

The case for regime shifts due to positive feedback loops that cause runaway processes is very convincing for some of these systems (e.g., lacustrine and terrestrial ecosystems) and remains more speculative for others (e.g., long-term evolution). The author concludes by describing very useful starting points for detecting the onset of critical transitions in real systems, although I found the section about how to manage such systems overly optimistic. It seems good to avoid large catastrophes, but there is a caveat to utility managing: in the end, what we want as humans, and what we think is good or bad, is a moral and philosophical question, not a scientific one, and any approach based solely on scientific utility concepts seems incomplete.

I find Scheffer's arguments that complex dynamics, and in particular critical transitions, do in fact occur in many real biological systems very convincing. But I think it is also important to not get carried away. For example, the author repeatedly refers to a study claiming the existence of power laws in the fossil record as evidence for complex long-term evolutionary dynamics, but the observed pattern is most likely an artifact due to the methods of data analysis (J. W. Kirchner and A. Weil. 1998. *Nature* 395:337–338). Nevertheless, it seems clear that the possibility of critical transitions must be taken seriously in empirical studies, and judging from a number of proposals that I have seen as a member of one of the review panels of the Natural Sciences and Engineering Research Council of Canada, and that explicitly incorporate the study of regime shifts into their research agenda, this view is shared by an increasing number of empirical and applied researchers. For them, as well as for many others interested in large-scale thinking, Scheffer's volume will be a fascinating read.

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THE SIMPLE SCIENCE OF FLIGHT: FROM INSECTS TO JUMBO JETS. *Revised and Expanded Edition.*

By Henk Tennekes. Cambridge (Massachusetts): MIT Press. \$21.95 (paper). xiv + 201 p.; ill.; index. ISBN: 978-0-262-51313-5. 2009.

This introduction to flight mechanics, a revised edition of a widely acclaimed treatment, provides conceptual background to and practical applications of the theory of flight. Through the use of simple equations, basic physical reasoning, and numerous biological and technological examples, the aeronauticist Henk Tennekes unifies themes of mechanical performance for flying machines as diverse as fruitflies and Boeing 747s. Size, speed, and air density are manipulated algebraically to yield the "great flight diagram" upon which cruis-

ing speeds and weights of all flying objects can be reasonably plotted and correlated with each other. This analysis then extends into discussions of power and flight energetics, the cost of transport, optimal strategies of migration, and the aerodynamics of flight control. Black-and-white drawings of diverse birds, insects, seeds, and airplanes are used to graphically indicate the kinds of morphologies relevant to flight performance, whereas data tables display the substantial range of relevant parameters as seen in both animal and mechanical systems. A healthy amount of both flight technology and basic biology (especially that relating to birds) is woven into the aerodynamic discussions. Given that a major theme of the book is the effect of body size, omission of the key concept of the Reynolds number is surprising. Similarly, the grand allometric curves exhibit sometimes shocking (i.e., ten-fold) deviation from mean values otherwise predicted by the overall linear regression and further discussion of those mechanical and biological factors underlying such variation would be helpful. Nonetheless, this serves as an excellent introduction to both the theory of flight aerodynamics as well as to its seemingly endless variants in both natural and technological domains. It would be excellent supplemental reading for undergraduates in biomechanics and engineering programs and, for general readers, it will serve as an informative and occasionally inspirational introduction to the marvels of flying machines.

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MATHEMATICAL METHODS IN BIOLOGY. *Pure and Applied Mathematics.*

By J. David Logan and William R. Wolessky. Hoboken (New Jersey): Wiley. \$84.95 (paper). xiii + 417 p.; ill.; index. ISBN: 978-0-470-52587-6. 2009.

