2010 IEEE International Symposium on Computer-Aided Control System Design
Part of 2010 IEEE Multi-Conference on Systems and Control
Yokohama, Japan, September 8-10, 2010

Investigating Stochastic Stability of Uncertain Genetic Networks via LMIs

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Abstract— **This paper addresses the problem of investigating stochastic stability of uncertain genetic networks with SUM regulatory functions. Specifically, the genetic network is assumed to be affected by Wiener processes, and its coefficients are parametrized by an unknown vector constrained in a hypercube. By using the square matricial representation (SMR) of matrix polynomials, it is shown that a condition for stochastic stability of the uncertain genetic network with disturbance attenuation guaranteed for all admissible values of the parameter can be derived in terms of linear matrix inequalities (LMIs). Some examples illustrate the proposed condition.**

I. INTRODUCTION

The study of genetic regulatory networks has become a fundamental challenge and accumulated a large amount of experimental data. It explains how genes and proteins interact to form a complex system that performs complicated biological functions [1]. Since genetic networks are biochemically dynamical systems, it is natural to model genetic networks by using dynamical system models which provide a powerful tool for studying gene regulation processes in living organisms. In the literature, genetic networks are classified into two types, i.e., the Boolean model (or discrete model) and the differential equation model (or continuous model) [2],[3],[4]. In Boolean models, the activity of each gene is expressed in one of two states, ON or OFF, and the state of a gene is determined by a Boolean function of the state of other related genes. In differential equation models, the variables describe the concentrations of gene products, such as mRNAs and proteins, as continuous values of the gene regulation system. See for example [5]-[10] and references therein for a wider categorization of genetic regulatory network models.

This paper focuses on the genetic regulatory networks which are described through differential equation models. In such models, the dynamics of each concentration is expressed by a function of all concentrations of the system. This function typically consists of two parts: a linear part which defines the natural decay rate of the concentration itself, and a nonlinear part which defines the influence by all the other concentrations. The nonlinear part can be described via SUM logic, where each transcription factor acts additively to regulate a gene, i.e., the regulatory function sums over all the inputs. Such a regulation by multiple promoters is indeed found in many gene systems. For further details see for example [11]-[13], [21], [22], [27], [28], [29].

Generally, gene regulation is an intrinsically noisy process, which is subject to intracellular and extracellular noise perturbations and environment fluctuations [14]-[18], [20]. Such stochastic noises may affect the dynamics of the entire biological system, both qualitatively and quantitatively. Moreover, some of the fluctuations in genetic networks are not entirely random, and the fluctuations are better described by the combination of noise perturbations and uncertainties, which makes the mathematical model uncertain. This means that one has to investigate the stability of an uncertain nonlinear system.

In this paper, we consider a genetic network model affected by stochastic noise and by parametric uncertainty. We assume that the noise is bounded by known functions, and that the uncertainty is constrained in a hypercube. We show that a condition for ensuring stochastic stability with disturbance attenuation for all admissible values of the uncertainty can be obtained in terms of a linear matrix inequality (LMI) feasibility test. This condition is derived by adopting polynomially parameter-dependent quadratic Lyapunov functions and the SMR of matrix polynomials introduced in [24]. See also [26] for details and algorithms about the SMR.

The paper is organized as follows. In Section II, we introduce some preliminaries about uncertain genetic regulatory network with stochastic noise, and the representation of matrix polynomials via the SMR. In Section III, we derive a sufficient condition for the stability of uncertain genetic networks with disturbance attenuation. In Section IV, we give several examples to illustrate the proposed condition. Finally, in Section V, we report some concluding remarks and possible extensions.

II. PRELIMINARIES

A. Problem formulation

Notation: I_n: $n \times n$ identity matrix; A^T: transpose of matrix A; $A > 0 (A \geq 0)$: symmetric positive definite (semidefinite) matrix A; $A \otimes B$: Kronecker product of matrices A and B; $\lceil c \rceil$: smallest integer greater than or equal to c; $\mathbf{E}(\cdot)$ denotes the expectation operator; $L_2[0,\infty)$ is the space of square-integrable vector functions over $[0,\infty)$; $\| \cdot \|$ stands for the Euclidean vector norm, and $\| \cdot \|_{L_2}$ stands for the usual $L_2[0,\infty)$ norm.

