Stability of Genetic Regulatory Networks with Interval Time-Varying Delays via Convex Combination Method

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Abstract—In this paper, asymptotical stability of genetic regulatory networks with interval time-varying delays is investigated. By choosing an appropriate new Lyapunov functional and employing convex combination method to estimate the derivative of the Lyapunov functional, some new delay-range-dependent and delay-derivative-dependent/independent stability criteria are presented in terms of linear matrix inequalities (LMIs). The important feature is that the obtained stability criteria are applicable to both fast and slow time-varying delays due to the ranges for the time-varying delays have been carefully considered. Three numerical examples are used to demonstrate the usefulness of the main results and less conservativeness of the presented results.

Index Terms—Genetic Regulatory Networks; Asymptotical Stability; Interval Time-Varying Delays; LMIs; Convex Combination Method

I. INTRODUCTION

Genetic regulatory networks have become an important new area of research in the biological and biomedical sciences [1]. A genetic regulatory network is a dynamic system to describe highly complex interactions among two main species of gene product: mRNAs and proteins, in the interactive transcriptional and translational processes. Nowadays, in systems biology, one of the main challenges is to understand the genetic regulatory networks, for example, how biological activities are governed by the connectivity of genes and proteins.

During the past few years, there are two basic models for genetic network models, the Boolean model and the differential equation model [2-6]. In Boolean models, the expression of each gene in the network is assumed to be either ON or OFF and the state of a gene is determined by a Boolean function of the states of other related genes [6-7]. Several typical genetic regulatory networks have been modeled and studied experimentally and/or theoretically see [1, 3, 8-11] for some recent results.

Due to the completion of the transcription and translation of DNA, mRNA and the diffusion to a certain place of a protein need time, time delay is an inevitable occurrence in modeling gene regulation processes [12-13]. Therefore, it is of great significance to consider the stability of genetic regulatory networks with time-varying delays and sufficient conditions have been proposed to guarantee the asymptotic or robust stability for genetic regulatory networks [3, 14-18].

In [3], the authors propose a system of nonlinear differential equations with delays as a uniform frame to describe the genetic regulatory networks and studied the stability of a general genetic network model with time delays by using local stability analysis and characteristic equation analysis. In [15], by using the Lyapunov method and the Lur’e system approach, some stability criteria of the genetic networks with time delays and/or stochastic perturbations are derived. In [16], the stability of the genetic networks with noise perturbations and time delays is studied.

In practice, a time-varying interval delay is often encountered, that is, a time delay varies in an interval in which the lower bound is not restricted to be 0. In this case, the criteria in the previous work [15-16] are conservative because they do not take into account the information of the lower bounds of delays. Furthermore, the time-varying delays and are required to be differentiable and must be less than 1 which means that the criteria only allows the time-delays to be slowly time-varying functions.

In [17], a genetic regulatory network with interval time-varying delay is addressed. The restrictions on the derivatives of the time-varying delays are removed, which means that fast time-varying delays (without any constraints on the delay derivative) (see e.g. [20, 22, 24] and the references therein) are allowed. In [14], discrete-time versions of the continuous-time genetic regulatory networks with SUM regulatory functions are formulated and studied. Sufficient conditions are derived to ensure
the global exponential stability of the discrete-time genetic networks with delays. In [27], the authors investigate the delay-probability-distribution-dependent stability problem of uncertain stochastic genetic regulatory networks with mixed time-varying delays. In [28], the robust stability problem of stochastic genetic regulatory networks with interval time-varying delays and Markovian jumping parameters is investigated.

Recently, by employing convex combination method to estimate the derivative of the Lyapunov functional, some new stability criteria are presented in terms of linear matrix inequalities for neural networks [29-30]. In [29], by using a convex polyhedron method to estimate the derivative of the Lyapunov functional, some new delay-dependent stability for neural networks with two additive time-varying delay components are derived. In [30], by using the first-order convex combination property, a novel method is developed for the stability problem of a class of neural networks with time-varying delay. Compared to some existing ones, the stability criteria for neural networks in [29-30] is less conservative due to the facts that the convex combination method is employed. Up to now, as far as we know to the best of our knowledge, convex combination method has not been widely used in stability of genetic regulatory networks.

Motivated by the above discussions, we aim to analyze the stability of genetic regulatory networks with SUM logic in the forms of differential equations. Besides the basic case, we will make contributions on the issues of asymptotical stability for genetic networks with interval time-varying delays. By choosing an appropriate new Lyapunov functional and employing convex combination method, some less conservative delay-range-dependent and delay-derivative-dependent/independent stability criteria are derived based on the consideration of ranges for the time-varying delays. All the obtained criteria are given in terms of LMIs and are applicable to both fast and slow time-varying delays. Finally, three numerical examples are given to demonstrate the effectiveness and the merit of the proposed method.

Notations: The notations used throughout the paper are fairly standard. The superscript “T” stands for matrix transposition; \( \mathbb{R}^n \) denotes the n-dimensional Euclidean space; the notation \( P > 0 \) means that \( P \) is real symmetric and positive definite; \( I \) and \( 0 \) represent identity matrix and zero matrix. In symmetric block matrices or long matrix expressions, 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.

