Guest Editorial for Special Section on the 14th International Conference on Intelligent Computing (ICIC)

De-Shuang Huang ⓘ, Vitoantonio Bevilacqua ⓘ, and Michael Gromiha ⓘ

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THIS special section includes a selection of eight papers presented at the Fourteenth International Conference on Intelligent Computing (ICIC) held in Wuhan, China, on August 15-18, 2018. 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 632 submissions from 19 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 275 research papers for presentation at ICIC 2018. 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, "Constructive Prediction of Potential RNA Aptamers for a Protein Target" by Wook Lee and Kyungsook Han, developed a new random forest (RF) model for finding potential RNA aptamers for a protein target. The potential RNA aptamers predicted by the method reveal similar secondary and protein-binding structures as the actual RNA aptamers. The RF model shows a reliable performance in both cross validations and independent testing. The approach will be useful in reducing time and money spent on in vitro experiments by substantially limiting the size of the initial pool of nucleic acid sequences.

The next paper, "Capsule Network for Predicting RNA-Protein Binding Preferences Using Hybrid Feature" by Zhen Shen, Su-Ping Deng, and De-Shuang Huang, proposed an improved capsule network to predict RNA-protein binding preferences, which can use both RNA sequence features and structure features. Experimental results show that the

proposed method iCapsule performs better than three baseline methods in this field. In addition, the paper also studied the impact of model structure on model performance by performing the proposed method with different number of convolution layers and different kernel sizes.

The paper "PASA: Identifying More Credible Structural Variants of Hedou12" by Huiqiang Jia, Haichao Wei, Daming Zhu, Jingjing Ma, Hai Yang, Ruizhi Wang, and Xiangzhong Feng devoted to detect deletions, insertions, inversions, in total of three kinds of structural variants occurring in Hedou12 genome in contrast to Williams82 genome. To find more potential structural variants, the paper tried to develop new principles to detect discordant and split read map sets supporting structural variants. Experimental results show that the method can be able to find deletions, insertions, and inversions in Hedou12 in contrast to Williams82 DELLY as well as LUMPY fails to find.

The paper "Jointly Integrating VCF-Based Variants and OWL-Based Biomedical Ontologies in MongoDB" by Jian Liu, Zhi Qu, Mo Yang, Jialiang Sun, Shuhui Su, and Lei Zhang, focused on exploring an effective method for the management of VCF-based genetic variants and OWL-based biological ontologies. The authors proposed a series of rules for the mapping from VCF and OWL files to JSON files, and then presented rule-based algorithms for transforming VCF-based genetic variants and OWL-based biological ontologies into JSON objects. This work was shown in experiments to have a well performance.

The next paper, "Learning Multimodal Networks from Heterogeneous Data for Prediction of lncRNA–miRNA Interactions" by Pengwei Hu, Yu-An Huang, Keith C.C. Chan, and Zhu-Hong You presented a novel computational approach for prediction of lncRNA–miRNA interactions. Using a set of real data, it was shown that the method can be a very effective one for the accurate prediction of lncRNA-miRNA interactions.

The paper "Efficient Classification of Hot Spots and Hub Protein Interfaces by Recursive Feature Elimination and Gradient Boosting" by Xiaoli Lin, Xiaolong Zhang, and Xin Xu presented the boosting algorithm and gradient boosting algorithm to classify hot spots with three common datasets and two hub protein datasets. Five datasets from different protein databases are used to verify the models in the experiments. Experimental results show that the proposed

- D.-S. Huang is with the Instute of Machine Learning and Systems Biology, Tongji University, Shanghai 201804, China. E-mail: dshuang@tongji.edu.cn.
- V. Bevilacqua is with the Electrical and Electronics Department, Polytechnic of BariVia Orabona, 70126 Bari, BA, Italy.
  E-mail: vitoantonio.bevilacqua@gmail.com.
- M. M. Gromiha is with the Department of Biotechnology, Indian Institute of Technology (IIT), Madras, Chennai, India. E-mail: gromiha@iitm.ac.in.

classification models have the competitive performance compared with existing classification methods.

The paper "A Novel Approach to Detecting Epistasis using Random Sampling Regularisation" by Jade Hind, Paulo Lisboa, Abir J. Hussain, and Dhiya Al-Jumeily, proposed a novel methodology for the detection of epistasis. Using a process of Random Sampling Regularisation which randomly splits and produces sample sets to conduct a voting system to regularise the significance and reliability of biological markers, SNPs. Results for the detection of epistasis, in the classification of breast cancer patients, indicated eight outlined risk candidate interactions from five variants and a singular candidate variant with high protective association.