A genetic regulatory network affected by time-invariant parametric uncertainties can be modeled as follows:

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$$\begin{cases} \dot{m}(t) = A(\theta)m(t) + G(\theta)g(p(t)) + l(\theta) \\ \dot{p}(t) = C(\theta)p(t) + D(\theta)m(t) \\ \theta \in \Theta \end{cases} \quad (1)$$

where $m(t)$ and $p(t) \in \mathbb{R}^n$ are concentrations of mRNA and protein of the ith node. The functions $A(\theta), C(\theta), D(\theta), G(\theta) \in \mathbb{R}^{n\times n}$ and $l(\theta) \in \mathbb{R}^n$ are linear, with $A(\theta), C(\theta)$ diagonal and Hurwitz for each $\theta \in \Theta$, and $D(\theta)$ diagonal and positive definite for each $\theta \in \Theta$. $A(\theta)$ and $C(\theta)$ contain the degradation rates of the mRNA and protein, $G(\theta)$ is the coupling matrix of the genetic network, that defines the coupling topology, direction, and the transcriptional rate of the genetic network, $l(\theta)$ is defined as a basal rate.

In the genetic network (1), $\theta \in \mathbb{R}^r$ is the time-invariant uncertainty vector and Θ is the uncertainty set described by the hypercube

$$\Theta = \{\theta \in \mathbb{R}^r : \theta_i \in [0,1] \quad \forall i\}. \quad (2)$$

The function $g(p(t))$ is monotonically increasing with respect to $p(t)$ and its ith entry is given by

$$g_i(p(t)) = \frac{p_i(t)^H}{\beta^H + p_i(t)^H} \qquad \beta > 0,\ p_i(t) > 0 \quad \forall i \quad (3)$$

where H is the Hill coefficient and β is a positive constant. See for example [21] for details and illustrations of the structure and regulation mechanism of this genetic network.

Let $(m^*(\theta), p^*(\theta))$ be an equilibrium point of (1), i.e., a solution of the nonlinear equations

$$\begin{cases} A(\theta)m^*(\theta) + G(\theta)g(p^*(\theta)) + l(\theta) = 0_n \\ C(\theta)p^*(\theta) + D(\theta)m^*(\theta) = 0_n. \end{cases} \quad (4)$$

Let us shift the origin to the unknown equilibrium point $(m^*(\theta), p^*(\theta))$ by defining

$$\begin{cases} x = m - m^*(\theta) \\ y = p - p^*(\theta). \end{cases} \quad (5)$$

Thus, system (1) becomes

$$\begin{cases} \dot{x}(t) = A(\theta)x(t) + G(\theta)f(y(t), p^*(\theta)) \\ \dot{y}(t) = C(\theta)y(t) + D(\theta)x(t) \\ \theta \in \Theta \end{cases} \quad (6)$$

where the ith entry of the function $f(y(t), p^*(\theta))$ is

$$f_i(y(t), p^*(\theta)) = \frac{(y_i(t) + p_i^*(\theta))^H}{\beta^H + (y_i(t) + p_i^*(\theta))^H} - \frac{p_i^*(\theta)^H}{\beta^H + (p_i^*(\theta))^H}. \quad (7)$$

Since $g(p(t))$ is a monotonically increasing function with saturation, it satisfies

$$0 \le \frac{g(a) - g(b)}{a - b} \le k,\ \forall a, b \ge 0,\ a \ne b. \quad (8)$$

For all a,b $\in \mathbb{R}^n$ with a $\neq$ b, from the relationship of $f(\cdot)$ and $g(\cdot)$, we know that $f(\cdot)$ satisfies the sector condition $0 \le f(a)/a \le k$, or equivalently

$$f_i(a)[f_i(a) - ka] \le 0 \quad \forall i = 1, \ldots, n. \quad (9)$$

Since gene regulation is an intrinsically noisy process, an uncertain genetic regulatory network with disturbance attenuation can be modeled as follows [22]

$$\begin{cases} dx(t) = [A(\theta)x(t) + G(\theta)f(y(t), p^*(\theta))]dt \\ \qquad + \varphi(x(t), y(t))d\omega_1(t) + v(t)d\omega_2(t) \\ dy(t) = [C(\theta)y(t) + D(\theta)x(t)]dt \\ \quad \theta \in \Theta \end{cases} \quad (10)$$

where $\theta \in \mathbb{R}^r$, $\varphi(x(t), y(t)) \in \mathbb{R}^n$ is the noise intensity matrix and $v(t) \in \mathbb{R}^n$ belongs to $L_2[0, \infty)$. The quantities $\omega_1(t)$ and $\omega_2(t)$ are two independent one-dimensional Wiener processes, and Θ is given in (2).

