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	Nota di contenuto	Measures of Codon Bias in Yeast, the tRNA Pairing Index and Possible DNA Repair Mechanisms -- Decomposing Metabolomic Isotope Patterns -- A Method to Design Standard HMMs with Desired Length Distribution for Biological Sequence Analysis -- Efficient Model-Based Clustering for LC-MS Data -- A Bayesian Algorithm for Reconstructing Two-Component Signaling Networks -- Linear-Time Haplotype Inference on Pedigrees Without Recombinations -- Phylogenetic Network Inferences Through Efficient Haplotyping -- Beaches of Islands of Tractability: Algorithms for Parsimony and Minimum Perfect

Phylogeny Haplotyping Problems -- On the Complexity of SNP Block Partitioning Under the Perfect Phylogeny Model -- How Many Transcripts Does It Take to Reconstruct the Splice Graph? -- Multiple Structure Alignment and Consensus Identification for Proteins -- Procrastination Leads to Efficient Filtration for Local Multiple Alignment -- Controlling Size When Aligning Multiple Genomic Sequences with Duplications -- Reducing Distortion in Phylogenetic Networks -- Imputing Supertrees and Supernetworks from Quartets -- A Unifying View of Genome Rearrangements -- Efficient Sampling of Transpositions and Inverted Transpositions for Bayesian MCMC -- Alignment with Non-overlapping Inversions in O(n 3)-Time -- Accelerating Motif Discovery: Motif Matching on Parallel Hardware -- Segmenting Motifs in Protein-Protein Interface Surfaces -- Protein Side-Chain Placement Through MAP Estimation and Problem-Size Reduction -- On the Complexity of the Crossing Contact Map Pattern Matching Problem -- A Fuzzy Dynamic Programming Approach to Predict RNA Secondary Structure -- Landscape Analysis for Protein-Folding Simulation in the H-P Model -- Rapid ab initio RNA Folding Including Pseudoknots Via Graph Tree Decomposition -- Flux-Based vs. Topology-Based Similarity of Metabolic Genes -- Combinatorial Methods for Disease Association Search and Susceptibility Prediction -- Integer Linear Programs for Discovering Approximate Gene Clusters -- Approximation Algorithms for Bi-clustering Problems -- Improving the Layout of Oligonucleotide Microarrays: Pivot Partitioning -- Accelerating the Computation of Elementary Modes Using Pattern Trees -- A Linear-Time Algorithm for Studying Genetic Variation -- New Constructive Heuristics for DNA Sequencing by Hybridization -- Optimal Probing Patterns for Sequencing by Hybridization -- Gapped Permutation Patterns for Comparative Genomics -- Segmentation with an Isochore Distribution.