Robust Stability of Discrete-time Genetic Regulatory Networks with Reaction Diffusion

Chengye Zou, Yongwei Yang, Haifeng Li, Yubao Shang, Yunong Liu

Abstract-In the realm of discrete-time modeling for gene regulatory networks, significant focus has been placed on addressing the time lags inherent in the process of DNA transcription to RNA and the subsequent translation of mRNA to proteins. These temporal delays have been consistently incorporated into discrete gene regulatory network models. However, true gene regulatory networks are also subject to spatial variables, due to the uneven distribution of protein and mRNA concentrations. The integration of reaction-diffusion terms is thus essential to fully represent the impact of spatial dynamics on gene regulatory networks. In such networks, reaction-diffusion dynamics highlight the complex interactions between neighboring spatial regions, where closeness leads to mutual influences on their functional activities. Based on this conceptual groundwork, this study introduces a discrete-time gene regulatory network model that includes the mutual interconnections between spatial areas. To guarantee the model's robust stability, we have established delay-dependent stability criteria using carefully designed Lyapunov-Krasovskii functions, framed within the context of linear matrix inequalities. The robustness and effectiveness of our approach are demonstrated through a numerical example presented in this work.

Index Terms—Discrete-time genetic regulatory networks; Robust stability; Reaction-diffusion; Linear matrix inequalities

I. INTRODUCTION

Historically, scientific inquiry predominantly centered on elucidating the functions of select genes, proteins, and molecules. However, contemporary understanding underscores that the orchestration of most biological functions transcends the control exerted by individual molecules or genes, instead arising from the intricate interplay among myriad components. This interaction entails the regulation of gene expression or function by the influence or activity of other genes, and conversely. With the

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Yunong Liu is a postgraduate of School of Information Science and Engineering, Yanshan University, Qinhuangdao 066004, China (e-mail: liutongxue888@163.com). progressive evolution of biological science, particularly the nuanced exploration of molecular mechanisms witnessed in recent years, there has emerged an increasingly profound appreciation among experts for the fundamental significance of genetic networks. Given the inherent complexity of authentic genetic networks, it becomes imperative to employ simplification strategies for effective comprehension. Genetic regulatory networks (GRNs) have emerged as potent tools in this regard, offering valuable insights into intricate biochemical processes such as gene transcription, translation, and protein diffusion within cellular microenvironments such as the cytosol and nucleus.

Researchers have made significant strides in the field of Genetic Regulatory Networks (GRNs), leading to the development of a diverse array of models. These include Bayesian models [1-3], Boolean models [4], and differential equations models [5-9]. Among them, the differential equations models stand out for their ability to capture the essence of GRNs through the representation of continuous values. However, the integration of delayed discrete-time GRNs is crucial for their practical deployment and use in simulation scenarios [10]. Scholars such as Sakthivel [11] have contributed significantly to the robustness evaluation of discrete-time GRNs, especially in dealing with various forms of delays.

Time delays are a fundamental aspect of numerous scientific disciplines, encompassing areas such as chemistry, physics, neural networks [12, 13], and GRNs. Within GRNs, these delays originate from the inherently slow pace of biochemical processes, including gene transcription and translation, or from the finite switching capabilities of amplifiers. Concurrently, uncertainties arise due to imperfections in modeling, the influence of external factors, and variations in parameters. In response to these complexities, a multitude of research efforts have been dedicated to performing robust stability analyses of GRNs, specifically addressing the intricacies of time delays and uncertainties.

As mentioned above, genetic regulatory processes require the migration of regulatory proteins or metabolites within cellular compartments such as the cytoplasm and nucleus. Recognition of the importance of protein diffusion has highlighted the need to incorporate reaction-diffusion phenomena into genetic regulatory network (GRN) models, rather than assuming spatial homogeneity. Several studies [14–16] have highlighted the key role of reaction-diffusion dynamics in shaping GRN behavior, emphasizing that models that ignore these effects may produce inaccurate predictions of protein and mRNA concentrations. Therefore, the integration of reaction-diffusion mechanisms is essential in GRN modeling. However, the literature on this aspect remains limited, especially regarding discrete-time GRNs within plant systems.