II. PROBLEM FORMULATION AND SOME PRELIMINARIES

Generally, a genetic regulatory network consists of a group of genes that interact and regulate the expression of other genes by proteins. The change in expression of a gene is controlled by the stimulation and inhibition of proteins in transcriptional, translational, and post-translational processes [11]. From [3], genetic regulatory networks with time delays containing of \( n \) mRNAs and \( n \) proteins can be described by the following equations:

\[
\begin{aligned}
\dot{m}_i(t) &= -a_im_i(t) + b_i(p_i(t - \sigma(t))) + \sum_{j=1}^{n}w_{ij}g_j(p_j(t - \sigma(t))) + u_i, \\
\dot{p}_i(t) &= -c_ip_i(t) + d_im_i(t - \tau(t)), \quad i = 1, 2, \ldots, n,
\end{aligned}
\]

where \( m_i(t), p_i(t) \in \mathbb{R}^+ \) are the concentrations of mRNA and protein of the \( i \)-th node. In this network, there is one output but multiple inputs for a single node or gene. In Eq.(1), \( a_i \) 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 \( i \)-th gene, which is a nonlinear function of the variables \( (p_1(t), p_2(t), \ldots, p_n(t)) \), but has a form of monotonicity with each variable [2, 5-6]. The gene activity is tightly controlled in a cell, and gene regulation function \( b_i(\cdot) \) plays an important role in the dynamics. Some genes can be activated by one of a few different possible transcription factors (“OR” logic). Other genes require that two or more transcription factors must all be bound for activation (“AND” logic). Here, we focus on a model of genetic networks where each transcription factor acts additively to regulate the \( i \)-th gene. The regulatory function \( b_i(p_i(t)) \) is a monotonic function of the Hill form [8, 23]. If transcription factor \( j \) is an activator of gene \( i \), then

\[
b_{ij}(p_i(t)) = \begin{cases} 
\frac{(p_i(t)/\beta_j)^{n_j}}{1 + (p_i(t)/\beta_j)^{n_j}}, & \text{if transcription factor } j \text{ is an activator of gene } i \\
\frac{1}{1 + (p_i(t)/\beta_j)^{n_j}}, & \text{if transcription factor } j \text{ is a repressor of gene } i
\end{cases}
\]

where \( H \) is the Hill coefficient, \( \beta_j \) is a positive constant, and \( a_{ij} \) is the dimensionless transcriptional rate of transcription factor \( j \) to gene \( i \), which is a bounded constant. Hence, Eq. (1) can be rewritten into the following form [15]:

\[
\begin{aligned}
\dot{m}_i(t) &= -a_im_i(t) + \sum_{j=1}^{n}w_{ij}g_j(p_j(t - \sigma(t))) + u_i, \\
\dot{p}_i(t) &= -c_ip_i(t) + d_im_i(t - \tau(t)), \quad i = 1, 2, \ldots, n,
\end{aligned}
\]

where \( g_j(x) = (x/\beta_j)^{n_j}/(1 + (x/\beta_j)^{n_j}) \), \( u_i = \sum_{j=1}^{n}a_{ij}V_{ij} \) and \( V_{ij} \) is the set of all the \( j \) which is a repressor of gene
The matrix is the coupling matrix $W = (w_{ij}) \in \mathbb{R}^{n \times m}$ of the genetic network, which is defined as follows: if transcription factor $j$ is an activator of gene $i$, $w_{ij} = \alpha_{ij}$; if there is no link from node $j$ to node $i$, $w_{ij} = 0$; if transcription factor $j$ is a repressor of gene $i$, $w_{ij} = -\alpha_{ij}$.

In other words, the matrix defines the coupling topology, direction, and the transcriptional rate of the genetic network.

In compact matrix form, Eq. (2) can be rewritten as

$$
\begin{align*}
\dot{m}(t) &= -Am(t) + Wg(p(t - \sigma(t))) + u, \\
\dot{p}(t) &= -Cp(t) + Dm(t - \tau(t)),
\end{align*}
$$

(3)

where

$$
m(t) = [m_{1}(t), m_{2}(t), ..., m_{n}(t)]^{T}, \\
p(t) = [p_{1}(t), p_{2}(t), ..., p_{l}(t)]^{T}, \\
A = \text{diag}\{a_{1}, a_{2}, ..., a_{l}\}, \\
C = \text{diag}\{c_{1}, c_{2}, ..., c_{n}\},
$$

(4)

$$
m(t - \tau(t)) = [m_{1}(t - \tau(t)), m_{2}(t - \tau(t)), ..., m_{n}(t - \tau(t))]^{T}, \\
g(p(t - \delta(t))) = [g_{1}(p_{1}(t - \sigma(t))), g_{2}(p_{2}(t - \sigma(t))), ..., g_{l}(p_{l}(t - \sigma(t)))]^{T}, \\
u = [u_{1}, u_{2}, ..., u_{l}]^{T}.
$$

