

Preface

This volume comprises the archived proceedings of the Second International Conference on Intelligent Systems for Molecular Biology (ISMB), held at Stanford University from August 15 to 17, 1994. The overwhelming success of the first conference produced high expectations for the quality and size of this year's meeting. The organizing committee is pleased to report some basic facts about the meeting that bode well for the future:

First, the response to our invitation for program committee membership was enthusiastic and swift. The program committee consists of biologists and computer scientists who are actively contributing to the interdisciplinary area of computational molecular biology. We note the truly international character of the program committee, as well as the increasing number of participating women scientists.

Second, the call for papers produced 86 submissions of high quality. These submissions were rigorously reviewed by three members of the program committee, and disagreements on the merits of individual papers were mediated by one of the organizers. The efforts of the program committee constitute strong evidence that the standards of productivity and communication in this field are high.

Third, the call for tutorial proposals produced nine accepted tutorials of high quality. Taught by distinguished members of the community (including many program committee members), the tutorials offered participants the opportunity to update or augment their knowledge of allied disciplines. The tutorials (and tutors) were *Information Science for Molecular Biologists* (Doug Brutlag), *Molecular Biology for Computer Scientists* (Gary Stormo), *Minimal Length Encoding in Molecular Biology* (Aleksandar Milosavljevic), *Machine Learning in Molecular Biology* (Pierre Baldi), *Computational Challenges for Intelligent Systems in Molecular Biology* (Russ Altman and Peter Karp), *Neural Networks* (David Bisant), *Constraint Satisfaction in Molecular Biology* (Christopher Rawlings and Dominic Clark), *Genetic Algorithms and Genetic Programming* (John Koza), and *Hidden Markov Models, SCFGs, and Related Models* (David Haussler).

Fourth, three outstanding speakers agreed to give the conference addresses: Bruce Buchanan, University of Pittsburgh, provided the keynote and

Lawrence Hunter, National Library of Medicine, and Richard Roberts, New England BioLabs, gave the plenary addresses.

Fifth, the response of funding agencies to our requests for support was uniformly enthusiastic. In particular, we were able to secure funds to support the travel of students, postdoctoral fellows, women and underrepresented minority scientists. We would like to thank the funding agencies that have supported the conference this year: the National Library of Medicine and National Center for Human Genome Research (both of the National Institutes of Health), the Computational Biology section of the National Science Foundation, and the Department of Energy, Office of Health and Environmental Research. The American Association for Artificial Intelligence has provided support for the publication of these Proceedings.

Finally, we have already identified a venue for ISMB-95: Cambridge, England. Dominic Clark and Christopher Rawlings, both of the Imperial Cancer Research Fund, will host the meeting, which will have been held in the eastern United States, western United States, and Europe. We hope that potential hosts from the Pacific Rim will consider organizing ISMB-96.

Preparation for this meeting has been a learning experience for all involved. One of the key issues that surfaced during the planning phases was the proper scope for the meeting. There can be conflict between the goals of computer scientists and those of biologists especially in the process of reviewing and organizing papers for presentation. The historical roots of this conference in artificial intelligence and molecular biology remain. There are, however, related disciplines that are also relevant to the production of complex computer systems for solving problems in molecular biology, including (but not limited to) mathematical biology, robotics, discrete mathematics, linguistics, systems engineering, theoretical physics, combinatorial chemistry, biochemistry, and biophysics. It is our hope that ISMB will become the major forum for computational molecular biology. The common denominator will be the expectation that new theoretical approaches are accompanied by computer implementations that allow evaluation, testing, and deployment of new technologies that

have an impact on biology. If this meeting continues to grow in importance, it will become a forum for presenting major innovations in computational molecular biology. We believe that many of these innovations will be, in some sense, "intelligent."

We have noted that there is a growing cadre of investigators whose discipline is neither computer science nor molecular biology, but is in the area of overlap between these. Lacking a clear niche within traditional disciplines, these investigators need opportunities to meet one another, establish a core literature, and develop a set of fundamental scientific premises. This should be the big conference for those who want to hear about major breakthroughs in dynamic programming, multiple sequence alignment, the federation of molecular biology databases, hidden Markov models for sequence analysis, constraint satisfaction techniques for map assembly or structure

definition, probabilistic modeling of biological structures and sequences, simulation of metabolic processes, heuristic ways to search large hypothesis spaces, the theory of neural networks, energy functions that fold protein structures more accurately, search algorithms for protein conformation, linguistic parsing techniques for sequence analysis, novel map reconstruction algorithms, computational geometry breakthroughs for drug design, robotic applications to molecular structure, and more.

We would like to thank the individuals whose efforts contributed to creating the meeting and the proceedings: Gustavo Galindo, Kevin Lauderdale, Irene Zagazeta, and Rosalind Ravasio have contributed to an excellent team effort. Mike Hamilton at AAAI Press has once again produced a proceedings of top quality.

—*Russ Altman, Douglas Brutlag, Peter Karp,
Rick Lathrop & David Searls*