Available online at www.sciencedirect.com

SCIENCE DIRECT®

ELSEVIER

Physics Letters A 344 (2005) 36–42

PHYSICS LETTERS A

www.elsevier.com/locate/pla

Stochastic coupling of two random Boolean networks

Ming-Chung Ho [a,*], Yao-Chen Hung [b,*], I-Min Jiang [b]

[a] *Department of Physics, National Kaohsiung Normal University, Kaohsiung, Taiwan*
[b] *Department of Physics, National Sun Yat-sen University, Kaohsiung, Taiwan*

Received 24 September 2004; received in revised form 24 May 2005; accepted 27 May 2005

Communicated by C.R. Doering

Abstract

We study the dynamics of two coupled random Boolean networks. Based on the Boolean model studied by Andrecut and Ali [Int. J. Mod. Phys. B 15 (2001) 17] and the stochastic coupling techniques, the density evolution of networks is precisely described by two deterministic coupled polynomial maps. The iteration results of the model match the real networks well. By using MSE and the maximal Lyapunov exponents, the synchronization phenomena of coupled networks is also under our discussion.

PACS: 02.50.-r; 05.45.Xt; 05.65.+b

Keywords: Boolean networks; Stochastic coupling; Synchronization

1. Introduction

In the past decades, the study of Boolean networks has attracted a lot of interest [1–6]. Besides being easy to deal with, the models are useful to understand the collective behavior and self-organized phenomena in complex systems. Actually, Boolean networks can be regarded as simplified models of real systems, such as biological networks, cellular automata, biochemical networks, and physical spin models [7–11]. Therefore, it is important to investigate the dynamics of Boolean networks for realization and prediction in real networks.

Recently, Andrecut and Ali show that there is an easier explication given to the generalized Rule 126 for elementary cellular automata: the system can be accurately described by a density map for a random Boolean network [12]. The authors consider a simple Boolean network with N cells in which each cell is connected to k randomly chosen cells and the parameter k is known as the connectivity of the network. The value of k is fixed, and the state of each cell obeying Rule 126 is influenced only by the k connections. The

---

[*] Corresponding authors.

E-mail addresses: t1603@nknucc.nknu.edu.tw (M.-C. Ho), d9123801@student.nsysu.edu.tw (Y.-C. Hung).

0375-9601/$ – see front matter © 2005 Elsevier B.V. All rights reserved.
doi:10.1016/j.physleta.2005.05.100

authors verify that the iterations of the density map are in good agreement with the numerical results of a real network when the parameters N and k are large enough. The density map of the random Boolean network is chaotic and exhibits extremely extensive dynamic behaviors. However, the problem is not solved completely. It is known that the number of connections is never identical for each cell in real networks. Lately, Matache and Heidel provided a generalized formula to model an inhomogeneous Boolean network [13]. In addition to the analysis of bifurcation diagrams and fixed points, the reversed bifurcations are reported and investigated further. Based on these studies, people can understand the characteristics of realistic Boolean networks much more clearly.

In this Letter, we are interested in the co-evolution of two coupled Boolean networks. The collective dynamic behavior, especially the synchronization phenomena, is a very important topic in nonlinear science. Owing to the discrete specialty of Boolean networks, the customary deterministic coupling applied in maps cannot be exercised. Thus, we introduce the stochastic coupling technique [14,15] to perform the interaction between two networks. As to the physical systems, the model possesses potential applications to investigate the synchronization in two lasers coupled face to face if the solid-state lasers are replaced by random lasers [16–19]. It would also be helpful when we study the dynamics of coupled gene networks [20]. Though the networks are stochastically coupled, our results show that two deterministic coupled polynomial maps can accurately describe their density evolution after statistic calculations. This outcome is important because the model provides predictions of real networks and allows analytical calculations. The iteration results of the model tally well with the real networks. Moreover, we investigate the synchronization phenomena of coupled networks and analyze it by using MSE and Lyapunov exponents.