In this study, we aim to incorporate reaction-diffusion dynamics into discrete-time GRNs and analyze the stability of discrete GRNs with reaction-diffusion terms, considering scenarios both with and without Brownian motion. Through computer simulations, we demonstrate the effectiveness of our theoretical findings and the impact of integrating reaction-diffusion dynamics into GRN modeling.

The main contributions of this work are summarized as follows:

(1) Integration of spatial diffusion: this study introduces the integration of spatial diffusion mechanisms into discrete GRNs, thus establishing a novel discrete coupled GRN incorporating reaction-diffusion dynamics.

(2) Stability theorem for Brownian motion and time delay: Taking into account Brownian motion and time delay, this study introduces a theorem aimed at determining the stability of discrete modeling GRNs incorporating reaction-diffusion processes. This theorem serves as an important tool for understanding the dynamic behavior of GRNs under the influence of these complex factors.

II. PROBLEM FORMULATION

Following nonlinear delayed genetic regulatory network [17]:

$$\begin{cases} X(m+1) = \tilde{A}X(m) + \tilde{B}F(Y(m - \theta(m))) + L\\ Y(m+1) = \tilde{C}Y(m) + \tilde{D}X(m - \theta(m)) \end{cases}$$
(1)

where

$$\begin{split} \tilde{A} &= diag\left\{\tilde{a}_{1}, \tilde{a}_{2}, \cdots, \tilde{a}_{N}\right\},\\ \tilde{C} &= diag\left\{\tilde{c}_{1}, \tilde{c}_{2}, \cdots, \tilde{c}_{N}\right\},\\ \tilde{D} &= diag\left\{\tilde{d}_{1}, \tilde{d}_{2}, \cdots, \tilde{d}_{N}\right\},\\ X(m) &= \begin{bmatrix} x_{1}(m), x_{2}(m), \cdots x_{N}(m) \end{bmatrix}^{T},\\ Y(m) &= \begin{bmatrix} y_{1}(m), y_{2}(m), \cdots, y_{N}(m) \end{bmatrix}^{T},\\ Y(m-\theta(m)) &= \begin{bmatrix} y_{1}(m-\theta(m)), y_{2}(m-\theta(m)),\\ &\cdots, y_{N}(m-\theta(m)) \end{bmatrix}^{T},\\ Y\left(m-\theta(m)\right) &= \begin{bmatrix} x_{1}(m-\theta(m)), \cdots, x_{N}(m-\theta(m)) \end{bmatrix}^{T},\\ X\left(m-\theta(m)\right) &= \begin{bmatrix} x_{1}(m-\theta(m)), \cdots, x_{N}(m-\theta(m)) \end{bmatrix}^{T}, \end{split}$$

$$F\left(Y\left(m-\theta(m)\right)\right) = \left[f_1\left(y_1\left(m-\theta(m)\right)\right), f_2\left(y_2\left(m-\theta(m)\right)\right) \\ \cdots, f_N\left(y_N\left(m-\theta(m)\right)\right)\right]^T$$
$$L = \left[L_1, L_2, \cdots, L_N\right]^T.$$

In Eq. (1), $x_i(m) \in \mathbb{R}^N$ $(i = 1, 2, \dots, N)$ and $y_i(m) \in \mathbb{R}^N$ represent the concentrations of mRNA and protein of the *i* node at time *m*, respectively. The parameters \tilde{a}_i and \tilde{c}_i denote the degradation rates of mRNA and protein, and \tilde{d}_i is the translation rate. The term L_i signifies the basal transcriptional rate of the repressor of gene *i*, and $f_i(\chi)$ is the Hill form regulatory function. This function represents the feedback regulation of the protein on transcription and is expressed as follows:

$$f_i(\chi) = \frac{\left(\frac{\chi}{v_i}\right)^{H_i}}{1 + \left(\frac{\chi}{v_i}\right)^{H_i}},$$

where H_i is the Hill coefficient, v_i is a positive constant, $\theta(m)$ and $\theta(m)$ are time-varying delays satisfying

$$\begin{cases} 0 < \theta_{\min} \le \theta(m) \le \theta_{\max} \\ 0 < \theta_{\min} \le \theta(m) \le \theta_{\max} \\ \tau_1 \le \dot{\theta} \le \mu_1 \\ \tau_2 \le \dot{\theta} \le \mu_2 \end{cases}$$
(2),

