1.

Record Nr.	UNISA996668469303316
Titolo	Advanced Intelligent Computing Technology and Applications : 21st International Conference, ICIC 2025, Ningbo, China, July 26–29, 2025, Proceedings, Part XXVI / / edited by De-Shuang Huang, Haiming Chen, Bo Li, Qinhu Zhang
Pubbl/distr/stampa	Singapore : , : Springer Nature Singapore : , : Imprint : Springer, , 2025
ISBN	981-9500-30-3
Edizione	[1st ed. 2025.]
Descrizione fisica	1 online resource (XXI, 515 p. 192 illus., 169 illus. in color.)
Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 15867
Disciplina	006.3
Soggetti	Computational intelligence Computer networks Machine learning Application software Computational Intelligence Computer Communication Networks Machine Learning Computer and Information Systems Applications
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	-- Cheminformatics. -- Topological Analysis of F-Multiplicity Corona Graphs: Zagreb Indices and Applications in Molecular Design. -- Graph-based Multi-scale Learning for Predicting Mass Spectra from Molecules. -- A Universal Periodicity Injection Module for Crystal Property Prediction. -- SM-CBNet: A Speech-Based Parkinson's Disease Diagnosis Model with SMOTE–ENN and CNN+BiLSTM Integration. -- Systems Biology. -- SpatialDSSC: Estimating Cell Type Abundance and Expression Profile from Spatial Transcriptomic Data. -- Cuproptosis-related genes are correlated with prognostic and immune infiltration in skin cutaneous melanoma patients. -- CS-Phylo: Accelerating Evolutionary Distance Estimation with Closed Syncmer-Enhanced MinHash. -- Aligning Histological Images and Spatial Gene Expression Profiles via Dynamic Convolution and Graph Transformers. -- SGAEMVN: a hybrid neighborhood-based graph attention autoencoder

for identifying spatial domains from spatial transcriptomics. -- MMF2Drug: A Multi-Modal Feature Fusion Method for Improving Targeted Drug Design. -- DFDGRU-DTI: Drug-Target Interaction Prediction Based on Random Walk Embeddings and Bidirectional GRU Neural Network. -- RDT-Net: A Novel Diffusion-Based Network for Intracranial Hemorrhage Segmentation. -- Feature Attribution-based Explanation Comparison of Magnetoencephalography Decoding Models. -- scAFC: Adaptive Fusion Clustering of Single-cell RNA-seq Data through Autoencoder and Graph Attention Networks. -- BIOFUSE-DDI: A Dual-Source Transformer Framework for Drug-Drug Interaction Prediction. -- MedMaskDiff: Mamba-based Medical Semantic Image Synthesis for Segmentation. -- Image Clarity Combination Method Based on Hybrid Sampling. -- PDA-PAGCN: Predicting Disease-Related piRNA Based on Proxy Attention Graph Convolutional Network. -- CALM-AcPEP: Predicting Anticancer Peptides using Cross-Attention and Pre-trained Language Model. -- ACP-TransLSTM: A Novel Deep Learning Framework for Anticancer Peptide Prediction Using Multi-Source Feature Integration. -- Multimodal GAN Integrating Hypergraph and Knowledge Graph Representations for Synthetic Lethality. -- EdgeViewDet: Dynamic Edge-Centric Fusion Network with Granger Causality for Neurological Disorders Detection. -- MOMTERL: Modeling Molecular Masking and Contrastive Learning Based on Motifs. -- Respiratory Sound Classification via Multi-View Feature Fusion with Enhanced Convolutional Neural Network and Audio Spectrogram Transformer. -- Multi-Scale Graph Regularized Deep Learning for Accurate Drug-Protein Interaction Prediction. -- DiffiT-HSFDA: Diffusion Based Source-Free Domain Adaptation for Histopathology. -- Dual-channel MiRNA Drug Resistance Prediction Model Based on Multimodal Feature Alignment. -- Whole Slide Images Based Cancer Survival Prediction Using Multi-Task Learning. -- Leveraging DermoGrabcut Segmentation for Improved CNN-Based Skin Lesion Classification. -- VirB: A Virus Hierarchical Classification Method Based on ModernBERT. -- FAPE-DTI: Enhancing Drug–Target Interaction Prediction with Focal Attention and Relative Positional Encoding. -- An Adaptive Multi-View Feature Fusion Framework Based on Multiple Graphs for Predicting Drug-drug Interactions. -- E-MSNGO: Explainable Multi-species Protein Function Prediction Model based on Aggregated Networks. -- PRNet: A Contrastive Ranking Model Based on 3D Convolution and Bi LSTM for ChRs Prediction. -- DeepGO-ESM: Improving the Protein Function Prediction of DeepGraphGO via the Evolutionary Scale Modeling Framework. -- scGECA: a Graph Embedded Representation Learning Approach with Dynamic Attention Mechanism for Single-cell Clustering. -- ChemTransGNN++: From Reactants to Products via Multiscale Graph Transformer Modeling of Reaction Pathways. -- ReAlign-Star: An Optimized Realignment Method for Multiple Sequence Alignment, Targeting Star Algorithm Tools. -- FMAlign3: A Scalable and Adaptive Framework for Large-Scale Multiple Sequence Alignment. -- Enough Consecutive Matches in k-Tuple Common Substrings. -- DeepCatl: A combination of channel attention mechanism and Transformer encoding to predict transcription factor binding sites. -- FDA-YOLO: Fast Domain Adaptation YOLO for Cross-Domain Brain Tumor Detection in Medical Imaging. -- Controllable Edge-Type-Specific Interpretation in Multi-Relational Graph Neural Networks for Drug Response Prediction.

Sommario/riassunto

The 20-volume set LNCS 15842-15861, together with the 4-volume set LNAI 15862-15865 and the 4-volume set LNBI 15866-15869, constitutes the refereed proceedings of the 21st International Conference on Intelligent Computing, ICIC 2025, held in Ningbo, China,

during July 26-29, 2025. The 1206 papers presented in these proceedings books were carefully reviewed and selected from 4032 submissions. They deal with emerging and challenging topics in artificial intelligence, machine learning, pattern recognition, bioinformatics, and computational biology. .