

Synchronization of the Time-Varying Discrete Biological Networks

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Abstract—The study of synchronization of population dynamics is extremely important for predicting and evaluating the risk of global extinctions. The migration in a network of patch populations (metapopulation) inevitably involves various environmental noises or outside disturbances, which make the migration is timely evolving and spatially extended. Thus the time-invariant discrete biological networks are often insufficient to capture the key features of real-world biological networks. Here, a time-varying discrete biological network is proposed to characterize the practical metapopulation for the first time. Based on this model, several novel local synchronous criteria are then attained, which provide some new insights into the ecological conservation and biological diversity. Moreover, these synchronous criteria are also applicable to the synchronization of complex networks in other biological and engineering systems.

I. INTRODUCTION

Biological networks are on our minds nowadays. There are various complex biological networks, such as genetic regulatory networks, food webs, metapopulations (networks of populations), and so on [1-10]. In particular, ecological networks are a kind of representative biological networks [1-5]. Hereafter, we will use the ecological networks as the typical examples to explore the synchronization of the complex biological networks.

Ecosystems are spatially extended and timely evolving dynamical systems [3]. Darwin used the metaphor of a ‘tangled bank’ to describe the complex interactions between species [1-5]. All such interactions can be visualized as ecological networks which reveal the underlying ecological mechanisms. A metapopulation comprises a network of spatially separated populations of the same species which interact at some level. Ecologists view the extinction of species as a danger and conservation of biological diversity as a goal.

Synchronization is an emerging collective behaviors in nature. Since some direct and indirect evidences indicate that synchronization is strongly correlated with global extinctions, the synchronization of population dynamics becomes one of major concern in the studies of ecological conservation [1-5].

Since the effects of migration in a metapopulation are very important for predicting the possibility of extinctions at the local scale, then the local asymptotic synchronization is extremely important for unraveling the underlying mechanics of global extinctions [1-5]. The most previous theoretical and experimental researches are concentrated on the synchronization of the time-invariant discrete ecosystems (biological networks) or coupled map lattices [1-5]. Since the ecosystems are spatially extended and timely evolving dynamical systems, the time-invariant discrete biological networks often can not capture some key features of the real-world ecosystems. As a result, the local asymptotic synchronization of time-invariant discrete biological network is often insufficient for understanding the risk of global extinctions. Also, there exist various environment noises in a metapopulation. Based on all reasons as above, it is very necessary to introduce a time-varying discrete biological network to characterize the network of patch populations. In the following, a time-varying discrete biological network is introduced and its local asymptotic synchronization is then further investigated. Based on this model, several local asymptotic synchronization criteria are then proposed for predicting the possibility of extinctions at a local scale.

The left paper is then organized as follows. A time-varying discrete biological network model and two necessary definitions are introduced in Section II. In Section III, several local asymptotic synchronization criteria for the time-varying discrete biological network are proposed. A simple example is then given to show the effectiveness of these synchronization criteria in Section IV. Conclusions are finally drawn in Section V.

II. A TIME-VARYING DISCRETE BIOLOGICAL NETWORK

In real-world biological context, such as metapopulation, many different factors, such as ages, genders and species, are often involved [1-5]. Therefore, it is necessary to use a multidimensional vector to characterize the population. The evolving rule of the population is then given by a multidimensional

iterative map

$$x^{t+1} = F(x^t), \quad t = 0, 1, \dots, \quad (1)$$

where $x \in \mathbb{R}^n$ and $F : X \rightarrow X$ ($X \subseteq \mathbb{R}^n$) is a fundamental reproductive (or birth-death) function. And the desired time-varying discrete biological (or ecological) network with N habitat patches (or populations) is described by

$$x_i^{t+1} = \sum_{j=1}^N c_{ij}^t F(x_j^t), \quad i = 1, 2, \dots, N, \quad t = 0, 1, \dots, \quad (2)$$

where $x_i^t \in X$ is the patch density of the i th habitat patch at time t , $\mathbf{C}(t) = (c_{ij}^t)_{N \times N}$ is the dispersal matrix at time t , representing the coupling strength and the connecting status between patches. Moreover, $\mathbf{C}(t)$ satisfies

