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Nota di contenuto	KNOWLEDGE DISCOVERY IN BIOINFORMATICS; CONTENTS; Contributors; Preface; 1 Current Methods for Protein Secondary-Structure Prediction Based on Support Vector Machines; 1.1 Traditional Methods; 1.1.1 Statistical Approaches; 1.1.2 Machine Learning Approaches; 1.2 Support Vector Machine Method; 1.2.1 Introduction to SVM; 1.2.2 Encoding Profile; 1.2.3 Kernel Functions; 1.2.4 Tertiary Classifier Design; 1.2.5 Accuracy Measure of SVM; 1.3 Performance Comparison of SVM Methods; 1.4 Discussion and Conclusions; References; 2 Comparison of Seven Methods for Mining Hidden Links 2.1 Analysis of the Literature on Raynaud's Disease2.2 Related Work; 2.3 Methods; 2.3.1 Information Measures; 2.3.2 Ranking Methods; 2.3.3 Seven Methods; 2.4 Experiment Results and Analysis; 2.4.1 Data Set; 2.4.2 Chi-Square, Chi-Square Association Rule, and Mutual Information Link ABC Methods Compared; 2.4.3 Chi-Square ABC Method: Semantic Check for Mining Implicit Connections; 2.4.4 Chi-Square and Mutual Information Link ABC Methods; 2.5 Discussion and

Conclusions; Acknowledgments; References; 3 Voting Scheme-Based Evolutionary Kernel Machines for Drug Activity Comparisons
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5.3.1 Microarray Data Descriptions5.3.2 Gene Selection Approaches; 5.3.3 Experimental Results; 5.4 Conclusions and Discussion; Acknowledgments; References; 6 Patient Survival Prediction from Gene Expression Data; 6.1 General Methods; 6.1.1 Kaplan-Meier Survival Analysis; 6.1.2 Cox Proportional-Hazards Regression; 6.2 Applications; 6.2.1 Diffuse Large-B-Cell Lymphoma; 6.2.2 Lung Adenocarcinoma; 6.2.3 Remarks; 6.3 Incorporating Data Mining Techniques to Survival Prediction; 6.3.1 Gene Selection by Statistical Properties; 6.3.2 Cancer Subtype Identification via Survival Information
6.4 Selection of Extreme Patient Samples

Sommario/riassunto

The purpose of this edited book is to bring together the ideas and findings of data mining researchers and bioinformaticians by discussing cutting-edge research topics such as, gene expressions, protein/RNA structure prediction, phylogenetics, sequence and structural motifs, genomics and proteomics, gene findings, drug design, RNAi and microRNA analysis, text mining in bioinformatics, modelling of biochemical pathways, biomedical ontologies, system biology and pathways, and biological database management.