This Letter is organized as follows. In Section 2, we introduce the model of the random Boolean networks and the stochastic coupling techniques. We provide the deterministic coupled maps to model the two stochastically coupled networks. Numerical results show the excellent agreement between the real system and the model. In Section 3, we investigate the synchronization phenomena of coupled networks and analyze it by using MSE and Lyapunov exponents. Finally, a brief conclusion and further works are given.

2. The model of stochastically coupled random Boolean networks

Consider two Boolean networks with N cells individually. Each cell c_n^i, where $i = 1, 2$, indicates network 1 or network 2 and $n = 1, 2, \dots, N$, is described by two values 1 or 0. The connections of a cell c_n^i could be assigned randomly from its belonged network, and the number of connections is denoted by k fixed for all cells during evolution. Suppose the states of the cells are updated simultaneously, and all are governed by the generalized Rule 126 from discrete time t to $t+1$: if the state of c_n^i and its connections are all 1 or 0, then $c_n^i(t+1) = 0$, otherwise, $c_n^i(t+1) = 1$. The density (the probability that a cell is in state 1) of a single network is given by

$$p^i(t) = N^{-1} \sum_{n=1}^{N} c_n^i(t),$$

and the iterations of density can be exactly formulated as in [12]:

$$\begin{aligned} p^i(t+1) &= f^i\bigl(p^i(t), k\bigr) \\ &= 1 - p^i(t)^{k+1} - \bigl[1 - p^i(t)\bigr]^{k+1}, \end{aligned} \tag{1}$$

where $i = 1, 2$ and the parameter $k \geqslant 1$.

Our purpose in this Letter is to study the interaction of the two networks, and provide a similar density function to model the dynamical behavior. Unlike typical systems, the deterministic coupling here is useless due to the discrete characteristics. Thus, we apply the stochastic coupling technique [14,15] to couple the networks 1 and 2. The techniques are shown as follows. Suppose two evolution operators

$$\mathbf{c}^{1,2}(t+1) = \hat{S} \circ \hat{R}\bigl(\mathbf{c}^{1,2}(t)\bigr)$$

govern the dynamics of coupled networks. The operator $\hat{R}$, as shown above, is the generalized Rule 126 which is applied to the both networks when they are not coupled. The role of the stochastic coupling operator $\hat{S}$ is to compare the states of all cells in each network. If $c_n^1(t) = c_n^2(t)$, both states will stay invariant. And if $c_n^1(t) \neq c_n^2(t)$, the coupling will not act and the states will be unchanged with the probability $1-g$ $(0 \leqslant g \leqslant 1)$ or the states of connected cells will be set to the same value with probability g. The values are set to equal to $c_n^1(t)$ or $c_n^2(t)$, with the same probability $1/2$ for each choice. Thus, the stochastic coupling operator can be expressed as [14]:

$$\hat{S}_n(\mathbf{c}^{1,2}) = \begin{cases} c_n^{1,2} & \text{if } c_n^1 = c_n^2, \\ c_n^{1,2} & \text{with probability } 1-g, \text{ if } c_n^1 \neq c_n^2, \\ c_n^1 & \text{with probability } g/2, \text{ if } c_n^1 \neq c_n^2, \\ c_n^2 & \text{with probability } g/2, \text{ if } c_n^1 \neq c_n^2. \end{cases} \tag{2}$$

