with their talents than make computer graphics. The final two chapters of the book deal with ecosystem function, demonstrating the utility of simply following the mass flow of conserved quantities through the complexities of an ecosystem; the novelty here is the definition of an intake rate (a pure rate with the dimensions of inverse time), which can be used to predict the reactions of components of an ecosystem to perturbations. The latter of these two chapters analyses human-modified ecosystems; as you might expect, it makes for somewhat depressing reading, but it does yield the most cogent argument I've seen for the necessity of limiting global human population.

No mathematics beyond algebra is required to follow the arguments in *Newton Rules Biology*, although many of the topics discussed would demand more advanced skills if a student were inspired to pursue them. This book is not a text of either mathematical biology or biomechanics, but, given the clear and engaging exposition, might be just the thing to convince reluctant biology undergraduates that they need to acquire mathematical skills or to give potential applied mathematicians some ideas on problems that would repay their attention.

MICHAEL LABARBERA
Department of Organismal Biology and Anatomy
The University of Chicago
1025 East 57th Street
Chicago, IL 60637, U.S.A.

---

*Trees and Proximity Representations*, Jean-Pierre Barthelemy and Alain Guenoche (translated from the French by Gregor Lawden). John Wiley and Sons, New York, 1991. xvi + 238 pp.

During the past decade impressive advances have been made with the credible estimation of evolutionary relationships among kinds of organisms. Much of this progress can be attributed to improved technical ability in measuring kinds of organisms at the molecular, chemical and genetic level. The data produced in this way are usually one of two basic types: (1) a collection of partitions of the various kinds of organisms or (2) a function assigning a number to each pair of kinds of organisms. In either case, to complete an inference about evolutionary relationships we need mathematical concepts and computational procedures to choose a tree that includes the kinds of organisms among its vertices. This book discusses such concepts and procedures applicable to the second type of

data. Data of this type arise from many sources, including DNA–DNA hybridization technology, reciprocal immunology technology, a variety of genetic distance techniques, as well as a variety of ways to convert type one data into type two data. Thus, the subject of this book is very relevant to understanding and practicing the estimation of evolutionary relationships.

The book approaches the subject from several points of view in parallel, making it relevant and accessible to a wide variety of readers. It defines concepts and proves propositions in a rigorous mathematical style. It shows figures to illustrate concepts. It discusses concepts and describes algorithms in natural language. It lists computer source code that implements algorithms and it presents "worked" examples with real data. This parallel, multiple approach to explanation and illustration is very effective.

The book begins by discussing the basic idea of a graph theoretic tree. Concepts of random trees are defined. Algorithms to drive a computer to draw trees in various styles are explicitly given and evaluated. The book continues with concepts of tree determining distances and presents techniques for finding tree distances, and the trees that they determine, that are close to data derived distances. As always, these algorithms are also described with computer source code and applied to real data. Next, ultrametric and centroid distances are described, with proofs, algorithms and examples presented in the same style. The special problems associated with constructing, representing and describing tree topologies are addressed. Finally, an overview of the various algorithms and methods earlier presented helps put ideas into a larger context and points to areas where future progress would be welcome.

Of special value to scholars in this and related fields are the extensive bibliographic citations and the explicit discussion, in several pages at the end of each chapter, of the history of the development of the ideas and results just presented. This unusually rich scholarship adds yet another parallel track to the variety of explanatory approaches, further broadening the already wide appeal of this work.

New results in this field are being published in a variety of places, in response to a variety of application motives. Although this book may not include every applicable algorithm, it is certainly a standard of excellence for clarity, accessibility and scholarship. I can recommend it with enthusiasm to anyone seeking an entry level understanding of trees and proximity representations.

GEORGE F. ESTABROOK
Professor of Botany
University of Michigan
Ann Arbor, MI 48019-1057, U.S.A.
*E.mail: USERECQM@UM.CC.UMICH EDU*