



Analysis of Biological Networks

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E-Book	ISBN: 978-1-118-20991-2	September 2011	£90.99
Hardcover	ISBN: 978-0-470-04144-4	April 2008	£101.00
O-Book	ISBN: 978-0-470-25348-9	August 2007	Available on Wiley Online Library

DESCRIPTION

An introduction to biological networks and methods for their analysis

Analysis of Biological Networks is the first book of its kind to provide readers with a comprehensive introduction to the structural analysis of biological networks at the interface of biology and computer science. The book begins with a brief overview of biological networks and graph theory/graph algorithms and goes on to explore: global network properties, network centralities, network motifs, network clustering, Petri nets, signal transduction and gene regulation networks, protein interaction networks, metabolic networks, phylogenetic networks, ecological networks, and correlation networks.

Analysis of Biological Networks is a self-contained introduction to this important research topic, assumes no expert knowledge in computer science or biology, and is accessible to professionals and students alike. Each chapter concludes with a summary of main points and with exercises for readers to test their understanding of the material presented. Additionally, an FTP site with links to author-provided data for the book is available for deeper study.

This book is suitable as a resource for researchers in computer science, biology, bioinformatics, advanced biochemistry, and the life sciences, and also serves as an ideal reference text for graduate-level courses in bioinformatics and biological research.

ABOUT THE AUTHOR

Björn H. Junker is a biologist with a strong background in bioinformatics. His current research activities include the quantitative analysis and modeling of metabolic networks, as well as pathway databases and visual data mining. Mr. Junker has been at the Leibniz Institute of Plant Genetics and Crop Plant Research in Germany since 2003. He worked at Brookhaven National Laboratory in New York during 2006 and was appointed as project leader at the Leibniz Institute in 2007.

Falk Schreiber is a computer scientist who has worked in bioinformatics for more than ten years. His current research areas include modeling, analysis, and visualization of biological networks; graph algorithms; and data exploration and information visualization in the life sciences. Since 2003, he has been head of the Network Analysis Research Group at the Leibniz Institute of Plant Genetics and Crop Plant Research. He was appointed professor of bioinformatics at the Martin Luther University Halle-Wittenberg, Germany, in 2007.

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