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Nota di contenuto	A Hybrid Random Subspace Classifier Fusion Approach for Protein Mass Spectra Classification -- Using Ant Colony Optimization-Based Selected Features for Predicting Post-synaptic Activity in Proteins -- Generating Linkage Disequilibrium Patterns in Data Simulations Using genomeSIMLA -- DEEPER: A Full Parsing Based Approach to Protein Relation Extraction -- Improving the Performance of Hierarchical Classification with Swarm Intelligence -- Protein Interaction Inference Using Particle Swarm Optimization Algorithm -- Divide, Align and Full-Search for Discovering Conserved Protein Complexes -- Detection of Quantitative Trait Associated Genes Using Cluster Analysis -- Frequent Subsplit Representation of Leaf-Labelled Trees -- Inference on Missing Values in Genetic Networks Using High-Throughput Data -- Mining Gene Expression Patterns for the Discovery of Overlapping Clusters -- Development and Evaluation of an Open-Ended Computational Evolution System for the Genetic Analysis of Susceptibility to Common

Human Diseases -- Gene Selection and Cancer Microarray Data Classification Via Mixed-Integer Optimization -- Detection of Protein Complexes in Protein Interaction Networks Using n-Clubs -- Learning Gaussian Graphical Models of Gene Networks with False Discovery Rate Control -- Enhancing Parameter Estimation of Biochemical Networks by Exponentially Scaled Search Steps -- A Wrapper-Based Feature Selection Method for ADMET Prediction Using Evolutionary Computing -- On the Convergence of Protein Structure and Dynamics. Statistical Learning Studies of Pseudo Folding Pathways.