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| Nota di contenuto | Cover; Table of Contents; Title page; Preface; List of Symbols; About the Authors; Part One: Introduction; 1 Introduction to Bioinformatics; 1.1 Introduction; 1.2 The "Omics" Era; 1.3 The Scope of Bioinformatics; 1.4 What Do Information Engineers and Biologists Need to Know?; 1.5 Discussion and Summary; References; 2 Computational Methods in Bioinformatics; 2.1 Introduction; 2.2 Machine Learning and Data Mining; 2.3 Optimisation; 2.4 Image Processing: Bioimage Informatics; 2.5 Network Analysis; 2.6 Statistical Analysis; 2.7 Software Tools and Technologies; 2.8 Discussion and Summary ReferencesPart Two: Introduction to Molecular Biology; 3 The Living Cell; 3.1 Introduction; 3.2 Prokaryotes and Eukaryotes; 3.3 Multicellularity; 3.4 Cell Components; 3.5 Discussion and Summary; References; 4 Central Dogma of Molecular Biology; 4.1 Introduction; 4.2 Central Dogma of Molecular Biology Overview; 4.3 Proteins; 4.4 DNA; 4.5 RNA; 4.6 Genes; 4.7 Transcription and Post-transcriptional Processes; 4.8 Translation and Post-translational Processes; 4.9 Discussion and Summary; References; Part Three: Data Acquisition and Pre-processing; 5 High-throughput Technologies; 5.1 Introduction 5.2 Microarrays5.3 Next-generation Sequencing (NGS); 5.4 ChIPon Microarrays and Sequencing; 5.5 Discussion and Summary; References; |

6 Databases, Standards and Annotation; 6.1 Introduction; 6.2 NCBI Databases; 6.3 TheEBIDatabases; 6.4 Species-specific Databases; 6.5 Discussion and Summary; References; 7 Normalisation; 7.1 Introduction; 7.2 Issues Tackled by Normalisation; 7.3 Normalisation Methods; 7.4 Discussion and Summary; References; 8 Feature Selection; 8.1 Introduction; 8.2 FS and FG - Problem Definition; 8.3 Consecutive Ranking; 8.4 Individual Ranking

8.5 Principal Component Analysis8.6 Genetic Algorithms and Genetic Programming; 8.7 Discussion and Summary; References; 9 Differential Expression; 9.1 Introduction; 9.2 Fold Change; 9.3 Statistical Hypothesis Testing - Overview; 9.4 Statistical Hypothesis Testing - Methods; 9.5 Discussion and Summary; References; Part Four: Clustering Methods; 10 Clustering Forms; 10.1 Introduction; 10.2 Proximity Measures; 10.3 Clustering Families; 10.4 Clusters and Partitions; 10.5 Discussion and Summary; References; 11 Partitional Clustering; 11.1 Introduction; 11.2 k-Means and its Applications

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16.4 Resources

Sommario/riassunto

Clustering techniques are increasingly being put to use in the analysis of high-throughput biological datasets. Novel computational techniques to analyse high throughput data in the form of sequences, gene and protein expressions, pathways, and images are becoming vital for understanding diseases and future drug discovery.   This book details the complete pathway of cluster analysis, from the basics of molecular biology to the generation of biological knowledge. The book also presents the latest clustering methods and clustering validation, thereby offering the reader a comprehensive review o