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Formato	Materiale a stampa
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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Biomolecular Structure: RNA, Protein and Molecular Comparison -- A Worst-Case and Practical Speedup for the RNA Co-folding Problem Using the Four-Russians Idea -- Sparse Estimation for Structural Variability -- Data Structures for Accelerating Tanimoto Queries on Real Valued Vectors -- Sparsification of RNA Structure Prediction

Including Pseudoknots -- Prediction of RNA Secondary Structure Including Kissing Hairpin Motifs -- Reducing the Worst Case Running Times of a Family of RNA and CFG Problems, Using Valiant's Approach -- Comparative Genomics -- Reconstruction of Ancestral Genome Subject to Whole Genome Duplication, Speciation, Rearrangement and Loss -- Genomic Distance with DCJ and Indels -- Listing All Sorting Reversals in Quadratic Time -- Haplotype and Genotype Analysis -- Discovering Kinship through Small Subsets -- Fixed-Parameter Algorithm for Haplotype Inferences on General Pedigrees with Small Number of Sites -- Haplotypes versus Genotypes on Pedigrees -- Haplotype Inference on Pedigrees with Recombinations and Mutations -- High-throughput Data Analysis: Next Generation Sequencing and Flow Cytometry -- Identifying Rare Cell Populations in Comparative Flow Cytometry -- Fast Mapping and Precise Alignment of AB SOLiD Color Reads to Reference DNA -- Design of an Efficient Out-of-Core Read Alignment Algorithm -- Estimation of Alternative Splicing isoform Frequencies from RNA-Seq Data -- Networks -- Improved Orientations of Physical Networks -- Enumerating Chemical Organisations in Consistent Metabolic Networks: Complexity and Algorithms -- Efficient Subgraph Frequency Estimation with G-Tries -- Phylogenetics -- Accuracy Guarantees for Phylogeny Reconstruction Algorithms Based on Balanced Minimum Evolution -- The Complexity of Inferring a Minimally Resolved Phylogenetic Supertree -- Reducing Multi-state to Binary Perfect Phylogeny with Applications to Missing, Removable, Inserted, and Deleted Data -- An Experimental Study of Quartets MaxCut and Other Supertree Methods -- An Efficient Method for DNA-Based Species Assignment via Gene Tree and Species Tree Reconciliation -- Sequences, Strings and Motifs -- Effective Algorithms for Fusion Gene Detection -- Swiftly Computing Center Strings -- Speeding Up Exact Motif Discovery by Bounding the Expected Clump Size -- Pair HMM Based Gap Statistics for Re-evaluation of Indels in Alignments with Affine Gap Penalties -- Quantifying the Strength of Natural Selection of a Motif Sequence.
