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Soggetti	Bioinformatics Pattern recognition systems Artificial intelligence Data mining Radiology Computational and Systems Biology Automated Pattern Recognition Artificial Intelligence Data Mining and Knowledge Discovery
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Nota di bibliografia	Includes bibliographical references at the end of each chapters and index.
Nota di contenuto	Introduction to Pattern Recognition and Bioinformatics -- Part I Classification -- Neural Network Tree for Identification of Splice Junction and Protein Coding Region in DNA -- Design of String Kernel to Predict Protein Functional Sites Using Kernel-Based Classifiers -- Part II Feature Selection -- Rough Sets for Selection of Molecular Descriptors to Predict Biological Activity of Molecules -- f -Information Measures for Selection of Discriminative Genes from Microarray Data -- Identification of Disease Genes Using Gene Expression and Protein-Protein Interaction Data -- Rough Sets for Insilico Identification of Differentially Expressed miRNAs -- Part III Clustering -- Grouping

Functionally Similar Genes from Microarray Data Using Rough-Fuzzy Clustering -- Mutual Information Based Supervised Attribute Clustering for Microarray Sample Classification -- Possibilistic Biclustering for Discovering Value-Coherent Overlapping d -Biclusters -- Fuzzy Measures and Weighted Co-Occurrence Matrix for Segmentation of Brain MR Images.

Sommario/riassunto

Recent advances in high-throughput technologies have resulted in a deluge of biological information. Yet the storage, analysis, and interpretation of such multifaceted data require effective and efficient computational tools. This unique text/reference addresses the need for a unified framework describing how soft computing and machine learning techniques can be judiciously formulated and used in building efficient pattern recognition models. The book reviews both established and cutting-edge research, following a clear structure reflecting the major phases of a pattern recognition system: classification, feature selection, and clustering. The text provides a careful balance of theory, algorithms, and applications, with a particular emphasis given to applications in computational biology and bioinformatics. Topics and features: Reviews the development of scalable pattern recognition algorithms for computational biology and bioinformatics Integrates different soft computing and machine learning methodologies with pattern recognition tasks Discusses in detail the integration of different techniques for handling uncertainties in decision-making and efficiently mining large biological datasets Presents a particular emphasis on real-life applications, such as microarray expression datasets and magnetic resonance images Includes numerous examples and experimental results to support the theoretical concepts described Concludes each chapter with directions for future research and a comprehensive bibliography This important work will be of great use to graduate students and researchers in the fields of computer science, electrical and biomedical engineering. Researchers and practitioners involved in pattern recognition, machine learning, computational biology and bioinformatics, data mining, and soft computing will also find the book invaluable.