Supplement A: Modeling and computation

Pulsed-resource mast systems and the movement, demographic storage, and diet breadth of consumers

JAMES S. CLARK[1,2], CHASE NŨNES[1], and BRADLEY TOMASEK[1]

March 5, 2018

[1] *Nicholas School of the Environment, Duke University, Durham NC 27708, USA*
[2] *Department of Statistical Science, Duke University, Durham NC 27708, USA*

Contents

SA1 Generative model and prediction

SA1.1 *Model elements*

Elements of the model summarized in *Model components* of the main text are described with additional detail here, with variable definitions from table 2:

- An *observation* consists of covariates for trees and seed traps, including $\{\mathbf{X}_{j,t}, \mathbf{W}_{j,t}, \mathbf{V}_{j,t}, \mathbf{Y}_{j,t}, \mathbf{z}_{j,t}, \mathbf{A}_{j,t}\}$ for plot $j, \dots, J$ in years $t, \dots, T_j$. There are $i = 1, \dots, n_{j,t}$ trees on plot j in year t. There are $s = 1, \dots, S_{j,t}$ seed traps in plot j in year t. The observation matrices are:

- *Sample effort* is contained in the diagonal $S_{j,t} \times S_{j,t}$ matrix $\mathbf{A}_{j,t}$ with diagonal elements holding the trap area (m^{-1}) times deployment time (proportion of the year, traps are occasionally damaged).
- *Predictors* that explain maturation occupy the $n_{j,t} \times q^v$ matrix $\mathbf{V}_{j,t}$. Predictors that explain fecundity occupy the $n_{j,t} \times q^x$ matrix $\mathbf{X}_{j,t}$. If there are random individual effects, they occupy the random effects design $\mathbf{W}_{j,t}$. The different species h are treated as factor levels in $\mathbf{V}_{j,t}, \mathbf{X}_{j,t}$, and $\mathbf{W}_{j,t}$ including all interactions with predictors. This design absorbs the species label into design matrices.
- The length-$n_{j,t}$ *maturation* vector $\mathbf{z}_{j,t}$ holds observed maturation states (often unknown).
- The $S_{j,t} \times M$ *response* matrix $\mathbf{Y}_{j,t}$ holds seed counts. It has one row for each seed-trap year and one column for each seed type m.

• Trap-to-tree distances enter the $S_{j,t} \times n_{j,t}$ *redistribution kernel* matrix $\mathbf{S}_{j,t}$. The distance from seed trap (sj) to tree (ij) is $d_{sij} = |\mathbf{s}_{sj,t} - \mathbf{s}_{ij,t}|$. The t subscript allows for ingrowth of new individuals, for mortality loss, and for the addition or loss of seed traps over time. $\mathbf{S}$ incorporates dispersal parameters $u_g, g = 1, \ldots G$, where g can correspond to species h or to random groups. The redistribution kernel has elements

$$\mathbf{S}_{si} = \frac{u_{h[i]}}{\pi \left(u_{h[i]} + d_{si}^2\right)^2} \quad \text{(SA1.1)}$$

for distance d_{si} and fitted dispersal parameter $u_{h[i]}$, where subscript $h[i]$ references the parameter value for the species h to which tree i belongs. This is a two-dimensional Student's t distribution (Clark et al. 1999).

SA1.2 *In- and out-of-sample prediction*

Seed data are generated by dispersal from mature and fecund trees. Estimates of these states and a dispersal kernel can be used to predict seed data,

$$\left[\mathbf{Y}|\hat{\mathbf{F}}, \mathbf{S}(\hat{\mathbf{u}})\right] \quad \text{(SA1.2)}$$

(variables are defined in table 2). This prediction is available where maturity, fecundity, and dispersal are known (or estimated). To predict out-of-sample, the conditioning variables must be predicted from the posterior distribution of parameters in the model,

$$\hat{\theta} = \left\{ \hat{\boldsymbol{\beta}}^{x}, \hat{\boldsymbol{\beta}}^{v}, \hat{\boldsymbol{\gamma}}, \hat{\sigma}^2, \hat{\mathbf{u}}, \hat{\mathbf{m}} \right\} \tag{SA1.3}$$

Here is the conditioning:

$$[\mathbf{Y}|\mathbf{F}, \mathbf{S}(\hat{\mathbf{u}})] \, [\mathbf{S}(\hat{\mathbf{u}})] \left[\mathbf{F}|\hat{\psi}, \hat{\rho}, \hat{\mathbf{m}}\right] \left[\hat{\psi}|\hat{\boldsymbol{\beta}}^{x}, \hat{\sigma}^2, \hat{\boldsymbol{\gamma}}, \mathbf{X}, \mathbf{W}\right] \left[\hat{\rho}|\hat{\boldsymbol{\beta}}^{v}, \mathbf{z}, \mathbf{V}\right] \left[\hat{\theta}\right] \tag{SA1.4}$$

From right to left, we have a posterior distribution of parameters, maturation status, conditional fecundity, actual fecundity, dispersal, and likelihood. [For model fitting, the posterior distribution is replaced with the prior distribution of parameters]. Predictions from eq. (SA1.2) will be more accurate than eq. (SA1.4), but, again, eq. (SA1.2) is only available for in-sample prediction. The fully generative eq. (SA1.4) can be used for fore- and backcasting. In-sample, it will be less accurate than eq. (SA1.2), because it relies on the capacity to predict maturation and fecundity from environmental variables as opposed to simply estimating them.

SA2 Posterior distribution

The posterior distribution for parameter values in eq. (SA1.4) is

$$[\boldsymbol{\theta}|\mathbf{X}, \mathbf{W}, \mathbf{V}, \mathbf{Y}, \mathbf{z}, \mathbf{A}] \propto \prod_{j,t} Poi(\mathbf{Y}_{j,t}|\mathbf{A}_{j,t}\mathbf{S}_{j,t}\mathbf{F}_{j,t}) \tag{SA2.5}$$

$$\times \prod_{ij} \prod_{t=1}^{T_j} [\psi_{ij,t}|\mathbf{x}'_{ij,t}\boldsymbol{\beta}^{x} + \mathbf{w}'_{ij,t}\boldsymbol{\beta}^{w}_{i}, \sigma^2, \rho_{ij,t}, \psi_{ij,t-p}, \ldots, \psi_{ij,t-1}] \tag{SA2.6}$$

$$\times \prod_{ij} \left(\prod_{t=1-p}^{-1} [\psi_{ij,t}] + \prod_{t=T_j+1}^{T_j+p} [\psi_{ij,t}] \right) \tag{SA2.7}$$

$$\times \prod_{ij} [\mathbf{z}_{ij}|\boldsymbol{\rho_{ij}}] \prod_{t=1}^{T_j} [\rho_{ij,t}|\mathbf{v}_{ij,t}\boldsymbol{\beta}^{v}, \rho_{ij,t-1}] \tag{SA2.8}$$

$$\times [\boldsymbol{\theta}]$$

The $n_{j,t} \times M$ matrix $\mathbf{F}_{j,t}$ has elements given by eq. (SA2.12). In eq. (SA2.6), latent fecundity ψ has a AR(p) representation, with the prior for the beginning and end of the series in eq. (SA2.7). If year effects were in use, the AR(p) terms would be replaced by γ_t on the right side of eq. (SA2.6).

SA2.1 *Dynamics*

The process is a multivariate dynamic (state-space) model for log fecundity and maturation, with a joint distribution of these latent states, $[\psi_{ij,t}, \rho_{ij,t}]$. Both state variables respond to environmental conditions.

