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Altri autori (Persone)	MoultonVincent SinghMona
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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.
Sommario/riassunto	We are pleased to present the proceedings of the 10th Workshop on Algorithms in Bioinformatics (WABI 2010) which took place in Liverpool, UK, Sept- ber 6-8, 2010. The WABI 2010 workshop was part of the four ALGO 2010 conference meetings, which, in addition to WABI, included ESA, ATMOS, and WAOA. WABI 2010 was hosted by the University of Liverpool Department of Computer Science, and sponsored by the European Association for Theoretical Computer Science (EATCS) and the International Society for Computational Biology(ISCB). Seehttp://algo2010.csc.liv.ac.uk/wabi/for more details. The Workshop in Algorithms in Bioinformatics highlights research in alrithmicworkforbioinformatics,computationalbiologyandsystemsbiology. The emphasis is mainly on discrete algorithms and machine-learning methods that address important problems in molecular biology, that are founded on sound models, that are computationally e'cient, and that havebeen implemented and tested in simulations and on real datasets. The goal is to present recent research results, including signi'cant work-in-progress,and to identify and explore dir- tions of future research.