Guest Editorial for Special Section on the 16th International Conference on Intelligent Computing (ICIC)

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THIS special section includes a selection of eight papers presented at the Sixteenth International Conference on Intelligent Computing (ICIC) held in Bari, Italy, on October 2-5, 2020. ICIC was formed to provide an annual forum dedicated to the emerging and challenging topics in artificial intelligence, machine learning, bioinformatics, and computational biology, etc. It aims to bring together researchers and practitioners from both academia and industry to share ideas, problems and solutions related to the multifaceted aspects of intelligent computing.

This year, the conference received 457 submissions from 21 countries and regions. All papers went through a rigorous peer review procedure and each paper received at least three review reports. Based on the review reports, the Program Committee finally selected 162 research papers for presentation at ICIC 2020. The authors of eight high quality papers were invited to submit an extended version to this special section. Following a rigorous review process, these eight papers were selected for publication.

The first paper in this section, "G Protein-Coupled Receptor Interaction Prediction Based on Deep Transfer Learning" by Tengsheng Jiang, Yuhui Chen, Shixuan Guan, Zhongtian Hu, Weizhong Lu, Qiming Fu, Yijie Ding, Haiou Li, and Hongjie Wu, proposes a transfer learning method based on sample similarity, using XGBoost as a weak classifier and using the TrAdaBoost algorithm based on JS divergence for data weight initialization to transfer samples to construct a data set. After that, the deep neural network based on the attention mechanism is used for model training. The existing GPCR is used for prediction. In short-distance contact prediction, the accuracy of the method is 0.26 higher than similar methods.

The next paper, "Novel Algorithm for Improved Protein Classification Using Graph Similarity" by Hsin-Hung Chou, Ching-Tien Hsu, Chin-Wei Hsu, Kai-Hsun Yao, Hao-Ching Wang, and Sun-Yuan Hsieh examines the problems of protein classification. The paper designs a classification algorithm, where auxiliary graphs are used to represent proteins, with every amino acid in a protein to a vertex in a graph. Moreover, the links between amino acids correspond to the edges between the vertices. The proposed algorithm classifies proteins according to the similarities in their graphical structures, which is efficient and accurate in distinguishing proteins from different families and outperformed related algorithms experimentally.

The paper "Predicting In-Vitro DNA Protein Binding With a Spatially Aligned Fusion of Sequence and Shape" by Qinhu Zhang, Yindong Zhang, Siguo Wang, Zhan-Heng Chen, Valeriya Gribova, Vladimir Fedorovich Filaretov, and De-Shuang Huang proposes a novel deep learning-based architecture, named hybridShape eDeepCNN, for TFBS prediction which integrates DNA sequence and shape information in a spatially aligned manner. The model utilizes the power of the multi-layer convolutional neural network and constructs an independent subnetwork to adapt for the distinct data distribution of heterogeneous features. Besides, the paper explores the usage of continuous embedding vectors as the representation of DNA sequences. Based on the experiments on 20 in-vitro datasets derived from universal protein binding microarrays (uPBMs), the superiority of the proposed method was demonstrated and the underlying design logic was validated.

The paper "DeepCLD: An Efficient Sequence-Based Predictor of Intrinsically Disordered Proteins" by Min Fang, Yufeng He, Zhihua Du, and Vladimir N. Uversky, proposes a novel algorithm, Deep CudnnLSTM Disorder (DeepCLD), for sequence-based prediction of intrinsically disordered proteins. This algorithm uses amino acid position specific scoring matrix (PSSM) to capture the intrinsic variability characteristic of sequence patterns, ResNet to preserve feature space structure, and bidirectional CudnnLSTM as recurrent layer to further improve the efficiency. Furthermore, DeepCLD also utilized the attention mechanism to solve the problem of gradient disappearing in deep network. Comparative analyses show that DeepCLD has faster training speed and higher prediction accuracy than comparable methods.

The paper "Predicting miRNA-Disease Associations via Combining Probability Matrix Feature Decomposition With Neighbor Learning" by Xinguo Lu, Jinxin Li, Zhenghao Zhu, Yue Yuan, Guanyuan Chen, and Keren He addresses probabilistic matrix decomposition combined with neighbor learning to identify miRNA-disease associations utilizing heterogeneous

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Date of current version 8 December 2022.
This work was supported in part by the National Key R&D Program of China under Grant 2018AAA0100100, and in part by the National Natural Science Foundation of China under Grant 61732012.
Digital Object Identifier no. 10.1109/TCBB.2022.3150232

data (PMDA). First, similarity networks for diseases and miRNAs were built, respectively, by integrating semantic information and functional interactions. Second, a neighbor learning model utilized the neighbor information of individual miRNA or disease to enhance the association relationship to tackle the spare problem. Third, the potential association between miRNAs and diseases via probability matrix decomposition was predicted. The experimental results show that PMDA is superior to other five methods in sparse and unbalanced data. The case study shows that the new miRNA-disease interactions predicted by the PMDA are effective and the performance of the PMDA is superior to other methods.