Dynamics start with maturation status. The maturation observation model recognizes uncertainty in the assignment of maturation (fruits are often unobservable in crowded canopies) and the fact that trees are not observed in many years. Let $z_{ij,t}$ be the observed status, which can be mature (fruits observed, $z_{ij,t} = 1$), uncertain (fruits not observed, canopy obscure), and immature (entire canopy visible in the fruiting season and fruits not observed, $z_{ij,t} = 0$). $t_{ij,l}$ is the last year in which individual ij was observed to be immature. $t_{ij,m}$ is the first year ij was observed in the mature state. True maturation status is the indicator $\rho_{ij,t} \in \{0, 1\}$, with $\rho_{ij,t} = 1$ being the event that individual ij is mature in year t. Maturation is a one-way process, $[\rho_{ij,t+1} = 1|\rho_{ij,t} = 1] = 1$, and $[\rho_{ij,t} = 1|\rho_{ij,t+1} = 0] = 0$. Status is known to be mature any time after first observed to be mature and to be immature any time before the last time it is established to have been immature. Between these times, the status is unknown and modeled with a probit:

$$\begin{aligned} z_{ij,t_m} = 0 \rightarrow & \quad \rho_{ij,t} = 0, \forall t \leq t_m \\ z_{ij,t_l} = 1 \rightarrow & \quad \rho_{ij,t} = 1, \forall t \geq t_l \\ t_l < t < t_m \rightarrow & \quad [\rho_{ij,t} = 1|\rho_{ij,t-1} = 0] = \Phi\left(\mathbf{v}'_{ijt}\beta^v\right) \end{aligned} \tag{SA2.9}$$

where t_l is an observation year earlier than t, and t_m is an observation year after year t. This relationship between $z_{ij,t}$ and $\rho_{ij,t}$ must be conditioned on past and future imputed states,

$$w_{ij,t}|\rho_{ij,t-1}, \rho_{ij,t+1} \sim N\left(\mathbf{v}'_{ij,t}\beta^v, 1\right) I(w_{ij,t} \in \mathbf{p}^v_{ij,t}) \tag{SA2.10}$$

with a partition

$$\mathbf{p}^{v}_{ij,t} = \begin{cases} (0, \infty) & \rho_{ij,t-1} = 1 \\ (-\infty, 0] & \rho_{ij,t+1} = 0 \\ (-\infty, \infty) & \text{otherwise} \end{cases}$$

that imposes the prior that maturation is a one-way process. The individual is mature, $\rho_{ij,t} = 1$, provided $w_{ij,t} > 0$, and $\rho_{ij,t} = 0$ otherwise.

Conditional fecundity is continuous, $\psi_{ij,t} \in (0, \infty)$, and depends on maturation status,

$$\psi_{ij,t} \in \begin{cases} (1, \infty) & \rho_{ij,t} = 1 \\ (0, 1] & \rho_{ij,t} = 0 \end{cases}$$

Note that fecundity here means the capacity to produce at least one seed. Mature individuals produce seeds at log fecundity

$$\log(\psi_{ij,t}) | \rho_{ij,t} \sim N\left(\mathbf{x}'_{ij,t}\beta^{x}, \sigma^{2}\right) I(\psi_{ij,t} \in \mathbf{p}^{x}_{ij,t}) \tag{SA2.11}$$

with the partition that imposes the prior that maturation is a one-way process,

$$\mathbf{p}^{x}_{ij,t} = \begin{cases} (0, \infty) & \rho_{ij,t-1} = 1 \\ (-\infty, 0] & \rho_{ij,t+1} = 0 \end{cases}$$

Additional terms in the fecundity submodel are given in *Model components* of the main text and summarized in table 2.

SA2.2 *Multiple seed types*

The observation model includes the uncertain assignment of seeds to species. Seed collections are classified as those that can be confidently assigned to a species and those that can only be assigned to genus or even family. There are $h = 1, \ldots, H$ species that might potentially contribute to $m = 1, \ldots, M$ seed types. For example, seed types in a data set might include three *Pinus* species plus a larger category, *Pinus* spp., which includes all seeds that could not be confidently identified to species. A prior seed-type composition matrix for $H = 3$ species might be organized like this:

$$\mathbf{m} = [\mathbf{m}_1, \mathbf{m}_2, \mathbf{m}_3]'$$

$$= \begin{array}{cccccc} & \textit{P. echinata} & \textit{P. taeda} & \textit{P. virginiana} & \textit{P. }\text{spp.} & \\ \left[\begin{array}{c} \\ \\ \\ \end{array}\right. & \begin{array}{c} 0.1 \\ 0 \\ 0 \end{array} & \begin{array}{c} 0 \\ 0.2 \\ 0 \end{array} & \begin{array}{c} 0 \\ 0 \\ 0.2 \end{array} & \begin{array}{c} 0.9 \\ 0.8 \\ 0.8 \end{array} & \left.\begin{array}{c} \\ \\ \\ \end{array}\right] \begin{array}{l} h = \textit{P. echinata} \\ h = \textit{P. taeda} \\ h = \textit{P. virginiana} \end{array} \end{array}$$

A row $\mathbf{m}_h$ represents the fraction of seeds produced by species h that are counted in each seed-type class. The rows accommodate observation errors, the fraction of species-h seed that is misclassified as seed type m. The vector corresponding to individual i is designated with the notation $\mathbf{m}_{h[i]}$. The expected fecundity on the seed-type basis is

$$\mathbf{F}_{ij,t}|\psi_{ij,t}, \rho_{ij,t} = \mathbf{m}_{i[h]}\rho_{ij,t}\psi_{ij,t} \tag{SA2.12}$$

Of course, $\mathbf{m}$ must be estimated.

SA3 Prior parameter values

The prior parameter distribution depends on which components are included in the model. *Maturation* and *conditional fecundity* parameters have the prior distributions $MVN(\boldsymbol{\beta}^v|\mathbf{0}, 10\times\mathbf{I}_{q^v})$, and $MVN(\boldsymbol{\beta}^x|\mathbf{0}, 10\times\mathbf{I}_q)$, both non-informative. Random effects have the prior distribution $\boldsymbol{\beta}_i^w \sim MVN(\mathbf{0}, \mathbf{B}_w)$ and $\mathbf{B}_w \sim IW(\mathbf{I}_{q^w}, df)$ with degrees of freedom $df = q^w + \sqrt{n}_+$, the second term being rounded to the nearest integer.

Year effects have the prior distribution $\prod_t N(\gamma_t|0, 10)$. For random groups, $\gamma_{g,t} \sim N(\gamma_t, \tau_t^2)$, with group variance $\tau_t^2 \sim IG(2, 2)$. *Autoregressive lag terms* have the prior distribution $(\alpha_1, \ldots, \alpha_L) \sim MVN(\mathbf{0}, \mathbf{A}_\alpha)$. If there are G random groups, they have the prior $(\alpha_{g,1}, \ldots, \alpha_{g,L}) \sim MVN(\mathbf{0}_G, \mathbf{A}_\alpha)$, with $IW(\mathbf{A}_\alpha|\mathbf{I}_p, p+1)$ (CHECK DIMENSION OF RANDOM LAG TERMS).

Seed composition vectors $\mathbf{m}_h$ have a Dirichlet prior distribution for the composition vectors.

Dispersal parameters have the prior distribution $N(u_h|\tilde{u}, \tilde{U})$. The next stage is $\tilde{u} \sim N(u^*, U^*)$ and $\tilde{U} \sim IG(v_1, v_2)$, where parameter values (u^*, U^*, v_1, v_2) are selected based on understanding of the species dispersal properties.

SA4 Data simulation

The simulator takes numbers of plots, trees, traps, and years as means for stochastic generation of sample size. The simulator follows these steps:

- Generate random species identities for trees.
- Draw random diameters for trees.
- Generate random locations of trees and traps.
- Draw coefficients for maturation, conditional fecundity, and dispersal parameters from a range that can generate patterns like observed data. Both maturation and conditional fecundity have an intercept and a slope for log diameter.
- Draw maturation status of each tree year from the probit submodel, subject to the constraint that this is a one-way transition (eq. (SA2.9)).
- For mature individuals, draw conditional fecundity from eq. (SA2.11).
- Assuming that only 20% of seeds can be assigned to species, construct the $\mathbf{m}_h$ vector for each species h and distribute seed production for each individual according to its species identity.
- Evaluate expected densities at seed trap locations (eq. (1)).
- Draw seed counts from the likelihood.

