THE SEVENTH INTERNATIONAL CONFERENCE ON INTELLIGENT SYSTEMS FOR MOLECULAR BIOLOGY (ISMB’99)

The Seventh International Conference on Intelligent Systems for Molecular Biology (ISMB’99), on August 6-10, 1999 in Heidelberg, Germany, was probably the largest meeting on computational biology to date. Over 650 scientists from 28 countries attended the meeting. This is 50% up from last year’s meeting in Montreal, Canada. In fact the organizers had to close registration 3 weeks early due to limited space at the conference site. Together with the large number of 167 conference posters and a notable industrial interest in the meeting, this is a strong indication that computational biology is continuing to boom. Of the participants, 31% came from the USA, 22% from Germany and 15% from the UK, followed by smaller attendance from other countries.

The conference featured a tutorial day, which was attended by about two in three conference participants, and had 10 half-day tutorials presenting both introductory and advanced topics in computational biology. Out of 91 submissions the program committee with 47 renowned scientists selected 34 papers that were presented at the conference. In eight additional keynote talks, cutting-edge research in bioinformatics was presented as well as new experimental projects and techniques that entail future challenges for bioinformatics. In the opening keynote address, Prof. Manfred Eigen, Nobel Laureate in Chemistry (1967), discussed the Origin of Biological Information, thus linking the quest of computational biology, which is studying the molecular structures and processes of life with methods of information technology, to the closely related question of how nature itself creates and handles information.

Outstanding contributed papers and posters received awards (checks and two SGI computers) that were donated by The Genomics and Computational Biology Program at Lawrence Berkeley National Laboratory and the University of California, Berkeley and Silicon Graphics, Inc., respectively.

An industrial exhibition with 13 exhibits featured software and print products for the field of computational biology. A job-fair allowed employers to seek prospective employees—and proved once again that computational biologists are hard to come by these days.

The meeting showed that present-day computational biology is driven by a number of challenges, among which the dominant three may be the following:

1. The incoming data from large-scale sequencing projects—a first rough draft of ~90% of the human genome was announced to be available before the middle of next year. Beyond generic genomes of different species, the available data increasingly allow (and demand) the analysis of genetic variability and differences between healthy and diseased states on the genomic level.

2. The quest to understand ever more high-level biological functions based on genomic data. While a few years ago the molecular sequence was still the focus of much of computational biology, molecular structure and molecular interactions, now even networks of metabolic and regulatory paths are being increasingly maintained, analyzed and predicted with the help of the computer.

3. New upcoming experimental techniques in genomics and proteomics. These include DNA-chips and proteomics based on 2-D gels, as well as MALDI-TOF mass spectrometry.

All of these factors were represented by both keynote talks and contributed papers and posters. The conference witnessed that the field of computational biology is composed of a healthy mix of basic research and application-oriented endeavors, eventually resulting in freely distributed or commercially marketed software. It is characterized by rapid development on the experimental side, creating a momentous influx of new data and research problems. Another observation is that the different disciplines that contribute to computational biology are quickly moving closer and the interdisciplinary coherence of this important scientific field is growing at a fast pace.

The ISMB conference series is organized by the International Society for Computational Biology (ISCB, www.iscb.org), which was founded in 1997. The mission of the society is the advancement of the scientific understanding of living systems through computation: its emphasis is on the role of computing and informatics in advancing molecular biology. The next sequel of the ISMB series will take place on August 20–23, 2000 at the University of California, San Diego, CA (ismb00.sdsc.edu).

On the day after the conference, an organized tour led ~300 conference participants into the path of totality of the solar eclipse of August 11, 1999, just 50 km south of Heidelberg. Despite generally adverse weather conditions the group was lucky enough to be able to view this rare and very impressive astronomic spectacle.

More information on ISMB’99 can be found on the internet (ismb99.gmd.de).

Thomas Lengauer
Chairman of the Organizing Committee of ISMB’99