$$y = \alpha_0 + \alpha + \beta x + e \tag{1}$$
$$\alpha \sim MVN(0, \sigma^2_{P\alpha}) \tag{2}$$
$$\beta \sim MVN(0, \sigma^2_{P\beta}) \tag{3}$$
$$e \sim normal(0, \sigma^2_y) \tag{4}$$
$$\sigma^2_{P\alpha} = \alpha_\alpha + \lambda_\alpha * \Sigma \tag{5}$$
$$\sigma^2_{P\beta} = \alpha_\beta + \lambda_\beta * \Sigma \tag{6}$$
$$\tag{7}$$

Where Σ is the phylogenetic structure, α_0 is a grand mean and species-level intercepts are partially pooled by phylogeny, scaled by λ_α and slopes are also are partially pooled by phylogeny, scaled by λ_β, and there is some residual error σ_y. Again, I ask what's wrong with this model?