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An Approximate Method of System Entropy in Discrete-Time Nonlinear Biological Networks

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Abstract: This study discusses the calculation of entropy of discrete-time stochastic biological systems. First, measurement methods of the system entropy of discrete-time linear stochastic networks are introduced. The system entropy is found to be characterized by system matrices of the discrete-time biological systems. Secondly, the system entropy of nonlinear discrete-time stochastic biological systems is discussed and is calculated based on a global linearization method. The approximation of the values of system entropy of nonlinear stochastic systems needs to solve an optimization problem that is constrained by a kind of linear matrix inequality (LMI). Finally, a practical biochemical system is provided to verify the effectiveness of the proposed calculation method.

Keywords: system entropy; system randomness; biological network; discrete-time nonlinear stochastic system; linear matrix inequality (LMI)

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1. Introduction

In general, entropy is considered as a measure of the randomness or disorder of a physical or biological system under intrinsic random fluctuations and environmental disturbances [1–5]. According to the second law of thermodynamics, entropy is used to describe the dispersion of energy in a thermally isolated system, in which energy has a natural tendency to spontaneously change toward states with higher entropy [6–8]. In order to maintain life, biological systems need to exchange material and energy with their environment in a continual process, so they are open systems [9].

In this exchange process, the entropy of biological systems can maintain a dynamic balance [10]. Under such a background, the calculation of biological system entropy is particularly important. In the past few decades, the system entropy in biological networks has been extensively studied [11–13]. The discrete-time model plays an important role in numerical calculation, stochastic simulation and numerical analysis [14–18]. For continuous-time stochastic systems, the authors of [16] calculated the system entropy of biological systems from their system matrices by the global linearization technique. In this way, the measurement of the system entropy of nonlinear biological networks could be transformed to solve an optimization problem constrained by a set of LMIs. In this paper, we follow the line of [16] and extend the LMI method to the calculation of the discrete-time system entropy of stochastic biological networks. With the aid of the Matlab software package, we solve the corresponding LMI-constrained optimization problem to measure the discrete-time system entropy of a nonlinear biological network.

This paper is organized as follows. In Section 2, we discuss how to calculate the entropy of the discrete-time linear network. Section 3 gives the system entropy measurement of the discrete-time nonlinear random biological network. Section 4 presents how to calculate

the system entropy in discrete-time nonlinear stochastic biological networks, which is approximated by the global linearization method. Lastly, in Section 5, an example is given to illustrate the measurement procedure and to validate the feasibility of the proposed system entropy measurement method.

2. System Entropy in Discrete-Time Linear Biological Networks

In this section, we consider a discrete-time linear network, which is described as follows:

$$\begin{cases} x_{t+1} = Ax_t + Bv_t, \\ y_t = Cx_t, t = 0, 1, 2, \cdots T_f \end{cases} \tag{1}$$

where $x_0 = 0$, $x_t \in \mathbb{R}^n$, $v_t \in \mathbb{R}^m$, $y_t \in \mathbb{R}^l$ denotes the biological network's state vector, random input and output, respectively. T_f is the finite terminal time. A, B and C are matrices with proper dimensions with the following formats:

$$A = \begin{bmatrix} a_{11} & \cdots & a_{1n} \\ \vdots & \ddots & \vdots \\ a_{n1} & \cdots & a_{nn} \end{bmatrix}, B = \begin{bmatrix} b_{11} & \cdots & b_{1m} \\ \vdots & \ddots & \vdots \\ b_{n1} & \cdots & b_{nm} \end{bmatrix}, C = \begin{bmatrix} c_{11} & \cdots & c_{1n} \\ \vdots & \ddots & \vdots \\ c_{l1} & \cdots & c_{ln} \end{bmatrix}.$$