We assume that $\varphi(x(t), y(t))$ satisfies

$$\varphi^T(x(t), y(t))\varphi(x(t), y(t)) \le x^T(t)H_1x(t) + y^T(t)H_2y(t). \quad (11)$$

for some positive definite matrices H_1, H_2.

For (10), if $v(t)$ does not vanish in the steady state, the network cannot achieve mean-square asymptotic stability. We give the definition below extending to the uncertain case the definition given in [22].

Definition: The network (10) is said to be stochastically stable with disturbance attenuation $\gamma(\theta)$ if the network is asymptotically stable in mean-square for $v(t) = 0$, and under zero initial conditions, we have

$$\| z(t) \|_{E_2} < \gamma(\theta) \| v(t) \|_{L_2} \quad (12)$$

for all nonzero $v(t)$, where

$$z(t) = \begin{bmatrix} x(t) \\ y(t) \end{bmatrix} \quad (13)$$

$$\| z(t) \|_{E_2} = \left[\mathbf{E} \left(\int_0^\infty \| z(t) \|^2 dt \right) \right]^{1/2}. \quad (14)$$

Problem 1: To establish if, for each $\theta \in \Theta$, the network (10) is stochastically stable with disturbance attenuation γ, i.e. to establish whether

$$\gamma(\theta) < \gamma \quad \forall \theta \in \Theta. \quad (15)$$

Problem 2: To find the worst case $\gamma(\theta)$, i.e.:

$$\gamma^* = \sup_{\theta \in \Theta} \gamma(\theta). \quad (16)$$

B. Representation of matrix polynomials

Let us introduce a key representation of polynomials. Let $s(x)$ be a polynomial in $x \in \mathbb{R}^q$ of degree $2m$. The square matricial representation (SMR) of $s(x)$ is defined as

$$s(x) = x^{\{m\}^T}(S + L(\alpha))x^{\{m\}}. \quad (17)$$

In (17), $x^{\{m\}} \in \mathbb{R}^{\sigma(q,m)}$ is a vector containing all monomials of degree less than or equal to m in x, S is any symmetric matrix $S \in \mathbb{R}^{\sigma(q,m)\times\sigma(q,m)}$ satisfying

$$s(x) = x^{\{m\}^T} S x^{\{m\}} \quad (18)$$

$L(\alpha)$ is a linear parameterization of the linear space.

$$\mathfrak{L} = \{L = L^T : x^{\{m\}^T} L x^{\{m\}} = 0 \quad \forall x \in \mathbb{R}^q\} \quad (19)$$

and $\alpha \in \mathbb{R}^{\mu(q,m)}$ is a vector of free parameters.

The length of $x^{\{m\}}$ is given by

$$\sigma(q,m) = \frac{(q+m)!}{q!m!} \tag{20}$$

whereas the length of α is given by

$$\mu(q,m) = \frac{1}{2}\sigma(q,m)[\sigma(q,m)+1] - \sigma(q,2m). \tag{21}$$

The SMR allows one to establish whether a polynomial $s(x)$ is a sum of squares of polynomials (SOS), indeed, $s(x)$ is SOS if and only if [19]

$$\exists \alpha : S + L(\alpha) \geq 0 \tag{22}$$

which is an LMI feasibility test, and hence a convex optimization problem.

