

1. Record Nr.	UNINA9910874669103321
Autore	Peng Wei
Titolo	Bioinformatics Research and Applications : 20th International Symposium, ISBRA 2024, Kunming, China, July 19-21, 2024, Proceedings, Part II
Pubbl/distr/stampa	Singapore : , : Springer Singapore Pte. Limited, , 2024 ©2024
ISBN	981-9751-31-4
Edizione	[1st ed.]
Descrizione fisica	1 online resource (515 pages)
Collana	Lecture Notes in Computer Science Series ; ; v.14955
Altri autori (Persone)	CaiZhipeng SkumsPavel
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Intro -- Preface -- Organization -- Contents - Part II -- Exploring Hierarchical Structures of Cell Types in scRNA-seq Data -- 1 Introduction -- 2 Related Work -- 2.1 Structural Entropy -- 2.2 Shared Nearest Neighbor -- 3 Method -- 3.1 The Framework of scHSD -- 3.2 Graph Construction -- 3.3 Hierarchy Tree Building via Structural Entropy Minimization -- 3.4 Cell Type Identification -- 4 Results and Discussion -- 4.1 Cell Type Hierarchy -- 4.2 Comparative Analysis of Clustering Results -- 4.3 Visualization -- 4.4 Comparative Analysis of Classifying Results -- 5 Conclusion -- References -- Predicting Frequencies of Drug Side Effects Using Graph Attention Networks with Multiple Features -- 1 Introduction -- 2 Materials and Methods -- 2.1 Benchmark Dataset -- 2.2 Drug Profile -- 2.3 Side Effect Profile -- 2.4 MFGAT -- 3 Result and Discussion -- 3.1 Evaluation Metrics -- 3.2 Comparision with Other Models -- 3.3 Ablation Experiments -- 4 Conclusion and Discussion -- References -- RabbitTrim: Highly Optimized Trimming of Illumina Sequencing Data on Multi-core Platforms -- 1 Introduction -- 2 Methods -- 2.1 Efficient I/O Strategy -- 2.2 Memory Reuse -- 2.3 Bitwise Operations -- 2.4 Vectorization -- 3 Results -- 3.1 Datasets and Platforms -- 3.2 Performance Results -- 4 Conclusion -- References -- A Hybrid Feature Fusion Network for Predicting HER2 Status on H& E-Stained Histopathology Images

