

COMPUTATIONAL BIOLOGY

The *Computational Biology* series publishes the very latest, high-quality research devoted to specific issues in computer-assisted analysis of biological data. The main emphasis is on current scientific developments and innovative techniques in computational biology (bioinformatics), bringing to light methods from mathematics, statistics and computer science that directly address biological problems currently under investigation.

The series offers publications that present the state-of-the-art regarding the problems in question; show computational biology/bioinformatics methods at work; and finally discuss anticipated demands regarding developments in future methodology. Titles can range from focused monographs, to undergraduate and graduate textbooks, and professional text/reference works.

The major difficulty many microbiologists face is simply that of too much information. As a result of sequencing technologies becoming so economical, there is a very real and pressing need for high-throughput computational methods to compare hundreds and thousands of bacterial genomes.

This accessible text/reference provides a coherent set of tools and a methodological framework for comparing raw DNA sequences and fully annotated genome sequences, then using these to build up and test models about groups of interacting organisms within an environment or ecological niche. Easy-to-follow, this introductory textbook is built around teaching computational / bioinformatics methods for comparison of microbial genomes, and includes detailed examples of how to compare them at the level of DNA, RNA, and protein, in terms of structural and functional analysis.

Topics and Features:

- Contains five introductory chapters each representing a specific scientific field, to bring all readers up to the same basic level
- Familiarizes readers with genome sequences, RNA sequences (transcriptomics), proteomics and regulation of gene expression
- Describes basic methods to compare genomes and visualize the results for easy interpretation
- Discusses microbial communities, providing a framework for analysing and comparing individual genomes or raw DNA derived from complete ecosystems
- Introduces various atlases, building up to the Genome Atlas
- Offers numerous helpful examples throughout
- Focuses on the use and interpretation of publicly available Web tools
- Provides supplemental resources, such as Web links, at <http://comparativemicrobial.com>

COMPUTER SCIENCE

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> springer.com

Developed from a set of lectures for a course in Comparative Microbial Genomics taught since 2001, and combined with a one-week workshop, this wide-ranging foundational textbook is aimed at advanced undergraduate and graduate students in Bioinformatics and Microbiology. The authors are from diverse backgrounds complementing the interdisciplinary nature of the topic and consequently have developed a common scientific language. Readers will find this text an invaluable reference for computational and bioinformatics tools.

Ussery • Wassenaar • Borini



Computing for Comparative Microbial Genomics

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Computing for Comparative Microbial Genomics

Bioinformatics for Microbiologists

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 Springer