For example, consider the polynomial of degree 4 in one variable

$$s(x) = 2 + 2x_1 + x_1^4. \tag{23}$$

Then, we have $m = 2$, $x^{\{m\}} = \begin{pmatrix} 1 \\ x_1 \\ x_1^2 \end{pmatrix}$ and

$$S = \begin{pmatrix} 2 & 1 & 0 \\ 1 & 0 & 0 \\ 0 & 0 & 1 \end{pmatrix}, \; L(\alpha) = \begin{pmatrix} 0 & 0 & -\alpha \\ 0 & 2\alpha & 0 \\ -\alpha & 0 & 0 \end{pmatrix}. \tag{24}$$

Similarly to what has been done for scalar polynomials, one can introduce the SMR for matrix polynomials. Let $M(x) \in \mathbb{R}^{n \times n}$ be a matrix polynomial of degree 2m in $x \in \mathbb{R}^q$. Then, $M(x)$ can be written as

$$M(x) = (x^{\{m\}} \otimes I_n)^T \bar{M} (x^{\{m\}} \otimes I_n) \tag{25}$$

where $\bar{M} \in \mathbb{R}^{n\sigma(q,m) \times n\sigma(q,m)}$ is a suitable matrix. Such a matrix is not unique and, indeed, all matrices $\bar{M}$ describing $M(x)$ are given by

$$\bar{M} + \bar{U} \qquad \bar{U} \in \mathscr{U} \tag{26}$$

where

$$\mathscr{U} = \{\bar{U} = \bar{U}^T \in \mathbb{R}^{n\sigma(q,m) \times n\sigma(q,m)} : (x^{\{m\}} \otimes I_n)^T \times \bar{U}(x^{\{m\}} \otimes I_n) = 0_{n \times n} \qquad \forall x \in \mathbb{R}^q\}. \tag{27}$$

The set $\mathscr{U}$ in (27) is a linear space of dimension

$$u(q,n,m) = \frac{1}{2} n \{\sigma(q,m)[n\sigma(q,m)+1] - (n+1)\sigma(q,2m)\}. \tag{28}$$

Let $\bar{U}(\alpha)$, $\alpha \in \mathbb{R}^{u(q,n,m)}$, be a linear parameterization of $\mathscr{U}$. The SMR of $M(x)$ is

$$M(x) = (x^{\{m\}} \otimes I_n)^T (\bar{M} + \bar{U}(\alpha))(x^{\{m\}} \otimes I_n). \tag{29}$$

The matrix polynomial $M(x)$ is said SOS if it can be written as

$$M(x) = \sum_i N_i(x)^T N_i(x) \tag{30}$$

for some matrix polynomials $N_i(x)$.

Then, $M(x)$ is SOS if and only if the following LMI holds [24]:

$$\exists \alpha : \bar{M} + U(\alpha) \geq 0. \tag{31}$$

See also [25], [26] for further details and for the gap between positive polynomials and SOS polynomials.

III. Stability conditions of uncertain genetic networks with noise perturbations

In this section, we study the stochastic stability of the uncertain genetic network model (10) via the SMR introduced in Section II-B.

Lemma 1: Given a scalar $\gamma > 0$, suppose that there are matrix functions $P_{11}(\theta)$, $P_{12}(\theta)$, $P_{22}(\theta)$, $\Lambda(\theta)$, and a function $\rho(\theta)$, such that the following conditions hold $\forall \theta \in \Theta$:

$$\begin{aligned}
&M(\theta) = \begin{bmatrix} (1,1) & (1,2) & P_{11}(\theta)G(\theta) \\ (1,2)^T & (2,2) & (2,3) \\ G^T(\theta)P_{11}(\theta) & (2,3)^T & -2\Lambda(\theta) \end{bmatrix} < 0 \\
&P(\theta) = \begin{bmatrix} P_{11}(\theta) & P_{12}(\theta) \\ P_{12}^T(\theta) & P_{22}(\theta) \end{bmatrix} > 0 \\
&P_{11}(\theta) \leq \rho(\theta) I \\
&\Lambda(\theta) = diag(\lambda_1(\theta), ..., \lambda_n(\theta)), \quad \lambda_i(\theta) > 0, \quad \forall i = 1, ..., n \\
&\rho(\theta) > 0
\end{aligned} \tag{32}$$

where

$$\begin{aligned}
(1,1) &= P_{11}(\theta)A(\theta) + A^T(\theta)P_{11}(\theta) + P_{12}(\theta)D(\theta) \\
&\quad + D(\theta)P_{12}^T(\theta) + \rho(\theta)H_1 + [\rho(\theta)/\gamma^2]I \\
(1,2) &= D(\theta)P_{22}(\theta) + A^T(\theta)P_{12}(\theta) + P_{12}(\theta)C(\theta) \\
(2,2) &= P_{22}(\theta)C(\theta) + C^T(\theta)P_{22}(\theta) + \rho(\theta)H_2 + [\rho(\theta)/\gamma^2]I \\
(2,3) &= P_{12}^T(\theta)G(\theta) + k\Lambda(\theta).
\end{aligned} \tag{33}$$

Then, the uncertain genetic network (10) is stochastically stable with disturbance attenuation γ.

