Class 9: Bayesian Hierarchical Models

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Learning outcomes:

- Start fitting hierarchical GLMs in `rstanarm`
- Know some of the different versions of Hierarchical GLMs
- Be able to expand and summarise fitted models

From LMs to HGLMs

- The Bayesian analogue of a mixed model is a *hierarchical model*.
- It's called a hierarchical model because the prior distributions come in layers, they depend on other parameters
- 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, and ordinal regression

Example 1: earnings data (again!)

- Very easy to convert quickly from `lmer` to `stan_lmer`:

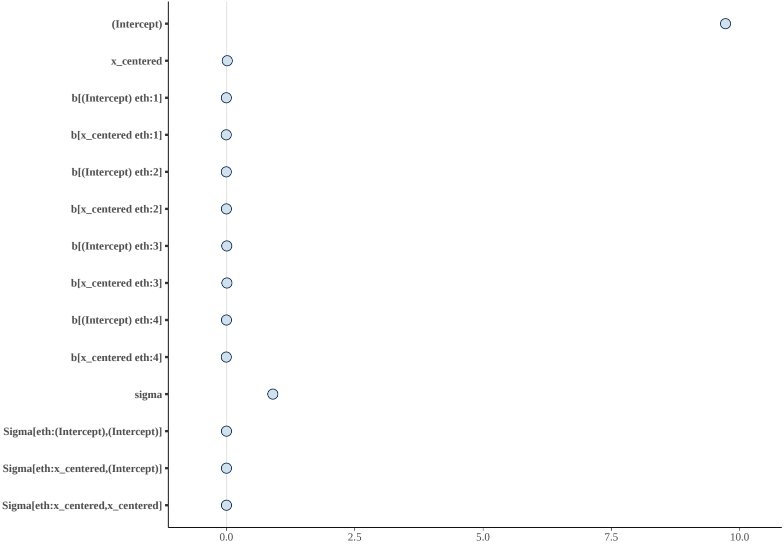
```
dat = read.csv('data/earnings.csv')
mod_1 = stan_lmer(y ~ x_centered + (x_centered | eth), data = dat)
```

```
round(posterior_interval(mod_1), 3)
```

```
##                                        5%   95%
## (Intercept)                         9.636 9.784
## x_centered                         -0.006 0.031
## b[(Intercept) eth:1]               -0.083 0.043
## b[x_centered eth:1]                -0.026 0.014
## b[(Intercept) eth:2]               -0.097 0.035
## b[x_centered eth:2]                -0.022 0.019
## b[(Intercept) eth:3]               -0.024 0.109
## b[x_centered eth:3]                -0.006 0.032
## b[(Intercept) eth:4]               -0.070 0.076
## b[x_centered eth:4]                -0.034 0.016
## sigma                               0.872 0.938
## Sigma[eth:(Intercept),(Intercept)]  0.000 0.016
## Sigma[eth:x_centered,(Intercept)]  -0.001 0.002
## Sigma[eth:x_centered,x_centered]    0.000 0.002
```

Earnings model output

```r
plot(mod_1)
```



Example 2: binomial-logit

- Earlier we met the Binomial-logit model for binary data:

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

  Here $logit(p_i)$ 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:

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

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

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
```

A hierarchical model

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

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

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 $logit(p_i)$ 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

rstanarm code

```
mod_2 = stan_glmer(cbind(y, N) ~ forest + (forest | alt),
                   data = swt,
                   family = binomial(link = 'logit'),
                   prior = normal(0, 0.1),
                   prior_intercept = normal(0, 5))
```

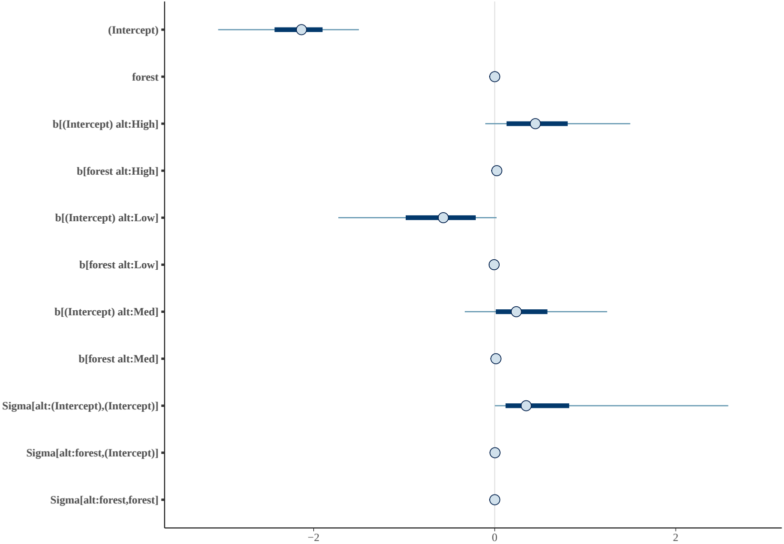
Model summary 1

