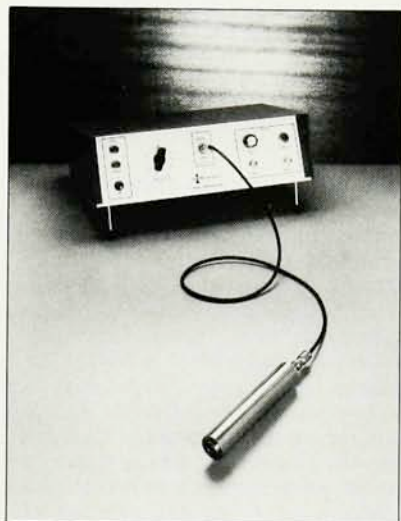


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able Cells (Clarendon Press, Oxford, 1975) by Julian Jack, Denis Noble and Richard Tsien. Along with these two books *Introduction to Theoretical Neurobiology* should be on the bookshelf (or beside the bed) of every student and researcher interested in neuronal modeling.

Elements of Differentiable Dynamics and Bifurcation Theory

David Ruelle

Academic, San Diego, Calif.,
1989. 187 pp. \$27.50 hc ISBN
0-12-601710-7

David Ruelle's book is a gem. For the last few weeks my desk has been covered with books on chaos, bifurcation, dynamical systems—and a request from PHYSICS TODAY to review several of them. Ruelle's book is so far superior to the others that any of them, reviewed alongside, would by contrast appear unsatisfactory.

Several colleagues perusing these books put down Ruelle's book after a cursory look, saying "Too sophisticated for me." Yes, one may need to read it slowly; yes, one may find in another book an example that explains an abstract statement. But as one savors each paragraph of Ruelle's book, one acquires the tools for studying differentiable dynamical systems, which then enables one to extract the highlights from the other books. As the author says, "The serious reader... should... be better equipped to enter the treacherous jungle of the literature on chaos."

This monograph is all that it intends to be: "An introduction to differentiable dynamics with emphasis on bifurcation theory and hyperbolicity, as needed for the understanding of complicated time evolutions occurring in nature (turbulence and 'chaos')." This is one of the rare books that does what its preface promises.

▷ *Coverage.* The first part of the book contains definitions of manifolds and differentiable dynamical systems; fixed points, periodic orbits and their invariant manifolds; attractors, bifurcations and generic properties. The second part is centered on bifurcations: elementary bifurcations for a fixed point or for a periodic orbit of a map, and related bifurcations for semiflows. It includes a study of hyperbolic invariant sets with applications to homoclinic intersections. Appendices and references constitute the third part.

▷ *Readership.* The author says the book is intended for "mathematicians

or mathematically inclined students of the natural sciences." I recommend it also to any theoretical physicist interested in dynamical systems. If one is not familiar with the mathematical language in Ruelle's book, one can refer to a more elementary book. His presentation, which may have seemed too abstract at first, will then reveal its perfection—and will clarify the confusion of discussions in other references that may have seemed more attractive at first sight.

▷ *Style.* Ruelle does not take one for an easy ride or a passive admiration of the scenery. He guides one on a mountain climb. And when the going gets rough, when one wonders at the need for so much intellectual discipline, or when the material seems dry, he offers "Notes" that relieve the thirst of the tired reader ("Note that the spirit of the above proof is the following..."). In his words, "In order to get to the heart of the matter quickly I emphasize ideas rather than proofs."

▷ *Price.* The price of \$27.50 for 187 pages is high. I am unhappy with publishers who price their books high when they expect a small market. This strategy is a self-fulfilling prophecy. Betting on a large market for Ruelle's book would be a negligible gamble. However, even at the present price, if one rates this book not in dollars per page but in dollars per unit of substance, Ruelle's book is a bargain.