-- 1 Introduction -- 2 Related Works -- 3 Materials and Methods --
3.1 Dataset -- 3.2 Overview of the Proposed Model -- 4 Experiments
and Results -- 4.1 Evaluation Metrics -- 4.2 Experimental Results --
4.3 Feature Fusion Weight Selection -- 5 Discussion -- 6 Conclusions
-- References -- scCoRR: A Data-Driven Self-correction Framework for
Labeled scRNA-Seq Data -- 1 Introduction -- 2 Method -- 2.1 Data
Preprocessing and Anchor Cell Identification.
2.2 Cell Representation Learning and Classification Based on a
Supervised Contrastive Learning -- 3 Results -- 3.1 Datasets -- 3.2
Validation on the Baron Dataset Revealed a Subset of Ductal Cells Were
Corrected to Acinar Cells -- 3.3 Validation on the Mammary Gland
Dataset Revealed a Subset of Stromal Was Corrected to Macrophage --
3.4 Evaluation of Clustering Results Before and After Cell Label
Correction -- 4 Discussion -- References -- KT-AMP: Enhancing
Antimicrobial Peptide Functions Prediction Through Knowledge
Transfer on Protein Language Model -- 1 Introduction -- 2 Materials
and Methods -- 2.1 Dataset -- 2.2 Overview of the Model Workflow --
2.3 Pre-trained Protein Language Model -- 2.4 Fine-Tuning Pre-trained
Model -- 2.5 MLP Classifier -- 3 Experiments and Results -- 3.1
Evaluation Metrics -- 3.2 Performance Evaluation -- 3.3 Feature
Representation Visualization -- 3.4 Ablation Study -- 4 Discussion and
Conclusion -- References -- A Multi-scale Attention Network for Sleep
Arousal Detection with Single-Channel ECG -- 1 Introduction -- 2
Methods -- 2.1 Data Preprocessing -- 2.2 Model Architecture -- 2.3
Loss Objective -- 2.4 Performance Metrics -- 3 Experiment Results and
Discussion -- 3.1 Experimental Setup -- 3.2 Arousal Detection
Performance Comparison -- 3.3 Arousal Index Performance
Comparison -- 3.4 Ablation Experiments -- 3.5 Visualized Analysis --
4 Conclusion and Future Work -- References -- RabbitSAlign:
Accelerating Short-Read Alignment for CPU-GPU Heterogeneous
Platforms -- 1 Introduction -- 2 Methods -- 2.1 Overview -- 2.2
Seeding Optimization -- 2.3 GPU Acceleration -- 3 Experimental
Results -- 3.1 Overview -- 3.2 Efficiency Evaluation -- 3.3 Accuracy
Evaluation -- 4 Conclusion -- References -- FedKD-DTI: Drug-Target
Interaction Prediction Based on Federated Knowledge Distillation -- 1
Introduction -- 2 Methods.
2.1 Drug-Target Interaction Prediction Model -- 2.2 Overview of
FedKD-DTI -- 3 Experiment -- 3.1 Experimental Setups -- 3.2 Results
-- 4 Conclusion -- References -- Accurately Deciphering Novel Cell
Type in Spatially Resolved Single-Cell Data Through Optimal Transport
-- 1 Introduction -- 2 Method -- 2.1 OT-Based Representation
Learning for Novel Cell Type Discovery -- 2.2 OT-Based Partial
Alignment for Seen Cell Type Identification -- 2.3 Re-weighted Entropy
Loss to Increase the Prediction Certainty -- 3 Results and Discussion --
3.1 Settings -- 3.2 Results -- 3.3 Ablation Study -- 4 Conclusion --
References -- Synthesis of Boolean Networks with Weak and Strong
Regulators -- 1 Introduction -- 2 Definitions -- 2.1 Strength of
Regulators -- 2.2 Regulation Conditions and Monotonic Definition -- 3
Synthesis Implementation -- 3.1 Variables -- 3.2 Constraints -- 3.3
DEFINE -- 3.4 Linear Temporal Logic Specification - LTLSPEC -- 3.5
Integration -- 4 Results -- 4.1 Application to Toy Example -- 4.2
Application to Mammalian Cell Cycle Modelling -- 5 Related Work --
References -- Patch-Based Coupled Attention Network to Predict MSI
Status in Colon Cancer -- 1 Introduction -- 2 Related Work -- 3
Materials and Methods -- 3.1 Dataset -- 3.2 Methodology -- 4
Experiments and Results -- 4.1 Experimental Setting -- 4.2
Comparison Experiments -- 4.3 Effects of Attention Mechanisms -- 4.4
Limitations -- 5 Conclusion -- References -- Predicting Blood-Brain

Barrier Permeability Through Multi-view Graph Neural Network with Global-Attention and Pre-trained Transformer -- 1 Introduction -- 2 Materials and Methods -- 2.1 Materials -- 2.2 Methods -- 3 Experiments and Results -- 3.1 Experimental Settings and Evaluation Metrics -- 3.2 Comparing with Different Methods in Hold-Out Validation -- 3.3 Comparing with Different Methods in 5-CV -- 4 Conclusion -- References.

