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Sangdun Choi. Introduction to systems biology. Totowa (NJ): Humana Press; 2007. 623 pages; ISBN: 1-58829-706-3; price: US $109.00

Field of medicine: Molecular medicine, bioinformatics, genetics.
Format: Hardcover book.
Audience: Medical students, students of biology or biochemistry, researchers in molecular biology.
Purpose: To present a broad overview of the field of systems biology and enable the generation of strategies for their application on the complex biological problems.

Content: The book is divided into four parts – Introduction, Experimental Techniques for Systems Biology, Theoretical and Modeling Techniques, and Methods and Software Platforms for Systems Biology, and ends with four appendices – Software, Databases, Web-sites for Systems Biology, and Glossary. Each part contains chapters written by a group of authors.

The first part consists of three chapters on scientific challenges in systems biology with an emphasis on metabolic networks. The reconstruction of metabolic networks allows an integration of different data types and provides a framework for the analysis of fluxomics data, metabolomics, and gene expression. Several analysis tools and predictive models are described and a special focus is given to transcriptome data analysis. Authors also sucessfully illustrate how systems biology approaches are being used in metabolic engineering to correlate the genotype with a phenotype.

The eight chapters of the second part discuss several tools that help in the analysis of gene groups from different high-throughput experiments and databases, eg, the software that uses Gene Ontology annotations and allows automated functional profiling of gene groups. Authors introduce the mouse cDNA encyclopedia project and transcriptome analysis, which opened a new research field of functional and proteome analysis.

Reconstructing how transcriptional networks function involves finding out which promoters are affected by which transcription factors, and the authors specifically focused on combining sequence analyses, microarray data analyses, and phylogenetic comparisons for the location of regulatory elements in genomes and classifying them. Some structural analysis methods and their application in the analysis of metabolic and transcriptional regulatory networks are also described in this part of the book. Authors showed how an expression profile comparison between species, with available tools, like global approaches and gene-centered approaches, helps to discover the functional annotation for unknown genes. Moreover, they described the two major methods for protein-protein interaction analysis, ie, mass spectrometry-based and yeast two-hybrid-based approach, which have so far succeeded in the generation of large data sets. It is explained how connections between genotype and phenotype can be obtained using transcriptomics, proteomics, fluxomics, and metabolomics and how their combining can compensate for the limitations of any single data type. At the end of this part, various approaches (feature-based analysis and pattern modeling) in investigating different image types and different cell types are introduced.

In the third part, divided into eight chapters, the authors explain the use of Linear-Gaussian state-space models, which attempt to "reverse engineer" regulatory networks from high-throughput data sources, such as microarray gene expression profiling. They present the simulation method and the supporting tools for capturing spatiotemporal dynamics of signaling networks. In this part, methods of dimension-restricted reaction kinetics modeling and the procedure of applying it for obtaining experimental results are introduced. The authors review the importance of ultrasensitivity in signal transduction and major mechanisms that generate ultrasensitivity, like zero-order kinetics and multisite phosphorylation. The spatiotemporal organization of mitogenic pathway is also analyzed here, as well as quantitative models that provide insight into the connection between external stimuli and the signaling outcome. Through oscillatory metabolism of human neutrophils, as a prototype biochemical subsystem, the ability of computational biology to explain and predict biochemical mechanisms is illustrated. The authors also review recent theoretical and experimental efforts in solving mathematical difficulties in understanding gene regulatory networks in system biology, giving lambda phage switch as a working example. The last chapter covers the data representation paradigms currently used to store and compute information about signaling pathways.

Through six chapters in the fourth part of the book, the authors discuss MathSBML, a tool-neutral, computer-readable format for representing models of biochemical reaction networks applicable to descriptions of cell signaling pathways, genomic regulatory networks, as well as metabolic networks, and others. The authors introduce CellDesigner, a process diagram editor, that helps understand the logic and dynamics of gene-regulatory and biochemical networks. They show how Difference-based regulation finding-minimum equivalent gene network method can be a powerful analytical tool for large-scale, as well as medium- or small-scale gene expression profiles. Authors present the Nonintegral Connectivity Method, a quantitative method, which systematically analyzes the dynamic phenotype of a set of network species and determines their local reaction connectivity, without the need to form differential equations. Authors introduce the challenges of storing, sharing, and querying proteomics data and outline the software requirements. They present two exemplars developed at the University of Manchester. The last chapter of the book discusses two important challenges – deriving appropriate conceptual frameworks for representing the data on biochemical networks and methods of analyzing various global and local properties of these networks.

Highlights: The book is well structured and easy to read. Each chapter begins with a brief overview and ends with key messages. It will provide an understanding of underlying biological meanings using key examples and typical approaches to experimental biology taken from both the "wet" and computational laboratories.

Limitations: Although all chapters include many schemes and diagrams and/or photographs, some of them are blurred or minuscule.

Related reading: A list of related readings is added at the end of each chapter, providing an insight into the sources of additional information. The readers may also enjoy: "An Introduction to Systems Biology: Design Principles of Biological Circuits" by Uri Alon (Chapman & Hall: 2006); "Life: An Introduction to Complex Systems Biology" by Kunihiko Kaneko, (Springer: 2006); or "Systems Biology: Properties of Reconstructed Networks" by Bernhard Palsson (Cambridge University Press: 2006).

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