

1. Record Nr.	UNISA996465893203316
Titolo	Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics [[electronic resource]] : 8th European Conference, EvoBIO 2010, Istanbul, Turkey, April 7-9, 2010, Proceedings // edited by Clara Pizzuti, Marylyn D. Ritchie, Mario Giacobini
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2010
ISBN	1-280-38605-3 9786613563972 3-642-12211-6
Edizione	[1st ed. 2010.]
Descrizione fisica	1 online resource (XII, 249 p. 63 illus.)
Collana	Theoretical Computer Science and General Issues, , 2512-2029 ; ; 6023
Classificazione	BIO 110f DAT 708f MAT 919f SS 4800 WC 7700
Disciplina	006.3
Soggetti	Bioinformatics Algorithms Database management Artificial intelligence Computer science Artificial intelligence—Data processing Computational and Systems Biology Database Management Artificial Intelligence Theory of Computation Data Science
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di bibliografia	Includes bibliographical references and index.
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.
