

1. Record Nr.	UNINA9910457007903321
Titolo	Clustering challenges in biological networks [[electronic resource] /] / editors, Sergiy Butenko, W. Art Chaovalitwongse, Panos M. Pardalos
Pubbl/distr/stampa	New Jersry, : World Scientific, c2009
ISBN	1-282-44130-2 9786612441301 981-277-166-2
Descrizione fisica	1 online resource (347 p.)
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Disciplina	570.1/5118
Soggetti	Biology - Mathematical models Cluster analysis Electronic books.
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	"This volume presents a collection of papers, several of which have been presented at DIMACS Workshop on Clustering Problems in Biological Networks that took place at Rutgers University on May-11, 2006"-- P. viii.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Fixed-parameter algorithms for graph-modeled data clustering / F. Huffner, R. Niedemeier and S. Wernicke -- Probabilistic distance clustering : algorithm and applications / C. Iyigun and A. Ben-Israel -- Analysis of regulatory and interaction networks from clusters of co-expressed genes / E. Yang ... [et al.] -- Graph-based approaches for motif discovery / E. Zaslavsky -- Statistical clustering analysis : an introduction / H. Zhang -- Diversity graphs / P. Blain ... [et al.] -- Identifying critical nodes in protein-protein interaction networks / V. Boginski and C.W. Commander -- Faster algorithms for constructing a concept (Galois) lattice / V. Choi -- A projected clustering algorithm and its biomedical application / P. Deng, Q. Ma and W. Wu -- Graph algorithms for integrated biological analysis, with applications to Type 1 diabetes data / J. D. Eblen ... [et al.] -- A novel similarity-based modularity function for graph partitioning / Z. Feng ... [et al.] --

Mechanism-based clustering of genome-wide RNA levels : roles of transcription and transcript-degradation rates / S. Ji ... [et al.] -- The complexity of feature selection for consistent biclustering / O. E. Kundakcioglu and P. M. Pardalos -- Clustering electroencephalogram recordings to study mesial temporal lobe epilepsy / C.-C. Liu ... [et al.] -- Relating subjective and objective pharmacovigilance association measures / R. K. Pearson -- A novel clustering approach : global optimum search with enhanced positioning / M. P. Tan and C. A. Floudas.

Sommario/riassunto

This volume presents a collection of papers dealing with various aspects of clustering in biological networks and other related problems in computational biology. It consists of two parts, with the first part containing surveys of selected topics and the second part presenting original research contributions. This book will be a valuable source of material to faculty, students, and researchers in mathematical programming, data analysis and data mining, as well as people working in bioinformatics, computer science, engineering, and applied mathematics. In addition, the book can be used as a sup
