

1. Record Nr.	UNISA996465879503316
Titolo	Bioinformatics Research and Applications [[electronic resource] ] : Fourth International Symposium, ISBRA 2008, Atlanta, GA, USA, May 6-9, 2008, Proceedings // edited by Ion Mandoiu, Rajshekhar Sunderraman, Alexander Zelikovsky
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2008
ISBN	1-281-85508-1 3-540-79450-6
Edizione	[1st ed. 2008.]
Descrizione fisica	1 online resource (XIX, 510 p.)
Collana	Lecture Notes in Bioinformatics ; ; 4983
Disciplina	570.285
Soggetti	Life sciences Computers Bioinformatics Pattern recognition Data mining Life Sciences, general Theory of Computation Computational Biology/Bioinformatics Computation by Abstract Devices Pattern Recognition Data Mining and Knowledge Discovery
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 and index.
Nota di contenuto	Invited Keynote Talk: Set-Level Analyses for Genome-Wide Association Data -- Hierarchical Clustering Using Constraints -- The Gene-Duplication Problem: Near-Linear Time Algorithms for NNI Based Local Searches -- A Distance-Based Method for Detecting Horizontal Gene Transfer in Whole Genomes -- An Approach for Determining Evolutionary Distance in Network-Based Phylogenetic Analysis -- Pairwise Statistical Significance Versus Database Statistical Significance for Local Alignment of Protein Sequences -- Estimating Pairwise

Statistical Significance of Protein Local Alignments Using a Clustering-Classification Approach Based on Amino Acid Composition -- Gapped Extension for Local Multiple Alignment of Interspersed DNA Repeats -- Improved Alignment of Protein Sequences Based on Common Parts -- Invited Keynote Talk: Computing P-Values for Peptide Identifications in Mass Spectrometry -- PFP: A Computational Framework for Phylogenetic Footprinting in Prokaryotic Genomes -- Accelerating the Neighbor-Joining Algorithm Using the Adaptive Bucket Data Structure -- Generalized Gene Adjacencies, Graph Bandwidth and Clusters in Yeast Evolution -- Physicochemical Correlation between Amino Acid Sites in Short Sequences under Selective Pressure -- HCV Quasispecies Assembly Using Network Flows -- A Dynamic Programming Algorithm for De Novo Peptide Sequencing with Variable Scoring -- Invited Keynote Talk: Haplotype Sharing for Genome-Wide Case-Control Association Studies -- Incorporating Literature Knowledge in Bayesian Network for Inferring Gene Networks with Gene Expression Data -- Integrative Network Component Analysis for Regulatory Network Reconstruction -- A Graph-Theoretic Method for Mining Overlapping Functional Modules in Protein Interaction Networks -- Identification of Transcription Factor Binding Sites in Promoter Regions by Modularity Analysis of the Motif Co-occurrence Graph -- Mean Squared Residue Based Biclustering Algorithms -- Sparse Decomposition of Gene Expression Data to Infer Transcriptional Modules Guided by Motif Information -- A Novel Metric for Redundant Gene Elimination Based on Discriminative Contribution -- Network-Based Inference of Cancer Progression from Microarray Data -- Invited Keynote Talk: Quiet Revolution: Connectivity in the Cancer Research Community -- Wavelet-Based 3-D Multifractal Spectrum with Applications in Breast MRI Images -- Accurate Inverse Consistent Non-rigid Image Registration and Its Application on Automatic Re-contouring -- GlycoBrowser: A Tool for Contextual Visualization of Biological Data and Pathways Using Ontologies -- Pattern Matching in RNA Structures -- The Use of a Conformational Alphabet for Fast Alignment of Protein Structures -- On-the-Fly Rotamer Pair Energy Evaluation in Protein Design -- Invited Keynote Talk: Integrative Viral Molecular Epidemiology: Hepatitis C Virus Modeling -- Multiple Kernel Support Vector Regression for siRNA Efficacy Prediction -- Hierarchical Clustering Support Vector Machines for Classifying Type-2 Diabetes Patients -- Computational Mutagenesis of E. coli Lac Repressor: Insight into Structure-Function Relationships and Accurate Prediction of Mutant Activity -- Evaluating Genetic Algorithms in Protein-Ligand Docking -- A Hidden Markov Model Approach for Prediction of Genomic Alterations from Gene Expression Profiling -- Evolutionary Algorithm for Feature Subset Selection in Predicting Tumor Outcomes Using Microarray Data -- Incorporating Knowledge of Topology Improves Reconstruction of Interaction Networks from Microarray Data -- Invited Keynote Talk: Data Mining and Statistical Methods for Analyzing Microarray Experiments -- Seven Variations of an Alignment Workflow - An Illustration of Agile Process Design and Management in Bio-jETI -- Supporting Computational Systems Science: Genomic Analysis Tool Federations Using Aspects and AOP -- BioDQ: Data Quality Estimation and Management for Genomics Databases -- Stepped Linear Regression to Accurately Assess Statistical Significance in Batch Confounded Differential Expression Analysis -- Bagging Multiple Comparisons from Microarray Data -- Human Blood-Brain Differential Gene-Expression Correlates with Dipeptide Frequency of Gene Products.

International Symposium on Bioinformatics Research and Applications, ISBRA 2008, held in Atlanta, GA, USA in May 2008. The 35 revised full papers presented together with 6 workshop papers and 6 invited papers were carefully reviewed and selected from a total of 94 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.

---