Optimal Control of Forest Disease Using Individual-Based Models

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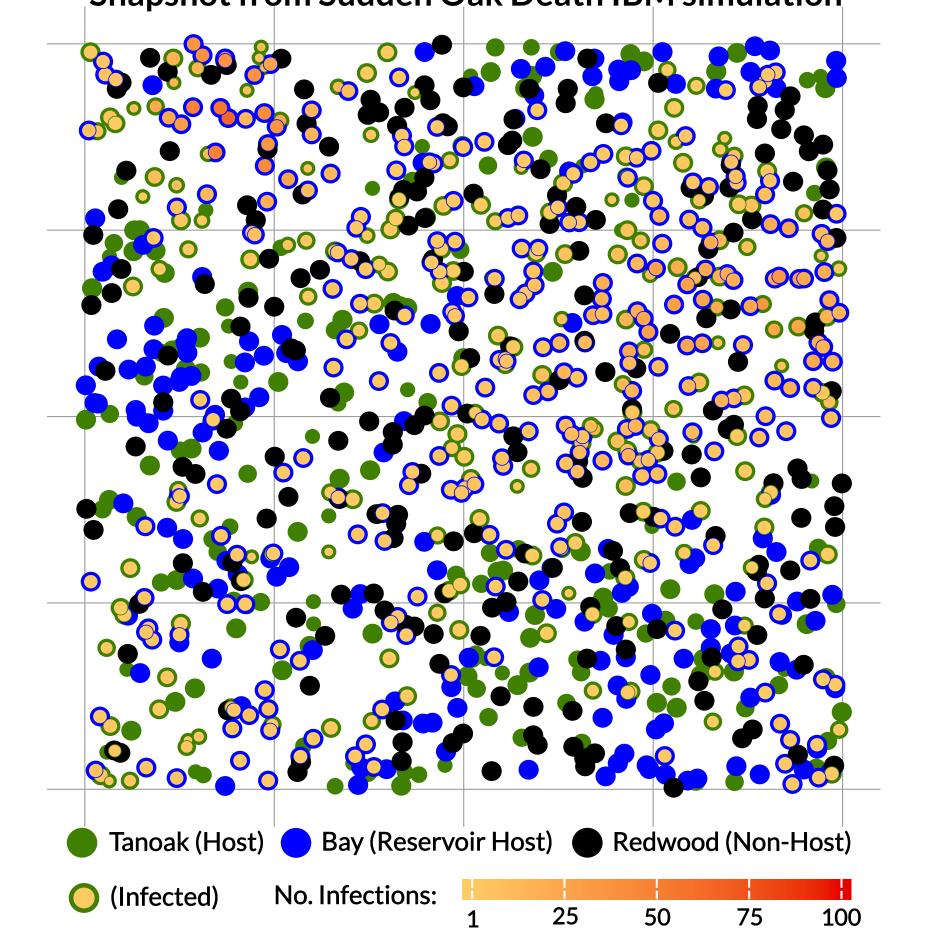
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Background:

Sudden Oak Death (SOD) is an invasive disease fatal to many oaks, especially tanoak (Notholithocarpus densiflorus), a species with important ecological and cultural values in coastal forests of California and Oregon.

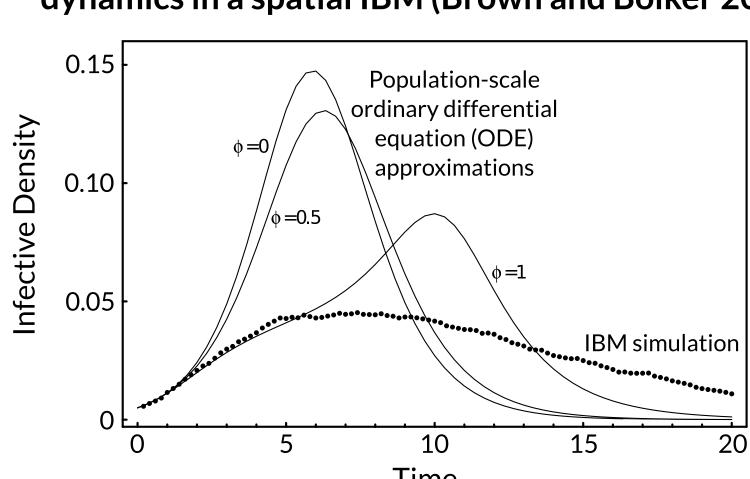
Epidemiology of SOD is complex. The effect of the pathogen (Phytophthora ramorum) varies widely by tree species and size (Cobb et al. 2012). Rain-splash dispersal and spatial heterogeneity of hosts leads to considerable spatial structure within stands. Thus, an **individual-based model (IBM)** is useful in simulating disease dynamics.

