1.

Record Nr.	UNISA996465681603316
Titolo	Algorithms in Bioinformatics [[electronic resource]] : 10th International Workshop, WABI 2010, Liverpool, UK, September 6-8, 2010, Proceedings / / edited by Vincent Moulton, Mona Singh
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2010
ISBN	1-280-38845-5 9786613566379 3-642-15294-5
Edizione	[1st ed. 2010.]
Descrizione fisica	1 online resource (XII, 376 p. 94 illus.)
Collana	Lecture Notes in Bioinformatics ; ; 6293
Classificazione	570
Disciplina	570
Soggetti	Life sciences Algorithms Computers Artificial intelligence Database management Bioinformatics Life Sciences, general Algorithm Analysis and Problem Complexity Computation by Abstract Devices Artificial Intelligence Database Management Computational Biology/Bioinformatics Kongress Liverpool <2010>
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.