Editorial: Computing with biomolecules

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This special issue contains extended full versions of selected papers presented at the *International Workshop on Computing with Biomolecules* held on August 27, 2008, in Vienna, Austria, in conjunction with the *7th International Conference on Unconventional Computation, UC 2008*. The topic of the workshop, and of this journal issue, lies within molecular and cellular computing, with special emphasis on membrane computing. The articles represent different approaches and cover a wide variety of research topics in these rapidly developing scientific areas, ranging from models of properties of DNA to different variants of P systems, i.e., membrane systems.

Additionally, one paper belonging to the general area of biocomputing was submitted specifically for this special journal issue. All contributions were thoroughly refereed and revised, according to the usual standards of *Natural Computing*. Below we provide a summary of each of the seven papers featured in the special issue. The articles are listed in alphabetical order according to the first author.

In the first paper, Bogdan Aman and Gabriel Ciobanu consider a new class of membrane systems (P systems), characterized by mutual mobile membranes with objects on the surface. The rules of this class are inspired by the pino, exo and phago operations. The authors investigate the computational power of this class of P systems and establish universality results already with a small number of membranes. In the last section the model is compared with brane calculi.

Mark Daley, Ian McQuillan, James M. McQuillan and Kalpana Mahalingam study formal-language-theoretic models for transposable genetic elements. The aim of their work is to improve our understanding of mathematical modeling of transpositions. The genetic transpositions are abstracted as operations on words and languages and the authors investigate the computational power of applying different types of transpositions iteratively.

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The paper by Giuditta Franco and Vincenzo Manca considers a novel DNA recombination mechanism called XPCR. This is a variant of polymerase chain reaction which has been much used in molecular biology as a technique for cyclic amplification of DNA segments. The authors propose several algorithms aimed at suggesting new methods for DNA manipulation in biotechnological procedures.

Rudolf Freund and Sergey Verlan investigate variants of maximally and minimally parallel computation (transition) modes in P systems. The set of rules is partitioned in a certain way and the parallel application of rules is guided by the partitioning, with the precise restrictions being different in, respectively, the maximally and the minimally parallel modes. In particular, the paper establishes a connection of the 1-restricted minimally parallel transition mode and the spiking neural P systems without delays.

Alexander Krassovitskiy, Yuri Rogozhin and Sergey Verlan consider a formal-language-theoretic model based on insertion and deletion operations for the mismatched annealing in DNA sequences. The paper focuses on one-sided insertion–deletion systems where at most two symbols may be present in the description of the rules. The authors establish that even very restricted types of systems of this form are able to generate non-regular languages. The second part of the paper deals with insertion–deletion rules within the framework of membrane computing, with the computational power of P systems employing insertion–deletion operations.

The paper by Matthew J. Patitz and Scott M. Summers considers computation in Winfree's abstract tile assembly model. As an extension of the wedge construction, the authors give a new characterization of decidable sets of natural numbers in terms of (weak) self-assembly. Furthermore, it is shown that the construction is robust with respect to certain types of geometrical constraints.

Finally, Elena Rivero-Gil, Miguel Á. Gutiérrez-Naranjo, Álvaro Romero-Jiménez and Agustín Riscos-Núñez describe a novel software tool, called JPLANT, for computing and representing the evolution of a P system. This tool is able to deal with complex P systems involving membrane creation and to represent graphically their evolution over time. The paper discusses several experiments that explore the graphical representation of P systems.

We thank all the authors of the papers whose contributions have made this issue possible. To conclude, we are grateful to Grzegorz Rozenberg, Editor-in-Chief of Natural Computing, for giving us the opportunity to publish this special issue.