Snapshot from Sudden Oak Death IBM simulation



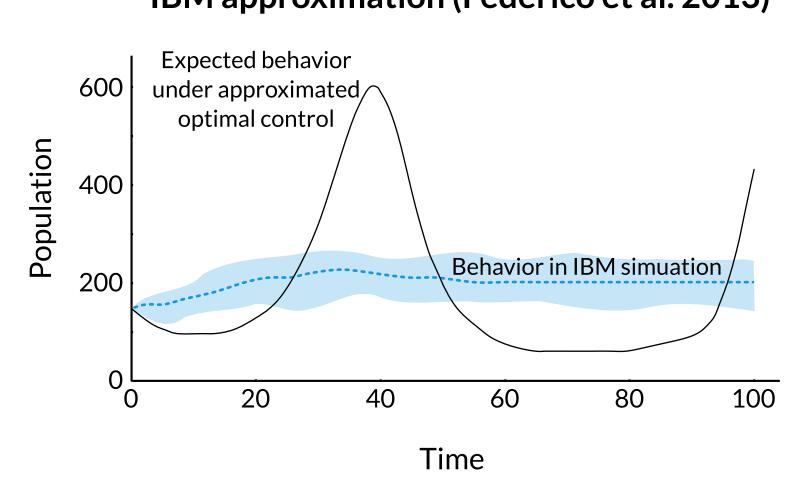
However, analysis of IBMs is challenging, as many are not well represented at the population scale with closed-form equations.

Closed-form approximations poorly capture disease dynamics in a spatial IBM (Brown and Bolker 2004)



In particular, IBMs challenge optimal control methods, as their state space is large and highly multidimensional. Control based on approximation can lead to incorrect outcomes.

Outcome of optimal control on an ODE-based IBM approximation (Federico et al. 2013)



Method: A Multi-Scale Approach to Dynamic Optimization

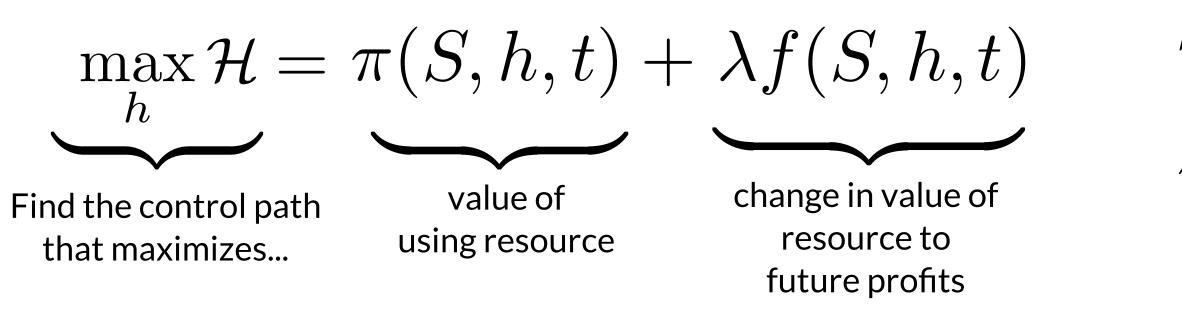
To solve optimal control problems in an IBM context, I am developing a method that combines the multi-scale or equation-free framework (Kevrekidis and Samaey 2009), with traditional dynamic optimization techniques from natural resource economics. This allows optimization of the mean behavior of an IBM, even if it can only be accessed as a "black box".

