
Editorial

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Biographical note: Professor Yi-Ping Phoebe Chen is Professor and Chair and Director of Research at the Department of Computer Science and Computer Engineering, La Trobe University, Melbourne Australia. Professor Chen is the Chief Investigator of ARC Centre of Excellence in Bioinformatics. Phoebe received her BInfTech degree with First Class Honours and PhD in Computer Science (Bioinformatics) from the University of Queensland. She is currently working on knowledge discovery technologies and is especially interested in their application to genomics and biomedical science. She has been working in the area of bioinformatics, health informatics, multimedia databases, query system and systems biology and co-authored over 180 research papers with many published in top journals and conferences. She is steering committee chair of Asia-Pacific Bioinformatics Conference (founder) and International conference on Multimedia Modelling. She has been on the program committees of over 100 international conferences, including top ranking conferences such as ICDE, ICPR, ISMB, CIKM etc.

This issue of the International Journal of Bioinformatics Research and Applications (IJBRA) features the selected papers at APBC2012, January 2012. The Asia Pacific Bioinformatics Conference (APBC) is a leading conference in the Bioinformatics community and has grown rapidly since its inception in 2003. The goal of the annual conference series is to enable high quality interaction on bioinformatics research.

The past APBC conferences were held in:

1. APBC 2003 4-7 Feb 2003: Adelaide, Australia
2. APBC 2004 18-22 Jan 2004: Dunedin, New Zealand
3. APBC 2005 17-21 Jan 2005: Singapore
4. APBC 2006 13-16 Feb 2006: Taipei, Taiwan
5. APBC 2007 15-17 Jan 2007: Hong Kong
6. APBC 2008 14-17 Jan 2008: Kyoto, Japan
7. APBC 2009 13-16 Jan 2009: Beijing, China
8. APBC 2010 18-21 Jan 2010: Bangalore, India
9. APBC 2011 11-14 Jan 2011: Incheon, Korea.

2012, of the 129 submitted full papers each paper was sent to three Program Committee members to review and with an acceptance rate of 32.5%. We wish to thank and acknowledge the Program Committee members and their contributions. These selected papers show of recent research that they have shown great teamwork in the completion of some challenging Bioinformatics' tasks and studies.

Sriganesh Srihari and Hon Wai Leong studied the employed functional interactions for characterization and detection of sparse complexes from yeast PPI networks. They proposed a novel approach to look beyond physical interactions and demonstrated that their approach was effective in enhancing the derivability of complexes.

Wilson Wen Bin Goh, Yie Hou Lee, Zubaidah M. Ramdzan, Maxey C.M. Chung, Limsoon Wong and Marek J. Sergot examined a network-based maximum link approach towards MS that identifies potentially important roles for undetected ARRB1/2 and ACTB in liver cancer progression. They proposed in building an integrated and comprehensive protein-protein interaction network (PPIN) by merging several major databases.

Hao Jiang, Wai-Ki Ching and Delin Chu proposed a Discriminated Analysis in Pairwise Kernel Learning for SVM Classification. They developed a new framework for determining the coefficients in learning pairwise kernels for classification in Support Vector Machines (SVM).

Sumit Kumar Jha, Raj Gautam Dutta, Christopher J. Langmead, Susmit Jha and Emily Sassano studied the Synthesis of Insulin Pump Controllers from Safety Specifications using Bayesian Model Validation. They proposed to introduce a new algorithm called RESERCHE that is specifically designed to quantify the likelihood of rare but physically, interesting behaviours in SDE models.

Wei-Chih Huang, Feng-Mao Lin, Tzu-Hao Chang, Kuang-Wen Liao and Hsien-Da Huang examined in identifying Cancer Highly-expressed Membrane Receptors for Targeted Drug Delivery. They proposed to collect 46 published cancer microarray datasets from GEO and analysed data by method of Significance Analysis of Microarray (SAM) for identifying differentially expressed genes.

Abu Z.M. Dayem Ullah, Sudhakar Sahoo, Kathleen Steinhofel and Andreas A. Albrecht examined derivative scores from site accessibility and ranking of miRNA target predictions. They proposed to obtain an average improvement of 13.6% (STD \pm 5.7%) for the new score-types.

Yan-Xia Lin studied the Algorithm of Equal Acceptance Region for Detecting Copy Number Alterations: Applications to Next-Generation Sequencing Data. They proposed an algorithm of equal acceptance regions for detecting copy number ratios. This algorithm can be used to determine a sufficient depth of sequencing data required for underlying copy number analysis.

Yang Zhao, Morihiro Hayashida, Jose Nacher, Hiroshi Nagamochi and Tatsuya Akutsu examined the protein complex prediction via improved verification methods using constrained domain-domain matching. They proposed an improved integer programming-based method based on the idea that a candidate complex should not be divided into many small complexes.

Zhenhua Li, Ying He, Longbing Cao, Limsoon Wong and Jinyan Li studied the conservation of water molecules in protein binding interfaces. They proposed to use the water information first, to label the residue. Then align the interfacial residues in fashion similar to normal sequence alignment.