For example, the dynamics of the repressilator which has been theoretically predicted and experimentally investigated in *Escherichia coli* [31] can be described. The repressilator is a cyclic negative-feedback loop comprising three repressor genes (*lacI*, *tetR* and *cl*) and their promoters. The kinetics of the system are determined by six coupled first-order differential equations. Taking into account the time delay for the proteins and mRNA, it has the form

$$
\begin{align*}
\dot{m}_{i}(t) &= -m_{i} + \frac{\alpha_{i}^{\text{rep}}}{1 + p_{j}^{\text{rep}}(t - \sigma(t))}, \\
\dot{p}_{i} &= -\beta_{i}^{\text{rep}}(p_{i} - m_{i}(t - \tau(t))).
\end{align*}
$$

(5)

where $m_{i}$ and $p_{i}$ are the concentrations of the three mRNAs and repressor-proteins, and $\beta > 0$ denotes the ratio of the protein decay rate to the mRNA decay rate. $n$ is the Hill coefficient. From above Eq. (4), we have,

$$
\begin{align*}
\dot{m}_{i}(t) &= -m_{i} + \frac{\alpha_{i}^{\text{rep}}}{1 + p_{j}^{\text{rep}}(t - \sigma(t))}, \\
\dot{p}_{i} &= -\beta_{i}^{\text{rep}}(p_{i} - m_{i}(t - \tau(t))).
\end{align*}
$$

In the following, we will always shift an inclined equilibrium point $(m^{*}, p^{*})$ of the system (3) to the origin by letting $x(t) = m(t) - m^{*}$, $y(t) = p(t) - p^{*}$. Hence, system (3) can be transformed into the following form:

$$
\begin{align*}
\dot{x}(t) &= -Ax(t) + Wf(y(t - \sigma(t))), \\
\dot{y}(t) &= -Cf(y(t)) + Df(x(t - \tau(t)),
\end{align*}
$$

(6)

where $x(t) = [x_{1}(t), x_{2}(t), ..., x_{n}(t)]^{T}$, $y(t) = [y_{1}(t), y_{2}(t), ..., y_{n}(t)]^{T}$, 

$$
f(y) = [f_{1}(y_{1}(t)), f_{2}(y_{2}(t)), ..., f_{n}(y_{n}(t))]^{T},
$$

with $f(y) = g(y(t) + p^{*}) - g(p^{*})$. Since $g_{i}$ is a monotonically increasing function with saturation, it satisfies, for all $x, y \in \mathbb{R}$ with $x \neq y$

$$
0 \leq \frac{g_{i}(x) - g_{i}(y)}{x - y} \leq k_{i}.
$$

(7)

From the relationship of $f(\cdot)$ and $g(\cdot)$, we know that $f(\cdot)$ satisfies the sector condition

$$
0 \leq f(x) \leq k_{i}.
$$

(8)

Thus, the genetic networks (6) can be seen as a kind of Lur’e system. By using the Lur’e system method in control theory, the genetic networks (3) can be investigated [23]. In this paper, we consider the following uncertain genetic networks with interval time-varying delays:

$$
\begin{align*}
\dot{x}(t) &= -Ax(t) + Wf(y(t - \sigma(t))), \\
\dot{y}(t) &= -Cy(t) + Dx(t - \tau(t)),
\end{align*}
$$

(9)

**Assumption 1.** The time-varying delays $\tau(t)$ and $\sigma(t)$ satisfy

$$
0 \leq \tau_{1} \leq \tau(t) \leq \tau_{2}, \quad 0 \leq \sigma_{1} \leq \sigma(t) \leq \sigma_{2},
$$

(10)

$$
(\dot{\tau}(t) \leq \mu, \quad \dot{\sigma}(t) \leq d),
$$

where $0 \leq \tau_{1} < \tau_{2}, 0 \leq \sigma_{1} < \sigma_{2}, \mu$ and $d$ are positive constants.

Now, we give the following lemmas that are useful in deriving our LMI-based stability criteria.

**Lemma 1.** [Schur complement] Given constant symmetric matrices $\Sigma_{1}, \Sigma_{2}$ and $\Sigma_{3}$, where $\Sigma_{i} = \Sigma_{i}^{T}$ and $0 < \Sigma_{1} \leq \Sigma_{2}$, then $\Sigma_{1} + \Sigma_{2} \Sigma_{1}^{-1} \Sigma_{3} < 0$ if and only if

$$
\begin{align*}
\Sigma_{1} &< 0, \\
\Sigma_{1}^{-1} &< 0.
\end{align*}
$$

**Lemma 2.** For any $z, y \in \mathbb{R}^{n \times m}$ and a positive scalar $\varepsilon$, the following inequality:

$$
2\varepsilon^{T} y \leq \varepsilon z^{T} z + \varepsilon^{2} y^{T} y
$$

holds.

**III. MAIN RESULTS**

Now, we are in the position to give the main results.

