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Preface

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The International Conference Series on DNA Computing and Molecular Programming has now become the premier forum for biomolecular computing research where scientists with diverse backgrounds come together with the common purpose of applying principles and tools of computer science, physics, chemistry and mathematics to advance molecular-scale computation and nanoengineering. Continuing this tradition, the 20th International Conference on DNA Computing and Molecular Programming (DNA20), organized under the auspices of the International Society for Nanoscale Science, Computation and Engineering (ISNSCE), focuses on important recent experimental and theoretical results.

This special issue contains a selection of six papers originally presented in preliminary form at DNA 20: the 20th International Conference on DNA Computing and Molecular Programming, held in September 2014 at Kyoto University, Kyoto, Japan. All papers herein were reviewed independently of the conference referee process and contain extensive additional material.

Implementing cellular automata by molecular computation is one of the recent research trends in the field of DNA computing and molecular programming. "Emulating Cellular Automata in Chemical Reaction–Diffusion Networks" Dominic Scalise and Rebecca Schulman is a milestone in that direction and won the best paper award in the conference. They show that chemical reactions with diffusion can emulate the dynamics of a deterministic cellular automaton by simulating the reaction–diffusion network for two 1-dimensional cellular automata. The research is expected to be followed by an experimental effort possibly using DNA molecules that interact via branch migration.

Chemical reactions and bio-operations have been attracting researchers in theoretical computer science. Two papers deal with their computational power measured in the formal language theory. In "The Computational Capability of Chemical Reaction Automata," Fumiya Okubo and Takashi Yokomori introduce a new computing model called chemical reaction automata (CRAs), which is obtained from Reaction Automata (RAs) by dropping inhibitor functioning in each reaction, and prove that CRAs in maximally parallel manner are Turing-computable while CRAs in sequential manner are equivalent to Petri nets. In "On Decidability and Closure Properties of Language Classes with Respect to Bio-Operations," by taking a general approach not based on reduction to the Post Correspondence Problem (PCP), Oscar Ibarra proves new decidability results and closure properties of some language classes under bio-operations such as hairpin-inversion.

Although CRAs provide an 'offline' model of computing by chemical reaction networks (CRNs), as Okubo and Yokmori write, two more theoretical papers directly concern CNRs. In "Minimal Output Unstable Configurations in Chemical Reaction Networks and Deciders," Robert Brijder analyzes chemical reaction deciders (CRDs), in which CRNs are used to define a predicate on initial configurations, and gives an algorithm to efficiently check output stability of configurations. While Brijder's paper assumes error-free computation and does not discuss probabilities, the other paper "Probability 1 Computation with Chemical Reaction Networks" by Rachel Cummings, David Doty and David Soloveichik deals with the computational power of stochastic CRNs. After introducing the notion of limit-stable computation, they show that limit-stable computation

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encompasses a superset of the set of Turing-computable predicates and characterize the functions computable by CRNs with probability 1.

"Classical, Quantum and Biological Randomness as Relative Unpredictability" by Cristian S. Calude and Giuseppe Longo is based on an invited talk of the conference, and also deals with randomness. It is expected to inspire researchers in DNA computing and molecular programing and in natural computing in general. They propose the thesis that randomness is unpredictability with respect to an intended theory and measurement, and discuss various forms of randomness in physics, mathematics and computing science, finally touching upon biological randomness.

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