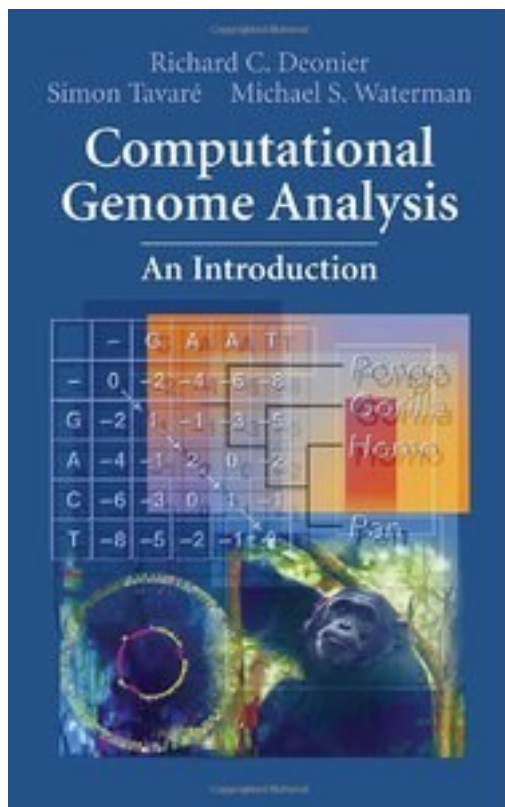


Computational genome analysis: an introduction



[Computational genome analysis: an introduction 下载链接1](#)

著者:Richard C. Deonier

出版者:Springer

出版时间:2005

装帧:HRD

isbn:9780387987859

Computational Genome Analysis : An Introduction presents the foundations of key problems in computational molecular biology and bioinformatics. It focuses on computational and statistical principles applied to genomes, and introduces the mathematics and statistics that are crucial for understanding these applications. The book is appropriate for a one-semester course for advanced undergraduate or beginning graduate students, and it can also introduce computational biology to computer scientists, mathematicians, or biologists who are extending their interests

into this exciting field. This book features: Topics organized around biological problems, such as sequence alignment and assembly, DNA signals, analysis of gene expression, and human genetic variation Presentation of fundamentals of probability, statistics, and algorithms Implementation of computational methods with numerous examples based upon the R statistics package Extensive descriptions and explanations to complement the analytical development More than 100 illustrations and diagrams (some in color) to reinforce concepts and present key results from the primary literature Exercises at the end of chapters

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.

Simon Tavar   holds the George and Louise Kawamoto Chair in Biological Sciences and is a Professor of Biological Sciences, Mathematics, and Preventive Medicine at the University of Southern California. Professor Tavar  's research lies at the interface between statistics and biology, specifically focusing on problems arising in molecular biology, human genetics, population genetics, molecular evolution, and bioinformatics. His statistical interests focus on stochastic computation. Among the applications are linkage disequilibrium mapping, stem cell evolution, and inference in the fossil record. Dr. Tavar   is also a professor in the Department of Oncology at the University of Cambridge, England, where his group concentrates on cancer genomics.

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.

作者介绍:

目录:

[Computational genome analysis: an introduction](#) [下载链接1](#)

标签

生物

评论

[Computational genome analysis: an introduction 下载链接1](#)

书评

Computational Genome Analysis: an Introduction Richard C. Deonier, Simon Tavaré and Michael S. Waterman Computational Genome Analysis: an Introduction Richard C. Deonier, Simon Tavaré and Michael S. Waterman Springer Manchestor; 2006; ISBN...

[Computational genome analysis: an introduction 下载链接1](#)