

# Preface

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This volume comprises the formal proceedings for the Eighth International Conference on Intelligent Systems for Molecular Biology (ISMB 2000) held on the campus of the University of California, San Diego from August 19-23, 2000. As has been true of previous ISMB meetings, ISMB provides a general forum for disseminating the latest developments in bioinformatics.

ISMB 2000 placed special emphasis on knowledge discovery from the modeling and simulation of complex biological systems. This included, but was not limited to, interpretation of large-scale gene expression data, whole genome comparative analysis, and mathematical modeling of biochemical pathways. This seemed appropriate given the completion of the human genome and thus the continual reference to the post-genomic era.

In keeping with the fast-growing interest in the field of bioinformatics in the interpretation of data generated in the pre- and post-genomic eras it is not surprising that this was the largest ISMB to date. More than 140 papers were received, with approximately 60% coming from the US, 30% from Europe and 10% from other parts of the world. Two or three members of the Program Committee or their designees reviewed each paper. Forty-one papers were selected for oral presentation. In addition keynote addresses were given by Gerald M. Edelman (The Neurosciences Institute), Leroy Hood (Institute for Systems Biology), Minoru Kanehisa (Kyoto University), J. Andrew McCammon (University of California, San Diego), Gene Myers (Celera Genomics Corp.) and Harold Scheraga (Cornell University). David Searls (SmithKline Beecham) gave a lecture honoring the memory of G. Christian Overton, who died on May 31, 2000. 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 was rounded out by 14 tutorials given on the first day, commercial and non-commercial exhibits and software demonstrations, birds-of-a-feather sessions, and a job fair.

ISMB 2000 is marked by two distinct changes over previous meetings—the size of the meeting and the complexity of the problems being addressed. Based on the number of submitted papers, this year's ISMB was 40% larger than any previous ISMB meeting. It would appear that the era of bioinformatics has truly arrived. Given the quality of the science submitted to the meeting there is every indication that the field will live up to its promise. That promise will be realized by a synergy among *in silico* biology and *in vivo* and *in vitro* biology. There was evidence of this synergy this year. Complexity came in two forms, from attempts to interpret ever more complex data sets particularly from DNA microarrays and from mass spectrometry experiments, but also from the scale of biological systems being addressed. Comparisons of complete genomes and attempts to model and understand whole biological pathways are examples of that complexity.

The completion of the human genome marks a unique point in time for biology, and for those new and not so new to the field, an increased excitement for what might be achieved in the future. As the first ISMB in the post (human) genome era we have a useful point of reference to the ISMB conferences of the future.

With size and complexity come added scientific and organizational needs. The Program Committee is to be commended for undertaking a large amount of work in a short time and the Organizing Committee is to be commended for taking on an ever-increasing amount of work up until the conference itself. Everyone should be very proud of his or her efforts.

Of special mention must be the staff of the San Diego Supercomputer Center (SDSC) who furthered their reputation for professionalism and excellence. It is certainly an ISMB that we will remember fondly; we hope you will, too.

Philip E. Bourne and Michael Gribskov  
*ISMB 2000 Cochairs*  
*University of California, San Diego*