

1. Record Nr.	UNINA9910874677403321
Autore	Peng Wei
Titolo	Bioinformatics Research and Applications : 20th International Symposium, ISBRA 2024, Kunming, China, July 19-21, 2024, Proceedings, Part I
Pubbl/distr/stampa	Singapore : , : Springer Singapore Pte. Limited, , 2024 ©2024
ISBN	9789819751280 9789819751273
Edizione	[1st ed.]
Descrizione fisica	1 online resource (531 pages)
Collana	Lecture Notes in Computer Science Series ; ; v.14954
Altri autori (Persone)	CaiZhipeng SkumsPavel
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Intro -- Preface -- Organization -- Contents - Part I -- Contents - Part II -- Contents - Part III -- Predicting Drug-Target Affinity Using Protein Pocket and Graph Convolution Network -- 1 Introduction -- 2 Materials and Methods -- 2.1 Representation of Protein Pocket -- 2.2 Representation of Molecule Structure -- 2.3 Model Architecture -- 2.4 Experimental Setup -- 2.5 Datasets -- 3 Results and Discussion -- 3.1 Evaluation Metrics -- 3.2 Comparison with Other Methods -- 3.3 Ablation Experiments -- 4 Conclusion -- References -- MSMK: Multiscale Module Kernel for Identifying Disease-Related Genes -- 1 Introduction -- 2 Materials -- 3 Methods -- 3.1 Multiscale Module Profile -- 3.2 Multiscale Module Kernel -- 3.3 Methods Integrating Multiscale Module Kernel -- 4 Experimental Results -- 4.1 Experimental Settings -- 4.2 Performance Analysis of Different Fusion Strategies -- 4.3 Performance Analysis of Different Kernel Sparseness -- 4.4 Performance Comparison of Different Algorithms -- 5 Conclusion -- References -- Flat and Nested Protein Name Recognition Based on BioBERT and Biaffine Decoder -- 1 Introduction -- 2 Related Work -- 2.1 Flat Protein Name Recognition -- 2.2 Nested Protein Name Recognition -- 3 Method -- 3.1 Overall Architecture -- 3.2 BioBERT Encoder -- 3.3 Biaffine Decoder -- 4 Experiments -- 4.1 Datasets --

4.2 Experimental Settings -- 4.3 Results -- 5 Discussion -- 5.1 Ablation Study -- 5.2 Impact of Smoothing Strategy -- 5.3 Visualization Example -- 5.4 Categorical Performances -- 6 Conclusions -- References -- RFIR: A Lightweight Network for Retinal Fundus Image Restoration -- 1 Introduction -- 2 Method -- 2.1 Dynamic Multi-head Self-Attention -- 2.2 Sparse Spatial Self-attention -- 2.3 Feed-Forward Network -- 3 Experiments -- 3.1 Datasets and Implementation Details -- 3.2 Ablation Study -- 3.3 Comparative Experiments.