```r
posterior_interval(mod_2)
```

```
##                                          5%          95%
## (Intercept)                    -3.0547350656 -1.500090318
## forest                         -0.0053117955  0.006815317
## b[(Intercept) alt:High]        -0.1039793407  1.497335796
## b[forest alt:High]              0.0131837840  0.033605020
## b[(Intercept) alt:Low]         -1.7271176612  0.020935355
## b[forest alt:Low]              -0.0292270906  0.015086361
## b[(Intercept) alt:Med]         -0.3306274126  1.242020299
## b[forest alt:Med]               0.0029792495  0.024435972
## Sigma[alt:(Intercept),(Intercept)]  0.0019747303  2.579853972
## Sigma[alt:forest,(Intercept)]  -0.0317051285  0.046441427
## Sigma[alt:forest,forest]        0.0001418906  0.025561489
```

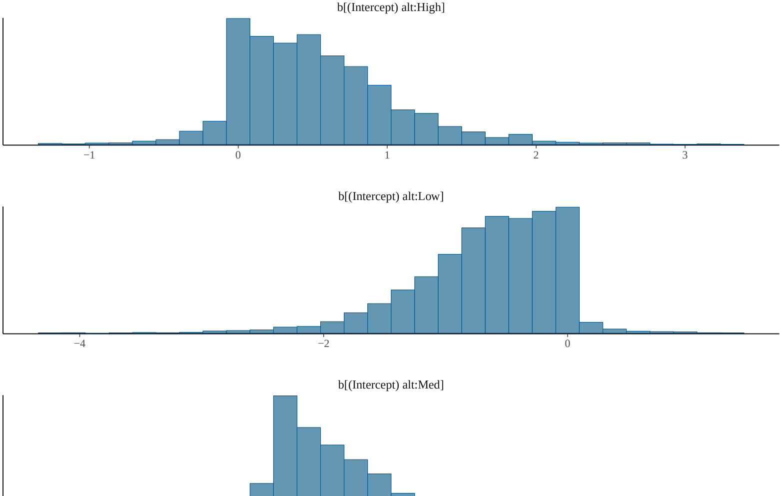
Model summary 2

```r
plot(mod_2)
```



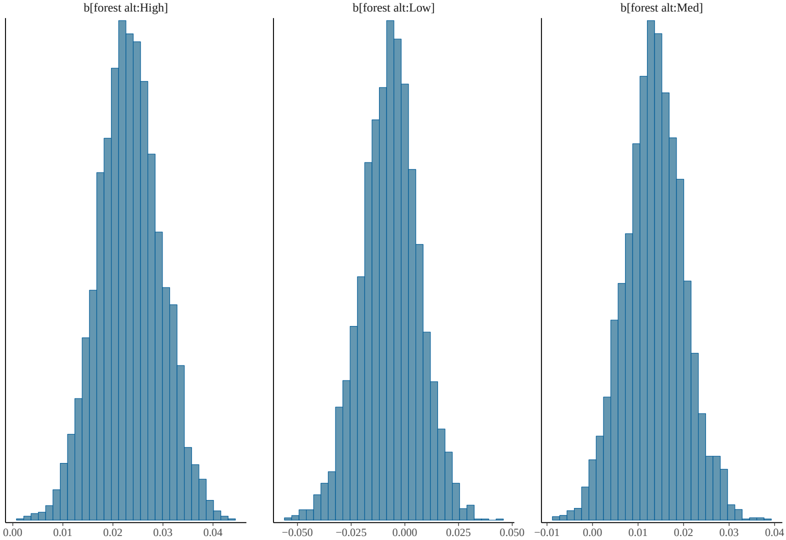
Model fit - intercepts

