

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

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THIS special section includes a selection of papers presented at the 12th International Symposium on Bioinformatics Research and Application (ISBRA), which was held at Belarusian State University in Minsk, Belarus on June 5-8, 2016. The ISBRA symposium provides a forum for the exchange of ideas and results among researchers, developers, and practitioners working on all aspects of bioinformatics and computational biology and their applications. In 2016, 73 papers were submitted in response to the call for papers, out of which 21 extended abstracts and 19 abridged abstracts appeared in the ISBRA proceedings published as volume 9,683 of Springer Verlag's *Lecture Notes in Bioinformatics* series.

A small number of authors were invited to submit extended versions of their symposium papers to this special section. Following a rigorous review process, four papers were selected for publication. The selected papers cover topics in phylogenetics, protein interaction networks, and drug resistance of tuberculosis strains.

The paper "The SCJ Small Parsimony Problem for Weighted Gene Adjacencies" by Luhmann et al. proposes a novel Fixed-Parameter Tractable exact algorithm for reconstruction of ancestral gene orders in a given phylogeny. The proposed algorithm allows for the sampling of co-optimal solutions and significantly reduces the fragmentation of the reconstructed ancestral gene order.

The paper "Efficient Local Search for Euclidean Path-Difference Median Trees" by Alexey Markin and Oliver Eulenstein considers a median tree reconstruction problem which seeks to synthesize a phylogenetic tree from a given collection of input trees under a specified tree distance. It proposes a time efficient local search algorithm for the euclidean median tree reconstruction problem that significantly outperforms the best-known solutions and improves their running time by a factor of n , where n is the size of the input trees.

The paper "Construction Of Refined Protein Interaction Network for Predicting Essential Proteins" by Min Li et al. explores refinement of protein interaction networks using gene expression profiles and subcellular location information. Ten network-based methods have been applied to predict essential proteins before and after refinement of protein interaction networks. It has been shown that all ten methods achieve better results when being applied to the refined protein interaction networks.

The paper "Genome-Wide Analysis of MDR and XDR Tuberculosis from Belarus: Machine-Learning Approach" by Sergeev et al. describes a novel framework for automated selection of the best performing statistical model for discovery of drug-resistance SNPs from whole-genome sequencing data. It also reports results from the application of the designed framework to the analysis of real tuberculosis strains isolated from infected hosts from Belarus.

We would like to thank the Program Committee members and external reviewers for volunteering their time to review the submissions to the symposium and the special section. We would also like to thank the Editor-in-Chief, Dr. Aidong Zhang, for continuing to provide us with the opportunity for wider dissemination of the exciting research presented at ISBRA in the *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. Last, but not least, we would like to thank all of the ISBRA authors—the symposium could not continue to thrive without their high-quality contributions.

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Guest Editors

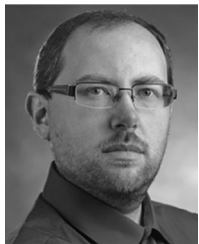
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Ion I. Măndoiu received the MS degree in computer science from Bucharest University, in 1992, and the PhD degree in computer science from the Georgia Institute of Technology, in 2000. He is a professor of computer science and engineering, University of Connecticut. His main research interests include the areas of bioinformatics and computational genomics, with a special focus on the development of high-performance computational methods for the analysis of high-throughput sequencing data. He has published more than 100 refereed articles in journals and conference proceedings and 15 book chapters. He has also co-edited nine conference proceedings and two books published in the Wiley Book Series on Bioinformatics. His research program has been funded by federal grants from NSF, NIH, and USDA, including the NSF Faculty Early Career Development (CAREER) award. He serves as an associate editor of *BMC Bioinformatics* and is on the editorial board of *Genes*, *In Silico Biology*, and the *International Journal of Bioinformatics Research and Applications*. He has served as guest editor for more than 20 special issues of *BMC Bioinformatics*, *BMC Genomics*, the *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, the *IEEE Transactions on NanoBioscience*, and *In Silico Biology*. He has also served as the program committee chair for numerous international conferences, including the International Symposium on Bioinformatics Research and Applications, IEEE International Conference on Bioinformatics and Biomedicine, and IEEE International Conference on Computational Advances in Bio and Medical Sciences.

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Pavel Skums received the BS and MS degrees in mathematics and the PhD degree in computer science from Belarussian State University, in 2004 and 2007, respectively. He is an assistant professor with the Department of Computer Science, Georgia State University. His research areas are computational genomics and computational biology, where his research focuses on studying epidemiology and the evolution of highly mutable RNA viruses, such as the human immunodeficiency virus (HIV) and the hepatitis C virus (HCV). Before joining Georgia State University in 2016, he was a regular fellow and associate service fellow in the National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention of the US Centers for Disease Control and Prevention (CDC), where his research was recognized by several CDC awards. He is the author of more than 70 refereed publications. He has served as a guest editor for four special issues of *BMC Bioinformatics*, *BMC Genomics*, the *IEEE Transactions on Nanobioscience*, and the *Journal of Computational Biology*. His research has been supported by NIH.

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Alexander Zelikovskiy received the PhD degree in computer science from the Institute of Mathematics of the Belorussian Academy of Sciences in Minsk (Belarus), in 1989 and was a research scientist with the Institute of Mathematics in Kishinev (Moldova) (1989-1995), University of Virginia (1995-1997), and UCLA (1997-1999). In 1999, he joined the Department of Computer Science, Georgia State University, where he is a distinguished University professor. Since 2018, he has also been affiliated with the Laboratory of Bioinformatics, I.M. Sechenov First Moscow State Medical University. His research interests include bioinformatics, discrete and approximation algorithms, combinatorial optimization, VLSI physical layout design, and ad-hoc wireless networks. He has published more than 200 refereed articles and 20 book chapters. His paper on approximation of Steiner trees was awarded the Society of Industrial & Applied Mathematics Outstanding Paper Prize in 2007. He has also coedited six conference proceedings and two books. He is founding co-chair of the International Symposium on Bioinformatics Research and Applications (ISBRA) and an associate editor-in-chief of Springer's *Human-Centric Computing and Information Sciences*. He has also served the editorial board of eight international scientific journals and edited 30 special issues in *BMC Bioinformatics*, *BMC Genomics*, the *Journal of Computational Biology*, the *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, the *IEEE Transactions on NanoBioscience*, and other journals. His research has been funded by multiple grants from NSF, NIH, and USDA.

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