$$\sum_{j=1}^N c_{ij}^t = 1, \quad i = 1, 2, \dots, N, \quad t = 0, 1, \dots, \quad (3)$$

i.e., $\mathbf{C}(t)$ has row sums 1 for $t = 0, 1, \dots$, which means that 1 is an eigenvalue of $\mathbf{C}(t)$ associated with eigenvector $\mathbf{e} = (1, 1, \dots, 1)^T$. And the row sum 1 is a precondition that makes a synchronous solution satisfy system (2), where the synchronous solution is defined by $x_i^t = x_j^t$ for all i and j at time t . System (2) can be recasted as follows:

$$x_i^{t+1} = F(x_i^t) + \sum_{j=1}^N \bar{c}_{ij}^t F(x_j^t), \quad i = 1, 2, \dots, N, \quad (4)$$

where $t = 0, 1, \dots$, $\bar{c}_{ij}^t = c_{ij}^t$ for $i \neq j$ and $\bar{c}_{ii}^t = c_{ii}^t - 1$ for $i, j = 1, 2, \dots, N$. Thus, $\bar{\mathbf{C}}(t) = \mathbf{C}(t) - \mathbf{E}_{N \times N}$, where $\mathbf{E}_{N \times N}$ is an $N \times N$ unit matrix. Furthermore, condition (3) implies

$$\bar{c}_{ii}^t = - \sum_{\substack{j=1 \\ j \neq i}}^N \bar{c}_{ij}^t, \quad i = 1, 2, \dots, N, \quad t = 0, 1, \dots, \quad (5)$$

i.e., $\bar{\mathbf{C}}(t)$ has zero row sums for $t = 0, 1, \dots$. In fact, system (2) (or (4)) is a diffusive coupling system, which can also describe many real-world networks, such as metabolic systems, genetic networks, food webs, Internet, communication networks, and the World Wide Web [6-10]. For constant matrix \mathbf{C} , system (2) becomes a time-invariant discrete biological network

$$x_i^{t+1} = \sum_{j=1}^N c_{ij} F(x_j^t), \quad i = 1, 2, \dots, N, \quad t = 0, 1, \dots \quad (6)$$

For convenience, several abbreviated notations are introduced as follows. Let an N -dimensional vector $\mathbf{e} = (1, 1, \dots, 1)^T$, $\lambda_1(t), \lambda_2(t), \dots, \lambda_N(t)$ be the eigenvalues of matrix $\mathbf{C}(t)$, $\bar{\lambda}_1(t), \bar{\lambda}_2(t), \dots, \bar{\lambda}_N(t)$ be the eigenvalues of matrix $\bar{\mathbf{C}}(t)$,

$$\bar{\mathbf{x}} = \begin{pmatrix} x_1 \\ \vdots \\ x_N \end{pmatrix} \in X^N, \quad F(\bar{\mathbf{x}}) = \begin{pmatrix} F(x_1) \\ \vdots \\ F(x_N) \end{pmatrix} \in X^N.$$

Then the complete map $\bar{\mathbf{F}} : \mathbb{R}^+ \times X^N \rightarrow X^N$ is described by

$$\bar{\mathbf{F}}(t, \bar{\mathbf{x}}) = \begin{pmatrix} \sum_{j=1}^N c_{1j}^t F(x_j) \\ \vdots \\ \sum_{j=1}^N c_{Nj}^t F(x_j) \end{pmatrix} = \mathbf{C}(t) \cdot F(\bar{\mathbf{x}}), \quad (7)$$

and network (2) can be rewritten as follows:

$$\bar{\mathbf{x}}^{t+1} = \mathbf{C}(t) \cdot F(\bar{\mathbf{x}}^t). \quad (8)$$

The trajectory of network (2) (or (8)) consists of the time series $\{\bar{\mathbf{x}}^t \mid \bar{\mathbf{x}}^t = \bar{\mathbf{F}}^t(t, \bar{\mathbf{x}}^0), t \geq 0\}$, where $\bar{\mathbf{F}}^0(0, \bar{\mathbf{x}}) = \bar{\mathbf{x}}$ and $\bar{\mathbf{F}}^t(t, \bar{\mathbf{x}}) = \bar{\mathbf{F}}^t(t, \bar{\mathbf{F}}^{t-1}(t-1, \bar{\mathbf{x}}))$ for $t \geq 1$.

