Guest Editorial
Data Mining in Bioinformatics and Biomedicine

This Special Issue is comprised of papers that are significantly extended version of papers presented at the IEEE Conference on Bioinformatics and Biomedicine (BIBM), 2008. The focus of the BIBM conference was to exchange research results and address open issues in all aspects of bioinformatics and biomedicine including databases, algorithms, interfaces, visualization, modeling, and simulation, as applied to life science problems.

The goal of this Special Issue is to present the applications of cutting-edge data mining methods to bioinformatics. Five papers accepted for this Special Issue cover a broad range of topics, from analytic methods for DNA/RNA sequences, gene expression analysis, to protein function predictions.

The issue starts with two papers on data mining methods for sequence analyses. Bucur *et al.* developed a frequency-sorting method for DNA spectrogram analysis, which could be applied for systematically investigating very long DNA sequences or entire genome. Chen and Chen developed a mining method that was based on a collection of predicted RNA secondary structures to discover inherent characteristics for secondary structures and to further detect association rules toward the identification of RNA secondary structures.

The advent of microarray techniques that allow for measuring the expression levels of tens of thousands of genes simultaneously has drawn increased interest in data mining community, covering a range of problems from biomarker detection to genetic regulatory network reconstruction. Two papers in this Special Issue address microarray applications. Wu and Zhang developed an autoregressive (AR) model for gene expression analysis. With a nonzero AR model for time-dependent expression profiles and a zero AR model for time-independent expression profiles, they identified a group of genes that are significantly expressed in terms of time-series expression data. Schaefer and Nakashima described a fuzzy-rule-based classification method for microarray data analyses.

As the gene products, proteins play an essential role in nearly all cellular functions. The fifth paper deals with issues in protein function prediction. Cho and Zhang used a frequent-labeled subgraph mining algorithm to detect the functional associations of frequent patterns in a protein interaction network and demonstrated its effectiveness.

The Guest Editors would like to thank all the authors for their high-quality work contributed to this Special Issue and all the reviewers for their hard work and expert comments in evaluating the manuscripts.

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He is currently an Associate Professor with the Department of Electrical Engineering and Computer Science, Information and Telecommunication Technology Center, University of Kansas, Lawrence, where he is also the Director of the Bioinformatics and Computational Life Sciences Laboratory. His research interest includes machine learning, data mining, bioinformatics, systems biology, and statistical modeling. He is the Coeditor-in-Chief of the *International Journal of Data Mining and Bioinformatics* (Science Citation Index indexed) and also serves in the editorial board in three other international journals.

Dr. Chen was the Chair (and Cochairs) for the IEEE International Conference on Bioinformatics and Biomedicine in 2009 and the International Conference in Machine Learning and Applications in 2008. He was a recipient of the prestigious National Science Foundation CAREER Award in 2007.

Hamid R. Arabnia received the Ph.D. degree in computer science from the University of Kent, Canterbury, England, in 1987.

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Dr. Arabnia has been a keynote Lecturer at international conferences; most recently at (since September 2008) the 14th IEEE International Conference on Parallel and Distributed Systems, Australia, 2008, the International Conference on Future Generation Communication and Networking, 2008/IEEE Computer Society, Sanya, China, and the 10th IEEE International Conference on High Performance Computing and Communications, Dalian, China, 2008. He was the recipient of an "Outstanding Achievement Award in Recognition of His Leadership and Outstanding Research Contributions to the Field of Supercomputing," formally presented at Harvard University Medical School.