2022 International Symposium on Nonlinear Theory and Its Applications,
NOLTA2022, Virtual, December 12-15, 2022

A Novel Ergodic Cellular Automaton Multi-Dimensional Gene Network Model

Shogo Shirafuji† and Hiroyuki Torikai‡

†Graduate School of Science and Engineering, Hosei University
3-7-2 Kajino-cho, Koganei-city, Tokyo 184-8584, Japan
Email: shogo.shirafuji.4i@stu.hosei.ac.jp, torikai@hosei.ac.jp

Extended Summary

The purpose of this study is to build a design method of efficient hardware-based gene network simulators. In this paper, as an example, a novel erogidc cellular automaton [1] multi-dimensional gene network model is presented. The model exhibits Hopf bifurcation relied on time delays [2]. Fig. 1 shows a schematic circuit diagram of the peresented model. As shown in Fig. 1, the presented model has registers, which store the following discrete state variables. $X \in Z_N = \{0, 1, \cdots, N-1\}, Y \in Z_N, M \in Z_N, W \in Z_N, S \in Z_N, Y_1 \in Z_N, Y_2 \in Z_N, \cdots, Y_D \in Z_N$, where the variables are saturated at 0 and $N-1$. As shown in Fig. 1, the presented model has other registers, which store the following discrete auxiliary variables, $A_X \in Z_A = \{0, 1, \cdots, A-1\}, A_Y \in Z_A, A_M \in Z_A, A_W \in Z_A, A_S \in Z_A$, where the variables are saturated at 0 and $A-1$. As shown in Fig. 1, the presented model receives the following clock $C(t) = \sum_{n=0}^{\infty} p(t-nT_C)$, where T_C is period of the clock, and p is an instantaneous pulse corresponding to a positive edge of a rectangular shaped clock. As shown in Fig. 1, the presented model receives the following binary switch signals $S_X = \sum_{n=0}^{\infty} q(t-nT_X-\Phi_X, \Omega_X), S_Y = \sum_{n=0}^{\infty} q(t-nT_Y-\Phi_Y, \Omega_Y), S_M = \sum_{n=0}^{\infty} q(t-nT_M-\Phi_M, \Omega_M), S_W = \sum_{n=0}^{\infty} q(t-nT_W-\Phi_W, \Omega_X)$, and $S_S = \sum_{n=0}^{\infty} q(t-nT_S-\Phi_S, \Omega_S)$, where $q(t, \Omega) \in \{0, 1\}$ is a rectagular shaped pulse with width Ω; T_X, T_Y, T_M, T_W, T_S are periods; and $\Phi_X, \Phi_Y, \Phi_M, \Phi_W, \Phi_S$ are initial phases. The clock C triggers the following transitions of the discrete state variables.

Transitions of discrete state variables:

If $C(t) = 1$,

$$\begin{cases} X(t^+) = X(t) + S_X(t)\mathcal{F}_X(X(t), M(t), S(t), A_X(t)), \\ Y(t^+) = Y(t) + S_Y(t)\mathcal{F}_Y(X(t), Y(t), M(t), S(t), A_Y(t)), \\ M(t^+) = M(t) + S_M(t)\mathcal{F}_M(Y_{delay}, M(t), S(t), A_M(t)), \\ W(t^+) = W(t) + S_W(t)\mathcal{F}_W(Y_{delay}, W(t), A_W(t)), \\ S(t^+) = S(t) + S_S(t)\mathcal{F}_S(W(t), S(t), A_S(t)), \end{cases} \quad (1)$$

where $\mathcal{F}_X, \mathcal{F}_Y, \mathcal{F}_M, \mathcal{F}_W, \mathcal{F}_S$ are discrete functions designed so that they reproduce nonlinear vector field of the oscillatory dynamics of p53 genetic network induced by feedback loops and time delays[2]. It is shown that the presented model can reproduce typical nonlinear phenomena observed in the oscillatory dynamics[2] (see Fig. 2). Furthermore, it is shown that the presented model consumes lower power and has fewer hardware components compared to a straightforward numerical integration method

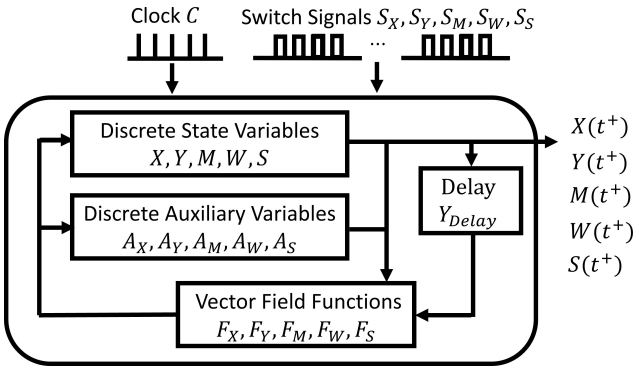

Figure 1: Schematic circuit diagram of the presented model.

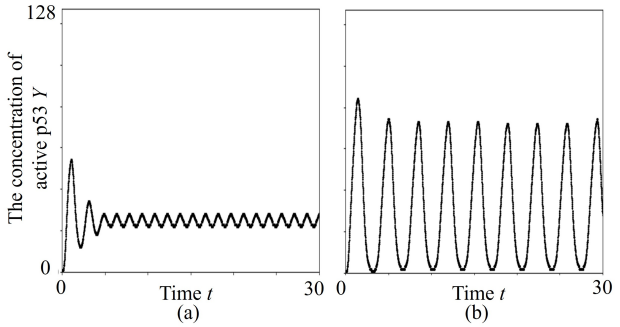

Figure 2: Typical time waveforms of the presented model for different values of time delay τ. (a) $\tau = 0.26$. (b) $\tau = 1.04$.

(forward Euler method) of [2]. Finally, future problems for designing more sophisticated hardware-based gene network simulators include (A) reproduction of more precise bifurcation phenomena and (B) comparison with many other hardware architectures. This work was supported by SCAT and KAKENHI Grant Numeber 21H3515.

References

[1] Shirafuji and Torikai, "A novel ergodic cellular automaton gene network model towards efficient hardware-based genome simulator," *Proc. EMBC*, 2022.

[2] Wang, Liu, and Zhou, "Oscillatory Dynamics of p53 Genetic Network Induced by Feedback Loops and Time Delays," *IEEE TNB*, 2019.