

Preface

Living cells and tissues are highly dynamic entities that carry out complex interconnected processes and functions that depend on both space and time. Dynamic analysis is required to connect cellular structure to function and to predict cellular behavior under different “environmental” conditions and stresses. Furthermore, many important cellular processes, such as chemotaxis, feed-back control loops, and clock reactions, are well-known to be non-linear dynamic events that further complicate analytical descriptions.

It is clear that a quantitative analysis of cellular behavior that connects structure to function requires a systematic analysis of the particular unit processes and their interactions in the living cell. This book was written in order to lay out the basic systems engineering approach to quantitatively describe the dynamic cell. An introduction to the essential biochemistry in living systems is given in Chapter 1, followed by a description of the particular engineering systems of the living cell in Chapter 2. These systems are

- Cellular communications and transport
- Biochemical production
- Motility, mechanical work, and structural support
- Reproduction or division
- Information systems, checkpointing, and reliability

The majority of cellular processes are carried out by so-called macromolecules, such as peptides and proteins, lipids, carbohydrates, and nucleotides and oligonucleotides. Although this may appear to complicate the description of the living cell, in some ways it simplifies things. In short, the overall dynamical

description of cellular processes involves large spatial and time scale separations between the behavior of the cellular solvent, i.e., water, dissolved ions, and small molecules, and that of the “workhorse” biological macromolecules. Chapters 3 and 4 develop the so-called multiple time scale methods that are used to exploit this disparity and simplify real-time macromolecular dynamics.

Finally, the last chapter of this book demonstrates the integration of system pathways to describe a cascade of cellular events that may lead to a particular phenotype. Although a full characterization of cellular processes along such rigorous lines is still a formidable goal, the last chapter explores some simplified examples of interconnected cellular system processes in order to illustrate the essential features of a rigorous approach in a revealing, analytical way.

In the future, large-scale computations will allow for the addition of more pathways and interconnectivity between systems in order to approach a more meaningful or useful total simulation of the dynamic living cell.

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