
## Inference for Bugs model at "5", fit using jags,
## 3 chains, each with 2000 iterations (first 1000 discarded)
## n.sims = 3000 iterations saved
##          mu.vect sd.vect  2.5%  25%  50%  75% 97.5%
## alpha    -1.082   0.200 -1.619 -1.172 -1.038 -0.945 -0.814 1
## beta      0.220   0.059  0.134  0.179  0.210  0.249  0.367 1
## sigma     0.537   0.123  0.363  0.449  0.515  0.597  0.842 1
## deviance  0.000   0.000  0.000  0.000  0.000  0.000  0.000 1
##
## For each parameter, n.eff is a crude measure of effective sam
## and Rhat is the potential scale reduction factor (at converge
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 0.0 and DIC = 0.0
## DIC is an estimate of expected predictive error (lower devian
```

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Summary

- ▶ We have now seen a number of different types of hierarchical GLM
- ▶ Many of the ideas of hierarchical linear models transfer over, but we can explore richer behaviour with hierarchical GLMs
- ▶ These have all used the normal, binomial or Poisson distribution at the top level, and have allowed for over-dispersion, robustness, and ordinal data, to name just three