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Genome-Scale Algorithm Design 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.

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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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However, genome-scale experiments are costly and laborious, yielding "big data" that are conceptually and statistically difficult to analyze. There is no obvious

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consensus regarding design or analysis. Here we discuss the relevant technical considerations to generate reproducible, statistically sound, and broadly useful genome-scale data.

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