

Preface

The essential question that fractal dimensions attempt to answer is about the *scales* in Nature. This is not exactly a new question. From Euclid to Poincare to Mandelbrot, many philosophers, mathematicians, physicists had thought about transformation, dilation and contraction of scales. This small book will attempt to investigate the diverse facets of the question: *Amongst the various protein surface properties, which ones are scale-invariant?* A detailed exploration of this problem will perhaps help us to investigate utilitarian questions like: *How can we apply the acquired knowledge about the nature of protein surface roughness to drug-discovery and other practical branches of science?*

Discussions on scale-invariance lead us to fractals. Unfortunately, elaborations on what are fractals and what are their historical roots—could not be made a part of this book. Interested readers may find these topics in my other book ‘Fractal Symmetry of Protein Interior’, which is being published by the same publisher. Any formal investigation of protein shape and protein surface necessarily leads us to the paradigm of (complex) mathematics. Studying scale-invariance of protein exterior properties, especially, demands a good command of mathematical constructs. But it was impossible to review these constructs within the tiny volume of this book. Thus, instead of being mathematically pedagogic, a qualitative approach has been adopted throughout the course of this book with clear onus on discussions related to biological aspects of the problem.

The book attempts to collate and classify the various fractal dimension-based approaches that have been employed over the years to study protein exterior biophysical properties, into distinct clusters. It then presents an account of cases where fractal dimension-based methodologies have successfully contributed to protein exterior research. In this context, a thorough documentation of accurate predictions made from the spectrum of fractal dimension-based studies has been provided. However, fractals are no panacea, and they cannot suggest magic solutions to all the problems of protein exterior biophysics. Consequently, the third aim of this book was to examine the intrinsic limitations of fractal dimension-based measures. Finally, with a balanced assessment of the entire framework, the book attempted to identify some of the outstanding questions, where application of fractal dimension-based investigations may prove to be helpful in deciphering deep and unexpected facets of protein exterior organization.

This book wouldn't have come into being without the direct or indirect support from the countably infinite number of well-wishers of mine. I thank them all. I take this opportunity to thank all those who asked me questions about fractals and proteins over the years and especially to those whom I could not answer for my lack of knowledge and/or conception. These questions stayed with me and forced me to spend more time in the library and in my work. In a way, it is through these interactions that I learned whatever little I've learned about fractals and proteins—Thank you all.

This preface will be incomplete if I do not mention the roles of the editors, Dr. Beatrice Menz and (later on) Dr. Jutta Lindenborn during the course of writing the book. They were always supportive, always encouraging. I thank Dr. Menz especially for entrusting me with the responsibility of writing this book.

There's nothing more helpful than to listen to constructive criticisms; thus, if you feel like criticizing and/or discussing and/or (in the unlikely case) appreciating any aspect of whatever that is written in the book, please drop me an email anirbanab@gmail.com. I'll be delighted to talk to you and learn from you.

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