

1. Record Nr.	UNISA996466257903316
Titolo	Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics [[electronic resource]] : 5th European Conference, EvoBIO 2007, Valencia, Spain, April 11-13, 2007, Proceedings / / edited by Elena Marchiori, Jason H. Moore, Jagath C. Rajapakse
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2007
ISBN	3-540-71783-8
Edizione	[1st ed. 2007.]
Descrizione fisica	1 online resource (XI, 302 p.)
Collana	Theoretical Computer Science and General Issues, , 2512-2029 ; ; 4447
Disciplina	572.80285/6
Soggetti	Artificial intelligence Computer programming Computer science Algorithms Bioinformatics Pattern recognition systems Artificial Intelligence Programming Techniques Theory of Computation Computational and Systems Biology Automated Pattern Recognition
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	Identifying Regulatory Sites Using Neighborhood Species -- Genetic Programming and Other Machine Learning Approaches to Predict Median Oral Lethal Dose (LD50) and Plasma Protein Binding Levels (% PPB) of Drugs -- Hypothesis Testing with Classifier Systems for Rule-Based Risk Prediction -- Robust Peak Detection and Alignment of nanoLC-FT Mass Spectrometry Data -- One-Versus-One and One-Versus-All Multiclass SVM-RFE for Gene Selection in Cancer Classification -- Understanding Signal Sequences with Machine Learning -- Targeting Differentially Co-regulated Genes by Multiobjective and Multimodal Optimization -- Modeling Genetic

Networks: Comparison of Static and Dynamic Models -- A Genetic Embedded Approach for Gene Selection and Classification of Microarray Data -- Modeling the Shoot Apical Meristem in *A. thaliana*: Parameter Estimation for Spatial Pattern Formation -- Evolutionary Search for Improved Path Diagrams -- Simplifying Amino Acid Alphabets Using a Genetic Algorithm and Sequence Alignment -- Towards Evolutionary Network Reconstruction Tools for Systems Biology -- A Gaussian Evolutionary Method for Predicting Protein-Protein Interaction Sites -- Bio-mimetic Evolutionary Reverse Engineering of Genetic Regulatory Networks -- Tuning ReliefF for Genome-Wide Genetic Analysis -- Dinucleotide Step Parameterization of Pre-miRNAs Using Multi-objective Evolutionary Algorithms -- Amino Acid Features for Prediction of Protein-Protein Interface Residues with Support Vector Machines -- Predicting HIV Protease-Cleavable Peptides by Discrete Support Vector Machines -- Inverse Protein Folding on 2D Off-Lattice Model: Initial Results and Perspectives -- Virtual Error: A New Measure for Evolutionary Biclustering -- Characterising DNA/RNA Signals with Crisp Hypermotifs: A Case Study on Core Promoters -- Evaluating Evolutionary Algorithms and Differential Evolution for the Online Optimization of Fermentation Processes -- The Role of a Priori Information in the Minimization of Contact Potentials by Means of Estimation of Distribution Algorithms -- Classification of Cell Fates with Support Vector Machine Learning -- Reconstructing Linear Gene Regulatory Networks -- Individual-Based Modeling of Bacterial Foraging with Quorum Sensing in a Time-Varying Environment -- Substitution Matrix Optimisation for Peptide Classification.

2. Record Nr.	UNINA9910691643103321
Autore	Brunner Daniel
Titolo	Enhanced gob gas recovery [[electronic resource]]
Pubbl/distr/stampa	[Washington, D.C.] : , : [U.S. Environmental Protection Agency], , [2000]
Soggetti	Coal mine waste - United States Longwall mining - United States
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	"June, 2000." Title from title screen.