

Simulating Self-replication of Linear Structures

Taisei Mori¹

taisei.mori.t6@dc.tohoku.ac.jp

Ibuki Kawamata^{1,2}

ibuki.kawamata@tohoku.ac.jp

Satoshi Murata¹

satoshi.murata.a4@tohoku.ac.jp

¹ Department of Robotics, School of Engineering, Tohoku University, 6-6-01, AramakiAzaAoba, Aoba, Sendai, Miyagi, 980-0845, Japan

² Natural Science Division, Faculty of Core Research, Ochanomizu University, 2-1-1 Ohtsuka, Bunkyo-ku, Tokyo 112-8610, Japan

Keywords: Self-replication, Virtual Spring Model, Transition rule, Autocatalysis

Self-replication is the process by which a system creates ones identical to itself without external operations from outside. A typical example of self-replication is that of living organisms, but its process is extremely complicated involving so many chemical reactions that it is difficult to see what is essential in the process. Simulation models of self-replication help us to find out what are the essential conditions for a system to replicate itself [1-3]. In order to describe the self-replication process, we have proposed the Virtual Spring Model [4], in which the bonds between the elements are regarded as spring-mass-damper systems. In this model, the state transition of each element is used to represent the chemical reactions among them.

By using this model, we were able to represent the self-replication system consisting of up to three interconnected elements. As for the self-replication procedure, the use of catalytic elements increased the success rate of self-replication, but the problem was that the number of transition rules was too large despite the simplicity of the system. In order to achieve scalable self-replication independent of the size of the system, the rules need to be redesigned.

Here, we propose a new self-replication procedure inspired by the concept of "complementarity of DNA", that only complementary base pairs (A and T, C and G) selectively bind to each other to form a double helix [5]. In DNA replication, an enzyme (polymerase) takes advantage of this property to make a complementary copy of the strand. By representing the DNA replication process with the use of autocatalytic procedure in the Virtual Spring Model, a scalable self-replication system for linear structures can be realized. Under this framework, we present a set of transition rules and simulation results of self-replication of a strand (linear structure) formed by interconnected elements with various sequences. We expect that the framework will be also useful to establish self-replication systems of more complex structures and dynamic mechanisms.

- [1] S. A. Kauffman, "Cellular Homeostasis, Epigenesis, and Replication in Randomly Aggregated Macromolecular Systems." *Journal of Cybernetics* 1, pp.71-96, 1971.
- [2] K. Tomita, H. Kurokawa, S. Murata, "Graph automata: natural expression of self-reproduction." *Physica D* 171, pp.197-210, 2002.
- [3] Z. Zeravcic, M. P. Brenner, "Self-replicating colloidal clusters." *PNAS* 111(5), pp.1748-1753, 2014.
- [4] K. Fujibayashi, S. Murata, K. Sugawara, M. Yamamura, "Self-Organizing Formation Algorithm for Active Elements." *IEEE*, pp.416-421, 2002.
- [5] J. D. WATSON, F. H. C. CRICK, "Molecular Structure of Nucleic Acids: A Structure for Deoxyribose Nucleic Acid." *Nature* 171, pp.737-738, 1953.