The randomness of this system's output y_t can be measured by

$$r_o = \mathbb{E}[\frac{1}{T_f}\sum_{t=0}^{T_f} y_t^T y_t]$$

while the randomness of input signals v_t is denoted as

$$r_i = \mathbb{E}[\frac{1}{T_f}\sum_{t=0}^{T_f} v_t^T v_t]$$

where $\mathbb{E}[\cdot]$ denotes the expectation. Similar to the definitions of entropy in [16], the entropy of the input signal or output signal for a discrete-time system is also defined by

$$s_i = -\log \mathbb{E}[\frac{1}{T_f}\sum_{t=0}^{T_f} v_t^T v_t]$$

and the entropy of y_t is defined by

$$s_o = -\log \mathbb{E}[\frac{1}{T_f}\sum_{t=0}^{T_f} y_t^T y_t].$$

Thus, it is natural to define the net signal entropy of a biological system as the discrete-time system entropy, i.e.,

$$s = s_i - s_o = \log \mathbb{E}[\frac{1}{T_f}\sum_{t=0}^{T_f} y_t^T y_t] - \log \mathbb{E}[\frac{1}{T_f}\sum_{t=0}^{T_f} v_t^T v_t]$$

$$s = \log \frac{\mathbb{E}[\sum_{t=0}^{T_f} y_t^T y_t]}{\mathbb{E}[\sum_{t=0}^{T_f} v_t^T v_t]} \tag{2}$$

Thus, if the system randomness r of System (1) is defined as the following

$$r = \frac{\mathbb{E}[\sum\limits_{t=0}^{T_f} y_t^T y_t]}{\mathbb{E}[\sum\limits_{t=0}^{T_f} v_t^T v_t]}$$

the system entropy is represented as

$$s = \log r.$$

In order to calculate the system entropy s in (1), we have to calculate or approximate the system randomness first. Of course, it is not easy to approximate such randomness directly. Therefore, we need to estimate the system randomness indirectly as follows:

$$r = \frac{\mathbb{E}[\sum\limits_{t=0}^{T_f} y_t^T y_t]}{\mathbb{E}[\sum\limits_{t=0}^{T_f} v_t^T v_t]} \leq \bar{r}$$

which is equivalent to

$$\mathbb{E}[\sum_{t=0}^{T_f} y_t^T y_t] \leq \bar{r}\mathbb{E}[\sum_{t=0}^{T_f} v_t^T v_t] \tag{3}$$

Here, $\bar{r}$ denotes the upper bound of r.

We will decrease the upper bound $\bar{r}$ to be as small as possible, to approach the randomness r of the discrete-time biological network (1), which is suggested in [16].

Proposition 1. *Suppose that a positive definite matrix $p > 0$ and a positive real number $\bar{r} > 0$ satisfy the following inequality:*

$$\begin{cases} A^T PA + C^T C - P + A^T PB(\bar{r}I - B^T PB)^{-1} B^T PA < 0 \\ \bar{r}I - B^T PB > 0 \end{cases} \tag{4}$$

Then, $\bar{r}$ is an upper bound of the system randomness of network (1).

Proof. Choose the Lyapunov function $V(x) = x^T Px$, then

$$\begin{aligned} V(x_{t+1}) - V(x_t) &= (x_t^T A^T + v_t^T B^T)P(Ax_t + Bv_t) \\ &= x_t^T (A^T PA - P)x_t + 2x_t^T A^T PBv_t + v_t^T B^T PBv_t \end{aligned}$$

Taking summation, and then taking expectation on both sides, we have

$$\mathbb{E}[V(x_{T_f+1})] - \mathbb{E}[V(x_0)] = \mathbb{E}\Big\{ \sum_{t=0}^{T_f} [x_t^T (A^T PA - P)x_t + 2x_t^T A^T PBv_t + v_t^T B^T PBv_t] \Big\}.$$

Recalling that $V(x) \geq 0$, $x_0 = 0$ and $V(0) = 0$, we have

$$0 \leq \mathbb{E}\Big\{ \sum_{t=0}^{T_f} [x_t^T (A^T PA - P)x_t + 2x_t^T A^T PBv_t + v_t^T B^T PBv_t] \Big\}.$$

