Guest Editorial for Special Section on the 7th National Conference on Bioinformatics and Systems Biology of China

Feng-Biao Guo, Xinglai Ji, and Jian Huang

It is our honor and great pleasure to present this special section of the *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. The special section includes eight papers, which were invited from the 7th National Conference on Bioinformatics and Systems Biology of China in 2016. The conference is the most influential conference of the Chinese scientific community of bioinformatics and systems biology. More than 1,000 scholars all over the world took part in the grand meeting this year. In total, 255 papers were submitted to the conference in 2016. Among them, eight were invited for this special section. These papers were significantly improved from their earlier versions and then went through a separate revision process. These papers cover a very broad spectrum of theoretical models, computational analyses, bioinformatic methods, and their applications, which have great potential to further bioinformatics and systems biology research.

In "Fast Prediction of Protein Methylation Sites Using a Sequence-Based Feature Selection Technique," Leyi Wei, Pengwei Xing, Gaotao Shi, Zhiliang Ji, and Quan Zou proposed MePred-RF, a new random-forest-based predictor for the fast prediction of protein methylation sites. The tool was based on sequence information alone and showed better performance than other state-of-the-art predictors.

In "Identifying Bacterial Essential Genes Based on a Feature-Integrated Method," Yan Lin, Fa-Zhan Zhang, Kai Xue, Yi-Zhou Gao, and Feng-Biao Guo developed a new feature-integrated approach to predict bacterial essential genes. The approach integrated homologous features, gene intrinsic features, protein domain feature, and network topological features. The results of *E. coli* are very successful with AUC near to 0.99, suggesting this approach can be widely used in accurately investigating essential genes from broad bacterial species.

In "Coupling Effect of Double Lungs on a VCV Ventilator with Automatic Secretion Clearance Function," a new secretion clearance method for VCV (volume-controlled ventilation) ventilator is put forward, and a secretion clearance system with a VCV ventilator and double lungs is designed by Yan Shi, Bolun Zhang, Maolin Cai, and Weiqing Xu. Finally, to illustrate the influence of key parameters of the respiratory system and secretion clearance system on the secretion clearance characteristics, coupling effects of two lungs on VCV secretion clearance system are studied by an orthogonal experiment

In "Identification and Functional Inference for Tumor-Associated Long Non-Coding RNA," Ying Li, Ye He, Siyu Han, and Yanchun Liang proposed a computational method to specify the relationship between lncRNA and gastric cancer by reusing the exon-based array of gastric cancer. They claimed that one specific lncRNAs LINC00365 and its target genes were candidates for a combined biomarker for gastric cancer.

In "Characteristics of Myosin V Processivity," Jun-Ping Zhang, Yi Liu, Wei Sun, Xiao-Yang Zhao, La Ta, and Wei-Sheng Guo used the 4-state mechanochemical model of the myosin V's processive movement to characterize its processivity quantitatively. The theoretical curves obtained were generally in line with the experimental data, providing a new insight for the characteristic of myosin V.

In the paper entitled "Predicting Antimicrobial Peptides by Using Increment of Diversity with Quadratic Discriminant Analysis Method," Pengmian Feng, Zhenyi Wang, and Xiaoyu Yu utilized the Increment of Diversity with Quadratic Discriminant analysis (IDQD) to classify antifungal and antibacterial peptides based on primary sequence information. In the jackknife test, the proposed IDQD model was superior to other state-of-the-art methods. The IDQD method proposed in this paper can also be expanded to other biological prediction problems.

In "HMMCAS: A Web Tool for the Identification and Domain Annotations of Cas Proteins," Guoshi Chai, Min Yu, Lixu Jiang, Yaocong Duan, and Jian Huang developed a special web service for finding and annotating Cas proteins from a set of protein sequences or a proteome. With the accumulation of hypothetical proteins derived from more and more metagenome projects, to identify novel Cas proteins quickly becomes possible due to the assistant from tools like HMMCAS. Both researches on bacteria immune system and studies on new scissors for genome editing can benefit from this tool.

In the paper entitled "Identifying Sigma70 Promoters with Novel Pseudo Nucleotide Composition," Hao Lin, Zhi-Yong Liang, Hua Tang, and Wei Chen designed a sequence-based

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predictor called "iPro70-PseZNC," which aimed to predict sigma70 promoters in prokaryotes. In this paper, they also proposed PseZNC, a new scheme of pseudo nucleotide composition covering the multi-window Z-curve composition and six local DNA structural properties. The PseZNC scheme can certainly be extended to other DNA-related problems.

As guest editors of this special section, we would like to thank the contributing authors, the CCBSB 2016 program committee, and the reviewers who critically reviewed the journal version of the papers for the *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. We are also very grateful to the former editor-in-chief of the *IEEE/ACM Transactions on Computational Biology and Bioinformatics* Prof. Ying Xu, the former associate editor-in-chief Prof. Dong Xu, and especially Ms Joyce Arnold for the professional editorial assistance and collaboration to produce the special section.

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