

Guest Editorial: Special Focus on Bioinformatics and Systems Biology

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WITH advances in biotechnologies, large-scale biological data has been and will continue to be produced. These large-scale biological data contain insightful information for understanding the mechanism of biological systems and have proven useful in the diagnosis, treatment, and drug design for genomic-alerted diseases. In this special section, five papers in their significantly extended versions were selected from the papers presented at the IEEE Conference on Bioinformatics and Biomedicine (BIBM), 2009. These papers present recent research in bioinformatics and systems biology to make sense from large-scale biological data.

In past decades, much attention has been paid to biomedical research. As a result, the biomedical literature is growing exponentially. To comprehensively utilize these biological text data, text data mining becomes a very important tool. Yanpeng Li, Xiaohua Hu, Hongfei Lin, and Zhihao Yang in "A Framework for Semisupervised Feature Generation and Its Applications in Biomedical Literature Mining" present a framework for creating new features for text data and show its applications to text mining tasks in biomedical domain.

With the complete sequences of many genomes, the tremendous amount of protein sequences is available now. It is challenging to predict protein functions from their sequences. Jong Cheol Jeong, Xiaotong Lin, and Xue-Wen Chen in "On Position-Specific Scoring Matrix for Protein Function Prediction" design some new features extracted from protein sequences only and propose machine learning-based methods for protein function prediction.

The classification can be used for classifying various biological data and for predicting the biological function from these data. However, imbalanced data can seriously affect the classification results and thus prediction performance. Sangyoon Oh, Min Su Lee, and Byoung-Tak Zhang in "Ensemble Learning with Active Example Selection for Imbalanced Biomedical Data Classification" present a method for the classification of imbalanced biological data.

In most (if not all) cases, it is prohibitive to directly do biological experiments on real-life biological systems. Therefore, modeling and simulation techniques become

very important for understanding the dynamical behavior of biological systems. Zina M. Ibrahim, Alioune Ngom, and Ahmed Y. Tawfik in "Using Qualitative Probability in Reverse-Engineering Gene Regulatory Networks" present a model for discovering monotonic relations among genes for constructing gene regulatory networks from gene expression data. Amit Sabnis and Robert W. Harrison in "A Continuous-Time, Discrete-State Method for Simulating the Dynamics of Biochemical Systems" propose a novel method for simulating biochemical networks based on a deterministic solution with a modification that permits the incorporation of stochastic effects.

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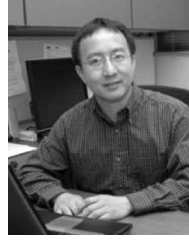
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