

Schematic description of ODE models & integro differential models



$$\begin{aligned} \frac{du}{dt} &= \underbrace{p_u(u,v)}_{\text{change in time}} - \underbrace{d_u(u,v)}_{\text{prolif.}} \pm \underbrace{f_u(u,v)}_{\text{death}} \pm \underbrace{h_u(u,v)}_{\text{differentiation}} \pm \underbrace{g_u(u,v)}_{\text{transport}} \\ \frac{dv}{dt} &= \underbrace{p_v(u,v)}_{\text{change in time}} - \underbrace{d_v(u,v)}_{\text{prolif.}} \pm \underbrace{f_v(u,v)}_{\text{death}} \pm \underbrace{h_v(u,v)}_{\text{differentiation}} \pm \underbrace{g_v(u,v)}_{\text{transport}} \end{aligned}$$

*continuous time

*nonspatial dynamics

*spatial dynamics: compartments=discrete patches

*could have stochastic components

with $u=(u_1, u_2)$
 $v=(v_1, v_2)$

Schematic description of PDE models & integro partial-differential models

compartment:
cell populations u, v



spatial domain

■ density of population u
■ density of population v

$$\begin{aligned} \frac{du}{dt} &= \underbrace{D_u \Delta u}_{\text{change in time (t)}} - \underbrace{B_u \nabla u}_{\text{change in space (x)}} + \underbrace{f_u(u,v)}_{\text{growth}} - \underbrace{d_u(u,v)}_{\text{decay}} \\ \frac{dv}{dt} &= \underbrace{D_v \Delta v}_{\text{change in time (t)}} - \underbrace{B_v \nabla v}_{\text{change in space (x)}} + \underbrace{f_v(u,v)}_{\text{growth}} - \underbrace{d_v(u,v)}_{\text{decay}} \end{aligned}$$

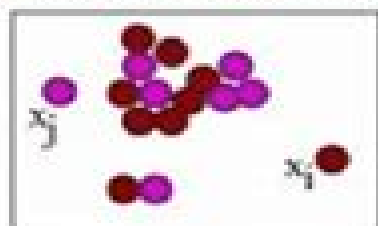
*continuous time

*spatial dynamics

*non-spatial dynamics: second variable can describe an "activity" space (x =activity)

Schematic description of agent-based (AB) & cellular automata (CA) models

lattice-free spatial domain:

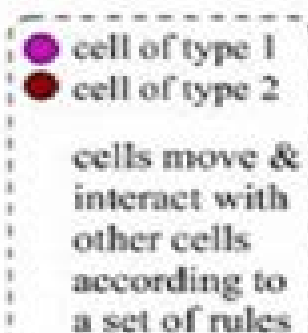


$i, j = 1..N$
 N =total cell nbrs.

cell position: $x_i(t+1) = x_i(t) + s v_i(t)$

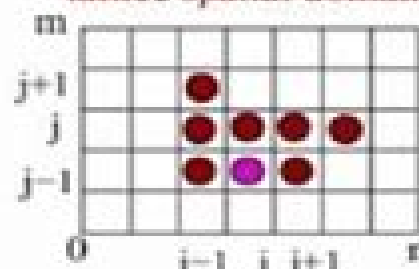
cell velocity: $v_i(t+1) = \underbrace{F(v_i(t))}_{\text{force that affects cell velocity}} + \underbrace{N_i}_{\text{noise}}$

*discrete time, space



*spatial dynamics

lattice spatial domain:



$i = 1..n$
 $j = 1..m$
domain size: $n \times m$

IF-THEN-ELSE rules for:

- cell division
- cell migration
- cell apoptosis
- cell differentiation

*deterministic or stochastic

Mathematical Models In Immunology

Amina Eladdadi, Peter Kim, Dann Mallet



Mathematical Models In Immunology:

Mathematical Models in Immunology Guriĭ Ivanovich Marchuk, 1983 *Mathematical Models in Immunology* Guriĭ I. Marčuk, 1983 **Mathematical Modelling of Immune Response in Infectious Diseases** Guri I. Marchuk, 2013-04-17

Beginning his work on the monograph to be published in English this author tried to present more or less general notions of the possibilities of mathematics in the new and rapidly developing science of infectious immunology describing the processes of an organism's defence against antigen invasions. The results presented in this monograph are based on the construction and application of closed models of immune response to infections which makes it possible to approach problems of optimizing the treatment of chronic and hypertoxic forms of diseases. The author, being a mathematician, had creative long lasting contacts with immunologists, geneticists, biologists and clinicians. As far back as 1976 it resulted in the organization of a special seminar in the Computing Center of Siberian Branch of the USSR Academy of Sciences on mathematical models in immunology. The seminar attracted the attention of a wide circle of leading specialists in various fields of science. All these made it possible to approach from a more or less united standpoint the construction of models of immune response, the mathematical description of the models and interpretation of results.

Mathematical Modeling of the Immune System in Homeostasis, Infection and Disease Gennady Bocharov, Burkhard Ludewig, Andreas Meyerhans, Vitaly Volpert, 2020-02-24

The immune system provides the host organism with defense mechanisms against invading pathogens and tumor development and it plays an active role in tissue and organ regeneration. Deviations from the normal physiological functioning of the immune system can lead to the development of diseases with various pathologies including autoimmune diseases and cancer. Modern research in immunology is characterized by an unprecedented level of detail that has progressed towards viewing the immune system as numerous components that function together as a whole network. Currently we are facing significant difficulties in analyzing the data being generated from high throughput technologies for understanding immune system dynamics and functions, a problem known as the curse of dimensionality. As the mainstream research in mathematical immunology is based on low resolution models, a fundamental question is how complex the mathematical models should be. To respond to this challenging issue we advocate a hypothesis driven approach to formulate and apply available mathematical modelling technologies for understanding the complexity of the immune system. Moreover, pure empirical analyses of immune system behavior and the system's response to external perturbations can only produce a static description of the individual components of the immune system and the interactions between them. Shifting our view of the immune system from a static schematic perception to a dynamic multi level system is a daunting task. It requires the development of appropriate mathematical methodologies for the holistic and quantitative analysis of multi level molecular and cellular networks. Their coordinated behavior is dynamically controlled via distributed feedback and feedforward mechanisms which altogether orchestrate immune system functions. The molecular regulatory loops inherent to the immune system that mediate cellular

behaviors e.g exhaustion suppression activation and tuning can be analyzed using mathematical categories such as multi stability switches ultra sensitivity distributed system graph dynamics or hierarchical control GB is supported by the Russian Science Foundation grant 18 11 00171 AM is also supported by grants from the Spanish Ministry of Economy Industry and Competitiveness and FEDER grant no SAF2016 75505 R the Mar a de Maeztu Programme for Units of Excellence in R D MDM 2014 0370 and the Russian Science Foundation grant 18 11 00171 Mathematical Methods in Immunology Jerome Kenneth Percus,2012 Any organism to survive must use a variety of defense mechanisms A relatively recent evolutionary development is that of the adaptive immune system carried to a quite sophisticated level by mammals The complexity of this system calls for its encapsulation by mathematical models and this book aims at the associated description and analysis In the process it introduces tools that should be in the armory of any current or aspiring applied mathematician in the context of arguably the most effective system nature has devised to protect an organism from its manifold invisible enemies **Killer**

