(such as the origin of the gnathostome jaw) are brushed over quickly. Paleoecological and evolutionary issues receive little coverage, and mainly appear as interesting anecdotes in the boxes. Similarly, punctuated equilibrium, which generated two decades of research and debate, is not mentioned, and the role of competition in the long-term succession of higher taxa is dismissed with little discussion. R L Carroll's *Patterns and Processes of Vertebrate Evolution* (1997. Cambridge (UK): Cambridge University Press) offers a stimulating application of vertebrate paleontology to problems in evolutionary biology.

Definitions and statements of fact are sometimes confusing, and some interpretations are questionable. For example, functional morphology is defined as "the interpretation of function from **morphology**" (p 28), ignoring analysis of the relationship between form and function, which is the basis for such interpretation. Cladistics and molecular phylogeny are erroneously contrasted as alternative systematic methods (p 30). Apatite, the mineral in bone, is defined incorrectly as calcium phosphate. We are told that the lobefins, *Dipterus* and *Osteolepis*, ate phytoplankton (p 64), for which their size and trophic morphology seem unsuitable. The Eocene *Hyracotherium* is characterized as "blending into the background" (p 342), although that cannot be known! Such details deserved more care. Despite these flaws, however, this book is a viable option as a textbook for an introductory course on vertebrate paleontology, and a useful reference because of its rich illustration, broad taxonomic scope, and up-to-date references on vertebrate paleontology.

MICHAEL A BELL, *Ecology & Evolution, State University of New York, Stony Brook, New York* and JOHN P HUNTER, *Anatomy, New York College of Osteopathic Medicine, New York Institute of Technology, Old Westbury, New York*

## MOLECULAR BIOLOGY

THE ART OF MOLECULAR DYNAMICS SIMULATION. *By D C Rapaport. Cambridge and New York: Cambridge University Press.* $69.95 (hardcover); $39.95 (paper). xiv + 400 p; ill.; function and subject indexes. ISBN: 0-521-44561-2 (hc); 0-521-59942-3 (pb). [First published in 1995. Reprinted with corrections in 1997.] 1995.

This excellent concise book, by a physicist, discusses the basic principles of molecular dynamics (MD) simulation. As advertised on the book's backcover, it is intended mainly for physicists, chemists, polymer and materials scientists. It is therefore not surprising that it does not contain as many biomolecular applications of MD as are found in books written for biomolecular modelers, such as Andrew R Leach's recent excellent text, *Molecular Modelling: Principles and Applications* (1996. Harlow (UK): Longman). Nonetheless, I believe Rapaport's book would be useful, and refreshing reading for biomolecular modelers as well.

Owing to the complexities of the systems they try to model, students of biomolecular modeling sometimes lose sight of the basic assumptions of MD, and treat certain software packages as if they represent ultimate reality. In this book, although not the least diminishing the importance and power of MD—it is "an indispensable part of the theorist's toolbox" (p xi)—the author clearly states the basic assumptions (Chapter 1) and the intrinsic limitations (Chapter 15) of the MD approach, with a presentation that leaves no room for mystery. Starting with the simplest of MD systems—solid-disk fluid (Chapter 2)—various aspects of MD (such as types of ensembles, geometric constraints on molecules, and forms of interaction potentials) are treated in 12 subsequent chapters. Essential details such as boundary and initial conditions, accuracy, convergence and computational efficiency are addressed.

Although not groundbreaking, the author's articulation of the philosophical underpinnings of MD is refreshing. "In the simulational context, understanding is achieved once a plausible model is able to reproduce and predict experimental observation" (p 3). He calls MD a "constructive approach" that "tries to reproduce the behavior using model systems" (p xi). I presume he is contrasting MD with a "deductive" approach, in which attempts are made to mathematically deduce experimental consequences from fundamental equations such as those by Schrödinger. He underscores the tentative, incremental, "experimental" and nonfundamental nature of the MD method. Truly reflecting his physicist tradition, he advocates liberal applications of Occam's razor (p 2), and states that in MD modeling, "despite any temptation to do otherwise, features should be added gradually" (p 4).

A very useful feature of this book is the computer programs embedded in the text, with a consistent set of global variables used throughout the book. Indeed, the author intends his work to be "a recipe book" (p xi). This is extremely helpful for MD beginners. In addition to the usual subject index, there is a useful index for functions used in the programs. The book also has several appendixes on other computational details.

HUE SUN CHAN, *Biochemistry and Medical Genetics & Microbiology, University of Toronto, Toronto, Ontario, Canada*