4 Conclusion -- A High-Resolution Figures -- References -- Gaussian Beltrami-Klein Model for Protein Sequence Classification: A Hyperbolic Approach -- 1 Introduction -- 2 Related Work -- 3 Proposed Approach -- 3.1 Beltrami-Klein Model -- 3.2 Kernel Matrix from Beltrami-Klein Distance -- 4 Results and Discussion -- 5 Conclusion -- References -- stEnTrans: Transformer-Based Deep Learning for Spatial Transcriptomics Enhancement -- 1 Introduction -- 2 Methods -- 2.1 Data Pre-processing -- 2.2 Self-supervised Learning -- 2.3 Details of StEnTrans -- 3 Experimental Results -- 3.1 StEnTrans Imputes the Gene Expression Accurately -- 3.2 StEnTrans Better Help to Discover Spatial Patterns -- 3.3 Ablation Study -- 4 Conclusions -- References -- Contrastive Masked Graph Autoencoders for Spatial Transcriptomics Data Analysis -- 1 Introduction -- 2 Methods -- 2.1 Data Preprocessing and Augmentation -- 2.2 GCNs Encoder and Decoder -- 2.3 Training Objective -- 2.4 Evaluation Criteria -- 3 Experimental Results -- 3.1 Experimental Datasets -- 3.2 Improved Spatial Domain Recognition Performance -- 3.3 Ablation Study -- 4 Conclusions -- References -- Spatial Gene Expression Prediction from Histology Images with STco -- 1 Introduction -- 2 Materials and Methods -- 2.1 Experimental Datasets -- 2.2 Data Pre-processing -- 2.3 Methods -- 3 Experimental Results -- 3.1 Evaluation Criteria -- 3.2 Comparison with Other Methods -- 3.3 Visualization of the Predicted Gene Expression -- 3.4 Spatial Region Detection -- 3.5 Ablation Study of the Proposed STco Model -- 4 Conclusions -- References -- Exploration and Visualization Methods for Chromatin Interaction Data -- 1 Introduction -- 2 Chromatin Interaction Data -- 2.1 Biological Interpretation -- 2.2 Formal Representation of Interaction Data Sets -- 2.3 Data Sets Used -- 3 Chromatin Data Visualization.

3.1 Data Visualization Module "Component Visualization" -- 3.2 Data Visualization Module "BioClique" -- 4 Using Data Visualization Tools for Deriving and Verification of Biological Hypotheses -- 5 Conclusions -- References -- A Geometric Algorithm for Blood Vessel Reconstruction from Skeletal Representation -- 1 Introduction -- 2 Method -- 2.1 Graph Construction -- 2.2 SDF Computation -- 2.3 Voxel Hashing and Mesh Extraction -- 3 Experimental Results -- 3.1 Datasets and Experiment Settings -- 3.2 Evaluation Metrics -- 3.3 Qualitative and Quantitative Analysis -- 4 Conclusion and Future Work -- References -- UFGOT: Unbalanced Filter Graph Alignment with Optimal Transport for Cancer Subtyping Based on Multi-omics Data -- 1 Introduction -- 2 Materials and Methods -- 2.1 fGOT -- 2.2 UFGOT -- 2.3 Optimization of UFGOT -- 2.4 Datasets -- 2.5 Benchmarking -- 3 Experimental Results -- 3.1 Selection of Filtering Operators -- 3.2 Combination of Omics Data -- 3.3 Alignment Performance of UFGOT -- 3.4 Clustering Performance of UFGOT -- 4 Discussion -- References -- Dendritic SE-ResNet Learning for Bioinformatic Classification -- 1 Introduction -- 2 Related Work -- 2.1 SE-ResNet -- 2.2 Dendritic Learning -- 3 Methodology -- 3.1 Squeeze-and-Excitation Structure -- 3.2 Dendritic Learning Module -- 4 Experiments and Results -- 4.1 Dataset -- 4.2 Model Hyper-