**Theorem 1.** For given scalars $0 \leq \tau_{1} < \tau_{2}, 0 \leq \sigma_{1} < \sigma_{2}, \mu$ and $d$, the system (8) is globally asymptotically stable, if there exist matrices

$$
P_{i} = P_{i}^{T} \geq 0, \quad k = 1, 2, 3, \quad Q_{i} = Q_{i}^{T} \geq 0, \quad r = 1, 2, 3, \quad R_{i} = R_{i}^{T} \geq 0, \quad i = 1, 2, 3, 4, \quad Z_{j} = Z_{j}^{T} > 0, \quad j = 1, 2, 3, 4
$$

$$
\Lambda = \text{diag}\{\lambda_{1}, \lambda_{2}, ..., \lambda_{m}\} \geq 0, \\
T_{j} = \text{diag}\{t_{j}, t_{j}, ..., t_{j}\} \geq 0, \quad j = 1, 2,
$$

$$
\begin{align*}
\dot{x}(t) &= -Ax(t) + Wf(y(t - \sigma(t))), \\
\dot{y}(t) &= -Cy(t) + Dx(t - \tau(t)),
\end{align*}
$$

(11)

where $x(t) = [x_{1}(t), x_{2}(t), ..., x_{n}(t)]^{T}$,
\( N_i, M_i, S_i, L_i, V_i, U_i, i = 1, 2, \ldots, 10 \) with appropriate dimensions, respectively, such that the following LMI

\[
\begin{bmatrix}
Y & \tau_i M & \tau_i L & \sigma_i S & \sigma_i V \\
* & -\tau_i Z_i & 0 & 0 & 0 \\
* & * & -\tau_i Z_2 & 0 & 0 \\
* & * & * & -\sigma_i Z_3 & 0 \\
* & * & * & * & -\sigma_i Z_4 \\
\end{bmatrix} < 0,
\]

(11) hold

\[
\begin{bmatrix}
Y & \tau_i M & \tau_i L & \sigma_i U & \sigma_i S \\
* & -\tau_i Z_i & 0 & 0 & 0 \\
* & * & -\tau_i Z_2 & 0 & 0 \\
* & * & * & -\sigma_i (Z_3 + Z_4) & 0 \\
* & * & * & * & -\sigma_i Z_4 \\
\end{bmatrix} < 0,
\]

(12)

where

\[ \tau_{i2} = \tau_i - \tau_1, \quad \sigma_{i2} = \sigma_i - \sigma_1, \]

\[
Y = \\
Y_{1,1} Y_{1,2} L_4 + M_3 - N_1 + M_4 S_1 + M_5 \quad Y_{1,6} \\
Y_{1,2} Y_{2,3} Y_{2,4} Y_{2,5} Y_{2,6} \\
Y_{2,3} - (1 - \mu_0) Q_1 + N_1 + N_1^T - L_4 - M_2 - M_2^T \\
Y_{2,3} = L_2 + N_3 - M_3 - L_7 \\
Y_{2,3} = N_2 + N_4 - M_4 - L_6 \\
Y_{2,3} = S_1 + P_2 D - M_5 + N_5 - L_7 \\
Y_{2,6} = U_2 - S_2 - V_2 - L_6 - M_6 + N_6 \\
Y_{3,3} = V_4 - L_7 - M_4 + N_7, Y_{3,8} = U_3 - L_8 - M_8 + N_8, \\
Y_{3,9} = Q_2 - M_4 - M_4^T, Y_{4,6} = U_4 - S_6 - V_4 - N_6, \\
Y_{3,6} = P C - C^T R_1 + R_2 + R_1, \\
Y_{5,6} = U_5 - S_5 - V_5 + S_5, \\
Y_{5,6} = -(1 - d) R_2 + U_6 + U_7 - S_6 - S_6^T - V_6 - V_7, \\
Y_{5,7} = V_6 + U_7 - S_7 - V_7, Y_{6,8} = U_8 - S_8 - V_8 - N_8, \\
Y_{6,9} = U_9 - S_9 - N_9, Y_{6,10} = K T_{12} + U_{10} - S_{10} - V_{10}, \\
Y_{10,10} = -(1 - d) R_2 - 2 T_1.
\]

**Proof.** The Lyapunov functional of system (8) is defined by:

\[
V(t) = V_1(t) + V_2(t) + V_3(t) + V_4(t),
\]

\[
\dot{V}_1(t) = x^T(t) P_1 x(t) + y^T(t) P_2 y(t) + 2 \sum_{i=0}^{\infty} \lambda_i \int_0^t f_i(s) ds,
\]

\[
\dot{V}_2(t) = \int_0^t \int_0^t x^T(s) Q_1 x(s) ds + \int_{-t}^0 x^T(\tau) Q_2 x(\tau) ds
\]

\[
+ \int_{-t}^0 \int_{-t}^0 x^T(\tau) Q_2 x(\tau) ds d\tau,
\]

\[
\dot{V}_3(t) = \int_{-t}^0 \int_{-t}^0 \int_{-t}^0 x^T(\tau) Z_3 x(s) ds d\tau d\theta.
\]

