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Nota di bibliografia	Includes bibliographical references at the end of each chapters and index.
Nota di contenuto	Papers -- Reversing Gene Erosion – Reconstructing Ancestral Bacterial Genomes from Gene-Content and Order Data -- Reconstructing Ancestral Gene Orders Using Conserved Intervals -- Sorting by Reversals with Common Intervals -- A Polynomial-Time Algorithm for the Matching of Crossing Contact-Map Patterns -- A 1.5-Approximation Algorithm for Sorting by Transpositions and Transreversals -- Algorithms for Finding Maximal-Scoring Segment Sets -- Gapped Local Similarity Search with Provable Guarantees -- Monotone Scoring of Patterns with Mismatches -- Suboptimal Local

Alignments Across Multiple Scoring Schemes -- A Faster Reliable Algorithm to Estimate the p-Value of the Multinomial llr Statistic -- Adding Hidden Nodes to Gene Networks -- Joint Analysis of DNA Copy Numbers and Gene Expression Levels -- Searching for Regulatory Elements of Alternative Splicing Events Using Phylogenetic Footprinting -- Supervised Learning-Aided Optimization of Expert-Driven Functional Protein Sequence Annotation -- Multiple Vector Seeds for Protein Alignment -- Solving the Protein Threading Problem by Lagrangian Relaxation -- Protein-Protein Interfaces: Recognition of Similar Spatial and Chemical Organizations -- ATDD: An Algorithmic Tool for Domain Discovery in Protein Sequences -- Local Search Heuristic for Rigid Protein Docking -- Sequence Database Compression for Peptide Identification from Tandem Mass Spectra -- Linear Reduction for Haplotype Inference -- A New Integer Programming Formulation for the Pure Parsimony Problem in Haplotype Analysis -- Fast Hare: A Fast Heuristic for Single Individual SNP Haplotype Reconstruction -- Approximation Algorithms for the Selection of Robust Tag SNPs -- The Minisatellite Transformation Problem Revisited: A Run Length Encoded Approach -- A Faster and More Space-Efficient Algorithm for Inferring Arc-Annotations of RNA Sequences Through Alignment -- New Algorithms for Multiple DNA Sequence Alignment -- Chaining Algorithms for Alignment of Draft Sequence -- Translation Initiation Sites Prediction with Mixture Gaussian Models -- Online Consensus and Agreement of Phylogenetic Trees -- Relation of Residues in the Variable Region of 16S rDNA Sequences and Their Relevance to Genus-Specificity -- Topological Rearrangements and Local Search Method for Tandem Duplication Trees -- Phylogenetic Super-networks from Partial Trees -- Genome Identification and Classification by Short Oligo Arrays -- Novel Tree Edit Operations for RNA Secondary Structure Comparison -- The Most Probable Labeling Problem in HMMs and Its Application to Bioinformatics -- Integrating Sample-Driven and Pattern-Driven Approaches in Motif Finding -- Finding Optimal Pairs of Patterns -- Finding Missing Patterns.