 $B = (b_{nn'}) \in \mathbb{R}^{N \times N}$ is described as

$$\tilde{b}_{nn'} = \begin{cases} \gamma_{nn'} \\ 0 \\ -\gamma_{nn'} \end{cases}$$

where $\gamma_{nn'}$ represent transcription factor $n' \in \{1, 2, 3 \dots, N\}$ is an activator of gene *n*, 0 represent that there is no link from node *n'* to *n*, $-\gamma_{nn'}$ represent transcription factor *n'* is an repressor of gene *n*.

Now, assuming that X^* and Y^* are the equilibrium point vectors of Eq. (1), let $x(m) = X(m) - X^*$, $y(m) = Y(m) - Y^*$, and $f(y(m - \theta(m))) = F(y(m - \theta(m)) + Y^*) - F(Y^*)$ then Eq. (1) can be expressed as follows:

$$\begin{cases} X(m+1) = \tilde{A}X(m) + \tilde{B}F(Y(m - \theta(m))) \\ Y(m+1) = \tilde{C}Y(m) + \tilde{D}X(m - \theta(m)) \end{cases}$$
(3).

Based on the fundamental discrete GRN model outlined in Eq. (1), we now advance to develop an enhanced discrete GRN model that integrates reaction-diffusion terms to capture the spatial-temporal dynamics more comprehensively.

$$\begin{cases} X(m+1,n) = \tilde{A}'X(m,n) + \tilde{B}F\left(Y\left(m-\theta(m),n\right)\right) + \Theta_{1} + L \\ Y(m+1,n) = \tilde{C}'y(m,n) + \Theta_{2} + \tilde{D}x\left(m-\theta(m),n\right) \end{cases}$$
(4),
Where
$$X(m,n) = \begin{bmatrix} x_{1}(m,n), \cdots, x_{N}(m,n) \end{bmatrix}^{T},$$
$$Y(m,n) = \begin{bmatrix} y_{1}(m,n), \cdots, y_{N}(m,n) \end{bmatrix}^{T},$$
$$Y\left(m-\theta(m),n\right) = \begin{bmatrix} y_{1}\left(m-\theta(m),n\right), \cdots, y_{N}\left(m-\theta(m),n\right) \end{bmatrix}^{T},$$
$$X\left(m-\theta(m),n\right) = \begin{bmatrix} x_{1}\left(m-\theta(m),n\right), \cdots, x_{N}\left(m-\theta(m),n\right) \end{bmatrix}^{T},$$
$$F\left(y\left(m-\theta(m)\right),n\right) = \begin{bmatrix} f_{1}\left(y\left(m-\theta(m),n\right)\right), \cdots, f_{N}\left(m-\theta(m),n\right) \end{bmatrix}^{T},$$

$$(m-\theta(m)),n) = \left[f_1(y(m-\theta(m),n)), \cdots, f_N(y(m-\theta(m),n)) \right]^T$$

In Eq. (4), $x_i(m,n)$ and $y_i(m,n)$ are the concentrations of mRNA and protein of the *i* th node at the time *m* and space *n*.

A typical continuous-time genetic regulatory networks with reaction-diffusion terms [15] is described as:

$$\begin{cases} \frac{\partial \hat{x}_{i}(t,r)}{\partial t} = \sum_{k=1}^{l} \frac{\partial}{\partial r_{k}} \left(D_{ik} \frac{\partial \hat{x}_{i}(t,r)}{\partial r_{k}} \right) - \hat{a}_{i} \hat{x}_{i}(t,r) + \\ \sum_{j=1}^{n} \omega_{ij} g_{j} \left(\hat{y}_{j}(t - \sigma(t), r) \right) + q_{i} \\ \frac{\partial \hat{y}_{i}(t,r)}{\partial t} = \sum_{k=1}^{l} \frac{\partial}{\partial r_{k}} \left(D_{ik}^{*} \frac{\partial \hat{y}_{i}(t,r)}{\partial r_{k}} \right) - \hat{c}_{i} \hat{y}_{i}(t,r) + \\ + \hat{b}_{i} \hat{x}_{i}(t - \theta(t), r), i = 1, 2, \cdots, n \end{cases}$$
(5)

