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Record Nr.	UNISA996465434003316
Titolo	Algorithms in Bioinformatics [[electronic resource]] : 4th International Workshop, WABI 2004, Bergen, Norway, September 17-21, 2004, Proceedings / / edited by Inge Jonassen, Junhyong Kim
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2004
ISBN	3-540-30219-0
Edizione	[1st ed. 2004.]
Descrizione fisica	1 online resource (IX, 477 p.)
Collana	Lecture Notes in Bioinformatics ; ; 3240
Disciplina	572.0285
Soggetti	Biochemistry Computer programming Algorithms Computers Data structures (Computer science) Computer science—Mathematics Biochemistry, general Programming Techniques Algorithm Analysis and Problem Complexity Computation by Abstract Devices Data Structures Discrete Mathematics in Computer Science
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di bibliografia	Includes bibliographical references at the end of each chapters and index.
Nota di contenuto	Papers -- Reversing Gene Erosion – Reconstructing Ancestral Bacterial Genomes from Gene-Content and Order Data -- Reconstructing Ancestral Gene Orders Using Conserved Intervals -- Sorting by Reversals with Common Intervals -- A Polynomial-Time Algorithm for the Matching of Crossing Contact-Map Patterns -- A 1.5-Approximation Algorithm for Sorting by Transpositions and Transreversals -- Algorithms for Finding Maximal-Scoring Segment Sets -- Gapped Local Similarity Search with Provable Guarantees -- Monotone Scoring of Patterns with Mismatches -- Suboptimal Local

Alignments Across Multiple Scoring Schemes -- A Faster Reliable Algorithm to Estimate the p-Value of the Multinomial llr Statistic -- Adding Hidden Nodes to Gene Networks -- Joint Analysis of DNA Copy Numbers and Gene Expression Levels -- Searching for Regulatory Elements of Alternative Splicing Events Using Phylogenetic Footprinting -- Supervised Learning-Aided Optimization of Expert-Driven Functional Protein Sequence Annotation -- Multiple Vector Seeds for Protein Alignment -- Solving the Protein Threading Problem by Lagrangian Relaxation -- Protein-Protein Interfaces: Recognition of Similar Spatial and Chemical Organizations -- ATDD: An Algorithmic Tool for Domain Discovery in Protein Sequences -- Local Search Heuristic for Rigid Protein Docking -- Sequence Database Compression for Peptide Identification from Tandem Mass Spectra -- Linear Reduction for Haplotype Inference -- A New Integer Programming Formulation for the Pure Parsimony Problem in Haplotype Analysis -- Fast Hare: A Fast Heuristic for Single Individual SNP Haplotype Reconstruction -- Approximation Algorithms for the Selection of Robust Tag SNPs -- The Minisatellite Transformation Problem Revisited: A Run Length Encoded Approach -- A Faster and More Space-Efficient Algorithm for Inferring Arc-Annotations of RNA Sequences Through Alignment -- New Algorithms for Multiple DNA Sequence Alignment -- Chaining Algorithms for Alignment of Draft Sequence -- Translation Initiation Sites Prediction with Mixture Gaussian Models -- Online Consensus and Agreement of Phylogenetic Trees -- Relation of Residues in the Variable Region of 16S rDNA Sequences and Their Relevance to Genus-Specificity -- Topological Rearrangements and Local Search Method for Tandem Duplication Trees -- Phylogenetic Super-networks from Partial Trees -- Genome Identification and Classification by Short Oligo Arrays -- Novel Tree Edit Operations for RNA Secondary Structure Comparison -- The Most Probable Labeling Problem in HMMs and Its Application to Bioinformatics -- Integrating Sample-Driven and Pattern-Driven Approaches in Motif Finding -- Finding Optimal Pairs of Patterns -- Finding Missing Patterns.