

Journal of Computers

Special Issue on Computational Systems Biology

FOREWORD

Computational systems biology is to develop and use efficient algorithms, data structures, visualization and communication tools to harmonize the integration of large quantities of biological data with the goal of computer modeling. It involves the use of computer simulations of biological systems, like cellular subsystems (such as the metabolites' networks and enzymes which comprise metabolism, gene regulatory networks and signal transduction pathways) to both analyze and visualize the complex connections of these cellular processes. Recently, computational systems biology had gained much attention from scholars in computer science, applied mathematics, statistics, engineering and biology fields. Without cooperating with scholars from different fields, it is difficult either to build computer models of biological systems or to interpret, classify and understand the biological datasets. Therefore, we need a forum for researchers to share their experiences in computational systems biology and to further foster research in this area.

The objective of this special issue is to present research and developments in various aspects of computational systems biology. We sincerely hope that this special issue would encourage the interested computer scientists in Taiwan to enter into this promising and active research area. After a very careful reviewing process, the editorial committee selected five outstanding papers, among many highly qualified submissions to be included in this special issue. The first paper, a work by Prof. Wen Bin Lee and Prof. Chuan Yi Tang, from National Tsing Hua University and Providence University. They propose a method to infer the gene network from time series microarray and literature mining. The second paper, a joint work by Prof. Kun-Mao Chao and his research team member, from National Taiwan University and National Chung Cheng University, proposes two hybrid methods, GTS1 and GTS2, to reduce the number of tag SNPs by both considering the extent of LD and block-like structure.. The third paper, a joint work by Prof. Kun-Mao Chao and his research team members, from National Taiwan University, proposes a linear-time algorithm for the DL-NNI LOCAL SEARCH problem. The fourth paper, a joint work by Prof. Chun Yuan Lin and his research team, from Chang Gung University, National Tsing Hua University, and Providence University, presents a re-sequencing tool designed for the Next Generation Sequencing (NGS) data. The final paper, co-worked by Fang Rong Hsu and research team from Feng Chia University and National Chunghua University of Education, presents their tissue-specific natural antisense transcripts database (ATTdb) and provides a user-friendly interface for visualization querying.

On behalf of the editorial committee, I would like to express my sincere thanks to all authors and reviewers for their great contribution to this special issue. I would also like to thank the editorial committee members for their excellent helps. Finally, I am grateful to Professor Chin-Chen Chang, the Editor-in-Chief, and the editorial staffs, for their kind helps. Without all of their great contribution and help, it is impossible to have this special issue.

Chuan Yi Tang and Chia-Chen Lin Guest Editors

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