Code is provided in the Supplemental vignette. For fig. 4, the specific algorithm is:

- Simulate a $n \times T$ fecundity matrix $\mathbf{F} \sim MVN(\boldsymbol{\psi}, \mathbf{C}_{\mathbf{F},n})$ (table SA5.1).
- Simulate random tree coordinates $\mathbf{s}^{\mathcal{N}} = (\mathbf{s}_{i1}, \mathbf{s}_{i2})_{i=1}^{n}$ and random trap coordinates, $\mathbf{s}^{\mathcal{S}} = (\mathbf{s}_{s1}, \mathbf{s}_{s2})_{s=1}^{S}$.
- Generate a distance matrix from the tree locations to the trap locations and evaluate a corresponding kernel matrix $\mathbf{S}(|\mathbf{s}^{\mathcal{S}} - \mathbf{s}^{\mathcal{N}}|; u)$ with dispersal parameter u.
- Evaluate intensities $\boldsymbol{\Lambda}_{\mathcal{S}}|\mathbf{f}_{\mathcal{N}}$ from eq. (1) and draw counts from $y_{s,t} \sim Poi(\lambda_{s,t})$. The variance in simulated $y_{s,t}$ is the horizontal axis in fig. 4. The vertical axis shows the prediction from eq. (6) and its two terms.

SA5 Means and covariances

This section summarizes means and covariances observed by a consumer in the canopy and on the forest floor.

SA5.1 *Space-lag covariance*

The *Tree-time and space-time covariance* of the main text starts with a space-time covariance matrix and moves immediately to summaries thereof. Here we provide additional explanation that is relevant to the interpretation of fig. 10.

We cannot estimate the $nT \times nT$ space-time covariance $\mathbf{C}$, because each (i, i', t, t') combination is observed once. However, we can estimate a lag matrix $\mathbf{C}_L$ consisting of vector blocks. For the simplest example of two individual trees or locations and one lag $(i = 1, i' = 2, p = 1)$, this structure is

$$\mathbf{C}_L = \begin{bmatrix} \mathrm{AC}_1 & \mathrm{CC}_{12} \\ \mathrm{CC}_{21} & \mathrm{AC}_2 \end{bmatrix} = \left[\begin{array}{ccc|ccc} L_{11,-1} & L_{11,0} & L_{11,+1} & L_{12,-1} & L_{12,0} & L_{12,+1} \\ \hline L_{21,-1} & L_{21,0} & L_{21,+1} & L_{22,-1} & L_{22,0} & L_{22,+1} \end{array}\right] \tag{SA5.13}$$

Blocks contain elements $L_{ii',l}, l = -p, \ldots, 0, \ldots, p$. Blocks along the diagonal are the symmetric auto-covariance (AC) vectors, $L_{ii,-l} = L_{ii,+l}$. Off-diagonal blocks are cross-covariance vectors (CC), which are asymmetric, because they depend on which individual leads the other. However, each element in $\mathrm{CC}_{ii'}$ has a counterpart in its mirror block $\mathrm{CC}_{i'i}$, where $L_{ii',-l} = L_{i'i,+l}$. In other words, $\mathbf{C}_L$ becomes block symmetric upon reversing the individual labels and the signs of lag indices in the upper (or lower) block.

Matrix $\mathbf{C}_L$ offers all combinations of tree-tree, year-year, and tree-year covariances. Tree-to-tree covariances are held in off-diagonal blocks (CC_{21} in eq. (SA5.13)). Center elements of the off-diagonal blocks hold the covariances between trees in the same year ($L_{21,0}$). These elements determine the resource heterogeneity that consumers abide by moving between trees, depending on their foraging ambits. The masting phenomenon is identified with episodic seed production in lagged year l', $(L_{ii,l'} > 0, l' > 1)$ and synchronicity $(L_{ii',0} > 0)$. The plots in fig. 10 show columns of $\mathbf{C}_L$ for sequential lags $0, 1, \ldots$.

SA5.2 *Means, covariances and resource scores*

Means, covariances, and aggregated means and variances are provided in table SA5.1. The subscript $\mathbf{A}$ on variables in the upper half of the table can apply to any of the three $n \times T$ matrices $\mathbf{F}, \mathbf{R}$, or $\mathbf{Q}$ (fecundity, resource quality, or their product). Those in the lower half only apply to the $S \times T$ matrix $\mathbf{Q}_G$.

Table SA5.1: Sums, means, and covariances associated that contribute to resource covariance.

Notation[a]	Description[a]	Function[b]	Dimensions[c]
		Canopy	
$\mathbf{c}_{\mathbf{A},T}$	year expectation	$n^{-1}\mathbf{A}'\mathbf{1}_n$	$T \times 1$
$\mathbf{c}_{\mathbf{A},n}$	tree expectation	$T^{-1}\mathbf{A}\mathbf{1}_T$	$n \times 1$
$c_{\mathbf{A},nT}$	total	$\mathbf{1}_n\mathbf{A}\mathbf{1}_T$	scalar
$\bar{c}_{\mathbf{A},nT}$	mean	$(nT)^{-1}c_{\mathbf{A},nT}$	scalar
$\mathbf{C}_{\mathbf{A},T}$	year covariance	$n^{-1}\left(\mathbf{A}-\mathbf{1}_n\mathbf{c}'_{\mathbf{A},T}\right)'\left(\mathbf{A}-\mathbf{1}_n\mathbf{c}'_{\mathbf{A},T}\right)$	$T \times T$
$\mathbf{C}_{\mathbf{A},n}$	tree covariance	$T^{-1}\left(\mathbf{A}-\mathbf{c}_{\mathbf{A},n}\mathbf{1}'_T\right)\left(\mathbf{A}-\mathbf{c}_{\mathbf{A},n}\mathbf{1}'_T\right)'$	$n \times n$
$C_{\mathbf{A},T}$	aggregate variance over years	$\mathbf{1}'_T\mathbf{C}_{\mathbf{A},T}\mathbf{1}_T$	scalar
$C_{\mathbf{A},n}$	aggregate variance over trees	$\mathbf{1}'_n\mathbf{C}_{\mathbf{A},n}\mathbf{1}_n$	scalar
		Forest floor	
$\mathbf{g}_T$	year expectation	$S^{-1}\mathbf{Q}'_G\mathbf{1}_S$	$T \times 1$
$\mathbf{g}_S$	site expectation	$T^{-1}\mathbf{Q}_G\mathbf{1}_T$	$S \times 1$
g_{ST}	total	$\mathbf{1}_S\mathbf{Q}_G\mathbf{1}_T$	scalar
$\bar{g}_{ST}$	mean	$(ST)^{-1}g_{ST}$	scalar
$\mathbf{G}_T$	year covariance	$S^{-1}\left(\mathbf{Q}_G-\mathbf{1}_T\mathbf{g}'_T\right)'\left(\mathbf{Q}_G-\mathbf{1}_S\mathbf{g}'_T\right)$	$T \times T$
$\mathbf{G}_S$	site covariance	$T^{-1}\left(\mathbf{Q}_G-\mathbf{g}_S\mathbf{1}'_T\right)\left(\mathbf{Q}_G-\mathbf{g}_S\mathbf{1}'_T\right)'$	$S \times S$
G_T	aggregate variance over years	$\mathbf{1}'_T\mathbf{G}_{\mathbf{Q},T}\mathbf{1}_T$	scalar
G_S	aggregate variance over sites	$\mathbf{1}'_S\mathbf{G}_{\mathbf{Q},S}\mathbf{1}_S$	scalar

[a] $\mathbf{A}$ represents a $n \times T$ matrix that can be fecundity $\mathbf{F}$, resource $\mathbf{R}$, or the product $\mathbf{Q} = \mathbf{F} \circ \mathbf{R}$.

[b] $\mathbf{Q}_G$ is the $S \times T$ seed quantity $\times$ quality matrix for the forest floor. $\mathbf{1}_j$ is a length-j vector of ones.

[c] Dimensions are T years, n trees, and S sites.

SA5.3 *Covariance on multiple seed types*

Where multiple seed types are included there is a covariance associated with the composition vector $\mathbf{m}_h$. When a fraction of fecundity $f_{ij,t}$ is allocated to each seed type m there is a a sum-to-$f_{ij,t}$ constraint. There is a $M \times M$ simplex covariance among seed types $\mathbf{M}_i$ produced by individual i, having diagonal elements

$$diag(\mathbf{M}_i) = \frac{\mathbf{m}_{i[h]}\left(1 - \mathbf{m}_{i[h]}\right)}{2}$$

where $\mathbf{m}_{i[h]}$ is the detection vector for species h corresponding to individual i. The off-diagonals (covariances) are

$$\mathbf{M}_{i,r,r'} = \frac{-\mathbf{m}_{i[h],m} \sum_{k \neq r'} \mathbf{m}_{i[h],k}}{2}$$

The covariance between seed types is negative, induced by the simplex.

