Oral Presentation 3

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『分子ロボティクス』
Molecular robotics

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O3-01

Automated exploration of CRN generating DNA structures

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Keywords: DNA nanostructures, chemical reaction networks, reaction enumeration, quality diversity

In recent years, a multitude of tools and models have been proposed for the rational design of specific DNA structures [1]. In particular, families of structures ranging from a tetrahedron to large structures ("buckyball") can be created by chemical reaction networks (CRNs) using only a few different strands [2].
However, predicting what particular set of strands leads to a CRN generating DNA structures exhibiting specific properties (size distribution, stability, and so) is challenging as it is an ill-defined and highly dimensional problem, making exhaustive or random search inadequate. Here, we tackle this problem through an automatic exploration of the range of possible DNA structures across a number of user-defined features of interests.
We use the MAP-Elites algorithm [3] to explore sets of initial strands: for each tested set of strands, we generate a CRN comprised of DNA structures and reaction paths among them with PepperCorn, an enumerator for DNA strand displacement reactions developed by Badelt et al. [4]. Promising results are complemented with NUPACK [5] analyses to identify which structures would be more prevalent for each tested CRN. Our framework can thus automatically provide suggestions for experimental validation.

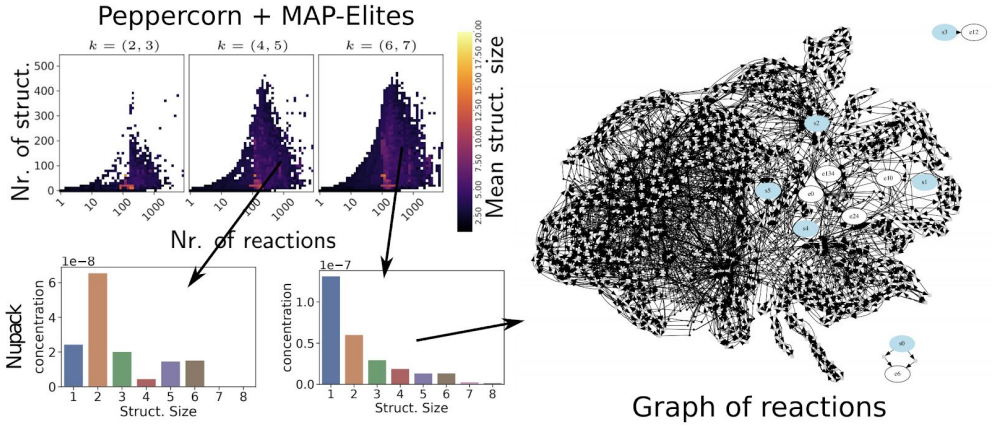

Figure: Workflow for automated discovery. The CRNs generated by sets of initial strands are evaluated automatically. Promising results are then forwarded to Nupack, which is used to annotate those CRNs.

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O3-02

Optimization of the multi-step DNA computing reaction using oxDNA MD simulation

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Keywords: DNA computing, State machine, Molecular Dynamics

Displacement Whiplash PCR (DWPCR) is a unique DNA computing reaction that implements a state machine [1]. In the DWPCR, each single-molecule DNA acts as a state transition machine by repeating hairpin structure formation, DNA polymerase extension, and hairpin structure deformation driven by primer extension under an isothermal condition. Each state transition is triggered upon addition of a 15-base DNA, called an operation signal. When the operation signal DNA binds to the loop region of the hairpin DNA, DNA polymerase extends the operation signal DNA as a primer and tears off the double-stranded stem region. The DWPCR, that can execute multi-step computation, is expected to be applied for medical diagnosis implemented within an aqueous solution. However, only up to two-step state transitions have been reported so far [2].

In this study, we investigated the efficiency of DWPCR for achieving state transition of three–step and more by using oxDNA simulation [3, 4]. oxDNA is a software tool for molecular dynamics (MD) simulation based on a coarse-grained model. At first, we performed MD simulation of an elementary process of the DWPCR and confirmed the DNA hairpin formation. Next, under the same condition, we performed MD simulation of the process in which an operation signal DNA was added to the hairpin DNA. As a result, the operation signal DNA did not bind to the loop region of the hairpin DNA. This result agrees with that in our biochemical experiment. In the presentation, we discuss the solution to the above problem and report the results of optimization of the reaction.

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O3-03

Analysis of wireframe DNA nanostructure based on coarse-grained molecular dynamics simulated on a web server with simple interface

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Keywords: Molecular Robotics, DNA origami, coarse-grained molecular dynamics, web server

DNA origami is one of the most successful methodologies using self-assembly to fabricate an object with a dimension about 100 nm and a resolution with a few nanometer [1,2]. Among various types of DNA nanostructures, wireframe structure is of interest thanks to its shape versatility, rigidity, simplicity, and the space-efficiency [3,4]. To utilize such DNA nanostructure for application, it is important to analyze the stability under thermal fluctuation, the cavity size of wireframe, and the effect of other molecules such as cationic ions [5]. To theoretically analyze those characteristics, varieties of simulation tools have been developed [6], some of which were not user-friendly due to its difficulty to setup.

