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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	MLMVFE: A Machine Learning Approach Based on Multi-View Features Extraction for Drug-Disease Associations Prediction -- STgcor: A Distribution-based Correlation Measurement Method for Spatial Transcriptome Data -- Automatic ICD Coding based on Multi-granularity Feature Fusion -- Effectively Training MRI Reconstruction Network via Sequentially Using Undersampled k-Space Data with Very Low Frequency Gaps -- Fusing Label Relations for Chinese EMR Named Entity Recognition with Machine Reading Comprehension -- Private Epigenetic PaceMaker Detector using Homomorphic Encryption - Extended Abstract -- NIDN: Medical Code Assignment via Note-Code Interaction Denoising Network -- Research on the prediction method of disease classification based on imaging features -- M-US-EMRs: A Multi-Modal Data Fusion Method of Ultrasonic Images and Electronic Medical Records Used for Screening of Coronary Heart Disease -- Transposition Distance Considering Intergenic Regions for Unbalanced

Genomes -- An SMT-based Framework for Reasoning about Discrete Biological Models -- ARGLRR: An Adjusted Random Walk Graph Regularization Sparse Low-rank Representation Method for Single-cell RNA-sequencing Data Clustering -- An Efficient and User-friendly Software for PCR Primer Design for Detection of Highly Variable Bacteria -- A Network-Based Voting Method for Identification and Prioritization of Personalized Cancer Driver Genes -- TDCOSR: A multimodality fusion framework for association analysis between genes and ROIs of Alzheimer's disease -- Policy-based Hypertension Monitoring using Formal Runtime Verification Monitors -- Deep learning-enhanced MHC-II presentation prediction and peptidome deconvolution -- MMLN: Leveraging Domain Knowledge for Multimodal Diagnosis -- Optimal sequence alignment to ED-strings -- Heterogeneous PPI network representation learning for protein complex identification -- A Clonal Evolution Simulator for Planning Somatic Evolution Studies -- Prediction of Drug-disease Relationship on Heterogeneous Networks Based on Graph Convolution -- t-SNE Highlights Phylogenetic and Temporal Patterns of SARS-CoV-2 Spike and Nucleocapsid Protein Evolution -- MPCDDI: A Secure Multiparty Computation-based Deep Learning Framework for Drug-drug Interaction Predictions -- A Multimodal Data Fusion-based Deep Learning Approach for Drug-Drug Interaction Prediction -- GNN-Dom: an unsupervised method for protein domain partition via protein contact map -- A Locality-Constrained Linear Coding-Based Ensemble Learning Framework for Predicting Potentially Disease-Associated MiRNAs -- Gaussian-enhanced Representation Model for Extracting Protein-Protein Interactions Affected by Mutations -- Distance Profiles of Optimal RNA Foldings -- 2D Photogrammetry Image of Adolescent Idiopathic Scoliosis Screening Using Deep Learning -- EMRShareChain: A Privacy-Preserving EMR Sharing System Model Based on the Consortium Blockchain -- Simulating Spiking Neural Networks based on SW26010pro -- Entropy Based Clustering of Viral Sequences -- A Tensor Robust Model Based on Enhanced Tensor Nuclear Norm and Low-Rank Constraint for Multi-view Cancer Genomics Data.

Sommario/riassunto

This book constitutes the proceedings of the 18th International Symposium on Bioinformatics Research and Applications, ISBRA 2022, held in Haifa, Israel, in November 14–17, 2022. The 30 full papers and 4 short papers presented in this book were carefully reviewed and selected from 72 submissions. They were organized in topical sections named: AI and disease; computational proteomics; biomedical imaging; drug screening and drug-drug interaction prediction; Biomedical data; sequencing data analysis.
