PROCEEDINGS OF THE 3RD ASIA-PACIFIC BIOINFORMATICS CONFERENCE

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Edited by

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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 Third Asia-Pacific Bioinformatics Conference, APBC2005, was held in Singapore during 17–21 January 2005. Taking advantage of the presence of APBC 2005 in Singapore, several related activities were also organized immediately before and after APBC 2005 as part of the "Singapore Bioinformatics Week" by the Association for Medical and Bio Informatics Singapore, the Institute for Infocomm Research, the Bioinformatics Institute of Singapore, the Nanyang Technological University of Singapore, and the National University of Singapore.

A total of 118 papers were submitted to APBC 2005. These submissions came from China, Hong Kong, India, Japan, Korea, Malaysia, Singapore, Taiwan, Australia, New Zealand, France, Norway, Portugal, Sweden, 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 289 reviews were received. As a result, there were 2.45 reviews per paper on average, and almost 45% of the papers have at least 3 reviews.

A total of 35 papers (30%) were accepted for presentation and publication in the proceedings of APBC 2005. All accepted papers had at least 2 positive recommendations and no negative recommendations from their reviewers. Based on the affiliation of the authors, 1.75 of the accepted papers were from China, 1.91 were from Hong Kong, 2.00 were from Japan, 7.17 were from Singapore, 4.00 were from Taiwan, 4.00 were from Australia, 5.00 were from Canada, 7.00 were from USA, 0.25 were from France, 0.75 were from Portugal, and 1.17 were from UK. In addition to the accepted papers, the scientific programme of APBC 2005 also included 3 keynote talks, 1 invited talk, 2 tutorials, as well as poster and demo sessions.

There is no doubt that very impressive scientific activities in bioinformatics and computational biology world-wide were demonstrated at APBC 2005. We had a great time in Singapore, 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: authors of the submitted papers, members of the programme commitee and additional external reviewers, members of the organizing committee, keynote speakers (Vladimir Bajic, Tao Jiang, and Haruki Nakamura), invited speaker (Santosh Mishra), and generous sponsors (World Scientific Publishing Company, Lilly Systems Biology Pte Ltd, and LION bioscience AG) and supporting organizations (Association for Medical and Bio-Informatics, Singapore; Bioinformatics Institute, Singapore; Genome Institute of Singapore; Institute for Infocomm Research, Singapore; Nanyang Technological University, Singapore; National University of Singapore; and Deakin University, Australia) for making APBC 2005 a success.

Yi-Ping Phoebe Chen
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