

# Methods

## Model

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

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

where

$$\mu_j = \alpha_j + \beta_{1,j}X_1 + \beta_{2,j}X_2 + \beta_{3,j}X_3 \quad (2)$$

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  $\alpha_j$ , are elements of the following normal random vectors:

$$\begin{aligned} \boldsymbol{\alpha} &= \{\alpha_1, \dots, \alpha_n\}^T \text{ such that } \boldsymbol{\alpha} \sim \mathcal{N}(\mu_{\boldsymbol{\alpha}}, \boldsymbol{\Sigma}_{\boldsymbol{\alpha}}) \\ \boldsymbol{\beta}_1 &= \{\beta_{1,1}, \dots, \beta_{1,n}\}^T \text{ such that } \boldsymbol{\beta}_1 \sim \mathcal{N}(\mu_{\boldsymbol{\beta}_1}, \boldsymbol{\Sigma}_{\boldsymbol{\beta}_1}) \\ \boldsymbol{\beta}_2 &= \{\beta_{2,1}, \dots, \beta_{2,n}\}^T \text{ such that } \boldsymbol{\beta}_2 \sim \mathcal{N}(\mu_{\boldsymbol{\beta}_2}, \boldsymbol{\Sigma}_{\boldsymbol{\beta}_2}) \\ \boldsymbol{\beta}_3 &= \{\beta_{3,1}, \dots, \beta_{3,n}\}^T \text{ such that } \boldsymbol{\beta}_3 \sim \mathcal{N}(\mu_{\boldsymbol{\beta}_3}, \boldsymbol{\Sigma}_{\boldsymbol{\beta}_3}) \end{aligned} \quad (3)$$

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:

$$\begin{bmatrix} \sigma_i^2 & \lambda_i \times \sigma_i \times \rho_{12} & \dots & \lambda_i \times \sigma_i \times \rho_{1n} \\ \lambda_i \times \sigma_i \times \rho_{21} & \sigma_i^2 & \dots & \lambda_i \times \sigma_i \times \rho_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ \lambda_i \times \sigma_i \times \rho_{n1} & \lambda_i \times \sigma_i \times \rho_{n2} & \dots & \sigma_i^2 \end{bmatrix} \quad (4)$$

where  $\sigma_i^2$  is the rate of evolution across a tree for trait  $i$  (here assumed to be constant along all branches),  $\lambda_i$  scales branch lengths and therefore is a measure of the “phylogenetic signal” within a species trait, and  $\rho_{xy}$  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:

$$\mu_j = \mu_\alpha + \mu_{\beta_1} X_1 + \mu_{\beta_2} X_2 + \mu_{\beta_3} X_3 + e_{\alpha_j} + e_{\beta_1,j} + e_{\beta_2,j} + e_{\beta_3,j} \quad (5)$$

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