Thus,

$$\mathbb{E}[\sum_{t=0}^{T_f} y_t^T y_t] - \bar{r}\mathbb{E}[\sum_{t=0}^{T_f} v_t^T v_t] \leq \mathbb{E}\Big\{ \sum_{t=0}^{T_f} [x_t^T (A^T PA + C^T C - P) x_t + 2x_t^T A^T PB v_t - v_t^T (\bar{r}I - B^T PB) v_t] \Big\}.$$

Completing the square on the right side, we obtain

$$\mathbb{E}[\sum_{t=0}^{T_f} y_t^T y_t] - \bar{r}\mathbb{E}[\sum_{t=0}^{T_f} v_t^T v_t] \leq \mathbb{E}\Big\{ \sum_{t=0}^{T_f} \Big[x_t^T \Big(A^T PA + C^T C - P + A^T PB \times (\bar{r}I - B^T PB)^{-1} B^T PA \Big) x_t - \| v_t - (\bar{r}I - B^T PB)^{-1} B^T PA x_t \|^2_{\bar{r}I - B^T PB} \Big] \Big\}.$$

where the notation $\| \cdot \|_A^2$ denotes $\|y\|_A^2 = y^T Ay$ with $A > 0$. By inequality (4), there exists

$$\mathbb{E}[\sum_{t=0}^{T_f} y_t^T y_t] - \bar{r}\mathbb{E}[\sum_{t=0}^{T_f} v_t^T v_t] \leq 0.$$

Thus, we have

$$\mathbb{E}[\sum_{t=0}^{T_f} y_t^T y_t] \leq \bar{r}\mathbb{E}[\sum_{t=0}^{T_f} v_t^T v_t]$$

This shows that the randomness r of System (1) has an upper bound $\bar{r}$. □

By the Schur lemma, we know that the matrix inequality (4) equals the following LMI:

$$\begin{bmatrix} C^T C + A^T PA - P & A^T PB \\ B^T PA & B^T PB - \bar{r}I \end{bmatrix} < 0. \tag{5}$$

Thus, we can obtain the following corollary described by LMI (5).

Corollary 1. *Suppose that there exists a positive definite matrix $p > 0$ and a positive real number $\bar{r} > 0$ that satisfy the inequality (5); then, $\bar{r}$ is an upper bound of the system randomness of network (1).*

Remark 1. *Compared with the results of Reference [16], the matrix inequality (4) that is obtained by the completing square method is different to the results of Proposition 2 of [16]. Moreover, the structure of LMI (5) for a discrete-time network is different to that of (12) for the continuous-time system discussed in [16].*

From Equation (3), we can see that the upper bound of the discrete-time system randomness r is $\bar{r}$, i.e., $r \leq \bar{r}$. Thus, the calculation of the system randomness of network (1) can be estimated by the following problem:

$$r = \min \bar{r} \tag{6}$$

with the constraint of LMI (5), where $p > 0$.

Based on (6), with the aid of Matlab's LMI toolbox, we can decrease $\bar{r}$ by the constraint of LMI in (5) until there is no positive matrix P appearing; then, the above LMI-constrained optimization problem can be solved, and the system randomness r can be estimated. Thus, the discrete-time system entropy of the linear stochastic System (1) can be obtained as

$s = \log r$. Moreover, the measurement of the system randomness r or system entropy s is dependent on matrices A, B and C in System (1) to some extent.

3. System Entropy in Discrete-Time Nonlinear Network

Nonlinear dynamic systems play an important role in biological networks, which causes the difficulty of estimating the entropy of such systems. Under this situation, the global linearized method is suggested [19–27], which is an interpolation method of local linearized systems of a nonlinear biological network. Suppose that the biological systems are described by the following discrete-time nonlinear stochastic biological network:

$$\begin{cases} x_{t+1} = f(x_t) + g(x_t)v_t, \\ y_t = h(x_t), t = 0, 1, 2, \cdots T_f \end{cases} \tag{7}$$

where $x_0 = 0$, f is a function, v_t denotes m external input signal and $g(x_t)$ denotes m nonlinear couplings between the biological network and environment. $h(x_t)$ denotes l nonlinear outputs.

