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Book Reviews

BOOK REVIEWS

This time, the Book Reviews section has a large portion of reviews on books devoted to applications—in particular medical and biological applications. The section starts with the featured review by Jessica M. Conway on the book *Mathematics of Epidemics on Networks*, by István Kiss, Joel C. Miller, and Péter L. Simon. As Jessica notes, it is a much needed book and provides a "good, comprehensive resource on the mathematics underlying the modeling of epidemics on networks."

Disease modeling is also the topic of the book *Infectious Disease Modeling. A Hybrid System Approach*, by Xinzhi Liu and Peter Stechlinski, which is reviewed by Odo Diekmann. Further biological topics in this section are biological systems and growth, modeling life, and the biomechanics of the human stomach.

We have three more insightful reviews on different topics. Here, I would like to put emphasis on the review by Daniel Luft on *A First Course in Computational Fluid Dynamics*, by Hassan Aref and Sivaramakrishnan Balachandar. The target audience of the book is senior undergraduate students and beginning graduate students. Thus, this review is written by a current Ph.D. student.

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Book Reviews

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Featured Review: Mathematics of Epidemics on Networks. *By István Z. Kiss, Joel C. Miller, and Péter L. Simon.* Springer, Cham, 2017. $89.99. xviii+413 pp., hardcover. ISBN 978-3-319-50804-7.

Mathematical modeling of infectious diseases has a long history of informing public policy to mitigate their impact. The earliest efforts were Daniel Bernoulli's work on smallpox in the 18th century and William Farr's work on rinderpest in the 19th century. But it was Ronald Ross' work on malaria near the turn of the 20th century that kick-started mathematical epidemiology as a field of study.

The most commonly used epidemic models are "compartmental," dividing the population into compartments based on infection status, using simple assumptions about mixing and movement between these compartments. While very successful, and offering significant insights into epidemics, they generally fail the "20/80 rule": the empirical observation that 20% of the individuals within any given population are thought to contribute at least 80% to the transmission potential of a pathogen [7]. Consider the 2003 SARS outbreak: Li et al. found that approximately 71% and 75% of the infections from Hong Kong and Singapore, respectively, were attributable to "superspreader" events [4]. Enter network modeling. In the late 1890s, Ferdinand Tönnies argued that social groups can exist as personal and direct social ties that can link individuals who share values and beliefs. It seems natural that individuals in these "networks" can share infectious diseases, too, spread through direct social ties, with well-connected nodes contributing more significantly to onwards disease transmission. The spread of infectious diseases between individuals in a network has been a central topic in the growing field of network sciences, which itself, in recent years, has advanced significantly.

The past couple of decades in particular have seen an acceleration of advancement in epidemic network modeling, with an over 500% increase in pubmed-posted publications in 1998–2007 vs. 2008–2017 (keywords: mathematical modeling infectious disease network), now representing about 10% of epidemic modeling studies. Network models occupy a middle ground in the field of mathematical epidemiology, allowing greater realism in the description of transmission patterns than compartmental models, but not reaching the full flexibility of generic agent-based models. Pedagogical resources for a newcomer are limited, primarily encompassing examples, or sections, in textbooks emphasizing mathematical epidemiology or network science —none of which captures the breadth of the field. Kiss, Miller, and Simon (KMS), experts who have already contributed significantly to the advancement of network epidemiology and related methods, fill that gap with this book.

Networks are computationally demanding to work with compared to compartmental models, so one focus of study of network epidemiology has been to find ap-

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proximating models that are analytically tractable and/or computationally efficient. Many such modeling approaches have been developed, and KMS covers the major differential equations-based models, also touching on a few stochastic approaches. In *Mathematics of Epidemics on Networks*, KMS state in Chapter 1 that they aim to

> make a contribution to modeling epidemics on networks by synthesizing a large pool of models, ranging from exact and stochastic to approximate differential equation models, so that we may:
> 1. recognize underlying model assumptions and the resulting model complexity;
> 2. provide a mathematical framework with which we can describe observed phenomena and predict future scenarios;
> 3. permit direct comparison of the main models and provide their hierarchy;
> 4. identify research gaps and opportunities for further rigorous mathematical exploration.

Note that in the text, the authors discuss "models," which I will call "network-models" as representations of disease dynamics on networks, and they neglect the underlying assumption that the network is, itself, intended to be a model of population structure through which the disease spreads.

Before discussing the book's aims, a note on the epidemic aspect. The authors emphasize two basic pictures of epidemics: "SIR" dynamics, wherein **s**usceptible individuals become **i**nfected through contact with other infected individuals, then are **r**emoved either by recovering and gaining immunity to infection or dying, and by contrast "SIS" dynamics, where recovered individuals are once again susceptible to infection. Thus, there are two nonnetwork related parameters, the mass-action rate at which contact between susceptible and infected individuals induces infection, and the rate at which infected individuals recover, with recovery exponentially distributed in time. For most of the text, they further assume no demography (no births, immigration, or natural deaths) or any further complexity to disease progression, e.g., an "exposed" period. Some realism is lost in this approach, and most applications will necessitate extensions. But the loss of realism comes at the massive gain of simplification and clarity of explanation; even for the simplest of epidemic models, the mathematics is already very complex. KMS provide in Chapter 9 tools to address some of those extensions.

The first aim of KMS is well met. Before wading into the network-models, a brisk explanation of these epidemic models and some basic network theory are provided (Chapter 1). KMS then launch into the stochastic models that fully capture network dynamics (Chapter 2). The authors clearly communicate not only the mathematics, but also how unwieldy they can be, thoroughly motivating the reader to advance to the differential equation network-models presented in subsequent chapters (Chapters 3–6). In each chapter, KMS describe different assumptions for how nodes, i.e., individuals, in the network may interact, and derive from those assumptions the resulting network-models. For example, from the assumption that all nodes of the same status (S, I, R) are interchangeable, one can derive the "homogeneous mean-field model." Restricting that assumption, by assuming that all nodes of the same status and degree, i.e., the other individuals to which they are connected, are interchangeable, one can derive the "heterogeneous mean-field model." KMS help their readers by sometimes leaving required proofs to the end of the chapters and providing excellent summary visualizations that demonstrate the various aspects of the network being modeled. The visualizations are very effectively tuned to aid in understanding the derivations.

