Table of Contents

Oral Contributions

Multiple Threshold Spatially Uniform ReliefF for the Genetic Analysis of Complex Human Diseases	1
Time-Point Specific Weighting Improves Coexpression Networks from Time-Course Experiments	11
Inferring Human Phenotype Networks from Genome-Wide Genetic Associations	23
Knowledge-Constrained K-Medoids Clustering of Regulatory Rare Alleles for Burden Tests	35
Feature Selection and Classification of High Dimensional Mass Spectrometry Data: A Genetic Programming Approach	43
Structured Populations and the Maintenance of Sex	56
Hybrid Multiobjective Artificial Bee Colony with Differential Evolution Applied to Motif Finding	68
ACO-Based Bayesian Network Ensembles for the Hierarchical Classification of Ageing-Related Proteins	80
Dimensionality Reduction via Isomap with Lock-Step and Elastic Measures for Time Series Gene Expression Classification	92
Supervising Random Forest Using Attribute Interaction Networks Qinxin Pan, Ting Hu, James D. Malley, Angeline S. Andrew, Margaret R. Karagas, and Jason H. Moore	104

Poster Contributions

Nandita Sharma and Tom Gedeon	117
Optimal Use of Biological Expert Knowledge from Literature Mining in Ant Colony Optimization for Analysis of Epistasis in Human Disease	129
Arvis Sulovari, Jeff Kiralis, and Jason H. Moore	
A Multiobjective Proposal Based on the Firefly Algorithm for Inferring Phylogenies	141
Mining for Variability in the Coagulation Pathway: A Systems Biology Approach	153
Improving the Performance of CGPANN for Breast Cancer Diagnosis Using Crossover and Radial Basis Functions Timmy Manning and Paul Walsh	165
An Evolutionary Approach to Wetlands Design	177
Impact of Different Recombination Methods in a Mutation-Specific MOEA for a Biochemical Application	188
Cell-Based Metrics Improve the Detection of Gene-Gene Interactions Using Multifactor Dimensionality Reduction	200
Emergence of Motifs in Model Gene Regulatory Networks	212
Author Index	217