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Nota di contenuto	Selected Articles -- Multi-label Hierarchical Classification of Protein Functions with Artificial Immune Systems -- Operon Prediction in Bacterial Genomes -- An Evaluation of the Impact of Side Chain Positioning on the Accuracy of Discrete Models of Protein Structures -- Top-Down Hierarchical Ensembles of Classifiers for Predicting G-Protein-Coupled-Receptor Functions -- A Hybrid Method for the Protein Structure Prediction Problem -- Detecting Statistical Covariations of Sequence Physicochemical Properties -- Molecular Models to Emulate Confinement Effects on the Internal Dynamics of Organophosphorous Hydrolase -- On the Toric Graph as a Tool to Handle the Problem of Sorting by Transpositions -- A Customized Class of Functions for Modeling and Clustering Gene Expression Profiles in Embryonic Stem Cells -- Extracting Information from Flexible Receptor-Flexible Ligand Docking Experiments -- Transposition Distance Based on the Algebraic Formalism -- Using BioAgents for Supporting Manual Annotation on Genome Sequencing Projects -- Application of Genetic Algorithms to the Genetic Regulation Problem --

Tests for Gene Clusters Satisfying the Generalized Adjacency Criterion
-- Extended Abstracts -- Identity Transposon Networks in D.
melanogaster -- Prediction of Protein-Protein Binding Hot Spots: A
Combination of Classifiers Approach -- AGN Simulation and Validation
Model -- A Practical Evaluation of BioProvider -- Evaluation of Models
for the Recognition of Handwritten Digits in Medical Forms.

Sommario/riassunto

This book constitutes the refereed proceedings of the Third Brazilian Symposium on Bioinformatics, BSB 2008, held in Sao Paulo, Brazil, in August 2008 - co-located with IWGD 2008, the International Workshop on Genomic Databases. The 14 revised full papers and 5 extended abstracts were carefully reviewed and selected from 41 submissions. The papers address a broad range of current topics in computational biology and bioinformatics featuring original research in computer science, mathematics and statistics as well as in molecular biology, biochemistry, genetics, medicine, microbiology and other life sciences.
