

Phylogenetic phylo-LMM (MCMCglmm) – three views

1. Index form

The per-observation reading: what happens for each row i of your data.

$$\begin{aligned} \text{Zr}_i \mid \mu_i, \sigma &\sim \text{Normal}(\mu_i, \sigma^2) \\ \mu_i &= \beta_0 + u_{\text{species}(i)} \\ \mathbf{u}_{\text{species}} &\sim \mathcal{N}(\mathbf{0}, \sigma_{\text{species}}^2 \mathbf{A}) \end{aligned}$$

Coefficient reading. On the response scale, $\hat{\beta}$ is the additive change in the mean of the response for a one-unit increase in the predictor (identity link – no back-transformation needed).

2. Matrix form

The same model in matrix notation. The structural contract every textbook past chapter 4 switches to.

$$\begin{aligned} \mathbf{zr} \mid \boldsymbol{\mu}, \boldsymbol{\sigma} &\sim \mathcal{N}(\boldsymbol{\mu}, \sigma^2 \mathbf{I}_n) \\ \boldsymbol{\mu} &= \mathbf{X}\boldsymbol{\beta} + \mathbf{u} \\ \mathbf{u}_{\text{species}} &\sim \mathcal{N}(\mathbf{0}, \sigma_{\text{species}}^2 \mathbf{A}_{116 \times 116}) \end{aligned}$$

3. Worked observation ($i = 1$)

The index-form equations evaluated at the first observation of your data, with coefficient estimates plugged in.

$$\hat{\mu}_1 = 0.366 + (-0.151) \approx 0.215$$

Observed $\text{Zr}_1 = 0.166$; predicted mean $\hat{\mu}_1 = 0.215$ (response scale); residual $\hat{\epsilon}_1 = -0.0485$ (observed = mean + residual).

Stacking the same response equation for all $n = 60$ observations:

$$\underbrace{\begin{bmatrix} 0.166 \\ 1.12 \\ 0.66 \\ 1.05 \\ 0.676 \\ \vdots \\ 0.172 \\ 0.0853 \end{bmatrix}}_{\mathbf{zr}_{60 \times 1} \text{ (observed)}} = \underbrace{\begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \\ \vdots \\ 1 \\ 1 \end{bmatrix}}_{\mathbf{X}_{60 \times 1}} \underbrace{\begin{bmatrix} 0.366 \end{bmatrix}}_{\hat{\boldsymbol{\beta}}_{1 \times 1} \text{ (estimated)}} + \underbrace{\begin{bmatrix} -0.0485 \\ 0.351 \\ 0.057 \\ 0.289 \\ 0.285 \\ \vdots \\ -0.178 \\ -0.0958 \end{bmatrix}}_{\hat{\boldsymbol{\epsilon}}_{60 \times 1} \text{ (residual)}}$$

And the structured-covariance prior on $\mathbf{u}$. The random effect that gives this model its structural-dependence character:

$$\text{Cov}(\hat{\mathbf{u}}) = \sigma_p^2 \cdot \underbrace{\begin{bmatrix} 0.161 & 0 & 0.161 & 0.161 & 0.161 & \cdots & 0 & 0 \\ 0 & 0.0946 & 0 & 0 & 0 & \cdots & 0.0946 & 0.0946 \\ 0.161 & 0 & 0.228 & 0.228 & 0.228 & \cdots & 0 & 0 \\ 0.161 & 0 & 0.228 & 0.298 & 0.298 & \cdots & 0 & 0 \\ 0.161 & 0 & 0.228 & 0.298 & 0.565 & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0.0946 & 0 & 0 & 0 & \cdots & 1 & 0.867 \\ 0 & 0.0946 & 0 & 0 & 0 & \cdots & 0.867 & 1 \end{bmatrix}}_{\mathbf{A}_{116 \times 116}}$$