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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	An Improved Model for Statistical Alignment -- Improving Profile-Profile Alignments via Log Average Scoring -- False Positives in Genomic Map Assembly and Sequence Validation -- Boosting EM for Radiation Hybrid and Genetic Mapping -- Placing Probes along the Genome Using Pairwise Distance Data -- Comparing a Hidden Markov Model and a Stochastic Context-Free Grammar -- Assessing the Statistical Significance of Overrepresented Oligonucleotides -- Pattern Matching and Pattern Discovery Algorithms for Protein Topologies -- Computing Linking Numbers of a Filtration -- Side Chain-Positioning as an Integer Programming Problem -- A Chemical-Distance-Based Test for Positive Darwinian Selection -- Finding a Maximum Compatible

Tree for a Bounded Number of Trees with Bounded Degree Is Solvable in Polynomial Time -- Experiments in Computing Sequences of Reversals -- Exact-IEBP: A New Technique for Estimating Evolutionary Distances between Whole Genomes -- Finding an Optimal Inversion Median: Experimental Results -- Analytic Solutions for Three-Taxon MLMC Trees with Variable Rates Across Sites -- The Performance of Phylogenetic Methods on Trees of Bounded Diameter -- (1+?)-Approximation of Sorting by Reversals and Transpositions -- On the Practical Solution of the Reversal Median Problem -- Algorithms for Finding Gene Clusters -- Determination of Binding Amino Acids Based on Random Peptide Array Screening Data -- A Simple Hyper-Geometric Approach for Discovering Putative Transcription Factor Binding Sites -- Comparing Assemblies Using Fragments and Mate-Pairs.

Sommario/riassunto

This book constitutes the refereed proceedings of the First International Workshop on Algorithms in Bioinformatics, WABI 2001, held in Aarhus, Denmark, in August 2001. The 23 revised full papers presented were carefully reviewed and selected from more than 50 submissions. Among the issues addressed are exact and approximate algorithms for genomics, sequence analysis, gene and signal recognition, alignment, molecular evolution, structure determination or prediction, gene expression and gene networks, proteomics, functional genomics, and drug design; methodological topics from algorithmics; high-performance approaches to hard computational problems in bioinformatics.
