

Guest Editors'

Introduction to the Special Section on Bioinformatics Research and Applications

THIS special section features a carefully curated collection of papers presented at the 17th International Symposium on Bioinformatics Research and Applications (ISBRA 2021), which took place in Shenzhen, China from November 26 to 28, 2021. ISBRA serves as a pivotal platform for researchers, developers, and practitioners to share and discuss their latest ideas and discoveries in the realms of bioinformatics and computational biology.

The symposium received a total of 135 submissions, resulting in the inclusion of 51 regular papers in the ISBRA proceedings, published as volume 12304 of Springer Verlag's Lecture Notes in the Bioinformatics series. A limited number of high-quality conference papers were invited to submit extended versions for consideration in this special issue. All invited papers underwent the standard peer-review process of the journal, resulting in the selection of four papers for publication.

This special issue encompasses a wide spectrum of bioinformatics topics, including research on Vaccine Distribution against Pandemic, Chronic Obstructive Pulmonary Disease Prediction, Microbe-Disease Association Identification, miRNA-disease Associations Prediction, and more.

In [A1], Hunmin Lee, Mingon Kang, Donghyun Kim, Daehee Seo, and Yingshu Li introduce the Epidemic Vulnerability Index (EVI) to assess the risk of individual infection, aiming to reduce infection and death rates efficiently during pandemics. By analyzing COVID-19 patient data and using an agent-based model, they validated EVI's effectiveness in nine vaccination scenarios. Vaccination based on EVI rankings resulted in significantly fewer infections, deaths, and lower death rates compared to other distribution methods.

In [A2], Qing Zhao, Jianqiang Li, Linna Zhao and Zhichao Zhu introduce a novel approach for better disease diagnosis using clinical data. It employs a knowledge-guided graph attention network, improving accuracy by considering semantic relations among medical concepts and utilizing mutual information from medical knowledge graphs. The method, using spatial and attention-based graph encoders, generates compact node embeddings for diagnosis. Experiments on a COPD EMR dataset outperform standard methods, showcasing its effectiveness.

In [A3], Yueyue Wang, Xiujuan Lei and Yi Pan present TNRGCN, a predictive model for microbe-disease associations.

It constructs a comprehensive microbe-disease-drug tripartite network and relation graph convolutional network (RGCN) and utilizes similarity networks for microbes, diseases, and drugs. TNRGCN outperforms other methods and proves effective in microbe-disease association prediction, contributing to disease prevention.

In [A4], Wei Peng, Zicheng Che, Wei Dai, Shoulin Wei and Wei Lan introduce miRNA-disease associations (HGCNMDA), a multi-relational Graph Convolutional Network model for predicting miRNA-disease associations. It incorporates a gene layer and heterogeneous network, considering both direct and indirect associations. HGCNMDA outperforms existing models in identifying missing miRNA-disease links and recommending related miRNAs/diseases for new cases.

In [A5], Sarwan Ali, Bikram Sahoo, Imdadullah Khan, Alexander Zelikovsky, Murray Patterson and Muhammad Asad Khan enhance the performance of approximate kernel methods for classifying coronavirus sequences, focusing on spike protein variants. By incorporating domain knowledge and efficient preprocessing techniques, the proposed approach outperforms existing methods in COVID-19 sequence classification and clustering, as demonstrated with multiple datasets and evaluation metrics.

In [A6], Yuxia Guan, Ying An, Jinrui Xu, Ning Liu, and Jianxin Wang introduce HA-ResNet, a neural network model that converts ECG signals into images for automatic arrhythmia detection. HA-ResNet uses SE blocks to enhance essential features and employs BConvLSTM to capture temporal dependencies. Evaluation on public datasets shows high accuracy and demonstrates the method's effectiveness and generalization.

We extend our gratitude to the Editor-in-Chief, Dr. Srinivas Aluru, and the Associate Editor-in-Chief, Dr. Jian Ma, for granting us the opportunity to showcase the exciting research presented at ISBRA 2021 in the IEEE/ACM Transactions on Computational Biology and Bioinformatics. We also express our appreciation to the Steering and General Chairs of ISBRA 2021 for their outstanding leadership and to the Finance, Publication, Publicity, and Local Organization Chairs for their diligent efforts in ensuring the success of ISBRA 2021. Additionally, we would like to acknowledge the Program Committee members and external reviewers for generously volunteering their time to review and discuss the symposium papers. Above all, we want to convey our sincere thanks to all the authors who contributed their high-quality work to ISBRA 2021.