Next, the coupled model can be formulated step by step. Let $N_1^{1,2}$ be the number of cell in state 1 for two networks and $N_0^{1,2}$ be the number of cell in state 0. The variables satisfy the condition $N_1^1 + N_0^1 = N_1^2 + N_0^2 = N$. After being acted by the evolution operator $\hat{R}$, which indicates the free evolution of individual networks, the network 1 (network 2) possesses the probability $f^1(p^1)$ $(f^2(p^2))$ of finding a cell in state 1. Therefore, after the first sub-step, $N_1^{1,2}$ will turn out to be

$$N_1^{1,2} = N f^{1,2}(p^{1,2}), \tag{3}$$

and $N_0^{1,2}$ will become

$$N_0^{1,2} = N\left[1 - f^{1,2}(p^{1,2})\right]. \tag{4}$$

Now, let us take the second sub-step of the evolution into consideration. When cell c_n^1 is in state 1, the corresponding cell c_n^2 may be in state 1 with probability $f^2(p^2)$ or in state 0 with probability $1 - f^2(p^2)$. Thus, for network 1, after being operated by $\hat{S}_n$ the number of cells staying in state 1 is

$$N_{1\to1}^1 = N f^1(p^1) f^2(p^2) + N f^1(p^1)\left[1 - f^2(p^2)\right]\left(1 - \frac{g}{2}\right). \tag{5}$$

The former part in the right-hand side of Eq. (5) corresponds to the condition $(c_n^1, c_n^2) = (1,1)$, and the states of c_n^1 will remain in state 1 under the action of $\hat{S}$. The latter part corresponds to the condition $(c_n^1, c_n^2) = (1,0)$, and the state of c_n^1 will remain in state 1 with probability $1 - g/2$. Similarly, the number of cells changing their states from 1 to 0 is

$$N_{1\to0}^1 = N f^1(p^1)\left[1 - f^2(p^2)\right]\frac{g}{2}, \tag{6}$$

where $g/2$ is the probability that c_n^1 will be set to equal to $c_n^2(t)$ (state 0).

When cell c_n^1 is in state 0, the corresponding cell c_n^2 may be in state 1 or in state 0. Using a similar argument as above for network 1, the number of cells that remain in state 0 after coupling is

$$N_{0\to0}^1 = N\left[1 - f^1(p^1)\right]\left[1 - f^2(p^2)\right] + N\left[1 - f^1(p^1)\right] f^2(p^2)\left(1 - \frac{g}{2}\right). \tag{7}$$

The number of cells that are changing their states from 0 to 1 is

$$N_{0\to1}^1 = N\left[1 - f^1(p^1)\right] f^2(p^2)\frac{g}{2}. \tag{8}$$

Obviously, the above equations satisfy the normalization condition:

$$N_{1\to1}^1 + N_{1\to0}^1 + N_{0\to0}^1 + N_{0\to1}^1 = N. \tag{9}$$

We can now construct the quantity

$$p^1(t+1) = N^{-1}\left[N_{1\to1}^1 + N_{0\to1}^1\right]$$

which represents the probability of finding a cell of network 1 in state 1 at time $t+1$. Inserting the results from Eqs. (5) and (8) into $p^1(t+1)$, we get the results:

$$p^1(t+1) = \left(1 - \frac{g}{2}\right) f^1(p^1) + \frac{g}{2} f^2(p^2). \tag{10}$$

Repeating the procedure above, the probability for network 2 will become

$$p^2(t+1) = \left(1 - \frac{g}{2}\right) f^2(p^2) + \frac{g}{2} f^1(p^1). \tag{11}$$

Thus, the final formula is as follows:

$$\begin{cases} p^1(t+1) = (1-\varepsilon) f^1(p^1) + \varepsilon f^2(p^2), \\ p^2(t+1) = (1-\varepsilon) f^2(p^2) + \varepsilon f^1(p^1), \end{cases} \tag{12}$$

where $\varepsilon = g/2$ $(0 \leqslant \varepsilon \leqslant 1/2)$ is the coupling strength.

