Mathematical Modeling for Epidemiology and Ecology

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Overview

- *Mathematical Modeling for Epidemiology and Ecology* is a reworking of my *Mathematics for the Life Sciences*. It should be out by April.

- The book was written as a textbook for an undergraduate course and **a source of problems and methods to supplement differential equations and modeling courses**.

- In this talk, I will
  - Identify important special features of the book.
  - Present an overview of the contents.
  - Highlight some topics in mechanistic modeling.
  - Highlight one topic in dynamical system analysis.

A Focus on Mathematical Modeling

- Many model derivations appear in the text and the problems.
- There are discussions of alternative choices for biological assumptions.
- Many problems contain symbolic parameters with analysis done in generality.
- Many problems ask for a biological interpretation of results.
- There are numerous projects that require modeling.

An Emphasis on Scientific Computation

Modeling requires simulation as well as analysis. Students need to learn to use a programming environment to create their own simulations.

- The book comes with 22 MATLAB programs.
- No prior programming experience is needed. Appendix A is a minimal MATLAB tutorial with line-by-line explanations of the two simplest programs.
- Programs are structured to make them easy to modify for new experiments or alter for different models.
  - All model-specific and scenario-specific code is in a small DATA section at the beginning of each program.

Contents

Chapter 3

3. Mechanistic Modeling

Chapter 4

Chapter 6

6. Nonlinear Dynamical Systems

6.1 Phase Plane Analysis

- Nullclines
- **See my talk at 2:30 EST on Saturday**

6.2 Linearized Stability Analysis with Eigenvalues

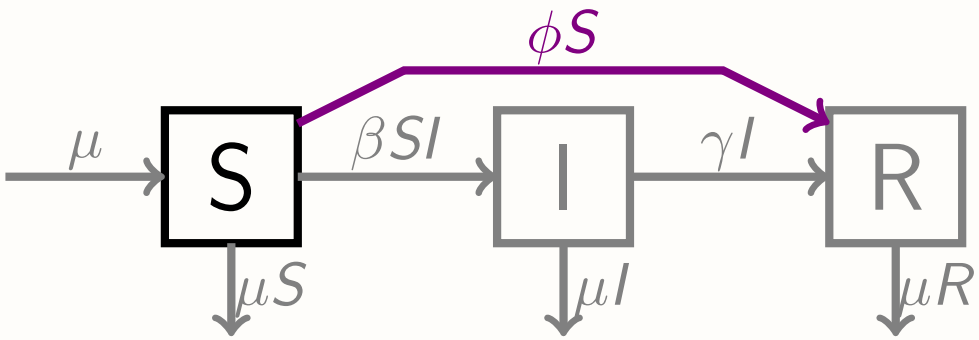
6.3 Stability Analysis with the Routh–Hurwitz Conditions

- **See my talk at 2:30 EST on Saturday**

6.4 Case Study: Onchocerciasis

6.5 Discrete Nonlinear Systems

Vaccination – Standard Model



(Birth rate is μ so that the equilibrium population is $N = 1$.)

Isolated Single Cohort Vaccination Model:

$$\frac{dS}{dt} = -\phi S, \qquad S(0) = 1$$

- What is wrong with this implementation of vaccination?
  - It is applied to the entire susceptible class.
  - It assumes unlimited supply.
  - It assumes instantaneous distribution.

Vaccination – Ledder Model – Limited Acceptance

$$\frac{dS}{dt} = -\phi S, \qquad S(0) = 1$$

- Model Modifications
  - **Limited acceptance**
  - Limited supply
  - Limited distribution capacity

Assume a fraction a of the population is willing and able to be vaccinated.

Let $W(t)$ be the population fraction that is waiting for vaccination.

$$\frac{dW}{dt} = -\phi W, \qquad W(0) = a$$

Vaccination – Ledder Model – Limited Supply

$$\frac{dW}{dt} = -\phi W, \qquad W(0) = a$$

- Model Modifications
  - Limited acceptance
  - **Limited supply**
  - Limited distribution capacity

Replace ϕ with $\phi g(t)$, where

$$g(0) = 0, \qquad g' \geq 0, \qquad g|_{t \geq \tau} = 1.$$

The simplest such model assumes that g is piecewise linear:

$$\frac{dW}{dt} = -\phi g(t) W\,, \qquad W(0) = a, \quad g(t) = \min\left(\frac{t}{\tau}, 1\right)$$

