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Titolo	Algorithms in bioinformatics : 10th international workshop, WABI 2010, Liverpool, UK, September 6-8, 2010 : proceedings // Vincent Moulton, Mona Singh (eds.)
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Descrizione fisica	1 online resource (XII, 376 p. 94 illus.)
Collana	Lecture notes in computer science ; ; 6293 Lecture notes in bioinformatics
Classificazione	570
Altri autori (Persone)	MoultonVincent SinghMona
Disciplina	570.285
Soggetti	Bioinformatics Computer algorithms
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	International conference proceedings.
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.
