

Your basic PMM (phylogenetic mixed model) ...as I understand it:

$$y = \alpha + \beta x + a + e \quad (1)$$

$$a \sim \text{normal}(0, \sigma_P^2 \Sigma) \quad (2)$$

$$e \sim \text{normal}(0, \sigma_R^2 I) \quad (3)$$

... where α and β , respectively, are the intercept and the slope for the co-factor x , a is the phylogenetic random effect, and e is the residual error. Σ is a phylogenetic correlation matrix.

What I would like to do is have the phylogenetic effect structure the species-level slopes (while also allowing partial pooling on the species given my uneven real data, that is, for some species I might have 3 observations, each at a different x value, and for other species, I have 30 observations). So here's my toy example

$$y = \beta x + e \quad (4)$$

$$\beta \sim MVN(0, \Phi \Sigma) \quad (5)$$

$$e \sim \text{normal}(0, \sigma_y) \quad (6)$$

$$(7)$$

In the Stan code, β is:

```
b_force ~ multi_normal(rep_vector(0, n_sp),
diag_matrix(rep_vector(null_intercepts_b, n_sp)) + lam_intercepts_b * Vphy;
```

To make this clearer (maybe), let α be `null_intercepts_b` and λ be `lam_intercepts_b`.

When `Vphy` is set to have 1s down the diagonal (e.g., `Vphy=vcv(phylo, corr=TRUE)`) the above simplifies to this:

$\Phi \Sigma =$

$$\begin{bmatrix} \alpha + \lambda & \lambda & \lambda \\ \lambda & \alpha + \lambda & \lambda \\ \lambda & \lambda & \alpha + \lambda \end{bmatrix} \quad (8)$$

Perhaps something similar to what happens in PGLS (as best I understand, next page) would be better? This would be something like:

$$\beta \sim MVN(\mu, \Phi \Sigma) \quad (9)$$

$$\Phi \Sigma = \begin{bmatrix} \sigma_\beta & \lambda \sigma_\beta & \lambda \sigma_\beta \\ \lambda \sigma_\beta & \sigma_\beta & \lambda \sigma_\beta \\ \lambda \sigma_\beta & \lambda \sigma_\beta & \sigma_\beta \end{bmatrix} \quad (10)$$

where μ is a single coefficient estimate. Though Will sent me code for this and it doesn't seem to work either