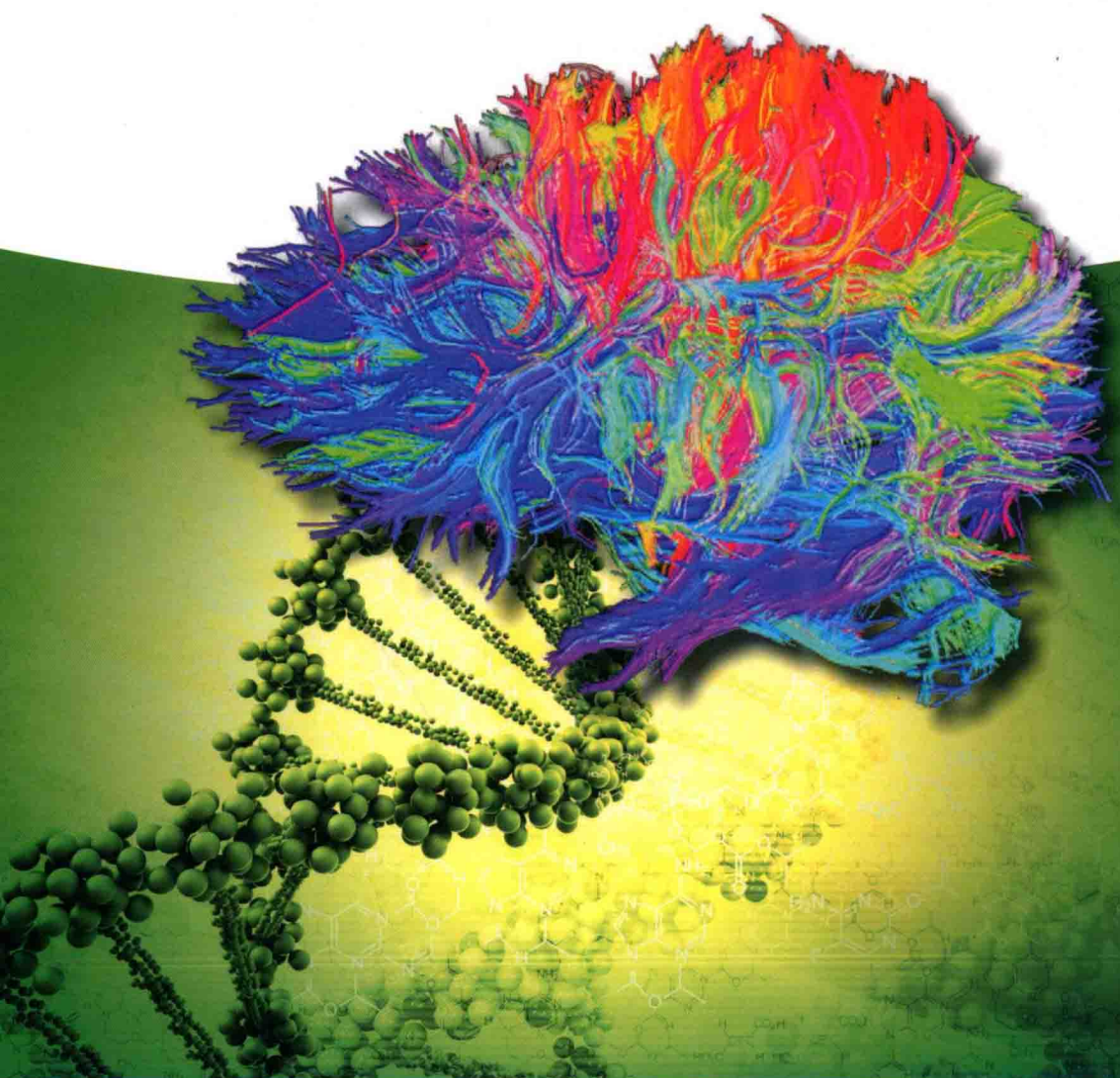


Edited by
Misha (Meyer) Z. Pesenson

Multiscale Analysis and Nonlinear Dynamics

From Genes to the Brain



Reviews of Nonlinear Dynamics and Complexity

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Multiscale Analysis and Nonlinear Dynamics

From Genes to the Brain



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Preface

“Those who study complex adaptive systems are beginning to find some general principles that underlie all such systems, and seeking out those principles requires discussions and collaboration among specialists in a great many fields.”

