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Autore	Dehmer Matthias <1968->
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Nota di contenuto	Statistical and Machine Learning Approaches for Network Analysis; Contents; Preface; Contributors; 1 A Survey of Computational Approaches to Reconstruct and Partition Biological Networks; 1.1 INTRODUCTION; 1.2 BIOLOGICAL NETWORKS; 1.2.1 Directed Networks; 1.2.2 Undirected Networks; 1.3 GENOME-WIDE MEASUREMENTS; 1.3.1 Gene Expression Data; 1.3.2 Gene Sets; 1.4 RECONSTRUCTION OF BIOLOGICAL NETWORKS; 1.4.1 Reconstruction of Directed Networks; 1.4.1.1 Boolean Networks; 1.4.1.2 Probabilistic Boolean Networks; 1.4.1.3 Bayesian Networks; 1.4.1.4 Collaborative Graph Model; 1.4.1.5 Frequency Method

1.4.1.6 EM-Based Inference from Gene Sets
1.4.2 Reconstruction of Undirected Networks; 1.4.2.1 Relevance Networks; 1.4.2.2 Graphical Gaussian Models; 1.5 PARTITIONING BIOLOGICAL NETWORKS; 1.5.1 Directed and Undirected Networks; 1.5.2 Partitioning Undirected Networks; 1.5.2.1 Kernighan-Lin Algorithm; 1.5.2.2 Girvan-Newman Algorithm; 1.5.2.3 Newman's Eigenvector Method; 1.5.2.4 Infomap; 1.5.2.5 Clique Percolation Method; 1.5.3 Partitioning Directed Networks; 1.5.3.1 Newman's Eigenvector Method; 1.5.3.2 Infomap; 1.5.3.3 Clique Percolation Method; 1.6 DISCUSSION; REFERENCES
2 Introduction to Complex Networks: Measures, Statistical Properties, and Models
2.1 INTRODUCTION; 2.2 REPRESENTATION OF NETWORKS; 2.3 CLASSICAL NETWORK; 2.3.1 Random Network; 2.3.2 Lattice Network; 2.4 SCALE-FREE NETWORK; 2.4.1 Degree Distribution; 2.4.2 Degree Distribution of Random Network; 2.4.3 Power-Law Distribution in Real-World Networks; 2.4.4 Barabasi-Albert Model; 2.4.5 Configuration Model; 2.5 SMALL-WORLD NETWORK; 2.5.1 Average Shortest Path Length; 2.5.2 Ultrasmall-World Network; 2.6 CLUSTERED NETWORK; 2.6.1 Clustering Coefficient; 2.6.2 Watts-Strogatz Model
2.7 HIERARCHICAL MODULARITY
2.7.1 Hierarchical Model; 2.7.2 Dorogovtsev-Mendes-Samukhin Model; 2.8 NETWORK MOTIF; 2.9 ASSORTATIVITY; 2.9.1 Assortative Coefficient; 2.9.2 Degree Correlation; 2.9.3 Linear Preferential Attachment Model; 2.9.4 Edge Rewiring Method; 2.10 RECIPROCITY; 2.11 WEIGHTED NETWORKS; 2.11.1 Strength; 2.11.2 Weighted Clustering Coefficient; 2.11.3 Weighted Degree Correlation; 2.12 NETWORK COMPLEXITY; 2.13 CENTRALITY; 2.13.1 Definition; 2.13.2 Comparison of Centrality Measures; 2.14 CONCLUSION; REFERENCES; 3 Modeling for Evolving Biological Networks; 3.1 INTRODUCTION
3.2 UNIFIED EVOLVING NETWORK MODEL: REPRODUCTION OF HETEROGENEOUS CONNECTIVITY, HIERARCHICAL MODULARITY, AND DISASSORTATIVITY
3.2.1 Network Model; 3.2.2 Degree Distribution; 3.2.3 Degree-Dependent Clustering Coefficient; 3.2.4 Average Clustering Coefficient; 3.2.5 Degree Correlation; 3.2.6 Assortative Coefficient; 3.2.7 Comparison with Real Data; 3.3 MODELING WITHOUT PARAMETER TUNING: A CASE STUDY OF METABOLIC NETWORKS; 3.3.1 Network Model; 3.3.2 Analytical Solution; 3.3.3 Estimation of the Parameters; 3.3.4 Comparison with Real Data
3.4 BIPARTITE RELATIONSHIP: A CASE STUDY OF METABOLITE DISTRIBUTION

Sommario/riassunto

"This book explores novel graph classes and presents novel methods to classify networks. It particularly addresses the following problems: exploration of novel graph classes and their relationships among each other; existing and classical methods to analyze networks; novel graph similarity and graph classification techniques based on machine learning methods; and applications of graph classification and graph mining. Key topics are addressed in depth including the mathematical definition of novel graph classes, i.e. generalized trees and directed universal hierarchical graphs, and the application areas in which to apply graph classes to practical problems in computational biology, computer science, mathematics, mathematical psychology, etc"--