

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 (β) only:

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

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

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:

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

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

Or this:

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

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

Or this:

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

$$\beta_1 \sim N(\mu_\beta, \sigma_\beta) \quad (10)$$

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 μ_β and σ_β , 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 β off μ and σ if you really wanted, but perhaps nice for clarity?

For the model `threelevelrandomslope3.stan`, which has one hierarchical level for species, nested within study, indexed, and partial pooling on the slopes (β) and intercepts (α) by study, but only pooling on species for the slopes (I think):

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

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

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

$$\mu_{\beta} \sim N(\mu_{\beta 2}, \sigma_{\beta 2}) \quad (16)$$

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

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

$$\sigma_{\beta 2} \sim N(0, 5) \quad (19)$$

$$\mu_{\beta 2} \sim \dots \text{no prior specified} \quad (20)$$

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:

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

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

$$\beta_k \sim N(\mu_{\beta[j]}, \sigma_{\beta[j]}) \dots \quad (23)$$

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