where $r = (r_1, r_2, \dots, r_l)^T \in \Omega \subset \mathbb{R}^C$, $\Omega = \{r | |r_k| < L'_k\}$, L'_k is constant, $k = 1, 2, \dots, l, D_{ik} > 0$, $D^*_{ik} > 0$ denote the diffusion rate matrices; $\hat{x}_i(t,r)$ and $\hat{y}_i(t,r)$ demonstrate the concentrations of mRNA and protein at the *i*th node respectively; \hat{a}_i and \hat{c}_i represent degradation rates of the mRNA and protein, respectively; \hat{b}_i is a constant; $g_j(*)$ is the activation function; $q_i = \sum_{j \in I_i} \alpha_{ij}$, I_i is the set of all the

nodes which are repressors of gene *I*; $W := (\omega_{ij}) \in \mathbb{R}^{n \times n}$ is coupling matrix, which is defined as

$$\omega_{ij} = \begin{cases} \alpha_{ij} \\ 0 \\ -\alpha \end{cases}$$

where α_{ij} represent transcription factor *j* is an activator of gene *i*, 0 represent that there is no link from node *j* to *i*, $-\alpha_{ij}$ represent transcription factor *j* is a repressor of gene *i*.

According to the form of the reaction-diffusion terms in Eq. (5), Θ_1 and Θ_2 are defined to represent the reaction diffusion terms of concentrations of mRNA and protein respectively as follows:

$$\begin{cases} \Theta_{1} = \xi_{1} \Big[X(m, n+1) - X(m, n) - (X(m, n) - X(m, n-1)) \Big] \\ \Theta_{2} = \xi_{2} \Big[Y(m, n+1) - Y(m, n) - (Y(m, n) - Y(m, n-1)) \Big] \end{cases}$$
(6),

where ξ_1 and ξ_2 are positive coupling coefficient.

After substituting Eq. (6) into Eq. (4) and simplifying, we obtain

$$\begin{cases} X(m+1,n) = \tilde{A}X(m,n) + \tilde{B}F\left(Y\left(m - \theta(m),n\right)\right) \\ + \xi_1\left(X(m,n+1) + X(m,n-1)\right) + L \\ Y(m+1,n) = \tilde{C}Y(m,n) + \xi_2\left(Y(m,n+1) + Y(m,n-1)\right) \\ + \tilde{D}X\left(m - \theta(m),n\right) \end{cases}$$
(7),

where $\tilde{A} = \tilde{A}' - 2\xi_1$ and $\tilde{C} = \tilde{C}' - 2\xi_2$.

Assuming that \hat{X} and \hat{Y} are the equilibrium point vectors of Eq. (7), let $x(m,n) = X(m,n) - \hat{X}$, y(m,n) = Y(m,n) $-\hat{Y}$ and $f(y(m - \theta(m), n)) = F(y(m - \theta(m), n) + \hat{Y}) - F(\hat{Y})$, then Eq. (7) can be expressed as follows:

$$\begin{cases} x(m+1,n) = \tilde{A}x(m,n) + \tilde{B}f\left(y\left(m - \theta(m),n\right)\right) \\ + \xi_1\left(x(m,n+1) + x(m,n-1)\right) \\ y(m+1,n) = \tilde{C}y(m,n) + \xi_2\left(y(m,n+1) + y(m,n-1)\right) \\ + \tilde{D}x\left(m - \theta(m),n\right) \end{cases}$$
(8)

Considering that the concentrations of mRNA and proteins are influenced by molecular Brownian motion, Eq. (8) is rewritten as

$$\begin{cases} x(m+1,n) = \tilde{A}x(m,n) + \tilde{B}f\left(y\left(m - \theta(m),n\right)\right) + \xi_1\left(x(m,n+1) + x(m,n-1)\right) + \sigma\left(y(m,n), y\left(m - \theta(m),n\right)\right)\omega(m,n) \\ y(m+1,n) = \tilde{C}y(m,n) + \xi_2\left(y(m,n+1) + y(m,n-1)\right) \\ + \tilde{D}x\left(m - \theta(m),n\right) \end{cases}$$
(9).

