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| Nota di contenuto | MLMVFE: A Machine Learning Approach Based on Muli-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 |

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| | 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. |