Calculating the derivative of \( V(t) \) with respect to \( t \) along the solutions of system (8), we get

\[
\dot{V}_1(t) = 2 x^T(t) P_1 x(t) + y^T(t) P_2 y(t) + 2 \sum_{i=0}^{\infty} \lambda_i \int_0^t f_i(s) ds,
\]

\[
\dot{V}_2(t) = \int_0^t \int_0^t x^T(s) Q_1 x(s) ds + \int_{-t}^0 x^T(\tau) Q_2 x(\tau) ds
\]

\[
+ \int_{-t}^0 \int_{-t}^0 x^T(\tau) Q_2 x(\tau) ds d\tau,
\]

\[
\dot{V}_3(t) = \int_{-t}^0 \int_{-t}^0 \int_{-t}^0 x^T(\tau) Z_3 x(s) ds d\tau d\theta.
\]
\[ V_i(t) = x^T(t)Q_i x(t) - (1 - \mu)x^T(t - \tau(t))Q_i x(t - \tau(t)) \\
+ y^T(t)R_i y(t) - (1 - d)y^T(t - \sigma(t))R_i y(t - \sigma(t)) \\
+ f^T(y(i))R_i f(y(i)) \\
- (1 - d)f^T(y(t - \sigma(t)))R_i f(y(t - \sigma(t))) \]

Thus for any \( T_j = \text{diag} \{ t_{i_1}, t_{i_2}, \ldots, t_{n_1} \} \geq 0, j = 1, 2 \), it follows that

\[ 0 \leq -2 \sum_{i=1}^{n} t_{i} f_i(y(i)) \left[ f_i(y(i)) - k_i y_i(t) \right] \\
-2 \sum_{i=1}^{n} t_{i} f_i(y(t - \sigma(t))) \left[ f_i(y(t - \sigma(t))) - k_i y_i(t - \sigma(t)) \right] \\
= -2 f^T(y(t))T_j f(y(t)) + 2y^T(t)KT_j f(y(t)) \\
-2 f^T(y(t))T_j f(y(t) - \sigma(t)) + 2y^T(t - \sigma(t))KT_j f(y(t) - \sigma(t)) \]

Combining (15)-(18) and adding the terms on the right side of (19)-(24) into the derivative of \( V(t) \)

\[ \dot{V}(t) \leq \xi^T(t) Y \xi(t) \]

\[ = -2 \xi^T(t) N \int_{t_{i_{\text{1}}}}^{t} \dot{x}(s) ds - 2 \xi^T(t) M \int_{t_{i_{\text{1}}}}^{t} \dot{x}(s) ds \\
-2 \xi^T(t) L \int_{t_{i_{\text{1}}}}^{t} \dot{y}(s) ds - 2 \xi^T(t) U \int_{t_{i_{\text{1}}}}^{t} \dot{y}(s) ds \\
-2 \xi^T(t) S \int_{t_{i_{\text{1}}}}^{t} \dot{y}(s) ds - 2 \xi^T(t) V \int_{t_{i_{\text{1}}}}^{t} \dot{y}(s) ds \\
-\int_{t_{i_{\text{1}}}}^{t} \dot{x}^T(s) \dot{z}_i(s) \dot{z}_i(s) ds \\
-\int_{t_{i_{\text{1}}}}^{t} \dot{y}^T(s) \dot{z}_i(s) \dot{z}_i(s) ds \\
= \xi^T(t) N \dot{x}(s) + \dot{z}_i(s) \dot{z}_i(s) ds \\
+ 2 \xi^T(t) \left[ (t_{i_{\text{1}}}) - (t_{i_{\text{1}}}) \right] M \dot{x}(s) ds \\
+ 2 \xi^T(t) \left[ (t_{i_{\text{1}}}) - (t_{i_{\text{1}}}) \right] U \dot{y}(s) ds \\
+ 2 \xi^T(t) \left[ (t_{i_{\text{1}}}) - (t_{i_{\text{1}}}) \right] S \dot{y}(s) ds \\
+ 2 \xi^T(t) \left[ (t_{i_{\text{1}}}) - (t_{i_{\text{1}}}) \right] V \dot{y}(s) ds \\
- \int_{t_{i_{\text{1}}}}^{t} \dot{x}^T(s) \dot{z}_i(s) \dot{z}_i(s) ds \\
- \int_{t_{i_{\text{1}}}}^{t} \dot{y}^T(s) \dot{z}_i(s) \dot{z}_i(s) ds \\
\leq \dot{V}(t) \left[ Y(t), \sigma(t) \right] \xi(t) \]

where \( Y(t) = Y + Y(t) + Y_{\sigma(t)} \) with
Thus, we have

\[ Y_1(\tau(t)) = (\tau_2 - \tau_1)N(Z_1 + Z_2)^{-1}N^T + \tau(t)MZ_1^{-1}M^T + (\tau(t) - \tau_1)LZ_2^{-1}L^T, \]

\[ Y_2(\sigma(t)) = (\sigma_2 - \sigma(t))U(Z_1 + Z_2)^{-1}U^T + \sigma(t)SZ_1^{-1}S^T + (\sigma(t) - \sigma_1)VZ_1^{-1}V^T. \]

If \( Y(\tau(t), \delta(t)) < 0 \), thus, we have

\[ V(t) \leq \zeta^T(t)Y(\tau(t), \sigma(t))\zeta(t) < 0 \] (27)

It follows from Lyapunov-Krasovskii stability theorem that the system (8) with interval time-varying delays is globally asymptotically stable.