Based on the ideas of the discrete-time system randomness of (3), we obtain the following proposition.

Proposition 2. *Suppose that there exists a positive definite matrix $p > 0$ and a positive real number $\bar{r} > 0$ that satisfy the following HJI:*

$$\begin{cases} f^T(x)Pf(x) - x^TPx + h^T(x)h(x) \\ \qquad + f^T(x)Pg(x)(\bar{r}I - g^T(x)Pg(x))^{-1}g^T(x)Pf(x) \leq 0 \\ \bar{r}I - g^T(x)Pg(x) > 0, \forall x \in \mathbb{R}^n \end{cases} \tag{8}$$

Then, $\bar{r}$ is an upper bound of the system randomness of network (7).

Proof. Let $V(x) = x^TPx$, then

$$V(x_{t+1}) - V(x_t) = f^T(x_t)Pf(x_t) - x_t^TPx_t^T + 2f^T(x_t)Pg(x_t)v_t + v_t^Tg^T(x_t)Pg(x_t)v_t.$$

Taking summation, and then taking expectation on both sides, we obtain

$$\mathbb{E}[V(x_{T_f+1})] - \mathbb{E}[V(x_0)] = \mathbb{E}\Big\{ \sum_{t=0}^{T_f} \Big[f^T(x_t)Pf(x_t) - x_t^TPx_t^T + 2f^T(x_t)Pg(x_t)v_t + v_t^Tg^T(x_t)Pg(x_t)v_t \Big] \Big\}.$$

Recalling that $V(x) \geq 0$, $x_0 = 0$ and $V(0) = 0$, we have

$$0 \leq \mathbb{E}\Big\{ \sum_{t=0}^{T_f} \Big[f^T(x_t)Pf(x_t) - x_t^TPx_t^T + 2f^T(x_t)Pg(x_t)v_t + v_t^Tg^T(x_t)Pg(x_t)v_t \Big] \Big\}.$$

Thus,

$$\mathbb{E}[\sum_{t=0}^{T_f} y_t^Ty_t] - \bar{r}\mathbb{E}[\sum_{t=0}^{T_f} v_t^Tv_t] \leq \mathbb{E}\Big\{ \sum_{t=0}^{T_f} \Big[f^T(x_t)Pf(x_t) - x_t^TPx_t^T + h^T(x)h(x) + 2f^T(x_t)Pg(x_t)v_t - v_t^T(\bar{r}I - g^T(x_t)Pg(x_t))v_t \Big] \Big\}.$$

Completing the square on the right side, we obtain

$$\mathbb{E}[\sum_{t=0}^{T_f} y_t^T y_t] - \bar{r}\mathbb{E}[\sum_{t=0}^{T_f} v_t^T v_t] \leq \mathbb{E}\Big\{ \sum_{t=0}^{T_f} \Big[f^T(x_t)Pf(x_t) - x_t^T P x_t^T + h^T(x)h(x) + f^T(x)Pg(x)(\bar{r}I - g^T(x)Pg(x))^{-1} g^T(x)Pf(x) - \|v_t - (\bar{r}I - g^T(x)Pg(x))^{-1} g^T(x)Pf(x)\|^2_{\bar{r}I - g^T(x)Pg(x)} \Big] \Big\}.$$

where the notation $\|\cdot\|_A^2$ denotes $\|y\|_A^2 = y^T A y$ with $A > 0$. By inequality (8), there exists

$$\mathbb{E}[\sum_{t=0}^{T_f} y_t^T y_t] - \bar{r}\mathbb{E}[\sum_{t=0}^{T_f} v_t^T v_t] \leq 0.$$

Thus, we have

$$\mathbb{E}[\sum_{t=0}^{T_f} y_t^T y_t] \leq \bar{r}\mathbb{E}[\sum_{t=0}^{T_f} v_t^T v_t] \tag{9}$$