I particularly valued the "recipe" boxes: following longer explanations or discussions of a concept or model, KMS provide text boxes with succinct algorithms showing how-to-actually-do-that.

To this reviewer, the second aim is less well met. To be sure, the network-models are well explained, providing a series of mathematical frameworks in which to investigate disease dynamics on some networks. For a reader who wants a single go-to tool, the "edge-based computation model" (Chapter 6), based largely on the work of coauthor Miller and collaborators [5, 6], is demonstrated to be a particularly useful, compact ODE framework to model epidemics on a network. Also, we are shown how one can use these network-models to make predictions such as final epidemic size (for SIR epidemics). However, mathematical epidemiology in itself and applied to public health policy is a field grounded in reality, and the connection to real diseases, epidemics, or population structure isn't well addressed, weakening the reader's ability to describe observed phenomena or predict realistic future scenarios. More on that follows below.

In contrast to their second aim, their third—permitting direct comparison of the main network-models and providing their hierarchy—is beautifully met. In any field, when there are multiple approaches to modeling phenomena, there can be significant confusion between approaches, their equivalence, or their disagreement. KMS dedicate an entire chapter to discussion and proofs showing the hierarchy of the network-models presented in the text. The relationships between models and model approximations are clearly delineated. To anyone using ODEs to model dynamics on networks who is new to the field, this is a must-read chapter. In the final chapter, KMS also provide a table showing the relationship between the mean-field SIR network-models and network properties captured, which is also a must-read.

Finally, network sciences and network epidemiology remain emerging fields, which KMS freely acknowledge as they satisfy their fourth aim. KMS note that network-models that consistently capture the "clustering" present in many realistic networks (essentially, the probability that two people connected to a randomly chosen individual are also connected to each other), which may have significant impact on disease spread, remain elusive. Dynamics on networks changing in time, discussed in the slim Chapter 8, is also identified as being in-development. KMS identify these and other knowledge gaps and make it clear that the toolbox to study network epidemic models is by no means complete.

The main weakness of this text is in bringing the mathematics back to the application. The model assumptions relating to how the network is approximated are clear, but this is a text on epidemic spread in networks: for a start, how well is the 20/80 rule captured? Chapter 9 addresses non-Markovian dynamics assumptions in network-models, noting, for example, that the assumption of exponentially distributed infectious periods with constant transmission rates underlying the SIR and SIS formulations is not correct. The natural discussion as to what the infectious or recovery periods may actually be for different diseases is absent. We are instead told how to implement a list of potential assumptions on, say, the recovery period, without motivation. Further, describing observations and making predictions for any phenomenon should be grounded in reality, but here I am left wondering: How do I use data to estimate parameters? How do I identify whether it is appropriate to use a stylized network, or a "real" network, given data on a particular disease or population structure? Chapter 11, "Disease Spread in Networks with Large-Scale Structure," does discuss a real network: the University of Oklahoma Facebook net-

work. Putting aside the verisimilitude of Facebook networks being a realistic network for disease spread—data on real networks is rare, and we do what we can—the assumptions upon which the mean-field and percolation-based network-models in the text were built fail because the network exhibits clustering. Some of these network-models reasonably approximate SIR and SIS dynamics on the network anyway (not the same models, I note), and though KMS discuss why that may be, we are left with little guidance when confronted with the next real network. This criticism is unfair: the title of the book focuses on the mathematics, and the aims quoted above do not explicitly include data. Still, I missed discussions of epidemiological aspects and implications of model assumptions.

Before closing this review, a few final notes. First, one of the primary benefits of the epidemic network-models over full network simulation or agent-based models is reduction of computational complexity. However, simulation remains integral to the mathematics of epidemics on networks. KMS have created, and provide for free, a Python module (which they call "nearly complete") providing tools for simulating epidemics in networks and for solving the many differential equation network-models described in the text. For those comfortable with Python, it is an excellent resource; documentation is fairly complete and the quick-start guide is useful, and it includes code for most of the figures in the text and additional examples. Users are invited to submit their own problems to the github/Springer-hosted "issues" board for help. The second author, Joel Miller, is active on the issues board. Second, for readers who would like to use this text for a class (which I myself plan to do!), note that there are exercises sprinkled throughout each chapter, but they are all fairly difficult, with no slow pitches to warm up with, for the targeted advanced undergraduate and graduate students.

In summary, there was a need for a text on network epidemiology, which Kiss, Miller, and Istvan more than meet. Their text is a solid contribution and a good, comprehensive resource on the mathematics underlying the modeling of epidemics on networks.

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Introduction to Linear Control Systems.
By Yazdan Bavafa-Toosi. Academic Press, Elsevier, 2017. $127.50. xxvi+954 pp., softcover. ISBN 978-01-281-2748-3.

Yazdan Bavafa-Toosi's *Introduction to Linear Control Systems* provides detailed treatment of the fundamentals of linear control systems theory. It is directed at senior and intermediate level undergraduate students and practicing engineers with no previous background in control theory. What is known about the author is that he graduated with B.Eng. and M.Eng. degrees from Ferdowsi University of Mashhad and K.N. Toosi University of Technology of Tehran (both in Iran), respectively, and with a Ph.D. from Keio University, Japan, and that he had research and teaching positions in Germany, Japan, and Iran.

The material presented is mostly along the lines of the textbooks [1, 2, 3, 4, 5, 6, 7], yet the present book is positioned as a comprehensive introduction to linear control systems, and in the reviewer's opinion it is both more basic and more comprehensive within the domain of fundamentals. Unlike some other textbooks, it does not cover design in the state space domain, digital, or sample-data control systems. However, the author mentions a number of times "the second course on state space methods," which has not been completed yet but which he is presumably preparing and is going to cover more advanced topics not included in the present book. We hope this endeavor will be accomplished in the future.

