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Nota di contenuto	Chapter 1. Molecular Biology for the Practical Bioinformatician -- Chapter 2. Strategy and Planning of Bioinformatics Experiments -- Chapter 3. DataMining Techniques for the Practical Bioinformatician -- Chapter 4. Techniques for Recognition of Translation Initiation Sites -- Chapter 5. How Neural Networks Find Promoters Using Recognition of Micro-Structural Promoter Components -- Chapter 6. Neural-StatisticalModel of TATA-Box Motifs in Eukaryotes -- Chapter 7. Tuning the Dragon Promoter Finder System for Human Promoter Recognition -- Chapter 8. RNA Secondary Structure Prediction -- Chapter 9. Protein Localization Prediction -- Chapter 10. Homology Search Methods -- Chapter 11. Analysis of Phylogeny: A Case Study on Saururaceae -- Chapter 12. Functional Annotation and Protein Families: From Theory to Practice -- Chapter 13. Discovering Protein-Protein Interactions -- Chapter 14. Techniques for Analysis of Gene Expression -- Chapter 15. Genome-Wide cDNA Oligo Probe Design and its Applications in Schizosaccharomyces Pombe -- Chapter 16. Mining New Motifs from cDNA Sequence Data -- Chapter 17. Technologies for Biological Data Integration -- Chapter 18. Construction of Biological Databases: A Case Study on the Protein Phosphatase DataBase (PPDB)

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Sommario/riassunto	Computer scientists have increasingly been enlisted as "bioinformaticians" to assist molecular biologists in their research. This book is a practical introduction to bioinformatics for these computer scientists. The chapters are in-depth discussions by expert bioinformaticians on both general techniques and specific approaches to a range of selected bioinformatics problems. The book is organized into clusters of chapters on the following topics: - Overview of modern molecular biology and a broad spectrum of techniques from computer science -- data mining, machine learning, mathematical modeling, sequence alignment, data integration, workflow development, etc. - In-depth discussion of computational recognition of functional and regulatory sites in DNA sequences. - Incisive discussion of computational prediction of secondary structure of RNA sequences. - Overview of computational prediction of protein cellular localization, and selected discussions of inference of protein function. - Overview of methods for discovering protein-protein interactions. - Detailed discussion of approaches to gene expression analysis for the diagnosis of diseases, the treatment of diseases, and the understanding of gene functions. - Case studies on analysis of phylogenies, functional annotation of proteins, construction of purpose-built integrated biological databases, and development of workflows underlying the large-scale-effort gene discovery.