The International Conference on Intelligent Systems for Molecular Biology (ISMB) 2005. The ISMB conference is the major conference that brings together scientists from biology, computer science, mathematics, and statistics. Its scope includes the development and evaluation of advanced computational methods for problems at the levels of sequences, cells, organs, and organisms.

The conference received a record of 428 full-length manuscripts from 374 institutions in 38 countries. Of these, 121 papers were chosen for presentation at the conference publication in this special issue of the journal. A Program Committee with over 300 distinguished scientists reviewed all the manuscripts. We split editors proposed a list of papers that were ‘clearly acceptable’ and a list of those that were ‘possibly acceptable’. Fifth, during an international telephone conference, all ACs and the Program Committee discussed the final list of manuscripts. A subsequent re-reviewing and email discussion of disputed cases yielded a selection of 56 manuscripts for which we invited the submission of revised, final versions. Sixth, the ACs reviewed the responses of the authors to the suggestions and decided on the final acceptance. This final step was introduced for the first time for ISMB 2005. However, no manuscript, for which the verdict had been ‘possibly accept after major changes,’ has been accepted. This final step did not filter out any manuscript. Another novelty was that ACs decided on editorial rejections for about 5% of all manuscripts.

The ten areas attracted very different numbers of submissions; the final percentage of accepted papers was proportional to this number, although this proportionality had not been explicitly enforced by us. The areas were (in parantheses: percentage of manuscript submissions and the ACs): genomics (18%; ACs: Steven Salzberg, TIGR, Rockville and Ying Xu, University of Georgia), pathways, networks and systems (15%; ACs: Alfonso Valencia, CNB, Madrid and Vincent Schachter, Hybrigenics, Paris), structural bioinformatics (14%; ACs: Nir Ben-Tal, Tel Aviv University and R. Sowdhamini, NCBS, Bangalore), transcriptomics (12%; AC: Martin Vingron, MPI, Berlin), Proteomics (10%; AC: Michal Linial, Hebrew University, Jerusalem), sequence analysis (9%; AC: Des Higgins, University College, Dublin), evolution and phylogeny (6%; ACs: Olivier Gascuel, LIRMM Montpellier and Dannie Durand, Carnegie Mellon, Pittsburgh), databases, data integration and ontologies (7%; ACs: Susan Davidson, University of Pennsylvania, Philadelphia and Carole Goble, University of Manchester), text mining (5%; AC: Dietrich Rebholz-Schuhmann, EBI, Hinxton), applications and others (4%; AC: Phil Bourne, UCSD, San Diego). Continuing a tradition started in 2004, the chairs responsible for coordinating peer review in each paper and abstract session will present a short overview introducing the session and placing the presentations in context.

New for 2005 are seven sessions devoted to oral presentation of pre-publication work in RNA and protein structural...
Editorial talks. Our keynote speakers reflect both the enormous scientific and technological advances in computational biology. H. V. Jagadish, David States and Burkhard Rost

ISMB 2005 Conference/Program Committee Co-Chairs

conference continues to spawn numerous special interest groups (SIG) many of which have been repeatedly presented and have grown into full international conferences in considerable sizes themselves. The educational tutorials (chaired by Shoba Ranganathan, Macquarie University) will present 14 tutorials in advance of the conference. Live software demonstrations have become an integral part of ISMB conferences growing in popularity over the years. New for 2005, is the introduction of an extended review process (chaired by Goran Neshich, NPTIA, Campinas, Brazil) to ensure that software and papers presented at the conference meet the academic standards expected of work presented at conferences.

We are extremely grateful to all the reviewers, and in particular to the editors, who assisted in determining the final program. An automated system for paper submission and review has been introduced this year (CyberChair). The editors, led by van der Stadt who managed the CyberChair system, found quick solutions when glitches arose. We also wish to thank Shiba Ikeda Santos and Jana Mitchell (both from Michigan University) for their secretarial help, and Vladimir Nekrutsy (Columbia University) for the crucial personal help with the invitation of the largest ever program committee. Particular thanks to the conference co-chair Brian Athey (Ann Arbor, Michigan University) for the organization of this important event.

The field of bioinformatics has grown tremendously and gone through radical changes in the last decade. The first ISMB conference was held in Bethesda, Maryland in July 1993. Larry Hunter, the ‘father’ of ISCB and one of the organizers of that meeting correctly predicted ‘that this would indeed be the inauguration of a continuing series of such meetings’. The conference has grown dramatically in the number of submissions (less than 70 papers were submitted the first year), in attendance, and in support and interest from industry and government sponsors. Although the word ‘computational biology’ may suggest a natural connection between the two disciplines, this merger is actually one of two very different scientific cultures. Biological sciences traditionally accept facts only if proven experimentally, whereas computational and physical sciences have established theoretical results as an independent evidence for truth. This simple reality generates frictions, not the least in the way scientific results are published and presented. Despite this continued clash in cultures, the field of computational biology has evolved over the years and is producing a new class of scientists who are bridging the gap between biology and computation. Major advancements, such as the completion of the sequencing of the human genome, have opened new areas of research and expanded the need for advanced computational solutions to complex biological problems. Over the last decades, computational biology has evolved into a ‘partner’ suggesting hypotheses to experimental biology that are usually statistical rather than analytical. Emergent properties of complex systems may indeed not be discoverable without strong impact from computational biology.

H. V. Jagadish, David States and Burkhard Rost

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