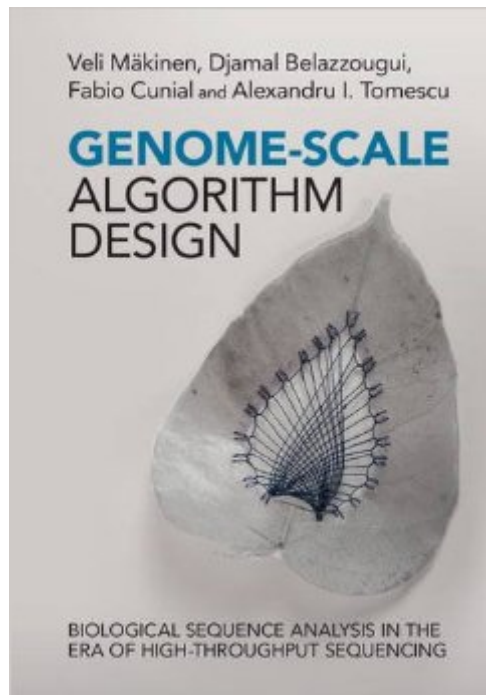# Genome-Scale Algorithm Design: Biological Sequence Analysis In The Era Of High-Throughput Sequencing

Synopsis

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.

Book Information

Hardcover: 413 pages

Publisher: Cambridge University Press; 1 edition (June 24, 2015)

Language: English

ISBN-10: 1107078539

ISBN-13: 978-1107078536

Product Dimensions: 6.8 x 0.9 x 9.7 inches

Shipping Weight: 2.1 pounds (View shipping rates and policies)

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