LLMDTA: Improving Cold-Start Prediction in Drug-Target Affinity with Biological LLM -- 1 Introduction -- 2 Materials and Methods -- 2.1 Datasets -- 2.2 Model -- 3 Experiments and Results -- 3.1 Experimental Setup -- 3.2 Experimental Results -- 3.3 Ablation Study -- 3.4 Case Study -- 4 Conclusion -- References -- DMSDR: Drug Molecule Synergy-Enhanced Network for Drug Recommendation with Multi-source Domain Knowledge -- 1 Introduction -- 2 Methods -- 2.1 Patient Representation Module -- 2.2 The Drug Molecular Synergy Module -- 2.3 Domain Knowledge Representation Module -- 2.4 Drug Prediction Module -- 2.5 Training and Inference -- 3 Experiments -- 3.1 Dataset and Preprocessing -- 3.2 Baseline and Evaluation Metrics -- 3.3 Results Analysis -- 3.4 Ablation Study -- 3.5 Case Study -- 4 Conclusion -- References -- A Graph Transformer-Based Method for Predicting LncRNA-Disease Associations Using Matrix Factorization and Automatic Meta-Path Generation -- 1 Introduction -- 2 Materials and Methods -- 2.1 Baseline Datasets -- 2.2 Similarity Networks -- 2.3 Fusion of Similarity Feature Matrices -- 2.4 LncRNA-Disease Heterogeneous Network -- 2.5 Generate Non-linear Features -- 2.6 Generate Linear Features -- 2.7 Generating Topological Features -- 2.8 Predicting Potential LDAs -- 3 Experiments and Results -- 3.1 Evaluation Metrics -- 3.2 Parameter Selection -- 3.3 Ablation Experiments -- 3.4 Comparison with Other Methods -- 3.5 Case Studies -- 4 Conclusion -- References -- The Dynamic Spatiotemporal Features Based on Rich Club Organization in Autism Spectrum Disorder -- 1 Introduction -- 2 Materials and Preprocessing -- 2.1 Participants -- 2.2 Diagnostic -- 2.3 fMRI Acquisition -- 2.4 Data Preprocessing -- 2.5 Construction of Dynamic Functional Connectivity Brain Network -- 3 Methods -- 3.1 Rich-Club Organization.

3.2 Dynamic Brain Networks Rich-Club Spatio-Temporal Similarity Metrics -- 3.3 Dynamic Rich-Club Brain Region Importance Assessment Indicator -- 3.4 Network Topology Characteristics -- 3.5 Construction and Classification of Dynamic Feature Sets Based on Rich-Club -- 4 Result -- 4.1 Temporal-Spatial Similarity Measurement of Dynamic Brain Networks -- 4.2 SVM Classification Results -- 4.3 Discussion -- 5 Conclusion -- References -- Integrated Analysis of Autophagy-Related Genes Identifies Diagnostic Biomarkers and Immune Correlates in Preeclampsia -- 1 Introduction -- 2 Materials and Methods -- 3 Results -- 4 Discussion -- References -- Multi-grained Cross-Modal Feature Fusion Network for Diagnosis Prediction -- 1 Introduction -- 2 Method -- 2.1 Fine-Grained Representation Learning Module -- 2.2 Fine-Grained Feature Fusion Module -- 2.3 Coarse-Grained Representation Learning Module -- 2.4 Coarse-Grained Feature Fusion Module -- 2.5 Prediction Module -- 3 Experiments and Results -- 3.1 Data Description -- 3.2 Implementation Details and Evaluation Metric -- 3.3 Baselines -- 3.4 Main Results -- 3.5 Ablation Study -- 3.6 Case Study -- 4 Conclusion -- References -- MOL-MOE: Learning Drug Molecular Characterization Based on Mixture of Expert Mechanism -- 1 Introduction -- 2 Method -- 2.1 Atomic and Functional Group Feature Fusion Based on Cross Attention -- 2.2 MOE for Drug Molecule Modeling -- 3 Results -- 3.1 Dataset -- 3.2 Experimental Setup -- 3.3 Experimental Results -- 3.4 Ablation Experiment -- 3.5 Comparative

Experiments -- 3.6 Case Study -- 4 Conclusion -- References -- A
Multimodal Federated Learning Framework for Modality Incomplete
Scenarios in Healthcare -- 1 Introduction -- 2 Methodology -- 2.1
Problem Definition -- 2.2 Overview -- 2.3 Cluster Stepwise
Aggregation -- 2.4 Prototype Contrastive Integration -- 3 Experiments.
3.1 Datasets and Data Preprocessing.