SA5.4 *Entropy*

To quantify the heterogeneity experienced by a consumer across trees, space, years, and hosts we evaluated entropy,

$$\frac{1}{2}\left[\log(2\pi) + \frac{\log|\mathbf{V}|}{d}\right] \tag{SA5.14}$$

where $|\mathbf{V}|$ is the determinant of a $d \times d$ matrix $\mathbf{V}$ that represents one of the covariance matrices $\mathbf{C}_{\mathbf{Q},T}, \mathbf{C}_{\mathbf{Q},n}, \mathbf{G}_T$ or $\mathbf{G}_S$ (table SA5.1). This entropy calculation is reported on a per-dimension basis (per d) due to the multiplicative effect of integrating volume over d dimensions.

SA6 Stability of the AR(p) process

The sequence of fecundities for each tree can be evaluated for its consistency with stable variation. Eigenvalues for time series quantify the tendency for quasi-periodic behavior. For the AR(p) model, we construct the matrix

$$\mathbf{E} = \begin{bmatrix} \psi_1 & \psi_2 & \dots & \psi_{p-1} & \psi_p \\ 1 & 0 & \dots & 0 & 0 \\ 0 & 1 & \dots & 0 & 0 \\ \vdots & \ddots & \ddots & \ddots & \vdots \\ 0 & 0 & \dots & 0 & 0 \\ 0 & 0 & \dots & 1 & 0 \end{bmatrix}$$

(West and Harrison, 1997). If there are random groups, then there is a matrix $\mathbf{E}_g$ for each group, combining the (global) fixed effect and the random effect for that group. A quasi-periodic process has complex eigenvalues. A stationary AR(p) process has all eigenvalues of less than unit modulus (real plus imaginary parts). Eigenvalues are evaluated for the fecundity of each mature tree and summarized by plot and species.

SA7 Dispersal kernel

Seeds arriving in seed traps need not all derive from within the inventory plot (Clark et al., 1998; Muller-Landau et al., 2008; Clark et al., 2004). This possibility suggests an intercept proportional to basal area in eq. (1) as a rough accommodation of long-distance dispersal. We do not include an intercept here, because it can have a large impact on estimates, without actually being sensitive to seeds outside the plot. An intercept has a large impact, because it provides an alternative to the dispersal kernel anytime data are noisy, which is always the case when seed recovery is low. It is insensitive to LDD, because the tail of kernel has no impact on estimates (**).

An approximate influence of LLD is available from eq. (SA1.1), with mean dispersal distance is obtained by integrating arc-wise and with distance,

$$\bar{d} = \frac{\pi\sqrt{u}}{2} \tag{SA7.15}$$

and the seed arriving at a location from beyond distance R is

$$S(R) = \int_R^\infty \oint_{2\pi} \frac{u}{\pi(u+r^2)^2} dr = 2u \int_R^\infty \frac{r}{(u+r^2)^2} dr = \frac{u}{u+2R^2} \tag{SA7.16}$$

(Clark et al. 1999), and a distance-specific intensity

$$l(r) = -\frac{d\log S}{dr} = \frac{4r}{u + 2r^2} \tag{SA7.17}$$

For perspective, if the average seed of a well-dispersed species moves 10 m from the parent in a forest of infinite area that is everywhere the same in composition, then $< 1\%$ of all seed derives from beyond 50 m. The insensitivity to distant sources is shown in the analysis of (Clark et al., 1998). It is consistent with the low scores associated of seed traps that collect few seeds.

In cases where fleshy-fruits are dispersed by songbirds, there is typically still substantial dispersal close to the source that cannot be estimated when an intercept is included in the model.

In addition to an undesirable effect on estimates, the intercept is costly. If we want to ask how much seed might be arriving at a location from outside a plot, we would not integrate arcwise, but rather would require Reimann sums for areas that differ in every direction from every seed trap. They would necessarily be truncated at some distance beyond which inputs would be assumed negligible. For MCMC, this would require reevaluation at each iteration, an extremely costly algorithm. Because estimates are dominated by the high values near parent trees, the effect of the intercept cannot be interpreted as an LDD contribution.

SA8 Data summary

Data come from 11 inventory plots initiated between the years of 1991 and ** and sampled until the present. Habitats range from southeastern Piedmont mixed pine-hardwoods (DFEE, DFEW, DFBW, BFHW), Appalachian foothills (CW118, CW119, MHF, MHP), and New England mixed hardwoods (HFBW, HFS). Numbers of trees, tree-years, seed and cone types, seed traps, trap-years are listed in section SA9.1.

As a fraction of basal area, seed production is comparable across plots, evaluated as

$$\frac{\text{seeds } \frac{1}{\text{ha yr}}}{\text{BA } \frac{\text{m}^2}{\text{ha}}} = \frac{\text{seeds}}{\text{BA m}^2\text{yr}} \tag{SA8.18}$$

In portions of plots with abundant trees, seed productivity extends to > 1000 seeds per m^2 of basal area.

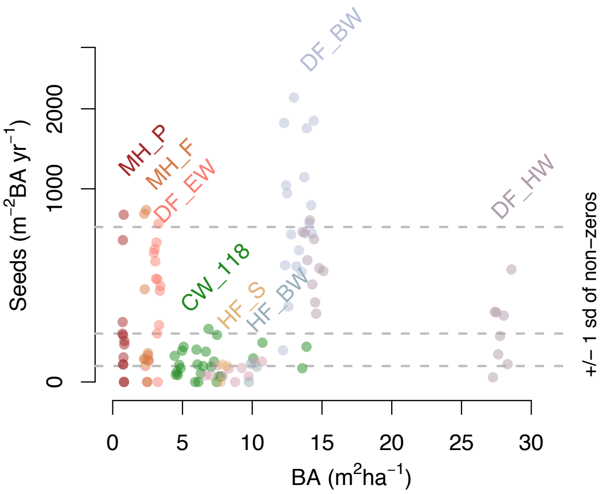

Figure SA8.1: Each dot represents a single plot-year mean, evaluated from eq. (SA8.18). Horizontal lines identify the median and ±1 standard deviation of non-zero values.

Table SA9.2: Sample size by plot.

	CW118	CW218	CWUG	DFBW	DFEE	DFEW	DFHW	HFBW	HFS	MHF	MHP	total
Trees												
pinuEchi	0	0	0	47	0	20	1	0	0	0	0	68
pinuRigi	32	0	0	0	0	0	0	0	0	0	0	32
pinuStro	3	29	0	0	0	0	0	174	145	82	22	455
pinuTaed	0	0	4	353	137	66	192	0	0	0	0	752
pinuVirg	0	0	0	10	6	11	1	0	0	0	0	28
Tree-years												
pinuEchi	0	0	0	793	0	228	18	0	0	0	0	1039
pinuRigi	838	0	0	0	0	0	0	0	0	0	0	838
pinuStro	58	508	0	0	0	0	0	484	391	896	248	2585
pinuTaed	0	0	64	5931	1353	722	3334	0	0	0	0	11404
pinuVirg	0	0	0	169	60	124	18	0	0	0	0	371
Traps	20	20	43	148	9	69	66	36	36	35	36	518
Trap-yrs	540	540	688	2516	90	828	1188	108	108	420	432	7458
Seed types												
pinuRigi	219	7	0	0	0	0	0	0	0	0	0	226
pinuStro	0	0	0	0	0	0	0	5	15	5	11	36
pinuTaed	0	0	0	0	0	0	0	0	0	0	2	2
UNKN	190	9	18	20479	49	1419	8853	0	0	520	179	31716
Cones												
pinuStro	0	0	0	0	0	0	0	1	0	0	0	1
UNKN	79	1	2	208	0	15	55	0	0	0	0	360
Immature	0	0	0	0	0	0	0	13	0	0	0	13

SA9 Diagnostics

SA9.1 *Simulated data*

Plots for simulation examples include coefficients (**), predictions (**), and ...