The paper "Extra Trees Method for Predicting LncRNA-Disease Association Based on Multi-Layer Graph Embedding Aggregation" by Qing-Wen Wu, Rui-Fen Cao, Jun-Feng Xia, Jian-Cheng Ni, Chun-Hou Zheng, and Yan-Sen Su proposes reconstructing similarity networks for both lncRNAs and diseases using top k similar information, and constructed a lncRNA-disease heterogeneous network (LDN). Then, Multi-Layer Graph Convolutional Network on LDN was applied to obtain latent feature representations of nodes. Finally, the Extra Trees was used to calculate the probability of association between disease and lncRNA. The results of extensive 5-fold cross-validation experiments show that MLGCNET has superior prediction performance compared to the state-of-the-art methods. Case studies confirm the performance of their model on specific diseases. All the experiment results prove the effectiveness and practicality of MLGCNET in predicting potential lncRNA-disease associations.

The paper "Predicting Cancer Lymph-Node Metastasis from LncRNA Expression Profiles Using Local Linear Reconstruction Guided Distance Metric Learning" byBo Li, Yihui Tian, Yang Tian, Shihua Zhang, and Xiaolong Zhang, puts forward a local linear reconstruction guided distance metric learning to handle lncRNA data for determination of cancer lymph-node metastasis. Taking the defined distance metric and lncRNA data supervised information into account, a local margin model is deduced to find a low dimensional subspace for lncRNA signature extraction. At last, a classifier is constructed to predict cancer lymph-node metastasis, where the learned distance metric is also adopted. Several experiments on lncRNA data sets have been carried out, and experimental results show the performance of the proposed method by making comparisons with some other related dimensionality reduction methods and the classical classifier models.

This section ends with the paper "Inferring Latent MicroRNA-Disease Associations on A Gene-Mediated Tripartite Heterogeneous Multiplexing Network" Wen Li, Shulin Wang, Junlin Xu, and Ju Xiang, creatively fused multiple similarity subnetworks from multi-sources for miRNAs, genes and diseases by multiplexing technology, respectively. Then, three multiplexed biological subnetworks are connected through the extended binary association to form a tripartite complete heterogeneous multiplexed network (Tri-HM). Finally, because the constructed Tri-HM network can retain subnetworks' original topology and biological functions and expand the binary association and dependence between the three biological entities, rich neighbourhood information is obtained iteratively from neighbours by a non-equilibrium random walk. Through cross-validation, the tri-HM-RWR model obtained an AUC value of 0.8657, and an AUPR value of 0.2139 in the global 5-fold cross-validation, which shows that the proposed model can more fully speculate disease-related miRNAs.

We would like to express our sincere thanks to the ICIC 2020 Program Committee members for their invaluable effort in making ICIC 2020 such a success. We would like to thank to the external reviewers for volunteering their time to review the submissions to the conference and the special section. We would like to thank Aidong Zhang, the former editor-in-chief of the IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB), for offering this opportunity for wider dissemination of the research presented at ICIC 2014 in TCBB. Last but not least, we would like to thank the authors of these eight articles for their time and effort in submitting their high quality work to ICIC and TCBB.

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De-Shuang Huang (Fellow, IEEE) is currently a professor with the Big Data and Intelligent Computing Research Center, Guangxi Academy of Science,China, and with the Department of Computer Science and the director of the Institute of Machine Learning and Systems Biology, Tongji University, China. He has authored or coauthored more than 470 papers in international journals, international conferences proceedings, and book chapters. Particularly, he has authored or coauthored more than 230 SCI indexed papers. His Google Scholar citation number is more than 18900 times and H index 73. His research interests include neural networks, pattern recognition, and bioinformatics. He is currently the fellow of the International Association of Pattern Recognition (IAPR Fellow) and senior member of INNS, Bioinformatics and Bioengineering technical committee member of IEEE CIS, Neural Networks technical committee member of IEEE CIS, a member of INNS, co-chair of Big Data Analytics Section within INNS, and an associate editor for *IEEE/ACM Transactions on Computational Biology & Bioinformatics* and *Neural Networks*. He founded the International Conference on Intelligent Computing (ICIC) in 2005. ICIC has since been successfully held annually with him serving as the general or steering committee chair. He was also the 2015 International Joint Conference on Neural Networks (IJCNN 2015) general chair, July 12-17, 2015, Killarney, Ireland, the 2014 11th IEEE Computational Intelligence in Bioinformatics and Computational Biology Conference (IEEE-CIBCBC) program committee chair, May 21-24, 2014, Honolulu, USA.

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