Mathematical Modeling of Biological Systems

VMB 631 (CRN 60561)

Spring Quarter 2020

Tuesdays 2:00PM–3:20PM & Thursdays 2:00PM–4:40PM

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Dryden 104

The course will introduce students to mathematical modeling to advance biological sciences. We will examine outstanding examples from the research literature across a broad range of biological disciplines. We will focus both on the contribution the modeling makes to the scientific application and on the modeling methods themselves. Substantial time will be devoted to implementing the models in the Python programming language.

Prerequisites: Graduate standing or permission of instructor

Fig. 6 The solid lines demarcate the stability domains for the density dependence parameter, $\beta$, and the population growth rate, $\lambda$, in equation (17); the dashed line shows where 2-point cycles give way to higher cycles of period 2. The solid circles come from analyses of life table data on field populations, and the open circles come from laboratory populations (from ref. 3, after ref. 39).

R.M. May, 1976

Fig. 1. (A) Plasma concentrations (copies per milliliter) of HIV-1 RNA (circles) for two representative patients (upper panel, patient 104; lower panel, patient 107) after intravenous treatment was begun on day 0. The theoretical curve (solid line) was obtained by nonlinear least squares fitting of Eq. 6 to the data. The parameters $\gamma$ (clearance rate), $\delta$ (rate of loss of infected cells), and $\nu$ (initial viral load) were simultaneously estimated. To account for the pharmacokinetics, we assumed $T = 0$ in Eq. 8 to correspond to the time of the pharmacokinetic delay (if measured) or selected 2, 4, or 6 hours as the best fit value (see Table 1). The log of the experimental data was fit to the log of Eq. 6 by a nonlinear least squares method with the use of the subroutine DNL51 from the Common Los Alamos Software Library, which is based on a finite-difference Levenberg-Marquardt algorithm. The best fit, with the smallest sum of squares per data point, was chosen after eliminating the worst (outlying) data point for each patient with the use of the multiple test rate (MTR) method. Plasma concentrations of HIV-1 RNA (upper panel, circles) and the plasma infectivity (lower panel, square) for patient 105. (Top panel) The solid curve is the best fit (Eq. 6) to the RNA data; the dotted line is the curve of the noninfectious pool of RNA, $n_0$; and the dashed line is the curve of the infectious pool of RNA, $n_0$. (Bottom panel) The dashed line is the best fit of the equation for $y(t)$ to the plasma infectivity data. TCI, total circulating infective.

A.S. Perelson et al., 1996