Network (2) with condition (3) implies that the synchronous solution $x_1^t = x_2^t = \dots = x_N^t = s^t$ is also a solution of the iterative map (1) of each population. Furthermore, a synchronous attractor may be an equilibrium, a periodic orbit, an aperiodic orbit, even or a chaotic attractor [1-10]. Before further investigating the local asymptotic synchronization of the time-varying discrete biological network (2), one firstly introduces the following two definitions.

Definition 1. $\mathbb{S} = \{\bar{\mathbf{x}} = (x_1^T, \dots, x_N^T)^T \in X^N \mid x_i = x_j = s \in X, i, j = 1, 2, \dots, N\}$ is called the synchronous manifold of the time-varying discrete biological network (2) and the time-invariant discrete biological network (6).

Definition 2. A trajectory $\{\bar{\mathbf{x}}^t \mid t = 0, 1, \dots\}$ is asymptotically synchronous if $\lim_{t \rightarrow \infty} \|\bar{\mathbf{x}}^t - s^t \mathbf{e}\| = 0$.

III. LOCAL ASYMPTOTIC SYNCHRONIZATION

It is well known that the local asymptotic synchronization is extremely important for unraveling the underlying mechanics of global extinctions [1-10]. This is because the effects of migration in a metapopulation (a network of populations) are very important for predicting the possibility of extinctions at the local scale. In the following, based on the proposed time-varying discrete biological network model (2), several novel local asymptotic synchronization criteria are presented for predicting the possibility of extinctions at a local scale.

Suppose that s^t is a solution of the single population dynamics $x^{t+1} = F(x^t)$. Let the error vectors be

$$\eta_i^t = x_i^t - s^t, \quad i = 1, 2, \dots, N. \quad (9)$$

Substitute system (9) into system (2) gets

$$\eta_i^{t+1} = \sum_{j=1}^N c_{ij}^t (F(s^t + \eta_j^t) - F(s^t)), \quad i = 1, 2, \dots, N. \quad (10)$$

Denote $\bar{\boldsymbol{\eta}} = \bar{\mathbf{x}} - s \mathbf{e} = (\eta_1^T, \eta_2^T, \dots, \eta_N^T)^T \in X^N$. Thus network (10) can be simplified as follows:

$$\bar{\boldsymbol{\eta}}^{t+1} = \bar{\mathbf{F}}(t, s^t \mathbf{e} + \bar{\boldsymbol{\eta}}^t) - \bar{\mathbf{F}}(t, s^t \mathbf{e}). \quad (11)$$

Since \mathbf{C} has 1 row sums, without loss of generality, let $\lambda_1 = 1$. Let $\lambda_{max} = \max_{2 \leq i \leq N} |\lambda_i|$, $r = \sup_{x \in X} \|D_x F\|$. For stating

simplification, one introduces a lemma and a hypothesis as follows.

Lemma 1: *If $\mathbf{C} = (c_{ij})_{N \times N}$ has 1 row sums and can be diagonalized, then there exists a nonsingular matrix $\Phi = (\phi_1, \phi_2, \dots, \phi_N)$ satisfying $\mathbf{C}^T \phi_i = \lambda_i \phi_i$ ($i = 1, 2, \dots, N$) with $\lambda_1 = 1$, and $\Phi^{-1} = (\varphi_1^T, \varphi_2^T, \dots, \varphi_N^T)^T$ with $\varphi_1 = (1, 1, \dots, 1)$.*

The proof is omitted here.

