

Proposed alternative model formulation

D. G. Gannon

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In the sparse Beverton-Holt model fits with varying slopes and intercepts for the linear model component for each species, we have

$$\log(\alpha_{jn}) = \beta_0 + b_{0j} + (\beta_1 + b_{1j})x_n$$

where I have dropped the i subscripts that would index the focal species, j indexes the competitor species, n is the index for the measurement unit (plot), and x_n is the n^{th} measurement for the environmental covariate. Equivalently,

$$\log(\alpha_{jn}) = \mathbf{x}_n^\top (\boldsymbol{\beta}_\alpha + \mathbf{b}_j)$$

where $\mathbf{x}_n = [1 \ x_n]^\top$ and $\mathbf{b}_j = [b_{0j} \ b_{1j}]^\top$. Thus, the model is equivalent to a regression model with slope β_1 and intercept β_0 and random/varying slopes and intercepts for each competing species.

To efficiently expand the model to incorporate more covariates as well as include flexibility in which environmental covariates may have species-specific values, we concatenate $\mathbf{b}_1, \mathbf{b}_2, \dots, \mathbf{b}_S$, where S is the total number of competing species that are not the focal species, into a matrix $\mathbf{B}_{(P_\delta \times S)}$, where P_δ is the number of covariates (including the intercept) that are allowed species-specific deviations from the mean. Also, let

$\mathbf{X}_{(N \times P_\alpha)}$ be a standard regression model matrix for a model with an intercept and $P_\alpha - 1$ covariates and $\mathbf{Z}_{(N \times P_\delta)}$ be a design matrix for the species-specific deviations from the mean effect. Then, we can have

$$\log(\boldsymbol{\alpha}) = \mathbf{X}\boldsymbol{\beta}_\alpha \mathbf{1}^\top + \mathbf{Z}\mathbf{B}$$

where $\mathbf{1}$ is a vector of ones with dimension S , $\boldsymbol{\alpha}_{(N \times S)}$ is a matrix of competition coefficients adjusted for the environment and species, and the logarithm is taken element-wise.

To complete the BH model and allow both intra-specific competition and low-density fecundity to vary with the environment, let

$$\begin{aligned} \log(\boldsymbol{\eta}) &= \mathbf{X}_\eta \boldsymbol{\beta}_\eta \\ &\text{and} \\ \log(\boldsymbol{\lambda}) &= \mathbf{X}_\lambda \boldsymbol{\beta}_\lambda, \end{aligned}$$

where $\boldsymbol{\eta}$ is an N -vector of intra-specific competition coefficients that vary with the environment, $\boldsymbol{\lambda}$ is the vector of low-density seed production values. Thus, both are allowed to vary with the environment, but we could include different environmental variables for the models on $\boldsymbol{\lambda}$ and $\boldsymbol{\eta}$. Finally, let \mathbf{c} be the vector of conspecific abundances in units $1, 2, \dots, N$ and \mathbf{A} be the $(N \times S)$ matrix of heterospecific abundances in each plot. Then, the model can be written as

$$\mu_n = \frac{\lambda_n}{1 + \eta_n c_n + \boldsymbol{\alpha}_n \cdot \mathbf{A}_n^\top},$$

$$f_n \sim \text{Poisson}(\mu_n)$$

where $\boldsymbol{\alpha}_n$ (\mathbf{A}_n) is the n^{th} row of $\boldsymbol{\alpha}$ (\mathbf{A}), treated as a row-vector.

Priors

Sparsity-inducing priors can be including for the species-specific deviations from mean effects by:

$$b_{p1}, b_{p2}, \dots, b_{pS} \stackrel{iid}{\sim} \mathcal{N}(0, \tau^2 \tilde{\xi}_p^2)$$

$$\tilde{\xi}_p^2 = \frac{c^2 \xi_p^2}{c^2 + \tau^2 \xi_p^2}$$

$$\xi_p \sim \mathcal{C}^+(0, 1)$$

$$c^2 \sim \text{inv-Gamma}\left(\frac{\nu}{2}, \frac{\nu s^2}{2}\right)$$

$$\tau \sim \mathcal{C}^+(0, \tau_0)$$

for $p = 1, 2, \dots, P_\delta$.