INTRODUCTION

The First IEEE Conference on Healthcare Informatics, Imaging, and Systems Biology HISB'11

The first IEEE HISB conference, organized by Tanveer Syeda-Mahmood (IBM, Conference Chair), Xue-wen Chen (University of Kansas, Conference Chair), Aziz Boxwala (University of California, San Diego, Program Chair), James Duncan (Yale University, Program Chair), and Satoru Miyano (Tokyo University, Program Chair), was held in San Jose, California, July 26–29, 2011. It brought together leading researchers in healthcare informatics, medical imaging, and systems biology to present the state-of-the-art research in their fields and to create synergies among the three communities in understanding diseases, treatments and outcomes from different but potentially complementary aspects. HISB review is double-blind with over 72 program committee members in three tracks of informatics, imaging, and systems biology. Twenty-nine oral papers (acceptance rate is less than 20%) and 23 posters were accepted for conference presentations. The participants came from all over the world, including, for example, Australia, Brazil, Canada, China, India, Portugal, Scotland, Singapore, South Korea, Spain, UK, and of course, USA.

The conference program consists of both peer-reviewed oral/poster sessions and invited sessions including plenary talks, special sessions talks, tutorials, and panels. The plenary talks include Nobel Laureate, Prof. Andrew Fire (Stanford University), who presented “sequence-based tracking of biological responses to foreign information”; Prof. Eric Grimson (Chancellor, MIT), who described “progress in biomedical imaging and its impact on healthcare”; and Prof. Charles Friedman (formerly with US Department of Health and Human Services, now with University of Michigan), who spoke about “the vision of a national ‘learning health system’”. In addition, in systems biology track, two invited speakers, Prof. Russ Altman (Stanford University) and Prof. Seyoung Kim (Carnegie Mellon University), presented their research progress in “computational methods for functional genomics and pharmacogenomics” and “modern statistical methods for genetic association study: structured genome–transcriptome–phenome association analysis”, respectively.

The four papers, featured in this special issue, were selected from the accepted oral papers reported at the conference in the systems biology track. Enzymes, typically with a few of residues actively involved in the catalytic reactions, play a significant role in cellular processes. Choi and Kim¹ developed a sequence-based catalytic domain prediction method by integrating clustering and information theory-based

approaches. To understand the genetic regulatory network that is involved in the stress response of the yeast to the agricultural fungicide mancozeb, Calcada *et al.*² developed an S-system formalism to model the gene network. Tang *et al.*³ proposed a compressed sensing based approach to analyze gene expression data for subtyping of leukemia. Finally, Desai *et al.*⁴ developed a systems biology approach to analyze a human protein network to detect proteins that are essential to link drug's target proteins to hematopoiesis-related proteins.

Xue-Wen Chen and Satoru Miyano
Guest Editors

References

1. Choi K, Kim S, Sequence-based enzyme catalytic domain prediction using clustering and aggregated mutual information content, *J Bioinform Comput Biol* **9**(5):597–611, 2011.
2. Calcada D, Vinga S, Freitas AT, Oliveira AL, Quantitative modeling of the *Saccharomyces cerevisiae* FLR1 regulatory network using an S-system formalism, *J Bioinform Comput Biol* **9**(5):613–630, 2011.
3. Tang W, Cao H, Duan J, Wang Y-P, A compressed sensing based-approach for subtyping of leukemia from gene expression data, *J Bioinform Comput Biol* **9**(5):631–645, 2011.
4. Desai K, Brott D, Hu X, Christianson A, A systems biology approach for detecting toxicity-related hotspots inside protein interaction networks, *J Bioinform Comput Biol* **9**(5):647–662, 2011.