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	Nota di contenuto	Algorithmic Approaches for Molecular Biology Problems -- Genotype Tagging with Limited Overfitting -- Constraint Programming Models for Transposition Distance Problem -- Comparison of Spectra in Unsequenced Species -- Micro-array Analysis -- BiHEA: A Hybrid Evolutionary Approach for Microarray Biclustering -- Using Supervised Complexity Measures in the Analysis of Cancer Gene Expression Data

Sets -- Quantitative Improvements in cDNA Microarray Spot Segmentation -- Machine Learning Methods for Classification -- SOM-PORTRAIT: Identifying Non-coding RNAs Using Self-Organizing Maps -- Automatic Classification of Enzyme Family in Protein Annotation -- Representations for Evolutionary Algorithms Applied to Protein Structure Prediction Problem Using HP Model -- Comparing Methods for Multilabel Classification of Proteins Using Machine Learning Techniques -- Comparative Study of Classification Algorithms Using Molecular Descriptors in Toxicological DataBases -- In Silico Simulation -- Influence of Antigenic Mutations in Time Evolution of the Immune Memory – A Dynamic Modeling -- Short Papers -- FReDD: Supporting Mining Strategies through a Flexible-Receptor Docking Database -- A Wide Antimicrobial Peptides Search Method Using Fuzzy Modeling -- Identification of Proteins from Tuberculin Purified Protein Derivative (PPD) with Potential for TB Diagnosis Using Bioinformatics Analysis -- Mapping HIV-1 Subtype C gp120Epitopes Using a Bioinformatic Approach -- MHC: Peptide Analysis: Implications on the Immunogenicity of Hantaviruses' N protein -- An Ontology to Integrate Transcriptomics and Interatomics Data Involved in Gene Pathways of Genome Stability.

Sommario/riassunto	This book constitutes the refereed proceedings of the 4th Brazilian Symposium on Bioinformatics, BSB 2009, held in Porto Alegre, Brazil, in July 2009 The 12 revised full papers and 6 extended abstracts were carefully reviewed and selected from 55 submissions. The papers are organized in topical sections on algorithmic approaches for molecular biology problems; micro-array analysis; machine learning methods for classification; and in silico simulation.