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Editorial

ISMB 2001

This volume comprises the formal proceedings for the Ninth International Conference on Intelligent Systems for Molecular Biology (ISMB 2001) held in the Tivoli Gardens in central Copenhagen, Denmark, from July 21–25, 2001. The ISMB conference is the annual meeting of the *International Society for Computational Biology* (ISCB). As has been true of previous ISMB meetings, ISMB provides a general forum for disseminating the latest developments in bioinformatics.

In all areas of biological and medical research, the role of the computer has been dramatically enhanced in the last five to ten year period. While the first wave of computational analysis focussed on sequence analysis, where many highly important unsolved problems still remain, the current and future needs will in particular concern sophisticated *integration* of extremely diverse sets of data. These novel types of data originate from a variety of experimental techniques of which many are capable of data production at the level of entire cells, organs or organisms.

Our ability in the future to make new biological discoveries will depend strongly on our ability to combine and correlate, rather than a continued effort which only addresses traditional data analysis in research areas on an individual basis. Basic research within bioinformatics will have to deal with these issues of *integrative biology*, in a situation where the amount of data will explode leading to the accumulation of for example:

- tens or hundreds of mammalian genomes,
- thousands of other eukaryotic and prokaryotic genomes,
- massive amounts of cDNA and EST data,
- data on world-wide single nucleotide polymorphisms,
- organism-wide gene expression profiles from many hundreds of organisms under many different experimental and environmental conditions,
- proteome snapshots characterizing translation products across time and tissues,
- organism-wide charaterization of protein structures (structural genomics) and protein-protein interaction,
- modeling of cellular processes and pathways, metabolomes, vaccinomes, phenomes, *etc.*,
- massive amounts of text data from abstracts and complete journal articles.

This situation calls for approaches which can deal with the problems of analysing data accross different domains. The 2001 ISMB meeting has indeed shown that methods which address many of these new challenges for bioinformatics are under development.

ISMB 2001 was the first meeting after the publication of the two human genome draft sequences. The encouragement to submit papers to this series of meetings has never been higher, a record high 180 papers were received, with approximately 60% coming from the US, 30% from Europe and 10% from other parts of the world. The Program Committee and their designees reviewed each paper and a total of more than 500 reports were submitted in all, meaning the large majority of all papers received three reviews. The reports were read by members of the Organizing Committee who initiated discussions among referees in the cases where reviews were inconsistent.

Thirty-eight papers were selected for oral presentation and included in this issue. In addition, the conference included keynote addresses by Christopher M. Dobson (University of Oxford), David Eisenberg (UCLA), Gunnar von Heijne (Stockholm University), Sean Eddy (Washington University), Bernardo Huberman (HP Sand Hill Labs), and Chris Sander (MIT Center for Genome Research), as well as a lecture honoring the memory of G. Christian Overton, who died on May 31, 2000. This year's recipient of the Chris Overton prize was Chris Burge, known—among many other things—for his work with the highly succesful GENSCAN gene finder. Overton was the founding director of the Center for Bioinformatics at the University of Pennsylvania and was a widely known and greatly respected leader in our field.

More than 300 posters were received and presented on three separate days. The program also includes 14 tutorials given on the first day, commercial and non-commercial exhibits and software demonstrations, birds-of-a-feather sessions, and a job fair.

A total of six satellite meetings/events took place before and after ISMB 2001: the Bioinformatics Open Source Conference (BOSC 2001), the Bio-pathways Consortium meeting, and the Special Interest Group for Biological Simulation (SIGSIM), the 4th Annual Bio-Ontologies Meeting, the Workshop of Education in Bioinformatics (WEB01), and the Information Extraction meeting (BRIE'01). Details on these workshops can be found from the links on the ISMB 2001 website (http://ismb01.cbs.dtu.dk/).

The planning and organization of a conference such as ISMB 2001 with the commitment to publishing a high quality refereed proceedings in a short time frame relies extensively on the enthusiasm and commitment of the program committee. The organising committee wishes to formally express their gratitude to all members of the program committee.

We would like to thank the sponsors of the meeting, whose contributions help make the meeting more enjoyable and reduce the registration fees.

In conclusion the organizing committee would like to thank Johanne Keiding at CBS in Lyngby for her exceptional engagement in all aspects of the conference preparation, including the web site and the many negotiations with sponsors. Thanks go also to Janine Hatchwell at CBS, for her help with the proceedings and many other aspects of the conference, to Kitte Fennestad for the ISMB 2001 design concept, and the staff at Oxford University Press for producing this first version of the ISMB proceedings in the form of a Bioinformatics special issue. Everyone should be very proud of his or her efforts.

Of special mention must be the staff of the Center for Biological Sequence Analysis (CBS) who furthered their reputation for professionalism and excellence.

Søren Brunak and Anders Krogh
ISMB 2001 co-chairs
Technical University of Denmark
May 2001

ISMB 2001 Organization

ISMB 2001 has been organized by the International Society for Computational Biology (ISCB)

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