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Preface

Biomolecular computing is an interdisciplinary field that draws together molecular biology, DNA nanotechnology, chemistry, physics, computer science and mathematics. The annual international meeting on DNA-based computation has been an exciting forum where scientists of different backgrounds who share a common interest in biomolecular computing can meet and discuss their latest results. The central goal of this conference is to bring together experimentalists and theoreticians whose insights can calibrate each others' approaches. The 9th Annual International Meeting on DNA Based Computers was held during June 1–4, 2003 in the University of Wisconsin, Madison, USA. The meeting had 106 registered participants from 12 countries around the world.

On the first day of the meeting, we had three tutorials: the first was on self-assembly of DNA nano structures which focused on the basic techniques of using designed DNA nano molecules to be self-assembled onto larger structures for computational purposes. This tutorial was given by Hao Yan of Duke University. The second tutorial was given by Chengde Mao of Purdue University in which Dr. Mao presented basic DNA biochemistry that was designed for non experimentalists. The third tutorial was given by Max Garzon of the University of Memphis. Dr. Garzon gave a lecture on computational complexity which was tailored for non-computer scientists. The next three days were for invited plenary lectures, and regular oral and poster presentations. Invited plenary lectures were given by Helen Berman of Rutgers University (USA), Giancarlo Mauri of the University of Milan (Italy), Guenter von Kiedrowski of Ruhr University (Germany), and Sorin Istrail of Celera/Applied Biosystems.

The organizers sought to attract the most significant recent research with the highest impact on the development of the discipline. Papers and posters with new experimental results were particularly encouraged. Authors who wished their work to be considered for either oral or poster presentation were asked to select from one of two submission "tracks": Track A, Full Paper; Track B, One-Page Abstract.

For authors with late-breaking results, or who were submitting their manuscript to a scientific journal, a one-page abstract, rather than a full paper, could be submitted in Track B. Authors could (optionally) include a preprint of their full paper for consideration by the program committee. The program committee received 48 submissions in Track A, and 12 submissions in Track B. These submissions were then reviewed by the program committee members. In principle, four committee members were allocated for each submission. In considering the returned review reports, all discussions pertaining to the final decisions were made online by the program committee members. We finally selected 32 oral presentations from Tracks A and B. The oral and poster presentations included all areas that relate to biomolecular computing, such as algorithms and applications, analysis of laboratory techniques/theoretical models, computational

processes in vitro and in vivo, DNA-computing-based biotechnological applications, DNA devices, error evaluation and correction, in vitro evolution, models of biomolecular computing, molecular design, and simulation tools.

The editors would like to acknowledge the help of the conference's Program Committee in reviewing the submitted abstracts. The editors thank the Organizing Committee for their superb organization skill. We are grateful for the generous support and sponsorship of the conference by GenTel Corporation, DARPA (IPTO Biocomputation), NSF (CISE QUBIC ITR), and the Chemistry Department of the University of Wisconsin, Madison. Finally, the editors would like to thank all of the participants in the DNA9 conference for making it a wonderful experience. We hope that this volume has captured the spirit and exhilaration that we experienced at the conference.

December 2003

Junghuei Chen
John Reif

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