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Nota di contenuto	Contents; Series Foreword; Preface; 1 Introduction; 2 Machine-Learning Foundations: The Probabilistic Framework; 3 Probabilistic Modeling and Inference: Examples; 4 Machine Learning Algorithms; 5 Neural Networks: The Theory; 6 Neural Networks: Applications; 7 Hidden Markov Models: The Theory; 8 Hidden Markov Models: Applications; 9 Probabilistic Graphical Models in Bioinformatics; 10 Probabilistic Models of Evolution: Phylogenetic Trees; 11 Stochastic Grammars and Linguistics; 12 Microarrays and Gene Expression; 13 Internet Resources and Public Databases; A Statistics B Information Theory, Entropy, and Relative EntropyC Probabilistic Graphical Models; D HMM Technicalities, Scaling, Periodic Architectures, State Functions, and Dirichlet Mixtures; E Gaussian

	Processes, Kernel Methods, and Support Vector Machines; F Symbols and Abbreviations; References; Index
Sommario/riassunto	An unprecedented wealth of data is being generated by genome sequencing projects and other experimental efforts to determine the structure and function of biological molecules. The demands and opportunities for interpreting these data are expanding rapidly. Bioinformatics is the development and application of computer methods for management, analysis, interpretation, and prediction, as well as for the design of experiments. Machine learning approaches (e. g., neural networks, hidden Markov models, and belief networks) are ideally suited for areas where there is a lot of data but little theory, which is the situation in molecular biology. The goal in machine learning is to extract useful information from a body of data by building good probabilistic models--and to automate the process as much as possible.In this book Pierre Baldi and Soren Brunak present the key machine learning approaches and apply them to the computational problems encountered in the analysis of biological data. The book is aimed both at biologists and biochemists who need to understand new data-driven algorithms and at those with a primary background in physics, mathematics, statistics, or computer science who need to know more about applications in molecular biology.This new second edition contains expanded coverage of probabilistic graphical models and of the applications of neural networks, as well as a new chapter on microarrays and gene expression. The entire text has been extensively revised.