

Model

We modeled the seedling survival for the dry and rainy seasons separately, in order to better understanding the seasonal dynamics of seedling community.

Neighbor densities

Since the effect of adult neighbors on seedling survival is nonlinear in the logistic scale (Detto et al., 2019), we performed a grid-search for the scaling parameter c between 0 and 1 in 0.01 increments that maximized the likelihood of the following survival model,

$$\text{logit}(p_i) = b_0 + b_1 Z_{1i}^c + b_2 Z_{2i}^c$$

where p_i is the individual survival probability in the i th census interval, and Z_1 and Z_2 are distance-weighted sums of basal areas of conspecifics and heterospecifics respectively. We found that $c = 0.24$ for the dry season and $c = 0.27$ for the rainy season were the best estimates for our dataset.

Survival model

We then build Bayesian hierarchical models that include variation among species in the effects of conspecific and heterospecific neighbours, and rainfall on survival. Survival (s) of seedling i of individual m for species j in census t in plot p was modeled using the Bernoulli distribution (\mathcal{B}):

$$s_{i,j,m,t,p} \sim \mathcal{B}(p_{i,j,m,t,p})$$

$$\text{logit}(p_{i,j,m,t,p}) = \beta_j \cdot \mathbf{z}_i + \phi_p + \omega_t + \psi_m$$

where $\beta_j = [\beta_{j,1}, \beta_{j,2}, \dots, \beta_{j,k}]$ is the coefficient k -vector for species j , k is the number of predictors for an individual seedling, $\mathbf{z}_i = [z_{1,i}, z_{2,i}, \dots, z_{k,i}]$ is the row vector of predictors of size k for an individual seedling, ϕ_p is the random effect for seedling plots, ω_t is the random effect for different census, and ψ_m is the random effect for the repeated observations of the same individuals (note that \cdot denotes dot product). The set of predictor variables ($z_{k,i}$) includes intercept, log of seedling heights, rainfall, densities of conspecific (CONS) and heterospecific (HETS) seedlings, densities of conspecific (CONA) and heterospecific (HETA) adult trees that are scaled by 0.24 for the dry season or 0.27 for the rainy season, and the interactions of rains with CONS, with HETS, with CONA and with HETA.

In the species-level regression, the vector of coefficients (β_{0-k}) of each species j were assumed to have a multivariate normal distribution (\mathcal{MVN});

$$\beta_j \sim \mathcal{MVN}(\mathbf{x}_j \cdot \boldsymbol{\gamma}_k, \boldsymbol{\Sigma}_\beta)$$

where $\mathbf{x}_j = [x_{j,1}, x_{j,2}, \dots, x_{j,l}]$ is the vector of predictors of size l for each species, l is the number of predictors for each species, $\boldsymbol{\gamma}_i = [\gamma_{1,k}, \gamma_{2,k}, \dots, \gamma_{l,k}]$ is the the coefficient l -vector for species j and $\boldsymbol{\Sigma}_\beta$ is the covariance matrix.

In the species-level regression, the vector of coefficients (β_{0-k}) of each species j were assumed to have a multivariate normal distribution through the Cholesky factorization,

$$\beta_j = \mathbf{x}_j \cdot \boldsymbol{\gamma}_k + (\text{diag}(\boldsymbol{\sigma}) \cdot \mathbf{L} \cdot \mathbf{u})^\top$$

where $\mathbf{x}_j = [x_{j,1}, x_{j,2}, \dots, x_{j,l}]$ is the vector of predictors of size l for each species, l is the number of predictors for each species, $\boldsymbol{\gamma}_i = [\gamma_{1,k}, \gamma_{2,k}, \dots, \gamma_{l,k}]$ is the the coefficient l -vector for species j , $\text{diag}(\boldsymbol{\sigma})$ is the diagonal matrix with the diagonal vector of coefficient scales, \mathbf{L} is the Cholesky factor of the original correlation matrix which can be derived using a Cholesky decomposition for the covariance matrix of the original multivariate normal distribution, \mathbf{u} is a $k \times j$ matrix of latent Gaussian variable, and \top denotes the conjugate transpose. The set of predictor variables ($x_{j,l}$) includes LDMC, SDMC, LA, SLA, Chl, LT, C13, C, N, CN, and tlp **(need to edit here according to a trait description section)**.