Hypothesis 1 (H1): *Assume that the zero solution of the discrete linear map $\xi^{t+1} = D_{st}F \xi^t$ is asymptotically stable, where $F : X \rightarrow X$ is differentiable at each $x \in X \subseteq \mathbb{R}^n$. And the asymptotic stability of zero solution of system (11) is equivalent to that of its corresponding linearized system. Suppose also that there exists $t_0 \geq 1$ satisfying $\lambda_i(t) \neq 1$ or $\lambda_i(t) \equiv 1$ for all $t \geq t_0$ and $i = 1, 2, \dots, N$.*

Condition (3) implies that $\mathbf{C}(t)$ has at least an eigenvalue 1 for all $t = 1, 2, \dots$, i.e., there exists at least an $1 \leq i \leq N$ satisfying $\lambda_i(t) = 1$ for each $t = 1, 2, \dots$. According to H1, there exists $t_0 \geq 1$ satisfying $\lambda_i(t) \equiv 1$ for any $t \geq t_0$. Without loss of generality, hereafter assume that $\lambda_1(t) \equiv 1$ for any $t \geq t_0$.

Theorem 1: *Suppose that H1 holds and $\mathbf{C}(t)$ is an $N \times N$ real matrix with 1 row sums for $t = 1, 2, \dots$. Suppose also that there exists a nonsingular real matrix $\Phi(t)$, such that $\Phi^{-1}(t)(\mathbf{C}(t))^T \Phi(t) = \text{diag}\{\lambda_1(t), \lambda_2(t), \dots, \lambda_N(t)\}$ and $\Phi^{-1}(t)\Phi(t+1) = \text{diag}\{\beta_1(t), \beta_2(t), \dots, \beta_N(t)\}$. Then the time-varying discrete biological network (2) (or synchronous manifold \mathbb{S}) is locally asymptotically synchronous if and only if the linear systems*

$$\xi_i^{t+1} = [\lambda_i(t)\beta_i(t)D_{st}F]\xi_i^t, \quad i = 2, 3, \dots, N \quad (12)$$

are asymptotically stable at the zero solution.

Proof: Linearizing system (11) at $\bar{\eta}^t = \mathbf{0}$ yields [12-15]

$$\vec{\zeta}^{t+1} = \mathbf{C}(t) \otimes D_{st}F \vec{\zeta}^t, \quad (13)$$

where $\vec{\zeta} = (\zeta_1^T, \zeta_2^T, \dots, \zeta_N^T)^T \in X^N$ and \otimes is the Kronecker product.

Rewrite system (13) as follows:

$$\begin{aligned} \zeta_i^{t+1} &= D_{st}F \left[\sum_{j=1}^N c_{ij}^t \zeta_j^t \right] \\ &= D_{st}F [(\zeta_1^t, \zeta_2^t, \dots, \zeta_N^t) \cdot (c_{i1}^t, \dots, c_{iN}^t)^T], \end{aligned} \quad (14)$$

where $i = 1, 2, \dots, N$. Thus one gets

$$(\zeta_1^{t+1}, \zeta_2^{t+1}, \dots, \zeta_N^{t+1}) = D_{st}F [(\zeta_1^t, \zeta_2^t, \dots, \zeta_N^t)(\mathbf{C}(t))^T]. \quad (15)$$

According to the assumption of Theorem 1, one has

$$\Phi^{-1}(t)(\mathbf{C}(t))^T \Phi(t) = \mathbf{\Lambda}(t), \quad (16)$$

where $\mathbf{\Lambda}(t) = \text{diag}\{\lambda_1(t), \lambda_2(t), \dots, \lambda_N(t)\}$. Consider the nonsingular linear transformation

$$(\zeta_1^t, \zeta_2^t, \dots, \zeta_N^t) = (\xi_1^t, \xi_2^t, \dots, \xi_N^t)\Phi^{-1}(t), \quad (17)$$

from (15), one gets

$$\begin{aligned} &(\xi_1^{t+1}, \xi_2^{t+1}, \dots, \xi_N^{t+1}) \\ &= D_{st}F [(\xi_1^t, \xi_2^t, \dots, \xi_N^t)\Phi^{-1}(t)(\mathbf{C}(t))^T \Phi(t)] \\ &[\Phi^{-1}(t)\Phi(t+1)] \\ &= D_{st}F [(\xi_1^t, \xi_2^t, \dots, \xi_N^t)\mathbf{\Lambda}(t)]\Gamma(t). \end{aligned} \quad (18)$$

where $\Gamma(t) = \text{diag}\{\beta_1(t), \beta_2(t), \dots, \beta_N(t)\}$.