Toward the end of his classic movie, *The Good, the Bad, and the Ugly* (1966), Sergio Leone taught us that there are two types of people in the world. For this review, they are mathematical scientists who want to learn about biology and biologists who want to acquire quantitative skills. I have taught such material to both groups for 30 years and written a number of books aimed toward the latter group. The former group is often looking toward biology as a source of problems in mathematics, but cannot find the problem. Biologists often have the problem in hand and get stuck on technical aspects. This volume, although aimed for both groups, is a much better fit for mathematicians who are trying to pick up some biology. The selection of topics is excellent, and the authors cover both deterministic and stochastic models, in what we might think of as the canon for quantitative methods in biology: foraging theory, diffusion, sin-

gle species population dynamics, structured populations, phase plane analysis, probability (including the Hardy-Weinberg law and the central limit theorem), statistical inference, random walks, birth and death processes, and stochastic differential equations. They suggest that only two semesters of calculus is needed to get into the book, along with some ability to reason quantitatively. However, even in the very first chapter, there are sophisticated mathematical ideas that will leave most neophytes in the intellectual dust (including solutions of differential equations and radii of convergence for Taylor polynomials) and little time is spent developing biological intuition about the mathematical ideas. This continues throughout the volume; for example, in Chapter 3, readers are supposed to know linear algebra, partial differentiation, and what a dominant eigenvalue is (although there is an appendix that provides this material, it might come too late for all but the most perseverant readers). I think that a typical upper-division undergraduate or graduate student in biological science would find it very tough going. Admirably, the volume is written with bits of MATLAB code inserted at appropriate places and has exercises interspersed throughout the text (as well as hints for solutions to the exercises at the end of the book). Overall, this is a nice volume that will be very helpful for mathematicians who are looking to use their skills on biological problems, and less helpful for biologists who want to learn these skills.

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REVERSE ENGINEERING BIOLOGICAL NETWORKS: OPPORTUNITIES AND CHALLENGES IN COMPUTATIONAL METHODS FOR PATHWAY INFERENCE. *Based on a workshop held in Wave Hill, Bronx, New York, 7–8 September 2006. Annals of the New York Academy of Sciences, Volume 1115.*

Edited by Gustavo Stolovitzky and Andrea Califano. Published by Blackwell Publishing, Boston (Massachusetts), on behalf of the New York Academy of Sciences, New York. \$125.00 (paper). xiv + 287 p.; ill.; index of contributors. ISBN: 978-1-57331-689-7. 2007.

Reverse engineering biological networks is the science of taking observational data to infer how different components, such as genes and proteins, of a biological system causally interact. Although the idea is not new, the computational techniques that use large datasets to do so have been well developed within the last decade. Research in this area is critical for the progression of the systems biology field, which relies on high-quality biological networks to draw conclusions at the level of an entire biological system.

This book is collection of articles that have emerged out of the DREAM (Dialogue on Reverse Engineering Assessment and Methods) workshop. It opens with reviews that could serve as an introduction to the field, including the particularly comprehensive chapter, Theory and Limitations of Genetic Network Inference from Microarray Data (by Margolin and Califano). The rest of the book consists of a diverse set of research articles that cover the methods, applications, and theories of constructing biological networks. Although several techniques are discussed and compared to construct biological networks, including Bayesian inference algorithms and differential equations, no particular one has yet proven to be the standard. The authors describe the variety of data available and numerous problems to be solved. Algorithms are discussed that use one or a combination of several different types of input data (including mRNA measurements, metabolites, and images) to build networks that range in size from tens to hundreds of genes. Despite the diversity of topics, there are several consistent themes that connect the research. One particular challenge is that of rigorously assessing and comparing these methods.

The depth and diversity of *Reverse Engineering Biological Networks*, much like the field itself, could make it difficult for someone who is not an expert in networks to understand completely. Because different articles approach the problem from different perspectives, there are portions of the book that will be useful to computer scientists, statisticians, or biologists. In this regard, the volume particularly excels at its primary goal, which is to honestly describe the progress made in network construction and the challenges still facing researchers.

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PALEONTOLOGY

DARWIN'S LOST WORLD: THE HIDDEN HISTORY OF ANIMAL LIFE.

By Martin Brasier. Oxford and New York: Oxford University Press. \$34.95. xiv + 304 p. + 16 pl.; ill.; index. ISBN: 978-0-19-954897-2. 2009.

The title of this volume refers to the apparent absence of fossils (in Darwin's day) in rocks older than those containing the familiar trilobites and brachiopods of the Cambrian. Darwin was concerned that this missing record might compromise his theory, given the need for time to allow such