Journal of Computers

Special Issue on Bioinformatics and Computational Biology

FOREWORD

When molecular biologists started to generate DNA sequence data some 30 years ago, it was natural that computer scientists and mathematicians would take a keen interest. This field of study gained a real identity, and the name bioinformatics, in the mid-1980s, as DNA sequencing became a fundamental tool for molecular biology and sequence data started to appear in significant volume. Bioinformatics is the recording, annotation, storage, analysis, and searching/retrieval of nucleic acid sequence (genes and RNAs), protein sequence and structural information. This includes databases of the sequences and structural information as well methods to access, search, visualize and retrieve the information. Typical techniques involved in this field include applied mathematics, informatics, statistics, computer science, artificial intelligence, chemistry, and biochemistry to solve biological problems usually on the molecular level. Major research efforts in the field include sequence alignment, gene finding, genome assembly, protein structure alignment, protein structure prediction, prediction of gene expression and protein-protein interactions, and the modeling of evolution.

The objective of this special issue is to present research and development in various areas of bioinformatics by putting together a collection of papers concerning the relevant topics. We wish the special issue can provide good starting points for interested computer scientists in Taiwan to enter in this promising and active research area. After a very careful reviewing process, the editorial committee accepts six outstanding papers, among many highly qualified submissions, to be included in this special issue. The first paper, by Prof. Fang Rong Hsu and Wei-Chung Shia from Feng Chia University, proposes multi-layer genome-wide unique marker positioning technology for the Single Nucleotide Polymorphism mapping problem. The second paper, by Chiou-Nan Chen, Kuan-Ching Li, Yaw-Ling Lin, and Hsiao-Hsi Wang from Providence University, presents a web-based GUI bioinformatics portal system that eases the deployment of well-known bioinformatics applications on large-scale cluster and grid computing environments. The third paper, by Sheng-Lung Peng and Jyun-Jhao Chen from National Dong Hwa University, show that the classification and identification problem of Human Papilloma Viruses (HPV) by be determined by a set of maximal common subsequences. The fourth paper, joint works by Hsiao Ping Lee, Tzu Fang Sheu, Yin Te Tsai and Chuan Yi Tang from Chung Shan Medical University, National Tsing Hua University, and Providence University, introduces famous and important

approaches in the context of searching homologous sequences in sequences in genomic databases. The fifth paper, another joint works by Austin H Chen, Zhi-En Chen and Pei-Chin Tsai from Tzu-Chi University and Yang-Ming University, presents an RNA silencing mechanism model and the application of the primate-specific model for validating and predicting the apolipoprotein B (APOB) mRNA suppression in a cynomolgus monkey's liver. The sixth paper, by Kuo-Tsung Tseng, Chang-Biau Yang and Kuo-Si Huang from National Sun Yat-sen University, presents mathematical scoring criteria with biological considerations for output biosequence alignments with biological meanings and yet   without increasing the computing complexity of the original LCS algorithm.

On behalf of the editorial committee, I would like to express my gratitude to all contributing authors and reviewers for their great efforts to this special issue. I wish to thank the editorial committee members for their excellent contributions. Furthermore, I am also grateful to Professor Chin-Chen Chang, the Editor-in-Chief, and Professor Jim-Min Lin, for their kind helps to make this issue possible.

Yaw-Ling Lin, Guest Editor

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