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DNA Based Computers II

DIMACS Workshop
June 10–12, 1996

Laura F. Landweber
Eric B. Baum
Editors

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Foreword

The Second Annual Workshop on DNA Based Computers was held on June 10–12, 1996 at Princeton University, N. J. We would like to express our appreciation to Eric Baum, Dan Boneh, Peter Kaplan, Richard Lipton, John Reif, and Nadrian Seeman for their efforts to organize and plan this successful workshop.

The Workshop was part of the broader Special Year on DNA Computing. We extend our thanks to Richard Lipton and Laura Landweber for their work over many months as Special Year organizers.

The Workshop was a forum for bringing together researchers working on all areas that relate directly to computing with DNA, including algorithms, applications, techniques, architectures, computational processes in vivo, and relevant ideas regarding biological evolution.

DIMACS gratefully acknowledges the generous support that makes these programs possible. The National Science Foundation, through its Science and Technology Center program, the New Jersey Commission on Science and Technology, and DIMACS’ partners at Rutgers, Princeton, AT&T Labs Research, Bell Labs, and Bellcore generously supported the Special Year.

Fred S. Roberts
Director

Bernard Chazelle
Co-Director for Princeton
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Introduction

DNA Computing has fueled a tremendous amount of excitement by offering a fresh paradigm for performing and viewing computations: this is biological mathematics, while also mathematical biology. Encoding of data in DNA strings coupled with the power of molecular biology now allows the execution of computational operations on single strands of DNA in the laboratory. As a small drop of solution can house several quadrillion DNA molecules, DNA computers use much less energy and space than traditional computers. Consequently, they offer the tantalizing potential of one day outperforming electronic computers. Computing with DNA is also massively parallel, with billions and trillions of molecules undergoing simultaneous chemical reactions and performing computations almost spontaneously.

The product of a radically different marriage of computer science to molecular biology, the fledgling field of DNA computers began in 1994, when Leonard Adleman surprised the scientific community by using DNA molecules, protein enzymes, and chemicals to solve an instance of a hard computational problem. These proceedings from the Second DIMACS Workshop on DNA Based Computers at Princeton University – held only one year and a half after the publication of Adleman’s seminal experiment – contain a set of refereed papers that highlight some of the exciting progress in this field and together build a strong foundation for the current theory of molecular computation.

This volume introduces such important advances as “mark and destroy” DNA algorithms and the use of surface chemistry in DNA computing. It also includes a healthy discussion of the myriad possibilities as well as potential pitfalls, means of error correction, and general practicality of building DNA based computers. Several articles draw on the analogy between DNA computing and other cutting edge fields of biology such as directed evolution. In principle, both types of experiments search for a single or unique class of molecules in a random or heterogeneous mixture. Such techniques have been enormously successful in discovering biological molecules with novel capacities for performing chemical reactions. As these molecules can even encode the solution to a mathematical problem, nucleic acid based computers may be viewed as a natural extension of test-tube evolution experiments that search a defined space of mathematical solutions. Indeed, they are “solutions of solutions!”

Laura F. Landweber, Princeton University
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Laura Landweber, Princeton University

Eric Baum, NEC
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