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Altri autori (Persone)	GuoXuan <1987-> MangulSerghei PattersonMurray ZelikovskyAlexander
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Nota di contenuto	Unveiling the Robustness of Machine Learning Models in Classifying COVID-19 Spike Sequences -- Efficient Sequence Embedding For SARS-CoV-2 Variants Classification -- On Computing the Jaro Similarity Between Two Strings -- Identifying miRNA-disease Associations based on Simple Graph Convolution with DropMessage and Jumping Knowledge -- Reconciling Inconsistent Molecular Structures from Biochemical Databases -- Deep Learning Architectures For the Prediction of YY1-Mediated Chromatin Loops -- Neurogenesis-associated Protein, a Potential Prognostic Biomarker in anti-PD-1 based kidney renal clear cell carcinoma patients therapeutics -- MPFNet: ECG Arrhythmias Classification Based on Multi-Perspective Feature Fusion --

PCPI: Prediction of circRNA and protein interaction using machine learning method -- Radiology Report Generation via Visual Recalibration and Context Gating-aware -- Using Generating Functions to Prove Additivity of Gene-Neighborhood Based Phylogenetics -- TCSA: A Text-guided Cross-view Medical Semantic Alignment Framework for Adaptive Multi-view Visual Representation Learning -- Multi-Class Cancer Classification of Whole Slide Images through Transformer and Multiple Instance Learning -- ricME: long-read based mobile element variant detection using sequence realignment and identity calculation -- scGASI: A graph autoencoder-based single-cell integration clustering method -- ABCAE: Artificial Bee Colony Algorithm with Adaptive Exploitation for Epistatic Interaction Detection -- USTAR: Improved Compression of k-mer Sets with Counters Using De Bruijn Graphs -- Graph-Based Motif Discovery in Mimotope Profiles of Serum Antibody Repertoire -- Sequence-Based Nanobody-Antigen Binding Prediction -- Approximating Rearrangement Distances with Replicas and Flexible Intergenic Regions -- The Ordered Covering Problem in Distance Geometry -- Phylogenetic Information as Soft Constraints in RNA Secondary Structure Prediction -- NeoMS: Identification of Novel MHC-I Peptides with Tandem Mass Spectrometry -- On Sorting by Flanked Transpositions -- Integrative analysis of gene expression and alternative polyadenylation from single-cell RNA-seq data -- SaID: Simulation-aware Image Denoising Pre-trained Model for Cryo-EM Micrographs -- Reducing the impact of domain rearrangement on sequence alignment and phylogeny reconstruction -- Identification and functional annotation of circRNAs in neuroblastoma based on bioinformatics -- SGMDD: Subgraph Neural Network-Based Model for Analyzing Functional Connectivity Signatures of Major Depressive Disorder -- PDB2Vec: Using 3D Structural Information For Improved Protein Analysi -- Hist2Vec: Kernel-Based Embeddings for Biological Sequence Classification -- DCNN: Dual-Level Collaborative Neural Network for Imbalanced Heart Anomaly Detection -- On the Realisability of Chemical Pathways -- A Brief Study of Gene Co-Expression Thresholding Algorithms -- Inferring Boolean Networks from Single-Cell Human Embryo Datasets -- Enhancing t-SNE Performance for Biological Sequencing Data through Kernel Selection -- Genetic Algorithm with Evolutionary Jumps -- HetBiSyn: Predicting Anticancer Synergistic Drug Combinations Featuring Bi-perspective Drug Embedding with Heterogeneous Data -- Clique-based topological characterization of chromatin interaction hubs -- Exploring Racial Disparities in Triple-Negative Breast Cancer: Insights from Feature Selection Algorithms -- Deep Learning Reveals Biological Basis of Racial Disparities in Quadruple-Negative Breast Cancer -- CSA-MEM: Enhancing Circular DNA Multiple Alignment through Text Indexing Algorithms -- A Convolutional Denoising Autoencoder for Protein Scaffold Filling -- Simulating tumor evolution from scDNA-seq as an accumulation of both SNVs and CNAs -- CHLPCA: Correntropy-Based Hypergraph Regularized Sparse PCA for Single-cell Type Identification.-.

Sommario/riassunto

This book constitutes the refereed proceedings of the 19th International Symposium on Bioinformatics Research and Applications, ISBRA 2023, held in Wrocaw, Poland, during October 9–12, 2023. The 28 full papers and 16 short papers included in this book were carefully reviewed and selected from 89 submissions. They were organized in topical sections as follows: reconciling inconsistent molecular structures from biochemical databases; radiology report generation via visual recalibration and context gating-aware; sequence-based nanobody-antigen binding prediction; and hist2Vec: kernel-based

embeddings for biological sequence classification.