vectors and on the very next line components of vectors. Toward the end of the same section, components of vectors are denoted $x^{(1)}, \ldots$. It's generally clear from the context, however. What's not so clear is that the authors at times mix row and column vectors (e.g., p. 26) and this is very confusing and seems to contradict p. 5. Similarly, using the notation $\langle x_1, \ldots, x_n \rangle$ to denote a column vector is also very confusing.

While everything is nicely done in the complex case, the sign of a scalar is defined only for real scalars (p. 6). Corollary 5.1.3 and the real version on p. 127 are classical and can be proved easily and directly from the Jordan canonical form. Interestingly, I know of no other proof. I also learned something new. The matrix I call the "reverse order identity matrix," the authors call the sip matrix (standard involutory permutation). Heavy use is made of it throughout the book.

I have a few quibbles about the conventions used. For example, in most mathematics books, either the range and nullspace of a matrix (or linear transformation) are used, or the image and kernel. These authors use one from each: range and kernel.

The index is a little skimpy. Most things appear only once and are not cross-listed. For example, Hamiltonian matrix appears as a subitem under matrix but not under Hamiltonian (matrix). Another little nitpick is that the word Hermitian appears throughout in lower case (hermitian). Perhaps because it's in adjectival form? But then Hamiltonian appears capitalized. It's better to be consistent.

All in all, I like this book. The concept of an indefinite inner product is by now well established in the linear algebra literature and this book goes a long way toward becoming the standard text on the subject. It culminates in a nice chapter on the algebraic Riccati equation (continuous-time case only; readers are urged to consult reference [67] for the discrete-time counterpart) which remains a source of intense research interest. The book is well worth having in one's library.

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Dynamic Models in Biology. *By Stephen P. Ellner and John Guckenheimer.* Princeton University Press, Princeton, NJ, 2006. $45.00. xxii+329 pp., softcover. ISBN 0-691-12589-9.

Those of us who came of age in the 1960s and 1970s have seen mathematical biology develop and mature to the point where it is now a distinct and important discipline (which somewhat compensates for the aging of other icons of the 1960s, and I write this on the day that Bob Dylan turns 65). We have also seen mathematical biology become an interdisciplinary field *par excellence*, in which one is most effective by mastering the core skills of applied mathematics and the core knowledge of the biological application. We are not there to do the sums for biologists; rather, we are there to solve scientific problems using mathematical methods. In their review of a different book, Bangham and Asquith [1] wrote:

> It is a widespread fallacy that what mathematics contributes to biology is quantification of an otherwise innumerate science. But experimental biologists have long been expert at measuring and quantifying. The real contribution of mathematics lies in a precise framework of reasoning. . . . Experiment, however, is in no sense superior to theory, nor vice versa: both are necessary ingredients of a proper understanding of nature. An experiment done with no theoretical framework to analyze or interpret the results. . . is meaningless; theory in the absence of experiment remains mere theory.

And Bruce Walsh [2] put it more succinctly: "Far from freeing molecular biologists from mathematics, the age of genomics has forced an appreciation of the importance of quantitative methods."

The challenge, however, is to figure out a way to make the key methods and ideas of dynamical modeling in biology accessible and exciting to students and postdocs in both biological and mathematical sciences. Ellner and Guckenheimer have produced a volume that will add to and complement existing books. The book is based on an undergraduate course taught at Cornell to a diverse audience of biologists, physical

scientists, mathematicians, and computer scientists. It is easy to read because it is written in a conversational style (a technical book is hard enough without the writing being turgid) and the book is exciting to read because it is clear that these particular applications interest and excite them—and that enthusiasm carries over into the written word.

The chapter headings are pretty much what one would hope for in an introductory volume: (1) "What Are Dynamic Models?," (2) "Matrix Models and Structured Population Dynamics," (3) "Membrane Channels and Action Potentials," (4) "Cellular Dynamics: Pathways of Gene Expression," (5) "Dynamical Systems," (6) "Differential Equation Models for Infectious Disease," (7) "Spatial Patterns in Biology," (8) "Agent-Based and Other Computational Models for Complex Systems," and (9) "Building Dynamic Models." This is a book about biology, where mathematics is the tool for understanding the biological system. And there is a lot here—Ellner and Guckenheimer note that the material could not be covered in a single semester, and give some suggestions about how the material could be used.

They are master craftsmen and emphasize the process of modeling (deciding what is essential and what is not in describing the problem at hand and understanding how much to trust the model), so that apprentices can learn from them (and indeed they make this analogy themselves toward the end of the book). The discussion of why one should bother at all to model is excellent, and another example of Richard Feynman's notion that there is nothing so practical as a good theory. They also weigh in on the issue of complex versus simple models, especially in the context of systems biology (Chapter 4; see below). Here, I think that they could have given more weight to Lander's [3] argument about the importance of exploring parameter spaces—which can indeed be followed in some sense regardless of the complexity of the model (see [4]). Ellner and Guckenheimer help the reader recognize that there are different kinds of models—as there should be when the problem is paramount—and in Chapter 8, after describing an individual-based model for

predation, they write, "This model is *theoretical* even though it is *computational.*"

In general, mathematical ideas are introduced as they are needed as tools to solve problems that arise in biology—the way it should be done—and students are expected to read primary biological literature. Thus, for example, in the chapter on membranes, energy landscapes (for membrane transport), Markov chains, coin-tossing, and the central limit theorem follow the motivation of the question and precede the solution of the problem for which they are needed. Similarly, data are shown when appropriate. Most importantly, the book is forward-looking: Ellner and Guckenheimer provide a description of current practice in the modeling of biological systems, and give a prescription of how to look forward in order to make new discoveries.

