

Modeling and Simulation Studies of Complex Biological Systems for Precision Medicine and Healthcare

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RECENTLY, big data driven precision medicine has become one of the frontiers in biomedical study, but the complex diseases caused by interactions between genes, environments, and lifestyles are still difficult to be understood by traditional methods. Although we have more and more high-throughput molecular data measured and accumulated, we are still lacking fine and personalized clinical phenotype data. There is a long way to go from data to precision medicine/healthcare, since the biomedical process is dynamic, evolutionary, and systematic. It is a big challenge to make these big data useful to the precision prognosis, diagnosis, and treatment of complex disease.

Modeling and simulation will be an essential and important method to the investigation of the mechanisms and dynamic evolution of complex diseases even with big data available. The prevention and the early diagnosis of complex diseases will be essential to the coming aging society. The shifting from clinical management to precision healthcare will be also the next challenge for scientific researches.

The special section on modeling and simulation studies of complex biological systems for precision medicine and healthcare solicited original and high quality articles on the genotype and phenotype level knowledge discovery for the future precision medicine and healthcare. The main obstacle for the translational biomedical study is the sharing and privacy of the big personalized data. We here present three articles on the private preservation of genome or electronic health record (EHR) data. Three articles focus on the algorithm developing for the analysis of GWAS and EHR-based phenotyping as well as electrocardiogram (ECG)-based disease recognition and classification. We also include an article developing an algorithm for repositioning of old drugs for their new applications. The articles in this special section proposed several computational model and simulation methods to address diverse medical and healthcare issues which will be helpful to

the promotion of the cross-disciplinary researches on the translational medicine and healthcare.

The first three articles are on the privacy protection of personal biomedical data from genotype to phenotype. The first paper entitled “SAFETY: Secure gwAs in Federated Environment through a hYbrid Solution” by Md Nazmus Sadat, Md Momin Al Aziz, Noman Mohammed, Feng Chen, Xiaoqian Jiang, and Shuang Wang. The paper introduces a hybrid framework combining both hardware and software secure primitives to protect data privacy for GWAS study in a distributed environment. The method demonstrated performance advantages over pure software solutions while providing stronger security guarantees than hardware solutions along.

The second paper is entitled “Are My EHRs Private Enough? Event-Level Privacy Protection” by Chengsheng Mao, Yuan Zhao, Mengxin Sun, and Yuan Luo. This paper quantifies the sensitivity of individual medical events within the trajectory of patient medical history and suggested suppression mechanisms to mitigate the privacy risks while greatly preserving the data utility.

The third one is entitled “SecureLR: Secure Logistic Regression Model via a Hybrid Cryptographic Protocol” by Yichen Jiang, Jenny Hamer, Chenghong Wang, Xiaoqian Jiang, Miran Kim, Yongsoo Song, Yuhou Xia, Noman Mohammed, Md Nazmus Sadat, and Shuang Wang. The authors propose a novel hybrid software and hardware solution to enable learning on encrypted data. Different from secure evaluation, this work demonstrated the feasibility of learning a logistic regression model from encrypted data efficiently and securely.

The fourth article is entitled “An Efficient Mixed-Model for Screening Differentially Expressed Genes of Breast Cancer based on LR-RF” by Mengmeng Sun, Tao Ding, Xu-Qing Tang, and Keming Yu. In this work, a hybrid logistic regression and random forest algorithm is proposed to precisely rank the gene’s importance in breast cancer. The hybrid strategy could be extended to the study of other complex diseases.

The fifth article is entitled “Arrhythmia Recognition and Classification Using ECG Morphology and Segment Feature Analysis” by Wenliang Zhu, Xiaohe Chen, Yan Wang, and Lirong Wang. They propose a novel method for accurate classification of cardiac arrhythmias using ECG features, which may have application in the future wearable sensor based detection of disease.

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The sixth article is entitled “Natural Language Processing for EHR-Based Computational Phenotyping” by Zexian Zeng, Yu Deng, Xiaoyu Li, Tristan Naumann, and Yuan Luo. This paper reviews the recent advances about the computational phenotyping based on the application of natural language processing to EHRs.

The last article is “DrPOCS: Drug Repositioning Based on Projection Onto Convex Sets” by Yin-Ying Wang, Chunfeng Cui, Liqun Qi, Hong Yan, and Xing-Ming Zhao. This paper introduces a computational approach based on projection onto convex sets, for drug repositioning with promising results.

Finally we thank all of the authors who contributed their high quality articles to this special section, and thanks to the reviewers for their precious comments and suggestions which helped improve this special section. Last, special thanks to the Dong Xu, Sun Kim, and Joyce Arnold, the editors of the *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)* for their efforts, and high quality work for the publication of the special section.

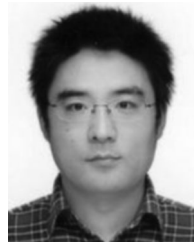
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Guest Editors



Bairong Shen received the PhD degree in physical chemistry from Fudan University, Shanghai, China, in 1997. He is currently a professor with the Center for Systems Biology, Soochow University, Suzhou, China. He started his bioinformatics research in June 1999 and got postdoctoral training from the University of Tampere, Finland. After that, he was recruited as an assistant professor in the beginning of 2014. From 2004 to 2008, he taught eight courses for graduated students and these covered most of the subfields in bioinformatics. He returned to China in June of 2008 and was appointed as a professor of systems biology with Soochow University. He then established the Center for Systems Biology at the university and acted as the director of the center. He is the founding chair for the International Conference on Translational Biomedical Informatics (ICTBI). His research interest is translational biomedical informatics for complex diseases.



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Xing-Ming Zhao received the PhD degree from the University of Science and Technology of China. He is a professor with the Institute of Science and Technology for Brain-Inspired Intelligence, Fudan University, China. His research focuses on data mining and computational systems biology. He has published more than 70 journal papers. He is an editorial board member of several journals. He is a senior member of the IEEE.

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