Vaccination – Ledder Model – Limited Distribution

$$\frac{dW}{dt} = -\phi g(t) W\,, \qquad W(0) = a, \quad g(t) = \min\left(\frac{t}{\tau}, 1\right)$$

- Model Modifications
  - Limited acceptance
  - Limited supply
  - **Limited distribution capacity**

Replace the linear function ϕW with a (bounded) Michaelis-Menten (Holling type 2) or Holling type 3 function.

$$\frac{dW}{dt} = -\frac{\phi g(t) W^p}{K^p + W^p}\,, \qquad W(0) = a, \qquad p \in \{1, 2\}$$

- Supply and distribution limits are only needed for scenarios with a new vaccine.

Vaccination – Ledder Model – Fit to Data

$$\frac{dW}{dt} = -\frac{\phi g(t) W^2}{K^2 + W^2}, \qquad W(0) = a \tag{1}$$

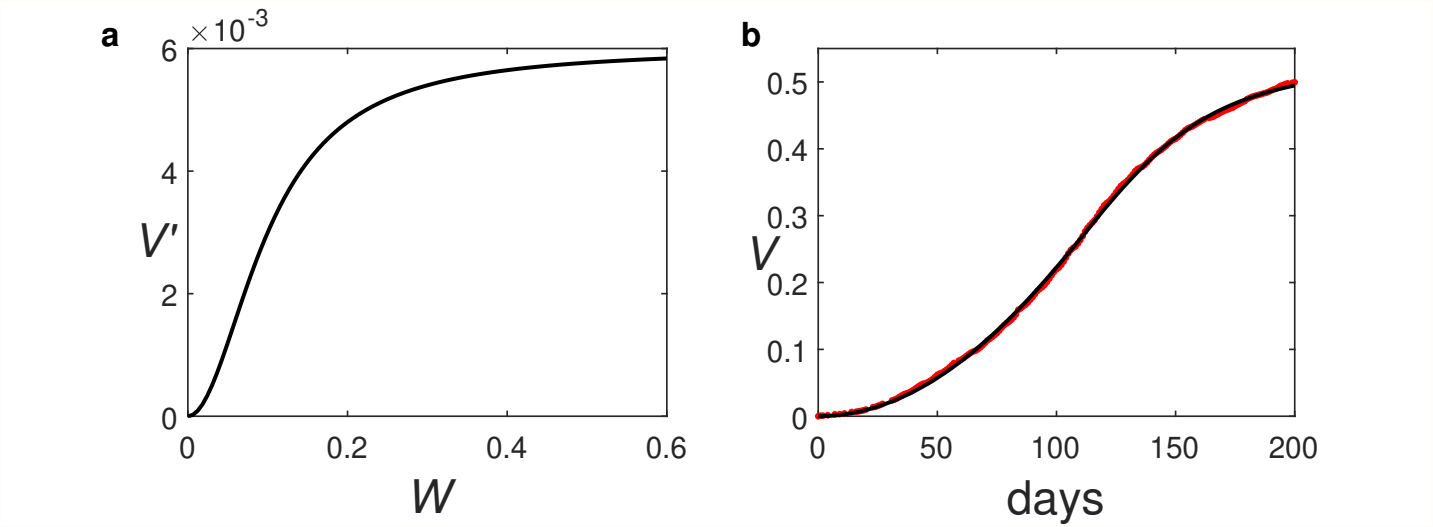


Figure: 3.1.1 (**a**): The vaccination rate $V' = -W'$ for (1) with $g = 1$ and best-fit parameters for ϕ, a, and K from CDC data; (**b**): The corresponding vaccinated population fraction V (black) for (1) with $g = \min(t/\tau, 1)$ and best-fit parameters for ϕ, a, τ and K from CDC data, along with the CDC data (red).

```
function Vaccination()
%% DATA
% Define parameters
avals = [0.6,0.8];
phi = 0.02;
interval = [0 100];
% Define the function that determines the derivatives.
function dWdt = rates(tt,WW)
    dWdt = -phi*WW;
end
%% INITIALIZATION (set up plots)
...
%% COMPUTATION and PLOTS (a loop pulls a value from
avals, runs ode45, and plots a curve)
...
%% END
end
```