An example MCMC chain for the dispersal parameter in the example described in the main text is shown converging to $u = 279 \pm 1.33$, CI $= (276, 282)$ m^2 in fig. SA9.2. The value used to simulate data is 253 m^2. Inaccuracies are expected due to the small number of trees of a given species per plot, ranging from 4 to 23 in this example. This concentration of seed production into a few individuals is typical of real data.

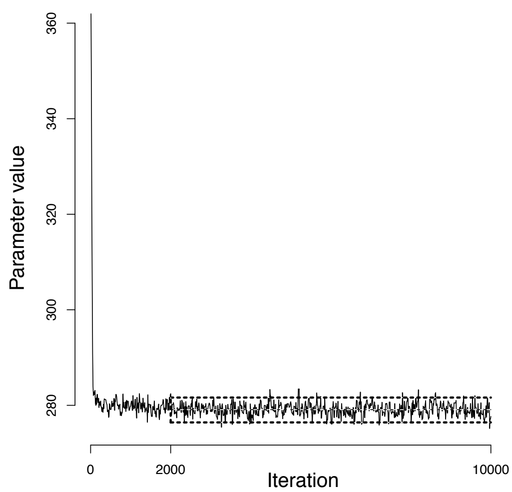

Figure SA9.2: MCMC chain for the dispersal parameter fitted to data simulated with $u = 253$ in the simulation example. Outlined are the post-burnin values used for estimates.

Maturation, fecundity, and seed composition parameters are plotted against true values in fig. SA9.3.

Wide predictive intervals in fig. SA9.4a reflect the fact that there is stochasticity in the prediction of fecundity from parameter value (fig. SA9.4c). The estimated fecundities predict seed data better (fig. SA9.4b) than does the full posterior fig. SA9.4a. In other words, tree size alone is not sufficient to predict fecundity.

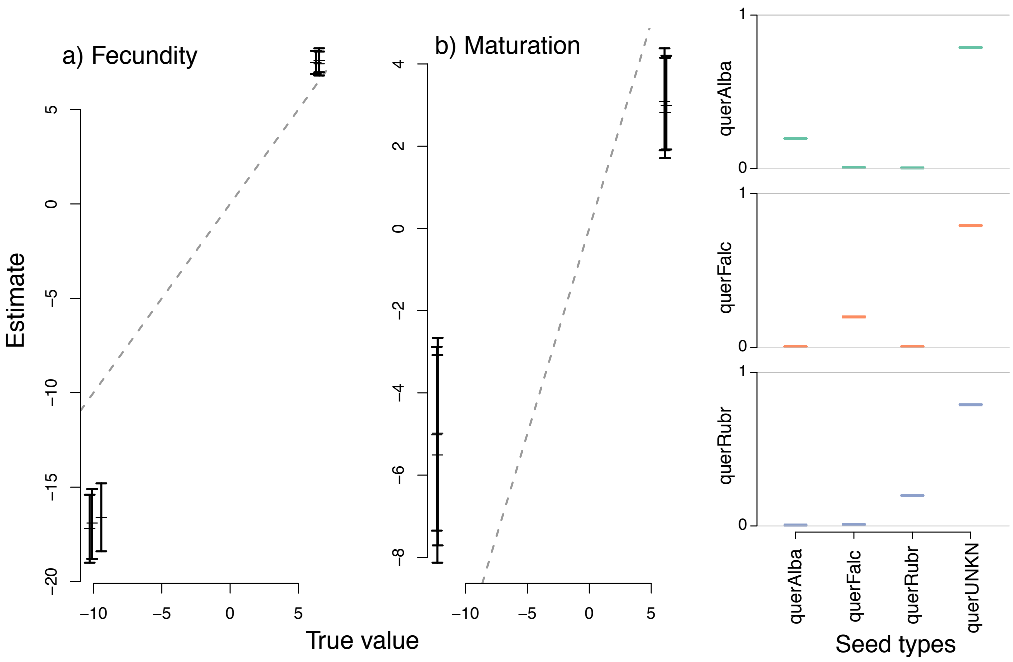

Figure SA9.3: Parameter estimates plotted against values used to simulate data for conditional fecundity (a) and maturation (b) of three species. In both panels, low values are intercepts and high values are slopes. c) ADD TO FIG. Estimates of the composition vectors $\mathbf{m}_h$ in simulation, where h refers to three species that can be classified as $M = 4$ seed types. For each species, only 20% were recorded to the correct species, the remainder counted as "querUNKN". Model fitting recovers estimates precisely (0.8 assigned to querUNKN).

SA9.2 *Application*

To make plot labels visible, resource scores shown in fig. 11 omit credible intervals. They are shown in fig. SA9.5.

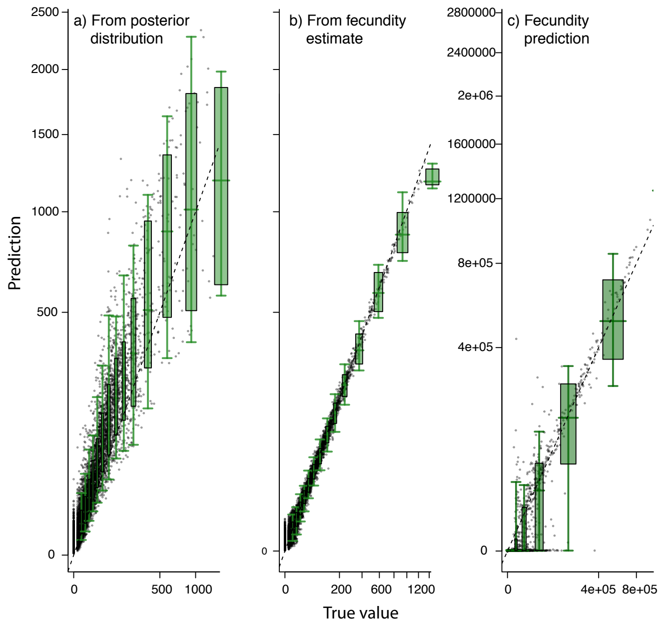

Figure SA9.4: Seed data prediction from the full posterior distribution (a) and from the maturation/fecundity estimates (b) compared with simulated observations ('Observed') for the simulated example. In (c) is the comparison of fecundity estimates with values used to simulate data ('True values').

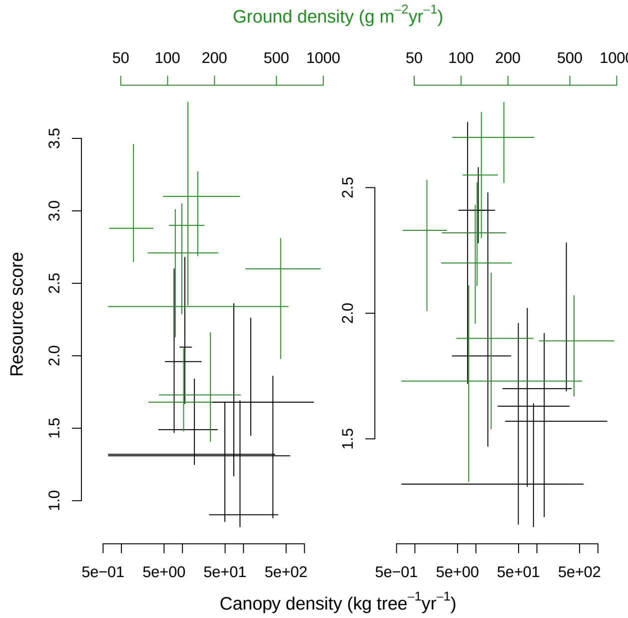

Figure SA9.5: The resource scores from fig. 11 with standard deviations added.

