

# Guest Editorial for Special Section on the 10th International Conference on Intelligent Computing (ICIC)

De-Shuang Huang, Vitoantonio Bevilacqua, and M. Michael Gromiha

THIS special section includes a selection of eight papers presented at the 10th International Conference on Intelligent Computing (ICIC) held in Taiyuan, China, on August 3–6, 2014. ICIC was formed to provide an annual forum dedicated to the emerging and challenging topics in artificial intelligence, machine learning, bioinformatics, 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 667 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 235 research papers for presentation at ICIC 2014. 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, “GeneNetFinder2: Improved Inference of Dynamic Gene Regulatory Relations with Multiple Regulators” by Kyungsook Han and Jeonghoon Lee, develops a method for identifying dynamic gene regulations of several types from the time-series gene expression data. The method can find gene regulations with multiple regulators that work in combination or individually as well as those with single regulators. Experimental evaluations show that their method finds regulatory relations as well as those with multiple, independent regulators or single regulators, and represents gene regulatory relations as a dynamic network in which different gene regulatory relations are shown in different stages of the cell cycle.

The next paper, “Hybrid Framework using Multiple-Filters and an Embedded Approach for an Efficient and Robust Selection and Classification of Microarray Data” by Edmundo Bonilla Huerta, Alberto Hernandez Montiel, Roberto Morales Caporal, and Marco Arjona Lopez presents a hybrid framework for gene selection and classification of

DNA microarray data. In this framework, traditional statistical methods are combined for preliminary gene selection. Then, different relevant gene subsets are selected by using an embedded method. By analyzing the frequency of each gene in the different gene subsets, a gene subset which consists of the most relevant genes is obtained from this process. From simulation study, it is observed that the proposed approach works better than other methods reported in the literature.

The paper “Predicting Hub Genes Associated with Cervical Cancer through Gene Co-expression Networks” by Su-Ping Deng, Lin Zhu, and De-Shuang Huang uses several bioinformatics tools to study the key genes resulting in the cervical cancer. Through comparing two differential co-expression networks (DCNs) at two different states, they found a common sub-network and two differential sub-networks as well as some hub genes in three sub-networks. The results can guide further experiments about the cervical cancer.

The paper “Predicting the Subcellular Localization of Proteins with Multiple Sites Based on Multiple Features Fusion” by Xumi Qu, Dong Wang, Yuehui Chen, Shanping Qiao, and Qing Zhao, focuses the problem of protein sub-cellular localization prediction. In contrast to traditional predictive methods which are mainly based on only one subcellular location, this paper studies proteins which have two or even more subcellular locations, which have useful implication for both basic biology and bioinformatics. By fusing together several feature extraction methods and multi-label learning scheme, their proposed method outperforms existing machine learning predictive tools on several benchmark datasets.

The next paper, “A Faster cDNA Microarray Gene Expression Data Classifier for Diagnosing Diseases” by Sun-Yuan Hsieh and Yu-Chun Chou, addresses the challenge of microarray data classification. This study enhanced a previously proposed gene expression graph (GEG)-based classifier to shorten the computation time. The modified classifier filters genes by using an edge weight to determine their significance, thereby facilitating accurate comparison and classification. The experimental results show that the proposed classifier is faster at detecting false-positives.

The paper “ChIP-PIT: Enhancing the Analysis of ChIP-Seq Data Using Convex-Relaxed Pair-Wise Tensor Decomposition” by Lin Zhu, Su-Ping Deng and De-Shuang Huang aims at enhancing the integrative analysis of ChIP-seq data by fusing together ChIP-seq data corresponding to a diverse collection of cell types, TFs, and genes by using the three-mode pair-wise interaction tensor (PIT)

- D.-S. Huang is with the Machine Learning and Systems Biology Laboratory, Tongji University. E-mail: dshuang@tongji.edu.cn.
- V. Bevilacqua is with the Electrical and Information Engineering Department, Polytechnic of Bari. E-mail: vitoantonio.bevilacqua@poliba.it.
- M. M. Gromiha is with the Department of Biotechnology, Indian Institute of Technology (IIT) Madras, Chennai, India. E-mail: gromiha@iitm.ac.in.

For information on obtaining reprints of this article, please send e-mail to: reprints@ieee.org, and reference the Digital Object Identifier below.  
Digital Object Identifier no. 10.1109/TCBB.2015.2491058

model, then formulates the prediction of unperformed ChIP-seq experimental results as a tensor completion problem. Experimental evaluation on the ENCODE data illustrate that they can accurately predict unavailable ChIP-seq datasets.

The paper “Practical Guidelines for Incorporating Knowledge-Based and Data-Driven Strategies into the Inference of Gene Regulatory Networks” by Yu-Ting Hsiao, Wei-Po Lee, Wei Yang, Stefan Müller, Christoph Flamm, Ivo Hofacker, and Philipp Kügler, addresses the problem of modeling gene regulatory networks (GRNs). This paper proposes an integrative modeling framework that combines knowledge-based and data-driven input sources to construct biological topologies with their corresponding network behaviors. The experimental results show that the proposed framework can successfully infer solutions that meet the requirements of both the network behaviors and biological structures.