Two-Phase Transition for a Single Cohort

Single-Phase Transition (mean time $1/\mu$):

$$\frac{dY}{dt} = -rY, \quad Y(0) = 1, \qquad r = \mu$$

$$Y = e^{-\mu t}$$

Two-Phase Transition
(mean time $1/\mu$, Y_k is the phase k population, $Y = Y_1 + Y_2$):

$$\frac{dY_1}{dt} = -rY_1, \quad Y_1(0) = 1, \qquad r = 2\mu$$

$$\frac{dY_2}{dt} = rY_1 - rY_2, \quad Y_2(0) = 0, \qquad r = 2\mu$$

$$Y = (1 + 2\mu t)\, e^{-2\mu t}$$

Multi-Phase Transitions for a Single Cohort

k-Phase Transition (mean time $1/\mu$, $Y = \sum_{i=1}^{k} Y_k$):

$$\frac{dY_1}{dt} = -rY_1, \qquad Y_1(0) = 1, \qquad r = k\mu$$
$$\frac{dY_2}{dt} = rY_1 - rY_2, \qquad Y_2(0) = 0, \qquad r = k\mu$$
$$\vdots$$
$$\frac{dY_k}{dt} = rY_{k-1} - rY_k, \qquad Y_k(0) = 0, \qquad r = k\mu$$

$$Y = \left(1 + T + \frac{1}{2}T^2 + \cdots + \frac{1}{(k-1)!}T^{k-1}\right)e^{-T}, \quad T = k\mu t$$

Multi-Phase Transitions for a Single Cohort

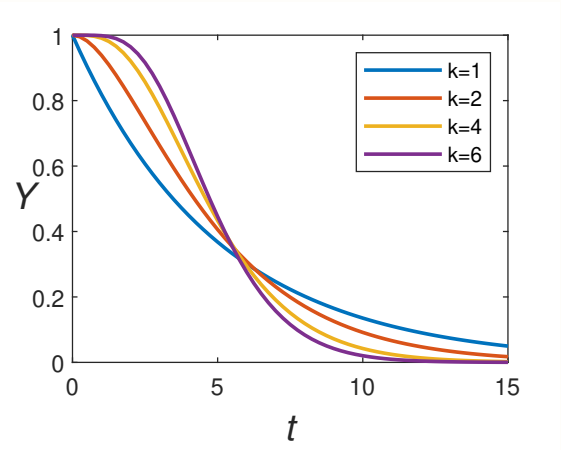


Figure: 3.1.2 Remaining fraction infected from an initial cohort for a k-phase recovery with mean recovery time $1/\mu = 5$.

- The single-phase transition is not good for disease recovery.
  - This doesn't matter for an endemic model, but it does throw off the results for epidemic models.
  - It is okay to use it for teaching, but a multi-phase transition should be considered for some research problems.
  - **This issue is explored in Project 3E in the book.**

Adding Demographics to a Disease Model

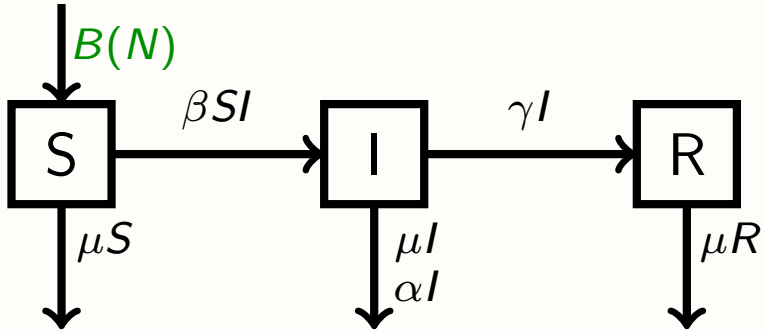


Figure: 3.9.1 (simplified) The generic SIR model with population demographics.

What do we use for $B(N)$?

- The usual choice is a constant rate Λ.
  - We choose μ for the rate so that the baseline population is 1.
    - Then we don't need to scale populations.
- $B(N) = \mu N$ can only compensate for natural deaths.
  - Doesn't work if $\alpha > 0$.

Birth Rate Based on Logistic Growth

- The logistic growth equation for total population is

$$\frac{dN}{dt} = rN\left(1 - \frac{N}{K}\right).$$

- The total death rate is

$$\mu S + \mu I + \mu R = \mu N.$$

- growth = birth - death, so

$$B(N) = rN\left(1 - \frac{N}{K}\right) + \mu N.$$

  - This is a better mechanistic model, but it only makes a noticeable difference if the death rate is high.