The proof of this lemma follows the same line of the certain case considered in [22]. Let us observe that the condition of Lemma 1 requires to test feasibility of an infinite family of LMIs. In order to solve this problem, we can restrict our attention to polynomial matrix functions in (32).

Hence, let us consider that the functions $P(\theta)$, $M(\theta)$, $\Lambda(\theta)$ and $\rho(\theta)$ are matrix polynomials, in particular:

$$P(\theta) = P(\theta)^T \in \mathbb{P}(\delta, 2n) \tag{34}$$

$$M(\theta) = M(\theta)^T \in \mathbb{P}(\delta + 1, 3n) \tag{35}$$

$$\Lambda(\theta) = \Lambda(\theta)^T \in \mathbb{P}(\delta + 1, n) \tag{36}$$

$$\rho(\theta) \in \mathbb{P}(\delta + 1, 1) \tag{37}$$

where $\mathbb{P}(\eta, \zeta)$ is the set of matrix polynomials of degree η and size $\zeta \times \zeta$. Thus, by using the SMR, we can express $P(\theta)$, $M(\theta)$, $\lambda_i(\theta)$ and $\rho(\theta)$ as:

$$P(\theta) = (\theta^{\{m_1\}} \otimes I_{2n})^T \bar{P} (\theta^{\{m_1\}} \otimes I_{2n}) \tag{38}$$

$$M(\theta) = (\theta^{\{m_2\}} \otimes I_{3n})^T \bar{M} (\theta^{\{m_2\}} \otimes I_{3n}) \tag{39}$$

$$\lambda_i(\theta) = (\theta^{\{m_2\}} \otimes I_n)^T \bar{\Lambda}_i (\theta^{\{m_2\}} \otimes I_n) \tag{40}$$

$$\rho(\theta) = \theta^{\{m_2\}^T} \bar{R} \theta^{\{m_2\}} \tag{41}$$

where $m_1 = \lceil \frac{\delta}{2} \rceil$, $m_2 = \lceil \frac{\delta+1}{2} \rceil$, and $\bar{P}$, $\bar{M}$, $\bar{\Lambda}_i$ and $\bar{R}$ are symmetric matrices of suitable dimension. The vector $\theta^{\{m_2\}} \in \mathbb{R}^{\sigma(r,m_2)}$ contains all monomials of degree m_2 in θ.

Let $L(\alpha)$ be a linear parameterization of

$$\begin{aligned} \mathscr{L} = \{ L = L^T \in \mathbb{R}^{n\sigma(r,m_2) \times n\sigma(r,m_2)} : (\theta^{\{m_2\}} \otimes I_{3n})^T \\ \times L(\theta^{\{m_2\}} \otimes I_{3n}) = 0_{3n \times 3n} \quad \forall \theta \in \mathbb{R}^r \}. \end{aligned} \tag{42}$$

Let us define the matrix polynomial

$$T(\theta) = \sum_{i=0}^{r} \theta_i (1-\theta_i) (\theta^{\{m_2-1\}})^T U (\theta^{\{m_2-1\}}) \tag{43}$$

where $U = U^T$, and let $Z(U) = Z(U)^T$ be a linear matrix function satisfying

$$T(\theta) = (\theta^{\{m_2\}} \otimes I_{3n})^T Z(U) (\theta^{\{m_2\}} \otimes I_{3n}). \tag{44}$$

We have the following result.

Theorem 1: If there exist symmetric matrices $\bar{P}$, $\bar{\Lambda}_i$, $\bar{R}$, U and a vector α satisfying the following LMIs:

$$\begin{aligned} &\bar{P} > 0, \quad \bar{\Lambda}_i > 0, \quad \bar{R} > 0, \quad U > 0 \\ &\bar{M} + L(\alpha) + Z(U) < 0 \end{aligned} \tag{45}$$

where $L(\alpha)$ is a linear parameterization of the linear space described in (42), then (15) holds.