"Lifting Function"

Generate a

distribution of

Define the Hamiltonian optimization problem at a coarse (population) scale



Population-scale variables, e.g. (infectious individuals) h = Control variable (e.g., rate of culling)Profit function "Shadow value" of resource (contribution to future profits)

Simulate each

IBM state forward

given h

"Restriction Function"

Calculate average

coarse-scale

Create a **coarse stepper** to simulate the system by repeated simulations of the IBM. The stepper samples from possible IBM states generated from the coarse-scale system state, and runs the IBM using the control variable as a parameter.

derivatives from the **IBM** states simulations dS dSdt, dt^2 Numerically optimize to find the control level (h) that maximizes time t. Use outputs of simulation

Control(h)

 $\mathsf{State}(S)$

Advance in time by using the previous outputs to integrate and produce the optimal path of the control parameter, shadow values, and average system state.

the value of the system (\mathcal{H}) at

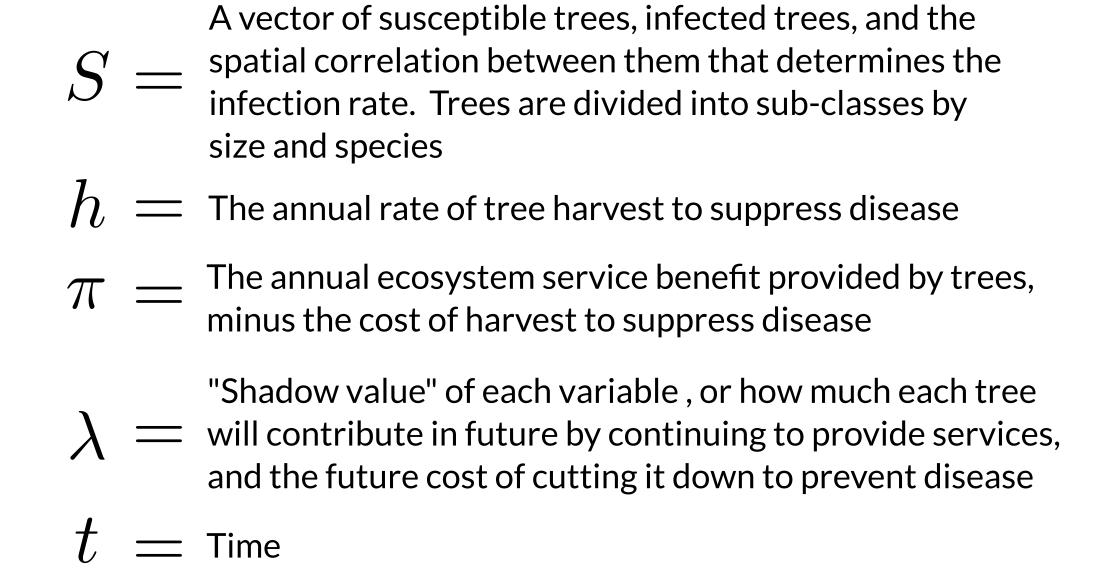
with h^* to determine $d\lambda/dt$.

Solve the **boundary value** problem by adjusting initial values to hit optimal final conditions.

Application: Thinning trees to slow disease spread Property managers seek to conserve host tree

populations under the threat of constant or increasing disease propagule pressure from the surrounding landscape. Culling or thinning to reduce disease must be balanced against loss of ecosystem services and threat of extinction of the host.

The optimization problem is to remove the correct number, size, species, and spatial configuration of trees to minimize host species loss from either disease, competition, or stochastic extinction. For this problem, I define the variables in the Hamiltonian equation as



$f(S,h) = {}^{ ext{Change in tree populations over time,} \atop ext{simulated by the IBM}}$

Ongoing work

The methods described here are being developed as an R/C++ package, eqnfree, which also implements methods described in Kevrekidis and Samaey (2009).

Works Cited

Brown, D. H., and B. M. Bolker. 2004. The effects of disease dispersal and host clustering on the epidemic threshold in plants. Bull. Math Bio. 66:341–71.

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Kevrekidis, I. G., and G. Samaey. 2009. Equation-free multiscale computation: algorithms and applications. Annual review of physical chemistry 60:321–44.



