Methods

Model

For each of n species, we assumed that data were generated from the following sampling distribution:

$$y_j \sim \mathcal{N}(\mu_j, \sigma_e^2) \tag{1}$$

where

$$\mu_j = \alpha_j + \beta_{1,j}X_2 + \beta_{2,j}X_2 + \beta_{3,j}X_3 \tag{2}$$

Predictors X_1, X_2, X_3 are standardized forcing, chilling, and photoperiod, and their effects on the phenology of species j are determined by parameters $\beta_{1,j}$, $\beta_{2,j}$, $\beta_{3,j}$ representing traits. These traits, including the species-specific intercept α_j, are elements of the following normal random vectors:

$$\begin{aligned}
\boldsymbol{\alpha} &= \{\alpha_1, \ldots, \alpha_n\}^T \text{ such that } \boldsymbol{\alpha} \sim \mathcal{N}(\mu_\alpha, \boldsymbol{\Sigma_\alpha}) \\
\boldsymbol{\beta_1} &= \{\beta_{1,1}, \ldots, \beta_{1,n}\}^T \text{ such that } \boldsymbol{\beta_1} \sim \mathcal{N}(\mu_{\beta_1}, \boldsymbol{\Sigma_{\beta_1}}) \\
\boldsymbol{\beta_2} &= \{\beta_{2,1}, \ldots, \beta_{2,n}\}^T \text{ such that } \boldsymbol{\beta_2} \sim \mathcal{N}(\mu_{\beta_2}, \boldsymbol{\Sigma_{\beta_2}}) \\
\boldsymbol{\beta_3} &= \{\beta_{3,1}, \ldots, \beta_{3,n}\}^T \text{ such that } \boldsymbol{\beta_3} \sim \mathcal{N}(\mu_{\beta_3}, \boldsymbol{\Sigma_{\beta_3}})
\end{aligned} \tag{3}$$

where the means of the multivariate normal distributions are root trait values (i.e., trait values prior to evolving across a phylogenetic tree) and $\boldsymbol{\Sigma_i}$ are $n \times n$ phylogenetic variance-covariance matrices of the form:

$$\begin{bmatrix}
\sigma_i^2 & \lambda_i \times \sigma_i^2 \times \rho_{12} & \ldots & \lambda_i \times \sigma_i^2 \times \rho_{1n} \\
\lambda_i \times \sigma_i^2 \times \rho_{21} & \sigma_i^2 & \ldots & \lambda_i \times \sigma_i^2 \times \rho_{2n} \\
\vdots & \vdots & \ddots & \vdots \\
\lambda_i \times \sigma_i^2 \times \rho_{n1} & \lambda_i \times \sigma_i^2 \times \rho_{n2} & \ldots & \sigma_i^2
\end{bmatrix} \tag{4}$$

where σ_i^2 is the rate of evolution across a tree for trait i (here assumed to be constant along all branches), λ_i is Pagel's D, which scales branch lengths and therefore is a measure of the "phylogenetic signal" within trait i (note: because estimates can be partitioned into phylogenetic and nonphylogenetic components in this model, $0 \leq \lambda \leq 1$; see Freckleton et al. 2002 Am Nat), and ρ_{xy} is the phylogenetic correlation between species x and y, or the fraction of the tree shared by the two species.

The above specification is exactly equivalent to writing equation 2 in terms of root trait values and residuals, such that:

$$\mu_j = \mu_\alpha + \mu_{\beta_1} X_1 + \mu_{\beta_2} X_2 + \mu_{\beta_3} X_3 + e_{\alpha_j} + e_{\beta_{1,j}} + e_{\beta_{2,j}} + e_{\beta_{3,j}} \tag{5}$$

where the residual error terms (e.g., e_{α_j}) are elements of normal random vectors from multivariate normal distributions centered on 0 with the same phylogenetic variance-covariance matrices as in equation 4.