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Nota di contenuto	 BIOMOLECULAR NETWORKS; CONTENTS; PREFACE; ACKNOWLEDGMENTS; LIST OF ILLUSTRATIONS; ACRONYMS; 1 Introduction; 1.1 Basic Concepts in Molecular Biology; 1.1.1 Genomes, Genes, and DNA Replication Process; 1.1.2 Transcription Process for RNA Synthesis; 1.1.3 Translation Process for Protein Synthesis; 1.2 Biomolecular Networks in Cells; 1.3 Network Systems Biology; 1.4 About This Book; I GENE NETWORKS; 2 Transcription Regulation: Networks and Models; 2.1 Transcription Regulation and Gene Expression; 2.1.1 Transcription and Gene Regulation; 2.1.2 Microarray Experiments and Databases 2.1.3 ChIP-Chip Technology and Transcription Factor Databases2.2 Networks in Transcription Regulation; 2.3 Nonlinear Models Based on Biochemical Reactions; 2.4 Integrated Models for Regulatory Networks; 2.5 Summary; 3 Reconstruction of Gene Regulatory Networks; 3.1 Mathematical Models of Gene Regulatory Network; 3.1.1 Boolean

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	 Networks; 3.1.2 Bayesian Networks; 3.1.3 Markov Networks; 3.1.4 Differential Equations; 3.2 Reconstructing Gene Regulatory Networks; 3.2.1 Singular Value Decomposition; 3.2.2 Model-Based Optimization; 3.3 Inferring Gene Networks from Multiple Datasets 3.3.1 General Solutions and a Particular Solution of Network Structures for Multiple Datasets3.3.2 Decomposition Algorithm; 3.3.3 Numerical Validation; 3.4 Gene Network-Based Drug Target Identification; 3.4.1 Network Identification Methods; 3.4.2 Linear Programming Framework; 3.5 Summary; 4 Inference of Transcriptional Regulatory Networks; 4.1 Predicting TF Binding Sites and Promoters; 4.2 Inference of Transcriptional Interactions; 4.2.1 Differential Equation Methods; 4.3 Identifying Combinatorial Regulations of TFs 4.4 Inferring Cooperative Regulatory Networks4.4.1 Mathematical Models; 4.4.2 Estimating TF Activity; 4.4.3 Linear Programming Models; 4.4.4 Numerical Validation; 4.5 Prediction of Transcription Factor Activity; 4.5.1 Matrix Factorization; 4.5.2 Nonlinear Models; 5.2 Prediction of Protein-Protein Interactions; 5.2.1 Association Methods; 5.2.2 Maximum-Likelihood Estimation; 5.2.3 Deterministic Optimization Approaches 5.3 Protein Interaction Prediction Based on Multidomain Pairs5.3.1 Cooperative Domains, Strongly Cooperative Domains, Superdomains; 5.3.2 Inference of Multidomain Interactions; 5.3.3 Numerical Validation; 5.3.4 Reconstructing Complexes by Multidomain Interactions; 5.4 Domain Interaction Prediction Methods; 5.4.1 Statistical Method; 5.4.2 Domain Interaction Prediction Methods; 5.4.1 Statistical Method; 5.4.2 Domain Interaction Prediction Methods; 5.4.1 Statistical Properties of Biomolecular Networks 6.2 Evolution of Protein Interaction Networks
Sommario/riassunto	Alternative techniques and tools for analyzing biomolecular networks With the recent rapid advances in molecular biology, high-throughput experimental methods have resulted in enormous amounts of data that can be used to study biomolecular networks in living organisms. With this development has come recognition of the fact that a complicated living organism cannot be fully understood by merely analyzing individual components. Rather, it is the interactions of components or biomolecular networks that are ultimately responsible for an organism's form and function. This book addresses the impor