

## 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, gene expression profiles of normal and diseased tissues are rapidly being generated for human and model organisms. Databases containing various kinds of biological networks, which include metabolic networks, protein-protein interaction networks and gene regulatory networks, are also being developed. 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 of 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, students, professionals, and industrial practitioners for interaction and exchange of knowledge and ideas. The Sixth Asia-Pacific Bioinformatics Conference, APBC 2008, was held in Kyoto, Japan, 14-17 January, 2008.

A total of 100 papers were submitted to APBC 2008. These submissions came from Australia, Belgium, Canada, China, Denmark, France, Germany, Hong Kong, India, Iran, Ireland, Israel, Italy, Japan, Latvia, Netherlands, Norway, Pakistan, Poland, Portugal, Saudi Arabia, Singapore, South Korea, Spain, Switzerland, Taiwan, Turkey, UK, 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 286 reviews were received, so that there were about three reviews per papers on average. It is to be mentioned that there were at least two reviews for each paper.

A total of 36 papers (36 %) were accepted for presentation and publication in the proceedings of APBC 2008. Based on affiliations of the authors, 3.75 of the accepted papers were from Australia, 2.67 were from Canada, 3.75 were from China, 0.25 were from France, 4.32 were from Germany, 2 were from Hong Kong, 0.5 were from Italy, 3.5 were from Japan, 1 were from Netherland, 2.75 were from Singapore, 0.5 were from Spain, 1.25 were from Switzerland, 1 were from Turkey, 0.18 were from UK and 8.33 were from USA. The topics of the accepted papers cover wide range of

bioinformatics, which includes population genetics/SNP/ haplotyping, comparative genetics, evolution and phylogeny, database and data integration, pathways and networks, text mining and data mining, prediction and analysis of RNA and protein structures, gene expression analysis, sequence analysis, and algorithms. In addition to the accepted papers, the scientific programme of APBC 2008 also included three keynote talks, by Andreas Dress, Minoru Kanehisa and Alfonso Valencia, as well as tutorial and poster sessions.

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

Lastly, we wish to express our gratitude to the authors of the submitted papers, the members of the programme committee and their subreferees, the members of the organizing committee, Phoebe Chen and Limsoon Wang (our liaisons in the APBC steering committee), the keynote speakers and our generous sponsors and supporting organizations, which include Bioinformatics Center (Kyoto University), Human Genome Center (University of Tokyo), The Telecommunications Advancement Foundation, Special Interest Group on Mathematical Modeling and Problem Solving (SIGMPS, IPSJ), Special Interest Group on Bioinformatics (SIGBIO, IPSJ) and Japanese Society for Bioinformatics, for making APBC 2008 a great success.

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