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APPENDIX RELATED ARTICLES

- [A1] H. Lee, M. Kang, D. Kim, D. Seo, and Y. Li, "Epidemic vulnerability index for effective vaccine distribution against pandemic," *IEEE/ACM Trans. Comput. Biol. Bioinf.*, vol. 20, no. 6, pp. 3332–3342, Nov./Dec. 2023.
- [A2] Q. Zhao, J. Li, L. Zhao, and Z. Zhu, "Knowledge guided feature aggregation for the prediction of COPD with chinese EMRs," *IEEE/ACM Trans. Comput. Biol. Bioinf.*, vol. 20, no. 6, pp. 3343–3352, Nov./Dec. 2023.
- [A3] Y. Wang, X. Lei, and Y. Pan, "Microbe-disease association prediction using RGCN through microbe-drug-disease network," *IEEE/ACM Trans. Comput. Biol. Bioinf.*, vol. 20, no. 6, pp. 3353–3362, Nov./Dec. 2023.
- [A4] W. Peng, Z. Che, W. Dai, S. Wei, and W. Lan, "Predicting miRNA-disease associations from miRNA-genedisease heterogeneous network with multi-relational graph convolutional network model," *IEEE/ACM Trans. Comput. Biol. Bioinf.*, vol. 20, no. 6, pp. 3363–3375, Nov./Dec. 2023.
- [A5] S. Ali, B. Sahoo, I. Khan, A. Zelikovsky, M. Patterson, and M. Asad Khan, "Efficient approximate kernel based spike sequence classification," *IEEE/ACM Trans. Comput. Biol. Bioinf.*, vol. 20, no. 6, pp. 3376–3388, Nov./Dec. 2023.
- [A6] Y. Guan, Y. An, J. Xu, N. Liu, and J. Wang, "HA-ResNet: Residual neural network with hidden attention for ECG arrhythmia detection using two-dimensional signal," *IEEE/ACM Trans. Comput. Biol. Bioinf.*, vol. 20, no. 6, pp. 3389–3398, Nov./Dec. 2023.



Zhipeng Cai received the BS degree from the Department of Computer Science and Engineering, Beijing Institute of Technology, in 2001, and the MS and PhD degrees from the Department of Computing Science, University of Alberta, in 2004 and 2008, respectively. He is currently an associate professor with the Department of Computer Science, Georgia State University. Prior to joining GSU, he was a research faculty with the School of Electrical and Computer Engineering, Georgia Institute of Technology. His research interests include areas focus on networking, big data, data security, and artificial intelligence. He has published more than 100 papers in top journals and conferences including more than 50 IEEE/ACM Transactions papers. His publications have been cited for more than 9700 times. He is an editor-in-chief for *Wireless Communications and Mobile Computing* and an associate editor-in-chief for *Elsevier High-Confidence Computing Journal* and serves as an editor for several prestigious journals including *IEEE Transactions on Knowledge and Data Engineering (TKDE)*, *IEEE Transactions on Vehicular Technology (TVT)*, *IEEE Transactions on Wireless Communications (TWC)*, *IEEE Internet of Things Journal*, etc.

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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 dean with the School of Computer Science and Engineering, Central South University, Changsha, Hunan, P.R. China. Her research interests include algorithms for computational biology and bioinformatics, mainly focus on algorithms and tools in de novo genome assembly, biological network analysis, protein bioinformatics, and AI based drug discovery, etc. She has published more than 100 technical papers in refereed journals and conferences, such as *Nature communications*, *Genome Research*, *Genome Biology*, *Nucleic Acids Research*, *Bioinformatics*, and *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. According to Google scholar, her paper has been cited for more than 11000 times and her H-index is 55.



Pavel Skums is an associate professor with the School of Computing of the University of Connecticut. His research interests include concentrates on computational genomics, molecular epidemiology, and evolutionary modelling. He has published more than 100 papers and book chapters, and has been a guest editor of more than 20 special issues of leading journals. He is a recipient of the NSF CAREER award, GSU Dean's of College of Arts and Sciences Early Career Award and US Centers for Disease Control and Prevention Charles C. Shepard Science Award.



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