math for IBM

Lisa Rosenthal

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Here's the math for a generic continuous time disease model with one species. C, S, and I are the number of individuals in states challenged, susceptible, and infected, respectively. Challenged individuals can become infected either through inoculum-plant transmission $(\alpha(t)C)$ or plant-plant transmission $(\beta(t)CI)$. We identify these two tranmission modes as "primary" and "secondary", respectively. The inoculum decays in virulence at a constant rate of δ; thus, challenged individuals transition to susceptibles at a rate of δC. Since we assume that inoculum can only infect individuals a short distance away (i.e. the "challenged" individuals), susceptible individuals can only be infected through secondary transmission $(\beta(t)SI)$.

$$\frac{dC}{dt} = -\delta C - \alpha(t)C - \beta(t)CI$$

$$\frac{dS}{dt} = \delta C - \beta(t)SI$$

$$\frac{dI}{dt} = \alpha(t)C + \beta(t)CI + \beta(t)SI$$

When I extend the above model to a multihost community, I need to account for the species-specific primary $\alpha_i(t)$ and secondary $\beta_{ij}(t)$ transmission coeffiecents. Since secondary transmission involves two plants, a donor and reciepent, every pairwise combination must be estimated. Here, each species i can be infected by all species j, where $j = 1, 2, ...s$ number of species.

$$\frac{dC_i}{dt} = -\delta C_i - \alpha_i(t)C_i - C_i \sum_j \beta_{ij}(t)I_j$$

$$\frac{dS_i}{dt} = \delta C_i - S_i \sum_j \beta_{ij}(t)I_j$$

$$\frac{dI_i}{dt} = \alpha_i(t)C_i + (C_i + S_i) \sum_j \beta_{ij}(t)I_j$$

In order to account for the spatial dynamics of disease spread, I must model space explicitly. The above models are spatially implicit and assume that all individuals are interacting equally and therefore have an equal probability of being infected. However, this assumption is oversimplifying, especially in small populations. To model space, I'm running an individual based model where each cell in a hexagonal lattice has an associated probability of transmission. An individual's infection probability is sensitive to the species identities of itself and its neighbors.

I have two models: one that assumes infections can only occur between nearest neighbors and one that assumes that contact rates decay with distance. For both, transmission varies with time. Currently, the $\alpha(t)$ and $\beta(t)$ curves originate from Otten et al. (2003), which were estimated from *Rhizoctonia solani* infections on radish. I am assuming that species with different competencies only changes the amplitude of those distributions.

To calculate $\beta(t, r)$, let $\beta(t, r) = c(r)p(t)$, where c is contact rate as a function of r distance and p is probability of transmission given contact. For the nearest neighbor model, we assume $r = 1$ for neighbors directly

adjacent and $r = 0$ for all others. For the model with distance decay, r is the pairwise distance between individuals.

I must discretize the continuous time equations above and have it recalculated at each time step.

*(**WARNING**: notation probably wrong!)* The probability of the following state transitions are. . .

C -> S: $1 - e^{-\delta}$

C -> I: $2 - e^{-\alpha_i(t)} - e^{-\sum_r \sum_j c(r) p_{ij}(t) I_j}$

C -> C: $1 - (1 - e^{-\delta}) - (2 - e^{-\alpha_i(t)} - e^{-\sum_r \sum_j c(r) p_{ij}(t) I_j})$

S -> I: $1 - e^{-\sum_r \sum_j c(r) p_{ij}(t) I_j}$

S -> S: $1 - (1 - e^{-\sum_r \sum_j c(r) p_{ij}(t) I_j})$

I-> I: 1

In the IBM simulation, I run a loop that says at every time step, for every individual, pull a number from 0 to 1 from a uniform distribution. The equations above estimate the probability of each event occuring and the random number decides the "fate" of each individual's state change. I record the states of all indivuals for the duration of the simulation.