This ends the proof. □

Remark 2. *Compared with the results of Proposition 4 in Reference [16], the HJI (8) in this paper does not depend on the input variables $v(t)$, but the HJIs in Proposition 4 of [16] include $v(t)$. Thus, the system randomness of network (7) can be obtained only by the coefficients $f(x)$, $g(x)$ and $h(x)$, which is defined on the state space.*

By Proposition 2, the system randomness r of network (7) can be approximated to solve the following optimization constrained by HJI:

$$r = \min \bar{r} \tag{10}$$

It is constrained by HJI in (8), where $p > 0$. Denote

$$\mathbb{V} = \Big\{ V(x) | V(x) = x^T P x, x \in \mathbb{R}^n, P > 0 \Big\}.$$

The system randomness r of network (7) could be estimated by solving the following optimization:

$$r = \min_{V(x) \in \mathbb{V}} \bar{r} \tag{11}$$

with the constraint of HJI in (8).

Based on the above results, it is easy to obtain the system entropy as

$$s = \log r.$$

We can obtain the system randomness r from the *HJI*-constrained optimization problem in (10) or (11). However, at present, there exists no efficient method to solve the HJI in (10) or (11) analytically or numerically. In this study, the global linearization method in [21,27] will be employed to interpolate several local linearized systems at the M matrices of the convex hull of the globalization systems to approach the nonlinear discrete-time biological systems in (7), to transform the difficult HJI-constrained optimization problem in (10) or (11) to an equivalent LMIs-constrained optimization problem for the calculation of system randomness in the following section.

4. The Global Linearization Method to Estimate System Entropy for Nonlinear Networks

In this section, the global linearization technique is suggested to help in estimating the system entropy of nonlinear stochastic systems in (7). The main idea of this method is described as follows: we convert the nonlinear system into a set of interpolated locally linearized networks in which the linear system's entropy is easy to calculate and approximate [16,21,27]. Therefore, the estimation of system randomness and entropy can be transformed to solve the *HJI*-constrained optimization problems (10) efficiently.

We prefer the detailed theory of the global linearization method to Reference [21]. According to this method, the global linearized systems are constructed by the convex hull of M vertices defined in Equation (12) as follows:

$$\begin{bmatrix} \frac{\partial f(x)}{\partial x} \\ \frac{\partial g(x)}{\partial x} \\ \frac{\partial h(x)}{\partial x} \end{bmatrix} \in C_0 \left(\begin{bmatrix} A_1 \\ B_1 \\ C_1 \end{bmatrix} \cdots \begin{bmatrix} A_i \\ B_i \\ C_i \end{bmatrix} \cdots \begin{bmatrix} A_M \\ B_M \\ C_M \end{bmatrix} \right), \forall x_t \tag{12}$$

Then, the state x_t in the discrete-time nonlinear System (7) can be represented by those states of local linearized biological networks with (12) as follows:

$$\begin{cases} x_{t+1} = A_i x_t + B_i v_t, \\ y_t = C_i x_t, t = 0, 1, 2, \cdots T \end{cases} \tag{13}$$

Thus, the combination of linearized systems in (13) can be represented as:

$$\begin{cases} x_{t+1} = \sum\limits_{i=1}^{M} \alpha_i(x_t)(A_i x_t + B_i v_t), \\ y_t = \sum\limits_{i=1}^{M} \alpha_i(x) C_i x_t, t = 0, 1, 2, \cdots T \end{cases} \tag{14}$$

where the interpolation function (for $x_t \neq x_i$)

$$\alpha_i(x_t) = \frac{\frac{1}{\|x_i - x_t\|_2^2}}{\sum\limits_{1=1}^{M} \frac{1}{\|x_i - x_t\|_2^2}} \tag{15}$$

and $\alpha_i(x_t) = 1$ for some $x_t = x_i$ satisfy $0 \leq \alpha_i(x) \leq 1$ and $\sum\limits_{i=1}^{M} \alpha_i(x_t) = 1$, while x_i denotes the ith local operation point with local linearization [27], i.e., the trajectory of the nonlinear System (7) can be represented by the trajectories of the interpolated biological network in (14).

