Guest Editorial Bioinformatics and Computational Biology Special Section

IN RECENT years, we have witnessed many successful applications of bioinformatics and computational biology methods in the field of Bionano to help us understand the biological system in the nanoscale, such as the BioNano next-generation mapping system to enhance the performance of physical map construction. Bioinformatics and computational tools and methods are essential to assemble, process, and analyze vast amounts of high-throughput datasets. In this Bioinformatics and Computational Biology Special Section, we have eight papers to reflect the latest developments and research in this exciting area.

In [A1], Peng et al. present an LRI-mediated CCC estimation framework (LRI-EnABCLG) by incorporating LRI collection, prediction and filtering, cell-to-cell communications (CCC) inference, and visualization. CCC is inferred by combining the filtered LRIs and scRNA-seq data. The CCC prediction framework is applied to CCC analysis in colorectal tumor tissues.

In [A2], Gong et al. first utilize the NeRV-3D to reconstruct the 3-D chromosome structure at a low resolution based on the nonlinear dimensionality reduction visualization algorithm, and then employ NeRV-3D-DC to reconstruct and visualize the 3-D chromosome structure at a high resolution based on the divide-and-conquer method. The results show that NeRV-3D and NeRV-3DDC perform better than existing methods by comparing the 3-D visualization effects and evaluation metrics on simulated and real Hi-C datasets.

In [A3], Tang and Ji present a new framework Pmli-TF to predict plant miRNA-lncRNA interactions. Pmli-TF provides a four-step process: input embedding, positional encoding, multi-head attention, and max pooling. The algorithm is compared with the existing models on two benchmark datasets. The results show that Pmli-TF performs better than other methods.

The research work by Guo et al. [A4] presents a new deep learning-based scoring function for ranking protein-ligand docking models based on Vision Transformer (ViT), named ViTRMSE. ViTRMSE can effectively capture the subtle differences between spatially and energetically favorable near-native conformations and unfavorable non-native decoys without needing extra information.

Peng et al. [A5] propose a novel method to predict personalized cancer driver genes of a single sample based on graph convolution networks, namely pDriverGCN. pDriverGCN utilizes the feature representations to reconstruct the association matrix between genes and samples through a linear correlation coefficient decoder.

In [A6], Zhao et al. propose a novel method to adaptively fuse functional and topological information between GO Terms. The proposed method is composed of a pre-trained language model for encoding protein sequences and an adaptive multi-view graph convolutional network (Multi-view GCN) for representing GO terms. Experimental results on the datasets of two species (i.e., humans and yeast) show that their method outperforms other state-of-the-art methods.

Wassan et al. [A7] propose a new classification method based on RF as guided by the evolutionary ancestry of microbial phylogeny, i.e., Phylogeny-RF. This method facilitates to capture the effects of phylogenetic relatedness in an ML classifier itself.

The last article by Ch et al. [A8] presents a new method for predicting both lymph node metastasis and distant metastasis. It identifies differential correlations of miRNAs and their target RNAs in cancer and builds prediction models using the differential correlations.

XIAOHUA HU, *Guest Editor*
College of Computing and Informatics
Drexel University
Philadelphia, PA 19104 USA
e-mail: xh29@drexel.edu

APPENDIX: RELATED ARTICLES

[A1] L. Peng et al., "CellEnBoost: A boosting-based ligand-receptor interaction identification model for cell-to-cell communication inference," *IEEE Trans. NanoBiosci.*, vol. 22, no. 4, pp. 705–715, Oct. 2023.

[A2] H. Gong et al., "A 3D chromosome structure reconstruction method with high resolution Hi-C data using nonlinear dimensionality reduction and divide-and-conquer strategy," *IEEE Trans. NanoBiosci.*, vol. 22, no. 4, pp. 716–727, Oct. 2023.

[A3] X. Tang and L. Ji, "Predicting plant miRNA-lncRNA interactions via a deep learning method," *IEEE Trans. NanoBiosci.*, vol. 22, no. 4, pp. 728–733, Oct. 2023.

[A4] L. Guo, T. Qiu, and J. Wang, "ViTScore: A novel three-dimensional vision transformer method for accurate prediction of protein-ligand docking poses," *IEEE Trans. NanoBiosci.*, vol. 22, no. 4, pp. 734–743, Oct. 2023.

[A5] W. Peng, P. Yu, W. Dai, X. Fu, L. Liu, and Y. Pan, "A graph convolution network-based model for prioritizing personalized cancer driver genes of individual patients," *IEEE Trans. NanoBiosci.*, vol. 22, no. 4, pp. 744–754, Oct. 2023.

[A6] Y. Zhao et al., "Protein function prediction with functional and topological knowledge of gene ontology," *IEEE Trans. NanoBiosci.*, vol. 22, no. 4, pp. 755–762, Oct. 2023.

[A7] J. T. Wassan, H. Wang, and H. Zheng, "Developing a new phylogeny-driven random forest model for functional metagenomics," *IEEE Trans. NanoBiosci.*, vol. 22, no. 4, pp. 763–770, Oct. 2023.

[A8] M. Ch, S. Lee, B. Park, and K. Han, "Prediction of cancer metastasis using correlations between miRNAs and competing endogenous RNAs," *IEEE Trans. NanoBiosci.*, vol. 22, no. 4, pp. 771–779, Oct. 2023.

Digital Object Identifier 10.1109/TNB.2023.3316485