

BOOK REVIEWS

Cellular Biophysics, by Thomas F. Weiss, MIT Press, Cambridge, MA, 1996. \$85.00 (cloth), 2 volumes.

Cellular Biophysics is a gigantic two-volume book about the theoretical basis for cellular transport and electrophysiology. The first volume concentrates on transport mechanisms, beginning with diffusion at the microscopic and macroscopic level, proceeding through carrier-mediated transport, ion transport, and the resting potential, and ending with models for cellular homeostasis and volume control. The second volume begins with linear electrical models of cells, and then moves on to Hodgkin-Huxley theory, saltatory conduction, and voltage-gated ion channels. All told, there are well over 1100 pages of text.

It is intended as a textbook for junior or senior undergraduates in bioengineering (or some such related discipline) and is based on the lecture notes of the author who taught such a course at The Massachusetts Institute of Technology for many years.

I approached the book with considerable excitement, as I have long believed in the necessity for a book of this kind. However, although the book has many excellent qualities, I was disappointed to find that it also has some serious deficiencies that make it rather less appealing. In the best tradition, let me start by describing the virtues of the book before describing what are, in my opinion, its flaws.

First, the book provides a wealth of physiological detail, including diagrams of experimental procedures, reproductions of experimental data, and detailed discussions of the background physiology. The amount of detail is (obviously) less than is found in a specialty physiology book, but is very much greater than that found in other books on physiological modeling, at least ones that I have read. For instance, the section on myelinated nerve fibers and saltatory conduction begins with a discussion of the physiology that includes a scanning electron micrograph of the node of Ranvier from the sciatic nerve of a rat, and several electron micrographs of sections through a myelinated nerve fiber. Experimental evidence for saltatory conduction is discussed, as are experimental tests. Throughout the book there is a similar interweaving of theory and experimental data which makes clear, as so few theoretical books do, their mutual interactions. Another excellent feature is the large number of exercises, most of which require real physiological understanding. Yet another virtue is the book's comprehensiveness; I could think of very few topics that were omitted. One exception to this general rule was the puzzling omission of Rall's equivalent cylinder theory. However, no doubt we all have our favorite topics, and we will never all agree on their relative importance, so this cannot really be construed as a serious defect.

What is far worse (and here we come to the flip side of the coin) is the method of presentation of some of the topics. In some places the presentation is so unusual as to border on downright error, and in other places I do not see how a student could avoid confusion. For example, in his discussion of the propagation of an action potential along a nerve axon the author correctly points out that such traveling waves are solutions of the form V(x,t) = V(x - ct), where V is the membrane potential and c is the wave speed. However, by differentiating V with respect to x and t, he then derives the fact that V must therefore satisfy the wave equation! This, surely, is a dangerous thing to tell students. The fundamental (mathematical) property of action potential propagation is that it is a nonlinear wave solution of a nonlinear reaction-diffusion equation. Of course, the wave equation has wave solutions also, but they are very different beasts; for a start, they are linear. This initial confusion leads the author into further difficulties when he derives the ordinary differential equation describing the wave solution in the traveling wave coordinate. Using the wave equation, the author derives an ordinary differential equation for V as a function of t only, instead of the usual traveling wave variable x - ct. Although the correct result is attained in the end, the method lacks rigor, to say the least.

Unfortunately, there are a number of places in the book where the method of presentation similarly obscures the underlying issues. In addition, excessive wordiness also causes problems. Often an argument is more difficult to follow when presented too slowly and with excessive detail, and I found this to be the case here. In many places, even though I was very familiar with the basic material, I found it hard work to read and absorb the arguments. In my opinion, the material would have been better presented in a single volume. (As a side issue, two large volumes can be demoralizing and frightening to students, not to mention expensive.)

In summary, although the book has some excellent features, I feel that I cannot recommend it unreservedly. I freely admit that some of my objections may be caused by a difference in approach between the engineer and the mathematician. I also admit that I have much less experience in teaching this kind of material than does the author, and it may well be that his style of slow presentation suits students much better than the approach

I personally prefer. Thus, it would be well to keep an open mind. Anyone teaching a course on quantitative physiology would be very well advised to read this book carefully. It is certainly a comprehensive and detailed view of the field, and, if approached with sufficient caution, may well prove valuable to many.

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Case Studies in Mathematical Modelling: Ecology, Physiology and Cell Biology, edited by Hans G. Othmer, Fred Adler, Mark Lewis and John Dallon, Prentice Hall, Upper Saddle River, NJ, 1997. \$33.33 (paperback), viii + 411 pp.