From Eq. (12), in the limit $N \to \infty$, we can use the deterministic coupled map to describe the dynamic behavior of coupled Boolean networks, regardless of the discrete nature of networks and the stochastic coupling methods. Actually, it is necessary to make sure that the coupled model tallies with the real system. Fig. 1 shows the numerical results of the model (mesh plot) and the actual coupled networks (points). Having $N = 1000$, $\varepsilon = 0.15$ and $k = 4$, we present the first

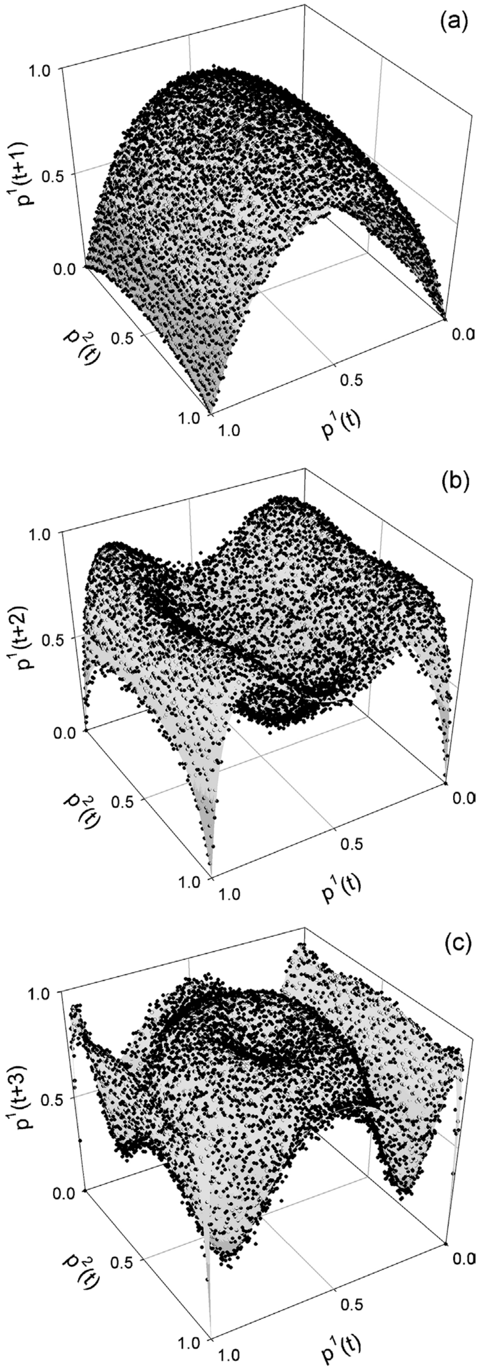

Fig. 1. The diagram presents the numerical results of the model (mesh plot) and the actual coupled networks (points) with $N = 1000$, $\varepsilon = 0.15$ and $k = 4$. The graphs (a), (b), (c) illustrate the first three iterations $p^1(t+1)$, $p^1(t+2)$, and $p^1(t+3)$ versus $p^1(t)$ and $p^2(t)$ individually.

three iterations of the model and the real networks. Fig. 1(a), (b), and (c) illustrate $p^1(t+1)$, $p^1(t+2)$, and $p^1(t+3)$ versus $p^1(t)$ and $p^2(t)$ individually. One can see the excellent agreement between the real Boolean system and the coupled maps. With the increase of N, the agreement will be approved further. Various parameter pairs and the relationship among $p^2(t+m)$ (where $m = 1, 2, 3$), $p^1(t)$, and $p^2(t)$ is also under our consideration (not presented). The match between the model and the real system is also excellent with other parameters.

3. Model dynamics and synchronization

In this section, we study the dynamics of the model and the synchronization phenomena.

Choosing the number of connections $k = 4$ and the initial condition $(p^1(0), p^2(0)) = (0.7, 0.1)$, the bifurcation diagrams for $p^1(t)$ and $p^2(t)$ versus different coupling strengths ε are illustrated in Fig. 2. One can observe that the chaotic behaviors of $p^1(t)$ and $p^2(t)$ is suppressed gradually with the increase of the coupling strength when ε is small. For $\varepsilon > 0.097$, chaos reappears and remains no matter what the value of ε is. Different initial conditions may alter the bifurcation in the region of weak coupling. However, when coupling strength is large enough, the dynamics are independent of the choices of $p^1(0)$ and $p^2(0)$. They depend only on the connectivity parameter k. The results of real networks ($N \geqslant 10000$) are similar to Fig. 2.

