# Generative equations of the Nee Soon IBM

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Let's write down the Nee Soon individual-based model (IBM) mathematically since we will inevitably need to do so in the manuscript. I tried my best to transcribe the R codes and our verbal communication mathematically but something may be incorrect. Need to double check.

1 Transitional diagram

A draft state diagram of the IBM. Initial seedling and adult numbers and diameters are determined [...] Edge labels are vital rates parameterised with regression and field data... Vital rates are influenced by stand competition, habitat mismatch, or both, as determined by model selection.
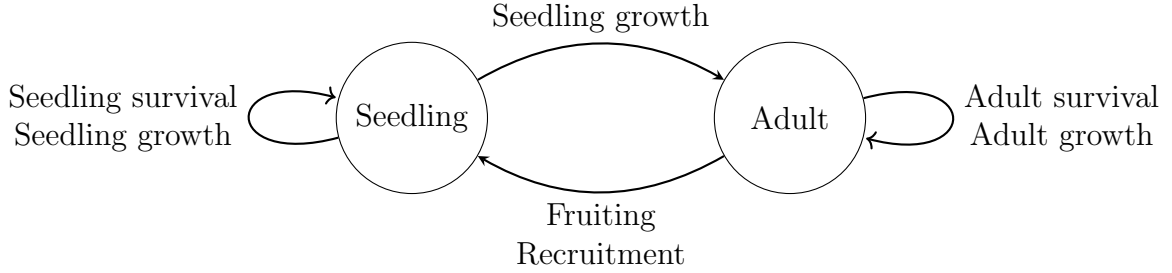
2 Fruiting incidence

For tree individual i of species j with diameter-at-breast-height, D_{ij}, in a spatial grid p with habitat index, H_p, at time point t, we model its fruiting incidence [yes or no] in the subsequent time point as a Bernoulli process with mean $p_{\text{fruit},ijp}$, which is a linear function of the species-specific potential fruiting incidence $\phi_{0,j}$, species-specific size dependence $\phi_{D,j}$, and overall effect of habitat mismatch, ϕ_H:

$$\Pr\left(\text{Fruiting}_{ij,p,t+1} = 1\right) \sim \text{Binomial}\left(1,\ p_{\text{fruit},ij,p,t+1}\right) \tag{1}$$

$$\text{logit}\left(p_{\text{fruit},ij,p,t+1}\right) = \phi_{0,j} + \phi_{D,j}D_{ij,p,t} + \phi_H \Delta H_{ij,p,t}. \tag{2}$$

The habitat mismatch, $\Delta H_{ij,p,t}$, of an individual is measured as [...]

3 Seedling recruitment

For each parent tree that fruited, we model its offspring count as a size-dependent power function with mean $r_{ij,t+1}$ and dispersion ψ_j:

$$R_{ij,t+1} \sim \text{NegBinom}\left(r_{ij,t+1},\ \psi_j\right) \tag{3}$$

$$r_{ij,t+1} = \rho_{0,j} D_{ij,t}^{\rho_{D,j}} \tag{4}$$

$$\log\left(r_{ij,t+1}\right) = \log \rho_{0,j} + \rho_{D,j} \log D_{ij,t} \tag{5}$$

4 Seedling location

We allow newly-recruited seedlings to follow a species-specific '2DT' dispersal kernel (REF), which has the probability density function (PDF):

$$\frac{\Sigma_j}{\pi \Lambda_j \left(1 + \frac{d^2}{\Lambda_j}\right)^{\Sigma_j+1}}, \tag{6}$$

where d is the distance from a parent tree. Because this PDF does not have a closed form, we numerically sample d from this PDF after normalising the PDF to sum to one for $d \in (0, 410)$ meters.

Note: changed latin letters to Greek to reserve S for survival

5 Seedling growth and survival

For each seedling we model its size-dependent survival $S_{\text{seedling},ij,p,t+1}$ following Needham et al. (2018):

$$\Pr(S_{\text{seedling},ij,t+1} = 1) \sim \text{Binomial}(1,\ s_{ij,t+1}) \tag{7}$$

$$s_{ij,t+1} = \frac{K_j}{1 + e^{-r_{1,j}(D_{ij} - p_{1,j})}}, \tag{8}$$

where seedling diameter D_{ij} is converted from height (because seedling growth is calculated as height increment, see below):

$$\log D_{ij} \sim \text{Normal}(\mu_{\log D,ij},\ \sigma_{\log D}) \tag{9}$$

$$\mu_{\log D,ij} = d_{0,j} + d_{H,j} \log H_{ij} \tag{10}$$

Note: currently diameter is not generated with variance, but only deterministically using the linear predictor!