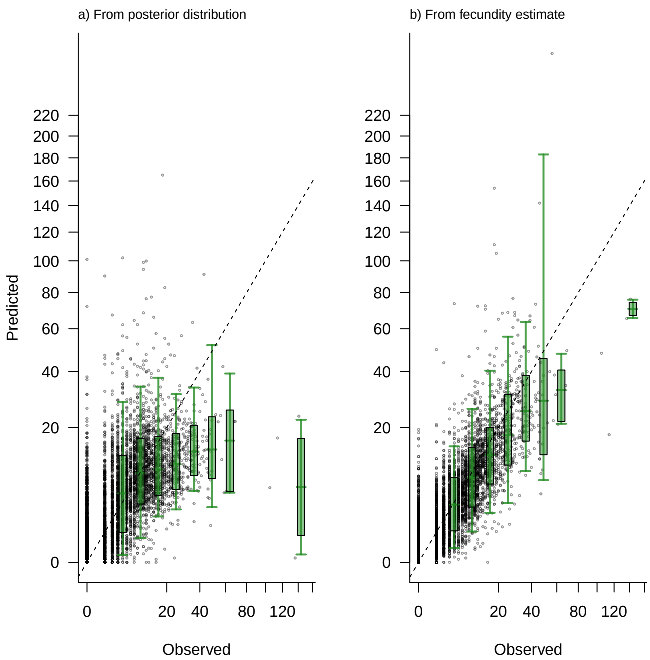

Figure SA9.6: Seed prediction from the AR(4) model fitted to *Pinus*. Predictions are from the full posterior distribution (a) and from the fecundity estimates (b).

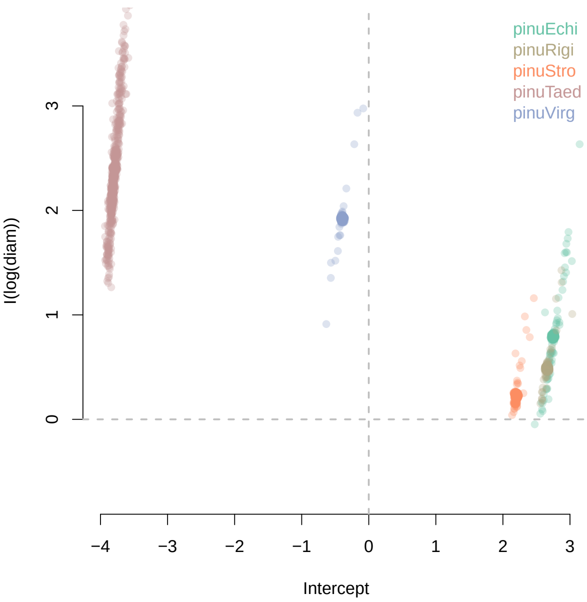

Figure SA9.7: Random slopes and intercepts for the AR(4) model

SA10 POSTERIOR SIMULATION: ALGORITHM NOTES

SA10.1 *Joint fecundity and maturation updates*

To impute states, fecundity and maturation status are proposed jointly as

$$[\psi^*_{ij,t}, \rho^*_{ij,t}] = [\psi^*_{ij,t}|\rho^*_{ij,t}][\rho^*_{ij,t}] \tag{SA10.19}$$

Maturation year is a random walk, centered on the currently imputed maturation year and subject to constraints imposed by observed or currently imputed states (mature individuals cannot become immature). Possible maturation years range from the last year in which an individual was observed in the immature state to the first year in which that individual was observed in the mature state. If there are no maturation observations, then all information on maturation status comes through the seed data. Maturation is proposed and accepted jointly with fecundity for all trees on a plot year. This blocking is necessitated by the fact that the likelihood for each trap-year conditionally depends on all tree-years for that plot (Clark et al. 2004).

Sampling of a plot-year block is summarized this way:

$$[\boldsymbol{\psi}_{j,t}, \boldsymbol{\rho_{j,t}}|\mathbf{y}_{j,t}, \mathbf{z}_{j,t}] \propto P_1 \times P_2 \times P_3 \tag{SA10.20}$$

where

$$P_1 = \prod_{s=1}^{S_j}\prod_{r=1}^{R} Poi\left(y_{rkj,t}|A_{sj}\lambda_{rsj,t}(\boldsymbol{\psi}_{j,t}, \boldsymbol{\rho}_{j,t}, \mathbf{r})\right)$$
$$P_2 = \prod_{i=1}^{n_i}[z_{ij,t}|\rho_{ij,t}]$$
$$P_3 = \prod_{i=1}^{n_i}[\psi_{ij,t}|\rho_{ij,t}]$$

(Conditioning on parameters is omitted to improve clarity.) Two methods are used, depending on the process model, both beginning with proposed $\{\rho^*_{ij,t}|\rho_{j,t-1}, \rho_{ij,t+1}\}_{i=1}^{n_j}$. Only cases where $\rho_{ij,t-1} = 0$ and $\rho_{ij,t+1} = 1$ can change state. We draw $w_{ij,t}$ from a normal distribution with censoring from (eq. (SA2.10)). If $w_{ij,t} > 0$ then $\rho^*_{ij,t} = 1$. Fecundity is then proposed from a normal distribution, with censoring imposed by the proposed $\rho^*_{ij,t}$. Then:

Method 1:

1. The proposed $\psi^*_{ij,t}|\rho^*_{ij,t}, \psi_{ij,t}$ come from a normal distribution centered on the currently imputed $\psi_{ij,t}$.

2. Accept/reject $\boldsymbol{\rho}^*_{j,t}, \boldsymbol{\psi}^*_{j,t}$ as a block with probability $P_1P_2P_3$.

Method 2:

1. The proposed $\psi^*_{ij,t}|\rho^*_{ij,t}$ come from the conditional normal distribution obtained from P_3. We discuss details only for the most complex case of the AR(p) model (section SA10.7.5).

2. Accept/reject $\boldsymbol{\rho}^*_{j,t}, \boldsymbol{\psi}^*_{j,t}$ as a block with probability $P_1 \times P_2$.

SA10.2 *Hamiltonian updates of conditional fecundity*

Hamiltonian updates cannot be used with discrete maturation status. However, by conditioning on maturation state, mixing of fecundity is accelerated with Hamiltonian updates for currently imputed mature individuals.

Each observation is a length-M vector $\mathbf{y}_{sj,t}$ with Poisson intensity $A_{sj}\lambda_{smj,t} = A_{sj}\sum_{i=1}^{n_{j,t}} \mathbf{S}_{[sjt,i]}e^{\psi_{ij,t}}\mathbf{m}_{i[h]}$, where $\mathbf{m}_{i[h],m}$ is the row vector $\mathbf{m}_h$ corresponding to the species of individual i and the column for seed type m. The Hamiltonian can be written as

$$H(\psi_{ij,t}, p) = B(\psi_{ij,t}) + C(p) \tag{SA10.21}$$

where $C(p) = \sum_{i=1}^{n_j} \frac{p_i^2}{2m_i}$ is the kinetic energy, taken as a quadratic function of momentum variables m_i, which are tuned to optimize performance (Neal 2011). The first term incorporates the conditional distribution,

$$B(\psi_{ij,t}) = -\log[\psi_{ij,t}|\mathbf{y}_{j,t}, \mu_{ij,t}, \sigma^2)] \tag{SA10.22}$$

$$\propto \sum_{m,s} (-y_{smj,t}\log\lambda_{smj,t} + A_{sj}\lambda_{smj,t}) + \frac{1}{2\sigma^2}(\psi_{ij,t} - \mu_{ij,t})^2 \tag{SA10.23}$$

The gradient is used to direct proposals efficiently:

$$\frac{\partial B}{\partial \psi_{ij,t}} = e^{\psi_{ij,t}} \sum_m \mathbf{m}_{h[i],m} \sum_s \mathbf{S}_{[sjt,i]} \left(-\frac{y_{smj,t}}{\lambda_{smj,t}} + A_{sj}\right) + \frac{1}{\sigma^2}(\psi_{ij,t} - \mu_{ij,t}) \tag{SA10.24}$$

Hamiltonian updates are individually slow, but affect larger steps then a Metrolis random walk, especially with large data sets. The two methods are mixed stochastically in the Gibbs sampler.

SA10.3 *Fecundity coefficients*

Direct sampling of coefficients in $\boldsymbol{\beta}^x$ and $\boldsymbol{\beta}^v$ is available from Gaussian conditional posterior distributions. Gaussian prior distributions are non-informative. For $\boldsymbol{\beta}^x$ conditional distributions marginalize random effects (see below). The variance σ^2 has an inverse gamma prior – and is sampled directly from the conjugate inverse gamma posterior.

