

Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications

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THIS special section consists of a selection of papers presented at the 15th International Symposium on Bioinformatics Research and Applications (ISBRA 2019), which was held at Technical University of Catalonia, Barcelona, Spain on June 3-6, 2019. The ISBRA symposium provides a forum for researchers, developers, practitioners, etc. to present and exchange innovative contributions and ideas on all aspects of Bioinformatics and Computational Biology and their applications. ISBRA 2019 received 95 submissions, among which 22 regular papers appeared in the ISBRA proceedings published as volume 11490 of Springer Verlag's Lecture Notes in the Bioinformatics series.

Extended versions of selected high-quality conference papers were invited to submit to this special section. All the invited papers have gone through a rigorous peer-review process of the journal and three papers were selected for publication. The topics of selected papers are Drug-drug Interactions Predication, Illicit Drug Ads Detection, and Threshold-free Hub Identification.

In the paper titled "Predicting Drug-Drug Interactions Based on Integrated Similarity and Semi-Supervised Learning" by Cheng Yan, Guihua Duan, Yayan Zhang, Fang-Xiang Wu, Yi Pan and Jianxin Wang, the authors proposed a novel method to predict drug-drug interaction based on the integrated similarity and semi-supervised learning. The drug chemical, biological and phenotype data are all taken into consideration to calculate the feature similarity of drugs with the cosine similarity method. The experimental results indicate the proposed method can achieve the better prediction performance than other cutting-edge methods.

In the paper titled "Computational Approaches to Detect Illicit Drug Ads and Find Vendor Communities Within Social Media Platforms" by Fengpan Zhao, Pavel Skums, Alex Zelikovsky, Eric L. Sevigny, Monica Haaavisto Swahn, Sheryl, M. Strasser, Yan Huang, and Yubao Wu, The authors

designed a computational framework with intention of automatically detecting illicit drug ads and communities of vendors. Three classification methods, The SVM- and CNN-based methods for detecting illicit drug ads, and a matrix factorization based method for discovering overlapping communities have been tested on three real-world large dataset from Google+, Flickr and Tumblr. The experimental results demonstrate that the proposed computational methods can identify illicit drug ads effectively and detect vendor-community accurately.

In the paper titled "A Refined 3-in-1 Fused Protein Similarity Measure: Application in Threshold-Free Hub Detection" by Sudipta Acharya, Laizhong Cui, and Yi Pan, The authors proposed a multi-objective clustering-based protein hub detection framework with FuSim-II working as the underlying proximity measure. The proposed framework does not require to follow any protein degree cut-off or threshold to define hubs and can be further extended to include other biological information to improve efficiency. The biological and statistical significance tests validate the effectiveness of the proposed framework.

First of all, we would like to thank the Editor-in-Chief, Dr. Aidong Zhang, and the Associate Editor-in-Chief, Dr. Sun Kim, for providing us the great opportunity to organize the special issue in the *IEEE/ACM Transactions on Computational Biology and Bioinformatics* for showcasing some of the exciting research presented at ISBRA 2019. Next, we want to thank the Steering and General Chairs of ISBRA 2019 for their leadership to make sure all the procedures are always on the right track, and to thank the Finance, Publication, Publicity, and Local Organization Chairs for their great efforts in making ISBRA 2019 a successful event. Furthermore, we would like to thank the Program Committee members and external reviewers for volunteering their time to review and discuss symposium papers. Most importantly, we want to thank all the ISBRA 2019 authors and attendees for their contribution.

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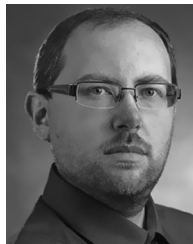
Zhipeng Cai received the BS degree from the Department of Computer Science and Engineering, Beijing Institute of Technology, and the MS and PhD degrees from the Department of Computing Science, University of Alberta. He was a research faculty with the School of Electrical and Computer Engineering, Georgia Institute of Technology. He is currently an associate professor with the Department of Computer Science, Georgia State University. He has authored or coauthored more than 100 papers in top journals and

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Min Li received the PhD degree in computer science from Central South University, China, in 2008. She is currently a professor and the vice dean with the School of Computer Science and Engineering, Central South University, Changsha, Hunan, China. She has more than 7000 paper citations, and her H-index is 45. She has authored or coauthored more than 100 technical papers in refereed journals, such as *Genome Research*, *Briefings in Bioinformatics*, *Bioinformatics*, *IEEE/ACM Transactions on Computational Biology and*

Bioinformatics, and *BMC Bioinformatics*, and conference proceedings, such as BIBM and ISBRA. Her research interests include algorithms for computational biology and bioinformatics, with focus on algorithms and tools in de novo genome assembly, biological network analysis and protein bioinformatics.



Pavel Skums is currently an assistant professor and the associate director of Graduate Studies with Computer Science Department, Georgia State University. He has authored or coauthored more than 50 papers and book chapters. His research interests include computational genomics, molecular epidemiology, and evolutionary modelling. He has been a guest editor for more than 20 special issues of leading journals. He was the recipient of NSF CAREER Award, the GSU Dean's of College of Arts and Sciences

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