This section ends with the paper, "Using Weighted Extreme Learning Machine Combined with Scale-invariant Feature Transform to Predict Protein-Protein Interaction from Protein Evolutionary Information" by Jianqiang Li, Xiaofeng Shi, Zhu-Hong You, Hai-Cheng Yi, Zhuangzhuang Chen, Qiuzhen Lin, and Min Fang presented a method to predict PPIs using protein sequences, where Scale-Invariant Feature Transform (SIFT) algorithm and Weighted Extreme Learning Machine (WELM) classifier were used to extract features and classify them respectively. In order to evaluate the proposed approach properly, some comparisons with Support Vector Machine (SVM) classifier and other recent-developed methods were made. The experiments found that the training time of the method is greatly shortened, which is obviously superior to the previous methods, such as SVM, ACC, PCVMZM and so on.

We would like to express our sincere thanks to the ICIC 2018 Program Committee members for their invaluable effort in making ICIC 2018 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 current 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 2018 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*.

De-Shuang Huang
Vitoantonio Bevilacqua
M. Michael Gromiha
Guest Editors

ACKNOWLEDGMENTS

De-Shuang Huang (Senior Members, IEEE) received the BSc degree from the Institute of Electronic Engineering, Hefei, China, in 1986, the MSc degree from the National Defense University of Science and Technology, Changsha, China, in 1989, and the PhD degree from Xidian University, Xian, China, in 1993, all in electronic engineering, . During 1993–1997 period he was a postdoctoral student respectively in the Beijing Institute of Technology and in the National Key Laboratory of Pattern Recognition, Chinese Academy of Sciences, Beijing, China. In September 2000, he joined the Institute of Intelligent Machines, Chinese Academy of Sciences as the Recipient of "Hundred Talents Program of CAS". In September 2011, he entered into Tongji University as chaired professor. From September 2000 to March 2001, he worked as research associate in Hong Kong Polytechnic University. From August to September 2003, he visited the George Washington University as visiting professor, Washington DC, USA. From July to December 2004, he worked as the university fellow, in Hong Kong Baptist University. From March, 2005 to March, 2006, he worked as research fellow, in the Chinese University of Hong Kong. From March to July, 2006, he worked as visiting professor, in the Queen's University of Belfast, U.K. In 2007, 2008, and 2009, he worked as visiting professor, in Inha University, Korea, respectively. From June 2015 to June 2018, he worked as visiting professor of the Liverpool John-Moore University, U.K. In addition, he is the director of the Institute of Machines Learning and Systems Biology, Tongji University. He is currently the fellow of the International Association of Pattern Recognition (IAPR Fellow), senior members of International Neural Network Society (INNS). He was the 2015 International Joint Conference on Neural Networks (IJCNN 2015) General Chair, July 12–17, 2015, Killarney, Ireland. He has published more than 220 journal papers. His current research interest includes bioinformatics, pattern recognition, and image processing.

Vitoantonio Bevilacqua received the the bachelor degree in electronic engineering and the PhD degree in electrical engineering both from the Polytechnic of Bari in 1996 and 2000. He is currently a tenured assistant professor in computing systems at the Department of Electrical and Electronic Engineering of Polytechnic of Bari. Since 1996 he has been working and investigating in the field of computer vision and image processing, neural networks, evolutionary algorithms, and hybrid expert systems. The main applications of his research are in real world, in biometry, in medicine and recently in bioinformatics and systems biology. He has published more than 70 papers in refereed journals, books, international conferences proceedings, and chaired several sessions such as *Speech Recognition*, *Biomedical Informatics*, *Intelligent Image Processing and Bioinformatics* in international conferences. He won the Best Paper Award at International Conference on Intelligent Computing held in Shanghai (ICIC 2008), he was program chair of ICIC 2009, publication chair of ICIC 2010, tutorial chair of ICIC 2011, and is publication chair of ICIC 2012.

M. Michael Gromiha received the PhD degree in physics from Bharathidasan University, Tiruchirappalli, India, in 1994. He pursued his postdoctoral research at the International Center for Genetic Engineering and Biotechnology (ICGEB), Trieste, Italy, and the Institute of Physical and Chemical Research (RIKEN), Tsukuba, Japan. Currently, he is working as a senior research scientist with the Computational Biology Research Center (CBRC) of the National Institute of Advanced Industrial Science and Technology (AIST), Tokyo, Japan. His main research interests are structural analysis, prediction, folding and stability of globular and membrane proteins, protein interactions and development of databases, and online tools in bioinformatics. He has published more than 120 research articles, 20 reviews, and a book.

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