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Soggetti	Bioinformatics Health informatics Pattern recognition Data mining Algorithms Artificial intelligence Computational Biology/Bioinformatics Health Informatics Pattern Recognition Data Mining and Knowledge Discovery Algorithm Analysis and Problem Complexity Artificial Intelligence
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Nota di contenuto	Robust Community Detection Methods with Resolution Parameter for Complex Detection in Protein Protein Interaction Networks -- Machine Learning Scoring Functions Based on Random Forest and Support Vector Regression -- A Genetic Algorithm for Scale-Based Translocon Simulation -- A Framework of Gene Subset Selection Using Multiobjective Evolutionary Algorithm -- Multiple Tree Alignment with Weights Applied to Carbohydrates to Extract Binding Recognition Patterns -- A Unified Adaptive Co-identification Framework for High-D

	Expression Data -- Protein Clustering on a Grassmann Manifold -- Improving the Portability and Performance of jViz.RNA – A Dynamic RNA Visualization Software -- A Novel Machine Learning Approach for Detecting the Brain Abnormalities from MRI Structural Images -- An Open Framework for Extensible Multi-stage Bioinformatics Software -- An Algorithm to Assemble Gene-Protein Reaction Associations for Genome-Scale Metabolic Model Reconstruction -- A Machine Learning and Chemometrics Assisted Interpretation of Spectroscopic Data – A NMR-Based Metabolomics Platform for the Assessment of Brazilian -- Principal Component Analysis for Bacterial Proteomic Analysis -- Application of the Multi-modal Relevance Vector Machine to the Problem of Protein Secondary Structure Prediction -- Cascading Discriminant and Generative Models for Protein Secondary Structure Prediction -- Improvement of the Protein–Protein Docking Prediction by Introducing a Simple Hydrophobic Interaction Model: An Application to Interaction Pathway Analysis -- Representation of Protein Secondary Structure Using Bond-Orientational Order Parameters -- Diagnose the Premalignant Pancreatic Cancer Using High Dimensional Linear Machine -- Predicting V(D)J Recombination Using Conditional Random Fields -- A Simple Genetic Algorithm for Biomarker Mining -- Finding Conserved Regions in Protein Structures Using Support Vector Machines and Structure Alignment -- Aligning Discovered Patterns from Protein Family Sequences -- Application of the Burrows-Wheeler Transform for Searching for Approximate Tandem Repeats -- Pattern Recognition for Subfamily Level Classification of GPCRs Using Motif Distillation and Distinguishing Power Evaluation.
Sommario/riassunto	This book constitutes the refereed proceedings of the 7th International Conference on Pattern Recognition in Bioinformatics, PRIB 2012, held in Tokyo, Japan, in November 2012. The 24 revised full papers presented were carefully reviewed and selected from 33 submissions. Their topics are widely ranging from fundamental techniques, sequence analysis to biological network analysis. The papers are organized in topical sections on generic methods, visualization, image analysis, and platforms, applications of pattern recognition techniques, protein structure and docking, complex data analysis, and sequence analysis.