To characterize the effects of coupling on the individual behavior more clearly, we analyze the dependence of the maximal Lyapunov exponent $\lambda_{\max}$ [21–23] on the coupling strength ε. The maximal Lyapunov exponent $\lambda_{\max}$ represents the exponential rate at which an arbitrarily small displacement is amplified, so $\lambda_{\max} > 0$ suffices to ensure the dynamic of coupled maps is chaotic. Fig. 3(a) shows the numerical result with $k = 4$ and $(p^1(0), p^2(0)) = (0.7, 0.1)$ under different values of ε. Comparing with the bifurcation diagrams in Fig. 2, it is easy to observe the excellent connections: the negative $\lambda_{\max}$ corresponds to the periodic windows in the bifurcation diagrams, and the positive $\lambda_{\max}$ corresponds to the chaotic regions. Thus, relating to what we have stated above, for $\varepsilon > 0.097$, $\lambda_{\max}$ is positive and remains no matter what the value of ε is.

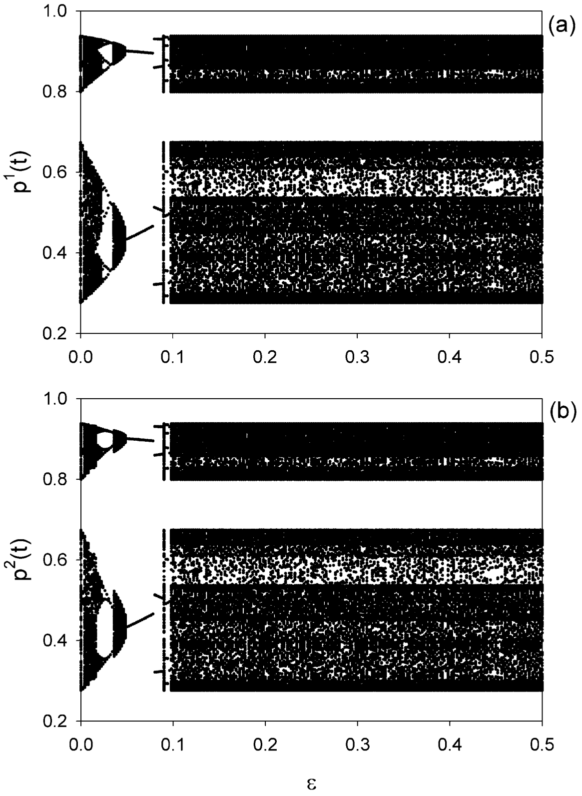

Fig. 2. The diagram shows the bifurcation diagrams for $p^1(t)$ and $p^2(t)$ versus different coupling strength ε when $k = 4$ and the initial condition $(p^1(0), p^2(0)) = (0.7, 0.1)$.

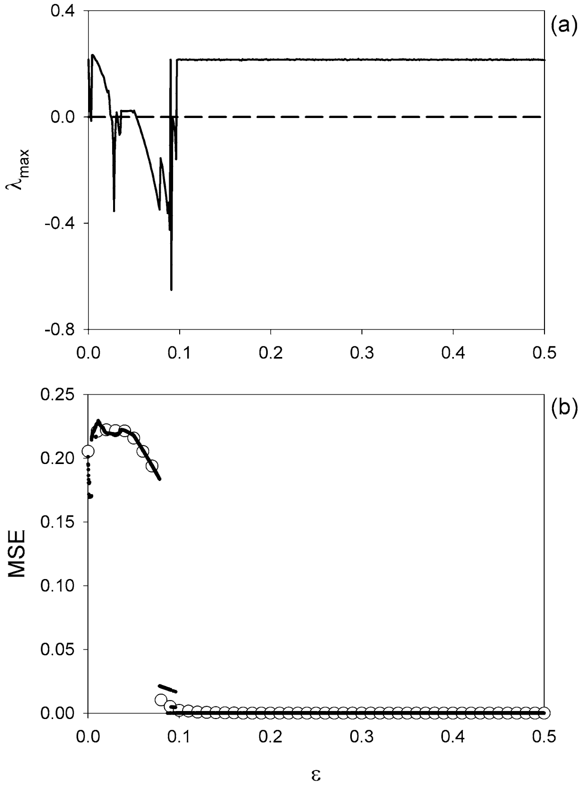

Fig. 3. In the condition $k = 4$ and $(p^1(0), p^2(0)) = (0.7, 0.1)$. (a) The relationship between the maximal Lyapunov exponent $\lambda_{\max}$ of coupled networks and the coupling strength ε. (b) The relationship between MSE and the coupling strength ε, where the results of model are denoted by solid circles and the results of real system are denoted by empty circles.

Now, we investigate the synchronization of two networks induced by the stochastic coupling. We evaluate the mean-square error (MSE) between $p^1(t)$ and $p^2(t)$ after controlling. The definition of MSE is

$$\mathrm{MSE} = \frac{1}{n}\sum_{t=1}^{n}\bigl(p^1(t) - p^2(t)\bigr)^2. \tag{13}$$

We illustrate the results of the coupled density maps in Fig. 3(b) marked with solid circles. When $\varepsilon < 0.050$, the coupling is too weak to overcome the divergent nature of nonlinearity. Thus, the MSE is much larger than zero and no synchronization is achieved. For $\varepsilon \in [0.050, 0.078]$, corresponding to the period-2 in bifurcations, the two coupled maps possess the same fixed points but different phase. Consequently, the value of MSE can be obtained easily by inserting the values of the two fixed points of the bifurcation diagram into $p^1(t)$ and $p^2(t)$ in Eq. (13). When $\varepsilon \in [0.078, 0.097]$, we get three possible values of MSE because the system possesses three possible stable solutions in this parameter region. The periodic iterations of the two maps may be in phase (corresponding to MSE = 0) or out of phase (corresponding to the other two values). The typical time series are presented in Fig. 4, where (a) corresponding to MSE = 0, (b) (period-4) corresponding to the largest MSE and (c) (period-8) corresponding to the value between (a) and (b). Finally, for $\varepsilon > 0.097$, MSE become zero and the complete synchronization is achieved. The results of real system ($N = 10^4$ and transition time steps are larger than 10^6) are denoted by empty circles.

We also study the situation for a different connectivity k. Choosing $k = 16$ and the initial condition used above, we illustrate the bifurcation diagram, the maxi-

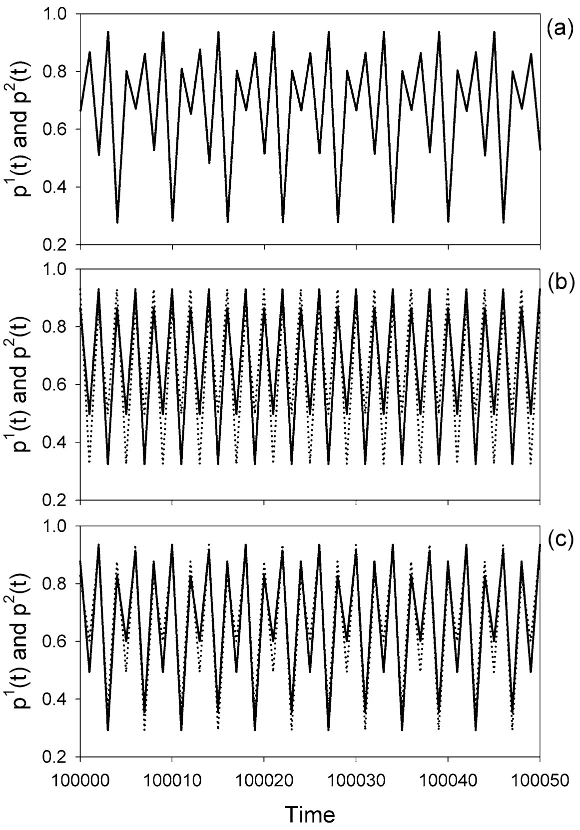

Fig. 4. The diagram presents the typical time series of the two maps when $\varepsilon \in [0.078, 0.097]$. (a) corresponds to MSE = 0, (b) (period-4) corresponds to the largest MSE in Fig. 3, and (c) (period-8) corresponds to the value between (a) and (b).

mal Lyapunov exponent and MSE versus various coupling strengths in Fig. 5. As what we expect, the $\lambda_{\max}$ connects to the bifurcation diagram well. For $\varepsilon > 0.23$, complete synchronization can be observed.

4. Conclusion and further works

In this Letter, we study the dynamics of two coupled random Boolean networks. Based on the Boolean model and the stochastic coupling techniques, the density evolution of networks is accurately described by two deterministic coupled polynomial maps. We show the excellent agreement between the model and the real system. Moreover, by using the MSE and the maximal Lyapunov exponents, we investigate the synchronization phenomena of coupled networks.

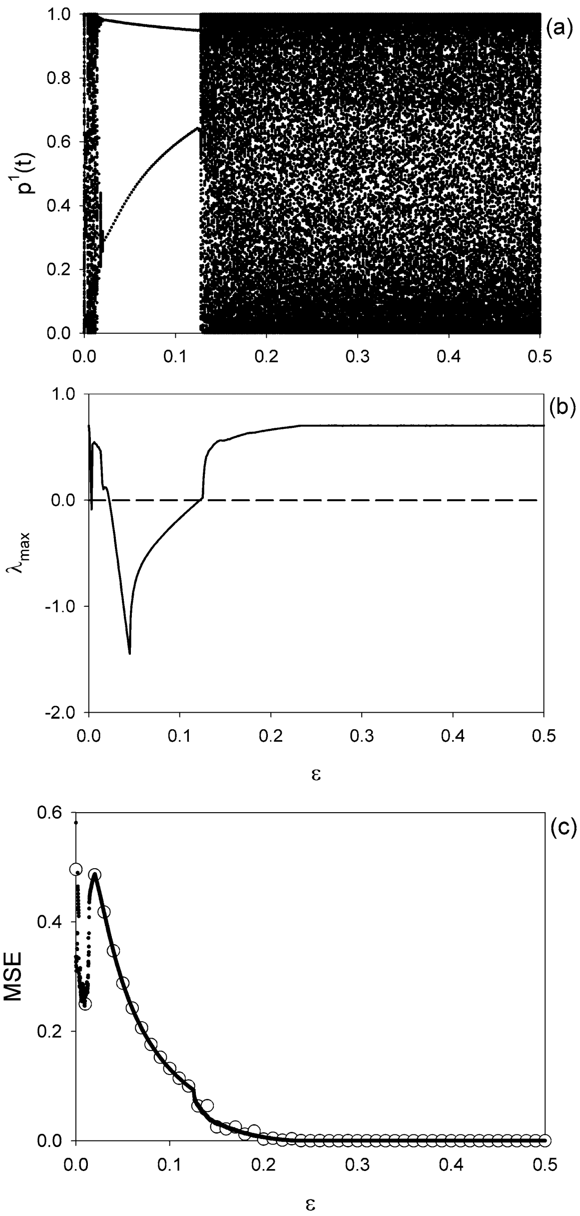

Fig. 5. In the condition $k = 16$ and $(p^1(0), p^2(0)) = (0.7, 0.1)$. (a) The bifurcation diagrams of $p^1(t)$. The result of $p^2(t)$ is similar with $p^1(t)$. (b) The relationship between $\lambda_{\max}$ and the coupling strength ε. (c) The relationship between MSE and ε, where the results of model are denoted by solid circles and the results of real system are denoted by empty circles.

The advantages our work offers are the model provides predictions of real networks and it allows analytical calculations. Actually, the deterministic coupled model in Eq. (12) is the typical formula used to describe the dynamics of globally coupled map lattice (GML) after the system falls in a two-cluster attractor [24,25]. The stochastic coupling techniques can be explored further to couple more than two Boolean networks. Depending on the coupling techniques, the present researches can be extended to locally coupled map lattice, globally coupled map lattice, or even power-law coupled map lattice. As we know, the simulations take a lot of time if we consider N_n coupled networks consisting of N cells, where N_n and N are sufficiently large. However, with the aid of the coupled model, it is relatively easy to investigate such problems. The topics will be investigated in our further studies.

Acknowledgements

The authors thank the National Science Council, Taiwan, ROC, for financially supporting this research under Contract No. NSC 93-2112-M-110-011.

References

[1] S.A. Kauffman, J. Theor. Biol. 22 (1969) 437;
S.A. Kauffman, Nature (London) 244 (1969) 177.
[2] R.A. Sherlock, Bull. Math. Biol. 41 (1979) 687.
[3] F. Fogelman-Soulie, Discrete Appl. Math. 9 (1984) 139.
[4] H. Flyvbjerg, N.J. Kjaer, J. Phys. A 21 (1988) 1695.
[5] U. Bastolla, G. Parisi, Physica D 98 (1996) 1.
[6] U. Bastolla, G. Parisi, Physica D 115 (1998) 203;
U. Bastolla, G. Parisi, Physica D 115 (1998) 219.
[7] S.A. Kauffman, The Origins of Order, Oxford Univ. Press, Cambridge, 1993.
[8] S. Wolfram, Rev. Mod. Phys. 55 (1983) 601.
[9] S. Wolfram, A New Kind of Science, Wolfram Media, Champaign, 2002.
[10] J.J. Fox, C.C. Hill, Chaos 11 (2001) 809.
[11] B. Derrida, H. Flyvbjerg, J. Phys. A 19 (1986) L1003.
[12] M. Andrecut, M.K. Ali, Int. J. Mod. Phys. B 15 (2001) 17.
[13] M.T. Matache, J. Heidel, Phys. Rev. E 69 (2004) 056214.
[14] L.G. Morelli, D.H. Zanette, Phys. Rev. E 58 (1998) R8.
[15] L.G. Morelli, D.H. Zanette, Phys. Rev. E 63 (2001) 036204.
[16] T. Ohtomo, K. Otsuka, A. Okamoto, J.-Y. Ko, Opt. Express 13 (2005) 358.
[17] J.L. Guisado, F. Jiménez-Morales, J.M. Guerra, Phys. Rev. E 67 (2003) 066708.
[18] X. Jiang, S. Feng, C.M. Soukoulis, J. Zi, J.D. Joannopoulos, H. Cao, Phys. Rev. E 69 (2004) 104202.
[19] N.M. Lawandy, R.M. Balachandran, S.S. Gomers, E. Sauvain, Nature (London) 368 (1994) 436.
[20] J.A. de Sales, M.L. Martins, D.A. Stariolo, Phys. Rev. E 55 (1997) 3262.
[21] S. Morita, Phys. Lett. A 226 (1997) 172.
[22] A.M. Batista, R.L. Viana, Phys. Lett. A 286 (2001) 134.
[23] A.M. Batista, S.E. de S. Pinto, R.L. Viana, S.R. Lopes, Phys. Rev. E 65 (2002) 056209.
[24] F. Xie, H.A. Cerdeira, Phys. Rev. E 54 (1996) 3235.
[25] G. Abramson, Europhys. Lett. 52 (2000) 615.