PROCEEDINGS OF THE FOURTH ASIA-PACIFIC BIOINFORMATICS CONFERENCE

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PREFACE

High-throughput sequencing and functional genomics technologies have given us a draft human genome sequence and have enabled large-scale genotyping and gene expression profiling of human populations. Databases containing large numbers of sequences, polymorphisms, and gene expression profiles of normal and diseased tissues in different clinical states 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 between genes and proteins, in the analysis the genetic variability of species, etc.

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 Fourth Asia-Pacific Bioinformatics Conference, APBC2006, was held in Taipei 13–16 February, 2006. Taking advantage of the presence of APBC 2006 in Taipei, several related activities were also organized immediately before or after APBC 2006, including the Third Association of Asian Societies for Bioinformatics Symposium.

A total of 118 papers were submitted to APBC 2006. These submissions came from China, Hong Kong, India, Japan, Korea, Singapore, Taiwan, Australia, Belgium, France, Germany, Italy, Norway, Russia, UK, Canada, and USA. We assigned each paper to at least 3 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 340 reviews were received. As a result, there were almost 2.9 reviews per paper on average, and more than 98% of the papers received at least 3 reviews.

A total of 35 papers (*i.e.* 30%) were accepted for presentation and publication in the proceedings of APBC 2006. Each accepted papers had at least 2 positive recommendations and no negative recommendations from their reviewers. Based on the affiliation of the authors, 1.80 of the accepted papers were from China, 4.50 were from Hong Kong, 3.00 were from India, 3.50 were from Japan, 0.75 were from Korea, 3.00 were from Singapore, 3.00 were from Taiwan, 2.00 were from Australia, 3.20 were from Canada, 7.25 were from USA, 1.00 were from France, 1.00 were from Germany, and 1.00 were from Norway. In addition to the accepted papers, the scientific programme of APBC 2006 also included 3 keynote talks, as well as tutorial and poster sessions. There is no doubt that the presentations covered a broad range of topics in bioinformatics and computational biology, and were of very high quality. We had a great time in Taipei, enhancing the interactions between many researchers and practioners of bioinformatics, and advancing bioinformatics into a more mature scientific discipline.

Lastly, 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, the keynote speakers, our generous sponsors, and supporting organizations for making APBC 2006 a great success.

Tao Jiang
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16 February 2006

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