Therefore, one has

$$\xi_i^{t+1} = [\lambda_i(t)\beta_i(t)D_{st}F]\xi_i^t, \quad i = 1, 2, \dots, N. \quad (19)$$

H1 indicates that the asymptotic stability of zero solution of system (11) is equivalent to that of system (13).

Since the linear transformation (17) is nonsingular, then $\zeta_i^t \rightarrow \mathbf{0}$ is equivalent to $\xi_i^t \rightarrow \mathbf{0}$. Thus the asymptotic stability of zero solution of system (11) is equivalent to that of system (19). Here, systems (19) and (12) have the same algebraic forms for $i = 2, \dots, N$.

From H1, there exists $t_0 \geq 1$ satisfying $\lambda_1(t) \equiv 1$ for any $t \geq t_0$. Denote $\Phi(t) = (\phi_1(t), \phi_2(t), \dots, \phi_N(t))$ and $\Phi^{-1}(t) = (\varphi_1^T(t), \varphi_2^T(t), \dots, \varphi_N^T(t))^T$. According to Lemma 1, $\varphi_1(t) = \varphi_1(t+1) = (1, 1, \dots, 1)$. Since $\Phi^{-1}(t+1)\Phi(t+1) = \mathbf{E}_{N \times N} = \text{diag}\{\varphi_1(t+1)\phi_1(t+1), \varphi_2(t+1)\phi_2(t+1), \dots, \varphi_N(t+1)\phi_N(t+1)\}$, then $\varphi_1(t+1)\phi_1(t+1) = 1$. From the assumption of Theorem 1, $\Phi^{-1}(t)\Phi(t+1) = \text{diag}\{\beta_1(t), \beta_2(t), \dots, \beta_N(t)\} = \text{diag}\{\varphi_1(t)\phi_1(t+1), \varphi_2(t)\phi_2(t+1), \dots, \varphi_N(t)\phi_N(t+1)\}$. Then $\beta_1(t) = \varphi_1(t)\phi_1(t+1) = (1, 1, \dots, 1)\phi_1(t+1) = \varphi_1(t+1)\phi_1(t+1) = 1$.

When $i = 1$, $\lambda_1(t)\beta_1(t) = 1$ for all $t \geq t_0$ and system (19) becomes

$$\xi_1^{t+1} = D_{st}F \xi_1^t.$$

H1 indicates that the above linear system is asymptotically stable at the zero solution. Therefore, the time-varying discrete biological network (2) (or synchronous manifold \mathbb{S}) is locally asymptotically synchronous if and only if the linear systems (12) are asymptotically stable at the zero solution. And the proof is thus completed.

Based on Theorem 1, we can easily get the following corollary.

Corollary 2: *Assume that H1 holds. Suppose the dispersal matrix $\mathbf{C}(t) = \mathbf{E}_{N \times N} + \alpha \sin(\arctan(t))\bar{\mathbf{C}}$ has 1 row sums and $\bar{\mathbf{C}}$ can be diagonalized. Then the time-varying discrete biological network (2) is locally asymptotically synchronous if $0 < \alpha \leq \frac{1}{\gamma}$ and*

$$\frac{-1 - e^{-\mu_0}}{\alpha \sin(\arctan 1)} < \bar{\lambda}_i < 0, \quad i = 2, 3, \dots, N, \quad (20)$$

or $-\frac{1}{\gamma} \leq \alpha < 0$ and

$$0 < \bar{\lambda}_i < \frac{-1 - e^{-\mu_0}}{\alpha \sin(\arctan 1)}, \quad i = 2, 3, \dots, N, \quad (21)$$

where $\bar{\lambda}_i$ ($i = 1, 2, \dots, N$) are the eigenvalues of matrix $\bar{\mathbf{C}}$, $\gamma = \max_{2 \leq i \leq N} |\bar{\lambda}_i|$, and $\mu_0 < 0$ is the largest Lyapunov exponent of population dynamical system (1).