```
mcmc_hist(as.data.frame(mod_2),
          regex_pars = 'b\\[\\(Intercept',
          facet_args = list(nrow = 3))
```



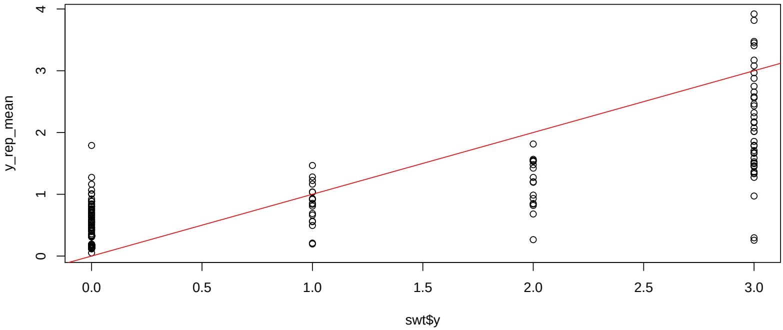
Model fit - Slopes

```
mcmc_hist(as.data.frame(mod_2), regex_pars = 'b\\[forest')
```



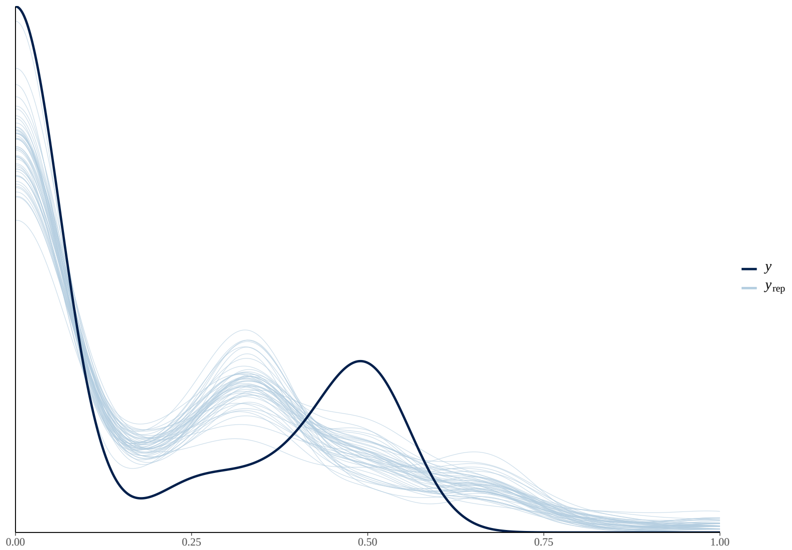
Model fit - posterior predictive check

```
y_rep = posterior_predict(mod_2)
y_rep_mean = apply(y_rep, 2, 'mean')
plot(swt$y, y_rep_mean)
abline(a = 0, b = 1, col = 'red')
```



Model fit - posterior predictive check 2

```
pp_check(mod_2)
```



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

An over-dispersed model

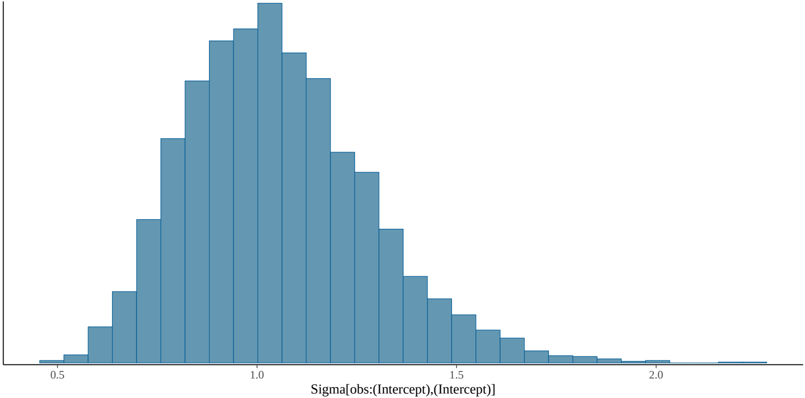
- The over-dispersed model looks like:

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

  where σ is the over-dispersion parameter
- We now need to estimate prior distributions for α, β, and σ
- We will use the horseshoe data again (see yesterday)

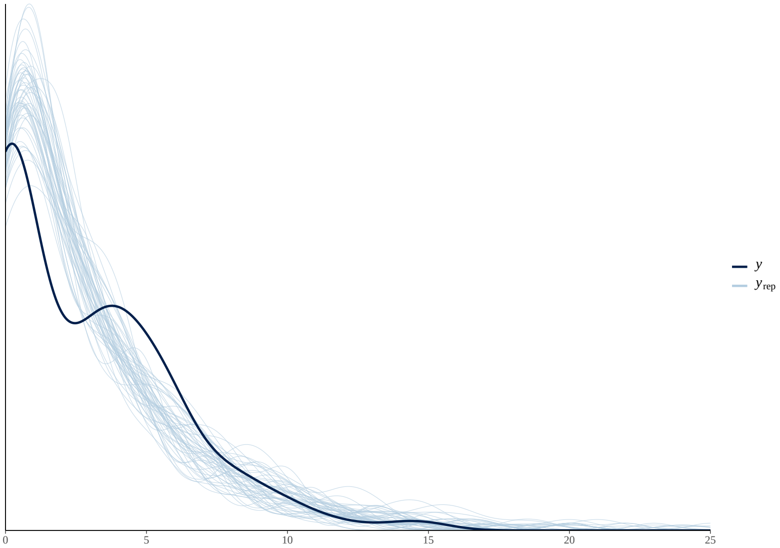
rstanarm code for OD Poisson

