# PROCEEDINGS OF THE FIFTH ASIA-PACIFIC BIOINFORMATICS CONFERENCE

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Hong Kong

Edited by

David Sankoff
University of Ottawa, Canada

Lusheng Wang
City University of Hong Kong, Hong Kong

Francis Chin
University of Hong Kong, Hong Kong

Organised by

Dept. of Computer Science, University of Hong Kong
Dept. of Computer Science, City University of Hong Kong

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# PREFACE

High-throughput sequencing and functional genomics technologies have given us the human genome sequence as well as those of other experimentally, medically and agriculturally important species, and have enabled large-scale genotyping and gene expression profiling of human populations. Databases containing large numbers of sequences, polymorphisms, structures and gene expression profiles of normal and diseased tissues are rapidly being generated for human and model organisms. Bioinformatics is thus rapidly growing in importance in the annotation of genomic sequences, in the understanding of the interplay among and between genes and proteins, in the analysis the genetic variability of species, in the identification of pharmacological targets and in the inference of evolutionary origins, mechanisms and relationships.

The Asia-Pacific Bioinformatics Conference series is an annual forum for exploring research, development, and novel applications of bioinformatics. It brings together researchers, professionals, and industrial practitioners for interaction and exchange of knowledge and ideas. The Fifth Asia-Pacific Bioinformatics Conference, APBC2007, was held in Hong Kong 15–17 January, 2007.

A total of 104 papers were submitted to APBC 2007. These submissions came from Bangladesh, China, Hong Kong, India, Japan, Korea, Malaysia, Singapore, Taiwan, Thailand, Australia, New Zealand, Denmark, France, Germany, Hungary, Italy, Israel, Portugal, UK, Canada, Mexico and USA. We assigned each paper to at least three members of the programme committee. Although not all members of the programme committee managed to review all the papers assigned to them, a total of 317 reviews were received, so that there were about three reviews per paper on average.

A total of 35 papers (33%) were accepted for presentation and publication in the proceedings of APBC 2007. Based on the affiliation of the authors, 1.25 of the accepted papers were from China, 1.46 were from Hong Kong, 3 were from Japan, 0.83 were from Korea, 1 were from Singapore, 2.30 were from Australia, 2 were from Denmark, 0.15 were from France, 4.5 were from Germany, 0.5 were from Italy, 1 were from Portugal, 1.66 were from UK, 4.57 were from Canada, 10.78 were from USA.

In addition to the accepted papers, the scientific programme of APBC 2006 also included three keynote talks, by Jennifer A. Marshall Graves, Joseph H. Nadeau and Pavel A. Pevzner, as well as tutorial and poster sessions. The presentations were of very high quality. Almost a third focused on evolution and phylogeny, largely at the genome level, a similar number dealt with protein structure and proteomics more generally, and a good proportion studied various aspects of pathways, networks, transcriptomics and microarray technology. A range of other topics in bioinformatics and computational biology were also covered, ranging from motif and gene recognition, through haplotypes and population genetics, to databases and text mining. Much of this work featured techniques of sequence analysis, while many of the papers included applications to biology and medicine.

We had a great time in Hong Kong, enhancing the interactions between many researchers and practitioners, and reuniting the Asia-Pacific bioinformatics community in the context of an international conference with worldwide participation.

Finally, we wish to express our gratitude to the authors of the submitted papers, the members of the programme commitee and their subreferees, the members of the organizing committee, Phoebe Chen and Limsoon Wong (our liaisons in the APBC steering committee), the keynote speakers, our generous sponsors, and supporting organizations for making APBC 2007 a great success.

David Sankoff
Lusheng Wang
Francis Chin

17 January 2007

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