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BOOK REVIEW

Haefner J.W.: MODELING BIOLOGICAL SYSTEMS: PRINCIPLES AND APPLICATIONS. Chapman & Hall, New York, 1996. 473 pp., hardcover. ISBN 0-412-04201-0. Price GBP 49.–.

It is no doubt that mathematical and simulation models are an important tool in description and investigation of biological systems. Contemporary approaches to modeling are based either on functional or individually based models. The functional approach is based on using some aggregative quantity (like population density), and it studies the evolution of this quantity in time and/or space. A typical example in population biology is the famous Lotka-Volterra system of predator-prey dynamics which is described by a system of ordinary differential equations governing population densities. Partial differential equations have been used, for example, in models of morphogenesis, or in models of the population growth with the age structure. Stochastic differential equations were used to model systems where external or internal uncertainties occur. Each of the above mentioned mathematical methods has been extensively studied during last decades and substantial progress has been made in these areas. The use of new methods based on individual oriented approach is rapidly increasing with the increasing computational capabilities. This approach deals directly with single individuals and, typically, it is connected with a heavy use of computers. Mathematical modeling in biological sciences thus covers nowadays a broad range of methods which have been applied to various biological problems. This textbook purports to survey the state-of-the-art of mathematical and simulation modeling of biological systems which could be used by students with one semester of calculus. It is divided into two parts – Principles and Applications. In Principles, methods are introduced and discussed, while in Applications they are applied to various biological problems.

Principles deals with model formulation and analysis. This part consists of the following chapters: models of systems, the modeling process, qualitative model formulation, quantitative model formulation, simulation paradigms, numerical techniques, parameter estimation, model validation, model analysis, stochastic models. Starting from Forrester diagrams, difference and differential equations are introduced together with some survey of differential and integral calculus. Some basics of qualitative analysis of such models are given together with numerical techniques for solving them. Methods for parameter estimation and model validation are discussed. Finally, stochastic models are reviewed.

Applications consists of the following chapters: photosynthesis and plant growth, hormonal control in mammals, populations and individuals, chemostats, spatial patterns and processes, scaling models, chaos in biology, cellular automata and recursive growth, evolutionary computation, and complex adaptive systems. The emphasis in this part is on the comparison of the results of models to quantitative data. Examples are taken mainly from ecology, but also from physiology and biochemistry.

The aim of the author was to write a text which would be accessible to a wide audience of people educated in biology (including students of biology) with minimum mathematical background. For this reason, the author keeps mathematical technicalities at a low level, and, where possible, he gives verbal or pictorial descriptions instead of mathematical formulas. The book will be useful for those readers who want to get a survey of the use of various types of models in biology.

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