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"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."

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Genome-Scale Algorithm Design by Veli Mäkinen

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

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Fundamental tasks, such as the assembly of numerous whole-genome shotgun fragments, the alignment of complementary DNA sequences with a long genome, and the design of gene-specific primers or oligomers, require efficient algorithms and state-of-the-art implementation techniques.

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6.1.3 Myers' bitparallel algorithm 6.2 Longest common subsequence 6.2.1 Sparse dynamic programming 6.3 Approximate string matching 6.4 Biological sequence alignment 6.4.1 Global alignment 6.4.2 Local alignment 6.4.3 Overlap alignment 6.4.4 Affine gap scores 6.4.5 The invariant technique 6.5 Gene alignment 6.6 Multiple alignment 6.6.1 Scoring ...

Genome-Scale Algorithm Design - Table of contents

However, genome-scale experiments are costly and laborious, yielding "big data" that are conceptually and statistically difficult to analyze. There is no obvious consensus regarding design or analysis. Here we discuss the relevant technical considerations to generate reproducible, statistically sound, and broadly useful genome-scale data.

Guidelines for Genome-Scale Analysis of Biological Rhythms.

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