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	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.