ARTIFICIAL INTELLIGENCE FOR BIOINFORMATICS AND BIOMEDICINE

With the development of high-throughput sequencing technology, large biological data sets are generated. How to effectively excavate the hidden meaning behind big data is very important to further understand the relationship between molecular biology and disease. In recent years, artificial intelligence technology has been widely studied and applied in bioinformatics and biomedicine, which has promoted the rapid development of these fields. This thematic series aims to bring together latest advances in artificial intelligence methods in bioinformatics and biomedicine.

Ali Ghulam et al. [1] described the necessary information related to pathway mechanisms, pathway characteristics and pathway databases feature annotations. Various difficulties related to data storage and data retrieval in biological pathway databases were discussed. These focus on different techniques for retrieving annotations, features, and methods of digital pathway databases for biological pathway analysis.

The main factors that drive proteins to form 3D structures are constrained between residues. A highly accurate prediction of inter-residue contacts and distance information is of great significance for protein tertiary structure computations. He Huang et al. [2] summarized some recent algorithms and show that they have obtained good results. Compared to contact map prediction, distance map prediction is in its infancy. There is a lot to do in the future, including improving distance map prediction precision and incorporating them into residue-residue distance-guided ab initio protein folding.

Liu Zhiping [3] provided a review of predicting IncRNA-protein interaction by machine learning. Firstly, a computational framework for predicting IncRNA-protein interactions was presented. Then, the author listed the currently available data resources for the predictions. Furthermore, the crucial steps of the existing methods were reviewed in the prediction framework. Finally, some important directions in bioinformatics for identifying essential IncRNA-protein interactions and deciphering the dysfunctional importance of IncRNA were discussed.

Different cell-constitutions of a sample could differentiate the expression profile and set considerable biases for downstream research. Matrix Factorization (MF) has contributed massively to deconvoluting genetic profiles at the expression level. Yuan Liu et al. [4] reviewed the usages of MF methods on heterogeneous problems of genetic data on expression level. Specifically, the manuscript presents separately into three sections: application scenarios, method categories and summarization for tools. Based on the investigation, this study presents a relatively global picture to assist researchers in achieving quicker access of deconvoluting genetic data in silico, further to help researchers in selecting suitable MF methods based on the different scenarios.

Although the spike-timing based neuronal codes have significant computational advantages over rate encoding scheme, the exact spike-timing-based learning mechanism in the brain remains an open question. Recently, many learning algorithms have been proposed to consider both synaptic weight plasticity and synaptic delay plasticity. Yawen Lan et al. [5] gave an overview of the existing synaptic delay-based learning algorithms in spiking neural networks, and described the typical learning algorithms and report the experimental results. Furthermore, they discussed the properties and limitations of each algorithm and made a comparison between them.

The segmentation of multiple abdominal organs of the human body from images with different modalities is challenging because of the inter-subject variance among abdomens, as well as the complex intra-subject variance among organs. Qiang Li et al. [6] reviewed the recent methods for Abdominal Multi-Organ Segmentation (AMOS) on medical images. The AMOS methods can be categorized into traditional and deep learning-based methods. First, various approaches and related problems under both segmentation categories are explained. Second, the advantages and disadvantages of these methods are discussed. Finally, AMOS remains an unresolved problem, and the combination of different methods can achieve improved segmentation performance.

The immunogenicity of T cell epitopes depends on their source and stability in combination with Major Histocompatibility Complex (MHC) molecules. Identification of epitopes is of great significance in the research of vaccine design and T cell immune response. Yang Liu et al. [7] introduced some recent methods for identifying peptide-MHC binding emerge to pre-select candidate peptides for experimental testing. Some of them employ matrix models or machine learning models based on the sequence characteristic embedded in peptides or MHC to predict the binding ability of peptides to MHC. Some others utilize the three-dimensional structural information of peptides or MHC.

High-density Genetic Linkage Map Construction in Sunflower (Helianthus annuus L.) use SNP and SSR Markers. Pin Lyu et al. [8] proposed the construction of a high-density genetic linkage map by the F7 population of sunflowers using SNP and SSR Markers. The SLAF-seq strategy was employed to further develop SNP markers with SSR markers to construct the high-density genetic map by the HighMap software. The final result demonstrated that the SLAF-seq strategy is suitable for SNP markers detection.
With the rapid growth of biological information, biological science technology has greatly enriched the biology and medicine data resources. The latest advantages of deep learning have achieved the state-of-the-art performance on high dimensional, non-structural and less explanatory biological data. Yongqing Zhang et al. [9] introduced an overview of deep learning techniques and some of the state-of-art applications in biology and medicine. Specifically, the fundamental of deep learning methods was introduced, and their successes in bioinformatics, biomedical image, biomedicine and drug discovery. Furthermore, the challenges, limitations and further improvement of this area were also discussed.

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REFERENCES


Dr. Yongqing Zhang
(Guest Editor)
School of Computer Science
Chengdu University of Information Technology
No. 24 Block 1, Xuefu Road
Chengdu, 610225, Sichuan
China
E-mail: zhangyq@cuit.edu.cn