Here, we developed a web server with a simple interface that can run a simulation and summarize the results of oxDNA [7], which is a software based on coarse-grained molecular dynamics. Fig.1 is a screenshot of typical examples on the web server that offers an easy-to-use experience. We further designed a simple wireframe DNA nanostructure and analyzed the behavior of it using the web server. In the presentation, we will show our new results of the simulation and discuss the potential benefit of our development.

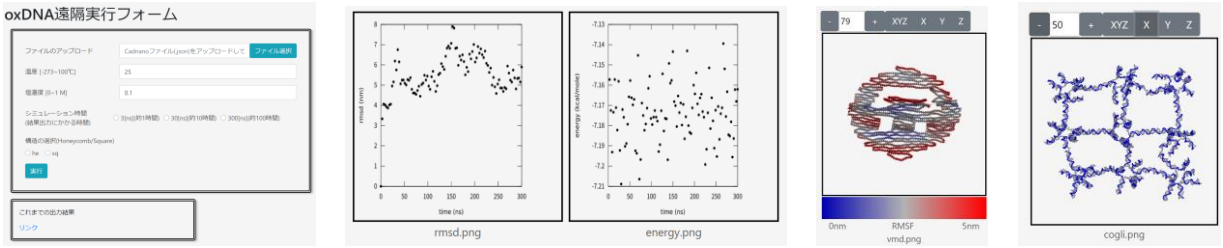

Figure 1. (From left to right) Interface of web server to launch an oxDNA simulation. Graphs of the simulation results. Snapshot of the simulation of smily face. Snapshot of the simulation of wireframe structure.

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O3-04

Simulation of Self-replication System with Virtual Spring Model

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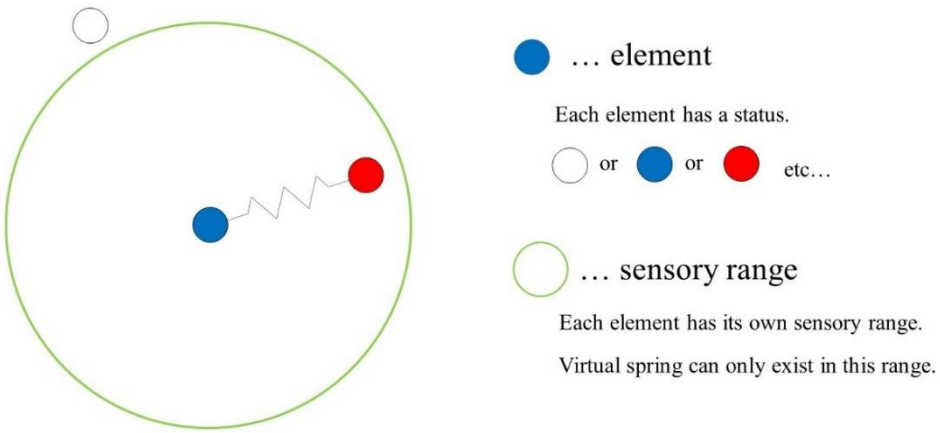
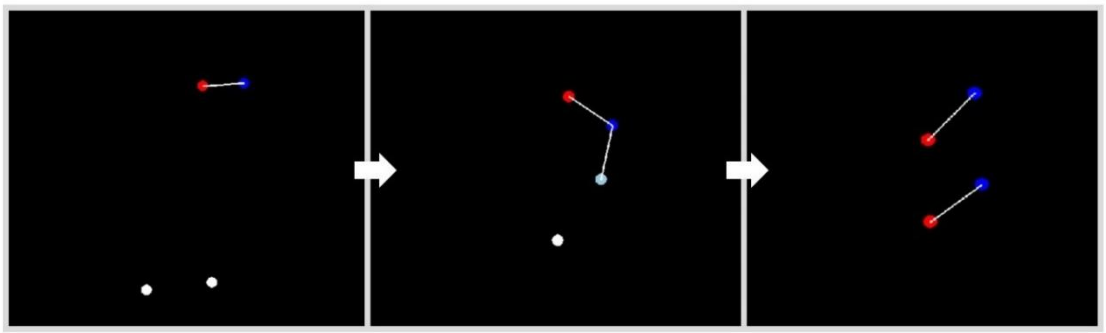
Chemical reactions play an important role in self-replication of biological organisms. Its process is complicated to some extent, so a simulation model gives a powerful tool to understand it. As a simple description of a chemical reaction system with various molecules, we consider a spring-mass-damper system[1] in which many elements interact with each other. In the past paper[1], an algorithm was proposed where the elements self-assemble into different shapes depending on parameters such as spring constant/natural length and state transition rule set based on the number of neighbors connected to the elements.

Here, we introduce the "state" as a new attribute of the simulation to improve the model's expressiveness, in order to simulate the process of self-replication. As the simplest example of self-replication, we deal with a string of few interconnected elements, each of which has a different "state". We examine how physical constants like a spring constant or a state transition rule influence the rate of self-replication.





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