Proof: Suppose that (45) holds. Since $\bar{P} > 0$, one gets from (38) that:

$$P(\theta) > 0 \quad \forall \theta. \tag{46}$$

Similarly, one gets that

$$\lambda_i(\theta) > 0, \quad \rho(\theta) > 0 \quad \forall \theta. \tag{47}$$

Let us consider now $M(\theta)$. From (45), pre- and post-multiplying by $(\theta^{\{m_2\}} \otimes I_{3n})^T$ and $(\theta^{\{m_2\}} \otimes I_{3n})$, one gets

$$\begin{aligned} 0 &> (\theta^{\{m_2\}} \otimes I_{3n})^T (\bar{M} + L(\alpha) + Z(U)) (\theta^{\{m_2\}} \otimes I_{3n}) \\ &= M(\theta) + T(\theta) \end{aligned} \tag{48}$$

since

$$(\theta^{\{m_2\}} \otimes I_{3n})^T L (\theta^{\{m_2\}} \otimes I_{3n}) = 0_{3n \times 3n} \quad \forall \theta \in \mathbb{R}^r. \tag{49}$$

Consider any $\theta \in \Theta$. Since $U > 0$, from (43) we have

$$\begin{cases} \theta_i (1-\theta_i) \geq 0 \quad \forall i \\ (\theta^{\{m_2-1\}})^T U (\theta^{\{m_2-1\}}) > 0. \end{cases} \tag{50}$$

This implies that:

$$T(\theta) \geq 0 \quad \forall \theta \in \Theta. \tag{51}$$

Therefore, from (48) and (51) it follows that:

$$M(\theta) < 0 \quad \forall \theta \in \Theta. \tag{52}$$

Consequently, the condition of Lemma 1 holds since there exist $P(\theta)$, $\Lambda(\theta)$, and $\rho(\theta)$ fulfilling (32). Hence, $\gamma(\theta) < \gamma \quad \forall \theta \in \Theta$. $\square$

Theorem 1 provides a sufficient condition for Problem 1 via a LMI feasibility test. This condition has been obtained by exploiting polynomially parameter-dependent quadratic Lyapunov functions and the SMR of matrix polynomials.

From Theorem 1 one can obtain an upper bound of γ^* via a one-parameter sequence of LMI feasibility test. Indeed, let us define

$$\hat{\gamma}^* = inf \ \{\gamma : \ (45) \ holds \ for \ some \ \bar{P}, \ \bar{\Lambda}_i, \ \bar{R}, \ U, \ \alpha\}. \tag{53}$$

We have from Theorem 1 that:

$$\hat{\gamma}^* \geq \gamma^*. \tag{54}$$

The upper bound $\hat{\gamma}^*$ can be found in various way, e.g., via a bisection algorithm on the scalar γ where (45) is tested at each step.

IV. Examples

In this section, we present three examples to illustrate the proposed contidion.

A. Example 1

Let us consider system (10) with $H = 2$, $\beta = 1$, $n = 2$, $r = 1$ and

$$\begin{aligned} A(\theta) &= diag(-1 + 0.3\theta, -1) \\ C(\theta) &= diag(-1 - 0.2\theta, -1) \\ D(\theta) &= diag(1 + 0.3\theta, 1 + 0.2\theta) \\ G(\theta) &= \begin{bmatrix} 0 & -0.1 - 0.3\theta \\ 0.3 + 0.2\theta & 0 \end{bmatrix}. \end{aligned} \tag{55}$$

It is easy to know that k is less than 0.65 in the sector condition (8). Similarly to [22], we set the noise intensity as

$$\varphi(x(t), y(t)) = \begin{bmatrix} \varphi_1(x(t), y(t)) \\ \varphi_2(x(t), y(t)) \end{bmatrix} \tag{56}$$

with $\varphi_i(x(t), y(t)) = 0.05[x_i(t) + \sum_{j=1}^{2} y_j(t)]$ for all i. Condition (11) can hence be satisfied by choosing $H_1 = 0.2I_2$, $H_2 = 0.2I_2$. From Theorem 1, with the simple choice $\delta = 1$, we obtain $\hat{\gamma}^* = 1.5$.

