Bayes Wrap-Up: Three other model examples:

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(1) Basic hierarchical - all groups exchangeable:

$$\hat{y}_i \sim \alpha_{[sp]}$$

$$\alpha_{[sp]} \sim normal(\mu_{sp}, \sigma_{sp})$$

$$y_i \sim normal(\hat{y}_i, \sigma_y)$$

Add covariance from evol. distance, geographical distance...

$$\hat{y}_i \sim \alpha_{[sp]}$$

repeating vector of same value

$$\alpha_{[sp]} \sim multinormal(\mu_{sp}, \Sigma_\alpha)$$

often = 1

$$\Sigma_\alpha = \begin{bmatrix} \rho_{1,1} & \rho_{1,2} & \cdots \\ \rho_{2,1} & \rho_{2,2} & \cdots \\ \rho_{3,1} & \rho_{3,2} & \rho_{3,3} \end{bmatrix} \times (\sigma_{sp})$$ will add this structure

$$\begin{bmatrix} \sigma & & \\ \rho(\sigma^2) & & \text{etc.} \end{bmatrix}$$

BUT! It will really force the structure & you likely would prefer the model fit the rel. role of covar.

one way to do that $\Rightarrow$

$$\Sigma_\alpha \begin{bmatrix} \sigma^2 & \cdot & \cdot \\ \lambda\rho_{2,1}\sigma & \sigma^2 & \cdot \\ \lambda\rho_{3,1}\sigma & \lambda\rho_{3,2}\sigma & \sigma^2 \end{bmatrix}$$

λ scales branches

$\lambda = 1$ returns above; $\lambda = 0$ covar matters not at all

See Morales-Castilla et al. 2024

Loughnan et al. 2024

Joint Model: Species' Traits (measured across spp. & studies, eg. TRY, BIEN etc.) predict spp.' response to °C

Trait model:

$$\hookrightarrow \hat{Y}_i = \alpha + \alpha_{sp_{trait}} + \alpha_{study_{trait}}$$

trait observation

$$\alpha_{sp_{trait}} \sim N(0, \sigma_{sp})$$

$$\alpha_{study} \sim N(0, \sigma_{study})$$

$$Y_i \sim N(\hat{Y}_i, \sigma_{y_{trait}})$$

$$* \alpha_{sp_{trait}} = \alpha + \alpha_{sp}$$

Response to °C model:

°C

latent predictor

$$\hat{y}_i = \alpha_{sp} + \beta_{sp}(x)$$

$$\beta_{sp} = \alpha_{\beta sp} + \beta_{trait_{sp}}(\alpha_{sp_{trait}})$$

$$\alpha_{\beta sp} \sim normal(\mu_{\beta sp}, \sigma_{\beta sp})$$

$$y_i \sim normal(\hat{y}_i, \sigma_y)$$

* You can have latent predictors & responses

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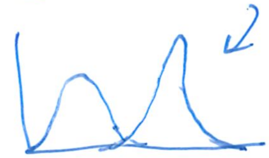
Mixture model

An example w/ a latent response is mixture models.

Z is the probability of an obs. y being part of same data generating model.

The simplest form of this is when z sorts into 2 normal distributions



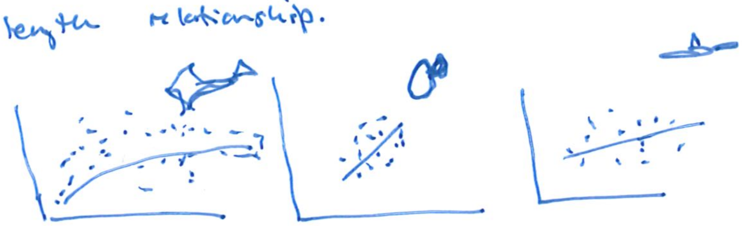
A mixture model will fit:

dist'n 1 $\sim$ normal (μ_1, σ_1)

dist'n 2 $\sim$ normal (μ_2, σ_2)

and λ — probability of sorting into either.

But you can have whatever alternative data generating models you want! For example, imagine 3 qualitative fish shapes that affect the bodymass ~ length relationship.



You could fit shape as a fixed or hierarchical component of your model but a mixture model would give you: (If time allows, ask class to guess.)

(1) Easy way to get different variances in each relationship

(2) Test your idea that shape matters (model decides for each observation) versus enforcing it.

But! Mixture models can be bad when you lack good prior information / domaine expertise. For example, in the fish example the # of shapes would define the # of diff. data generating models you allow & that is very helpful to avoid model degeneracy.