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Finite-time state observer for delayed reaction-diffusion genetic regulatory networks

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ABSTRACT

This paper focus on the finite-time state estimation problem for delayed reaction-diffusion genetic regulatory networks (DRDGRNs) under Dirichlet boundary conditions. The purpose is to design a finite-time state observer which is used to estimate the concentrations of mRNAs and proteins via available measurement outputs. By constructing a Lyapunov–Krasovskii functional (LKF) concluding quad-slope integrations, we establish a reaction-diffusion-dependent and delay-dependent finite-time stability criterion for the error system. The derivative of LKF is estimated by employing the Wirtinger-type integral inequality, Gronwall inequality and convex (reciprocally convex) technique. The stability criterion is to check the feasibility of a set of linear matrix inequalities (LMIs), which can be easily realized by the toolbox YALMIP of MATLAB. In addition, the expected finite-time state observer gain matrices can be represented by a feasible solution of the set of LMIs. Finally, two numerical examples are presented to illustrate the effectiveness of the theoretical results.

1. Introduction

In recent years, genetic regulatory networks (GRNs) has become a hot topic in many disciplines, for example, mathematics, statistics, biology and medicine, and aroused the attention of experts and scholars. As a result, a great deal of very important research results (see [1–7] and the references therein) have been achieved. GRNs, as highly complex network models, describe genetic expression and regulation behavior. The transcription and translation are the most important and most complex processes in the GRNs.

Currently, mathematical models have been one of the main tools to analyze GRNs. Due to the different forms of the GRNs and the different research purpose and methods, several GRN models have been established. For example, the Bayesian model [8], the Boolean model [7,9] and the functional differential equations model [5,10,11]. A functional differential equation model describes the continuous change of mRNA and protein concentrations which have two merits: (i) the slow processes of the transcription and translation are characterized by time delays; and (ii) the continuous change of mRNA and protein concentrations are expressed as the derivatives of the unknown functions. So, functional differential equation models have been widely applied to understand the nonlinearity and complexity of GRNs. It should be emphasized that time delays are one of main sources for causing instability and/or poor performance [12–15]. Accordingly, stability analysis of functional differential equation models has aroused increasing research interests, and a great number of outstanding results have been reported (see [6,7,16–24] and the references therein). The stability criteria presented in these literature are divided into two kinds: delay-dependent stability ones and delay-independent stability ones. In general, delay-dependent stability criteria are less conservative than delay-independent ones. Please refer to [25–32] for effective approaches to establish delay-dependent stability criteria.

In some mathematical modeling, it is assumed that GRNs are spatially homogeneous, namely, the concentrations of mRNAs and proteins are homogenous in space at all times. However, in some cases, it is need to introduce reaction-diffusion terms into models [19,33–39]. Especially, it is necessary to consider the diffusion of mRNAs and proteins [19,37–39]. Thus, it is imperative to introduce reaction-diffusion terms into the continuous-time GRN models. To the best of authors' knowledge, the stability problem for delayed reaction-diffusion genetic regulatory networks (DRDGRNs) has been only studied in [19,22–24]. Ma et al. [24] introduced DRDGRNs for the first time and established delay-dependent asymptotic stability criteria. Ma et al.'s results have been gradually improved in [19,23] by introducing novel LKF and utilizing Wirtinger-type integral inequality approach. The problem of finite-time robust stochastic stability analysis for uncertain stochastic DRDRNs has been studied in [22].

With the change of environment, the usual feedback loops existing in GRNs may be destroyed. This will make GRNs' performance worse, and eventually lead to some fatal disease like cancer [40]. Therefore, it

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is necessary to adjust the feedback loops by artificial input control. For this end, the exact concentrations of the mRNAs and proteins (that is, the states of continuous GRN models) are needed. However, due to the complexity of GRNs, it is almost impossible to measure the exact concentrations. Hence, the state estimation for GRNs has been one of available methods to investigate dynamical behaviors; see, eg., [41–44]. To the best knowledge of authors, the state estimation problem for DRDGRNs is only in [45], although the reaction-diffusion-free case has been researched (see [5,41,46–49] and the references therein). This motivates our research interests.