Notice that \( Y_1(\tau(t)) \) is a convex combination of matrices \( N(Z_1 + Z_2)^{-1}N^T, MZ_1^{-1}M^T \) and \( LZ_2^{-1}L^T \) on \( \tau(t) \) satisfying \( 0 \leq \tau_1 < \tau(t) < \tau_2 \) and \( Y_2(\sigma(t)) \) is a convex combination of matrices \( U(Z_1 + Z_2)^{-1}U^T, SZ_1^{-1}S^T \) and \( VZ_1^{-1}V^T \) on \( \sigma(t) \) satisfying \( 0 \leq \sigma_1 < \sigma(t) < \sigma_2 \). Then

\[ Y(\tau(t), \delta(t)) < 0 \] only if

\[ Y(\tau_1, \delta_1) = Y + \tau_1MZ_1^{-1}M^T + (\tau_2 - \tau_1)LZ_2^{-1}L^T + \delta_1SZ_1^{-1}S^T \]

\[ + \delta_1SZ_1^{-1}S^T \]

\[ Y(\tau_2, \delta_1) = Y + \tau_1MZ_1^{-1}M^T + (\tau_2 - \tau_1)LZ_2^{-1}L^T + (\delta_2 - \delta_1)U(Z_1 + Z_2)^{-1}U^T + (\delta_2 - \delta_1)SZ_1^{-1}S^T < 0, \]

\[ Y(\tau_1, \delta_2) = Y + (\tau_2 - \tau_1)N(Z_1 + Z_2)^{-1}N^T + \tau_1MZ_1^{-1}M^T + \delta_2U(Z_1 + Z_2)^{-1}U^T + \delta_2SZ_1^{-1}S^T \]

\[ + (\delta_2 - \delta_1)U(Z_1 + Z_2)^{-1}U^T + (\delta_2 - \delta_1)SZ_1^{-1}S^T < 0. \]

Applying the Schur complement to the four inequalities above, we arrive at the LMIs (11)-(13).

**Remark 1.** Compared to some existing ones [27-28], the estimation of \( V(\tau_1) \) in the proof of Theorem 1 is less conservative due to the facts that the integrals terms. Therefore, the delay-dependent stability criterion is less conservative than the result in [17, 26, 28], in our Theorem 1, we choose the Lyapunov functional as

\[ V(t) = V_1(t) + V_2(t) + V_3(t) + V_4(t), \]

where

\[ V_1(t) = \dot{x}^T(t)P_1x(t) + \dot{y}^T(t)P_2y(t) + \sum_{i=1}^{n} \lambda_i \int_{0}^{\tau_i} f_i(s) ds, \]

\[ V_2(t) = \int_{0}^{\tau_1} \dot{x}^T(s)Q_1x(s) ds + \int_{0}^{\tau_1} \dot{y}^T(s)Q_2y(s) ds, \]

\[ V_3(t) = \int_{0}^{\tau_1} \dot{x}^T(s)Q_3x(s) ds + \int_{0}^{\tau_1} \dot{y}^T(s)Q_4y(s) ds + \int_{0}^{\tau_1} \dot{y}^T(s)R_1y(s) ds, \]

\[ V_4(t) = \int_{0}^{\tau_1} \dot{x}^T(s)R_2x(s) ds + \int_{0}^{\tau_1} \dot{y}^T(s)R_3y(s) ds. \]

Then, along a similar line as in the derivation of Theorem 1, we can derive the following stability result.

**Corollary 1.** For given scalars \( 0 < \tau_2, 0 < \sigma_2, \mu \) and \( d \), the system (8) is globally asymptotically stable, if there exist matrices \( P = P_1^T \geq 0, k = 1,2, \)

\[ Q_k = Q_k^T \geq 0, \quad r = 2,3, \quad R_k = R_k^T \geq 0, \quad i = 2,3,4, \]

\[ Z_j = Z_j^T > 0, \quad j = 1,3 \]

\[ \Lambda = diag \{ \lambda_1, \lambda_2, \ldots, \lambda_n \} \geq 0, \quad T_j = diag \{ t_1, t_2, \ldots, t_{\tau_j} \} \geq 0, \quad j = 1,2, \]

\[ N_j, M_j, S_j, U_j, i = 1,2,8 \] with appropriate dimensions, respectively, such that the following LMIs (28)-(31) hold

\[ \Upsilon \left[ \begin{array}{c} \tau_2M \quad \sigma_S \\ * -\tau_2Z_1 \quad 0 \\ * \quad -\sigma_Z_1 \end{array} \right] < 0, \] (28)

\[ \Upsilon \left[ \begin{array}{c} \tau_2M \quad \sigma_U \\ * -\tau_2Z_2 \quad 0 \\ * \quad -\sigma_Z_2 \end{array} \right] < 0, \] (29)

\[ \Upsilon \left[ \begin{array}{c} \tau_1N \quad \sigma_S \\ * -\tau_1Z_3 \quad 0 \\ * \quad -\sigma_Z_3 \end{array} \right] < 0, \] (30)