The book is divided into ten chapters, grouped into three parts, and is concluded with appendices. The subject matter can be divided into seven major topics: basic concepts and system models, stability analysis, performance in the time domain, root locus method, frequency-domain analysis, frequency-domain design, and advanced issues. Each topic is reviewed as follows.

1. *Basic concepts and system models* are covered in Chapters 1 and 2. The author starts with the history of control and continues with the principles of feedback, open-loop, and closed-loop control; he then reviews the relationship of control with the engineering disciplines, highlights the challenges of the control theory, and introduces such system characteristics as stability, performance, robustness, sensitivity, disturbance rejection quality, and others. The author then continues with mathematical representations of systems. Both chapters are concluded with worked problems and references.

2. Chapter 3 presents *stability analysis.* The author starts with definitions of the two types of stability, for the zero-input response, referred to in the book as Lyapunov stability, and for the zero-initial-state response or bounded-input-bounded-output (BIBO) stability. A few stability criteria are presented: Routh's test, Hurwitz's test, and Liennard and Chipart's test. The notions of relative stability, gain and phase margins, and D-stability are introduced. Kharitonov's stability theory is presented too. Chapter 3 concludes with a section on stability of linear time-varying (LTV) systems, which by means of examples illustrates the complexity of stability analysis in LTV systems.

3. *Performance in the time domain* is presented in Chapter 4, which demonstrates clearly how the time-domain metrics of a system characterize its performance. Test input signals such as step, ramp, and parabolic signals are considered. Sections on model reduction, the effect of the addition of a pole or zero, and the inverse response, which are seldom included in textbooks, are presented. In the reviewer's opinion what is missing are the plots showing step responses of first- and second-order systems for various damping ratios that are usually given in textbooks.

4. Chapter 5 covers the *root locus method.* The approach is explained from the conceptual point of view. Simple rules for drawing the root locus from open-loop zeros and poles are given. A problem in which more than one parameter varies is considered too. The problem of finding an appropriate value of the gain from the root locus, for the satisfactory performance of the sys-

tem, is also addressed. The examples throughout the chapter and problems included at the end illustrate applications of the root locus method.

5. *Frequency-domain analysis* is discussed in Chapters 6, 7, and 8. Chapter 6 does an excellent job of presenting and explaining the important and often difficult material on the principle of argument, complex values mapping, and the Nyquist stability criterion. Chapter 7 proceeds with the frequency-domain analysis using Bode diagrams and links this material with the previously presented root locus and Nuquist plot. It further extends the presentation to the rules of drafting of Bode diagrams and aspects of analysis such as stability, steady-state error, nonminimum phase systems, gain, phase, and delay margins. In Chapter 8, Krohn–Manger–Nichols charts (commonly known as Nichols diagrams) are studied. The author concisely presents the S, M, and N circles and M- and N-contours. Numeric examples are extensive and serve as an excellent illustration of the presented theories.

6. *Frequency-domain design* is discussed in Chapter 9. Design of phase-lead, phase-lag, and lead-lag compensators as well as PID controllers is considered in the context of Nyquist and Bode plots and root loci. Some specific ideas used for PID controller design (pole placement, direct synthesis, IMC structure, Skogestad tuning rules) are described in detail.

7. Chapter 10 covers *advanced issues*, which includes time- and frequency-domain relationships, fundamental constraints, and actuator and sensor limitations. In the reviewer's opinion, these topics are very useful for understanding of the practical aspects of the control system design. The chapter further includes controller design via sensitivity functions, eigenstructure assignment by the feedback, regulation and tracking, noninteractive performance, robust stabilization, and positive systems. Again, examples are

extensive and illustrate well the theoretical material.

The book is concluded with seven appendices: on Laplace transform, dynamics, MATLAB programming, stability, genetic algorithms, and a sample exam.

Some topics lack the systematic coverage typical of a textbook: in Chapter 1, for example, the introduction to control is done with the use of the transfer function and state space concepts prior to their introduction; the material on transfer functions is too concise; the introduction of the state space concept is sketchy; and gain scheduling as a method of handling nonlinear properties is referred to without sufficient explanation. However, the book definitely has strong points, including numerous worked problems, examples, and exercises. Despite its length, the book's scope is limited only to the study of linear time-invariant systems in the continuous time domain, without coverage of state-space domain design methods. This relatively narrow scope combined with its increased depth can also be viewed as a strong feature. In the reviewer's opinion, even the author's personal views, at some points debatable, of the history of control, the various contributions to the control theory, and the important control problems, and his attempts to restore historical validity by mentioning names that are not well remembered now, make it interesting to read.

Overall, given the fact that a number of excellent textbooks on control are available that are very suitable for undergraduate teaching (see [1, 2, 3, 4, 5, 6, 7]), the publication of a book that is different from those listed above with such features as deeper coverage of the basics and an abundance of examples and exercises is a good thing and a successful endeavor. Over 600 examples and worked problems, as well as about 1800 unsolved exercises, should be very helpful in using the text in teaching. Although as the only reference it would be less convenient for an undergraduate course, the abovementioned features make it an excellent supplementary text for students studying undergraduate control or a great reference book for practising engineers and graduate students, who, in addition to the material usually included in textbooks, may

also find a number of techniques that are seldom available.

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Infectious Disease Modeling. A Hybrid System Approach. *By Xinzhi Liu and Peter Stechlinski.* Springer, Cham, 2017. $119.99. xvi+271 pp., hardcover. Nonlinear Systems and Complexity Series. Vol. 19. ISBN 978-3-319-53206-6.

Models thrive when they are based on the right simplifications, but deciding what simplifications are right is not a simple matter. It therefore makes sense to question simplifications that are customarily made and to investigate whether dropping them leads to new or improved insights.

In this spirit, the present monograph focuses on coefficients in epidemic models being piecewise constant rather than constant. Even though time is a continuous variable, the intervals of time in between changes of the coefficients then introduce a discrete time element, whence the word "hybrid." In connection with (human) childhood diseases one can think about seasonality in contact opportunities caused by the school system. In the case of mosquito-borne diseases,

think of seasonal fluctuations in mosquito abundance.

An impulsive perturbation is a more extreme form of nonconstant coefficients. In many natural animal populations the inflow of new susceptibles is concentrated in a narrow period of time, so occurs as a pulse; see [1]. In intensive farming of chickens or pigs a cohort of fattened animals in a farm building is often entirely replaced by a new cohort of juveniles (while some of the pathogen stays attached to the walls, floor, or equipment).

I mention these examples in order to demonstrate that the subject of the book is well chosen and that its overall aim is worthwhile, so I started reading with high expectations. However, while reading I became rather disappointed.

Hybrid systems are the bread and butter of the authors, and they explain the formalism, as well as some technical aspects, in an early chapter on hybrid and switched systems, without using any examples with an epidemiological background. Hybrid variants of classical epidemic models are introduced and analyzed in Part II. The focus is on deriving criteria that distinguish between elimination, i.e., (global) asymptotic stability of the disease-free steady state, and persistence of the disease. Usually these criteria involve a basic reproduction number R_0. The emphasis is on technical aspects, rather than on conceptual issues, modeling itself, or epidemiological insights (this reviewer believes that analysis is most powerful when it reinforces (or even instills) common sense and intuition, and that motivation and interpretation therefore deserve lots of attention; but admittedly this is just an opinion). Most likely both the criteria and their justification are a bit misleading, since the crucial variable is one-dimensional (if the book provides a warning about the intricacies, both conceptual and technical, arising from the noncommutativity of matrix multiplication, I missed it). Somewhat implicitly, the book focuses on humans as the hosts that are exploited by the pathogen and animal or plant diseases are not considered. The last chapter, A Case Study: Chikungunya Outbreak in Réunion," pays some attention to modeling and to interpreting mathematical statements in order

to provide epidemiologial insights. Yet all in all I am inclined to call this book a missed opportunity to write an inspiring account of an epidemiologically very relevant subject.

To illustrate what I miss in the book, consider the final size of an epidemic outbreak when there is a strong seasonal influence on transmission. In an inspiring paper [2], Bacaër and Gomes have shown that the point in the cycle at which the infectious disease is introduced in the host population can have a very large impact on the final size. A related timing issue concerns the release of *Wolbachia* infected mosquitoes for dengue control. Here Allee effects are possibly reinforced by seasonal effects and the caption of Figure 12 in [3] meaningfully starts with "To wait or not to wait?" Clearly, then, the *timing* of control efforts is of utmost importance, too. Yet when discussing switched control, the book over and over again derives criteria for disease elimination versus persistence, while taking the switch points as given and not as to be chosen in a clever way (it is tempting to say "in an optimal way," but choosing the functional that one wants to optimize is an art in itself).

So if you have a serious interest in the epidemiology of infectious diseases and are eager to roll up your sleeves, please consult this book and then embark on one of the many challenges that are not (yet) covered.

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The Mathematics and Mechanics of Biological Growth. *By Alain Goriely.* Springer, New York, 2017. $159.00. xii+646 pp., hardcover. ISBN 978-0-387-87709-9.

I was asked to review this book around the same time I started a project investigating mechanical interactions in growing populations of rod-shaped bacteria. As I was unfamiliar with the mathematics used in models of mechanical interactions between cells, I sifted through many texts to find some that could provide a solid foundation on basic concepts. When I was approached to review this particular text, I saw it as the perfect opportunity to learn the math and, as a young mathematical biologist and biophysicist, to be introduced to an assortment of research questions that these mathematical tools could help answer.

I was not disappointed. Goriely's book is self-contained and provides sufficient review of the background material necessary to understand the mathematics employed in the study of phenomena he describes. Even in those areas where background material is not comprehensively covered, it points to a large number of references that provide the in-depth background development required for those unfamiliar with the basic theory of the mechanics of growth. Furthermore, the primary focus of this book is the mathematical description of the mechanics of growth of several different biological structures as a first step in developing a general theory of the mechanics of biological growth. More specifically, it instructively delineates previous theoretical work on biological growth and then poses several questions and challenges that need to be addressed. Indeed, it is surprising how limited the literature on the mechanics of biological growth is relative to the vast amount of work done in mathematical biology. Goriely appears to have presented here the first major technical book on biological growth in 100 years (see D'Arcy Wentworth Thompson's *On Growth and Form*).

The text itself is very well written and richly illustrated. Its structure is similar to that of Strogatz's classic *Nonlinear Dynamics and Chaos*. In particular, theory and examples in one dimension are described completely before moving on to problems and theory in two and, subsequently, three dimensions.

Part I describes the history behind scientific investigations of biological growth and broadly introduces the reader to basic concepts that are central to the book. The latter include a description of the relationship between growth and stress on various biological structures such as stems, axons, and soft tissues and a brief introduction to the questions addressed by the theory of morphoelasticity. This section finishes by providing an overview of various discrete computational models (e.g., cellular automata) that have been previously used to study biological growth. This section is a joy to read, as the writing unfolds as if it were a narrative history. Chapter 1, which describes the history of scientific studies of biological growth, is particularly excellent. I thoroughly enjoyed the story of how Galileo disproved that the discovery of giant bones (dinosaur bones) was evidence for the existence of prehistoric human giants through a simple scaling argument.

Part II begins the technical portion of the text. It describes the one-dimensional theory of filament growth and introduces the reader to elasticity, viscoelasticity, and plasticity, which are central ideas in the mathematical theory of biological mechanics. Chapter 4 kicks off the section by developing theory for growing rods on the line. The benefit of choosing this as a starting point is that rods can only stretch in one dimension, whereas in general they support bending, stretching, twisting, and shearing. Under this constraint, Goriely proceeds to describe a plethora of examples and applications for rod growth on the line. Chapter 5 builds on the ideas developed earlier and considers growing filaments embedded in space. Following a brief review of the calculus of space curves, the mechanics of elastic rods are described in great detail. The chapter finishes with a wonderful geometric example of helical rods. Chapter 6 incorporates all the theory developed in this section and further develops it by including the interaction of mechanical properties with growth—the theory of morphoelastic rods.

Chapters 4 and 5 of Part II were very instructional for me as a newbie to the field of mechanics. They provided great intuition and a firm grounding in the fundamental ideas underlying elastic filaments. Goriely

masterfully incorporates growth into the language of mechanics. However, it might have been more beneficial if the text did not try to be so self-contained in terms of the development of mechanical ideas before delving into how biological growth manifests itself in mechanics equations. The result is a very long monograph that may be exhausting to read. Furthermore, Goriely can be a bit wordy with his prose. This is my only complaint with the book—it is simply too long.

On the other hand, Part II plays an essential role in developing the mathematical theory of filament growth. In particular, it develops a general theory for filament growth, which is a novel contribution to the mathematical biology community.

Part III generalizes the concepts developed in Part II to two-dimensional geometries, with discussions of accretive growth for seashells and systems such as fungi representing tip growth. The final chapter in this section introduces the reader to the general theory of morphoelastic plates, but only briefly.

Part IV makes up the meat of the book and presents a general theory of growth for three-dimensional bodies. A description of the theory of nonlinear elasticity begins the section. This chapter is enormously helpful for those readers (like this one) who are not acquainted with large deformations mechanics theory. Here, however, I again question the necessity for a review chapter, especially in such a large monograph. Although I did find the chapter helpful, I would have liked the discussion on growth to come more quickly and the background material to be outsourced to the references within the text. More than 1300 references are listed.

This background chapter leads to the best-written chapter in the text, Chapter 12 on the kinematics of growth. Here the reader is introduced to the notion of incompatibility in a growing body and the different tensorial objects needed to quantify it. How growth tensors manifest themselves naturally in this setting is elucidated by leading the reader through a thought experiment wherein a stressed elastic tube is progressively sliced into small, potentially infinitesimal, pieces that are stress-free. This idea is given a mathematical

formalism. Specifically, the reader is introduced to an elegant differential geometry perspective on the above thought experiment, drawing from results in the theory of the geometry of differentiable manifolds. It is exciting to see the use of differential geometry in addressing biological problems; moreover, as geometry is a central aspect of biological growth, it may be the driving force behind the full development of a general theory of biological growth.

This chapter is followed by a general discussion on growth laws, stability, and dynamics. The section ends with detailed descriptions of applications in spherical and cylindrical growth.

Part V consists of a single chapter entitled "Ten Challenges." Here, Goriely describes in great detail problems he believes require significant attention from biologists, biophysicists, and mathematical biologists alike and shape the future of interdisciplinary research on the problem of biological growth. He concludes each description with a concise question posed to the scientific community. The tenth listed challenge concerns the mathematical formalism for the theory of biological growth. Here, it becomes clear that Goriely's intention for this book is to spark a movement toward a general theory and mathematical framework of biological growth.

To summarize, *The Mathematics and Mechanics of Biological Growth* serves not as a complete treatise on the title subject, but rather teaches the reader how to elegantly incorporate growth into the language of mechanics and introduces the vast variety of research questions that may be addressed by the theory described within the text. It is a first step toward a general theory of the mechanics of biological growth, as intended by Goriely. It is not suitable as a text for a standard class, as the topics are specialized and there are no exercises provided for the reader to ascertain whether or not they have grasped the theory presented. However, it may be suitable for a special topics course. Probably it is better suited for an individual to read through alone and learn the material. It is best suited as a reference text for basic mechanical ideas and overviews of potential future research projects. Overall, the text is well written, richly illustrated,

and enjoyable to read, although the monograph is lengthy. I applaud Prof. Goriely on his impressive text.

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Modeling Life: The Mathematics of Biological Systems. *By Ian Garfinkel, Jane Shevtsov, and Yina Guo.* Springer, Cham, 2017. $64.99. xvi+454 pp., hardcover. ISBN 978-3-319-59730-0.

If you teach mathematics to students in the life sciences, this book deserves a place on your (electronic) bookshelf. I am currently preparing such a course and *Modeling Life* is serving to guide my thinking about how to employ simple language to introduce a topic, how to pace the layering of technical material, how to raise natural mathematics-based questions in the minds of students, and how to integrate answers to those questions so that the mathematics becomes both habitual in the generality of its application and informative with respect to the particulars of the topic. Garfinkel, Shevtsov, and Guo excel at these things.

The self-proclaimed purpose of *Modeling Life* is to teach the art of making mathematical models of natural phenomena so that students will learn how to predict behavior from them. The book represents the authors' response to the "Scientific Foundations for Future Physicians," "Bio 2010," and "Vision and Change in Undergraduate Biology" reports and its approach is through the language and methods of dynamical systems. The featured systems are neural dynamics, ecological population dynamics, and immune system dynamics. The material has been classroom tested in a (20-week, 5-hour-per-week) course for first- and second-year life science students at UCLA for which there is no calculus prerequisite. The software package used in the course is SageMath, though reliance on this package is not so strong as to preclude the use of others.

The authors (and students) jump right into the study of systems. Beginning with well-chosen examples, the conceptual emphasis of the first chapter is on state vari-

ables, arithmetic and geometry in state space, change equations whose expressions in words lead to both time series for each state variable, and vector fields whose trajectories in state space are the predictions. The role of system feedback is prominent throughout this chapter and permeates the entire book. Calculus underpinnings appear succinctly in Chapter 2: the derivative measures sensitivity and provides a local linear approximation to a time series; more importantly, change equations express relationships between the derivatives and values of the state variables, while knowledge of those relationships enables the implementation of Euler's method, the basic computational tool for simulating systems and for computing model trajectories. In contrast with conventional calculus for life sciences textbooks, limits are barely mentioned. The symbolic rules for differentiation are stated rather than derived, occupying a scant four pages.

Chapters 3–5 contain the essentials of the dynamical systems approach and are entitled "Equilibrium Behavior," "Nonequilibrium Dynamics: Oscillation," and "Chaos." Chapter 4 is pivotal. While a typical calculus sequence includes discussion of equilibrium solutions to differential equations, these authors exclaim, "But are systems in nature really governed by equilibrium dynamics? No!" A sequence of examples, complete with data and figures from scientific papers, is used to convince the reader that an expectation of oscillatory behavior is more realistic and to posit that negative feedback and time delays combine to produce this behavior. A reasonably ambitious goal for a 14 week, 3 hour per week course would be to reach the characterization of Hopf bifurcation as the destruction of a stable equilibrium point and its replacement by an unstable equilibrium point and a stable limit cycle attractor. For students to emerge with an understanding of those words enriched by the several concrete examples provided in the text would be a notable accomplishment. The lovely chapter on chaos can wait.

Exercises in *Modeling Life* are of two types: between-paragraph questions test the student's understanding of what they are reading, while end-of-section exercises may involve mathematics of a new model, experimentation with model parameters, or extending model principles to explain their application in new scenarios, e.g., "Use your understanding of feedback loops and oscillations to suggest [ways to help a yo-yo dieter] to stabilize their weight." The exercises and the hand-drawn quality of the informative figures make for a lively text and contribute substantially to student learning.

The linear algebra required for further understanding is presented in Chapter 6. Students learn the mechanics of matrix algebra while performing computations that arise naturally in a Leslie matrix model for a population of black bears. Emphasis is placed on the units involved in sums of products. The authors achieve good balance between computation and description in their section on "eigenbehavior" for both discrete time models and linear systems of ODE. The final chapter includes enough multivariable calculus to enable stability analysis using the Jacobian. This paves the way for the more complete statement of the Hopf bifurcation theorem with which the book concludes.

My primary criticism of the print edition is that, despite a pattern of exposition in which the same terminology and models recur over the course of several chapters, the index lists only the first page on which an item appears. For this reason, I recommend the searchable electronic version. For some instructors and students, inclusion of an appendix introducing SageMath might also be useful.

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Biomechanics of the Human Stomach. *By Roustem N. Miftahof.* Springer, Cham, 2017. $199,00. xxii+279 pp., hardcover. ISBN 978-3-319-59676-1.

> People who have tried it, tell me that a clear conscience makes you very happy and contented; but a full stomach does the business quite as well, and is cheaper, and more easily obtained.
> –Jerome K. Jerome

This book caught my attention because of its focus on the stomach—an organ that I

find most fascinating, second only to my first love, the kidney. I have always found it quite amazing that our stomach, with the constant renewal of its lining, can withstand hydrochloric acid, which is strong enough to dissolve most metals. I also find it amazing that we can survive without a stomach. Apparently, a total gastrectomy, combined with the removal of the spleen, three quarters of the liver, most of our intestines, one of our kidneys (ouch), a lung, and all the organs from the groin area, won't kill us. Isn't biology truly fascinating?

I should note that I didn't learn any of the above tidbits from the book. It gets right down to business, so to speak. . . .

Potential Audiences. Let's talk about the book. It concerns the mathematical modeling of the human stomach, based on soft shell theory. As you can imagine, this is a highly interdisciplinary and rather specialized book, with prerequisites including a knowledge of the "anatomy, morphology, and physiology of the human stomach along with familiarity of basic principles of biochemistry, pharmacology, numerical methods, and the mechanics of solids." Quite a long list! Given this set of prerequisites, I find it difficult to agree with the author's assertion, in the preface, that "the book should serve as a text in computational systems biology classes at advanced undergraduate and/or first-year graduate levels." I respectfully disagree. Many of the topics are simply too advanced, even for a graduate program. For a math graduate student, the learning curve in physiology, biochemistry, and pharmacology is simply too steep. How many math graduate students know what an acetylcholinesterase inhibitor is? For a biology graduate student, soft shell theory and the numerical methods are probably too much. However, if you are a researcher seeking to develop or apply a computational model of the human stomach, this book would certainly make a great first (or second) point of reference.

Structure and Content. The book puts forward a holistic modeling of the human stomach as a soft biological active shell. The math involved in the description of the active soft shell is complex enough. But on top of that, the author also includes

the dynamic interplay of coupled electrical, chemoelectrical, and mechanoelectrical cellular and tissue events, all of which makes the modeling more fun! The author has done a good enough job of explaining most of the details.

Now, if I were to use this book for a class, I would want to see a description of multiple approaches for modeling the stomach. Preferably, the textbook would start with a simple approach (not soft shells), which students can easily grasp, and then would point out things that the simple model can capture and those that it can't. Then it would build on that simple model, see what the next-level model can do, and then build on it some more and then perhaps take an entirely different approach. Seeing how a simple model fails can help a student appreciate a more comprehensive model that is a pain to learn. In contrast, this book focuses on one single modeling approach: soft shell. That's it. Indeed, the first five chapters are dedicated to the foundations of the theory of soft shell (geometry, thin shell theory, boundary conditions, etc.). At times the book reads like a much extended version of a research article.

One thing the reader can get out of reading this book, provided that they go through at least the first five chapters, is a reasonable foundation of soft shell modeling, with the stomach as an application. That is, no doubt, a useful technique to learn. However, that learning process may be somewhat hampered the lack of end-of-chapter problem sets, which I consider to be a significant drawback. I always believe that I understand something until I have to work out a few problems.

The next few chapters focus on the constitutive relations for the wall of the human stomach under uniaxial and biaxial loading, modeling of the tissue as a chemically reactive mechanical continuum, and the cellular signaling networks. These eventually cumulate in a model of the human stomach as a soft bioshell in Chapter 11. While there is much for the reader to learn in these chapters, I also feel that some teaching opportunities might have been missed. For instance, some of the regulatory signals exhibit sustained oscillations. Wouldn't this be a great moment for the

author to introduce analytical techniques whereby one can determine when (i.e., with what parameters) the system may exhibit oscillations, and when it may not (e.g., as in [1])? But that wasn't done. The author simply presents the models and moves on.

Relation to Other Publications. In addition to this stomach book, the author has also published monographs on the mathematical modeling and numerical simulations of the digestive tract, human urinary bladder [2], and gravid human uterus [3]. All these models are based on the theory of thin shells, so the materials are somewhat repetitive. Indeed, the beginning chapters in all these books have many similarities. If I wanted to learn how to apply soft shell theory to model complex biological systems, I would much prefer *one* book that explains the soft shell theory and then shows the reader how to apply that theory to a number of organs, including the stomach, digestive tract, uterus, and bladder. More is not always better.

> By swallowing evil words unsaid, no one has ever harmed his stomach.
> –Winston Churchill

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A First Course in Computational Fluid Dynamics. *By H. Aref and S. Balachandar.* Cambridge University Press, Cambridge, UK, 2017. $59.99. x+394 pp., hardcover. ISBN 978-13-166-3096-9.

Yet another book about computational fluid dynamics (CFD) in the seemingly endless swirling current of computational science literature. The authors of this book, *A First Course in Computational Fluid Dynamics*, Hassan Aref and Sivaramakrishnan Balachandar, specifically target late undergraduate and early graduate students. So as a beginning Ph.D. student in numerical mathematics, I may not fall into their target audience. Nevertheless, this was my first experience in CFD, so this review is a first contact beginner's review.

A First Course in Computational Fluid Dynamics starts out very gently, and only a basic familiarity with concepts of theoretical and numerical linear algebra and differential equations is needed. Immediately the authors hit you with a good dose of passion about the topic of CFD, which certainly makes the read easier and boosts enthusiasm for further developments.

They begin with a brief refresher on numerical concepts such as rounding errors, some thoughts about hardware and software, binary numbers, and some more CFD-specific overviews on concepts such as general modeling aspects and turbulence. Next, the authors start by defining numerical methods as mappings and build on them by giving algorithms for solving ODE initial value, boundary value, and eigenvalue problems. Taking their time on this topic, the authors present a vast variety of finite difference methods, ranging from the basic Runge–Kutta and Adams–Bashforth–Moulton schemes to compact finite differences and finite differences in spectral spaces.

This is one of the things a potential reader has to be aware of. The book places its entire focus around discretization of differential equations on finite difference methods. Finite volumes are covered only on a few pages and finite elements are omitted entirely. This has the advantage that the authors are able to present different approaches to constructing finite difference schemes tailored with the specific application in mind. And since other approaches are not covered, the authors proposed a large body of further literature covering alternative methods, such as finite volumes, in greater detail.

In general, this is an aspect where the book shines; it takes the reader by the hand and avoids overwhelming him with many

new technical concepts at once, while pointing to further literature, both historical and current papers and educational books, for those interested.

Due to this, proofs of theorems are omitted almost entirely, and mathematical theorems are rarely seen in this book. This might be an advantage for students with backgrounds in both IT and engineering, but mathematicians seeking definition/theorem/proof based literature should look elsewhere.

Students with weak or no background in numerical techniques will be delighted to find an additional chapter devoted solely to basic techniques of numerical differentiation, integration, and interpolation, as well as various types of discretization. These barely need any prerequisites, and additional marked comments for beginners, which can be skipped by the more familiar reader, are included by the authors.

The examples the authors provide are chosen to fit into the current point of focus. So ABC-Flow is introduced to highlight aspects of different finite difference methods, and Prandtl–Meyer flow to serve as a guinea pig for different numerical methods for differentiating and integrating. These examples are supported by convincing graphical presentation, highlighting the properties of the governing equations at hand. Nevertheless, as a student of mathematics without background in physics, it was not always easy to grasp the physical interpretation of both model parameters as well as the physical phenomena themselves which are governed by the many different examples given by the authors. Thus, extensive research in secondary literature and online were needed to gain more intuition on the physical interpretations of Mach and Reynolds numbers, viscosity, turbulence, and visualization of the flows. Of course, covering all the basics of the physical side of CFD would have blown out the size of the book, so the authors compensate for this by pointing to additional literature for this aspect as well. Furthermore, students of engineering might even benefit of the lack of introductory level physical interpretation. Another benefit of this is that shortly after the brief discussion of the underlying phenomena, the authors resume their focus

on the mathematical and computational aspects of handling the equations.

One of the dominant focal points of such issues is the analysis of the stability of a given equation and numerical method. Stability concepts are introduced from the very beginning, and are discussed in great detail for various scenarios using different techniques, without giving any formal proofs. So von Neumann stability analysis and matrix methods are introduced, and strong emphasis is placed on differentiating between temporal and absolute instability, as well as the difference and interaction of accuracy and stability of the various methods. The authors succeed in making these aspects intuitively accessible, which is a highlight of the book. To complement these aspects and techniques, several pen-and-paper and programming exercises are spread throughout the book. These are mainly intended to apply techniques introduced in the previous chapters, both analyzing and deriving equations and numerical schemes and their properties, as well as implementing different numerical techniques for different problems. The exercises do not involve finding proofs, as in pure math lectures, but instead involve learning to apply various techniques useful for designing and analyzing algorithms and their respective implementations. This goes hand in hand with the authors' intentionally dialectic attitude toward weighing advantages and disadvantages of certain methods in the realm of practical applications. So fun passages like "first shoot, then relax," as in the context of shooting and relaxation methods for ODE boundary value problems, accomplish this goal and are presented in the aforementioned enthusiastic but sober way. The programming exercises and corresponding topics are well suited for seminars following lectures on either fluid dynamics or numerics, giving students the option to implement nontrivial problems. Speaking of nontrivial problems, the authors include interesting fluid dynamical problems at the end of chapters, so readers eager to see results from actual published papers will be satisfied. As an example, after introducing techniques for ODE eigenvalue problems, the reader is encouraged to reproduce the results shown in [1] concerning the hydrodynamic stability

of the plane Poiseuille–Couette flow, i.e., to implement the necessary software to solve the corresponding eigenvalue problems for varying Reynolds numbers.