The aim of this paper is to design a finite-time state observer for estimating concentrations of the mRNAs and proteins of DRDGRNS. A novel LKF is first constructed. Then its derivative is estimated by employing Wirtinger-type integral inequality [50], Gronwall inequality [51], convex technique and reciprocally convex technique [52]. As a result, a reaction-diffusion-dependent and delay-dependent sufficient condition is given to ensure that the error system is finite-time stable. This is different from [45] wherein the asymptotic stability of error systems are involved. The stability criterion is given in the form of linear matrix inequalities (LMIs), which can be solved by applying the Toolbox LMI or YALMIP of MATLAB. Thereby, we design a finite-time state observer whose gain matrices are described based on a feasible solution to these LMIs. In addition, two numerical examples are presented to illustrate the theoretical results obtained in this paper.

Notation: Throughout the paper, for given real symmetric matrices X and Y, $X > Y$ ($X \geq Y$) means that $X - Y$ is positive definite (positive semi-definite). I is the identity matrix of appropriate dimension, A^{T} represents the transpose of matrix A. Set $\langle l\rangle = \{1, 2, \ldots, l\}$ for any positive integer l. Ω is a compact set in the vector space $\mathbb{R}^n$ with smooth boundary $\partial\Omega$. Let $C^1(X, \mathbb{R}^n)$ be the Banach space of functions which map X into $\mathbb{R}^n$ and have the continuous first derivatives. We define a pair of norms on $C^1(X, \mathbb{R}^n)$ and $C^1([-d, 0] \times \Omega, \mathbb{R}^n)$ by $\|\cdot\|$ as follows:

$$\| y(x)\| = \left(\int_{\Omega} y(x)^{\mathrm{T}} y(x)\mathrm{d}x \right)^{1/2}$$

and

$$\| \phi(t, x)\|_d = \max\left\{ \sup_{-d\leq t\leq 0} \| \phi(t, x)\|, \sup_{-d\leq t\leq 0} \left\| \frac{\partial \phi(t, x)}{\partial t} \right\|, \max_{1\leq k\leq n} \sup_{-d\leq t\leq 0} \left\| \frac{\partial \phi(t, x)}{\partial x_k} \right\| \right\},$$

respectively. Let $\mathrm{diag}(\cdots)$ and $\mathrm{col}(\cdots)$ be the (block) diagonal matrix and column matrix formed by the elements in brackets, respectively.

2. Problem formulation and preliminaries

This paper considers the following DRDGRNs [19]:

$$\begin{cases} \dfrac{\partial \widetilde{m}(t, x)}{\partial t} = \sum_{k=1}^{l} \frac{\partial}{\partial x_k}\left(D_k \dfrac{\partial \widetilde{m}(t, x)}{\partial x_k} \right) - A\widetilde{m}(t, x) + Wg(\widetilde{p}(t - \sigma(t), x)) + q, \\ \dfrac{\partial \widetilde{p}(t, x)}{\partial t} = \sum_{k=1}^{l} \frac{\partial}{\partial x_k}\left(D_k^* \dfrac{\partial \widetilde{p}(t, x)}{\partial x_k} \right) - C\widetilde{p}(t, x) + B\widetilde{m}(t - \tau(t), x), \end{cases} \tag{1}$$

where

$A = \mathrm{diag}(a_1, a_2, \ldots, a_n)$, $B = \mathrm{diag}(b_1, b_2, \ldots, b_n)$, $C = \mathrm{diag}(c_1, c_2, \ldots, c_n)$,

$q = \mathrm{col}(q_1, q_2, \ldots, q_n)$, $W := [w_{ij}] \in \mathbb{R}^{n\times n}$, $D_k = \mathrm{diag}(D_{1k}, D_{2k}, \ldots, D_{nk})$,

$D_k^* = \mathrm{diag}(D_{1k}^*, D_{2k}^*, \ldots, D_{nk}^*)$;

$\widetilde{m}(t, x) = \mathrm{col}(\widetilde{m}_1(t, x), \widetilde{m}_2(t, x), \ldots, \widetilde{m}_n(t, x))$,

$\widetilde{p}(t, x) = \mathrm{col}(\widetilde{p}_1(t, x), \widetilde{p}_2(t, x), \ldots, \widetilde{p}_n(t, x))$,

$g(\widetilde{p}(t, x)) = \mathrm{col}(g(\widetilde{p}_1(t, x)), g(\widetilde{p}_2(t, x)), \ldots, g(\widetilde{p}_n(t, x)))$;