B. Example 2

In this example we illustrate the application of the proposed results to an existing biological system, the repressilator investigated in *Escherichia coli* [23]. In this system, the repressilator is a cyclic negative-feedback loop comprising three repressor genes ($lacl, tetR$ and cl) and their promoters. The system has the form

$$\begin{cases} \dot{m}_i = -m_i + \dfrac{\alpha_i^{rep}}{1+p_j^H} \\ \dot{p}_i = -\beta_i^{rep}(p_i - m_i) \\ i = lacl, tetR, cl \\ j = cl, lacl, tetR \end{cases} \tag{57}$$

where m_i and p_i are the concentrations of the three mRNAs and repressor-proteins. In [21] this system has been investigated for a specific choice of the coefficients α_i^{rep} and β_i^{rep}. Here we consider the case of uncertain coefficients, in particular

$$\begin{array}{ll} \alpha_1^{rep} = 0.5 & \beta_1^{rep} = 1.5 \\ \alpha_2^{rep} = 1 & \beta_1^{rep} = 2.5 \\ \alpha_3^{rep} = 2.5 - 2.5\theta & \beta_1^{rep} = 3.5 \end{array} \tag{58}$$

Let us rewrite this repressilator in the form of the genetic network (10): we have $n = 3$, $r = 1$ and

$$A(\theta) = diag(-1,-1,-1)$$

$$G(\theta) = \begin{bmatrix} 0 & 0 & -0.5 \\ -1 & 0 & 0 \\ 0 & -2.5+2.5\theta & 0 \end{bmatrix}$$

$$C(\theta) = diag(-1.5,-2.5,-3.5)$$

$$D(\theta) = -C(\theta).$$

From Theorem 1, with the simple choice $\delta = 1$, we obtain $\hat{\gamma}^* = 2.1$.

C. Example 3

In this example we consider a more difficult case with larger state dimension. Let us consider (10) with $H = 2$, $\beta = 1$, $n = 4$, $r = 1$ and

$$A(\theta) = diag(-0.3, -0.8 - 0.5\theta, -1.5 - 0.4\theta, -0.8)$$

$$G(\theta)_{i,j} = \begin{cases} 0.5 + 0.5\theta & if(i,j) = (1,2) \\ -0.4 - 0.2\theta & if(i,j) = (2,3) \\ -0.3 - 0.1\theta & if(i,j) = (3,1) \\ 0.5 + 0.5\theta & if(i,j) = (4,3) \\ 0 & otherwise \end{cases}$$

$$C(\theta) = diag(-1.1 + 0.3\theta, -1.5, -0.8 - 0.3\theta, -1.3)$$

$$D(\theta) = diag(1, 1.4 + 0.2\theta, 0.6, 0.7 + 0.1\theta).$$

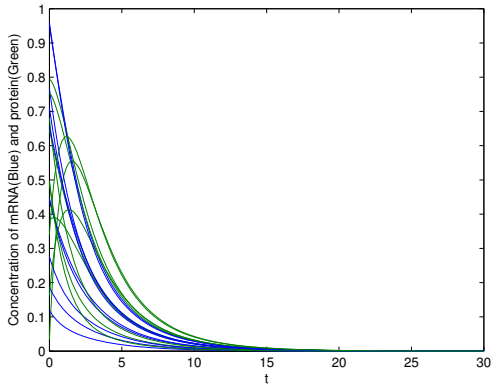

Fig. 1. Trajectories of the concentrations of mRNA and protein of the genetic network.

With the simple choice of $H = 2$, $\beta = 1$, $r = 1$, the trajectories of $m(t)$ and $p(t)$ of the uncertain genetic network are shown in Fig. 1 with different uncertainty parameter θ and different concentrations of mRNA and protein.

According to Theorem 1, with the simple choice $\delta = 1$, we easily obtain $\hat{\gamma}^* = 3.0$.

V. Conclusions

In this paper, we have addressed the problem of establishing stochastic stability of the uncertain genetic networks with SUM regulatory function. Specifically, by using the SMR of matrix polynomials, it has been shown that a condition for establishing stochastic stability of the uncertain genetic network with disturbance attenuation can be derived in terms of an LMI feasibility test.

Future work will be devoted to extend the proposed condition to the presence of time delays.

Acknowledgement

The authors would like to thank the Associate Editor and the Reviewers for their useful comments.

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