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PREFACE IN BIOINFORMATICS

Bioinformatics has emerged as a new disciplinary research area for advancing fundamental concepts and creating knowledge from biochemical to molecular to living organism levels. It can be found in the intersection among the research fields of biology, chemistry and computer science. Bioinformatics is involved in developing innovative computationally biological processes for drug design, and computational software tools and methods for detecting, monitoring, and signaling the evolution of disease; developing imaging and visualization tools for understanding the connection between biochemical processes and engineering; treating disease; developing new bio-computing models; and interpreting complex biological processes.

Bioinformatics is a very important and active interdisciplinary research area that offers promising new computational models for solving or contributing to complex medical and biological problems as well as practical applications to other professions in industry and government. Especially, NIH supports bioinformatics research and consortia and dedicated to communicating to and supporting researchers in the community. Bioinformatics has been considered one of the three new interactive research areas (bio-informatics, medical-informatics, nano-informatics) that will dominate this century.

This area has rapidly increasing impact on our society relating to important health issues and commercial applications such as drug development, disease detection, understanding of the living organisms at the molecular and higher levels of interactions, etc. The combination of these fields offers a medium for publishing high-quality original work from DNA computing, genomics, proteomics to drug design, bio-imaging and visualization, and disease monitoring (biosensors and nanostructures) and their associations. In response to this demand, a number of related periodicals have been published worldwide.

In response to this intrigue research call in bioinformatics with promise of great scale, these special issues in Bioinformatics I & II include articles selected after a peer review process (3 reviews per paper) from the IEEE Symposium on Bio-Informatics and BioEngineering (BIBE). These articles deal with topics, such as *Predicting Peptide Interactions with Model Class II MHC Structures* by Martin T. Swain, Anthony J. Brooks and Graham J. Kemp, *Interrelated Two-way Clustering and Its Application on Gene Expression Data* by Chun Tang and Aidong Zhang, *Mining Genome Variation to Associate Genetic Disease with Mutation Alterations and Ortho/Paralogous Polimorphysms in Transcription Factor Binding*

Site by Julia V. Ponomarenko, Galina V. Orlova, Tatyana Merkulova, Gennady Vasiliev and Mikhail Ponomarenko, *Discovering Common Structural Motifs of Ribosomal RNA Secondary Structures in Prokaryotes* by Hsien-Da Huang, Jorng-Tzong Horng and Shu-Fen Fang, *Gene Classification Using Expression Profiles: A Feasibility Study* by Michihiro Kuramochi and George Karypis, *P-DCFold or How to Predict All Kinds of Pseudoknots in RNA Secondary Structures* by Fariza Tahi, Engelen Stefan and Mireille Regnier, *A Collapsing Method for the Efficient Recovery of Optimal Edges in Phylogenetic Trees* by Michael Hu, Paul Kearney, Jonathan Badger, *Sequence Similarity Search Using Discrete Fourier and Wavelet Transformation Techniques* by S. Alireza Aghili, Divyakant Agrawal and Amr El Abbadi, *Time Series Analysis of Gene Expression and Location Data* by Chen-Hsiang Yeang, Tommi Jaakkola, *An Improved Biclustering Method for Analyzing Gene Expression Profiles* by Jiong Yang, Haixun Wang, Wei Wang, Philip S. Yu, *Hierarchical Clustering for Complex Data* by Latifur Khan and Feng Luo, *Vector Space Indexing for Biosequence Similarity Searches* by Ozgur Ozturk and Hakan Ferhatosmanoglu, *Towards SCALEable Protein Structure Comparison and Database Search* by Chern-Hooi Chionh, Zhiyong Huang, Kian-Lee Tan and Zhen Yao, *Prediction of Contact Maps Using Support Vector Machines* by Ying Zhao and George Karypis, *An Assessment of a Metric Space Database Index to Support Sequence Homology* by Rui Mao, Weijia Xu, Neha Singh and Daniel P. Miranker.

The guest editors wish to express their appreciation to the IEEE BIBE organizers, the authors, the reviewers, and to World Scientific Publishing, especially to Ms Linda Kwan, for making these two special issues possible.

With great appreciation.

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