SA10.4 *Random individual effects*

Let $\mathbf{w}_{ij,t}$ be a design vector holding all or some of the columns in $\mathbf{x}_{ij,t}$. There is an individual-effects coefficient matrix $\boldsymbol{\beta}^w_{ij}$,

$$\psi_{ij,t} \sim N\left(\mathbf{x}'_{ij,t}\boldsymbol{\beta}^x + \mathbf{w}'_{ij,t}\boldsymbol{\beta}^w_{ij}, \sigma^2\right) \tag{SA10.25}$$

The prior distribution includes

$$\boldsymbol{\beta}^w_{ij}|\mathbf{B}_w \sim MVN(\mathbf{0}, \mathbf{B}_w) \tag{SA10.26}$$

$$\mathbf{B}_w \sim IW\left(\tilde{\mathbf{B}}, df\right) \tag{SA10.27}$$

where $df = Q^w + 2$, Q^w is the number of columns in $\mathbf{w}_{ij,t}$, and $\tilde{\mathbf{A}} = \mathbf{I}_r$ is a prior diagonal matrix. The conditional posterior matrix is

$$\boldsymbol{\beta}^w_{ij}|\boldsymbol{\beta}^x, \mathbf{B}_w \sim MVN(\mathbf{V}_{ij}\mathbf{v}_{ij}, \mathbf{V}_{ij}) \tag{SA10.28}$$

where

$$\mathbf{v}_{ij} = \frac{1}{\sigma^2}\sum_{t\in\{t_i\}} \mathbf{w}_{ijt}(\psi_{ijt} - \mathbf{x}'_{ijt}\boldsymbol{\beta}^x) \tag{SA10.29}$$

$$\mathbf{V}_{ij} = \frac{1}{\sigma^2}\sum_{t\in\{t_i\}} \mathbf{w}_{ijt}\mathbf{w}'_{ijt} + \mathbf{B}_w^{-1} \tag{SA10.30}$$

The summations are taken over all observation years for an individual i, the set $\{t_i\}$ for which the individual is mature. Here is the conditional for the covariance,

$$\mathbf{B}_w|\{\boldsymbol{\beta}^w_{ij}\} \sim IW\left(\sum \boldsymbol{\beta}^w_{ij}\boldsymbol{\beta}^{w\prime}_{ij} + df \times \tilde{\mathbf{B}}, \sum_j n_j + df\right) \tag{SA10.31}$$

SA10.5 *Random groups in the year and AR(*p*) models*

The year and AR(p) models allow for group random effects on year and lag coefficients, respectively–if groups are defined by the user, they will be treated as random. This is done, because year and lag terms across groups are highly unbalanced. Plot-species groups can hold different numbers of plots and trees in different years. Plots can be established at different times, have different plot areas, and support very different communities of species. For a given species, abundance across plots may range from zero to high. Within plots, numbers of mature individuals vary across years with recruitment, maturation, and death. Within posterior simulation, their imputed maturation statuses change by tree and year. The sizes of design matrices are thus dynamic.

Given this imbalance, treating groups as random provides the advantage that no arbitrary rules are needed to catch computation errors that would result from plot-years that are at some iterations imputed to have mature trees and other iterations not.

SA10.6 *Year effects*

For a single group, years effects are fixed, drawn from the conditional

$$\gamma_t \sim N(V_t v_t, V_t) \tag{SA10.32}$$

$$V_t^{-1} = \frac{n_t}{\sigma^2} + 1/\tau^2 \tag{SA10.33}$$

$$v_t = \frac{1}{\sigma^2}\sum_i(\psi_{i,t} - \mu_{i,t}) \tag{SA10.34}$$

With multiple groups, there are random year effects across groups:

$$\gamma_{g,t} \sim N(V_t v_t, V_t) \tag{SA10.35}$$

$$V_{g,t}^{-1} = \frac{n_{g,t}}{\sigma^2} + 1/\tau_t^2 \tag{SA10.36}$$

$$v_{g,t} = \frac{1}{\sigma^2} \sum_{i \in g} (\psi_{i,t} - \mu_{i,t} - \gamma_t) \tag{SA10.37}$$

Years have a sum-to-zero constraint imposed in Gibbs sampling. The intercept for a given year is the overall intercept plus the year effect for that year.

The variance for random effects:

$$\tau_t^2 \sim IG\left(2 + \frac{n_t}{2}, 1 + \frac{1}{2} \sum \gamma_{g,t}^2\right) \tag{SA10.38}$$

where n_t is the number of groups available in year t, i.e., those having mature individuals in that year.

SA10.7 *AR(*p*) model*

The AR(p) model allows for the dependence of the current states of ψ_t on p previous states. The process is homogeneous in time, because the lag coefficients α_p are constant. I start with a few words on structure.

SA10.7.1 *Imputed past, predicted future*

AR models handle the early years in different ways. There is no AR(p) estimate for years $t \in \{1, \ldots, p\}$. One of the more common ways to deal with these years is to simply condition on them. This seems like a big price to pay. Because 'mastif' is a state-space model, and we are imputing fecundity and maturation anyway, it makes sense to imput fecundity/maturation for years $t - p, \ldots, t - 1$.

So while we are imputing the past, it makes sense to predict the future. Conditionally, fecundity in the final year T_i depends on the future, up to year $T_i + p$. To accommodate past and future, MASTIF imputes backward p years from the first observation and predicts forward p years beyond the last observed year.

A consistent treatment would appear to demand that AR effects be restricted to individuals that have been mature for the past $t - p$ years. Note that this would not be a concern if maturation state was known. We adopt this rule, so lag effect estimates are not biased downward by the inclusion of trees that might have immature during one or more of years $t-p, \ldots, t-1$. Although fecundity is imputed for all years, including before observations began, sampling of coefficients for fixed effects and lag effects is restricted to years in which trees were observed and mature.

SA10.7.2 *AR(p) model structure*

To avoid further notation, the description that follows applies only to tree-years for which the mature state extends back to $t-p$ years. Also to simplify notation we initially the subscript j. Note that multiple plots j might fall within a group g.

Conditionally, the model for an individual i in group $g \in \{1, \ldots, G\}$ can be written as

$$\psi_{ig,t}|\mu_{ig,t}, \boldsymbol{\alpha}, \boldsymbol{\alpha}_g[i], \tilde{\boldsymbol{\psi}}_{ig,t} \sim N\left(m_{ig,t}, \sigma^2\right) \tag{SA10.39}$$

where

$$m_{ig,t} = \mu_{ig,t} + \sum_{l=1}^{p}(\alpha_l + \alpha_{g[i]l})\psi_{ig,t-l} \tag{SA10.40}$$

$$= \mu_{ig,t} + (\boldsymbol{\alpha} + \boldsymbol{\alpha}_{g[i]})'\tilde{\boldsymbol{\psi}}_{ig,t} \tag{SA10.41}$$

$\mu_{ig,t} = \mathbf{x}'_{ig,t}\boldsymbol{\beta}^x$ is the fixed effect, $\tilde{\boldsymbol{\psi}}_{ig,t} = (\psi_{ig,t-1}, \ldots, \psi_{ig,t-p})'$ is the vector of lagged fecundities for (ig, t), $\boldsymbol{\alpha} = (\alpha_1, \ldots, \alpha_p)'$ is the vector of fixed effects for lag $l = 1, \ldots, p$, and $\boldsymbol{\alpha}_g = (\alpha_{g1}, \ldots, \alpha_{gp})$ is the random effect for group g with prior distribution

$$\boldsymbol{\alpha}_g \sim MVN(\mathbf{0}, \mathbf{A}_{(l)}) \tag{SA10.42}$$

$$\mathbf{A}_{(l)} \sim IW\left(\tilde{\mathbf{A}}_{(l)}, df\right) \tag{SA10.43}$$