Interestingly, and contrary to my expectations, the authors do not put heavy emphasis on numerics for PDEs. Rather, only the last third of the book with concerned with the PDE case, focusing mostly on the difficult aspects of generalizing the techniques shown in the first two thirds of the book. The advection-diffusion and Burgers equations serve as the main examples here, and later on the incompressible Navier–Stokes equation becomes the center of attention for the last sixth of the book. All the previously learned aspects come together to show aspects of handling Navier–Stokes. The main technique shown is the time splitting and pressure correction in various forms, including spectral versions. To round off the presentation of PDEs, some techniques for simulations in complex geometries are touched upon, giving a glimpse of body fitted grids and, especially of immersed boundary conditions using Lagrangian markers, to illustrate that the reader is not too far away from full blown CFD. So all in all, *A First Course in Computational Fluid Dynamics* offers a good introduction to ODE and PDE techniques, especially, but not solely, suited for fluid dynamics, with the focus on practical implementation and ideally suited for enngineering and math students in their late undergraduate studies. If you are looking for a book for more advanced PDE solvers, the use of finite volume, advanced grid techniques, or a book which is heavy on theory, this is not the right choice for you.

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Pyomo: Optimization Modeling in Python. *By William E. Hart, Carl D. Laird, Jean-Paul Watson, David L. Woodruff, Gabriel A. Hackebeil, Bethany Nicholson, and John D. Siirola.* Springer, Cham, 2017. $69.99. xiv+266 pp., hardcover. ISBN 978-3-319-58819-3.

Pyomo (Python Optimization Modeling Objects) is a Python-based open-source modeling language which is and can be used for a wide range of optimization problems, e.g., linear, nonlinear, quadratic, mixed-integer, stochastic, disjunctive, and bilevel problems. Thereby, Pyomo provides a solid platform on which to formulate and numerically model your problem. For the solution of your formulated optimization problems, external solvers are used. This book provides a detailed guide to Pyomo for beginners and advanced users from undergraduate students to academic researchers to practitioners. The book is an extended revision of an earlier volume published in 2012. It is published in the "Springer Optimization and Its Applications Series." This book is a case sui generis with its specific reference to Pyomo, apart from the earlier version mentioned above. The main problem classes supported by Pyomo are discussed within the book, which has two main parts. The first part gives an introduction to Pyomo and the second part provides more insight into advanced features and extensions. The book is well structured and explanatory, and all the explanations are underlined by code excerpts and illustrative examples.

The authors start with a general introduction giving some background on existing modeling languages in optimization and comparing Pyomo to these mostly commercial modeling languages. They give an overview of Pyomo's role and goals when dealing with optimization problems and start with a few examples and software requirements. Chapter 2 gives an overview of mathematical modeling and optimization formulations and their embedding in Pyomo, providing several instances from formulating the optimization problem to solving it with different external solvers. An illustrative example of the association of happiness with ice cream is given. Chapter 3 is devoted to the explanation of the Pyomo syntax, giving an introduction to its core modeling components and capabilities.

This chapter is especially useful for learning how to handle data files with Pyomo and it shows the different options doing so. As the illustrative example for this entire chapter, a warehouse location problem is chosen. All of this is explained in more detail in Chapter 4 which mainly provides a short outlook into other modeling components discussed in detail later in the book. Chapter 5 reveals how to run, check, or solve the models with Pyomo from the command line and how to analyze the output. In Chapter 6 we learn how to deal with data files and how to embed them in Pyomo. This is illustrated by a classic diet problem. Thereby, Chapters 2–6 belong to the first part of the book and provide a good introduction for Pyomo beginners.

The second part of the book consists of Chapters 7–14. Chapter 7 covers more details on the treatment of nonlinear programming (NLP) formulations within Pyomo, also providing some useful examples such as the Rosenbrock problem, a deer population dynamics problem, estimation problems for infectious diseases, and a classic reactor design problem. Moreover, this chapter gives some important notes regarding redefined Python operators within Pyomo and shows the right way to import Python's math package taking the redefined structure into account. In Chapter 8 we learn about structured modeling with blocks, which can be especially useful for models with repeating related components and a certain hierarchical order. This is illustrated by an optimal multiperiod optimization problem for optimal lot-sizing where the optimal production is supposed to be determined with the demands given. For users dealing with generalized disjunctive programming formulations, Chapter 9 clarifies their expression and solution within Pyomo. In the case of working with stochastic programming formulations, Chapter 10 will be very helpful as it explains their expression within Pyomo as an extension of a deterministic model. Chapter 11 deals with the formulation and solution of optimization problems with differential and algebraic equations as equality constraints included in the pyomo.dae package. For the newest features the reader is referred to the online Pyomo documentation. The

formulation of mathematical programs with equilibrium constraints (MPECs) from the formulation of complementarity conditions to MPEC transformations is highlighted in Chapter 12. In Chapter 13 the formulation of bilevel programs is discussed. A big advantage of Pyomo over other modeling languages is that you can use Python scripts and in this way connect all kind of problems and subproblems or even just embed and preprocess data files. The power of scripting in Python is shown in Chapter 14, where an example for implementing the Sudoku problem is given. Furthermore, the warehouse problem introduced in Chapter 3 is taken up again. As Pyomo is Python-based it is very useful but not required to have some prior Python knowledge. A brief Python tutorial is placed at the reader's disposal in the appendix and more references are provided.

All in all, the book provides a good introduction to Pyomo and a good overview of the capabilities of the software. The provided examples make Pyomo with all its different packages very accessible to all levels of users. The selection of examples covers a wide range with some very interesting applications, which makes them very useful. Personally, I started looking into Pyomo about two years ago and I have acknowledged its existence and development more and more, such that I am still working with it. I guess I am not the only one who feels that way, since the Pyomo community is continuously growing. So far, I have mainly used it for NLP problems, such as parameter estimation problems, optimal control problems, and nonlinear model predictive control problems using Ipopt as the solver of choice. From this book and its previous version I got some good additional input for challenges faced during the formulation of my particular NLPs. From my point of view, the gray boxes with the additional remarks and comments included in the book are exceptionally useful. For more advanced users looking for something in particular, they might not find what they are looking for in this book as it mainly provides the basics of the expressions and solution approaches for the specific problem formulations. Those users might find more help on the official Pyomo website or on the Pyomo

software github site. Nevertheless, the book is a good software guide which I strongly recommend to anybody interested in looking for an alternative to commercial modeling languages in general or in learning or intensifying their Pyomo skills in particular. It provides a good supplement to the on-line documentation for undergraduate and graduate students as well as researchers in academics and industry, including specialists in the relevant research and practical fields.

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