

Guest Editorial for Special Section on BIBM 2013

Feng Luo and Xintao Wu

THIS special section includes a selection of seven papers presented at the IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2013) held in Shanghai, China, on December 18-21, 2013. BIBM is a premier research conference that covers all aspects of bioinformatics, biomedicine, and healthcare informatics. The scientific program highlights five research themes: (1) genomics and molecular structure, function, and evolution; (2) computational system biology; (3) medical informatics and translational bioinformatics; (4) cross-cutting computational methods and bioinformatics infrastructure; and (5) healthcare informatics.

BIBM 2013 had an international program committee of 312 members. All 306 research paper submitted to the conference were reviewed by at least three independent reviewers. After the review process, 115 papers were accepted, of which 60 papers were regular research papers and 55 were short papers. The authors of seven high quality papers were invited to submit an extended version to this special section. Following a rigorous review process, these seven papers were selected for publication.

The paper “Predicting Microbial Interactions using Vector Autoregressive Model with Graph Regularization” by Xingpeng Jiang, Xiaohua Hu, Weiwei Xu, and E.K. Park develops a graph-regularized vector autoregressive model to infer causal relationships among microbial entities. The new proposed model is promising in large-scale applications for exploring microbial dynamics and can also be used in other multivariate time series analysis tasks.

The paper “Predicting the Pro-Longevity or Anti-Longevity Effect of Model Organism Genes with New Hierarchical Feature Selection Methods” by Cen Wan, Alex A. Frietas, and João Pedro de Magalhães develops new hierarchical feature selection methods for the classification task of data mining and applies them to ageing-related data from several model organisms. The developed methods exploit hierarchical relationships in the set of Gene Ontology terms in order to improve the predictive accuracy of the naive Bayes classifier when the classifier is used to classify model organisms’ genes into pro-longevity or anti-longevity genes.

The paper “UDoNC: An Algorithm for Identifying Essential Proteins based on Protein Domains and Protein-protein Interaction Networks” by Wei Peng, Jianxin Wang, Yingjiao Cheng, Yu Lu, Fangxiang Wu, and Yi Pan analyzes

the correlation between the essentiality of proteins and their domain features and finds that the proteins containing more protein domain types which rarely occur in other proteins tend to be essential. The authors develop a new prediction method by combining the domain features of proteins with their topological properties in protein-protein interaction network.

The paper “ENISI SDE: A New Web-based Tool for Modeling Stochastic Processes” by Yongguo Mei, Adria Carbo, Stefan Hoops, Raquel Hontecillas, and Josep Bassagany-Riera presents a web-based modeling tool with stochastic differential equations. The tool provides user-friendly web user interfaces to facilitate adoption by immunologists and computational biologists. The case study conducted in the paper also shows the effectiveness of stochastic differential equations modeling in biology in general and immunology in particular.

The paper “An Integrated Approach to Sequence Independent Local Alignment of Protein Binding Sites” by Bin Pang, David Schlessman, Xingyan Kuang, Nan Zhao, Daniel Shyu, Dmitry Korin, and Chi-Ren Shyu integrates multiple techniques and properties to align protein-protein binding sites. Their new method, called PBSalign, can accurately detect similar homologous and analogous binding sites. The PBSalign outperforms existing protein-protein interface comparison tools according to average match index (MI), similarity index (SI), and structural alignment score (SAS).

The paper “P-Finder: Reconstruction of Signaling Networks from Protein-Protein Interactions and GO Annotations” by Young-Rae Cho, Yanan Xin, and Greg Speegle develops two computational approaches to reconstruct directed signaling networks by integrating genome-wide protein-protein interaction data and ontological annotation data. The first approach uses network motifs based on the assumption that a signaling cascade has typical low patterns whereas the second approach adopts an information propagation algorithm which iteratively updates edge orientations for a signaling cascade using user-specified path strength parameters. The proposed two approaches are demonstrated to achieve higher accuracy than previous computational methods.

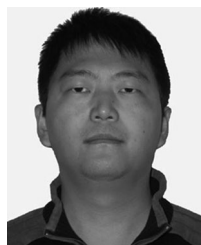
The paper “A New Semantic Functional Similarity over Gene Ontology” by Jong Cheol Jeong and Xuewen Chen develops an method that effectively integrates information from Gene Ontology, functional domain, sequence, structure and phylogenetic profiles, and clustering analysis of disease genes clusters to measure the similarities between genes and gene products. Their evaluation shows that these new methods clearly outperform traditional methods. They also demonstrate that their method can be used to identify disease related gene and gene products.

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We would like to express our sincere thanks to the BIBM 2013 Program Committee members for their invaluable effort in making BIBM 2013 such a success. We also 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 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 BIBM 2013 in *TCBB*. We also would like to thank Ms. Joyce Arnold for her kind help throughout the process. Last but not least, we would like to thank the authors of these seven articles for their time and effort in submitting their high quality work to BIBM and *TCBB*.

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Guest Editors



Feng Luo received the PhD degree from the University of Texas at Dallas in 2004. He is an associate professor in the School of Computing at Clemson University. He was a postdoctoral senior research associate in the Department of Pathology, University of Texas Southwestern Medical Center at Dallas. He served program committee for several international conferences. His research interests include bioinformatics, medical informatics, machine learning, big data analysis, and distributed computing. He is a member of the IEEE.



Xintao Wu received the BS degree in information science from the University of Science and Technology of China in 1994, the ME degree in computer engineering from the Chinese Academy of Space Technology in 1997, and the PhD degree in information technology from George Mason University in August 2001. He is a professor and the Charles D. Morgan/Axiom Endowed Graduate Research chair in Database in Computer Science and Computer Engineering Department, University of Arkansas. He was an assistant professor (August 2001-June 2007), an associate professor (July 2007-June 2012), and a professor (July 2012-June 2014) in College of Computing and Informatics, University of North Carolina at Charlotte. His major research interests include data mining, privacy and security, big data analysis. He has developed privacy preserving techniques for mining tabular, social network, healthcare, and genetic data. He is an editor of *Springer's Journal of Intelligent Information Systems*, *InderScience Publisher's International Journal of Social Network Mining*, and *Spanish Higher Research Council's Transaction on Data Privacy*, and serves program committees of top international conferences, including ACM KDD, CIKM, IEEE ICDM, BIBM, SIAM SDM, PKDD, and PAKDD. He is a member of the IEEE.

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