

Genome-Scale Algorithm Design: Biological Sequence Analysis in the Era of High-Throughput Sequencing

By Veli Mäkinen, Djamal Belazzougui, Fabio Cunial, Alexandru I. Tomescu

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High-throughput sequencing has revolutionised the field of biological sequence analysis. Its application has enabled researchers to address important biological questions, often for the first time. This book provides an integrated presentation of the fundamental algorithms and data structures that power modern sequence analysis workflows. The topics covered range from the foundations of biological sequence analysis (alignments and hidden Markov models), to classical index structures (k-mer indexes, suffix arrays and suffix trees), Burrows-Wheeler indexes, graph algorithms and a number of advanced omics applications. The chapters feature numerous examples, algorithm visualisations, exercises and problems, each chosen to reflect the steps of large-scale sequencing projects, including read alignment, variant calling, haplotyping, fragment assembly, alignment-free genome comparison, transcript prediction and analysis of metagenomic samples. Each biological problem is accompanied by precise formulations, providing graduate students and researchers in bioinformatics and computer science with a powerful toolkit for the emerging applications of high-throughput sequencing.

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Editorial Review

Review
"Genome-Scale Algorithm Design is a well-thought-out ... book that fills a gap in the recent literature ... [on algorithms] for bioinformatics. It offers a sound, clear, and rich overview of computer science methods for the challenge of today's biological sequence analysis. I [recommend] it to students as well as to researchers in the field."
Nadia Pisanti, University of Pisa

"This book will be a new reference text for string data structures and algorithms, and their applications in computational molecular biology and genome analysis. The technically precise style, illustrated with a great collection of well-designed examples and many exercises makes it an ideal resource for researchers, students and teachers."
Jens Stoye, Universität Bielefeld

"I think the book is really great and could envision using it in courses in bioinformatics and data compression. The book's scope, clarity, and mathematically precise, compelling explanations make the advanced topics in genome-wide bioinformatics accessible to [a] wide audience."
Christina Boucher, Colorado State University

"This book is a timely, rigorous and comprehensive systematization of the concepts and tools at the core of post-genome bioinformatics. By choosing to incorporate the principles of algorithms design most pertinent to the topic, the authors have created a rare, self-contained reference that will smoothly introduce the neophyte and assist the seasoned researcher as well as anybody who needs to understand these issues at a fundamental level. The organization of the material, the clarity of exposition and rigor of treatment make the book an ideal textbook for courses directed at a mixed audience coming from diverse, even distant backgrounds."
Alberto Apostolico, Georgia Institute of Technology

"A very timely textbook covering many recently established techniques and applications at a level of rigor befitting a computer science audience."
Paul Medvedev, Pennsylvania State University

About the Author
Veli Mäkinen is a Professor of Computer Science at the University of Helsinki, Finland, where he heads a research group working on genome-scale algorithms as part of the Finnish Center of Excellence in Cancer Genetics Research. He has taught advanced courses on string processing, data compression, biological sequence analysis, along with introductory courses on bioinformatics.

Djamal Belazzougui is a postdoctoral researcher at the University of Helsinki. His research topics include hashing, succinct and compressed data structures and string algorithms.

Fabio Cunial is a postdoctoral researcher at the University of Helsinki. His research focuses on string algorithms and genome analysis.

Alexandru I. Tomescu is a postdoctoral researcher at the University of Helsinki. His current research

interests lie at the intersection of computational biology and computer science.

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