Dmitry A. Kondrashov, Quantifying Life: A Symbiosis of Computation, Mathematics, and Biology, 2016, The University of Chicago Press, ISBN-13: 978-0-226-37176-4, 418 pp., $35.00 (paperback)

The history of numerical investigation into biological patterns and processes has traditionally set off down two roads, that of biostatistics and that of mathematical biology. These two approaches are obviously interconnected, but rely on somewhat different "philosophies." Biostatistics basically consists in the analysis of biological data using statistical methods. The aim of mathematical biology is to represent biological phenomena through mathematical models. Of course, in many cases, these two approaches largely overlap, so the distinction is sometimes a matter of taste and tradition or training. Many textbooks on biostatistics and mathematical biology exist that cover virtually all aspects of these disciplines with differing emphases on specialties. This volume, however, is an intriguing addition to the literature because of its hybrid nature: it combines some arguments typically addressed in textbooks of biostatistics with others that are usually found in textbooks of mathematical biology. This approach is useful because it allows students to understand links between issues that are generally discussed in separate courses and to develop a more open mind in the numerical analysis of biological data.

Chapter 1 presents the scope of the book and introduces readers to the R programming language, which is a great merit because of the increasing popularity of R for statistical analysis and simulations. Chapters 2 is dedicated to presenting some common functions and their graphical

representation. Chapters 3 to 9 address some arguments typical of a basic course in biostatistics, such as statistics used to express central values and variability, probability distributions and calculation (with a brief discussion of Bayesian probabilities), confidence intervals, tests for association between variables, correlation and regression analysis. All these arguments are presented in a quite unconventional and attractive way. Chapters 10 to 13 are dedicated to Markov models. I found this part of the book particularly intriguing, because this argument is usually not addressed in basic courses. Chapters 14-17 deal with difference equations, which is a typical argument of mathematical biology.

Although the book is written in a very clear and conversational style, I think it cannot replace more traditional and more comprehensive textbooks for introductory courses in data analysis. And, of course, it cannot replace more advanced texts devoted to specific arguments. However, I think that this book may be a very useful complement to both categories. For example, chapters about Bayesian inference and Markov chains may be used to introduce these arguments also in a basic course. The programming component may be useful to make students familiar with R and, more in general, with simulation approaches. Other parts, such as those dealing with linear difference equations, may be used not only as an introduction to more advanced courses, but also as a useful mathematical guide for students that encounter these models in other courses (e.g. in ecology, population biology, physiology, etc.). Also, the entire book may represent pleasant reading for people that already possess some background in biostatistics and mathematical biology and who want to deepen certain themes or to look at them from a different perspective. The book is not focused on conservation, but it encompasses techniques and approaches that are commonly used in conservation biology. Because it is easy to read and inexpensive this book deserves a space in the bookcase of people that want an introductory text to mathematical modelling in life sciences.

Simone Fattorini

Department of Life, Health and Environmental Sciences, University of L'Aquila, Via Vetoio,

Coppito, 67100, L'Aquila, Italy and CE3C – Centre for Ecology, Evolution and Environmental

Changes / Azorean Biodiversity Group, Universidade dos Açores, 9700-042, Angra do Heroísmo,

Açores, Portugal

E-mail address: simone.fattorini@uivaq.it