My only concern is about the level of mathematical expertise required. Although the book starts with a model based on difference equations (for chinook salmon), already by page 9 students will really have to have mastered calculus and introductory ordinary differential equations because the classic Michaelis–Menten kinetics for enzymatic reactions are analyzed and a very simple phase plane constructed. Although it could have been given here, with a bit of respite for the reader, the authors save the Lineweaver–Burke plot until very late in the book. By page 17, they are using Newton's second law of motion in differential form—making me a bit concerned about the level of difficulty. Similarly, the chapter on matrix models ranges in mathematical level from analysis of 2×2 matrices to the recent projection kernel methods that Ellner and his colleagues have worked on. In the chapter on gene expression, scaling and nondimensionalization are introduced as a footnote. In the chapter on dynamical systems, I appreciate what they are trying to do in giving the existence and uniqueness theorem for differential equations, but fear that biologists will run in fright and mathematicians will be unsatisfied because the proof is not given—thus leaving everyone unhappy. (Admittedly, this is in the most mathematical chapter of the book.) I expect that this material can surely be taught effectively, but it may be difficult for self-study

unless the student is given some guidance about what to cover and what to ignore.

I liked the exercises, which are a mixture of mathematical analysis, numerical or data analysis, and writing—something that all of our students need to work on. The exercises are scattered throughout the text, not just at the end of the chapter. This is also a good thing, because it will encourage students to think about those questions before moving on. Computational tools can be found at the website associated with the book. The reference lists at the end of each chapter represent good coverage and can lead readers into new territory. I also liked that there are pictures of animals in the book—reminding the reader of the motivation for the mathematics.

In summary, this is a great book and I expect that it will play an important role in the teaching of mathematical biology and the development of the next generation of mathematical biologists for many years to come.

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Heights in Diophantine Geometry. By Enrico Bombieri and Walter Gubler. Cambridge University Press, New York, 2006. $130.00. xvi+652 pp., hardcover. ISBN 0-521-84615-3.

The purpose of this book is to give a detailed introduction, accessible to beginning graduate students, to many of the results and conjectures in Diophantine geometry (the study of equations in integer and rational numbers). The authors succeed beautifully; most of this book requires only basic algebra and arithmetic geometry, as well as patience and careful reading; the choice of topics and level of detail illuminate a vast and popular landscape.

There are several good books on Diophantine geometry [1, 2, 3, 4], and this book is a welcome addition to that list. The distinguishing feature here is the incredible wealth of detail. There are no exercises for the reader in the book. Instead, the authors provide proofs for what would have been exercises elsewhere, as well as additional comments and suggestions for further reading. The book is mostly self-contained, and their approach is a great aid to the nonexpert who wants an in-depth analysis of certain subjects. As a further aid to the beginner, many side topics not used elsewhere in the book or material requiring more advanced knowledge of algebra and geometry appear in a smaller font.

There are three main parts of the book. The first (Chapters 1–7) develops the theory of heights, with applications to proving finiteness results on solutions to Diophantine equations. Let $\overline{\mathbb{Q}}$ be an algebraic closure of $\mathbb{Q}$, and consider the projective space $\mathbb{P}^n_{\overline{\mathbb{Q}}}$. The height of a nonzero point $P = (x_0 : x_1 : \cdots : x_n) \in \mathbb{P}^n_{\overline{\mathbb{Q}}}$ with coordinates in a number field K is $h(P) = \sum_{v \in M_K} \max_j \log |x_j|_v$. Here $|\ |_v$ is the normalized absolute value (as well as the extension to the completion K_v) associated to a place $v \in K$, and M_K is a set of nontrivial inequivalent absolute values on K such that for any nonzero $x \in K$, there are only finitely many v with $|x|_v \neq 1$. For example, if $K = \mathbb{Q}$ and v is a prime p, then for $m/n = p^a m'/n'$ (with $(p, m'n') = 1$) we have $|m/n|_p = p^{-a}$, and $M_{\mathbb{Q}} = \{|\ |_p : p \text{ prime or } p = \infty\}$. It is often convenient to study the absolute exponential height, $H(\alpha) = e^{h(\alpha)}$. One application of the theory of heights is a proof of Roth's theorem over number fields (finite extensions of $\mathbb{Q}$).

ROTH'S THEOREM. *Let K be a number field with a finite set S of places. For each $v \in S$ let $\alpha_v \in K_v$ be K-algebraic. Let $\kappa > 2$. Then there are only finitely many $\beta \in K$ such that*

$$\prod_{v \in S} \min(1, |\beta - \alpha_v|_v) \leq H(\beta)^{-\kappa}.$$