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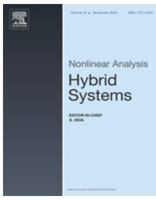

Stability analysis of the differential genetic regulatory networks model with time-varying delays and Markovian jumping parameters

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ABSTRACT

In this paper, we investigate the stability and robust stability criteria for genetic regulatory networks with interval time-varying delays and Markovian jumping parameters. The genetic regulatory networks have a finite number of modes, which may jump from one mode to another according to the Markov process. By using Lyapunov–Krasovskii functional, some sufficient conditions are derived in terms of linear matrix inequalities to achieve the global asymptotic stability in the mean square of the considered genetic regulatory networks. Two numerical examples are provided to illustrate the usefulness of the obtained theoretical results.

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1. Introduction

In the two decades, Genetic Regulatory Networks (GRNs) have been playing an important role in biological and biomedical sciences as they explain the interactions between genes and proteins. With the study of GRNs, scientists gain insight into the underlying process of living systems at the molecular level in order to possibly control the complex mechanisms that regulate biological functions in living organisms. Accordingly, the dynamic behaviors of the GRNs in living organisms have recently received increasing attention [1–3]. GRNs can be described by two types of models, the Boolean networks models [4,5] and differential equation models [6,7]. Recently, the differential models have received an increasing amount of research attention since it can provide detailed understanding of the nonlinear behavior exhibited by biological systems.

For a living cell to function efficiently there should be a tight control on its gene expression for translating the genetic information (nucleic acids) to a gene product (protein). Normally, the gene regulatory network (GRN), which comprises different segments of DNA, interacts directly/indirectly through gene products and other substances (inputs) in a cell for its gene expression as mRNAs and proteins (outputs). GRN controls the rate and level of informational processing of gene expression within cells through feedback and/or feed-forward regulatory inputs and thereby controls the cellular metabolic and functional behaviors. The increased output signal (gene product) leads to feed-back inhibition of GRN and the excess of input signal (molecules and proteins) governs the feed-forward process of GRN [8]. Therefore, a significant attention has been given to dynamical behaviors of GRNs (see e.g., [9–15]).

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On the other hand, many dynamical systems depend not only on their present states but also involve the past ones, which are called as time-delay systems. Some recent work on delay-dependent stability analysis for neural networks and bidirectional associative memory neural networks have been studied in [16–18]. Due to slow biochemical reactions in gene regulation processes such as transcription, translation and translocation, time-delay is commonly encountered. We should mention here that several important results for GRN with time-delays have been reported in the existing literature (see, e.g. [19,20]). In [21], the authors studied stochastic delay differential equations to describe the dynamics of GRNs with time-delay and developed a delayed chemical master equation to represent the biological reactions. On the other hand, when constructing a dynamical model, the intrinsic noise and extrinsic noise may transport the parameter uncertainties. Such parameter uncertainties could be external perturbations, parameter fluctuation or data error which make changes on the dynamical behaviors of the model. In this regard, many researchers studied the stability analysis of uncertain GRNs with time-delays.

Recently, the dynamical system with Markovian jumping becomes an interesting topic due to random changes in their structure, such as component failures/repairs, sudden environmental disturbance, and changing subsystem interconnections. The jumping system, a category of the stochastic hybrid system, has two components $x(t)$ and $r(t)$. $x(t)$ denotes the state and $r(t)$ is a continuous-time Markov chain with a finite state space $\mathcal{S} = \{1, 2, \ldots, N\}$, which is usually regarded as the mode. Recently, some researchers draw attention to studying the stochastic stability problem of GRN with Markovian jumping (see e.g., [22–27]). In this regard, the authors in [23–25] proposed delay-dependent sufficient conditions that guarantee the stability of GRNs with Markovian jumping parameters. Moreover, the problem of state estimation and H_∞ filter design of GRNs with Markovian jumping parameters are reported in [1,27].

