

‘Joint’ modeling notes and thoughts

For modeling trait values estimated at the species-level from one model for a giant trait database (TRY, which has a lot of noise to it) to help predict phenology at the species-level, with data from OSPREE (our in-house phenology database of experiments of leafout dates in response to forcing (F), chilling, daylength etc.).

Update thoughts, 26 March 2020

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

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