

Cat's Ranges Model

A 3 level Hierarchical model with ncp

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1 Data and question

This model takes what I assume is OSPREE forcing and photoperiod data for lots of studies and species. There is an additional level of variation in this data, which is the population the species comes from. I think it is possible for different species to come from the same population, but Cat you should correct me if I'm wrong. The question we focus on is whether there is greater variation within a species (in terms of variation between populations) than between species.

2 Model

This model differs a bit from Cat's original one. Maybe we will get time to discuss how they differ at the end of the meeting. The original code is in *stan* `/nointer_3levelwpop_force&photo_ncp.stan`, and the modified code I refer to in this documents is in *stan* `/nointer_3levelwpop_force&photo_ncp_FaithExample.stan`

$$\tilde{y}_i \sim normal(\mu_i, \sigma_y) \tag{1}$$

$$\mu_i = \alpha + \alpha_{study} + \alpha_{sppop} + force_i * \beta_{force,sppop} + photo_i * \beta_{photo,sppop} \tag{2}$$

Study intercept

$$\alpha_{study} = \sigma_{\alpha,study} * \alpha_{rawstudy} \tag{3}$$

Species intercept

$$\alpha_{species} = \sigma_{\alpha,species} + \alpha_{raw_{species}} \quad (4)$$

Subpopulation intercept

$$\alpha_{sppop} = \alpha_{species} + \sigma_{\alpha,sppop} * \alpha_{raw_{sppop}} \quad (5)$$

Species forcing slope

$$\beta_{force,species} = \beta_{force} + \sigma_{\beta_{force,species}} * \beta_{raw_{force}} \quad (6)$$

Subpopulation forcing slope

$$\beta_{force,sppop} = \beta_{force,species} + \sigma_{\beta_{force,sppop}} * \beta_{raw_{force,sppop}} \quad (7)$$

Species photoperiod slope

$$\beta_{photo,species} = \beta_{photo} + \sigma_{\beta_{photo,species}} * \beta_{raw_{photo}} \quad (8)$$

Subpopulation photoperiod slope

$$\beta_{photo,sppop} = \beta_{photo,species} + \sigma_{\beta_{photo,sppop}} * \beta_{raw_{photo,sppop}} \quad (9)$$

