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	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; 4.2.2 Bayesian Approaches; 4.2.3 Data Mining and Other 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; 4.6 Summary; II PROTEIN INTERACTION NETWORKS; 5 Prediction of Protein-Protein Interactions; 5.1 Experimental Protein-Protein Interactions; 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 Pair Exclusion Analysis; 5.4.3 Parsimony Explanation Approaches; 5.4.4 Integrative Approaches; 5.5 Summary; 6 Topological Structure of Biomolecular Networks; 6.1 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