Foreword

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This special issue of Natural Computing contains a selection of extended versions of papers presented at the 14th International Meeting on DNA Computing, held on June 2–9 in 2008, in Prague, Czech Republic.

The DNA computing conference now traditionally is one of the two large meetings of the International Society of Nanoscale Science, Computing, and Engineering (ISNSCE, <http://www.isnsce.org>). It has developed considerably from its beginnings, and today encompasses a broad range of topics from theoretical computer science to the theory of self-assembly, molecular and cellular computing and even synthetic biology. It therefore regularly brings together a unique blend of scientific personalities with a highly multi-disciplinary background, which is also reflected in the paper contributions to the meeting.

We wish to express our gratitude to the members of the Program Committee, the local organizers, and the Steering Committee who made DNA14 a great success. In particular, we would like to thank Prof. Petr Sosik, the chair of the organizing committee.

We are pleased to present in this special issue six considerably extended and enhanced versions of selected papers presented at the meeting. Three of the papers deal with the theory of self-assembly, one paper utilizes DNA-assembly principles for the optimization of operon structures, and two papers are devoted to DNA computing by whiplash PCR.

- *Polyomino-Safe DNA Self-Assembly Via Block Replacement* (by Chris Luhrs): DNA tile assembly is a prototypic system for the study of bottom-up assembly of molecular nanostructures. An important problem here is the occurrence of errors during assembly, for instance through the unwanted attachment of pre-formed, multiply connected DNA tiles (“polyominoes”). This paper introduces an assembly scheme that avoids errors caused by polyomino attachment.

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- *Robust Self-Assembly of Graphs* (by Stanislav Angelov, Sanjeev Khanna and Mirkó Visontai): This paper investigates the robust self-assembly problem for accretive graphs, which deals with the question whether every feasible sequence of vertex additions to a seed vertex results in the assembly of the complete graph. One major result of the paper is that the robust self-assembly problem is co-NP-complete even on planar graphs with two distinct edge weights.
- *Self-Assembly of Discrete Self-Similar Fractals* (by Matthew Patitz and Scott Summers): Another important self-assembly problem is the question, whether a given target structure can be produced by self-assembly or not. This paper deals with limitations of the Tile Assembly Model (TAM) and investigates, whether certain self-similar fractals can self-assemble in the TAM. The authors show that a particular class of well-behaved fractals has a “fibered” version that strictly self-assembles in the TAM.
- *Operon Structure Optimization by Random Self-assembly* (by Yusuke Nakagawa, Katsuyuki Yugi, Kenji Tsuge, Mitsuhiro Itaya, Hiroshi Yanagawa and Yasubumi Sakakibara): In this experimental paper, random self-assembly of gene sequences is used for the construction of operon structures. Random assembly results in different operons with permutations of the operon genes. As the efficiency of an operon is non-trivially dependent on the order and orientation of the genes, this method can be used to experimentally optimize such operon structures.
- *Isothermal Reactivating Whiplash PCR for Locally Programmable Molecular Computation* (by John Reif and Urmi Majumder): Whiplash PCR (WPCR) is a molecular computing technique, in which computational state transitions are realized with single-stranded DNA molecules, DNA polymerase and thermal denaturation and annealing steps. This paper introduces three distinct protocols for isothermal and autocatalytic WPCR, which effectively transform WPCR into an autonomous computing technique. A computational program can therefore be executed over several cycles without external interference or assistance.
- *Experimental Validation and Optimization of Signal Dependent Operation in Whiplash PCR* (by Ken Komiya, Masayuki Yamamura and John A. Rose): The original WPCR-technique suffers from the problem of back-hybridization, in which the DNA sequence representing the current state of the WPCR device hybridizes to a rule sequence that has already been executed. This limits WPCR computations to only a few steps. The rule-protect operation introduces primers during the computation, which are extended by DNA polymerase and thereby mask already executed rule sequences. In this paper, the fundamental feasibility of the rule protect operation is shown experimentally, and it is also proposed to utilize this operation for sensing and signaling.