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	Nota di contenuto	Association Study between Gene Expression and Multiple Relevant Phenotypes with Cluster Analysis -- Gaussian Graphical Models to Infer Putative Genes Involved in Nitrogen Catabolite Repression in S. cerevisiae -- Chronic Rat Toxicity Prediction of Chemical Compounds Using Kernel Machines -- Simulating Evolution of Drosophila Melanogaster Ebony Mutants Using a Genetic Algorithm -- Microarray Biclustering: A Novel Memetic Approach Based on the PISA Platform -- F-score with Pareto Front Analysis for Multiclass Gene Selection -- A Hierarchical Classification Ant Colony Algorithm for Predicting Gene Ontology Terms -- Conquering the Needle-in-a-Haystack: How

	Correlated Input Variables Beneficially Alter the Fitness Landscape for Neural Networks -- Optimal Use of Expert Knowledge in Ant Colony Optimization for the Analysis of Epistasis in Human Disease -- On the Efficiency of Local Search Methods for the Molecular Docking Problem -- A Comparison of Genetic Algorithms and Particle Swarm Optimization for Parameter Estimation in Stochastic Biochemical Systems -- Guidelines to Select Machine Learning Scheme for Classification of Biomedical Datasets -- Evolutionary Approaches for Strain Optimization Using Dynamic Models under a Metabolic Engineering Perspective -- Clustering Metagenome Short Reads Using Weighted Proteins -- A Memetic Algorithm for Phylogenetic Reconstruction with Maximum Parsimony -- Validation of a Morphogenesis Model of Drosophila Early Development by a Multi-objective Evolutionary Optimization Algorithm -- Refining Genetic Algorithm Based Fuzzy Clustering through Supervised Learning for Unsupervised Cancer Classification.
Sommario/riassunto	This book constitutes the refereed proceedings of the 7th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2009, held in Tübingen, Germany, in April 2009 colocated with the Evo* 2009 events. The 17 revised full papers were carefully reviewed and selected from 44 submissions. EvoBio is the premiere European event for experts in computer science meeting with experts in bioinformatics and the biological sciences, all interested in the interface between evolutionary computation, machine learning, data mining, bioinformatics, and computational biology. Topics addressed by the papers include biomarker discovery, cell simulation and modeling, ecological modeling, uxomics, gene networks, biotechnology, metabolomics, microarray analysis, phylogenetics, protein interactions, proteomics, sequence analysis and alignment, as well as systems biology.