

For the model `twolevelrandomslope2.stan`, which has one hierarchical level for species, represented here by  $j$ , each observation is  $i$ , and partial pooling on the slopes ( $\beta$ ) only:

$$y_i = \alpha_{j[i]} + \beta_{j[i]}X_i + \epsilon_i \quad (1)$$

$$\beta_j \sim N(\mu_\beta, \sigma_\beta) \quad (2)$$

Which is the same as this:

$$y_i = \alpha_{sp[i]} + \beta_{sp[i]}X_i + \epsilon_i \quad (3)$$

$$\beta_{sp} \sim N(\mu_\beta, \sigma_\beta) \quad (4)$$

Or this:

$$y_i = a_{j[i]} + b_{j[i]}X_i + \epsilon_i \quad (5)$$

$$b_j \sim N(\mu_b, \sigma_b) \quad (6)$$

Or this:

$$y_i = \alpha_{j[i]} + \beta_{j[i]}(Year_i - 1981) + \epsilon_i \quad (7)$$

$$\beta_j \sim N(\mu_\beta, \sigma_\beta) \quad (8)$$

Or this:

$$y_i = \beta_{0j[i]} + \beta_{1j[i]}(Year_i - 1981) + \epsilon_i \quad (9)$$

$$\beta_{1j} \sim N(\mu_\beta, \sigma_\beta) \quad (10)$$

My personal favorite of all possible combinations:

$$y_i = \alpha_{sp[i]} + \beta_{sp[i]}(Year_i - 1981) + \epsilon_i \quad (11)$$

$$\beta_{sp} \sim N(\mu_\beta, \sigma_\beta) \quad (12)$$

Note that I did not write out the priors on  $\mu_\beta$  and  $\sigma_\beta$  and the  $\alpha_j$ , which are not specified and thus are uniform. I think you could just say in the text that we used the default priors. Also note that I think you could leave the  $\beta$  off  $\mu$  and  $\sigma$  if you really wanted, but perhaps nice for clarity?

For the model `threelevelrandomslope3.stan`, which has a hierarchical level for species, nested within (another hierarchical level) study, and partial pooling on the slopes ( $\beta$ ) and intercepts ( $\alpha$ ) by species, but only pooling on study for the slopes; also, note that all species share a common  $\sigma$  (for intercepts,  $\sigma_\alpha$ , and slopes,  $\sigma_{\beta_1}$ ):

$$y_i = \alpha_{study[sp[i]]} + \beta_{study[sp[i]]}X_i + \epsilon_i \quad (13)$$

$$\alpha_{study[sp]} \sim N(\alpha_{study}, \sigma_\alpha) \quad (14)$$

$$\beta_{study[sp]} \sim N(\beta_{study}, \sigma_{\beta_1}) \quad (15)$$

$$\beta_{study} \sim N(\mu_\beta, \sigma_{\beta_2}) \quad (16)$$

$$\sigma_\alpha \sim N(0, 5) \quad (17)$$

$$\sigma_{\beta_1} \sim N(0, 5) \quad (18)$$

$$\sigma_{\beta_2} \sim N(0, 5) \quad (19)$$

$$\mu_\beta \sim \dots \text{no prior specified} \quad (20)$$

Again, many variants of this possible (see above). For example, you could do species, indexed here by  $j$ , nested within study, indexed by  $k$  and get:

$$y_i = \alpha_{k[j[i]]} + \beta_{k[j[i]]}X_i + \epsilon_i \quad (21)$$

$$\alpha_{k[j]} \sim N(\alpha_k, \sigma_\alpha) \quad (22)$$

$$\beta_{k[j]} \sim N(\beta_k, \sigma_{\beta_1}) \dots \quad (23)$$

$$\beta_k \sim N(\mu_\beta, \sigma_{\beta_2}) \dots \quad (24)$$

See also: 12.5 in Gelman & Hill, pages 262-265.