1.

Record Nr.	UNISA996396168503316
Autore	T. H
Titolo	A true and exact narrative of the proceedings of the Parliaments fleet, against the island of Barbadoes [[electronic resource]] : With the maner of the reducing thereof: together with the submitting of the islands of St. Christophers, Antego, and St. Mevis, to the Commonwealth of England. Written by an eye-witnesse, Mr. T.H. from aboard the Amity, in Carlisle Bay, and sent to a friend in London, to be published for satisfaction, and printed verbatim by the same copy
Pubbl/distr/stampa	London, : printed for Richard Harper in Smithfield, 1652
Descrizione fisica	12 p
Soggetti	Great Britain History, Naval Stuarts, 1603-1714 Early works to 1800 Barbados History Early works to 1800 Antigua History Early works to 1800 Leeward Islands (West Indies) History Early works to 1800
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Reproduction of original in the John Carter Brown Library.
Sommario/riassunto	eebo-0114

2.	Record Nr.	UNINA9910830613203321
	Titolo	Genomics and proteomics engineering in medicine and biology [[electronic resource] /] / edited by Metin Akay
	Pubbl/distr/stampa	Piscataway, New Jersey : , : IEEE Press, , c2007
	ISBN	1-280-73984-3 9786610739844 0-470-05219-8 1-60119-504-4 0-470-05218-X
	Descrizione fisica	1 online resource (317 p.)
	Collana	IEEE press series on biomedical engineering ; ; 25
	Altri autori (Persone)	AkayMetin
	Disciplina	572.86 572/.6 660.65
	Soggetti	Proteomics Genomics Bioinformatics
	Lingua di pubblicazione	Inglese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Note generali	"IEEE Engineering in Medicine and Biology Society, sponsor."
	Nota di bibliografia	Includes bibliographical references and index.
	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. Stamatakos, 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.