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comprises the formal proceedings for the Thirteenth International Conference on Intelligent Systems for Molecular Biology (ISMB 2005). The ISMB conference is organized by the International Society for Computational Biology (ISCB). ISMB provides a general forum for the latest developments in bioinformatics. It is an annual conference that brings together scientists from biology, medicine, computer science, mathematics and statistics. Its scope includes the development and application of advanced computational methods for solving problems at the levels of sequences, cells, organs, and organisms.

The computational techniques considered at ISMB 2005 include machine learning, data mining, text analysis, pattern recognition, knowledge representation, databases, combinatorial optimization, stochastic modeling, string and graph algorithms, robotics, constraint satisfaction, data parallelism and parallel computation. Biological areas of interest include protein structure, protein function, genomics, molecular sequence analysis, evolution and molecular interactions, molecular structure, metabolism, metabolic pathways, regulatory networks, systems control and systems biology. Underlying this diversity is a blend of different scientific cultures and languages that have been channeled into the following broad areas: (1) genomics, (2) pathways, networks and systems, (3) structural biology, (4) transcriptomics, (5) proteomics, (6) data analysis, (7) evolution and phylogeny, (8) data integration and ontologies, (9) text mining as well as other areas.

This year we received a record of 428 full-length manuscripts from 374 institutions in 38 countries. Of these, 100 were chosen for presentation at the conference and 100 were published in this special issue of the journal. A Program Committee with over 300 distinguished members 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 parentheses: percentage of manuscript submissions and the ACs): genomes (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

ynote speakers reflect both the enormous sci-
ographic diversity of research in computational
n Birney (EBI/Ensembl, Hinxton; genomics
analysis), Howard Cash (CEO GeneCodes Inc.
forensic informatics), Peter Hunter (Univer-
nd; computational physiology), Jill Mesirov
te MIT Cambridge; high-throughput biology),
o (University of Tokyo; gene expression net-
Pevzner (UCSD; computational biology), Janet
BI Hinxton; structural biology) and Gunnar
Stockholm Bioinformatics Center; membrane

conference continues to spawn numerous spe-
roups (SIG) many of which have been repeated
rs and have grown into full international con-
siderable sizes themselves. The educational
ired by Shoba Ranganathan, Macquarie Uni-
ey) will present 14 tutorials in advance of the
elf. Live software demonstrations have been
SMB conferences growing in popularity over
al years. New for 2005, is the introduction of
review process (chaired by Goran Neshich,
NPTIA, Campinas, Brazil) to ensure that soft-
trations presented at the conference meet the
ademic standards expected of work presented
ts.

emely grateful to all the reviewers, and in partic-
ior editors, who assisted in determining the final
lly automated system for paper submission and
introduced this year (CyberChair). The editors
l van der Stadt who managed the CyberChair
found quick solutions when glitches arose. We
ri Ikeda Santos and Jana Mitchell (both from
Michigan University) for their secretarial help
Kernytsky (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 meet-
ings’. 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 differ-
ent 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 gener-
ates frictions, not the least in the way scientific results are
published and presented. Despite this continued clash in cul-
tures, 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, com-
putational biology has evolved into a ‘partner’ suggesting
hypotheses to experimental biology that are usually statistical
rather than analytical. Emergent properties of complex sys-
tems may indeed not be discoverable without strong impact
from computational biology.

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ISMB 2005 Conference/Program Committee Co-Chairs