*M. Gell-Mann*¹⁾

Modern science and engineering deal with problems that involve wide ranges of spatial and temporal scales. Moreover, data-intensive sciences such as Systems Biology and Systems Neuroscience, besides dealing with complex physical, chemical, and biological phenomena, need to handle enormous amounts of high-dimensional data produced by modern high-throughput experimental technologies. All this creates a critical need for modeling sophisticated, natural/artificial systems and analyzing modern high-dimensional data across multiple scales ranging from molecules to macroscales. However, traditional mathematical approaches to modeling/analyzing complex phenomena/data are often limited because of the multiscale nature of the problems. At the same time, it is well known that biological systems solve computationally demanding problems with many scales and process multiscale information deftly. Indeed, in order to resolve a broad range of spatial/temporal scales present in input signals, perception systems perform sophisticated multiscale encoding, analysis, and decoding in real time. A second example is related to data dimension reduction (which is intimately connected with feature extraction, recognition and learning). In fact, the input signals to all mammalian perception systems, despite their coming from low-dimensional Euclidian space, are transformed internally into extremely high-dimensional representations. This counterintuitive drastic increase in complexity is followed by a concealed, effortless and perpetual nonlinear dimension reduction, that is, converting the complex representations back into low-dimensional signals to be, ultimately, executed by the motor system. Another example comes from Systems Biology where embryonic development is, in fact, an immense information processing task in which DNA sequence data generate and direct the system level spatial deployment of specific cellular functions [2]. These examples indicate that the theoretical understanding of biological computational mechanisms and their experimental implementation can

1) Cited in Ref. [1].

greatly enhance our ability to develop efficient artificial information processing systems. An important advance in the engineering of biological computing systems has recently been achieved and the first network of artificial neurons made from DNA was created, suggesting that DNA strand displacement cascades could endow biochemical systems with the capability of recognizing patterns [3]. Pattern recognition and multiresolution are quintessential for information processing, which, in turn, is closely connected with learning and adaptivity.

Complex biological systems capable of adaptive behavior and effective information processing are often governed by mechanisms operating simultaneously on multiple spatial and temporal scales. Thus, in order to analyze the machinery that underlies biological information processing and computations in general, this book focuses on modeling multiscale phenomena in Synthetic/Systems Biology and Systems Neuroscience, as well as on mathematical approaches to multiresolution analysis. Because of the inherently interdisciplinary nature of this task, the editor of this book invited experts (theoreticians and experimentalists) in bioengineering, chemistry, cardiology, neuroscience, computer science, and applied mathematics, to provide their perspectives ("seeking out those principles requires . . . collaboration among specialists in a great many fields."). The contributions to this book may broadly be categorized as belonging to mathematical methods, Systems Biology, and Systems Neuroscience. Multiscale analysis is the major integrating theme of this book, as indicated by its title. The subtitle does not call for bridging the scales all the way from genes to behavior, but rather stresses the unifying perspective provided by the concepts referred to in the title. The contributions emphasize the importance of taking into account the *interplay* between *multiscale structure* and *multiscale dynamics*. One of our goals is to attract the attention of scientists working in Systems Biology and Systems Neuroscience by demonstrating that some of the seemingly unrelated problems from these disciplines may be modeled using virtually identical powerful mathematical methods from the inclusive paradigms emphasized here. Each chapter provides a window into the current state of the art in the areas of research discussed. This book is thus intended for advanced researchers interested in recent developments in these areas. It is believed that the interdisciplinary perspective adopted here will be beneficial for all the above-mentioned disciplines. The roads between different sciences, "while often the quickest shortcut to another part of our own science, are not visible from the viewpoint of one science alone" [4].

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Pasadena, 2013

Misha Z. Pesenson

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