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Nota di contenuto	GFBA: A Biclustering Algorithm for Discovering Value-Coherent Biclusters -- Significance Analysis of Time-Course Gene Expression Profiles -- Data-Driven Smoothness Enhanced Variance Ratio Test to Unearth Responsive Genes in 0-Time Normalized Time-Course Microarray Data -- Efficiently Finding the Most Parsimonious Phylogenetic Tree Via Linear Programming -- A Multi-Stack Based Phylogenetic Tree Building Method -- A New Linear-Time Heuristic Algorithm for Computing the Parsimony Score of Phylogenetic Networks: Theoretical Bounds and Empirical Performance -- A Bootstrap Correspondence Analysis for Factorial Microarray Experiments with Replications -- Clustering Algorithms Optimizer: A Framework for Large Datasets -- Ranking Function Based on Higher Order Statistics (RF-HOS) for Two-Sample Microarray Experiments -- Searching for Recombinant Donors in a Phylogenetic Network of Serial Samples -- Algorithm for Haplotype Inferring Via Galled-Tree Networks with Simple Galls -- Estimating Bacterial Diversity from Environmental DNA: A Maximum Likelihood Approach -- Invited Talk: Modern Homology Search -- Statistical Absolute Evaluation of Gene Ontology Terms with Gene Expression Data -- Discovering Relations Among GO-Annotated Clusters by Graph Kernel Methods -- An Empirical Comparison of Dimensionality Reduction Methods for Classifying Gene

and Protein Expression Datasets -- NEURONgrid: A Toolkit for Generating Parameter-Space Maps Using NEURON in a Grid Environment -- An Adaptive Resolution Tree Visualization of Large Influenza Virus Sequence Datasets -- Wavelet Image Interpolation (WII): A Wavelet-Based Approach to Enhancement of Digital Mammography Images -- High Level Programming Environment System for Protein Structure Data -- Finding Minimal Sets of Informative Genes in Microarray Data -- Noise-Based Feature Perturbation as a Selection Method for Microarray Data -- Efficient Generation of Biologically Relevant Enriched Gene Sets -- Space and Time Efficient Algorithms to Discover Endogenous RNAi Patterns in Complete Genome Data -- A Fast Approximate Covariance-Model-Based Database Search Method for Non-coding RNA -- Extensions of Naive Bayes and Their Applications to Bioinformatics -- The Solution Space of Sorting by Reversals -- A Fast and Exact Algorithm for the Perfect Reversal Median Problem -- Genomic Signatures from DNA Word Graphs -- Enhancing Motif Refinement by Incorporating Comparative Genomics Data -- Mining Discriminative Distance Context of Transcription Factor Binding Sites on ChIP Enriched Regions -- Enhanced Prediction of Cleavage in Bovine Precursor Sequences -- Invited Talk: A Computational Study of Bidirectional Promoters in the Human Genome -- The Identification of Antisense Gene Pairs Through Available Software -- Inferring Weak Adaptations and Selection Biases in Proteins from Composition and Substitution Matrices -- Markov Model Variants for Appraisal of Coding Potential in Plant DNA -- Predicting Palmitoylation Sites Using a Regularised Bio-basis Function Neural Network -- A Novel Kernel-Based Approach for Predicting Binding Peptides for HLA Class II Molecules -- A Database for Prediction of Unique Peptide Motifs as Linear Epitopes -- A Novel Greedy Algorithm for the Minimum Common String Partition Problem -- An Efficient Algorithm for Finding Gene-Specific Probes for DNA Microarrays -- Multiple Sequence Local Alignment Using Monte Carlo EM Algorithm -- Cancer Class Discovery Using Non-negative Matrix Factorization Based on Alternating Non-negativity-Constrained Least Squares -- A Support Vector Machine Ensemble for Cancer Classification Using Gene Expression Data -- Combining SVM Classifiers Using Genetic Fuzzy Systems Based on AUC for Gene Expression Data Analysis -- A BP-SCFG Based Approach for RNA Secondary Structure Prediction with Consecutive Bases Dependency and Their Relative Positions Information -- Delta: A Toolset for the Structural Analysis of Biological Sequences on a 3D Triangular Lattice -- Statistical Estimate for the Size of the Protein Structural Vocabulary -- Co-clustering Based Parcellation of Human Brain Cortex Using Diffusion Tensor MRI -- An Algorithm for Hierarchical Classification of Genes of Prokaryotic Genomes -- Using Multi Level Nearest Neighbor Classifiers for G-Protein Coupled Receptor Sub-families Prediction -- Invited Talk: Ab Initio Gene Finding Engines: What Is Under the Hood -- Reconstruction of 3D Structures from Protein Contact Maps -- A Feature Selection Algorithm Based on Graph Theory and Random Forests for Protein Secondary Structure Prediction -- DNA Sites Buried in Nucleosome Become Accessible at Room Temperature: A Discrete-Event-Simulation Based Modeling Approach -- Comparative Analysis of Gene-Coexpression Networks Across Species -- Comparative Pathway Prediction Via Unified Graph Modeling of Genomic Structure Information -- Extending the Calculus of Looping Sequences to Model Protein Interaction at the Domain Level.
