Guest Editorial for Selected Papers From ACM-BCB 2019

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The ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB) is the flagship conference of SIGBio, which is the ACM Special Interest Group in Bioinformatics, Computational Biology, and Biomedical Informatics. The 10th annual ACM-BCB conference was held in Niagara Falls, NY in the United States on September 7-10, 2019. The conference continued the main focus of fostering scientific interactions of important research questions at the interface of computer science, statistics, biology, biomedicine, and health informatics. After rigorous peer review from the program committee members, the conference accepted 42 full research papers and 19 short research papers to the conference proceedings.

This special issue of the *IEEE/ACM Transactions on Computational Biology and Bioinformatics* features four papers presented in ACM-BCB 2019. All four invited papers underwent additional careful reviews and revisions with substantially more materials compared to the conference version.

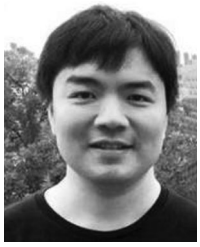
The first paper, titled "SAU-Net: A Unified Network for Cell Counting in 2D and 3D Microscopy Image," is from Yue Guo, Oleh Krupa, Jason Stein, Guorong Wu, and Ashok Krishnamurthy. This work is focused on developing computational method for image-based cell counting, which is broadly applicable to a wide range of biological contexts but still has many unsolved challenges. The authors developed a new deep-learning based method to unify both 2D and 3D image analysis. Specifically, the new SAU-Net extends the segmentation method U-Net by incorporating a self-attention module. An additional component also allows training with small datasets. Extensive evaluation demonstrated the effectiveness of the proposed SAU-Net.

The second paper, titled "Majority Vote Cascading: A Semi-Supervised Framework for Improving Protein Function Prediction," is from John Lazarsfeld, Jonathan Rodríguez, Mert Erden, Yuelin Liu, and Lenore J. Cowen. This paper is motivated by a significant question in the context of protein function prediction. Specifically, the new method "majority vote cascade" employs a semi-supervised scheme that uses the high confidence scores of predicted labels to predict the labels of other proteins in the protein-protein interaction (PPI) network. Real data evaluations showed the advantage of this new functional labeling voting framework in yeast and fly. Highly confident new label predictions were also presented, which could become a useful resource for the community.

The third paper, titled "G4detector: Convolutional Neural Network to Predict DNA G-quadruplexes," is from Mira Barshai, Alice Aubert, and Yaron Orenstein. This paper introduces a machine learning method G4detector that predicts nucleic acid secondary structure G-quadruplexes (G4s) from DNA or RNA sequences based on convolutional neural network. The authors extensively evaluated G4detector using experimental data from the G4-seq assay and demonstrated the advantage of the new method, including its effectiveness by applying a predictive model trained in human to non-human species. This method adds to the growing toolbox of applying deep learning architectures to predict biologically important features from nucleic acid sequences.

The fourth paper, titled "Predicting Drug Synergism by Means of Non-Negative Matrix Tri-Factorization," is from Pietro Pinoli, Gaia Ceddia, Stefano Ceri, and Marco Masseroli. This work reports a computational method to predict drug-pair synergies based on non-negative matrix tri-factorization (NMTF) by integrating different data types, where the data types are modeled as association matrices of a large multilayer graph. Both cross-validation and literature-based evaluation showed the effectiveness of the method that predicts drug combinations and their synergy scores in different cell lines.

We greatly appreciate the time and effort from the authors, the program committee of ACB-BCB 2019, and the reviewers for this special issue of TCBB. We are also grateful to the TCBB staff for their support.



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