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   Disciplina   570

   Soggetti   Life sciences
                         Data mining
                         Computer graphics
                         Bioinformatics
                         Life Sciences
                         Data Mining and Knowledge Discovery
                         Computer Graphics
                         Computational and Systems Biology

   Lingua di pubblicazione Inglese

   Formato   Materiale a stampa

   Livello bibliografico Monografia

   Note generali   International conference proceedings.

   Nota di bibliografia Includes bibliographical references and index.

   Nota di contenuto   Evolution of Regulatory Systems in Bacteria (Invited Keynote Talk) -- Integrating Multiple-Platform Expression Data through Gene Set Features -- Practical Quality Assessment of Microarray Data by Simulation of Differential Gene Expression -- Mean Square Residue Biclustering with Missing Data and Row Inversions -- Using Gene Expression Modeling to Determine Biological Relevance of Putative Regulatory Networks -- Querying Protein-Protein Interaction Networks -- Integrative Approach for Combining TNF?-NF?B Mathematical Model to a Protein Interaction Connectivity Map -- Hierarchical Organization of Functional Modules in Weighted Protein Interaction Networks Using Clustering Coefficient -- Bioinformatics Challenges in Translational Research -- Untangling Tanglegrams: Comparing Trees by Their

Drawings -- An Experimental Analysis of Consensus Tree Algorithms for Large-Scale Tree Collections -- Counting Faces in Split Networks -- Relationship between Amino Acids Sequences and Protein Structures: Folding Patterns and Sequence Patterns -- Improved Algorithms for Parsing ESLTAGs: A Grammatical Model Suitable for RNA Pseudoknots -- Efficient Algorithms for Self Assembling Triangular and Other Nano Structures -- Motif Construction from High–Throughput SELEX Data -- Rearrangement Phylogeny of Genomes in Contig Form -- Prediction of Contiguous Regions in the Amniote Ancestral Genome -- Pure Parsimony Xor Haplotyping -- A Decomposition of the Pure Parsimony Haplotyping Problem -- Exact Computation of Coalescent Likelihood under the Infinite Sites Model -- Imputation-Based Local Ancestry Inference in Admixed Populations -- Interpreting Population Sequencing Data -- Modeling and Visualizing Heterogeneity of Spatial Patterns of Protein-DNA Interaction from High-Density Chromatin Precipitation Mapping Data.-A Linear-Time Algorithm for Analyzing Array CGH Data Using Log Ratio Triangulation -- Mining of cis-Regulatory Motifs Associated with Tissue-Specific Alternative Splicing -- Analysis of Cis-Regulatory Motifs in Cassette Exons by Incorporating Exon Skipping Rates -- A Class of Evolution-Based Kernels for Protein Homology Analysis: A Generalization of the PAM Model -- Irreplaceable Amino Acids and Reduced Alphabets in Short-Term and Directed Protein Evolution -- A One-Class Classification Approach for Protein Sequences and Structures -- Prediction and Classification of Real and Pseudo MicroRNA Precursors via Data Fuzzification and Fuzzy Decision Trees.

| Sommario/riassunto | This book constitutes the refereed proceedings of the 5th International Symposium on Bioinformatics Research and Applications, ISBRA 2009, held in Fort Lauderdale, FL, USA, in May 2009. The 26 revised full papers presented together four invited papers were carefully reviewed and selected from a total of 55 submissions. The papers cover a wide range of topics, including clustering and classification, gene expression analysis, gene networks, genome analysis, motif finding, pathways, protein structure prediction, protein domain interactions, phylogenetics, and software tools. |