\[ \Upsilon \left[ \begin{array}{c} \tau_1N \quad \sigma_U \\ * -\tau_1Z_4 \quad 0 \\ * \quad -\sigma_Z_4 \end{array} \right] < 0, \] (31)
with
\[
Y_{11} = -P_1 A - A^T P_2 + Q_1 + Q_2 + M_1 + M_1^T, \\
Y_{12} = N_1 - M_1 + M_2 + Y_{1,5} = U_1 + M_5, \\
Y_{21} = -(1 - \mu) Q_2 + N_2 + N_2^T - M_2 - M_2^T, \\
Y_{22} = N_2 + N_3 - M_3, \ \\
Y_{3,3} = U_2 - S_2 - M_3 + N_4, \ \\
Y_{2,5} = -M_2 - \Delta D + N_7, \ \\
Y_{4,5} = U_4 - S_2 + S_1 + S_5, \ \\
Y_{5,5} = -(1 - \delta) R_2 + U_5 + U_5^T - S_1 - S_1^T, \\
Y_{6,6} = -U_6 + S_6 - N_6. \ \\
\]

**Remark 4.** By choosing \( Q_5 = R_5 = R = 0 \) in Theorem 1, we choose the Lyapunov functional as
\[
\bar{V}(t) = \bar{V}_1(t) + \bar{V}_2(t) + \bar{V}_3(t),
\]
where
\[
\bar{V}_1(t) = x^T(t) P_1 x(t) + y^T(t) P_2 y(t) + 2 \sum_{i=1}^{\infty} \lambda_i \int_0^t f_i(s) ds,
\]
\[
\bar{V}_2(t) = \int_0^t x^T(s) Q_1 x(s) ds + \int_0^t y^T(s) Q_2 y(s) ds
+ \int_{t-\delta}^t y^T(s) R_1 y(s) ds + \int_{t-\delta}^t y^T(s) R_1 y(s) ds
\]
\[
\bar{V}_3(t) = \int_{t-\delta}^t \bar{x}^T(s) Z_1 \bar{x}(s) ds \mathrm{d}s + \int_{t-\delta}^t \bar{y}^T(s) Z_2 \bar{y}(s) ds \mathrm{d}s
+ \int_{t-\delta}^t \bar{y}^T(s) \bar{y}(s) ds \mathrm{d}s.
\]

Then, along a similar line as in the derivation of Theorem 1, we can derive the following stability result.

**Corollary 2.** For given scalars \( 0 \leq \tau_1 < \tau_2, 0 \leq \sigma_1 < \sigma_2 \), the system (8) is globally asymptotically stable, if there exist matrices \( P_2 = P_2^T > 0, k = 1,2 \), \( Q = Q^T > 0 \), \( r = 1,2 \), \( R = R^T > 0 \), \( i = 1,2 \), \( Z_i = Z_i^T > 0 \), \( j = 1,2,3,4 \)

where
\[
\tau_2 = \tau_2 - \tau_1, \ \\
\sigma_2 = \sigma_2 - \sigma_1.
\]
with
\[ Y_{1,1} = -P_1A - A^T P_1 + Q_1 + Q_2 + M_1^T M_1, \]
\[ Y_{1,2} = -L_1 + N_1 - M_1 + M_2, \]
\[ Y_{1,6} = U_1 - S_1 - V_1 + M_6, \]
\[ Y_{2,3} = N_2 + N_2^T L_2 - L_2^T M_2 - M_2^T, \]
\[ Y_{2,4} = N_2 + N_4 - M_4 - L_4, \]
\[ Y_{2,5} = U_2 - S_2 - V_2 - L_6 - M_6 + N_6, \]
\[ Y_{2,7} = V_3 - L_4 - M_7 + N_7, \]
\[ Y_{2,8} = U_2 - L_4 - M_8 + N_8, \]
\[ Y_{2,9} = -M_9 - L_9 + AD + N_9, \]
\[ Y_{2,10} = -M_{10} - L_{10} + N_{10}, \]
\[ Y_{3,6} = U_3 - S_3 - V_3 + L_6, \]
\[ Y_{4,6} = U_4 - S_4 - V_4 - N_6, \]
\[ Y_{5,5} = -P_2C - C^T P_2 + R_1 + R_2 + S_5, \]
\[ Y_{5,6} = U_5 - S_5 - V_5 + S_6, \]
\[ Y_{6,6} = U_6 + U_6^T - S_6 - V_6 - V_6^T, \]
\[ Y_{6,7} = V_6 + U_7 - S_7 - V_7, \]
\[ Y_{6,8} = -U_6 + U_8 - S_8 - V_8 - N_8, \]
\[ Y_{6,9} = U_9 - S_9 - N_9, \]
\[ Y_{6,10} = KT_2 + U_{10} - S_{10} - V_{10}. \]

IV. NUMERICAL EXAMPLES

In this section, three examples are given to show the effectiveness and less conservativeness of our theoretical results.

