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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.

Sommario/riassunto	It gives us great pleasure to present the proceedings of the 4th Workshop on Algorithms in Bioinformatics (WABI 2004) which took place in Bergen, Norway, September 17-21, 2004. The WABI 2004 workshop was part of a ?- conference meeting, which in addition to WABI, included ESA, WAOA, IWPEC, and ATMOS, hosted by the University of Bergen, Norway. See http://www.ii.uib.no/algo2004/ for more details. TheWorkshoponAlgorithmsinBioinformaticscoversresearchonallaspects of algorithmic work in bioinformatics. The emphasis is on discrete algorithms that address important problems in molecular biology. These are founded on sound models, are computationally e'cient, and have been implemented and tested in simulations and on real datasets. The goal is to present recent research results, including sign'cant work in progress, and to identify and explore dir- tions of future research. Original research papers (including signi'cant work in progress) or sta- of-the-art surveys were solicited on all aspects of algorithms in bioinformatics, including, but not limited to: exact and approximate algorithms for genomics, genetics, sequence analysis, gene and signal recognition, alignment, molecular evolution, phylogenetics, structure determination or prediction, gene expression and gene networks, proteomics, functional genomics, and drug design. We received 117 submissions in response to our call for papers, and were able to accept 39 of these. In addition, WABI hosted one invited distinguished lecture, given to the entire ALGO 2004 conference, by Dr. Marie France Sagot of