```
horseshoe = read.csv('data/horseshoe.csv')
horseshoe$obs <- 1:nrow(horseshoe)
mod_3 = stan_glmer(satell ~ weight + (1 | obs),
              family = poisson, data = horseshoe)
mcmc_hist(as.data.frame(mod_3), regex_pars = 'Sigma')
```



Posterior predictive check

```r
pp_check(mod_3)
```



Notes about OD Poisson model

- The way to think about OD models is via the data generating process. You could draw a DAG and think about how these processes might arise
- We could compare this model to one without over dispersion via the PPC (or if time, WAIC, LOO, or cross validation).
- In general, the parameter values (i.e. the intercepts and slopes) tend to be more uncertain when you add in over dispersion

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

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 :

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

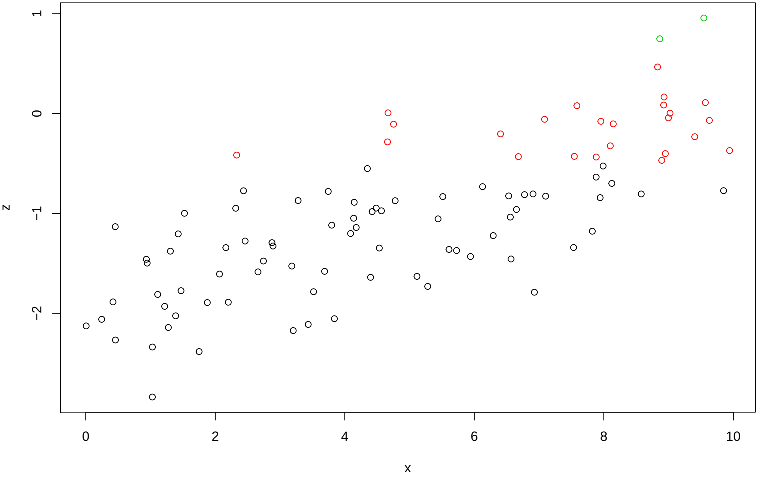
- We then give z_i a prior distribution, e.g. $N(\beta_0 + \beta_1 x_i, \sigma^2)$

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)
dat = data.frame(y = as.factor(y),
                 x = x)
```

Simulated data - plot

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



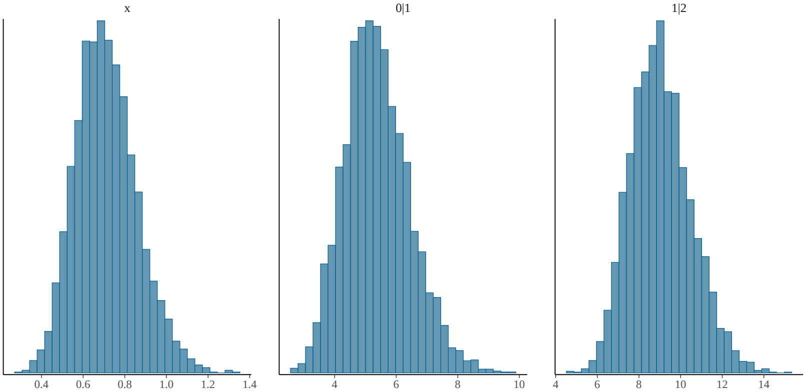
Fitting in rstanarm

```
mod_4 = stan_polr(y ~ x,
                  data = dat,
                  prior = R2(0.5, "mean"),
                  prior_counts = dirichlet(1))
```

Output

```
mcmc_hist(as.data.frame(mod_4))
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwi
```



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