3 Priors

Grand intercept

$$\sigma_{\alpha,study} \sim normal(0, 20) \quad (10)$$

Study intercept

$$\sigma_{\alpha,study} \sim normal(0, 20) \quad (11)$$

$$\alpha_{raw_{study}} \sim normal(0, 1) \quad (12)$$

Species intercept

$$\alpha_{raw_{species}} \sim normal(0, 1) \quad (13)$$

$$\sigma_{\alpha,species} \sim normal(0, 20) \quad (14)$$

Subpopulation intercept

$$\sigma_{\alpha,sppop} \sim normal(0, 20) \quad (15)$$

$$\alpha_{raw_{sppop}} \sim normal(0, 1) \quad (16)$$

Grand forcing slope

$$\beta_{force} \sim normal(0, 20) \quad (17)$$

Species forcing slope

$$\beta_{raw_{force}} \sim normal(0, 1) \quad (18)$$

$$\sigma_{\beta_{force,species}} \quad (19)$$

Subpopulation forcing slope

$$\sigma_{\beta_{force,sppop}} \sim normal(0, 20) \quad (20)$$

$$\sigma_{\beta_{force,sppop}} \quad (21)$$

Grand photoperiod slope

$$\beta_{photo} \sim normal(0, 20) \quad (22)$$

Species photoperiod slope

$$\sigma_{\beta_{photo,species}} \quad (23)$$

$$\beta_{raw_{photo}} \sim normal(0, 1) \quad (24)$$

Subpopulation photoperiod slope

$$\sigma_{\beta_{photo,sppop}} \quad (25)$$

$$\beta_{raw_{photo,sppop}} \sim normal(0, 1) \quad (26)$$

General variance

$$\sigma_y \sim normal(0, 10) \quad (27)$$

3.1 Priors on parameters made up of hyperparameters

I have changed the structure of Cat's model mostly in terms of priors. I think, and we should discuss this, that priors should generally go parameters that are on the right side of the equals sign. Each prior parameter then interacts with the other prior parameters to get a new combination prior distribution. For example, in the case of the study level effect on the intercept, $\alpha_{study} = \sigma_{\alpha,study} * \alpha_{raw_{study}}$, the priors should be on $\sigma_{\alpha,study}$ and $\alpha_{raw_{study}}$ rather than on α_{study} . Theoretically you could put the prior on α_{study} , but then how does the model know how to partisan information?

4 Model explained in words

$$\tilde{y}_i \sim normal(\mu_i, \sigma_y) \quad (28)$$

Every \tilde{y}_i value is centered around a mean predicted value μ_i with a normal distribution of width σ_y

$$\mu_i = \alpha + \alpha_{study} + \alpha_{sppop} + force_i * \beta_{force,sppop} + photo_i * \beta_{photo,sppop} \quad (29)$$

Each mean predicted value μ_i has intercept which is a combination of a grand intercept (α), an intercept based on the study of value i (α_{study}), and intercept variation due to the species and

population combination (α_{sppop}). There are also two slopes that relate forcing ($\beta_{force,sppop}$) and photoperiod ($\beta_{photo,sppop}$) of value i to its predicted μ_i value. These slope values depend on the species and subpopulation of value i , meaning a different species and subpopulation combination may react faster or slower to forcing and photoperiod.

$$\alpha_{study} = \sigma_{\alpha,study} * \alpha_{raw_{study}} \quad (30)$$

Each study deviates somewhat from the grand mean intercept α ; we call this value α_{study} . Sometimes you might see this written as $\alpha_{study} \sim normal(\alpha, \sigma_{\alpha,study})$.

$$\alpha_{sppop} = \alpha_{species} + \sigma_{\alpha_{force,sppop}} * \alpha_{raw_{force,sppop}} \quad (31)$$

Each population deviates somewhat from its species mean value ($\alpha_{species}$). The amount they deviate a normal distribution with a width of $\sigma_{\alpha_{force,sppop}}$.

$$\alpha_{species} = \sigma_{\alpha,species} * \alpha_{raw_{species}} \quad (32)$$

How much each species deviates from the grand mean α value is called $\alpha_{species}$, and is drawn from a normal distribution of width $\sigma_{\alpha,species}$.

$$\beta_{force,sppop} = \beta_{force,species} + \sigma_{\beta_{force,sppop}} * \beta_{raw_{force,sppop}} \quad (33)$$

Each population's rate of change due to an amount of forcing, that is the slope of forcing, is somewhat different. We describe this as the population values being centered around its species mean slope $\beta_{force,species}$ and has a distribution of width $\sigma_{\beta_{force,sppop}}$.

$$\beta_{force,species} = \beta_{force} + \sigma_{\beta_{force,species}} * \beta_{raw_{force}} \quad (34)$$

Each species's slope value for the effect of forcing is drawn from a normal distribution centred around the grand beta slope β_{force} and a width of $\sigma_{\beta_{force,species}}$.

$$\beta_{photo,sppop} = \beta_{photo,species} + \sigma_{\beta_{photo,sppop}} * \beta_{raw_{photo}} \quad (35)$$

Each population's rate of change due to an amount of photoperiod, that is the slope of photoperiod, is somewhat different. We describe this as the population values being centered around its species mean slope $\beta_{photo,species}$ and has a distribution of width $\sigma_{\beta_{photo,sppop}}$.

$$\beta_{photo,species} = \mu_{\beta_{photo,species}} + \sigma_{\beta_{photo,species}} * \beta_{raw_{photo,sppop}} \quad (36)$$

Each species's slope value for the effect of photoperiod is drawn from a normal distribution centred around the grand beta slope β_{photo} and a width of $\sigma_{\beta_{photo,species}}$.