CÉCILE DEWITT-MORETTE
University of Texas at Austin

Proteins: A Theoretical Perspective of Dynamics, Structure and Thermodynamics

C. L. Brooks III, M. Karplus
and B. Montgomery Pettitt

Wiley, New York, 1988. 259 pp.
\$55.00 hc ISBN 0-471-62801-8

Many of us went into physics because it advertises itself as a discipline that unifies and codifies a large body of seemingly incoherent data into a highly predictive, satisfying and consistent set of rules. What then are we to make of a field such as biophysics with its enormous and low-resolution set of seemingly incoherent data? Many physicists, both theoretical and experimental, are quite proud of their total ignorance of biological systems; after all, how can anything that is good to eat be worthy of serious study? I suspect that most experimentalists understand their personal computers better than the fundamentals of the

beast that conceived and built it.

There is of course a reason for this attitude among the anointed. Dirac pointed out in his famous statement (quoted in the foreword of *Proteins*) that all the fundamentals are in quantum mechanics so everything else is "just" chemistry, understood in principle but intractable in practice. Thus only the most overly simplified models can be applied to biological systems. Predictive power goes out the window.

There is, however, hope that massive supercomputers might somehow be able to keep track of the myriad interactions and trace the flow of energy and conformation in biomolecules. This book is a detailed account of such attempts to follow the dynamics of proteins via computer simulations. Martin Karplus, the senior author, has been one of the pioneers in protein dynamics simulations, and his mastery of the field shows in the book.

Although the subtitle of this book is "A Theoretical Perspective of Dynamics, Structure and Thermodynamics," the main emphasis is on computer dynamics. There is no mention of more exotic concepts such as Davydov solitons or similar theoretical ideas beloved of physicists. For those interested in getting an overview of what we understand about the dynamics of proteins this is not a good book on which to start. It is written in a dry, dense style with exhaustive references to the literature. If you are a practicing molecular dynamicist then this is a great book to have handy, but the casual reader will find it extremely easy to put down. A better introduction to the major concepts involved in molecular dynamics is *Dynamics of Proteins and Nucleic Acids* by Andrew McCammon and Stephen Harvey (Cambridge University Press, New York, 1987), which takes a more pedagogical view of the field and contains the kind of simple figures that help in understanding the ideas.

Proteins, on the other hand, is all business, and makes a good companion to McCammon and Harvey's book if your interest deepens. The text by McCammon and Harvey is more likely to give you a feeling for why a calculation is done, while *Proteins* tells you how it was done and who did it. You learn from *Proteins* that a great deal of dynamics can be done on isolated proteins in a vacuum over a picosecond time scale, but the more daunting problem of handling the protein-solvent system over the nanosecond-to-microsecond range still lies beyond the reach of present algorithms and raw computational

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power. The authors have been deeply interested in this important work in their own research, and do an excellent job discussing the difficulties. Further, they also discuss important issues of configurational entropy calculations and structural relaxation.

The most interesting—and disturbing—section of the book occurs in the "Concluding Discussion." The authors clearly address in this well-written section the basic problem that physicists have with biomolecules: We like to make unifying models. For example, Hans Frauenfelder has stressed the utility of the hierarchical description of protein dynamics, with a Caley-tree-like branching of progressively smaller amplitudes and motions. Like John Muir's Sierra wilderness, pull on one part of it and you find that it is connected to everything else.

The authors of *Proteins* are doubtful about the utility of this idea. For example, they cite aromatic ring flips in proteins that occur very slowly in spite of the small physical size of the displacement. In their view the ring-flip motion is disconnected from other parts of the protein, and thus each motion must be treated individually. Frauenfelder would like to say that it is not the Euclidean distance but the configurational distances—the generation number—between conformations that determines the rates of seemingly small events. Can the computer simulations reach out long enough in time to test that hypothesis? I'll quote the authors' response based upon their experience with computer dynamics: "An alternative possibility, far less pleasing, is that the specifics of each motion determine its character and no such general scaling relation holds. . . . Since each motion then becomes a problem in itself . . . a conceptual approach to protein dynamics would have to include the complexity that is embodied in chemistry rather than the simplicity that is often assumed in physics." Say it ain't so, Joe.

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Princeton University

The Michelson Era in American Science: 1870-1930

Stanley Goldberg and
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AIP Conference Proceedings
179, AIP, New York, 1988.

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