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Nota di contenuto	Preface. -- Contributors. -- 1. Qualitative Knowledge Models in Functional Genomics and Proteomics (Mor Peleg, Irene S. Gabashvili, and Russ B. Altman). -- 1.1. Introduction. -- 1.2. Methods and Tools. -- 1.3. Modeling Approach and Results. -- 1.4. Discussion. -- 1.5. Conclusion. -- References. -- 2. Interpreting Microarray Data and Related Applications Using Nonlinear System Identification (Michael Korenberg). -- 2.1. Introduction. -- 2.2. Background. -- 2.3. Parallel Cascade Identification. -- 2.4. Constructing Class Predictors. -- 2.5. Prediction Based on Gene Expression Profiling. -- 2.6. Comparing Different Predictors Over the Same Data Set. -- 2.7. Concluding Remarks. -- References. -- 3. Gene Regulation Bioinformatics of Microarray Data (Gert Thijs, Frank De Smet, Yves Moreau, Kathleen Marchal, and Bart De Moor). -- 3.1. Introduction. -- 3.2. Introduction to Transcriptional Regulation. -- 3.3. Measuring Gene Expression Profiles. -- 3.4. Preprocessing of Data. -- 3.5. Clustering of Gene

Expression Profiles. -- 3.6. Cluster Validation. -- 3.7. Searching for Common Binding Sites of Coregulated Genes. -- 3.8. Inclusive: Online Integrated Analysis of Microarray Data. -- 3.9. Further Integrative Steps. -- 3.10. Conclusion. -- References. -- 4. Robust Methods for Microarray Analysis (George S. Davidson, Shawn Martin, Kevin W. Boyack, Brian N. Wylie, Juanita Martinez, Anthony Aragon, Margaret Werner-Washburne, Monica Mosquera-Caro, and Cheryl Willman). -- 4.1. Introduction. -- 4.2. Microarray Experiments and Analysis Methods. -- 4.3. Unsupervised Methods. -- 4.4. Supervised Methods. -- 4.5. Conclusion. -- References. -- 5. In Silico Radiation Oncology: A Platform for Understanding Cancer Behavior and Optimizing Radiation Therapy Treatment (G. Stamatakis, D. Dionysiou, and N. Uzunoglu). -- 5.1. Philosophiae Tumoralis Principia Algorithmica: Algorithmic Principles of Simulating Cancer on Computer. -- 5.2. Brief Literature Review. -- 5.3. Paradigm of Four-Dimensional Simulation of Tumor Growth and Response to Radiation Therapy In Vivo. -- 5.4. Discussion. -- 5.5. Future Trends. -- References. -- 6. Genomewide Motif Identification Using a Dictionary Model (Chiara Sabatti and Kenneth Lange). -- 6.1. Introduction. -- 6.2. Unified Model. -- 6.3. Algorithms for Likelihood Evaluation. -- 6.4. Parameter Estimation via Minorization-Maximization Algorithm. -- 6.5. Examples. -- 6.6. Discussion and Conclusion. -- References. -- 7. Error Control Codes and the Genome (Elebeoba E. May). -- 7.1. Error Control and Communication: A Review. -- 7.3. Reverse Engineering the Genetic Error Control System. -- 7.4. Applications of Biological Coding Theory. -- References. -- 8. Complex Life Science Multidatabase Queries (Zina Ben Miled, Nianhua Li, Yue He, Malika Mahoui, and Omran Bukhres). -- 8.1. Introduction. -- 8.2. Architecture. -- 8.3. Query Execution Plans. -- 8.4. Related Work. -- 8.5. Future Trends. -- References. -- 9. Computational Analysis of Proteins (Dimitrios I. Fotiadis, Yorgos Goletsis, Christos Lampros, and Costas Papaloukas). -- 9.1. Introduction: Definitions. -- 9.2. Databases. -- 9.3. Sequence Motifs and Domains. -- 9.4. Sequence Alignment. -- 9.5. Modeling. -- 9.6. Classification and Prediction. -- 9.7. Natural Language Processing. -- 9.8. Future Trends. -- References. -- 10. Computational Analysis of Interactions Between Tumor and Tumor Suppressor Proteins (E. Pirogova, M. Akay, and I. Cosic). -- 10.1. Introduction. -- 10.2. Methodology: Resonant Recognition Model. -- 10.3. Results and Discussions. -- 10.4. Conclusion. -- References. -- Index. -- About the Editor.

Sommario/riassunto

Current applications and recent advances in genomics and proteomics. Genomics and Proteomics Engineering in Medicine and Biology presents a well-rounded, interdisciplinary discussion of a topic that is at the cutting edge of both molecular biology and bioengineering. Compiling contributions by established experts, this book highlights up-to-date applications of biomedical informatics, as well as advancements in genomics-proteomics areas. Structures and algorithms are used to analyze genomic data and develop computational solutions for pathological understanding. Topics discussed include: . Qualitative knowledge models. Interpreting micro-array data. Gene regulation bioinformatics. Methods to analyze micro-array. Cancer behavior and radiation therapy. Error-control codes and the genome. Complex life science multi-database queries. Computational protein analysis. Tumor and tumor suppressor proteins interactions.
