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Soggetti	Database management Bioinformatics Medical informatics Artificial intelligence Algorithms Database Management Computational and Systems Biology Health Informatics Artificial Intelligence
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Invited Papers -- Differential Gene Expression in the Auditory System -- Searching for Non-coding RNA -- Cyberinfrastructure for PathoSystems Biology -- Analysis of Genomic Tiling Microarrays for Transcript Mapping and the Identification of Transcription Factor Binding Sites -- Full Papers -- Perturbing Thermodynamically Unfeasible Metabolic Networks -- Protein Cellular Localization with Multiclass Support Vector Machines and Decision Trees -- Combining One-Class Classifiers for Robust Novelty Detection in Gene Expression Data -- Evaluation of the Contents of Partitions Obtained with Clustering Gene Expression Data -- Machine Learning Techniques for Predicting Bacillus subtilis Promoters -- An Improved Hidden Markov

Model Methodology to Discover Prokaryotic Promoters -- Modeling and Property Verification of Lactose Operon Regulation -- YAMONES: A Computational Architecture for Molecular Network Simulation -- Structure Prediction and Docking Studies of Chorismate Synthase from Mycobacterium Tuberculosis -- Analysis of the Effects of Multiple Sequence Alignments in Protein Secondary Structure Prediction -- Tests of Automatic Annotation Using KOG Proteins and ESTs from 4 Eukariotic Organisms -- Diet as a Pressure on the Amino Acid Content of Proteomes -- A Method for Comparing Three Genomes -- Comparison of Genomic DNA to cDNA Alignment Methods -- Segmentation and Centromere Locating Methods Applied to Fish Chromosomes Images -- Extended Abstracts -- Sequence Motif Identification and Protein Family Classification Using Probabilistic Trees -- Prediction of Myotoxic and Neurotoxic Activities in Phospholipases A2 from Primary Sequence Analysis -- Genomics and Gene Expression Management Tools for the Schistosoma Mansoni cDNA Microarray Project -- SAM Method as an Approach to Select Candidates for Human Prostate Cancer Markers -- New EST Trimming Strategy -- A Modification of the Landau-Vishkin Algorithm Computing Longest Common Extensions via Suffix Arrays -- The BioPAUÁ Project: A Portal for Molecular Dynamics Using Grid Environment -- Analysis of Structure Prediction Tools in Mutated MeCP-2 -- Protein Loop Classification Using Artificial Neural Networks -- VIZ – A Graphical Open-Source Architecture for Use in Structural Bioinformatics -- Selection of Data Sets of Motifs as Attributes in the Process of Automating the Annotation of Proteins' Keywords -- Bioinformatics Tools for HIV-1 Identification in Southern Brazilian States -- Fact and Task Oriented System for Genome Assembly and Annotation -- A Clustering Strategy to Find Similarities in Mycoplasma Promoters -- Gene Prediction by Syntenic Alignment -- Real Time Immersive Visualization and Manipulation of the Visible Human Data Set.

Sommario/riassunto

This book constitutes the refereed proceedings of the Brazilian Symposium on Bioinformatics, BSB 2005, held in Sao Leopoldo, Brazil in July 2005. The 15 revised full papers and 10 revised extended abstracts presented together with 3 invited papers were carefully reviewed and selected from 55 submissions. The papers address a broad range of current topics in computational biology and bioinformatics.
