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Descrizione fisica	1 online resource (396 pages)
Disciplina	570.285
Soggetti	Data mining Expert systems (Computer science) Machine learning Bioinformatics Big data Medical informatics Data Mining and Knowledge Discovery Knowledge Based Systems Machine Learning Computational and Systems Biology Big Data Health Informatics Bioinformàtica Aprentatge automàtic Sistemes experts (Informàtica) Informàtica mèdica Mineria de dades Dades massives Llibres electrònics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
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Nota di contenuto	Chapter1:Computer science for Molecular biology -- Chapter2: Introduction to association analysis -- Chapter3:Introduction to computational linguistics and biology structure -- Chapter4:Matrix

decomposition for dimensionality deduction -- Chapter5:Discovering conserved RNA secondary structures with structure similarity -- Chapter6:Gene ontology for non-coding RNAs classification -- Chapter7:Learning frequent sub-structure by graph mining -- Chapter8:Editing distance and its application to biology graph analytics -- Chapter9:Sequence assembly and applications -- Chapter10:Classifying protein structures by measuring structural similarity -- Chapter11:Identification of metabolic pathways with embedding network -- Chapter12:Emerging Knowledge integration-based approach with multi-sources data for bioinformatics -- Chapter13: Conclusion and Future Work.

Sommario/riassunto

Advances in experimental technologies have given rise to tremendous amounts of biology data. This not only offers valuable sources of data to help understand biological evolution and functional mechanisms, but also poses challenges for accurate and effective data analysis. This book offers an essential introduction to the theoretical and practical aspects of association analysis, including data pre-processing, data mining methods/algorithms, and tools that are widely applied for computational biology. It covers significant recent advances in the field, both foundational and application-oriented, helping readers understand the basic principles and emerging techniques used to discover interesting association patterns in diverse and heterogeneous biology data, such as structure-function correlations, and complex networks with gene/protein regulation. The main results and approaches are described in an easy-to-follow way and accompanied by sufficient references and suggestions for future research. This carefully edited monograph is intended to provide investigators in the fields of data mining, machine learning, artificial intelligence, and bioinformatics with a profound guide to the role of association analysis in computational biology. It is also very useful as a general source of information on association analysis, and as an overall accompanying course book and self-study material for graduate students and researchers in both computer science and bioinformatics. .