Someone somewhere once wrote of a certain green mathbiology book something along the lines of, "It is a book to be read and savoured of an evening, sitting by a fire with a glass of malt whisky." I thought that these were pretty good instructions for reviewing a book, and so sitting by an open fire with a "wee dram" (viz. small whisky) by my side, I set about reading the above book. A little bit of my own elementary mathematical modeling, using conservation of mass, and the laws of fluid dynamics ("...a sip every few pages; 400 pages; approximately 200 sips...") led me to believe I would have a fine evening. Upon reaching the end of the book, however, I was thoroughly disappointed—I had hardly touched a drop, a testament to the uniform quality of this unassuming volume.

This book is the outcome of a special educational program, "A Special Year in Mathematical Biology," which took place at the University of Utah in 1995–1996, and is a collection of case studies presented by 26 leading mathbiology researchers in three particular areas of mathbiology: ecology, physiology, and cell biology, designed to introduce the student to the overlooked and oft-taken-for-granted art of mathematical modeling. Each chapter of the book aims to take the reader from the stage of formulating an initial mathematical model through testing and refining of the model to

the cutting edge of research. In this, it is very largely successful. The mathematical techniques employed in the book are mainly ordinary differential equations and linear algebra. Other techniques included at various parts of the book include partial differential equations, stochastic processes, and statistics.

The book is naturally divided into three sections, with each section being prefaced by one of the editors detailing specific themes and characteristics of that particular section. The section on ecology contains chapters on ESS, niche evolution, epidemiology, biomass dynamics, and DNA sequence data; that on cell biology, chapters on signal transduction, the cell cycle, hematopoietic cell replication, delayed feedback control, and pancreatic β -cells: while the final section, physiology, deals with muscle crossbridge mechanics, phase resetting and limit cycles, cardiac muscle modeling, fluid dynamics of the heart, and bioconvention. Although all of the chapters are well written and interesting, chapters which I personally would single out as being particularly excellent are those by Othmer (signal transduction), Mackey (hematopoietic cells), and Glass (phase resetting), with the chapter by Peskin and McQueen (heart fluid dynamics) being quite outstanding. The figures and illustrations are reproduced to a high quality, as is the typeface and excellent referencing—three cheers for EMACS and LaTeX!

At the end of the book are three appendices (A, B, and C) devoted to, respectively, age-structured models, qualitative theory of odes, and an introduction to pdes. Two of these (age-structure and pdes) are very short. Indeed, the pde appendix is really an introduction to vector calculus rather than the theory of pdes. Appendix B (ode theory) is more comprehensive and indeed reflects the overall bias of the book. From a personal point of view, I would have preferred to see more attention to partial differential equation modeling, especially in the section on cell biology. (Where were the reaction-diffusion equations, mechanisms of cell migration such as chemotaxis, pattern formation, traveling wave theory, etc?)

In my experience, it is very difficult to teach students (both undergraduate and graduate) mathematical modeling. Rather, modeling must be learned by experience and not rote example, since each new biological problem brings new and different challenges for the modeler. This is a book which will serve as an excellent volume of how to apply mathematics to problems in biology, how to construct mathematical models, and how to test and improve them. However, importantly it also conveys the sense of excitement and fun that is associated with mathbiology. The spirit of fun, informality, and enthusiasm which undoubtedly permeated the yearlong program shines through all the underlying mathematics (cf. M. Mackey, p. 163: "After that wordy digression, let's assume that $z(t) \approx e^{\lambda t}$ in (8.49). If we make this substitution ... then we are left with the equation ..."). It is a book that is well worth having as part of one's mathbiology collection, providing an insight into the diversity of modeling techniques used and the richness of the field of study.

And now for that glass of (single) malt whisky...

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Null Models in Ecology, by Nicholas J. Gotelli and Gary R. Graves, Smithsonian Institution Press, Washington, DC, 1996. \$30.00 (paperback) and \$65.00 (cloth), xvi + 368 pp.

Ecologists have long been fascinated by community-wide patterns in the geographical distribution and morphology of species. Much of the literature on these patterns focuses on illustrating the ubiquity of pattern in community-wide data, and on interpreting pattern to imply the operation of specific mechanistic biological processes. On the other hand, a considerable literature has also developed that attempts to understand the statistical properties of the largely ad hoc numerical indices that are used as metrics of these patterns, and hence whether the extent of pattern in data is an expected property of the metric or constitutes sufficient patterning to require biological explanation. This latter approach involves the use of so-called "null models" to attempt to generate the expected properties of these metrics in the absence of any putative biological process-in the null case-so that pattern due solely to the statistical properties of the metric may be distinguished from the more interesting biological processes. Gotelli and Graves' Null Models in Ecology is a comprehensive, balanced, and informative compendium and critical examination of the use, formulation, and interpretation of null models largely in the field of community ecology.