If the nonlinear biological network in Equation (7) could be approximated by the global linearization system in Equation (14), then we obtain the following result.

Proposition 3. *Suppose that a positive definite matrix* $\mathrm{p} > 0$ *and a real number* $\bar{r} > 0$ *satisfy the following* LIMs*:*

$$\begin{bmatrix} A_i^T P A_i + C_i^T C_i - P & A_i^T P B_i \\ B_i^T P A_i & B_i^T P B_i - \bar{r} I \end{bmatrix} \leq 0, \quad for \quad i = 1, \cdots, M \tag{16}$$

Then, $\bar{r}$ *is an upper bound of the system randomness of network (7).*

Proof. Let Lyapunov function $V(x) = x_t^T P x_t$, and the approximation of $f(x_t)$ and $g(x_t)$ are

$$f(x_t) = \sum_{i=1}^{M} \alpha_i(x_t) A_i x_t$$

and

$$g(x_t) = \sum_{i=1}^{M} \alpha_i(x_t) B_i.$$

Then, we have

$$\mathbb{E}[V(x_0)] - \mathbb{E}[V(x_t)] + \mathbb{E}[\sum_{t=0}^{T_f} (y_t^T y_t - \bar{r} v_t^T v_t + \Delta V(x_t))] \leq 0$$

where

$$\Delta V(x_t) = \sum_{i=1}^{M} \alpha_i(x_t)[x_t^T A_i^T + v_t^T B_i^T P(A_i x_t + B_i v_t)] - x_t^T P x_t^T$$

Thus, we obtain the following result:

$$\mathbb{E}\left\{ \sum_{i=1}^{M} \alpha_i(x_t) \begin{bmatrix} x_t^T & v_t^T \end{bmatrix} \begin{bmatrix} \Pi & A_i^T P B_i \\ B_i^T P A_i & \Xi \end{bmatrix} \begin{bmatrix} x_t \\ v_t \end{bmatrix} \right\} \leq 0 \tag{17}$$

where $\Pi = A_i^T P A_i + C_i^T C_i - P$, $\Xi = B_i^T P B_i - \bar{r} I, i = 1, \cdots, M$.

This ends the proof. □

Based on this technique, the system randomness r of network (7) or (14) can be approximated by solving the following optimization problem:

$$r = \min_{P>0} \bar{r} \tag{18}$$

with the constraint of LMIs in (16) and $p > 0$. The system randomness r in (18) could be obtained by decreasing its upper bound $\bar{r}$ until there exists no $p > 0$.

5. Example and Simulation

In this section, we consider a phosphorelay system in yeast, discussed in [16,23]; see Figure 1. This signal transduction pathway includes seven state variables: Sln1, Sln1H-P, Sln1D-P, Ypd1, Yod1-P, Ssk1, Ssk1-P. We prefer to References [16,23,25], for detailed information.

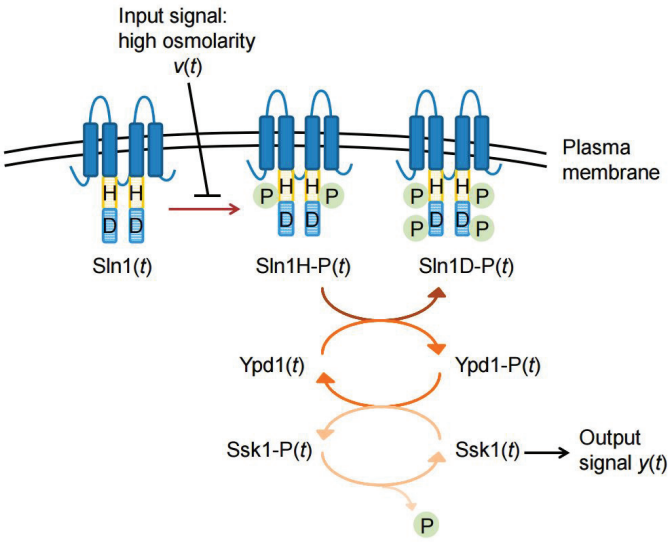

Figure 1. Schematic representation of phosphorelay system.