This section ends with the paper, “The Intrinsic Geometric Structure of Protein-Protein Interaction Networks for Protein Interaction Prediction” by Yi Fang, Mengtian Sun, Guoxian Dai, and Karthik Ramani developed an intrinsic geometry structure (IGS) for predicting protein-protein interaction (PPI), which exploits the intrinsic and hidden relationship among proteins in network through a heat diffusion process. Experimental results indicate that, under different levels of the missing and spurious PPIs, IGS is able to robustly exploit the intrinsic and hidden relationship for PPI prediction.

The authors would like to express our sincere thanks to the ICIC 2014 Program Committee members for their invaluable effort in making ICIC 2014 such a success. They would like to thank to the external reviewers for volunteering their time to review the submissions to the conference and the special section. They would like to thank Ying Xu, 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 2014 in *TCBB*. Last but not least, they would also 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



**De-Shuang Huang** received the BSc, MSc, and PhD degrees all in electronic engineering from the Institute of Electronic Engineering, Hefei, China, National Defense University of Science and Technology, Changsha, China, and Xidian University, Xian, China, in 1986, 1989, and 1993, respectively. During 1993-1997, he was a postdoctoral student, respectively, in Beijing Institute of Technology and in 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 Tongji University as a chaired professor. From September 2000 to March 2001, he was a research associate at Hong Kong Polytechnic University. From August to September 2003, he visited the George Washington University as visiting professor, Washington DC. From July to December 2004, he was a University fellow at Hong Kong Baptist University. From March 2005 to March 2006, he was a research fellow at the Chinese University of Hong Kong. From March to July 2006, he was a visiting professor at Queen’s University of Belfast, United Kingdom. In 2007-2009, he was a visiting professor at Inha University, Korea. He is currently a visiting professor at the Liverpool John-Moore University, United Kingdom. In addition, he is the director in the Institute of Machines Learning and Systems Biology, Tongji University. He was the 2015 International Joint Conference on Neural Networks (IJCNN 2015) General Chair, July 12-17, 2015, Killarney, Ireland. He has published over 190 journal papers. His current research interest includes bioinformatics, pattern recognition, and image processing. He is currently a fellow in the International Association of Pattern Recognition (IAPR fellow), and a senior member of the IEEE and International Neural Network Society (INNS).



**Vitoantonio Bevilacqua** received the bachelor’s degree in electronic engineering and the PhD degree in electrical engineering from Polytechnic, where he is currently tenured assistant professor of human computer interaction in the Department of Electrical and Information Engineering and taught also expert systems, medical informatics, and image processing. 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. On July 2011, he was invited as a lecturer at the International School on Medical Imaging using Bio-inspired and Soft Computing-Miere (Spain) MIBISOC FP7-PEOPLE-ITN-2008. GA N. 238819—where he presented his research on Intelligent Tumors Computer Aided Early Diagnosis and Therapy: Neural Network and Genetic Algorithms frameworks. He won the Best Paper Award at the International Conference on Intelligent Computing held in Shanghai (ICIC 2008), he was a program chair of ICIC 2009, Publication Chair of ICIC 2010, Tutorial Chair of ICIC 2011, Publication Chair of ICIC 2012 and ICIC 2013, Award Committee Chair of ICIC 2014, Special Issue Chair of ICIC 2015, and was General Chair of HMISS 2015.



**M. Michael Gromiha** received the PhD degree in physics from Bharathidasan University, India, and served as a STA fellow, RIKEN researcher, research scientist, and senior scientist at Computational Biology Research Center, AIST, Japan, till 2010. He is currently an associate professor at the Indian Institute of Technology (IIT) Madras, India. His main research interests are structural analysis, prediction, folding and stability of globular and membrane proteins, protein interactions and development of bioinformatics databases and tools. He

has published over 150 research articles, 40 reviews, five editorials, and a book entitled *Protein Bioinformatics: From Sequence to Function* by Elsevier/Academic Press. His papers received more than 7,000 citations and h-index is 47. He is an associate editor of *BMC Bioinformatics* as well as editorial board member of *Scientific Reports*, *Biology Direct*, the *Journal of Bioinformatics and Computational Biology*, and *Current Computer Aided Drug design*. He has received several awards including the Oxford University Press Bioinformatics prize, Okawa Science Foundation Research Grant, Young Scientist Travel awards from ISMB, JSPS, AMBO, ICTP, etc., Best Paper Award at ICIC2011, ICTP Associateship award, ICMR International fellowship for Senior Biomedical Scientists, INSA Senior Scientist Award, Best Paper Award in Bioinformatics by Department of Biotechnology, India, and Outstanding Performance award from Initiative for Parallel Bioinformatics (IPAB), Tokyo Institute of Technology, Japan.

▷ For more information on this or any other computing topic, please visit our Digital Library at [www.computer.org/publications/dlib](http://www.computer.org/publications/dlib).