Gotelli and Graves illustrate that the use of null models has been highly instructive in many ecological endeavors, although not without controversy. Perhaps the first widely acknowledged application of a null model was in determining the expected ratio of the number of species to the number of genera (S/G) in a biota. Elton (1946) found that the S/G ratio was almost always lower for insular communities than for mainland biotas, and postulated that this pattern was the result of interspecific competition and

competitive exclusion of closely related species on resource poor islands. However, Williams (1951, 1964), and later, Simberloff (1970) demonstrated that because of the hierarchical nature of the classification of species into genera, the expected S/G ratio should be an increasing function of the number of species sampled. Thus, islands with fewer species should be expected to have lower S/G ratios than more speciose mainlands. Comparisons of expected S/G ratios to the observed data indicated that the observed ratios on islands were predominately larger than expected, forcing a reexamination of both the pattern and hypotheses regarding its cause.

Gotelli and Graves' synthesis clearly and forcefully demonstrates that such ad hoc statistics as the S/G ratio are not solely a construct of our ecological past. Because community-wide ecological patterns are very complex, by necessity ecologists often begin their exploration using derived numerical indices whose distributional properties are unknown. This is in part a consequence of the difficulty, or for large-scale patterns, the impossibility of performing replicated field experiments that would result in metrics whose distributions may be derived from the traditions of parametric and nonparametric statistical inference. For many areas of inquiry in ecology, the examination and interpretation of nonexperimental evidence has been and will remain an important, if not central, component to understanding how nature works. However, the use of nonexperimental evidence and its accompanying ad hoc numerical indices requires that we understand the statistical properties of, as well as how, biological and geographical processes affect the metric we use.

A null model is an attempt to place data derived from nonexperimental research into the context of statistical hypothesis testing. As such, a null model is contrived to generate the probability distribution of a variable of interest under the null hypothesis of no experimental effect. Null models are statistical models tailored to serve as the "control" case when examining a specific set of nonexperimental evidence (Connor and Simberloff, 1986).

All null models derive from the statistical tradition of tests of independence as manifested in the analysis of contingency tables. As in contingency tables, one asks if the observed value of some metric is unlikely under a hypothesis of independence, and one generates the probability distribution of the metric under a hypothesis of independence by examining the population of contingency tables with the same marginal totals. Although the convention of using fixed marginal totals derived from the observed data to constrain the population of possible tables is commonplace in statistics, it has been at the center of the controversy over the use of null models in ecology.

Operationally, one implements a hypothesis of independence via the selection or placement of species at random with respect to the putative causal process of interest. For example, Beven et al. (1984) attempted to generate the expected geographical distributions of bird species in the Amazon basin under the hypothesis that the distributions of bird species were not influenced by specific Pleistocene forest refugia as had been proposed (Haffer, 1969). To do so, Beven et al. placed the observed number of species, with each species having the observed area of its geographical range, at random on a map of the Amazon basin subject to the constraint that all ranges occur in the basin. In this null model, the fixed marginal constraints were the number of species and the areas of their geographic ranges. The shapes and locations of each species' geographic range were allowed to vary. Beven et al. contended that this random placement algorithm permitted them to compare the actual geographical distribution of bird species in the Amazon to that expected if those geographical distributions developed independent of the hypothesized forest refugia. Hence, a random placement or selection algorithm is used to synthesize data expected under a hypothesis of independence.

I emphasize that in null models, randomization algorithms are merely vehicles to generate the expected properties of numerical indices under a hypothesis of independence. The hypothesis tested in a null model is one of independence, not that the data at hand or the nature in general are random, as has been interpreted by many of the critics of the use of null models (Gilpin and Diamond, 1984; Harvey and Ralls, 1985; Roughgarden, 1983). That null models test a hypothesis of independence, "...not a hypothesis that the world has no structure" (italics added) (Roughgarden, 1983), is crucial to understanding null models, and is a point that Gotelli and Graves did not make as clearly and emphatically as I believe necessary. Hence, the reason I belabor this point here.

Just as for nonnull or process models, null models are fraught with assumption. In null models, the assumptions are embedded in the selection of the marginal constraints used in defining the population of synthetic data sets over which the distribution of any ad hoc metric will be evaluated. Much of the early debate about the utility and appropriateness of null models revolved around these marginal constraints. Gotelli and Graves trace the course of these debates by presenting an overview in Chapter 1 and through all subsequent chapters when discussing the details for specific null models. Gotelli and Graves take all criticisms of the assumptions used in specific null models seriously and present a fair, if not overly patient assessment of them.

Gotelli and Graves chronical the diversity of questions to which null models have been applied, and in so doing provide testimony to their widespread use, if not grudging acceptance by the community of ecologists. Their treatment is technical but quite understandable to a statistically literate reader, since in most instances the probability distributions of metrics are obtained by simulation rather than by recourse to mathematical statistics.

