



# Computational Genome Analysis: An Introduction (Statistics for Biology & Health S)

By Richard C. Deonier, Simon Tavaré, Michael S. Waterman

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This book 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 features a free download of the R software statistics package and the text provides great crossover material that is interesting and accessible to students in biology, mathematics, statistics and computer science. More than 100 illustrations and diagrams reinforce concepts and present key results from the primary literature. Exercises are given at the end of chapters.

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## **Editorial Review**

Review

From the reviews:

"The book is useful for its breadth. An impressive variety of topics are surveyed...." *Short Book Reviews of the ISI, June 2006*

"It is a very good book indeed and I would strongly recommend it both to the student hoping to take this study further and to the general reader who wants to know what computational genome analysis is all about." *Mark Bloom for the JRSS, Series A, Volume 169, p. 1006, October 2006*

"Richard C. Deonier, Simon Tavaré and Michael S. Waterman provide us with a 'roll up your sleeves and get dirty' (as the authors phrase it in their preface) introduction to the field of computational genome analysis...The book is carefully written and carefully edited..." *Ralf Schmid for Genetic Research, Volume 87, p. 218, 2006*

"This book provides an introduction to a broad spectrum of the biological and computation background required for genome analysis. Topics are illustrated with examples and exercises. ... The computational problems encourage the reader to investigate concepts using R. The book is very useful for its breadth. An impressive variety of topics are surveyed ... . This book is a useful starting point." (D. F. Andrews, *Short Book Reviews*, Vol. 26 (1), 2006)

"This book provides a practical introduction to computational molecular biology and bioinformatics. One of the strengths of the text is the breadth of the material ... . The mathematical and statistical concepts ... are presented clearly with the necessary detail. The book is nicely organized with a useful glossary and many informative tables and figures. The text is highly recommended for a course for upper level undergraduates or beginning graduate students, or as a reference for researchers ... ." (Sharon M. Crook, *Mathematical Reviews*, Issue 2006 i)

"This book is broad and deep in its coverage, with chapters on genome assembly and comparative genomics (including gene prediction) as well as more common topics. ...Overall, this book and the book by Jones and Pevzner (2004) are the best texts that I have seen in the area..." (Paul Havlak, *Journal of the American Statistical Association*, Vol. 102, No. 477, 2007)

"'Computational Genome Analysis: an introduction' is a new teaching book aimed at master and PhD students. ... As stated in its preface, this book is an introduction to the computational side of genomics and bioinformatics. In my opinion the authors largely succeed in providing just that. ... the book should help physicists and computational scientists to simultaneously learn what type of computational problems are addressed in bioinformatics and what the biology behind these problem is." (Berend Snel, *Mathematical Biosciences*, Vol. 208, 2007)

"The goal of computational genomics is the understanding and interpretation of information encoded and expressed from the entire genetic complement of biological organisms: the genome. This book provides an introduction to the subject, on the level of a senior or first-year graduate-level course, to students from a variety of backgrounds. It is addressed to biologists, applied mathematicians, computer scientists, and

persons working in the biotechnology industry." (Quarterly of Applied Mathematics, Vol. 66 (2), 2008)

From the Back Cover

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.

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.

Simon Tavaré 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 Tavaré'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. Tavaré is also a professor in the Department of Oncology at the University of Cambridge, England, where his group concentrates on cancer genomics.

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.

#### About the Author

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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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