In the existing literature, most of the authors considered the range of the time-delay $\tau(t)$ is varying from 0 to an upper bound τ^* $(0 \le \tau(t) \le \tau^*)$ [28–30]. However, in many practical cases, the delay may typically exist in an interval, that is, the range of delay varies in an interval for which the lower bound is not restricted to 0. For this reason many researchers have investigated the stability analysis of GRNs with interval time-varying delays, (see e.g., [31–35]). However, only few authors provided “improved” stability conditions for a GRN with time-varying delays. The authors in [31] derived a new stability criterion for uncertain genetic networks with interval time-varying delays by choosing an appropriate Lyapunov functional and employing some free-weighting matrices. Subsequently, improved stability criteria have been proposed for GRNs with interval time delays in [32]. Recently, the authors in [34,35] addressed a new type of uncertainty namely linear fractional uncertainty for the GRN. Also, the authors in [36] provided a less conservative result for static neural networks with interval time-varying delay. The Lyapunov functional that contains more information about the lower bound of the delay is proposed in [36]. However, to the best of our knowledge, there is no work dealing with the stability analysis of GRNs with linear fractional uncertainties, interval time-varying delays and Markovian jumping parameters available in the existing literature.

Motivated by the above discussions and to fill this gap, in the present paper, we study the stability analysis of the delayed differential GRNs model with linear fractional uncertainties and Markovian jumping parameters. We establish a suitable Lyapunov–Krasovskii functional which involves double and triple integral terms. The derived sufficient stability conditions are expressed in terms of linear matrix inequalities (LMIs) that can be easily solved by the MATLAB LMI control toolbox. The information about the lower bound of the delay is fully used in the Lyapunov–Krasovskii functional.

To ease the analysis, we introduce the following notations:

Notations 1. *$\mathbb{R}^n$ and $\mathbb{R}^{n\times n}$ denote the n-dimensional Euclidean space and the set of all $n \times n$ real matrices respectively. The superscript T denotes the transposition and the notation $X \ge Y$ (similarly, $X > Y$), where X and Y are symmetric matrices, means that $X - Y$ is positive semi-definite (similarly, positive definite). For a matrix A, $\lambda_{\min}(A)$ denotes the minimum eigenvalues of A. For $\tau > 0$, $C([-\tau, 0]; \mathbb{R}^n)$ denotes the family of continuous functions φ from $[-\tau, 0]$ to $\mathbb{R}^n$ with the norm $\varphi = \sup_{-\tau\le s\le 0} \|\varphi(s)\|$. Let $(\Omega, \mathcal{F}, \{\mathcal{F}_t\}_{t\ge 0}, \mathcal{P})$, be a complete probability space with a filtration $\{\mathcal{F}_t\}_{t\ge 0}$ satisfying the usual conditions and $\mathcal{E}$ stands for the mathematical expectation. Denote by $L^2_{\mathcal{F}_0}([-\tau, 0], \mathbb{R}^n)$ the family of all bounded, $\mathcal{F}_0$-measurable, $C([-\tau, 0], \mathbb{R}^n)$-valued random variables $\xi = \{\xi(\theta) : -\tau \le \theta \le 0\}$ such that $\int_{-\tau}^{0} |\mathcal{E}(s)|^2 ds < \infty$. Matrices, if their dimensions are not explicitly stated, are assumed to be compatible for algebraic operations.* diag$\{\cdots\}$ *stands for a block diagonal matrix. The notation $*$ always denotes the symmetric block in one symmetric matrix.*

2. Problem description and preliminaries

Consider the differential GRNs model with time delays, containing n mRNAs and n proteins, of the form [9]:

$$\begin{cases} \dot{m}_i(t) = -a_i m_i(t) + b_i(p_1(t-h(t)), p_2(t-h(t)), \ldots, p_n(t-h(t))), \\ \dot{p}_i(t) = -c_i p_i(t) + d_i m_i(t-\tau(t)), \quad i = 1, 2, \ldots, n, \end{cases} \tag{1}$$

where $m_i(t), p_i(t)$ are the concentrations of mRNA and protein of the ith node at time t, respectively. In this network, there is one output but multiple inputs for a single node or gene. a_i and c_i are the degradation rates of the mRNA and protein, respectively. d_i is the translation rate, and $b_i(\cdot)$ is the regulatory function of the ith gene. The regulatory function is of the form $b_i(p_1(t), p_2(t), \ldots, p_n(t)) = \sum_{j=1}^{n} b_{ij}(p_j(t))$, which is also called SUM logic [10,11]. The function $b_{ij}(p_j(t))$ is a monotonic

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