The state x_t is denoted by the following vector:

$$x_t = \begin{bmatrix} x_1(t) \\ x_2(t) \\ x_3(t) \\ x_4(t) \\ x_5(t) \\ x_6(t) \\ x_7(t) \end{bmatrix} = \begin{bmatrix} Sln1(t) \\ Sln1H - P(t) \\ Sln1D - P(t) \\ Ypd1(t) \\ Ypd1 - P(t) \\ Ssk1(t) \\ Ssk - P(t) \end{bmatrix} \tag{19}$$

Suppose that the dynamic behavior of this system can be represented by discrete-time difference equations, which are seen as the discrete-time type of phosphorelay system discussed in [25]:

$$\begin{cases} x_1(t+1) = (1-k_1)x_1(t) + k_3x_3(t)x_4(t) + k_0v_t \\ x_2(t+1) = k_1x_1(t) + (1-k_2)x_2(t) \\ x_3(t+1) = k_2x_2(t) + (1-k_3x_4(t))x_3(t) \\ x_4(t+1) = k_4x_5(t)x_6(t) + (1-k_3x_3(t))x_4(t) \\ x_5(t+1) = (1-k_4x_6(t))x_5(t) + k_3x_3(t)x_4(t) \\ x_6(t+1) = k_5x_7(t) + (1-x_4(t)x_5(t))x_6(t) \\ x_7(t+1) = (1-k_5)x_7(t) + x_4(t)x_5(t)x_6(t) \\ y = x_6(t) \end{cases} \tag{20}$$

where k_0, k_1, k_2, k_3, k_4 and k_5 are the systematic characteristics, and v_t is the random fluctuation. Figure 2 shows the trajectories of x with the systematic characteristics $k_0 = 0.5, k_1 = 0.4, k_2 = 0.1, k_3 = 50, k_4 = 50, k_5 = 0.5$ and v_t, which is the standard Gaussian white noise with zero mean.

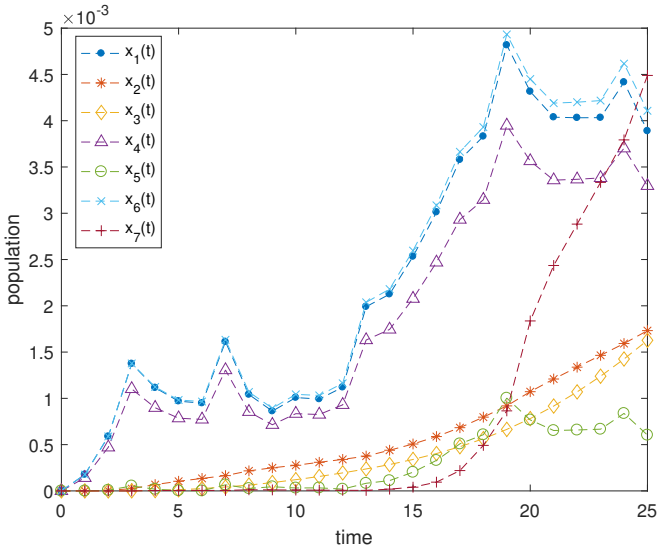

Figure 2. Temporal profiles of the state variables of Sln-1-phosphorelay system in (20) at the systematic characteristic case: $k_0 = 0.5, k_1 = 0.4, k_2 = 0.1, k_3 = 50, k_4 = 50, k_5 = 0.5$ with $v_t \sim N(0, 0.01^2)$.

In order to show the effects of systematic characteristics on system entropy, we take the three different systematic characteristics given in Table 1.

Table 1. Systematic characteristics in three cases.

