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Titolo	Research in Computational Molecular Biology [[electronic resource] ] : 10th Annual International Conference, RECOMB 2006, Venice, Italy, April 2-5, 2006, Proceedings // edited by Alberto Apostolico, Concettina Guerra, Sorin Istrail, Pavel Pevzner, Michael Waterman
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Collana	Lecture Notes in Bioinformatics ; ; 3909
Disciplina	572.8
Soggetti	Algorithms Data structures (Computer science) Computer science—Mathematics Database management Artificial intelligence Bioinformatics Algorithm Analysis and Problem Complexity Data Structures Discrete Mathematics in Computer Science Database Management Artificial Intelligence
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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Integrated Protein Interaction Networks for 11 Microbes -- Hypergraph Model of Multi-residue Interactions in Proteins: Sequentially--Constrained Partitioning Algorithms for Optimization of Site-Directed Protein Recombination -- Biological Networks: Comparison, Conservation, and Evolutionary Trees -- Assessing Significance of Connectivity and Conservation in Protein Interaction Networks -- Clustering Short Gene Expression Profiles -- A Patient-Gene Model for Temporal Expression Profiles in Clinical Studies -- Global Interaction Networks Probed by Mass Spectrometry -- Statistical Evaluation of Genome Rearrangement -- An Improved Statistic for Detecting Over-

Represented Gene Ontology Annotations in Gene Sets -- Protein Function Annotation Based on Ortholog Clusters Extracted from Incomplete Genomes Using Combinatorial Optimization -- Detecting MicroRNA Targets by Linking Sequence, MicroRNA and Gene Expression Data -- RNA Secondary Structure Prediction Via Energy Density Minimization -- Structural Alignment of Pseudoknotted RNA -- Stan Ulam and Computational Biology -- CONTRAlign: Discriminative Training for Protein Sequence Alignment -- Clustering Near-Identical Sequences for Fast Homology Search -- New Methods for Detecting Lineage-Specific Selection -- A Probabilistic Model for Gene Content Evolution with Duplication, Loss, and Horizontal Transfer -- A Sublinear-Time Randomized Approximation Scheme for the Robinson-Foulds Metric -- Algorithms to Distinguish the Role of Gene-Conversion from Single-Crossover Recombination in the Derivation of SNP Sequences in Populations -- Inferring Common Origins from mtDNA -- Efficient Enumeration of Phylogenetically Informative Substrings -- Phylogenetic Profiling of Insertions and Deletions in Vertebrate Genomes -- Maximal Accurate Forests from Distance Matrices -- Leveraging Information Across HLA Alleles/Supertypes Improves Epitope Prediction -- Improving Prediction of Zinc Binding Sites by Modeling the Linkage Between Residues Close in Sequence -- An Important Connection Between Network Motifs and Parsimony Models -- Ultraconserved Elements, Living Fossil Transposons, and Rapid Bursts of Change: Reconstructing the Uneven Evolutionary History of the Human Genome -- Permutation Filtering: A Novel Concept for Significance Analysis of Large-Scale Genomic Data -- Genome-Wide Discovery of Modulators of Transcriptional Interactions in Human B Lymphocytes -- A New Approach to Protein Identification -- Markov Methods for Hierarchical Coarse-Graining of Large Protein Dynamics -- Simulating Protein Motions with Rigidity Analysis -- Predicting Experimental Quantities in Protein Folding Kinetics Using Stochastic Roadmap Simulation -- An Outsider's View of the Genome -- Alignment Statistics for Long-Range Correlated Genomic Sequences -- Simple and Fast Inverse Alignment -- Revealing the Proteome Complexity by Mass Spectrometry -- Motif Yggdrasil: Sampling from a Tree Mixture Model -- A Study of Accessible Motifs and RNA Folding Complexity -- A Parameterized Algorithm for Protein Structure Alignment -- Geometric Sieving: Automated Distributed Optimization of 3D Motifs for Protein Function Prediction -- A Branch-and-Reduce Algorithm for the Contact Map Overlap Problem -- A Novel Minimized Dead-End Elimination Criterion and Its Application to Protein Redesign in a Hybrid Scoring and Search Algorithm for Computing Partition Functions over Molecular Ensembles -- 10 Years of the International Conference on Research in Computational Molecular Biology (RECOMB) -- Sorting by Weighted Reversals, Transpositions, and Inverted Transpositions -- A Parsimony Approach to Genome-Wide Ortholog Assignment -- Detecting the Dependent Evolution of Biosequences -- Detecting MicroRNA Targets by Linking Sequence, MicroRNA and Gene Expression Data.

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