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	Nota di contenuto	Particle Swarm Optimization-based Power Allocation Scheme for Secrecy Sum Rate Maximization in NOMA with Cooperative Relaying -- A Discrete Particle Swarm Optimization for PairwiseSequence Alignment -- A Diversity based Competitive Multi-Objective PSO for Feature Selection -- A Decomposition-based Hybrid Estimation of Distribution Algorithm for Practical Mean-CVaR Portfolio Optimization -- CBLNER: a multi-models biomedical named entity recognition system based on machine learning -- Dice Loss in Siamese Network for Visual Object Tracking -- Fuzzy PID Controller for Accurate Power Sharing in DC

Microgrid -- Precipitation Modeling and Prediction Based on Fuzzy-control Multi-cellular Gene Expression Programming and Wavelet Transform -- Integrative Enrichment Analysis of Intra- and Inter-Tissues’ Differentially Expressed Genes Based on Perceptron -- Identifying differentially expressed genes based on differentially expressed edges -- Gene functional module discovery via integrating geneexpression and PPI network data -- A novel framework for improving the prediction of disease-associated microRNAs -- Precise Prediction of Pathogenic Microorganisms using 16S rRNA Gene Sequences -- Learning from Deep Representations of Multiple Networks for Predicting Drug–Target Interactions -- Simulation of Complex neural firing patterns based on improved deterministic Chay model -- Knowledge based helix angle and residue distance restraint free energy terms of GPCRs -- Improved Spectral Clustering Method for Identifying Cell Types from Single-Cell Data -- A Novel Weight Learning Approach Based on Density for Accurate Prediction of Atherosclerosis -- An effective approach of measuring disease similarities based on the DNN regression model -- Herb Pair Danggui-Baishao:Pharmacological Mechanisms Underlying Primary Dysmenorrhea by Network Pharmacology Approach -- End-to-end learning based compound activity prediction using binding pocket information -- A novel approach for predicting lncRNA-disease associations by structural perturbation method -- Improved Inductive Matrix Completion Method for Predicting MicroRNA-Disease Associations -- A link and Weight-Based Ensemble Clustering for Patient Stratification -- HGMDA: HyperGraph for Predicting MiRNA-disease Association -- Discovering Driver Mutation Profiles in Cancer with A Local Centrality Score -- LRMDA: Using Logistic Regression and Random Walk with Restart for MiRNA-Disease Association Prediction -- Distinguishing driver missense mutations from benign polymorphisms in breast cancer -- A novel method to predict protein regions driving cancer through integration of multi-omics data -- In Silico Identification of Anticancer Peptides with Stacking Heterogeneous Ensemble Learning Model and Sequence Information -- Effective Analysis of Hot Spots in Hub Protein Interfaces Based on Random Forest -- Prediction of human lncRNAs based on integrated information entropy features -- A Gated Recurrent Unit Model for Drug Repositioning by Combining Comprehensive Similarity Measures and Gaussian Interaction Profile Kernel -- A Novel Approach to predicting miRNA-disease associations -- Hierarchical Attention Network for Predicting DNA-Protein Binding Sites -- Motif discovery via convolutional networks with k-mer embedding -- Whole-Genome Shotgun Sequence of Natronobacterium Gregoryi SP2 -- The detection of gene modules with overlapping characteristic via integrating multi-omics data in six cancers -- Combining High Speed ELM with a CNN Feature Encoding to Predict LncRNA-Disease Associations -- A prediction method of DNA-binding proteins based on evolutionary information -- Research on RNA Secondary Structure Prediction Based on Decision Tree -- Improving hot region prediction by combining gaussian naïve Bayes and DBSCAN -- An efficient LightGBM model to predict protein selfinteracting using Chebyshev moments and bi-gram -- Combining Evolutionary Information and Sparse Bayesian Probability Model to Accurately Predict Self-Interacting Proteins -- Identification of DNA-Binding Proteins via Fuzzy Multiple Kernel Model and Sequence Information -- Research on HP Model Optimization Method Based on Reinforcement Learning -- EnsembleKQC: An Unsupervised Ensemble Learning Method for Quality Control of Single Cell RNA-seq Sequencing Data -- Regulatory sequence architecture of stress responsive genes in (Oryza sativa) --

Identifying Cancer Biomarkers from High-throughput RNA sequencing Data by Machine Learning -- Identification of prognostic and heterogeneous breast cancer biomarkers based on fusion network and multiple scoring strategies -- A Novel Differential Essential Genes Prediction Method Based on Random Forests Model -- Identification of candidate biomarkers and pathways associated with liver cancer by bioinformatics analysis -- Real-Time Pedestrian Detection in Monitoring Scene Based on Head Model -- CNN and Metadata for classification of benign and malignant melanomas -- An Application of Using Support Vector Machine Based on Classification Technique for Predicting Medical Data sets -- Fully Convolutional Neural Networks for 3D Vehicle Detection based on Point Clouds -- Illegally Parked Vehicle Detection Based on Haar-Cascade Classifier -- Graph-SLAM Based Hardware-in-the-loop-simulation for Unmanned Aerial Vehicles Using Gazebo and PX4 open source -- Evaluating CNNs for Military Target Recognition -- Detection and Segmentation of Kidneys from Magnetic Resonance Images in Patients with Autosomal Dominant Polycystic Kidney Disease -- Research of Formal Analysis Based on Extended Strand Space Theories -- The Application of Artificial Intelligence in Music Education -- Single-machine green scheduling problem of multi-speed machine -- Whale Optimization Algorithm with Local Search for Open Shop Scheduling Problem to Minimize Makespan -- Water Wave Optimization for the Multidimensional Knapsack Problem -- A Complex-valued Firefly Algorithm -- Gene Expression Prediction Based on Hybrid Evolutionary Algorithm -- MPdeep: the medical procession with deep learning -- Predicting potential Drug-Target Interactions with Multi-label learning and ensemble learning -- Robust Circulating Tumor Cells Detection in Scanned Microscopic Images with Cascaded Morphological and Faster R-CNN Deep Detectors -- Electrocardiogram Diagnosis Based on SMOTEENN and Random Forest -- Complex leaves classification with features extractor -- IDP - OPTICS: Improvement of Differential Privacy Algorithm in Data Histogram Publishing Based on Density Clustering.

Sommario/riassunto

This two-volume set of LNCS 11643 and LNCS 11644 constitutes - in conjunction with the volume LNAI 11645 - the refereed proceedings of the 15th International Conference on Intelligent Computing, ICIC 2019, held in Nanchang, China, in August 2019. The 217 full papers of the three proceedings volumes were carefully reviewed and selected from 609 submissions. The ICIC theme unifies the picture of contemporary intelligent computing techniques as an integral concept that highlights the trends in advanced computational intelligence and bridges theoretical research with applications. The theme for this conference is “Advanced Intelligent Computing Methodologies and Applications.” Papers related to this theme are especially solicited, including theories, methodologies, and applications in science and technology.