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Nota di contenuto	Chapter 1: Introduction to Multiomics Technology, Ahmed Hajyasien -- Chapter 2: Multi-omics Data Integration Applications and Structures, Ammar El-Hassa -- Chapter 3: Machine learning approaches for multi-omics data integration in medicine, Fatma Hilal Yagin -- Chapter 4: Multimodal methods for knowledge discovery from bulk and single-cell multi-omics data, Yue Li, Gregory Fonseca, and Jun Ding -- Chapter 5: Negative sample selection for miRNA-disease association prediction models, Yulian Ding, Fei Wang, Yuchen Zhang, Fang-Xiang Wu -- Chapter 6: Prediction and Analysis of Key Genes in Prostate Cancer via MRMR Enhanced Similarity Preserving Criteria and Pathway Enrichment Methods, Robert Benjamin Eshun, Hugette Naa Ayele Aryee, Marwan U. Bikdash, and A.K.M Kamrul Islam -- Chapter 7: Graph-Based Machine Learning Approaches for Pangenomics, Indika Kahanda, Joann Mudge, Buwani Manuweera, Thiruvarangan Ramaraj, Alan Cleary, and Brendan Mumey -- Chapter 8: Multiomics-based tensor decomposition for

characterizing breast cancer heterogeneity, -- Qian Liu, Shujun Huang, Zhongyuan Zhang, Ted M. Lakowski, Wei Xu and Pingzhao Hu -- Chapter 9: Multi-Omics Databases, Hania AlOmari, Abedalrhman Alkhateeb, and Bassam Hammo.

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## Sommario/riassunto

The advancement of biomedical engineering has enabled the generation of multi-omics data by developing high-throughput technologies, such as next-generation sequencing, mass spectrometry, and microarrays. Large-scale data sets for multiple omics platforms, including genomics, transcriptomics, proteomics, and metabolomics, have become more accessible and cost-effective over time. Integrating multi-omics data has become increasingly important in many research fields, such as bioinformatics, genomics, and systems biology. This integration allows researchers to understand complex interactions between biological molecules and pathways. It enables us to comprehensively understand complex biological systems, leading to new insights into disease mechanisms, drug discovery, and personalized medicine. Still, integrating various heterogeneous data types into a single learning model also comes with challenges. In this regard, learning algorithms have been vital in analyzing and integrating these large-scale heterogeneous data sets into one learning model. This book overviews the latest multi-omics technologies, machine learning techniques for data integration, and multi-omics databases for validation. It covers different types of learning for supervised and unsupervised learning techniques, including standard classifiers, deep learning, tensor factorization, ensemble learning, and clustering, among others. The book categorizes different levels of integrations, ranging from early, middle, or late-stage among multi-view models. The underlying models target different objectives, such as knowledge discovery, pattern recognition, disease-related biomarkers, and validation tools for multi-omics data. Finally, the book emphasizes practical applications and case studies, making it an essential resource for researchers and practitioners looking to apply machine learning to their multi-omics data sets. The book covers data preprocessing, feature selection, and model evaluation, providing readers with a practical guide to implementing machine learning techniques on various multi-omics data sets.

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