

Spatiotemporal Modeling of Influenza

Partial Differential Equation Analysis in R

Synthesis Lectures on Biomedical Engineering

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John D. Enderle, *University of Connecticut*

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Partial Differential Equation Analysis in R

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SYNTHESIS LECTURES ON BIOMEDICAL ENGINEERING #57

ABSTRACT

This book has a two-fold purpose:

- (1) An introduction to the computer-based modeling of influenza, a continuing major world-wide communicable disease.
- (2) The use of (1) as an illustration of a methodology for the computer-based modeling of communicable diseases.

For the purposes of (1) and (2), a basic influenza model is formulated as a system of partial differential equations (PDEs) that define the spatiotemporal evolution of four populations: susceptibles, untreated and treated infecteds, and recovered. The requirements of a well-posed PDE model are considered, including the initial and boundary conditions. The terms of the PDEs are explained.

The computer implementation of the model is illustrated with a detailed line-by-line explanation of a system of routines in R (a quality, open-source scientific computing system that is readily available from the Internet). The R routines demonstrate the straightforward numerical solution of a system of nonlinear PDEs by the method of lines (MOL), an established general algorithm for PDEs.

The presentation of the PDE modeling methodology is introductory with a minimum of formal mathematics (no theorems and proofs), and with emphasis on example applications. The intent of the book is to assist in the initial understanding and use of PDE mathematical modeling of communicable diseases, and the explanation and interpretation of the computed model solutions, as illustrated with the influenza model.

KEYWORDS

communicable disease, influenza, computer-based mathematical model, partial differential equation (PDE), method of lines (MOL), R coding, spatiotemporal solutions, traveling wave solutions

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Preface

This book has a two-fold purpose:

- (1) An introduction to the computer-based modeling of influenza, a continuing major world-wide communicable disease.
- (2) The use of (1) as an illustration of a methodology for the computer-based modeling of communicable diseases.

For the purposes of (1) and (2), the influenza model by Zhang [2] was selected which has the following general features:

- The model is an introduction to the quantitative analysis of influenza.
- It has the basic elements of a model for communicable diseases such as transmission between susceptibles and untreated/treated infecteds.
- Through the partial differential equation (PDE) formulation it provides the spatiotemporal features of disease evolution.
- Since it is basic (with minimal complexity), the model is well suited as an introduction to numerical methods and computer implementation of PDE models.
- The methodology for PDE model formulation and computer implementation is illustrated with a detailed derivation of the influenza model equations and a line-by-line explanation of associated routines in R¹.
- The R routines are available from a download so that the reader/analyst/researcher can readily execute them to confirm the solutions reported in the book, then experiment with the model, for example, by varying parameter values and PDE terms, on modest computers.

In summary, the presentation of the PDE modeling methodology is introductory with a minimum of formal mathematics (no theorems and proofs), and with emphasis on example applications. The intent of the book is to assist in the initial understanding and use of mathematical modeling, and the explanation and interpretation of the computed model solutions, as illustrated with the influenza model.

¹R is a quality, open-source scientific computing system that is readily available from the Internet [1].

I hope these objectives are fulfilled, and I would welcome hearing about experiences with the use of the book (directed to wes1@lehigh.edu).

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May 2019

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