Posterior distributions of all parameters were estimated using the Hamiltonian Monte Carlo algorithm (HMC) implemented in Stan (Carpenter et al., 2017) using the weakly-informative priors (Gelman et al., 2008). See supplement X for more detail. The Stan code use to fit models is available from Github at: XXXX. Convergence of the posterior distribution was assessed with the Gelman-Rubin statistic with a convergence threshold of 1.1 for all parameters (Gelman et al., 2013).

SI text

Model estimation

We fitted the parameters using laten Gaussian variables for the species-level coefficient

$$s_{i,j,m,t,p} \sim \mathcal{B}(p_{i,j,m,t,p}) \quad (1)$$

$$\beta_j \sim \mathcal{MVN}(\mathbf{x}_j \cdot \gamma_k, \Sigma_\beta) \quad (2)$$

$$\gamma \sim \mathcal{N}(0, 5) \quad (3)$$

$$L \sim \text{LkjCholesky}(2) \quad (4)$$

$$\tilde{\phi}_p, \tilde{\omega}_t, \tilde{\psi}_m, u \sim \mathcal{N}(0, 1) \quad (5)$$

$$\tau_{1-3}, \sigma_{1-3} \sim \mathcal{U}(0, \pi/2) \quad (6)$$

$$\beta = x \cdot \gamma + (\text{diag}(\sigma) \cdot L \cdot u)^\top \quad (7)$$

$$\tau_{1-3} = 2.5 \times \tan(\tau_{1-3}) \quad (8)$$

$$\sigma_{1-3} = 2.5 \times \tan(\sigma_{1-3}) \quad (9)$$

$$\phi_p = \tau_1 \tilde{\phi}_p \quad (10)$$

$$\omega_t = \tau_2 \tilde{\omega}_t \quad (11)$$

$$\psi_m = \tau_3 \tilde{\psi}_m \quad (12)$$

$$(13)$$

50 parameter

$$\text{logit}(p_{i,j,m,t,p}) = \beta_j \cdot \mathbf{z}_i + \phi_p + \omega_t + \psi_m,$$

$$\tau_{1-3} = 2.5 \times \tan(\tau_{1-3}),$$

$$\sigma_{1-3} = 2.5 \times \tan(\sigma_{1-3}),$$

$$\beta = x \cdot \gamma + (\text{diag}(\sigma) \cdot L \cdot u)^\top,$$

$$\phi_p = \tau_1 \tilde{\phi}_p,$$

$$\omega_t = \tau_2 \tilde{\omega}_t,$$

$$\psi_m = \tau_3 \tilde{\psi}_m \quad (14)$$

51 likelihood

$$s_{i,j,m,t,p} \sim \mathcal{B}(p_{i,j,m,t,p}),$$

$$\beta_j \sim \mathcal{MVN}(\mathbf{x}_j \cdot \gamma_k, \Sigma_\beta),$$

$$\tilde{\phi}_p, \tilde{\omega}_t, \tilde{\psi}_m, u \sim \mathcal{N}(0, 1),$$

$$\tau_{1-3}, \sigma_{1-3} \sim \mathcal{U}(0, \pi/2),$$

$$\gamma \sim \mathcal{N}(0, 5),$$

$$L \sim \text{LkjCholesky}(2) \quad (15)$$

The covariance matrix Σ_β can be decomposed as $\Sigma = \text{diag}(\sigma)\Omega\text{diag}(\sigma) = \text{diag}(\sigma)\mathbf{L}\mathbf{L}^\top\text{diag}(\sigma)$ using a Cholesky decomposition (Alvarez et al., 2014), where \mathbf{L} is a Cholesky factor of a correlation matrix (Ω), \mathbf{L}^\top is the conjugate transpose of \mathbf{L} , and σ is the vector of coefficient scales.

References

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