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	Nota di contenuto	Classification of Biological Sequences -- Sequence-Based Prediction of Protein Secretion Success in Aspergillus niger -- Machine Learning Study of DNA Binding by Transcription Factors from the LacI Family -- Joint Loop End Modeling Improves Covariance Model Based Non-coding RNA Gene Search -- Structured Output Prediction of Anti-cancer Drug Activity -- SLiMSearch: A Webserver for Finding Novel Occurrences of Short Linear Motifs in Proteins, Incorporating Sequence Context -- Towards 3D Modeling of Interacting TM Helix Pairs Based on Classification of Helix Pair Sequence -- Optimization Algorithms for Identification and Genotyping of Copy Number Polymorphisms in Human Populations -- Preservation of Statistically Significant Patterns in Multiresolution 0-1 Data -- Novel Machine Learning Methods for MHC Class I Binding Prediction -- Unsupervised Learning Methods for Biological Sequences -- SIMCOMP: A Hybrid Soft Clustering of Metagenome Reads -- The Complexity and Application of Syntactic Pattern Recognition Using Finite Inductive Strings -- An Algorithm to

Find All Identical Motifs in Multiple Biological Sequences -- Discovery of Non-induced Patterns from Sequences -- Exploring Homology Using the Concept of Three-State Entropy Vector -- A Maximum-Likelihood Formulation and EM Algorithm for the Protein Multiple Alignment Problem -- Polynomial Supertree Methods Revisited -- Enhancing Graph Database Indexing by Suffix Tree Structure -- Learning Methods for Gene Expression and Mass Spectrometry Data -- Semi-Supervised Graph Embedding Scheme with Active Learning (SSGEAL): Classifying High Dimensional Biomedical Data -- Iterated Local Search for Biclustering of Microarray Data -- Biologically-aware Latent Dirichlet Allocation (BaLDA) for the Classification of Expression Microarray -- Measuring the Quality of Shifting and Scaling Patterns in Biclusters -- Frequent Episode Mining to Support Pattern Analysis in Developmental Biology -- Time Series Gene Expression Data Classification via L 1-norm Temporal SVM -- Bioimaging -- Sub-grid and Spot Detection in DNA Microarray Images Using Optimal Multi-level Thresholding -- Quantification of Cytoskeletal Protein Localization from High-Content Images -- Pattern Recognition for High Throughput Zebrafish Imaging Using Genetic Algorithm Optimization -- Consensus of Ambiguity: Theory and Application of Active Learning for Biomedical Image Analysis -- Semi-supervised Learning of Sparse Linear Models in Mass Spectral Imaging -- Molecular Structure Prediction -- A Matrix Algorithm for RNA Secondary Structure Prediction -- Exploiting Long-Range Dependencies in Protein ?-Sheet Secondary Structure Prediction -- Alpha Helix Prediction Based on Evolutionary Computation -- An On/Off Lattice Approach to Protein Structure Prediction from Contact Maps -- Protein Protein Interaction and Network Inference -- Biological Protein-Protein Interaction Prediction Using Binding Free Energies and Linear Dimensionality Reduction -- Employing Publically Available Biological Expert Knowledge from Protein-Protein Interaction Information -- SFFS-MR: A Floating Search Strategy for GRNs Inference -- Revisiting the Voronoi Description of Protein-Protein Interfaces: Algorithms -- MC4: A Tempering Algorithm for Large-Sample Network Inference -- Flow-Based Bayesian Estimation of Nonlinear Differential Equations for Modeling Biological Networks.