parameters Setting -- 4.3 Evaluation Metrics -- 4.4 Result and Discussion -- 5 Conclusion -- References -- GSDRP: Fusing Drug Sequence Features with Graph Features to Predict Drug Response -- 1 Introduction -- 2 Methods -- 3 Results -- 3.1 Experimental Settings and Model Evaluation -- 3.2 Results of Single-Omics and Multi-Omics Comparison Experiments -- 3.3 Performance Comparison of Our Method and Existing Methods -- 3.4 Ablation Study. 3.5 Performance Comparison of Our Method for Predicting Different Cancers -- 3.6 Blind Drugs/Cell-Lines Test -- 3.7 Case Study -- 4 Conclusion and Discussion -- References -- CircMAN: Multi-channel Attention Networks Based on Feature Fusion for CircRNA-Binding Protein Site Prediction -- 1 Introduction -- 2 Materials and Methods -- 2.1 Benchmark Dataset -- 2.2 Feature Encoding Scheme -- 2.3 Deep Neural Network Architecture -- 2.4 Performance Evaluation -- 3 Experimental Settings -- 4 Results -- 4.1 Comparison with Other Methods -- 4.2 Ablation Experiment -- 5 Conclusion -- References -- Machine Learning-Driven Discovery of Quadruple-Negative Breast Cancer Subtypes from Gene Expression Data -- 1 Introduction -- 2 Data -- 3 Methods -- 3.1 Data Preparation -- 3.2 Dimensionality Reduction -- 3.3 Clustering Methodology -- 3.4 Analyzing Cluster Features -- 3.5 Assessing Cluster Performance -- 4 Results -- 4.1 Patient Cluster Identification -- 4.2 Analyzing Cluster Features -- 4.3 Initial Cluster Assessment -- 5 Conclusion -- References -- A Novel Combined Embedding Model Based on Heterogeneous Network for Inferring Microbe-Metabolite Interactions -- 1 Introduction -- 2 Materials and Methods -- 2.1 Dataset -- 2.2 The Overall Flow of the Model -- 2.3 Node Embedding -- 2.4 Paired Embedding -- 2.5 Combined Embedding Model -- 3 Results and Discussion -- 3.1 Evaluation Criteria -- 3.2 Comparison of Algorithms -- 3.3 Ablation Study -- 3.4 Hyperparametric Study -- 3.5 Case Study -- 4 Conclusion -- References -- Central Feature Network Enables Accurate Detection of Both Small and Large Particles in Cryo-Electron Tomography -- 1 Introduction -- 2 Methods -- 2.1 Central Feature Network (CFN) -- 2.2 Gradient Descent Tracing -- 3 Experiments -- 3.1 Dataset and Experimental Settings -- 3.2 Performance Comparison -- 3.3 Benefits of Adding MLP-Mixer. 3.4 Implementation Details -- 4 Discussions and Conclusions -- References -- LncRNA-Disease Association Prediction Based on Integrated Application of Matrix Decomposition and Graph Contrastive Learning -- 1 Introduction -- 2 Materials and Methods -- 2.1 Data Collection -- 2.2 The Overall Flow of the Model -- 2.3 Disease Semantic Similarity -- 2.4 Functional Similarity of LncRNA (miRNA) -- 2.5 Gaussian Interaction Spectral Kernel Similarity of LncRNAs/miRNAs and Diseases -- 2.6 Similarity Matrix Fusion -- 2.7 LncRNA-miRNA-Disease Graph Construction -- 3 Matrix Decomposition -- 3.1 Nonnegative Matrix Factorization and Matrix Reconstruction -- 3.2 Extracting Linear Features of Nodes by Singular Value Decomposition -- 4 Extracting Node Embeddings by Graph Contrastive Learning -- 4.1 Encoder Based on Graph Convolutional Networks -- 4.2 Constructing Global Representation -- 4.3 Constructing Negative Samples Based on Destructor Function -- 4.4 Discriminator -- 5 Experiments -- 5.1 Experiment Settings -- 5.2 Comparison with Other Baseline Methods -- 5.3 Ablation Experiment -- 6 Case Studies -- 7 Conclusion -- References -- Predictive Score-Guided Mixup for Medical Text Classification -- 1 Introduction -- 2 Related Work -- 3 The Proposed Method -- 3.1 Encoding Layer and Multi-head Scoring Layer -- 3.2 Score Guided Mixup Layer -- 3.3 The Loss Function -- 4 Experimental Results -- 4.1 Dataset -- 4.2 Evaluation Metrics -- 4.3 Baseline -- 4.4

Experimental Environment -- 5 Results -- 5.1 Comparison Experiment -- 5.2 Impact of Dimensionality on Model Performance -- 5.3 Ablation Experiment -- 5.4 Case Study -- 6 Conclusions -- References -- CHASOS: A Novel Deep Learning Approach for Chromatin Loop Predictions -- 1 Introduction -- 2 Materials and Methods -- 2.1 The Workflow of the Model -- 2.2 Construction of Anchor Score Prediction Model.  
2.3 Construction of OCR Score Prediction Model.

---