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Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 5462
Classificazione	BIO 110f BIO 180f DAT 718f SS 4800
Altri autori (Persone)	RajasekaranSanguthevar
Disciplina	570
Soggetti	Life sciences Computer science Data mining Bioinformatics Artificial intelligence Information storage and retrieval systems Life Sciences Theory of Computation Data Mining and Knowledge Discovery Computational and Systems Biology Artificial Intelligence Information Storage and Retrieval
Lingua di pubblicazione	Inglese
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Livello bibliografico	Monografia
Note generali	International conference proceedings. Includes index.
Nota di contenuto	Invited Talks -- Association Analysis Techniques for Bioinformatics Problems -- Analyzing and Interrogating Biological Networks (Abstract) -- From Architecture to Function (and Back) in Bio-networks -- A New Machine Learning Approach for Protein Phosphorylation Site Prediction in Plants -- Assembly of Large Genomes from Paired Short Reads --

	Amino Acid Classification and Hash Seeds for Homology Search -- Genotype and Haplotype Reconstruction from Low-Coverage Short Sequencing Reads -- Gene Networks Viewed through Two Models -- Identifying Evolutionarily Conserved Protein Interaction Modules Using GraphHopper -- The 2-Interval Pattern Matching Problems and Its Application to ncRNA Scanning -- Refereed Papers -- RNA Pseudoknot Folding through Inference and Identification Using TAGRNA -- Comparing Bacterial Genomes by Searching Their Common Intervals -- Generalized Binary Tanglegrams: Algorithms and Applications -- Three-Dimensional Multimodality Modelling by Integration of High-Resolution Interindividual Atlases and Functional MALDI-IMS Data -- Detecting Motifs in a Large Data Set: Applying Probabilistic Insights to Motif Finding -- A Biclustering Method to Discover Co-regulated Genes Using Diverse Gene Expression Datasets -- Computational Protocol for Screening GPI-anchored Proteins -- Towards Large-Scale Molecular Dynamics Simulations on Graphics Processors -- An Agent-Based Model of Solid Tumor Progression -- Deciphering Drug Action and Escape Pathways: An Example on Nasopharyngeal Carcinoma -- Selection of Multiple SNPs in Case-Control Association Study Using a Discretized Network Flow Approach -- Biclustering Expression Data Based on Expanding Localized Substructures -- Constrained Fisher Scores Derived from Interaction Profile Hidden Markov Models Improve Protein to Protein InteractionPrediction -- Improving Protein Localization Prediction Using Amino Acid Group Based Physichemical Encoding -- The Impact of Gene Selection on Imbalanced Microarray Expression Data -- Spatial Information and Boolean Genetic Regulatory Networks -- Modeling of Genetic Regulatory Network in Stochastic ?-Calculus -- fMRI Activation Detection by MultiScale Hidden Markov Model -- cnF2freq: Efficient Determination of Genotype and Haplotype Probabilities in Outbred Populations Using Markov Models -- A Comprehensive Analysis Workflow for Genome-Wide Screening Data from ChIP-Sequencing Experiments -- A Fitness Distance Correlation Measure for Evolutionary Trees -- Alignment and Analysis of Closely Related Genomes -- Computational Prediction of Genes Translationally Regulated by Cytoplasmic Polyadenylation Elements -- Multiple Sequence Alignment System for Pyrosequencing Reads -- A Bayesian Approach to High-Throughput Biological Model Generation -- Parallel Selection of Informative Genes for Classification -- Simulation Methods in Uncovering New Regulatory Mechanisms in Signaling Pathways -- GridSPiM: A Framework for Simple Locality and Containment in the Stochastic ?-Calculus -- Mutual Information Based Extrinsic Similarity for Microarray Analysis -- Graph Spectral Approach for Identifying Protein Domains.
Sommario/riassunto	This book constitutes the refereed proceedings of the First International on Bioinformatics and Computational Biology, BICoB 2007, held in New Orleans, LA, USA, in April 2007. The 30 revised full papers presented together with 10 invited lectures were carefully reviewed and selected from 72 initial submissions. The papers address current research in the area of bioinformatics and computational biology fostering the advancement of computing techniques and their application to life sciences in topics such as genome analysis sequence analysis, phylogenetics, structural bioinformatics, analysis of high-throughput biological data, genetics and population analysis, as well as systems biology.