Characteristics	k_0	k_1	k_2	k_3	k_4	k_5
Case 1	0.5	0.4	0.1	50	50	0.5
Case 2	0.3	0.1	0.2	1	1	0.6
Case 3	0.01	0.02	0.03	10	10	0.04

Due to the global linearization in (14), the approximation of discrete-time nonlinear network (20) can be presented by:

$$X_{t+1} = \sum_{t=1}^{M} \alpha_i(x_t)(A_i X_t + B_i v_t) \tag{21}$$

where $\alpha(x_t)$ denotes the the interpolation functions. X_t denotes the M states of local linearization systems [26].

By solving the LMI-constrained optimization problem in Equation (18) for the above three system characteristic cases in Table 1, the positive definite matrices P_1, P_2 and P_3 are obtained as follows:

$$P_1 = \begin{bmatrix} 2.7010 & 0.4458 & -0.0177 & -0.1448 & 0.0034 & 0 & 0 \\ 0.4458 & 2.8184 & -0.0063 & -0.0032 & -0.0006 & 0 & 0 \\ -0.0177 & -0.0063 & 3.0983 & -0.0006 & -0.0249 & 0 & 0 \\ -0.1448 & -0.0032 & -0.0006 & 3.0790 & 0.0352 & 0 & 0 \\ 0.0034 & -0.0006 & -0.0249 & 0.0352 & 3.0920 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 3.9651 & -0.0001 \\ 0 & 0 & 0 & 0 & 0 & -0.0001 & 5.2752 \end{bmatrix},$$

$$P_2 = \begin{bmatrix} 16.2540 & -0.1773 & -0.0102 & -0.0034 & 0.0000 & 0 & 0 \\ -0.1773 & 17.5868 & -0.0025 & 0.0001 & -0.0000 & 0 & 0 \\ -0.0102 & -0.0025 & 16.2441 & 0.0000 & -0.0001 & 0 & 0 \\ -0.0034 & 0.0001 & 0.0000 & 16.2445 & 0.0001 & 0 & 0 \\ 0.0000 & -0.0000 & -0.0001 & 0.0001 & 16.2445 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 17.2443 & -0.0006 \\ 0 & 0 & 0 & 0 & 0 & -0.0006 & 35.0822 \end{bmatrix},$$

$$P_3 = \begin{bmatrix} 119.4032 & -0.0239 & -0.0001 & -0.0005 & -0.0000 & 0 & 0 \\ -0.0239 & 119.6182 & -0.0007 & -0.0000 & -0.0000 & 0 & 0 \\ 0.0001 & -0.0007 & 119.4032 & -0.0000 & -0.0240 & 0 & 0 \\ -0.0005 & 0.0000 & 0.0000 & 119.4032 & 0.00000 & 0 & 0 \\ 0.0000 & -0.0000 & -0.0000 & 0.0000 & 119.4032 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 120.40 & -0.00 \\ 0 & 0 & 0 & 0 & 0 & -0.0000 & 119.78 \end{bmatrix}.$$

Corresponding system entropy is calculated, and the result is shown in following Table 2.

Table 2. System entropy of systems with three different systematic characteristics.

Characteristics	P	r	$s = \log r$
Case 1	P_1	3.6404	1.2921
Case 2	P_2	20.3077	3.0110
Case 3	P_3	149.2539	5.0056

By the estimation results of Table 2, we see that the different systematic characteristics in (20) can affect the system entropy of the biological network.

6. Conclusions

In this paper, the system entropy measurement of discrete-time nonlinear biological system is discussed. In order to overcome the nonlinear Hamilton-Jacobi inequality(HJI) in the measurement precedure, we extend the global linearization method in continuous-time system to the discrete-time system, so that the HJI-constrained optimization for the measurement of system entropy of discrete-time nonlinear biological system can be transformed to LMIs-constrained optimization problem to efficiently calculate the system entropy easily with the help of LMI Toobox in MATLAB. Moreover, the calculation methods of system entropy of more complex systems such as the nonlinear system with intrinsic randomness, stochastic systems driven by Markov processes are worth further study.

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