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Preface

David Doty[1] · Hendrik Dietz[2]

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The International Conference on DNA Computing and Molecular Programming, held under the auspices of the International Society for Nanoscale Science, Computation, and Engineering (ISNSCE), is the premier conference for research investigating the possibility of programming molecules to carry out computation. The conference features contributed and peer-reviewed talks, poster presentations, and invited talks of leading scientists. The conference attracts a wide range of scientists from many backgrounds such as mathematics, computer science, physics, chemistry, biology, bioengineering, electrical engineering, and nanotechnology.

This special issue of Natural Computing is associated with the 24th International Conference on DNA Computing and Molecular Programming, held October 8–12, 2018 at Shandong Normal University in Jinan, China. Six papers were invited from the conference that had been presented in preliminary form at the conference. Each was subjected to a thorough review independent of the DNA 24 reviewing process. One paper was withdrawn, and this issue contains the five remaining papers.

The paper "Transcript Design Problem of Oritatami Systems", by Yo-Sub Han, Hwee Kim, and Shinnosuke Seki, investigates a recently developed model of RNA cotranscriptional folding, based on experimentally demonstrated programming of such folding by Geary et al. They study the problem of, given a certain conformation, create a transcript that folds into it under the model. This problem is shown to be NP-hard in general, but solvable in polynomial time in certain special cases.

The paper "Self-Assembly of 3-D Structures Using 2-D Folding Tiles", by Jérôme Durand-Lose, Jacob Hendricks, Matthew J. Patitz, Ian Perkins, and Michael Sharp, studies a relaxation of the well-studied tile assembly model based on experimentally implemented DNA tiles, which acknowledges the experimental reality that 2D tiles are not perfectly rigid and may fold into the third dimension. Imagining that such flexibility could be intentionally engineered into the tiles, they demonstrate how to form certain target 3D structures from folding 2D tiles, and how this flexibility allows "efficient" reconfiguration. As with many computationally powerful systems, they also show that certain prediction problems are therefore intractable.

The paper "Hierarchical Growth is Necessary and (Sometimes) Sufficient to Self-Assemble Discrete Self-Similar Fractals" by Jacob Hendricks, Joseph Opseth, Matthew J. Patitz, and Scott M. Summers, shows that certain infinite fractal shapes cannot be assembled in the standard "single-tile accretion" tile assembly model based on experimentally implemented DNA tiles, but *can* be assembled if hierarchical growth is allowed, that is, if large assemblies may attach to each other in a single step. The impossibility result that the standard model cannot assemble such fractals is significant in that it goes beyond the simple "information theoretic bottleneck" arguments used to show that the discrete Sierpinski triangle cannot self-assemble.

The paper "Forming Tile Shapes with Simple Robots", by Robert Gmyr, Kristian Hinnenthal, Irina Kostitsyna, Fabian Kuhn, Dorian Rudolph, Christian Scheideler, and Thim Strothmann, studies a form of tile assembly different from the tile assembly papers elsewhere in this issue, in which the "actors" that move the tiles are separate from the tiles themselves. In this case, nanoscale "robots" are modeled, which pick up and carry hexagonal tiles to different positions in the plane. It is shown that such a distributed system of robots can build certain shapes from tiles efficiently in terms of the amount of time required.

The paper "CRN++: Molecular Programming Language", by Marko Vasic, David Soloveichik, and Sarfraz Khurshid, introduces an imperative programming language for programming chemical reaction networks. The

✉ David Doty
doty@ucdavis.edu

Hendrik Dietz
dietz@tum.de

[1] University of California, Davis, USA

[2] Technical University of Munich, Munich, Germany

language systematically composes a variety of modules that perform basic calculations on values stored as concentrations, utilizing a chemical clock for synchronization. A number of classical algorithms such as GCD are demonstrated by implementation in the language. Furthermore, error-analysis tools for chemical reaction programs are shown.

The guest editors thank the authors for contributing papers and the referees who agreed to review the submissions. All papers had significant suggestions made by referees, which significantly improved the quality of the papers. The guest editors warmly thank Joost Kok, Grzegorz Rozenberg, and the staff of Natural Computing for their effort in creating this special issue. Finally, the guest editors are grateful to the conference organizers, authors of track A, B, and C submissions, and attendees at DNA 24. It was a truly magnificent conference.