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Robust stability analysis of stochastic delayed genetic regulatory networks with polytopic uncertainties and linear fractional parametric uncertainties ☆

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ABSTRACT

This study examines the problem of robust stability of uncertain stochastic genetic regulatory networks with time-varying delays. The system's uncertainties are modeled as both polytopic form and structured linear fractional form. Based on a novel augmented Lyapunov–Krasovskii functional and different integral approaches, new stability conditions have been derived. Furthermore, these stability criteria can be applicable to both fast and slow time-varying delays. Finally, a numerical example is presented to illustrate the effectiveness of the proposed stability conditions.

1. Introduction

Genetic regulatory networks (GRNs) explicitly explain how a genomic sequence encodes the regulation of gene expression. Genes codes are essential for the development and functioning of an organism. Therefore, GRNs have received great attention over the past few years [1–4].

It is a well known fact that the processes of transcription and translation are not instantaneous, hence they introduce time delays in the GRNs. In order to have a more accurate model, time delays need to be included in the genetic regulatory processes [5–17,20,21]. So far in the literatures, the delay stability criteria are often classified into two categories according to their dependence on the size of the delays, namely, delay-independent stability criteria and delay-dependent stability criteria. The delay-independent condition is more conservative, especially for small delays.

Besides, there are many stochastic perturbations that affect the stability of GRNs, such as an intrinsic noise which is derived from the random births and deaths of individual molecules, and an extrinsic noise which is due to environment fluctuations. Therefore, it is of a great significance to study the stochastic effects on the stability of GRNs [5,13,14,16,18].

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Moreover, an uncertainty in the mathematical modeling is unavoidable due to external perturbations, parameter fluctuations, data errors, etc. That is to say we should investigate the stability of GRNs with parameter uncertainties. The most common uncertainty considered in GRNs is a norm bounded one which has been investigated in [5,6,9,12,13,16,17]. The other two important types of uncertainties are polytopic uncertainties and linear fractional uncertainties. Recently, Ref. [19] have studied the polytopic uncertainties and linear fractional uncertainties have been investigated in [22].

Motivated by the above discussion, we construct a new differential equation model for the delayed stochastic GRNs with both polytopic uncertainties and linear fractional parametric uncertainties. In this study, we choose an appropriate new Lyapunov–Krasovskii functional and use different approaches for handling different types of integral terms. Finally, a numerical example is given to demonstrate the effectiveness and advantages of the proposed results via the Matlab LMI toolbox.

The main contributions of this paper are listed in the following. The first one is the choose of Lyapunov–Krasovskii functional $V_1(t,x_t,y_t,\lambda)$ and $V_2(t,x_t,y_t,\lambda)$ which are more general than the common ones. We consider the integral terms $\int_{t-\tau_1}^{t} x(s)\mathrm{d}s$, $\int_{t-\tau_2}^{t-\tau_1} x(s)\mathrm{d}s$, $\int_{t-\sigma_1}^{t} y(s)\mathrm{d}s$ and $\int_{t-\sigma_2}^{t-\sigma_1} y(s)\mathrm{d}s$ as augmented terms. In this way, more information on state variables for the Lyapunov–Krasovskii functional can be utilized. Second, we employ different approaches to deal with different integral terms according to their dissimilarity. Last but not the least, we aim at introducing polytopic uncertainty and linear fractional parametric uncertainty in GRNs. As it is introduced in Ref. [29], polytopic uncertainty exist in many real systems. When we have some prior structural information on the uncertainty, the polytopic uncertainty can arise. Therefore, the polytopic type uncertainty can be regarded as an important class of parameter uncertainty. On the other hand, the linear fractional parametric uncertainty include the norm bounded uncertainty as a special case. Thus, the linear fractional uncertainties are more general than the norm bounded uncertainty. To the best of our knowledge, there is no existing result concerning GRNs with both polytopic uncertainties and linear fractional parametric uncertainties.

Notations: The notations used throughout the paper are fairly standard. The superscript 'T' stands for matrix transposition; R^n denotes the n-dimensional Euclidean space; $R^{n\times m}$ is the set of all $n\times m$ real matrices; the notation $P>0$ means that P is a positive definite matrix; I_n and $0_{n\times n}$ represent identity matrix and zero matrix with dimension n, respectively; diag $\{\cdot\}$ denotes the diagonal matrix; $E\{\cdot\}$ denotes the expectation operator; $col\{\cdot\}$ means a column vector. In symmetric block matrices, we use an asterisk $(*)$ to represent a term that is induced by symmetry. Matrices, if their dimensions are not explicitly stated, are assumed to be compatible for algebraic operations.

2. Problem formulation and some preliminaries

Generally, a GRN consists of a group of genes which interact and regulate the expression of other genes by proteins. A change in expression of a gene is controlled by the stimulation and inhibition of proteins in transcriptional, translational and post-translational processes. In [23], a single gene auto-regulatory genetic network with time delays containing n mRNAs and n proteins can be described by the following equations:

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

where $m_i(t), p_i(t)$ are 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. In (1), a_i and c_i are the degradation rates of the mRNA and protein, respectively. d_i is the translation rate, $b_i(\cdot)$ 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 called SUM logic [24]. The function $b_{ij}(p_j(t))$ is a monotonic function of the Hill form, that is,

$$b_{ij}(p_j(t)) = \begin{cases} \alpha_{ij}\dfrac{\left(p_j(t)/\beta_j\right)^{H_j}}{1+\left(p_j(t)/\beta_j\right)^{H_j}} & \text{if transcription factor } j \text{ is an activator of gene } i \\ \alpha_{ij}\dfrac{1}{1+\left(p_j(t)/\beta_j\right)^{H_j}} & \text{if transcription factor } j \text{ is a repressor of gene } i \end{cases}$$

where H_j is the Hill coefficient, β_j is a positive constant, and α_{ij} is the dimensionless transcriptional rate of transcription factor j to gene i, which is a bounded constant. Therefore, (1) can be rewritten into the following form:

$$\begin{cases} \dot{m}_i(t) = -a_i m_i(t) + \sum_{j=1}^{n} w_{ij} h_j(p_j(t-\sigma(t))) + u_i \\ \dot{p}_i(t) = -c_i p_i(t) + d_i m_i(t-\tau(t)), \quad i=1,2,\ldots,n. \end{cases} \tag{2}$$

where $h_j(x) = (x/\beta_j)^{H_j}/(1+(x/\beta_j)^{H_j})$, u_i is defined as a basal rate, $u_i = \sum_{j\in I_i}\alpha_{ij}$ and I_i is the set of all the j which is a repressor of gene i. The matrix $W=(w_{ij})\in\mathbb{R}^{n\times n}$ of the genetic network is defined as follows:

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

Rewriting the system (2) into a compact matrix form, we obtain