Preface

The ISMB-97 conference took place in Halkidiki, Greece, from June 21-25, 1997. The conference consisted of one day of tutorials followed by four days of technical presentations, and included a workshop on genome annotation.

The organizing committee received eighty-five submitted papers. Each paper was reviewed by three members of the program committee. Based on those reviews, the organizers accepted thirty-two papers for publication in the proceedings and oral presentation at the meeting. An additional twenty-two papers were accepted for publication in short form, and for presentation as posters. These short papers allow dissemination of important research results despite the time constraints of the conference.

The invited speakers at this year's conference were Professors Fotis C. Kafatos, Director General, EMBL, Heidelberg, Germany; Richard Lathrop, University of California at Irvine, Irvine California, USA; Marcie McClure, University of Nevada, Las Vegas, Nevada, USA; and Hans V. Westerhoff, Vrije Universiteit, Amsterdam, The Netherlands.

In the past two years, bioinformatics has changed from a backwater to a tidal wave. The ISMB conference, now in its fourth year, has proven to be a driving force behind that wave. Surprisingly, the advances in bioinformatics and computer power that deliver faster, more accurate processing of biological data continue to be equally matched by the abilities of experimentalists to generate these data at an ever-increasing rate. The ongoing challenge of capturing that data, and extracting biological meaning from it, is considerable. Thus, our clearest goal is to continue applying the latest computational methods to the problems of managing and analyzing molecular-biology data. However, as well as generating traditional types of data at an accelerating pace (such as sequences and maps), experimentalists are also developing high-throughput techniques for generating novel types of data, such as gene-expression and protein-interaction data. A second challenge to the ISMB community is to integrate these novel types of data into a larger bioinformatics framework that infers correlations among diverse types of measurements. A final goal is to fully exploit the interdisciplinary nature of bioinformatics problems by using these problems to drive the development of more powerful computer-science techniques.

--The ISMB Organizing Committee