Cell Dynamics Dominik Wodarz,2007-04-05 Systems biology and computational biology have recently become prominent areas of research in the biomedical community especially in the area of cell biology Given that much information on genes and their protein products has become available the big question is how the individual components interact and work together and how this determines the functioning of cells organs and organisms Long before the popularity of systems biology in biomedicine however such approaches have been used successfully in a di erent area of biology population ecology Research in the area of population dynamics vestigated complex interactions between di erent populations of organisms such as the dynamics of competition and predation food webs community structure as well as the epidemiology of infectious diseases In this eld t oretical biology and mathematical modeling have become an integral part of research Mathematical models allowed people to obtain interesting and counter intuitive insights into how complex interactions among di erent p ulations can play out Such mathematical studies not only gave rise to teresting theoretical ideas but also provided the basis for the design of new experimental work and de ned major questions and directions of research Around 1990 such population dynamic concepts and the use of mathema cal computational approaches started to be applied to the in vivo dynamics between viruses and the immune system These interactions have many s ilarities to ecological epidemiological and evolutionary principles Consider theepidemiologicalspreadofapathogen suchasthecommoncold througha population of hosts

Mathematical Models and Immune Cell Biology Carmen Molina-París,Grant Lythe,2011-05-05 Whole new areas of immunological research are emerging from the analysis of experimental data going beyond statistics and parameter estimation into what an applied mathematician would recognise as modelling of dynamical systems Stochastic methods are increasingly important because stochastic models are closer to the Brownian reality of the cellular and sub cellular world

Mathematical Modeling of the Immune Response Daniela Prikrylova,Milos Jilek,Jacek Waniewski,1992-07-27 Mathematical Modeling of the Immune Response presents a comprehensive examination of the history of development of

mathematical models in immunology and discusses how these models are used by biologists The book features the results of work done by the authors using a model showing the potential of interleukin 2 as an agent responsible for the proper control of the range of the immune response Additional work by the authors regarding modeling autoimmunity and its treatment are discussed as well

Mathematical Models of Tumor-Immune System Dynamics Amina Eladdadi, Peter Kim, Dann Mallet, 2014-11-06 This collection of papers offers a broad synopsis of state of the art mathematical methods used in modeling the interaction between tumors and the immune system These papers were presented at the four day workshop on Mathematical Models of Tumor Immune System Dynamics held in Sydney Australia from January 7th to January 10th 2013 The workshop brought together applied mathematicians biologists and clinicians actively working in the field of cancer immunology to share their current research and to increase awareness of the innovative mathematical tools that are applicable to the growing field of cancer immunology Recent progress in cancer immunology and advances in immunotherapy suggest that the immune system plays a fundamental role in host defense against tumors and could be utilized to prevent or cure cancer Although theoretical and experimental studies of tumor immune system dynamics have a long history there are still many unanswered questions about the mechanisms that govern the interaction between the immune system and a growing tumor The multidimensional nature of these complex interactions requires a cross disciplinary approach to capture more realistic dynamics of the essential biology The papers presented in this volume explore these issues and the results will be of interest to graduate students and researchers in a variety of fields within mathematical and biological sciences

Mathematical Immunology of Virus Infections Gennady Bocharov, Vitaly Volpert, Burkhard Ludewig, Andreas Meyerhans, 2018-06-12 This monograph concisely but thoroughly introduces the reader to the field of mathematical immunology The book covers first basic principles of formulating a mathematical model and an outline on data driven parameter estimation and model selection The authors then introduce the modeling of experimental and human infections and provide the reader with helpful exercises The target audience primarily comprises researchers and graduate students in the field of mathematical biology who wish to be concisely introduced into mathematical immunology

Mathematical Models In Immunology Book Review: Unveiling the Magic of Language

In an electronic era where connections and knowledge reign supreme, the enchanting power of language has are more apparent than ever. Its capability to stir emotions, provoke thought, and instigate transformation is truly remarkable. This extraordinary book, aptly titled "**Mathematical Models In Immunology**," written by a very acclaimed author, immerses readers in a captivating exploration of the significance of language and its profound affect our existence. Throughout this critique, we will delve in to the book is central themes, evaluate its unique writing style, and assess its overall influence on its readership.

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