For each surviving seedling we model its subsequent log height $\log H_{ij,t+1}$ as a function of previous log height, conspecific competition, heterospecific competition, and their interactions:

$$\log H_{ij,t+1} \sim\ \text{Normal}(\mu_{\log H,ij,t+1},\ \sigma_{\log H}) \tag{11}$$

$$\mu_{\log H,ij,t+1} =\ h_{0,j} + h_{H,j} \log H_{ij,t+1} + h_{\text{intra},j}\text{Consp}_{i,t} + h_{\text{inter},j}\text{Hetsp}_{i,t} \tag{12}$$

$$+ h_{\text{intra}H,j} \log H_{ij,t+1}\text{Consp}_{i,t} + h_{\text{inter}H,j} \log H_{ij,t+1}\text{Hetsp}_{i,t} \tag{13}$$

$$\text{Consp}_{i,t} =\ ??? \tag{14}$$

$$\text{Hetsp}_{i,t} =\ ??? \tag{15}$$

6 Adult growth and survival

Next, we model the size-dependent growth $G_{ij,p,t}$ and survival $(S_{\mathrm{adult},ij,p,t+1})$ of adult individuals, which include 'saplings' and 'trees'. Adult survival model is similar to that of seedlings, except that the function has a discontinuity at 1-cm DBH:

$$\Pr(S_{\mathrm{adult},ij,p,t+1} = 1) \sim \mathrm{Binomial}(1,\ s_{\mathrm{adult},ij,p,t+1}) \tag{16}$$

$$s_{\mathrm{adult},ij,p,t+1} = \begin{cases} \dfrac{K_j}{1 + e^{-(r_{10,j}+r_{11,j}\cdot\mathrm{interA}_{i,t}\cdot\Delta H_{ip,t})[D_{ij}-(p_{10,j}+p_{11,j}\cdot\mathrm{intraA}_{i,t})]}}, & D_{ij} \leq 1 \\[4mm] \dfrac{K_j}{1 + e^{-r_{2,j}[D_{ij}-(p_{20,j}+p_{21,j}\cdot\mathrm{intraA}_{i,t}+p_{22,j}\cdot\mathrm{interA}_{i,t})]}}, & D_{ij} > 1 \end{cases} \tag{17}$$

$$\mathrm{intraA}_{i,t} = ??? \tag{18}$$

$$\mathrm{interA}_{i,t} = ??? \tag{19}$$

Adult growth model follows Kohyama et al. (2020):

$$D_{ij,p,t+1} = D_{ij,p,t} + G_{ij,p,t} \tag{20}$$

$$G_{ij,p,t} \sim \mathrm{Normal}(\mu_{G,ij,p,t}, \sigma_G) \tag{21}$$

$$\mu_{G,ij,p,t} = a D_{ij,p,t}^b e^{-c D_{ij,p,t}} \tag{22}$$

$$a = a_j \tag{23}$$

$$b = b_j + b_{\mathrm{intraA}}\mathrm{intraA}_{i,t} + b_{\mathrm{interA}}\mathrm{interA}_{i,t} \tag{24}$$

$$c = c_j + c_{\mathrm{intraA}}\mathrm{intraA}_{i,t} + c_{\mathrm{interA}}\mathrm{interA}_{i,t} \tag{25}$$

Note: some random intercepts potentially are missing from all the equations above; need to double check

7 References

Kohyama, T. S., Potts, M. D., Kohyama, T. I., Niiyama, K., Yao, T. L., Davies, S. J., & Sheil, D. (2020). Trade-off between standing biomass and productivity in species-rich tropical forest: Evidence, explanations and implications. *Journal of Ecology*, 108(6), 2571–2583. doi: 10.1111/1365-2745.13485

Needham, J., Merow, C., Chang-Yang, C.-H., Caswell, H., Mcmahon, S. M., & Needham, J. (2018). Inferring forest fate from demographic data: from vital rates to population dynamic models. *Proceedings of the Royal Society B: Biological Sciences*, 285(1874), 20172050. doi: 10.1098/rspb.2017.2050