Why Structures for Phase Line Analysis?

In Section 4.5, we derive a model for a resource subjected to harvesting by a fixed number of consumers:

$$x' = f(x) = x(1-x) - \frac{cx^2}{p+x^2}, \qquad p, c > 0.$$

- The usual way to make a phase line is to plot $f(x)$ and see where f changes sign.
  - This f is a complicated function with two parameters, so we'll need to select specific pairs (p, c).
    - We'll have to start over if we change **either** parameter.
- There are other options. We could think of f as

$$\text{total change} = \text{increase} - \text{decrease}.$$

  - Then we only need to know which term is bigger.

Using a Structure for Phase Line Analysis

$$x' = f(x) = x(1-x) - \frac{cx^2}{p+x^2}, \qquad p, c > 0.$$

- We could think of the function f as

  $$\text{total change} = \text{increase} - \text{decrease}.$$

- Better yet, we can remove a common non-negative factor:

  $$\text{total change} = \text{non-negative} \times (\text{'increase'} - \text{'decrease'}).$$

  $$f(x) = w(x)[\,g(x) - h(x)\,], \qquad w(0) = 0, \quad w' > 0.$$

  - Equilibria have $g(x) = h(x)$ or $w(x) = 0 \to x = 0$.
  - x increases if $g(x) > h(x)$.

Two Structures for the Phase Line Example

$$x' = f(x) = x\,(1-x) - \frac{cx^2}{p+x^2}\,, \qquad p, c > 0.$$

$$f(x) = w(x)[\,g(x) - h(x)\,], \qquad w(0) = 0, \quad w' > 0.$$

$$x' = f(x) = x\left(1 - x - \frac{cx}{p+x^2}\right) \tag{1}$$

$$x' = f(x) = \tfrac{x}{p+x^2}\left[(1-x)(p+x^2) - cx\right] \tag{2}$$

- (2) is slightly better than (1).
  - Easy to graph for fixed p with a family of c values.

Using a Structure for the Phase Line Example

$$x' = f(x) = \frac{x}{p+x^2}\left[(1-x)(p+x^2) - cx\right], \quad p = 0.01 \qquad (2)$$

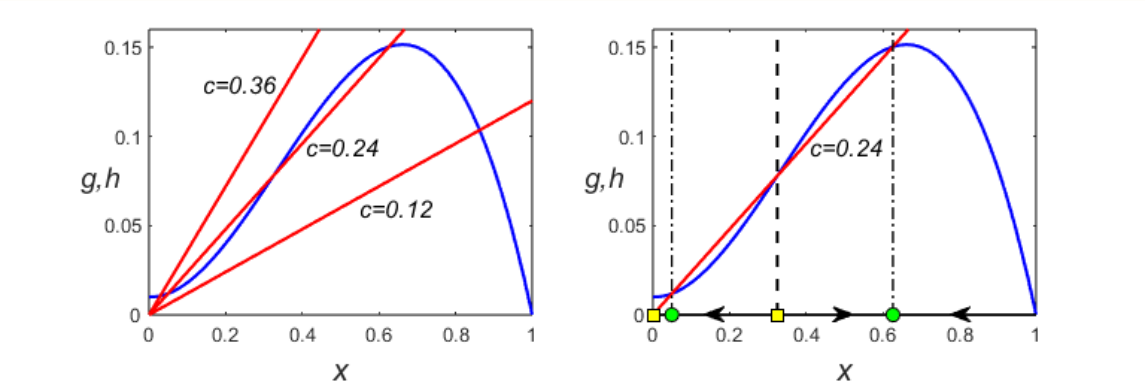


Figure: 4.5.2 (simplified) g and h from (2). (**a**): $c = 0.12, 0.24, 0.36$; (**b**): $c = 0.24$, with phase line on x axis. Arrows point to the right when $g > h$. Equilibria are green (stable) or yellow (unstable). The point $x = 0$ satisfies $w(x) = 0$.

Shameless Self Promotion

- *Mathematical Modeling for Epidemiology and Ecology* is a new Springer text by Glenn Ledder. It should be out by April.
- The book features linked problem sets that are like distributed projects. **I will present two of these in my talk at 2:30 EST tomorrow.**
- Find me during the Expo if you want to chat.
- Or contact me at gledder@unl.edu.
  - (If anyone wants to have me visit, I'm interested.)