by Bohr. It is the one found in most texts and is usually presented without criticism. Never fully explicated and in many respects left ambiguous by Bohr and his collaborators, the Copenhagen interpretation has encountered considerable conceptual difficulties upon closer examination. The potentiality view was proposed by Werner Heisenberg and is sometimes called quantum realism (to be clearly distinguished from the classical realism advocated by Albert Einstein). These three views violate different definitions of locality; each view requires nonlocality in a different sense. The author does not advocate one particular view but leaves the choice to the reader.

This very carefully written book clears the metaphysical fog where most needed. Redhead has managed to squeeze a great deal into less than 200 pages. But I would have liked a longer book. The author excluded the problem of the reduction of states—the collapse of the wavefunction—beyond a very clear mathematical statement of it; that is understandable given the difficulty of that yet unsolved problem. But I can see no good reason for the author to exclude his own very attractive proof of the peaceful coexistence of the apparently contradictory concepts of nonlocality and special relativity (which demands a finite propagation velocity of signals). But this is not a serious criticism. The book is attractive and remarkably free of misprints (I found only four), but it is expensive. In summary, I believe that Redhead's book belongs in the collection of everyone seriously interested in the foundations of quantum mechanics.

Fritz Rohrlich
Syracuse University

Dynamics of Proteins and Nucleic Acids

J. Andrew McCammon and Stephen C. Harvey
Cambridge U. P., New York, 1987. 234 pp.
$39.50 hc ISBN 0-521-30750-3; $19.95 pb ISBN 0-521-35654-0

Our picture of biological matter has undergone many revolutions since the last century, when even the discrete molecular nature of proteins was in doubt. By the 1970s, through the techniques of x-ray crystallography, an architecturally beautiful, but static, picture of proteins and nucleic acids had come into being and indeed made contributions to central problems of biology. What was lacking was a description of the four-dimensional structure of biomolecules as moving, fluctuating collections of atoms. A little over a decade ago such a new picture began to emerge. It is based on the application of the ideas of condensed matter and chemical physics to proteins and nucleic acids. *Dynamics of Proteins and Nucleic Acids* by Andrew McCammon and Stephen Harvey is an authoritative survey of this new paradigm, leading us from the structural foundations and theoretical underpinnings to the most modern work in this extremely active area of inquiry.

Like earlier revolutions in the understanding of biological molecules, the dynamical picture was made possible by new developments in technology. The key tool for investigating biomolecular dynamics is computer simulation based on the molecular dynamics approach. Despite earlier speculations and inferences from experiment by insightful prophets, the revolution was taken to the masses only when McCammon, along with Martin Karplus and other collaborators at Harvard, carried out large-scale simulations of the dynamics of a protein in 1978. What distinguished that study from other essays in biomolecular physics was its use of the sophisticated language and viewpoint that had been developed in the statistical mechanics community for describing the fluctuations of many-body systems. The same thoughtful style characterizes this book. [See also the article by Karplus in PHYSICS TODAY, October 1987, page 68.]

The complexity of biomolecules is daunting to many a physicist. A nice feature of this book is that it leads the reader patiently from the fundamentals onward. It provides a simple and rapid introduction to basic structures of biological molecules. There is also a good orientation to the kinds of biochemical processes that biomolecules take part in. Similarly, the book gives a lucid introduction to the various techniques of computer simulation and statistical mechanics that are used in the field. Excessive formalism is avoided, but enough information is given to make the subject understandable.

A major part of the book is a tour through the enormous quantity of information that has resulted from theoretical studies on biomolecules. The authors have done a good job of organizing this tour and of guiding the reader to the literature for still more detail. The main problem here is that because the picture is new it is still hard to discern a unifying theme for understanding biomolecular dynamics.

McCammon and Harvey do a good job of explaining the interplay between experiment and theory in biomolecular dynamics. This is a difficult task because of the many experimental techniques in use—they include photochemical studies, nmr and other spectroscopic techniques.

Where is the dynamical picture of biomolecules leading? McCammon and Harvey give us some of their views, but—properly—they hold speculation to a minimum. Certainly no great biological puzzle has yet succumbed to analysis with the new paradigm. Insights into the extreme facility and specificity of enzymatic catalysis may someday be expected from this picture. The solution of the great structural problems of how the genetic information of DNA encodes the three-dimensional structures of proteins may be achieved with computer simulation techniques like those discussed in the book. We are far from these goals. Anyone who wishes to take part in the adventure of achieving them should read this book.

PETER G. WOLYNES
University of Illinois, Urbana–Champaign

Quantum Theory of Finite Systems

Jean-Paul Blaizot and Georges Ripka
MIT P., Cambridge, Mass., 1985. 657 pp. $47.50 hc ISBN 0-262-02214-1

Quantum Many-Particle Systems

John W. Negele and Henri Orland
Addison–Wesley, Redwood City, Calif., 1987. 459 pp. $46.25 hc ISBN 0-201-12593-5

Both of these excellent books are well suited for a graduate course in many-body theory; both are characterized by mathematical elegance. *Quantum Theory of Finite Systems* is "admittedly influenced by the prevailing style at the Service de Physique Théorique in Saclay." That style is a legacy of Augustin Louis Cauchy, who was a professor at the Ecole Polytechnique, from which most of the Saclay physicists come (though not the book's authors). Although *Quantum Many-Particle Systems* originated from lectures at MIT, it is, if anything, more elegantly mathematical than the first book.

Both books have excellent discussions on coherent states. John Negele and Henri Orland use Feynman path-