To facilitate sampling, the fecundity values are organized into a vector $\boldsymbol{\psi} = \{\psi_{ig,t}|i = 1, \ldots, n, g = 1, \ldots, G, t = 1, \ldots, T_i\}$ and a corresponding matrix of p lag terms. For example, a vector with these subscripts

$$\boldsymbol{\psi} = (\psi_{i,g,t}, \psi_{i,g,t+1}, \ldots, \psi_{i,g,T_i}, \psi_{i+1,g,t}, \ldots,) \tag{SA10.44}$$

has the lag matrix with matching rows and p columns,

$$\tilde{\mathbf{\Psi}} = \begin{pmatrix} \psi_{i,g,t-1} & \cdots & \psi_{i,g,t-p} \\ \psi_{i,g,t} & \cdots & \psi_{i,g,t+1-p} \\ \vdots & \vdots & \vdots \\ \psi_{i,g,T_i-1} & \cdots & \psi_{i,g,T_i-p} \\ \psi_{i+1,g,t} & \cdots & \psi_{i+1,g,t+1-p} \\ \vdots & \vdots & \vdots \end{pmatrix} \tag{SA10.45}$$

SA10.7.3 *Sample fixed effects*

To sample fixed effects, I move a few terms to the left,

$$\mathbf{m} = \tilde{\mathbf{\Psi}}\boldsymbol{\alpha} \tag{SA10.46}$$

where $\mathbf{m}$ has elements $\psi_{ig,t} - \mu_{ig,t} - \boldsymbol{\alpha}'_{g[i]}\tilde{\boldsymbol{\psi}}_{ig,t}$, and, again, $\boldsymbol{\alpha}_{g[i]}$ indicates the vector of lags for the group to which individual i belongs. The conditional posterior matrix for fixed effects is

$$\boldsymbol{\alpha}|\{\boldsymbol{\alpha}_g\} \sim MVN(\mathbf{V}\mathbf{v}, \mathbf{V}) \tag{SA10.47}$$

$$\mathbf{v} = \sigma^{-2}\tilde{\mathbf{\Psi}}'\mathbf{m} \tag{SA10.48}$$

$$\mathbf{V}^{-1} = \sigma^{-2}\tilde{\mathbf{\Psi}}'\tilde{\mathbf{\Psi}} + \mathbf{A}^{-1} \tag{SA10.49}$$

SA10.7.4 *Random group effects*

For random effects, make a slight change in $\mathbf{m}$,

$$\boldsymbol{\alpha}_g \sim MVN(\mathbf{V}_g\mathbf{v}_g, \mathbf{V}_g) \tag{SA10.50}$$

$$\mathbf{v}_g = \frac{1}{\sigma^2}\sum_{i,t}\tilde{\boldsymbol{\psi}}'_{ig,t}m_{ig,t} \tag{SA10.51}$$

$$\mathbf{V}_g = \frac{1}{\sigma^2}\sum_{i,t}\tilde{\boldsymbol{\psi}}_{ig,t}\tilde{\boldsymbol{\psi}}'_{ig,t} + \mathbf{A}^{-1}_{(l)} \tag{SA10.52}$$

where $m_{ig,t} = \psi_{ig,t} - \mu_{ig,t} - \boldsymbol{\alpha}'\tilde{\boldsymbol{\psi}}_{ig,t}$. The summations are taken over all observation years in which individual i has been in the mature state for the previous p years, for all individuals in group g. Here is the conditional for the covariance,

$$\mathbf{A}_{(l)}|\{\boldsymbol{\alpha}_g\} \sim IW\left(\sum_{g=1}^{G} \boldsymbol{\alpha}_g \boldsymbol{\alpha}_g' + df \times \tilde{\mathbf{A}}_{(l)}, G + df\right) \tag{SA10.53}$$

SA10.7.5 *Latent states*

Latent states in the AR(p) model are sampled by proposing from the conditional posterior for the fecundity/maturation submodel $\psi_t, z_t|\psi_{\{-t\}}, z_{t-1}, z_{t+1}$, where $\psi_{\{-t\}}$ is the set of all fecundity values except t, and accepting from the likelihood (Method 2 in section SA10.1). To reduce clutter, we now omit subscripts ijg. If there are random groups in the model, then everything below is handled at the group level, with lag coefficient α_l being replaced with $\alpha_l + \alpha_{gl}$ for group g.

To isolate the terms in ψ_t the AR(p) model can be written as

$$\psi_t \sim N\left(m_t, \sigma^2\right) \tag{SA10.54}$$

where

$$m_t = \mu_t + \sum_{l=1}^{p} \alpha_l \psi_{t-l} \tag{SA10.55}$$

The exponent of the conditional distribution $\psi_t|\psi_{\{-t\}}$ can be factored this way:

$$\frac{1}{\sigma^2}\left[(\psi_t - m_t)^2 + \sum_{k=1}^{p} (n_{t,k} - \alpha_k \psi_t)^2\right] \tag{SA10.56}$$

where

$$n_{t,k} = \psi_{t+k} - \mu_{t+k} - \sum_{l=1}^{p} \alpha_l \psi_{t+k-l} I(l \neq k) \tag{SA10.57}$$

To sample latent states, we propose from

$$\psi_t \sim N\left(V v_t, V\right) \tag{SA10.58}$$

where

$$v_t = \frac{1}{\sigma^2}\left(m_t + \sum_{k=1}^{p} n_{t,k}\alpha_k\right) \tag{SA10.59}$$

$$V^{-1} = \frac{1}{\sigma^2}\left(1 + \sum_{k=1}^{p} \alpha_k^2\right) \tag{SA10.60}$$

Proposals are accepted as a block for each plot-year in the data set, based on the likelihood for seed data (see Method 2).

SA10.8 *Covariance effects*

$$v_t = \Omega^{-1}\left(\mathbf{m}_t + \mathbf{n}_t\boldsymbol{\alpha}\right) + \mathbf{A}^{-1}f^0 \tag{SA10.61}$$

$$V^{-1} = \Omega^{-1}\mathbf{I}_n\left(1 + \boldsymbol{\alpha}'\boldsymbol{\alpha}\right) + \mathbf{A}^{-1} \tag{SA10.62}$$

SA10.9 *Other parameters*

The error variance σ^2 is sampled from the conditional inverse gamma posterior distribution.

If there are no random groups, the dispersal parameter u is sampled with Metropolis, with an adaptive proposal variance and truncated normal prior distribution,

$$[u] \propto L \times N(u|u_0, U_0) I(u > 0) \tag{SA10.63}$$

where the likelihood L is $\prod_{r,s,j,t} Poi\left(y_{rsj,t}|A_{sj}\lambda_{rsj,t}(u, \boldsymbol{\psi}_{j,t}, \boldsymbol{\rho}_{j,t}, \mathbf{r})\right)$, u_0 and U_0 are the prior mean and variance dispersal parameters.

If there are random groups, then an additional stage for the global mean. The previous distribution applies to u_g for group g,

$$[u_g] \propto L \times N(u_g|u, U) \tag{SA10.64}$$

The u_g are proposed and accepted as a block.

The global mean and variance have conditional distributions:

$$u|u_1,\ldots,u_G,u_0,U,U_0 \sim N\left(Vv,V\right) \tag{SA10.65}$$

$$V^{-1} = \frac{G}{U} + \frac{1}{U_0} \tag{SA10.66}$$

$$v = \frac{1}{U}\sum_g u_g + \frac{u_0}{U_0} \tag{SA10.67}$$

$$U|u_1,\ldots,u_G,u \sim IG\left(2+\frac{G}{2}, 1+\frac{1}{2}\sum_g (u_g-u)^2\right) \tag{SA10.68}$$

References

Clark, J., S. LaDeau, and I. Ibanez. 2004. Fecundity of trees and the colonization-competition hypothesis. Ecological Monographs **74**:415–442.

Clark, J., E. Macklin, and L. Wood. 1998. Stages and spatial scales of recruitment limitation in southern Appalachian forests. Ecological Monographs **68**:213–235.

Muller-Landau, H. C., S. J. Wright, O. Calderon, R. Condit, and S. P. Hubbell. 2008. Interspecific variation in primary seed dispersal in a tropical forest. Journal of Ecology **96**:653–667. URL `<GotoISI>://WOS:000256635800010`.

West, M., and J. Harrison. 1997. Bayesian Forecasting and Dynamic Models. 2nd edition. Springer.