

1. Record Nr.	UNINA9910298425303321
Titolo	Soft Computing for Biological Systems // edited by Hemant J. Purohit, Vipin Chandra Kalia, Ravi Prabhakar More
Pubbl/distr/stampa	Singapore : , : Springer Singapore : , : Imprint : Springer, , 2018
ISBN	981-10-7455-0
Edizione	[1st ed. 2018.]
Descrizione fisica	1 online resource (301 pages) : illustrations
Disciplina	570.285
Soggetti	Bioinformatics Gene expression Biomedical engineering Medical genetics Gene Expression Biomedical Engineering/Biotechnology Computational Biology/Bioinformatics Gene Function
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references at the end of each chapters and index.
Nota di contenuto	1. Diagnostic prediction based on gene expression profiles and artificial neural networks -- 2. Soft-Computing Approaches to Extract Biologically Significant Gene Network Modules -- 3. A Hybridization of Artificial Bee Colony with Swarming Approach of Bacterial Foraging Optimization for Multiple Sequence Alignment -- 4. Construction Gene Networks Using Gene Expression Profiles -- 5. Bioinformatics tools for shotgun metagenomic data analysis -- 6. Prediction of protein-protein interactions using machine learning techniques -- 7. Protein structure prediction using machine learning approaches -- 8. Drug-transporters as Therapeutic targets: Computational Models, Challenge and Opportunity -- 9. Module-Based Knowledge Discovery for Multiple-Cytosine-Variant Methylation Profile -- 10. Outlook of various soft computing data pre-processing techniques to study the pest population dynamics in Integrated Pest Management -- 11. Genomics for Oral Cancer Biomarker research -- 12. Soft-computing methods

and tools for Bacteria DNA Barcoding data analysis -- 13. Fish DNA Barcoding: A comprehensive survey of the Bioinformatics tools and databases.

Sommario/riassunto

This book explains how the biological systems and their functions are driven by genetic information stored in the DNA, and their expression driven by different factors. The soft computing approach recognizes the different patterns in DNA sequence and try to assign the biological relevance with available information. The book also focuses on using the soft-computing approach to predict protein-protein interactions, gene expression and networks. The insights from these studies can be used in metagenomic data analysis and predicting artificial neural networks.
