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Nota di contenuto	Variable Genetic Operator Search for the Molecular Docking Problem -- Variable Genetic Operator Search for the Molecular Docking Problem -- Role of Centrality in Network-Based Prioritization of Disease Genes -- Parallel Multi-Objective Approaches for Inferring Phylogenies -- An Evolutionary Model Based on Hill-Climbing Search Operators for Protein Structure Prediction -- Finding Gapped Motifs by a Novel Evolutionary Algorithm -- Top-Down Induction of Phylogenetic Trees -- A Model

Free Method to Generate Human Genetics Datasets with Complex Gene-Disease Relationships -- Grammatical Evolution of Neural Networks for Discovering Epistasis among Quantitative Trait Loci -- Grammatical Evolution Decision Trees for Detecting Gene-Gene Interactions -- Identification of Individualized Feature Combinations for Survival Prediction in Breast Cancer: A Comparison of Machine Learning Techniques -- Correlation-Based Scatter Search for Discovering Biclusters from Gene Expression Data -- A Local Search Approach for Transmembrane Segment and Signal Peptide Discrimination -- A Replica Exchange Monte Carlo Algorithm for the Optimization of Secondary Structure Packing in Proteins -- Improving Multi-Relief for Detecting Specificity Residues from Multiple Sequence Alignments -- Using Probabilistic Dependencies Improves the Search of Conductance-Based Compartmental Neuron Models -- Posters -- The Informative Extremes: Using Both Nearest and Farthest Individuals Can Improve Relief Algorithms in the Domain of Human Genetics -- Artificial Immune Systems for Epistasis Analysis in Human Genetics -- Metaheuristics for Strain Optimization Using Transcriptional Information Enriched Metabolic Models -- Using Rotation Forest for Protein Fold Prediction Problem: An Empirical Study -- Towards Automatic Detecting of Overlapping Genes - Clustered BLAST Analysis of Viral Genomes -- Investigating Populational Evolutionary Algorithms to Add Vertical Meaning in Phylogenetic Trees.
