

1. Record Nr.	UNINA9910484378703321
Titolo	Bioinformatics Research and Applications : 10th International Symposium, ISBRA 2014, Zhangjiajie, China, June 28-30, 2014, Proceedings // edited by Mitra Basu, Yi Pan, Jianxin Wang
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2014
ISBN	3-319-08171-3
Edizione	[1st ed. 2014.]
Descrizione fisica	1 online resource (XVIII, 409 p. 115 illus.)
Collana	Lecture Notes in Bioinformatics ; ; 8492
Disciplina	570.285
Soggetti	Bioinformatics Data mining Pattern recognition Biomathematics Computational Biology/Bioinformatics Data Mining and Knowledge Discovery Pattern Recognition Mathematical and Computational Biology Conference papers and proceedings.
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 author index.
Nota di contenuto	Predicting Disease Risks Using Feature Selection Based on Random Forest and Support Vector Machine -- Phylogenetic Bias in the Likelihood Method Caused by Missing Data Coupled with Among-Site Rate Variation: An Analytical Approach -- An Eigen decomposition Method for Protein Structure Alignment -- Functional Interplay between Hemagglutinin and Neuraminidase of Pandemic 2009 H1N1 from the Perspective of Virus Evolution -- Predicting Protein Submitochondrial Locations Using a K-Nearest Neighbors Method Based on the Bit-Score Weighted Euclidean Distance -- Algorithms Implemented for Cancer Gene Searching and Classifications -- Dysregulated microRNA Profile in HeLa Cell Lines Induced by Lupeol -- A Simulation for Proportional Biological Operational Mu-Circuit -- Computational Prediction of Human Saliva-Secreted Proteins -- A Parallel Scheme for Three-

Dimensional Reconstruction in Large-Field Electron Tomography -- An Improved Correlation Method Based on Rotation Invariant Feature for Automatic Particle Selection -- An Effective Algorithm for Peptide de novo Sequencing from Mixture MS/MS Spectra -- Identifying Spurious Interactions in the Protein-Protein Interaction Networks Using Local Similarity Preserving Embedding -- Multiple RNA Interaction with Sub-optimal Solutions -- Application of Consensus String Matching in the Diagnosis of Allelic Heterogeneity (Extended Abstract) -- Continuous Time Bayesian Networks for Gene Network Reconstruction: A Comparative Study on Time Course Data -- Drug Target Identification Based on Structural Output Controllability of Complex Networks -- NovoGMET: De Novo Peptide Sequencing Using Graphs with Multiple Edge Types (GMET) for ETD/ECD Spectra -- Duplication Cost Diameters -- Computational Identification of De-Centric Genetic Regulatory Relationships from Functional Genomic Data -- Classification of Mutations by Functional Impact Type: Gain of Function, Loss of Function and Switch of Function -- Network Analysis of Human Disease Comorbidity Patterns Based on Large-Scale Data Mining -- Identification of Essential Proteins by Using Complexes and Interaction Network -- GenoScan: Genomic Scanner for Putative miRNA Precursors -- Searching SNP Combinations Related to Evolutionary Information of Human Populations on HapMap Data -- 2D Pharmacophore Query Generation -- Structure-Based Analysis of Protein Binding Pockets Using Von Neumann Entropy -- A New Mathematical Model for Inbreeding Depression in Large Populations -- dSpliceType: A Multivariate Model for Detecting Various Types of Differential Splicing Events Using RNA-Seq -- Conformational Transitions and Principal Geodesic Analysis on the Positive Semidefinite Matrix Manifold -- Joint Analysis of Functional and Phylogenetic Composition for Human Microbiome Data -- schematikon: Detailed Sequence-Structure Relationships from Mining a Non-redundant Protein Structure Database (Extended Abstract) -- PNIModeler: Web Server for Inferring Protein Binding Nucleotides from Sequence Data -- A MCI Decision Support System Based on Ontology -- Context Similarity Based Feature Selection Methods for Protein Interaction Article Classification -- Network Propagation Reveals Novel Genetic Features Predicting Drug Response of Cancer Cell Lines -- Splice Site Prediction Using Support Vector Machine with Markov Model and Codon Information -- Exploiting Topic Modeling to Boost Metagenomic Sequences Binning -- Network-Based Method for Identifying Overlapping Mutated Driver Pathways in Cancer -- Completing a Bacterial Genome with in silico and Wet Lab Approaches -- Protein Function Prediction: A Global Prediction Method with Multiple Data Sources -- A microRNA-Gene Network in Ovarian Cancer from Genome-Wide QTL Analysis -- K-Profiles Nonlinear Clustering -- Estrogen Induced RNA Polymerase II Stalling in Breast Cancer Cell Line MCF7 -- A Knowledge-Driven Approach in Constructing a Large-Scale Drug-Side Effect Relationship Knowledge Base for Computational Drug Discovery -- Systems Biology Approach to Understand Seed Composition -- Prediction of the Cooperative cis-regulatory Elements for Broadly Expressed Neuronal Genes in *Caenorhabditis Elegans* -- Improving the Mapping of the Smith-Waterman Sequence Database Search Algorithm onto CUDA GPUs -- VFP: A Visual Tool for Predicting Gene-Fusion Base on Analyzing Single-end RNA-Sequence -- A Novel Method for Identifying Essential Proteins from Active PPI Networks -- RAUR: Re-alignment of Unmapped Reads with Base Quality Score -- PIGS: Improved Estimates of Identity-by-Descent Probabilities by Probabilistic IBD Graph Sampling -- Clustering PPI Data through Improved Synchronization-Based

Hierarchical Clustering Method -- Order Decay in Transcription Regulation in Type 1 Diabetes -- Simulated Regression Algorithm for Transcriptome Quantification.

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Sommario/riassunto

This book constitutes the refereed proceedings of the 10th International Symposium on Bioinformatics Research and Applications, ISBRA 2014, held in Zhangjiajie, China, in June 2014. The 33 revised full papers and 31 one-page abstracts included in this volume were carefully reviewed and selected from 119 submissions. The papers cover a wide range of topics in bioinformatics and computational biology and their applications including the development of experimental or commercial systems.

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