Example 1. Consider system (8) with the parameters [17] listed as follows:
\[ A = diag \{3,3,3\}, \quad C = diag \{2.5,2.5,2.5\}, \]
\[ D = diag \{0.8,0.8,0.8\}, \]
\[ W = \begin{bmatrix} -2.5 & 0 & 0 \\ 0 & -2.5 & 0 \end{bmatrix}, \quad K = diag \{0.65,0.65,0.65\}, \]
\[ \tau = 17.53, \quad \sigma = 6.47. \]

It is noteworthy that the condition (24) in [17] and condition (44) in [26] is infeasible. However, solving LMI s (28)-(31) in Corollary 1, we can find that the system (8) described by Example 3 is globally asymptotically stable and get the feasible solution. Therefore it is clear to see that our method is less conservative and more effective than Ref. [17] and Ref. [26]. Limited to the length of the paper, we only provide a part of the feasible solution here.

\[
\begin{bmatrix}
1.3084 & 0.0011 & 0.0011 \\
0.0011 & 1.3084 & 0.0011 \\
0.0011 & 0.0011 & 1.3084
\end{bmatrix},
\end{equation}

\[
P_1 = 0.7240 -0.0006 -0.0006,
\]
\[
P_2 = -0.0006 0.7240 -0.0006.
\]

Example 3. Consider system (8) with the following parameters:
\[ A = diag \{4,2,2\}, \quad C = diag \{2,2,2\}, \quad D = diag \{1,1,1\}, \]
\[ W = \begin{bmatrix} -0.5 & 0 & 0 \\ 0 & -0.5 & 0 \end{bmatrix}, \quad K = diag \{0.65,0.65,0.65\}, \]
\[ \tau_1 = 2, \quad \tau_2 = 0.2, \quad \sigma_1 = 1.9, \quad \sigma_2 = 0.1. \]

Using LMI Control Toolbox, by our Theorem 1, we can find that the system (8) is globally asymptotically stable. Furthermore, we present the comparison with results obtained in [17] and [26] in following Table 1 and Table 2. Therefore it is clear to see that our method is less conservative and more effective than existing ones.

Example 2. Consider system (8) with the following parameters:

Using LMI Control Toolbox, by our Theorem 1, we can find that the system (8) described by Example 3 is globally asymptotically stable and get the feasible solution. As mentioned above, we only show a part of the feasible solution here.

\[
P_1 = \begin{bmatrix}
3.7636 & 0.0083 & 0.0160 \\
0.0083 & 5.4552 & 0.0107 \\
0.0160 & 0.0107 & 5.4536
\end{bmatrix},
\]
\[
P_2 = \begin{bmatrix}
2.8941 & 0.0216 & 0.0085 \\
0.0216 & 3.1982 & 0.0174 \\
0.0085 & 0.0174 & 3.1959
\end{bmatrix}.
\]

### Table I. Stability bounds of time-delay \( \tau \) for different \( \tau \) (\( \sigma_1 = 0.125, \sigma_2 = 0.25 \)).

<table>
<thead>
<tr>
<th>Method</th>
<th>( \tau_1 = 0.25 )</th>
<th>( \tau_1 = 0.5 )</th>
<th>( \tau_1 = 0.75 )</th>
<th>( \tau_1 = 1 )</th>
<th>( \tau_1 = 1.25 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ref[17]</td>
<td>0.52</td>
<td>0.77</td>
<td>1.02</td>
<td>1.27</td>
<td>1.52</td>
</tr>
<tr>
<td>Theorem 1</td>
<td>17.37</td>
<td>17.62</td>
<td>17.87</td>
<td>18.12</td>
<td>18.37</td>
</tr>
</tbody>
</table>

### Table II. Stability bounds of time-delay \( \sigma \) for different \( \sigma \) (\( \tau_1 = 0.25, \tau_2 = 0.5 \)).

<table>
<thead>
<tr>
<th>Method</th>
<th>( \sigma_1 = 0.5 )</th>
<th>( \sigma_1 = 1 )</th>
<th>( \sigma_1 = 1.5 )</th>
<th>( \sigma_1 = 2 )</th>
<th>( \sigma_1 = 2.5 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ref[17]</td>
<td>0.64</td>
<td>1.14</td>
<td>1.64</td>
<td>2.14</td>
<td>2.64</td>
</tr>
<tr>
<td>Ref[26]</td>
<td>4.23</td>
<td>4.28</td>
<td>4.72</td>
<td>5.22</td>
<td>5.72</td>
</tr>
<tr>
<td>Theorem 1</td>
<td>8.37</td>
<td>8.49</td>
<td>8.93</td>
<td>9.47</td>
<td>9.98</td>
</tr>
</tbody>
</table>
V. CONCLUSIONS

This paper presents some new results of stability analysis for genetic regulatory networks with interval time-varying delays. An appropriate Lyapunov functional is proposed to investigate the delay-range-dependent and delay-derivative-dependent/independent stability problem. The present results improve the existing ones due to a method to estimate the upper bound of the derivative of Lyapunov functional without ignoring some useful terms and the introduction of convex combination method into the proposed Lyapunov functional, which takes into account the relationship between the time-varying delays and their lower and upper bounds. The supplementary requirements that the time derivatives of time-varying delays must be less than one are removed. As a result, the new stability criteria in term of LMIs are applicable to both fast and slow time-varying delays. Three numerical examples show that the proposed criteria are effective and are an improvement over some existing results in the literature.

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