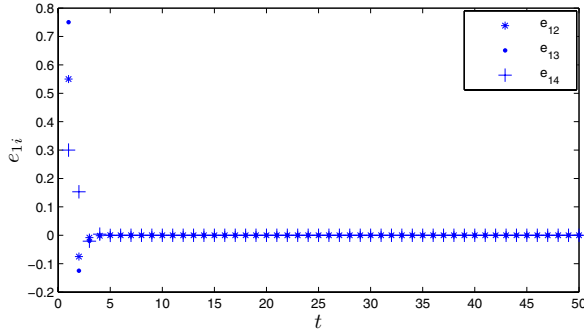


Fig. 1. Synchronous errors e_{1i} ($i = 2, 3, 4$) between the population densities of the patches, where $e_{1i} = x_i^t - x_1^t$.

IV. AN EXAMPLE

To verify the effectiveness of the proposed synchronous criteria, one analyzes a simple spatially structured discrete time metapopulation model (2) with four patches.

Hereafter, x_i^t is the population density of the i th patch at time t . $F(x_i)$, such as logistic map [3,5], characterizes the birth-death processes of the local population x_i , which is described by

$$x^{t+1} = a x^t (1 - x^t), \quad (22)$$

where a is the net growth rate of the local population.

Let $a = 2.5$, then system (22) has a asymptotically stable solution $x^t = 1 - \frac{1}{a}$ and $\mu_0 = -\ln 2 < 0$.

The time-varying dispersal matrix $\mathbf{C}(t)$ is given by $\mathbf{C}(t) = \mathbf{E}_{N \times N} + \sin(\arctan(t))\bar{\mathbf{C}}$, where

$$\bar{\mathbf{C}} = \begin{pmatrix} -0.4 & 0.2 & 0 & 0.2 \\ 0.8 & -0.8 & 0 & 0 \\ 0.8 & 0 & -0.8 & 0 \\ 0.25 & 0 & 0.25 & -0.5 \end{pmatrix}. \quad (23)$$

The eigenvalues of matrix $\bar{\mathbf{C}}$ are described by $\bar{\lambda}_1 = 0$, $\bar{\lambda}_2 = -0.7382$, $\bar{\lambda}_3 = -0.8$, $\bar{\lambda}_4 = -0.9618$.

Then $\gamma = \max_{2 \leq i \leq 4} |\bar{\lambda}_i| = 0.9618$ and $0 < \alpha = 1 < \frac{1}{0.9618}$. Moreover, one has

$$-3\sqrt{2} = \frac{-1 - e^{-\mu_0}}{\sin(\arctan(1))} < \bar{\lambda}_i < 0, \quad i = 2, 3, 4. \quad (24)$$

According to *Corollary 2*, the spatially structured discrete time metapopulation model (2) with four patches is locally asymptotically synchronous.

The synchronous errors between the population densities of the patches are defined by $e_{1i} = x_i^t - x_1^t$ for $i = 2, 3, 4$. Fig. 1 shows the synchronous errors e_{1i} ($i = 2, 3, 4$) between the population densities of the patches for 8,000 iterations. It is very clear from Fig. 1 that the spatially structured discrete time metapopulation model (2) with four patches is locally asymptotically synchronous. Therefore, our numerical simulations are well consistent with our theoretical analysis.

V. CONCLUSIONS

We have introduced a novel time-varying discrete biological network and further investigated its local asymptotic synchronization. Moreover, several fundamental criteria are also proposed for the local asymptotic synchronization of the time-varying discrete biological network (2). These criteria are essentially important and provide some new insight for the prediction and evaluation of the risk of global extinctions. These synchronous criteria are also suitable to the local asymptotic synchronization of other complex dynamical systems, such as the secure communication, synchronous satellite, swarming in the battlefield, collective motion in animal groups, and the eradication of infectious diseases, etc.

These synchronous criteria provide the powerful tools for evaluating and predicting the risk of global extinctions in ecosystems. They also offer some new views on the conservation of biological diversity and endangered species, such as the weak couplings (few migration) or same fixed couplings (uniform migration) between populations do not means the low risk of global extinctions. Our results show that the heterogeneous migration is more likely to decrease the risk of global extinctions.

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