$x = \mathrm{col}(x_1, x_2, \ldots, x_l) \in \Omega \subset \mathbb{R}^l$, $\Omega = \{x \| x_k\| \leq L_k, k \in \langle l\rangle\}$, $L_1, L_2, \ldots, L_l$ are constants; $D_{ik} > 0$ and $D_{ik}^* > 0$ denote the diffusion rate matrices; $\widetilde{m}_i(t, x)$ and $\widetilde{p}_i(t, x)$ are the concentrations of mRNA and protein of the ith node, respectively; a_i and c_i are degradation rates of the mRNA and protein, respectively; b_i is a constant; W represents the coupling matrix, which is defined as follows:

$$w_{ij} = \begin{cases} \gamma_{ij}, & \text{if } j \text{ is an activator of gene } i, \\ -\gamma_{ij}, & \text{if } j \text{ is a repressor of gene } i, \\ 0, & \text{if there is no link from gene } j \text{ to } i, \end{cases}$$

here γ_{ij} is the dimensionless transcriptional rate of transcription factor j to gene i; g_j is the activation function of the form $g_j(s) = \frac{s^H}{1+s^H}$, where H is the Hill coefficient; $q_i = \Sigma_{j\in I_i}\gamma_{ij}$, I_i is the set of all the nodes which are repressors of gene i; $\sigma(t)$ and $\tau(t)$ are time-varying delays satisfying

$$0 \leq \tau(t) \leq \overline{\tau}, \quad \dot{\tau}(t) \leq \mu_\tau, \quad 0 \leq \sigma(t) \leq \overline{\sigma}, \quad \dot{\sigma}(t) \leq \mu_\sigma, \tag{2}$$

where $\overline{\tau}$, $\overline{\sigma}$, μ_τ and μ_σ are non-negative real numbers.

Let $(m^*(x), p^*(x))$ is the unique equilibrium solution of DRDGRN (1), that is,

$$\begin{cases} 0 = \sum_{k=1}^{l} \dfrac{\partial}{\partial x_k}\left(D_k \dfrac{\partial m^*(x)}{\partial x_k} \right) - Am^*(x) + Wg(p^*(x)) + q, \\ 0 = \sum_{k=1}^{l} \dfrac{\partial}{\partial x_k}\left(D_k^* \dfrac{\partial p^*(x)}{\partial x_k} \right) - Cp^*(x) + Bm^*(x). \end{cases}$$

Set $m(t, x) = \widetilde{m}(t, x) - m^*(x)$ and $p(t, x) = \widetilde{p}(t, x) - p^*(x)$. Then DRDGRN (1) is transformed to

$$\begin{cases} \dfrac{\partial m(t, x)}{\partial t} = \sum_{k=1}^{l} \dfrac{\partial}{\partial x_k}\left(D_k \dfrac{\partial m(t, x)}{\partial x_k} \right) - Am(t, x) + Wf(p(t - \sigma(t), x)), \\ \dfrac{\partial p(t, x)}{\partial t} = \sum_{k=1}^{l} \dfrac{\partial}{\partial x_k}\left(D_k^* \dfrac{\partial p(t, x)}{\partial x_k} \right) - Cp(t, x) + Bm(t - \tau(t), x), \end{cases} \tag{3}$$

where

$$\begin{aligned} f(p(s, x)) &= \mathrm{col}(f_1(p_1(s, x)), \ldots, f_n(p_n(s, x))), f_i(p_i(s, x)) \\ &= g_i(p_i(s, x) + p_i^*) - g_i(p_i^*), \quad i \in \langle n\rangle. \end{aligned}$$

In this paper, the following initial conditions and Dirichlet boundary conditions associated with DRDGRN (3) are considered:

$$\begin{aligned} &m_i(t, x) = \phi_i(t, x), \quad p_i(t, x) = \phi_i^*(t, x), \quad x \in \Omega, \quad t \in [-d, 0], \\ &i \in \langle n\rangle, m_i(t, x) = 0, \quad p_i(t, x) = 0, \quad x \in \partial\Omega, \quad t \in [-d, +\infty), \\ &i \in \langle n\rangle, \end{aligned}$$

where $d = \max\{\overline{\sigma}, \overline{\tau}\}$, and $\phi_i(t, x)$, $\phi_i^*(t, x) \in C^1([-d, 0] \times \Omega, \mathbb{R}^n)$.

As shown in Introduction, it is important to estimate the exact concentrations of the mRNAs and proteins based on the available measurement. For this end, in the following we assume that the network outputs are

$$z_m(t, x) = Mm(t, x), \quad z_p(t, x) = Np(t, x), \tag{4}$$

where M and N are known constant matrices of appropriate sizes, and $z_m(t, x)$ and $z_p(t, x)$ are the network outputs.

The aim of this paper is to estimate the states of DRDGRN (3) by employing the following state observer: