

Editorial

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THIS special section gives the opportunity to know recent advances in the application of intelligent optimization algorithms in genomics and precision medicine. Precision medicine is designed to optimize the pathway for diagnosis, therapeutic intervention, and prognosis by using multidimensional biological datasets that capture individual variability in genes, function, and environment. Recent advances in -omics technologies provide substantial novel opportunities to study and/or identify biomarkers of chronic diseases by interpreting multi-omics data, including transcriptomics, epigenomics, genomics, and proteomics, that, together may improve understanding of precision medicine. Precision medicine is drugs or treatments designed for small groups, rather than large populations, based on characteristics, such as medical history, genetic makeup, and data recorded by wearable devices. The use of genomic data can support precision medicine to enable clinicians to predict the most appropriate course of action quickly, efficiently, and accurately for a patient. This offers clinicians the opportunity to tailor early interventions to each patient more carefully.

The advancements in intelligent algorithms will enable techniques to process multimodal, multi-scale genomic data, handle heterogeneity in space and time, and accurately quantify uncertainty in the results. Recent years have seen a surge in approaches, such as deep learning, that have shown broad utility in uncovering new biology and contributing to new discoveries in precision medicine. Intelligent algorithms, especially machine learning algorithms, have proven to be promising in predicting disease risk from available multidimensional clinical and biological data. Therefore, there is a strong need to discuss and foster these advances systematically to give support both to researchers and practitioners. Our goal for this special section was to bring together researchers working in different areas related to novel breakthroughs towards artificial intelligence and genome-based precision medicines.

This special section presents seven original, high-quality articles, clearly focused on theoretical and practical aspects of the interaction between artificial intelligence and genomics and precision medicine. Each of the papers was

reviewed by three experts in the area of the presented study. The candidates for acceptance had to undergo one or more thorough revisions. In the remainder of this editorial, we briefly describe the contribution made by each accepted paper.

The paper “DiaDeL: An Accurate Deep Learning-Based Model with Mutational Signatures for Predicting Metastasis Stage and Cancer Types” by Sina Abdollahi, Peng-Chan Lin, and Jung-Hsien Chiang investigated the trinucleotide mutational pattern of cancers and proposed a deep learning-based binary classifier that uses mutational signatures as input features and distinct a cancer type from the others. The proposed model outperforms six state-of-the-art methods with better accuracy and AUC.

The paper “Construction and Evaluation of Robust Interpretation Models for Breast Cancer Metastasis Prediction” by Nahim Adnan, Maryam Zand, Tim H. M. Huang, and Jianhua Ruan proposed a breast cancer metastasis prediction model using a very small number of biologically interpretable features, and a simple yet novel model interpretation approach that can provide personalized interpretations. It is the first method to quantitatively compare different interpretation algorithms. Experimental results show that the proposed model achieved competitive prediction accuracy and higher inter-classifier interpretation consistency than state-of-the-art interpretation methods.

The paper “Unsupervised Feature Selection Using an Integrated Strategy of Hierarchical Clustering with Singular Value Decomposition: An Integrative Biomarker Discovery Method with Application to Acute Myeloid Leukemia” by Tapas Bhadra, Saurav Mallik, Amir Sohel, and Zhongming Zhao developed a novel unsupervised feature selection by combining hierarchical feature clustering with singular value decomposition. The experimental results demonstrated that the proposed algorithm performed well against state-of-the-art methods of feature selection in terms of various evaluation criteria through the analysis of Acute Myeloid Leukemia multi-omics data.

The paper “Heterogeneity in Blood Biomarker Trajectories After Mild TBI Revealed by Unsupervised Learning” by Lien A. Bui, Dacosta Yeboah, Louis Steinmeister, Sima Azizi, Daniel B. Hier, Donald C. Wunsch II, Gayla R. Olbricht, and Tayo Obafemi-Ajayi applied a Locality-Sensitive Hashing model enhanced by varied statistical methods to cluster blood biomarker level trajectories acquired over multiple time points. Additional features derived from demographics, injury context, neurocognitive assessment, and postural stability assessment were extracted using an autoencoder to augment the model. The ability to cluster blood biomarker trajectories

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enhances the possibilities for precision medicine approaches to mTBI.

The paper “Genetic Analysis of Coronary Artery Disease Using Tree-Based Automated Machine Learning Informed by Biology-Based Feature Selection” by Elisabetta Manduchi, Trang Le, Weixuan Fu, and Jason H. Moore assessed the applicability of Tree-based Pipeline Optimization Tool to genomics and identified combinations of single nucleotide polymorphisms (SNPs) associated with coronary artery disease (CAD). Importance analysis uncovered functional relevance of the identified SNPs to genes whose association with CAD is supported by other resources.

The paper “An Ensemble of U-Net Models for Kidney Tumor Segmentation with CT images” by Jason Causey, Jonathan Stubblefield, Jake Qualls, Jennifer Fowler, Lingrui Cai, Karl Walker, Yuanfang Guan, and Xiuzhen Huang summarized the Arkansas AI-Campus solution method for the 2019 Kidney Tumor Segmentation Challenge (KiTS19). The proposed solution is an ensemble of U-Net models developed after testing many model variations. The model achieved Dice scores 0.9470 and 0.6099 kidney and tumor segmentation in the final competition test.

The paper “Age Prediction by DNA Methylation in Neural Networks” by Lechuan Li, Chonghao Zhang, Shiyu Liu, Hannah Guan, and Yu Zhang proposed a Correlation Pre-Filtered Neural Network (CPFNN) that uses Spearman Correlation to pre-filter the input features before feeding them into neural networks. CPFNN outperformed state-of-the-art models by at least 1 year in term of Mean Absolute Error (MAE), with a MAE of 2.7 years.

We would like to thank the external reviewers for volunteering their time to review the submissions. We would like to thank Yi Pan, the editor-in-chief of this *TCCB* special section, for offering this opportunity for wider dissemination of the research in genomics and precision medicine. 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 *TCCB*.

Conflicts of Interest

The editors declare that they have no conflicts of interest.

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Guest Editors

Xiuzhen Huang completed the doctorate degree in computer science from Texas A&M University. She is currently a professor of computer science with Arkansas State University. She conceived and defined the concept of No-Boundary Thinking (NBT). She founded the Arkansas Artificial Intelligence (AI) Campus and Joint Translational Research Lab on the campuses of Arkansas State University and St. Bernard's Medical Center's Internal Medicine Residency Program. Her research interests include bioinformatics and biomedical informatics, artificial intelligence, machine learning, deep learning, graph theory and algorithms, parameterized computation and complexity, and theory of computation. Her research projects are supported by funding agents including NSF and NIH. Dr. Huang. She was named the Arkansas Research Alliance fellow. She is currently an associate editor for *IEEE/ACM Transactions on Computational Biology and Bioinformatics*.

Yu Zhang is currently a professor and the chair of computer science with Trinity University. Her research interests include agent-based modeling and simulation with the applications in bioinformatics and social network analysis. From 2011 to 2017, she was the editor-in-chief of the *International Journal of Agent Technologies and Systems* and the editor-in-chief of the Newsletter of the Society for Modeling and Simulation International. She is currently on the editorial board of the *SCS Transaction of Simulation* and is the general chair of agent directed simulation in SCS SpringSim 2018 and the co-program chair of agent directed simulation in European Modeling and Simulation Symposium 2018. She is currently the co-editor for the *No Boundary Thinking in Bioinformatics* book which will be published by Cambridge in 2020. She was the recipient of the 2013 Outstanding Service Award of the Society for Modeling & Simulation International, 2008 Trinity Distinguish Junior Faculty Award, 2007 IEEE Central Texas Chapter Service Recognition, and Best Paper Award of the 2008 IEEE Region 5 Student Paper Competition.

Xuan Guo is currently an assistant professor of computer science and engineering with the University of North Texas. His research interests include machine learning, big data mining, and high-performance computing and their applications in the environment, food, and health sectors. He founded the Biocomputing Research Laboratory, Center for Computational Epidemiology and Response Analysis, University of North Texas. His research projects have been supported by funding agents, including DOD, DOE, NSF, and NIH. He was the editorial board member of the *International Journal of Bioinformatics Research and Applications*, the guest editor of *MDPI Genes*, and the program chair of BDCloud 2016 and DataCloud 2017.

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