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Nota di contenuto	Experimental Tools -- An Object Oriented Simulation of Real Occurring Molecular Biological Processes for DNA Computing and Its Experimental Verification -- Towards Optimization of PCR Protocol in DNA Computing -- DNASquenceGenerator: A Program for the Construction of DNA Sequences -- DNA Computing in Microreactors -- Cascadable Hybridisation Transfer of Specific DNA between Microreactor Selection Modules -- Theoretical Tools -- Coding Properties of DNA Languages -- Boundary Components of Thickened Graphs -- Probabilistic Computational Models -- Population Computation and Majority Inference in Test Tube -- DNA Starts to Learn Poker -- PNA-mediated Whiplash PCR -- Computer Simulation and Sequence Design --

Biomolecular Computation in Virtual Test Tubes -- Developing Support System for Sequence Design in DNA Computing -- The Fidelity of the Tag-Antitag System -- PUNCH: An Evolutionary Algorithm for Optimizing Bit Set Selection -- Algorithms -- Solving Knapsack Problems in a Sticker Based Model -- A Clause String DNA Algorithm for SAT -- A Proposal of DNA Computing on Beads with Application to SAT Problems -- Experimental Solutions -- Aqueous Solutions of Algorithmic Problems: Emphasizing Knights on a 3×3 -- Solutions of Shortest Path Problems by Concentration Control -- Another Realization of Aqueous Computing with Peptide Nucleic Acid -- Experimental Confirmation of the Basic Principles of Length-only Discrimination -- Experimental Construction of Very Large Scale DNA Databases with Associative Search Capability -- Nano-tech Devices -- Operation of a Purified DNA Nanoactuator -- DNA Scissors -- Biomimetic Tools -- A Realization of Information Gate by Using *Enterococcus faecalis* Pheromone System -- Patterns of Micronuclear Genes in Ciliates -- Peptide Computing - Universality and Complexity -- Programmed Mutagenesis Is a Universal Model of Computation -- New Computing Models -- Horn Clause Computation by Self-assembly of DNA Molecules -- DNA-based Parallel Computation of Simple Arithmetic -- Splicing Systems and Membranes -- On P Systems with Global Rules -- Computing with Membranes: Variants with an Enhanced Membrane Handling -- Towards an Electronic Implementation of Membrane Computing: A Formal Description of Non-deterministic Evolution in Transition P Systems -- Insertion-Deletion P Systems -- A Universal Time-Varying Distributed H System of Degree 1 -- A Note on Graph Splicing Languages.

Sommario/riassunto

Biomolecular computing is an interdisciplinary field that draws together molecular biology, chemistry, physics, computer science, and mathematics. DNA technology and molecular biology are key relevant experimental areas, where knowledge increases with each passing year. 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 meet and discuss their latest results. The central goal of this conference is to bring together experimentalists and theoreticians whose insights can calibrate each other's approaches. DNA7, The Seventh International Meeting on DNA Based Computers, was held at The University of South Florida in Tampa, FL, USA, June 10-13, 2001. The organizers sought to attract the most significant research, with the highest impact on the development of the discipline. The meeting had 93 registered participants from 14 countries around the world. The program committee received 44 abstracts, from which 26 papers were presented at the meeting, and included in this volume. In addition to these papers, the Program Committee chose 9 additional papers from the poster presentations, and their revised versions have been added to this volume. As is now a tradition, four tutorials were presented on the first day of the meeting. The morning started with general tutorials by Erik Winfree (Caltech) and Junghuei Chen (University of Delaware), designed to bridge between their respective areas of expertise, computer science and molecular biology. More specialized tutorials on encoding DNA sequences and on non-standard DNA motifs and interactions were given in the afternoon by Anne Condon (University of British Columbia) and Nadrian C. Seeman (New York University), respectively.
