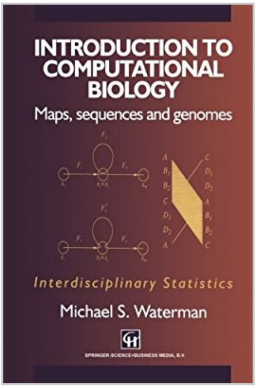

Introduction to Computational Biology: Maps, Sequences and Genomes (Chapman & Hall/CRC Interdisciplinary Statistics)

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Biology is in the midst of a era yielding many significant discoveries and promising many more. Unique to this era is the exponential growth in the size of information-packed databases. Inspired by a pressing need to analyze that data, Introduction to Computational Biology explores a new area of expertise that emerged from this fertile field- the combination of biological and information sciences.

This introduction describes the mathematical structure of biological data, especially from sequences and chromosomes. After a brief survey of molecular biology, it studies restriction maps of DNA, rough landmark maps of the underlying sequences, and clones and clone maps. It examines problems associated with reading DNA sequences and comparing sequences to finding common patterns. The author then considers that statistics of pattern counts in sequences, RNA secondary structure, and the inference of evolutionary history of related sequences.

Introduction to Computational Biology exposes the reader to the fascinating structure of biological data and explains how to treat related combinatorial and statistical problems. Written to describe mathematical formulation and development, this book helps set the stage for even more, truly interdisciplinary work in biology.

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Review
"I very much enjoyed the book, and was delighted to recommend itthe use of molecular biology to introduce and illustrate application of sophisticated mathematical theory was excellentas an illustration of the challenges and rewards of collaborative work, it is ideal." -Statistics: Monash University

About the Author
Richard C. Deonier is Professor Emeritus in the Molecular and Computational Biology Section of the Department of Biological Sciences at the University of Southern California. Originally trained as a physical biochemist, His major research has been in areas of molecular genetics, with particular interests in physical methods for gene mapping, bacterial transposable elements, and conjugative plasmids. During 30 years of active teaching, he has taught chemistry, biology, and computational biology at both the undergraduate and graduate levels.

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Michael S. Waterman is a University Professor, a USC Associates Chair in Natural Sciences, and Professor of Biological Sciences, Computer Science, and Mathematics at the University of Southern California. A member of the National Academy of Sciences and the American Academy of Arts and Sciences, Professor Waterman is Founding Editor and Co-Editor in Chief of the Journal of Computational Biology.His research has focused on computational analysis of molecular sequence data. His best-known work is the co-development of the local alignment Smith-Waterman algorithm, which has become the foundational tool for database search methods. His interests have also encompassed physical mapping, as exemplified by the Lander-Waterman formulas, and genome sequence assembly using an Eulerian path method.

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