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Nota di contenuto	Multiple Threshold Spatially Uniform ReliefF for the Genetic Analysis of Complex Human Diseases -- Time-Point Specific Weighting Improves Coexpression Networks from Time-Course Experiments -- Inferring Human Phenotype Networks from Genome-Wide Genetic -- Knowledge-Constrained K-Medoids Clustering of Regulatory Rare Alleles for Burden Tests -- Feature Selection and Classification of High Dimensional Mass Spectrometry Data: A Genetic Programming Approach -- Structured Populations and the Maintenance of Sex -- Hybrid Multiobjective Artificial Bee Colony with Differential Evolution Applied to Motif Finding -- ACO-Based Bayesian Network Ensembles for the Hierarchical Classification of Ageing-Related Proteins -- Dimensionality Reduction via Isomap with Lock-Step and Elastic Measures for Time Series Gene Expression Classification -- Supervising Random Forest Using Attribute Interaction Networks -- Hybrid Genetic

Algorithms for Stress Recognition in Optimal Use of Biological Expert Knowledge from Literature -- Mining in Ant Colony Optimization for Analysis of Epistasis in Human Disease -- A Multiobjective Proposal Based on the Firefly Algorithm for Inferring Phylogenies -- Mining for Variability in the Coagulation Pathway: A Systems Biology Approach -- Improving the Performance of CGPANN for Breast Cancer Diagnosis Using Crossover and Radial Basis Functions -- An Evolutionary Approach to Wetlands Design -- Impact of Different Recombination Methods in a Mutation-Specific MOEA for a Biochemical Application -- Cell–Based Metrics Improve the Detection of Gene-Gene Interactions Using Multifactor Dimensionality Reduction -- Emergence of Motifs in Model Gene Regulatory Networks.

| Sommario/riassunto | This book constitutes the refereed proceedings of the 11th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2013, held in Vienna, Austria, in April 2013, colocated with the Evo* 2013 events EuroGP, EvoCOP, EvoMUSART and EvoApplications. The 10 revised full papers presented together with 9 poster papers were carefully reviewed and selected from numerous submissions. The papers cover a wide range of topics in the field of biological data analysis and computational biology. They address important problems in biology, from the molecular and genomic dimension to the individual and population level, often drawing inspiration from biological systems in oder to produce solutions to biological problems. |