

1. Record Nr.	UNINA9910741159203321
Titolo	Bioinformatics Research and Applications : 9th International Symposium, ISBRA 2013, Charlotte, NC, USA, May 20-22, 2013, Proceedings // edited by Zhipeng Cai, Oliver Eulenstein, Daniel Janies, Daniel Schwartz
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2013
ISBN	3-642-38036-0
Edizione	[1st ed. 2013.]
Descrizione fisica	1 online resource (XIV, 312 p. 102 illus.)
Collana	Lecture Notes in Bioinformatics ; ; 7875
Classificazione	004 BIO 110f SS 4800
Disciplina	570.285
Soggetti	Bioinformatics Data mining Application software Algorithms Pattern recognition Bioinformatics Computational biology Computational Biology/Bioinformatics Data Mining and Knowledge Discovery Information Systems Applications (incl. Internet) Algorithm Analysis and Problem Complexity Pattern Recognition Computer Appl. in Life Sciences Kongress2013.Charlotte, NC Conference 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	Peptide Identification from Mass Spectrometry -- Identifying Critical Transitions of Biological Processes by Dynamical Network Biomarkers

-- Computational Behavioral Ecology -- Unusual RNA Structures: Information Content in RNAs from the "Prebiotic Ribosome" to Modern Viruses -- The Radiation Hybrid Map Construction Problem Is FPT -- Reconstructing Ancestral Genomic Orders Using Binary Encoding and Probabilistic Models -- Computational Methods for the Parallel 3D Simulation of Biochemical Kinetics at the Microscopic Scale -- A Tool for Non-binary Tree Reconciliation -- Patterns of Chromatin-Modifications Discriminate Different Genomic Features in Arabidopsis -- Inferring Time-Delayed Gene Regulatory Networks Using Cross-Correlation and Sparse Regression -- A Simulation of Synthetic agr System in E.coli -- Gene Regulatory Networks from Gene Ontology -- Partitioning Biological Networks into Highly Connected Clusters with Maximum Edge Coverage -- Reconstructing k-Reticulated Phylogenetic Network from a Set of Gene Trees -- LCR Finder: A de Novo Low Copy Repeat Finder for Human Genome -- Heuristic Algorithms for the Protein Model Assignment Problem -- Alignment of DNA Mass-Spectral Profiles Using Network Flows -- A Context-Driven Gene Prioritization Method for Web-Based Functional Genomics -- Exploiting Dependencies of Patterns in Gene Expression Analysis Using Pairwise Comparisons -- Cloud Computing for De Novo Metagenomic Sequence Assembly -- Protein Closed Loop Prediction from Contact Probabilities -- A Graph Approach to Bridge the Gaps in Volumetric Electron Cryo-Microscopy Skeletons -- Measure the Semantic Similarity of GO Terms Using Aggregate Information Content -- Scalable and Versatile k-mer Indexing for High-Throughput Sequencing Data -- POMAGO: Multiple Genome-Wide Alignment Tool for Bacteria -- Effect of Incomplete Lineage Sorting on Tree-Reconciliation-Based Inference of Gene Duplication -- Ellipsoid-Weighted Protein Conformation Alignment -- Construction of Uncertain Protein-Protein Interaction Networks and Its Applications -- Does Accurate Scoring of Ligands against Protein Targets Mean Accurate Ranking?.

Sommario/riassunto

This book constitutes the refereed proceedings of the 9th International Symposium on Bioinformatics Research and Applications, ISBRA 2013, held in Charlotte, NC, USA, in May 2013. The 25 revised full papers presented together with 4 invited talks were carefully reviewed and selected from 46 submissions. The papers cover a wide range of biomedical databases and data integration, high-performance bio-computing, biomolecular imaging, high-throughput sequencing data analysis, bio-ontologies, molecular evolution, comparative genomics and phylogenomics, molecular modeling and simulation, pattern discovery and classification, computational proteomics, population genetics, data mining and visualization, software tools and applications.
