

1. Record Nr.	UNINA9910874672303321
Autore	Peng Wei
Titolo	Bioinformatics Research and Applications : 20th International Symposium, ISBRA 2024, Kunming, China, July 19-21, 2024, Proceedings, Part III
Pubbl/distr/stampa	Singapore : , : Springer Singapore Pte. Limited, , 2024 ©2024
ISBN	981-9750-87-3
Edizione	[1st ed.]
Descrizione fisica	1 online resource (159 pages)
Collana	Lecture Notes in Computer Science Series ; ; v.14956
Altri autori (Persone)	CaiZhipeng SkumsPavel
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Intro -- Preface -- Organization -- Contents - Part III -- Feddaw: Dual Adaptive Weighted Federated Learning for Non-IID Medical Data -- 1 Introduction -- 2 Method -- 2.1 Client-Side Classification Layer Probability Weighting Factor Adjustment Module -- 2.2 Server-Side Accuracy-Based Adaptive Weight Aggregation Module -- 3 Experiments and Results -- 3.1 Data Description -- 3.2 Non-IID Dataset Segmentation -- 3.3 Baselines and Implementation Details -- 3.4 Performance Comparison with Baseline Methods -- 4 Conclusion -- References -- LoopNetica: Predicting Chromatin Loops Using Convolutional Neural Networks and Attention Mechanisms -- 1 Introduction -- 2 Results -- 2.1 LoopNetica: Effectively Combines Convolutional Neural Networks and Attention Mechanisms -- 2.2 LoopNetica Can Accurately Predict Chromatin Loops -- 2.3 The LoopNetica Model Performs Exceptionally Well in Scenarios with Extremely Imbalanced Positive and Negative Samples -- 2.4 LoopNetica Successfully Captures Sequence Features and Discovers Type-Specific Motifs -- 3 Methods -- 3.1 Data Preparation -- 3.2 LoopNetica Model -- 3.3 Training Strategy -- 4 Discussion -- 5 Conclusion -- References -- Probabilistic and Machine Learning Models for the Protein Scaffold Gap Filling Problem -- 1 Introduction -- 2 Methodology -- 2.1 Data Collection -- 2.2 Data Preprocessing -- 2.3 The Proposed Models for

the PSGF Problem with Known Gap Size -- 2.4 A Probabilistic Algorithm for the PSGF Problem with Known Gap Mass -- 3 Experimental Results -- 3.1 Results for PSGF with Known Gap Size Using ML Models -- 3.2 Results for PSGF with Known Gap Masses Using the Probabilistic Algorithm -- 4 Conclusions -- References -- Patient Anticancer Drug Response Prediction Based on Single-Cell Deconvolution -- 1 Introduction -- 2 Materials -- 3 Methods -- 3.1 Gene Expression Data Deconvolution.

3.2 Domain Invariant Feature Extraction -- 3.3 Training Classifier -- 4 Experiment -- 4.1 Drug Response Prediction for Clinical TCGA Dataset -- 4.2 Results of Ablation Experiments -- 5 Conclusion -- References -- A Data Set of Paired Structural Segments Between Protein Data Bank and AlphaFold DB for Medium-Resolution Cryo-EM Density Maps: A Gap in Overall Structural Quality -- 1 Introduction -- 2 Methods -- 3 Results and Discussion -- 3.1 The Dataset of Matched Structural Segments in the PDB/AlphaFold DB -- 3.2 Evaluation of Matched Structural Segments Using MolProbity -- 3.3 Differences in Local Quality Between the Four Models Derived from Medium-Resolution Cryo-EM Maps and Those Predicted with AlphaFold -- 4 Conclusion -- References -- PmmNDD: Predicting the Pathogenicity of Missense Mutations in Neurodegenerative Diseases via Ensemble Learning -- 1 Introduction -- 2 Materials and Methods -- 2.1 Overall Workflow -- 2.2 Dataset Construction -- 2.3 Feature Extraction -- 2.4 PmmNDD Model Training -- 2.5 Evaluation Metrics -- 3 Results and Discussion -- 3.1 Performance of Different Ensemble Models of PmmNDD -- 3.2 Analysis of Feature Importance -- 3.3 Comparison with Existing Prediction Methods -- 3.4 Predictions for 3 Million Missense Mutations in NDDs -- 4 Conclusions -- References -- Improved Inapproximability Gap and Approximation Algorithm for Scaffold Filling to Maximize Increased Duo-Preservations -- 1 Introduction -- 2 Preliminaries -- 3 An Improved Inapproximability Gap for SF-MIDP -- 4 Approximation Algorithms for SF-MIDP -- 4.1 An Approximation Algorithm for the SF-MIDP -- 4.2 Proof of the Approximation Ratio -- 5 Experimental Results -- 6 Conclusion -- References -- Residual Spatio-Temporal Attention Based Prototypical Network for Rare Arrhythmia Classification -- 1 Introduction -- 2 Methods.

2.1 Residual Spatio-Temporal Attention Feature Extractor -- 2.2 Meta Training Based on Prototype Network -- 2.3 Meta Test -- 3 Experiments and Results -- 3.1 Dataset -- 3.2 Experiment Settings -- 3.3 Performance Comparison with Other ECG Few-Shot Methods -- 3.4 Ablation Experiments -- 3.5 Feature Extractor Performance on Common Classes Comparison with Baselines -- 3.6 Meta Test with Different Classifier -- 3.7 Visualization Analysis -- 4 Conclusion -- References -- SEMQuant: Extending Sipros-Ensemble with Match-Between-Runs for Comprehensive Quantitative Metaproteomics -- 1 Introduction -- 2 Methods -- 2.1 Overview of SEMQuant -- 2.2 Implementation and Software Test -- 3 Experiments and Results -- 3.1 Evaluation Measures -- 3.2 Benchmark Datasets and Experiment Design -- 3.3 Parameters for Benchmarking Software -- 3.4 Assessment of the False Positives of Transferred Peptides Using the Two-Organism Dataset -- 3.5 Assessment of the Identification and Quantification Results Using the Yeast-UPS1 Datasets -- 3.6 Assessment of the Identification and Quantification Results Using the In-House Dataset of a Four-Bacteria Mixed Culture -- 3.7 Assessment of the Identification and Quantification Results Using Two Mock Community Datasets -- 4 Conclusion -- 5 Data Availability -- References -- PrSMBooster: Improving the Accuracy of Top-Down Proteoform Characterization Using Deep Learning Rescoring Models --

1 Introduction -- 2 Method -- 2.1 Basic Feature Extraction -- 2.2 Rescoring Model -- 3 Result and Discussion -- 3.1 Dataset and Preprocessing -- 3.2 Evaluation Criteria -- 3.3 Comparison of PrSM Results Before and After Rescoring -- 4 Conclusion -- References -- FCMEDriver: Identifying Cancer Driver Gene by Combining Mutual Exclusivity of Embedded Features and Optimized Mutation Frequency Score -- 1 Introduction -- 2 Materials and Methods. 2.1 Datasets and Resources -- 2.2 Networks Construction and Network Embedding -- 2.3 Gene Clustering to Detect the Modules of Highly Correlated Genes -- 2.4 Module Importance Score with Mutual Exclusivity -- 2.5 Comprehensive Scoring to Prioritize Driver Genes -- 3 Results and Conclusion -- References -- Author Index.
