Model

We modeled the seedling survival for the dry and rainy seasons separately. Since the effect of tree neighbors on seedling survival is nonlinear on a 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 ith 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.

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

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

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

where $\boldsymbol{\beta_j} = [\beta_{j,1}, \beta_{j,2}, \ldots, \beta_{j,K}]$ is the coefficient *K*-vector for species *j*, *K* is the number of predictors for an individual seedling, $\boldsymbol{x_i} = [x_{1,i}, x_{2,i}, \ldots, x_{K,i}]$ 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 ($\boldsymbol{x_i}$) includes intercept, log of seedling heights, rainfall, densities of conspecific (*ConS*) and heterospecific (*HetS*) seedlings, densities of conspecific (*ConA*) and heterospecific (*HetA*) 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 ($\boldsymbol{\beta_{1-K}}$) of each species *j* were assumed to have a multivariate normal distribution through the Cholesky factorization (Stan Development Team 2021),

$$\boldsymbol{\beta_j} = \boldsymbol{u_j} \cdot \boldsymbol{\gamma_k} + (\text{diag}(\boldsymbol{\sigma}) \cdot \boldsymbol{L} \cdot \boldsymbol{z})^\top,$$

where $\boldsymbol{u_j} = [u_{j,1}, u_{j,2}, \ldots, u_{j,L}]$ is the vector of predictors of size *L* for species *j*, *L* is the number of predictors for each species (i.e., the number of traits including an intercept), $\boldsymbol{\gamma_k} = [\gamma_{1,k}, \gamma_{2,k}, \ldots, \gamma_{L,k}]$ is the the coefficient *L*-vector for *k*th predictor in the individual-level regression, $\text{diag}(\boldsymbol{\sigma})$ is the diagonal matrix with the diagonal vector of coefficient scales, $\boldsymbol{L}$ 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, $\boldsymbol{z}$ is a $K \times J$ matrix of latent Gaussian variables, J is the number of species, and $\top$ denotes the conjugate transpose. The set of predictor variables ($\boldsymbol{u}_j$) includes LDMC, SDMC, RDMC, LA, SLA, Chl, LT, δC_{13}, C, N, CN, and π_{tlp} To allow comparisons among parameter estimates, all the predictor variables ($\boldsymbol{x}_i$ and $\boldsymbol{u}_j$) were scaled to a mean of 0 and standard deviation of 1.

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). 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).

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