Towards Persistent Molecular Computers for Molecular Robots

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Although a large number of models for molecular computers have been proposed and many of them have actually been implemented typically by using DNA molecules with or without modifications, most of those models are restricted in the sense that computational resources are consumed by each instance of computation and cannot be reused iteratively. Models based on strand displacement of DNA, such as that of seesaw gates by Qian et al. [1], are not exceptions. On the other hand, the idea of molecular robots is now commonly accepted [2], and computers for molecular robots are expected to be reusable and sustainable. The model of dynamical systems by Rondelez et al. is one of few such models [3]. We envision that molecular computers for molecular robots should have the following properties. They 1) receive input from the environment, 2) adapt to the environment by solving some optimization (or learning) problems, and finally 3) save the result of computation (solutions to the problems) for handling the next input from the environment.

In this ongoing and preliminary work, we take the k-SAT problem as an optimization problem whose clauses model input from the environment. The molecular computer solves the problem, and re-solves it when its clauses are modified or new ones are added. As in the work by Sakamoto et al. [4], each clause of an instance of the k-SAT problem is represented by a computational unit. While one literal is chosen from a clause in advance in [4], a computational unit in this work takes one of the literals in its corresponding clause as a state, and changes the state for solving or re-solving the problem.

In this poster, we propose and compare three molecular implementations of the above abstract scheme. 1) Implementation by a molecular complex whose conformational changes realize progression of state transitions by alternating irradiation of two kinds of light [5]. 2) Implementation by polymerase extension and digestion by nicking enzymes, which can be considered as an extension of DWPCR [6]. 3) Implementation by a dynamical system of Montagne et al. [3].

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