parameters' importance in interpretation of macromolecular dynamical calculations. The chapter goes on to review a comprehensive range of techniques in use for calculating these quantities, and also includes what may be reliably inferred from these data and what may not. Poring through the text, another chapter by Kutteh and Straatsma introduced this reviewer to the usage of holonomic constraints in molecular dynamic calculations. From a clear, pleasant-to-read introduction on the benefits of applying holonomic constraints to calculations on biomolecular systems, to a through overview of exactly how to implement and utilize them, this chapter inspired me to try to apply this method to some of my own calculations. Subsequent chapters were equally useful and thorough, and overall pleasant to read.

In conclusion, I believe this series has a place in every computational chemists library. This volume is no exception. Future volumes, I trust, will also continue to have the same high level of clarity and quality that computational chemists have come to expect from this series.

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Fractals in Molecular Biophysics. By T. Gregory Dewey (University of Denver). Oxford University Press: Oxford, New York. 1997. xii + 276 pp. $65.00. ISBN 0-19-508447-0.

While it does not provide exercises or problems at the ends of chapters, *Fractals in Molecular Biophysics* is written in a nicely unified and pedagogical manner, and could certainly be used for an advanced course in this subject. It is very well-referenced, both to the literature of biophysical chemistry and to the relevant mathematical sources. The author must use a word processor that objects to long sentences, because the prose seems to this reader to be annoyingly choppy, but it is nevertheless clear. As a conventional physical chemist (not the "bio" kind), I was eager to read about what fractal analytical methods can do in the biophysical area. This book did not disappoint me. T. Gregory Dewey makes the case, through numerous practical examples, that fractal measures and methods should be considered part of the standard repertoire of the biophysical chemist. In fact, there may not be a scientific area in which fractals will have more applications.

In the first chapter (What Are Fractals?), the author briefly reviews the mathematics of fractals. The exposition is quite condensed; a complete novice would surely want to begin by reading elsewhere. This chapter also introduces the nomenclature that is used later, reminds the reader of the phenomena to which fractals have been applied and, most importantly, emphasizes the connection between fractals and renormalization group theory. The renormalization group is used throughout the book, providing a very useful recurring theme.

Chapters Two through Four show how fractal measures provide an alternative to the traditional primary, secondary, and tertiary structure classifications of proteins, and their connection to the statistical mechanics of biomacromolecules in general. The fractal dimension seems to be a natural measure of protein structure, and one more closely related to physical measurements than are the traditional ones. In Chapter Five (Fractal Diffusion and Chemical Kinetics) the focus shifts from static to dynamical properties of biopolymers, and it remains largely in that realm through the end of the book. The fractal character of protein dynamics is described in Chapter 6, and Chapter 7 discusses fractons and vibrational relaxation in proteins. Percolation is the subject of Chapter 9 and, in Chapter Ten, Dewey explains the connection between fractals and chaos. This subject is dealt with in a brief fashion, similar to the way Chapter One is written, but the most important phenomena are mentioned and plentiful references make the treatment useful to readers looking for more depth. This volume is likely to be of interest to many readers, and should be on the bookshelf of every biophysical chemist.

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