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Book Reviews

J. Hofbauer and K. Sigmund: *The Theory of Evolution and Dynamical Systems*, Cambridge University Press, 1988 viii + 341pp., £35.00 (hardback), £12.95 (paperback).

N. MacDonald: *Biological Delay Systems: Linear Stability Theory*, Cambridge University Press, 1989, xi + 235pp., £30.00 (hardback).

J. Mazumdar: *An Introduction to Mathematical Physiology and Biology*, Cambridge University Press, 1989, xi + 208pp., £27.50 (hardback), £9.95 (paperback).

Here are three books from the same publisher, all dealing with changes over time of biological quantities. The application of mathematics to biology and, what is equally important, biologically motivated mathematical investigations (think, for example, of Thom's catastrophe theory instigated by the problems of morphogenesis), have come a long way since Fibonacci counted his rabbits. Both the range and depth of the mathematics that turns out to be useful, as well as the range and depth of biological problems that these days are thought about in a mathematical way, have grown tremendously in the last twenty or thirty years. Biomathematics, whatever that word signifies, has come to stay. The field has become so large that for many years now it is impossible to even hint at a complete overview. Fibonacci could not write a textbook of mathematical biology (because what was there to tell?), nowadays one cannot write even an introduction to mathematical biology without scratching only the top of the iceberg. Apart from pure research monographs, there seems to be a call for only two kinds of introductory textbooks in biomathematics: the kind that lures people to 'the field' and stimulates them to roll up their sleeves and start digging, and the kind intended for people already 'in the field' who are looking for mathematical methods to solve problems they have encountered in the course of their research. A perfect example of the first is Hofbauer and Sigmund, an example of the second is provided by MacDonald. Mazumdar strengthens this criterion by exclusion. Although, in itself, the above can already be called a review, let me digress on this nutshell-characterization.

MacDonald's book deals with delays from a methodological problem solving point of view. Delays are an essential feature of many biological processes and MacDonald devotes twenty pages to a diverse range of examples. Two types of delay are considered: discrete delay (where the change at time t depends on the state at some earlier time $t - T$), and distributed delay (where the present change depends on a weighted integral over all past times). The book deals with the analysis of the effect of these delays on the local stability of steady states, which means that it is devoted largely to the location of roots of transcendental equations in one complex variable.

For a system with one distributed delay, the characteristic equation is given by, say, $Q(z) = H(z) + K(z)F(z)$ for some polynomials H and K , where $F(z)$ is the Laplace transform of the delay kernel (in the discrete case, the kernel is a Dirac δ -'function'). Direct methods for locating roots are treated, as are methods that transform $Q(z)$ into a polynomial which can subsequently be treated using the Routh—Hurwitz criteria. There are chapters on systems with two delays and on stability independently of the delays. Nearly all of the ten chapters end with a series of exercises with a strong view towards applications of the theory and detailed answers are provided. Mathematical prerequisites that go beyond standard calculus and some ordinary differential equations are treated in the appendices which makes the book reasonably self-contained. Much attention is paid to the geometry of stability by studying intersections of the *ratio curve* $-H(is)/K(is)$, ($s \in [0, \infty)$), with the *delay curve* (in the discrete one delay case, this is the unit circle that are associated with $Q(z)$). Most of the material appears here for the first time in book form and a large part of it is based on the author's own contributions to the subject. The book will certainly be useful to researchers from applied mathematics disciplines.

The book by Mazumdar is not, as the title suggests, an introduction to mathematical biology, nor is it, as the preface suggests, suitable to acquaint mathematically sophisticated students who have not previously encountered applications of mathematics to biology with models in this field. Eight out of ten chapters are devoted to dimension theory, diffusion, pharmacokinetics, fluid dynamics, bloodflow, mechanics of heart valves, heart valve vibrations, and medical devices (?). This suggests that 'Introduction to Medical Physics', would have been a better title. The two remaining chapters seem only to be included to ensure the intended broad scope of the book. One chapter, on biogeography, is no more than a collection of examples from the literature and the reader does not get the impression that this subject ever rises above curve-fitting (which it certainly does). The other chapter, on population biology, uses 20 of the 28 pages for stability analysis of two coupled autonomous differential equations which the intended audience should already be familiar with. Little is said about more complex interactions than a goat and a sheep eating from the same meadow (I'm not making these things up), let alone chaotic behaviour or bifurcations. The completely shallow nature of these chapters is in stark contrast to the rest of the book with such section headings as: 'Analysis for increased time-averaged pressure drop across an arterial stenotic segment'. All in all, there is too much emphasis on the author's own research subject: the heart. Although parts of the book are really nice, for example the chapter on dimension analysis (rarely found in a 'biomathematics' text), as a text for mathematics students looking for applications in biology, this book does not serve its purpose.

If a student wants to see sophisticated mathematics combined with sophisticated biology in a way that makes your mouth water and hungry for more, he or she should leave Mazumdar to gather dust, close this journal now, **run to the nearest bookstore and buy Hofbauer and Sigmund. Because the book by Hofbauer and Sigmund is a beauty. It is a thoroughly reworked translation of their 1984 German book:**

istic equation is given by, say, $F(z) = K$, where $F(z)$ is the Laplace transform of $Q(z)$ (kernel is a Dirac δ -function'). The methods that transform $Q(z)$ into $F(z)$ are the Routh—Hurwitz criteria. The stability is determined independently of the number of exercises with a strong view of exercises are provided. Mathematical methods and some ordinary differential equations are treated reasonably self-consistently by studying intersections of curves (in the discrete one delay case). Most of the material appears to be based on the author's own work and will be useful to researchers from

an introduction to mathematical models to acquaint mathematically minded applications of mathematics. Ten chapters are devoted to dynamics: bloodflow, mechanics, devices, etc. This suggests that a better title. The two remaining chapters cover the broad scope of the book. A collection of examples from the literature that this subject ever rises above the level, on population biology, uses coupled autonomous differential equations which will be familiar with. Little is said about chaotic behaviour or bifurcations. There is a stark contrast to the rest of the book. The increased time-averaged pressure here is too much emphasis on the later parts of the book are really nice, especially found in a 'biomathematics' applications in biology. This book

is combined with sophisticated and hungry for more, he or she should now, run to the nearest bookstore. The book by Hofbauer and Sigmund is a translation of their 1984 German book:

Evolutionstheorie und Dynamische Systeme, Mathematische Aspekte der Selection. The book can be read as an introduction to dynamical systems theory by way of the study of differential equations that arise from examples in evolutionary biology. At the same time, it brings the reader rapidly from first principles to recent advances in four branches of evolutionary biology: population genetics, population ecology, (prebiotic) evolution of macromolecules, and game theoretic modelling of animal behaviour.

The book is divided into seven parts, a set of four and a set of three separated by an interlude. The first four parts span 17 chapters, almost all of which include exercises and conclude with notes to the literature. The parts deal consecutively with the above-mentioned branches of evolution theory. Each part starts with a clear introduction to the biology involved. Along the way, many important notions connected to dynamical systems and the qualitative theory of ordinary differential equations (with the emphasis on stability theory) are introduced, all motivated by the biological background. The emphasis here is on the biology. The interlude, almost halfway through the book, connects parts I to IV by pointing out that one equation, called the replicator equation, is common to them all. In its general form, it is the system

$$\frac{dx_i}{dt} = x_i \left(f_i(x) - \sum_{i=1}^n x_i f_i(x) \right), \quad i = 1, \dots, n, \quad (1)$$

on the $(n - 1)$ -simplex

$$\Delta^{(n-1)} = \{x = (x_1, \dots, x_n) \in \mathbb{R}^n \mid \sum x_i = 1, x_i \geq 0, i = 1, \dots, n\}.$$

In the special case of a linear function $f_i(x) = \sum a_{ij}x_j$, it appears as the continuous time version of Fisher's selection equation from Part I, in population ecology as the Lotka–Volterra system, in molecular evolution it describes catalytic reactions in closed loops of n molecules where every molecule catalyses the replication of the next one in the cycle (these loops are called hypercycles), and in sociobiology it occurs as the game dynamical equation modelling the evolution of behavioural phenotypes. The mathematical properties of (1) are the subject of the last three parts of the book comprising 12 chapters. The emphasis now shifts to the mathematics. In these chapters, the exercises are sometimes very difficult and begin to look more like a collection of results.

In the most difficult and longest part of the book, Part V, notions from topology like the Brouwer degree and index are introduced to prove an index theorem for the fixed points of (1), and one of the central ideas from the book, permanence, is studied in detail. Permanence means that the boundary of $\Delta^{(n-1)}$ is a repeller for the dynamical system. Chapter 19 gives necessary and sufficient conditions for permanence in the case that the rates f_i in the replicator system (1) are linear. Particularly nice in Part V is also Chapter 21 where the stability of n -species communities is classified using algebraic properties of the matrices that describe the interactions between the species.

A second central idea in the book, the Shahshahani metric, is introduced in Part VI, Chapter 24. It turns out that for some restrictions on the rates f_i , the replicator system

is a gradient vector field if one does not take the Euclidean inner product on the tangent space of $\Delta^{(n-1)}$ but the Shahshahani inner product which attaches more weight to changes near the boundary. The last part of the book, Part VII, returns to the game dynamics of Part IV, but this time we have enough machinery to include sex. The book concludes with some interesting deliberations on the battle of the sexes (where at the last moment the important notion of a Poincaré map is introduced).

I should perhaps emphasize that the parts following the interlude are definitely mathematically more advanced. In most cases, the nonstandard concepts are nicely introduced (like degree and index) but sometimes (like manifolds and tangent spaces with Riemannian metrics) this could be too quickly to grasp for those readers unfamiliar with the concepts. But these are details, for the largest part the exposition is very clear, and all mathematics is motivated by the biology. This is a textbook example of the kind of textbooks 'we' need to have more of.

In these days where biomathematics books appear on the market with a frequency that pales the reproductive success of Fibonacci's rabbits, and both libraries and researchers are faced with a battle of the books and the struggle for budgets, I would hazard the following summary: Hofbauer and Sigmund is not to be missed, a gem (five stars); MacDonald is useful and belongs in the library (three stars); Mazumdar I give only one star, my heart just isn't in it.

*Centre for Mathematics and Computer Science,
Amsterdam,
The Netherlands.*

HANS HEESTERBEEK

R. J. Rivers: *Path Integral Methods in Quantum Field Theory*, Cambridge Monographs on Mathematical Physics, Cambridge University Press, London, New York, New Rochelle, Melbourne, Sydney, 1987, 340 pp., \$69.50.

The path integral method is widely used in modern theoretical physics, especially in quantum field theory (see, e.g., [1-3]) and almost all results here can be obtained by using such techniques. The path integral method can be considered as a method for the quantization of systems with nonflat phase spaces such as non-Abelian gauge theories and as the instrument for perturbative calculations such as the summation of leading terms.

The path integral is a very effective tool due to the fact that it allows us to naturally consider the symmetry of the system, the topology of the phase or configuration space, and so on, despite the lack of the mathematical foundation. Unfortunately, it is well based in rather simple situations only (see, e.g., [4, 5]), contrary to the so-called Wiener or Euclidean path integral which corresponds to imaginary time [6].

The book at hand is a textbook which successfully combines a great number of