It is certainly my hope that there will come a day when it is second nature for ecologists to study the distributional properties of any ad hoc metrics they invent. I feel sure that a careful reading of *Null Models in Ecology* by students and practitioners will hasten that day considerably. Furthermore, when combined with the null model software package *EcoSim*, which is currently under development by Gotelli and Entsminger (1997) with some modules already available free to users (http:// www.uvm.edu/~biology/Faculty/EcoSim/), *Null Models in Ecology* will become a widely used reference.

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The Theory and Applications of Reaction-Diffusion Equations: Patterns and Waves, by Peter Grindrod, Clarendon Press, Oxford, 1996. 55.00 (cloth), x + 275 pp.

I have not written a book report since the eighth or ninth grade, so I must admit that I have faced the task of reviewing Peter Grindrod's *The Theory* and Applications of Reaction-Diffusion Equations: Patterns and Waves with more than a little bit of trepidation. However, the editors of the Bulletin, like good teachers, have provided reviewers with clear instructions regarding the form of review that is desired, and I shall endeavor to accommodate.

Professor Grindrod comes from the fine and venerable British tradition of applied mathematics and his book is a definite reflection of this fact, both in content and in style. His goal is to provide a thorough introduction to the types of pattern formation and wave propagation phenomena that may be discerned via reaction-diffusion models. The results range from the now classical (pattern formation from spatially homogeneous equilibria due to diffusion driven instability, first established by Turing in the early 1950s) to subjects of current research interest (results on nonplanar wave propogation from recent articles by the author and his collaborators). Grindrod aims to reach an audience that includes mathematicians, mathematical biologists, and chemists, and his principal mathematical tool is that of asymptotic expansions. As a consequence, Patterns and Waves is probably as accessible as any serious book on reaction-diffusion systems is likely to be. Indeed, the book for the most part can be read with the equivalent of senior undergraduate courses in ordinary and partial differential equations. The author also courts the nonmathematician in at least three other ways. First, he provides a number of well-documented models from other disciplines (e.g., morphogenesis, population biology) as motivation. Second, his approach is to use representative but particular examples of reaction-diffusion models to exhibit the general phenomena in question (e.g., excitable system, planar wave), thus providing paradigms that the nonmathematician may follow. Third, he demonstrates a certain commonality in how patterns and waves arise, emerging from spatially homogeneous equilibria or from a simpler system which results when some system parameter tends to zero. This last exploits the fact that the underlying physical systems frequently work on fast and slow time scales.

Some comparisons may be useful in identifying more closely the "niche" of *Patterns and Waves*. First, although Grindrod includes some work at the level of current research interest, as previously noted, his book is intended primarily as an introduction to pattern formation and wave propogation in reaction-diffusion equations, rather than as a theoretical or applied break-

through on the order of, say, Dan Henry's Geometric Theory of Semilinear Parabolic Equations or Paul Fife's Mathematical Aspects of Reacting and Diffusing Systems. Patterns and Waves is also by design far more limited in scope, both in terms of topics covered and range of mathematical tools employed, than is Joel Smoller's Shock Waves and Reaction-Diffusion Equations. It is also less elegant mathematically than Smoller's book. Moreover, while there is substantial overlap in mathematical approach and style with portions of J. D. Murray's Mathematical Biology, the focus of Patterns and Waves is not on the biology, per se, and so the book attempts few if any new biological insights. However, what Patterns and Waves does offer in one place is a very detailed examination of the phenomena of pattern formation and wave propogation via reaction-diffusion equations ranging, as noted, from classical results to current research topics.

The preceding comparisons are intended as a guide to the nature of the book. The question remains as to its value. I think that the answer is that the book (which is now in its second edition) is a worthwhile resource for the interested mathematician and nonmathematician alike. As previously noted, *Patterns and Waves* is quite accesible mathematically and possesses a coherent focus. It is also relaxed in its style and very well annotated. Grindrod is very knowledgeable about the literature, mathematical and otherwise, and he is generous in sharing his knowledge. He also provides a useful primer to the subject of reaction-diffusion equations in his first chapter. Consequently, the book provides a good jumping off point for a mathematician interested in starting research in the area or for a quantitative bioligist in need of well-wrought examples of how to look for pattern formation or wave propogation in reaction-diffusion models.

Patterns and Waves has six chapters. Following the introductory chapter, there is an initial chapter on pattern formation, including Turing bifurcation and Hopf bifurcation. The topic turns to wave propagation in Chapter 3 (planar waves) and Chapter 4 (nonplanar waves). Chapter 5 returns to pattern formation, this time with patterns arising in response to nonlinear dispersal mechanisms. This book concludes with a chapter (new to this edition) on flux driven waves in geochemistry.

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