Mathematical Modeling of Biological Systems

VMB 631 (CRN 40115)

Winter Quarter 2014

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

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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 R software package.

Prerequisites: Graduate standing or permission of instructor

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Fig. 1. A. Plasma concentrations (copies per milliliter) of HIV-1 RNA (circles) for two representative patients (upper panel, patient 104; lower panel, patient 103) after antiretroviral 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 z (clearance rate), \( k \) (rate of loss of infected cells), and \( V_m \) (maximal end load) were simultaneously estimated. To account for the pharmacokinetic delay, we assumed \( h = 0 \) in Eq. 6 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 logarithm of the experimental data was fitted to the logarithm of Eq. 6 by a nonlinear least squares method with the use of the subroutine DNLS3 from the Common Lisp Numerical Software Library, which is based on a modified difference Levenberg-Marquardt algorithm. The best fit, with the smallest sum of squares per data point, was selected after eliminating the worst fitting data point for each patient with the use of the jackknife method. B. 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 of Eq. 5 to the RNA data; the dotted lines are the curve of the negative log of the viral load, and the dashed line is the curve of the log of the viral load. (Top panel) The dashed line is the best fit of the equation for \( y(t) \) to the plasma infectivity data. TCD50: 50% tissue culture infective dose.

A.S. Perelson et al., 1996

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Fig. 6. The solid lines demarcate the stability domains for the density dependence parameter, \( B \), 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 from laboratory populations (from ref. 3, after ref. 39).

R.M. May, 1976

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J.D. Murray, 1981