

Joint modeling notes and thoughts

For modeling trait values estimated at the species-level from one model to help predict phenology data from OSPREE, which model makes the most sense?

Update thoughts, 26 March 2020



Joint trait and phenology model formulated like this:

$$\begin{aligned}\hat{y}_{trait,i} &= \alpha_{trait,grand} + \alpha_{trait,sp[i]} + \alpha_{study[i]} \\ \alpha_{trait,sp} &\sim N(0, \sigma_{\alpha,trait}) \\ \alpha_{study} &\sim N(0, \sigma_{\alpha,study}) \\ y_{trait} &\sim N(\hat{y}_{trait}, \sigma_{trait,y}^2) \\ \hat{y}_{pheno,i} &= \alpha_{pheno,sp[i]} + \beta_{forcing_{sp[i]}} * F_i \\ \beta_{forcing_{sp}} &= \alpha_{forcing_{sp}} + \beta_{trait:pheno} * \alpha_{trait,sp} \\ \alpha_{pheno,sp} &\sim N(\mu_{\alpha,pheno}, \sigma_{\alpha,pheno}) \\ \alpha_{forcing_{sp}} &\sim N(\mu_{\alpha,forcing}, \sigma_{\alpha,forcing}) \\ y_{pheno} &\sim N(\hat{y}_{pheno}, \sigma_{y,pheno}^2)\end{aligned}$$

Side note ... this model:

$$\begin{aligned}\hat{y}_{trait,i} &= \alpha_{trait,grand} + \alpha_{trait,sp[i]} + \alpha_{study[i]} \\ \alpha_{trait,sp} &\sim N(0, \sigma_{\alpha,trait}) \\ \alpha_{study} &\sim N(0, \sigma_{\alpha,study}) \\ y_{trait} &\sim N(\hat{y}_{trait}, \sigma_{trait,y}^2)\end{aligned}$$

And this model:

$$\begin{aligned}y_{trait,i} &= \alpha_{trait,sp[i]} + \alpha_{study[i]} + \epsilon_{trait,i} \\ \alpha_{trait,sp} &\sim N(\mu_{\alpha,trait}, \sigma_{\alpha,trait}) \\ \alpha_{study} &\sim N(\mu_{\alpha,study}, \sigma_{\alpha,study}) \\ \epsilon_{trait} &\sim N(0, \sigma_{trait,y}^2)\end{aligned}$$

I believe are the same, but I was clearer about \hat{y}_{trait} (predicted y) versus the data (y_{trait}) in the first version, and in the first version I showed that you need to break out $\alpha_{trait,grand}$ when you have multiple intercepts.