where $\omega(m,n)$ is a vector-form scalar Brownian motion with $\varepsilon \{\omega(m,n)\} = 0$,

$$\varepsilon \left\{ \omega(m,n)^T \omega(m,n) \right\} = 1,$$

$$\varepsilon \left\{ \omega(m,n)^T \, \omega(m',n) \right\} = 0(m' \neq m) \,,$$

and $\sigma(y(m,n), y(m-\theta(m), n))$ is the noise intensity matrix satisfying

$$\sigma^{T}(y(m,n), y(m-\theta(m),n))\sigma(y(m,n), y(m-\theta(m),n))$$

$$\leq v^{T}(m,n)H(y(m,n)+v^{T}(m-\theta(m),n)H(y(m-\theta(m),n))$$

$$\leq y(m,n)H_1y(m,n) + y(m-\theta(m),n)H_2y(m-\theta(m),n)$$

where H_1 and H_2 are known constant matrices with appropriate dimensions.

Nonlinear function $f_i(\cdot)$ satisfies the Ineq. (11), because $f_i(\cdot)$ is a monotonically increase function with saturation

$$0 \le \frac{f_i(\chi_i)}{\chi_i} \le \mathcal{G}'_i, \chi_i \ne 0, i = 1, 2, \cdots, n \tag{11}.$$

(10).

Ineq. (11) is reformulated in matrix notation, thereby engendering

$$f^{T}(\boldsymbol{\chi})(f(\boldsymbol{\chi}) - \boldsymbol{K}\boldsymbol{\chi}) \le 0$$
(12)

where $K = \text{diag}(\kappa_1, \kappa_2, \cdots, \kappa_n), \forall \chi \in \mathbb{R}^n$.

In this study, we contemplate the imposition of Dirichlet boundary conditions, articulated as follows:

$$\begin{cases} x(m,n) = 0, n \in \partial \Omega \\ y(m,n) = 0, n \in \partial \Omega \end{cases}$$

where $\partial \Omega$ represents boundary.

Lemma 1 [16]. For any constant matrix $W = W^T > 0$, scalar r' > 0, exist

$$r'\sum_{l=t'-r'}^{t'-1} \bar{x}^{T}(l)W\bar{x}(l) \ge \sum_{l=t'-r'}^{t'-1} \bar{x}^{T}(l)W\sum_{l=t'-r'}^{t'-1} \bar{x}(l)$$
(13)

Lemma 2 [18]. For any vectors \vec{X} , $\vec{Y} \in \mathbb{R}^n$, H > 0 is any positive definite matrix, exist following Ineq.

$$2\vec{X}^{T}H\vec{Y} \le \vec{X}^{T}H\vec{X} + \vec{Y}^{T}H^{-1}\vec{Y}$$
(14).
III. STABILITY CRITERIA

In this section, we will investigate a stability criterion for Eq. (8).

Theorem 1 For given scalars θ_{\min} , θ_{\max} , θ_{\min} and θ_{\max} satisfying Ineq. (2), $\omega(m,n) = 0$, the trivial solution of Eq. (9) is stability if there exist scalars $\gamma > 0$, matrices $\Lambda_h^T = \Lambda_h > 0$ (h = 1, 2), $P_{h'}^T = P_{h'} > 0$, $R_{h'}^T = R_{h'} > 0$ and $Q_{h'}^T = Q_{h'} > 0$ $(h' = 1, \dots, 4)$, $T_1^T = T_1 > 0$, $S_1^T = S_1 > 0$ and $S_2^T = S_2 > 0$, such that the following linear matrix Ineq. (LMI) holds:

$$\Xi = \begin{bmatrix} \Xi_1 & \Xi_2 \\ * & \Xi_3 \end{bmatrix} < 0 \tag{15}.$$

Where

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$$\begin{split} \Omega_{10,12} &= \tilde{B}^T P_1 \xi_1 + \mathcal{G}_{\min} \tilde{B}^T R_1 \xi_1 + (\mathcal{G}_{\max} - \mathcal{G}_{\min}) \tilde{B}^T R_2 \xi_1 ,\\ \Omega_{11,11} &= \xi_1^T P_1 \xi_1 + \mathcal{G}_{\min} \xi_1^T R_1 \xi_1 + (\mathcal{G}_{\max} - \mathcal{G}_{\min}) \xi_1^T R_2 \xi_1 - S_1 ,\\ \Omega_{11,12} &= \xi_1^T P_1 \xi_1 + \mathcal{G}_{\min} \xi_1^T R_1 \xi_1 + (\mathcal{G}_{\max} - \mathcal{G}_{\min}) \xi_1^T R_2 \xi_1 ,\\ \Omega_{12,12} &= \xi_1^T P_1 \xi_1 + \mathcal{G}_{\min} \xi_1^T R_1 \xi_1 + (\mathcal{G}_{\max} - \mathcal{G}_{\min}) \xi_1^T R_2 \xi_1 - S_1 ,\\ \Omega_{13,13} &= \xi_2^T P_2 \xi_2 + \mathcal{G}_{\min} \xi_2^T R_3 \xi_2 + (\mathcal{G}_{\max} - \mathcal{G}_{\min}) \xi_2^T R_4 \xi_2 - S_2 ,\\ \Omega_{13,14} &= \xi_2^T P_2 \xi_2 + \mathcal{G}_{\min} \xi_2^T R_3 \xi_2 + (\mathcal{G}_{\max} - \mathcal{G}_{\min}) \xi_2^T R_4 \xi_2 - S_2 ,\\ \Omega_{14,14} &= \xi_2^T P_2 \xi_2 + \mathcal{G}_{\min} \xi_2^T R_3 \xi_2 + (\mathcal{G}_{\max} - \mathcal{G}_{\min}) \xi_2^T R_4 \xi_2 - S_2 .\\ \end{split}$$

$$\begin{cases} \mu_1(m,n) = x(m+1,n) - x(m,n) \\ \mu_2(m,n) = y(m+1,n) - y(m,n) \end{cases}$$
(16).

Define a Lyapunov-Krasovskii functional candidate for Eq. (17) as

$$V(m,n) = \sum_{g=1}^{5} V_g(m,n)$$
(17),

Where

$$V_1(m,n) = x^T(m,n)P_1x(m,n) + y^T(m,n)P_2y(m,n)$$
(18),

$$V_{2}(m,n) = \sum_{l=m-\theta(m)}^{m-1} x^{T}(m,n)P_{3}x(l,n) + \sum_{l=m-\theta(m)}^{m-1} y^{T}(l,n)P_{4}y(l,n)$$
(19)

$$V_{3}(m,n) = \sum_{l=m-\theta_{\min}}^{m-1} x^{T}(l,n)Q_{1}x(l,n) + \sum_{l=m-\theta_{\max}}^{m-\theta_{\min}-1} x^{T}(l,n)Q_{2}x(l,n) + \sum_{l=m-\theta_{\min}}^{m-1} y^{T}(l,n)Q_{3}y(l,n) + \sum_{l=m-\theta_{\max}}^{m-\theta_{\min}-1} y^{T}(l,n)Q_{4}y(l,n)$$
(20),

 $V_4(m,n) =$

$$\sum_{\theta=-\theta_{\min}}^{-1} \sum_{l=m+\theta}^{m-1} \mu_{1}^{T}(l,n)R_{1}\mu_{1}(l,n) + \sum_{\theta=-\theta_{\max}+\theta_{\min}}^{-1} \sum_{l=m-\theta_{\min}+\theta}^{m-1} \mu_{1}^{T}(l,n)R_{2}\mu_{1}(l,n) + \sum_{\theta=-\theta_{\max}+\theta_{\min}}^{-1} \sum_{l=m-\theta_{\min}+\theta}^{m-1} \mu_{2}^{T}(l,n)R_{4}\mu_{2}(l,n) + \sum_{\theta=-\theta_{\max}+\theta_{\min}}^{-1} \sum_{l=m-\theta_{\min}+\theta}^{-1} \mu_{2}^{T}(l,n)R_{4}\mu_{2}(l,n) + \sum_{\theta=-\theta_{\max}+\theta_{\min}}^{-1} \sum_{l=m-\theta_{\min}+\theta}^{-1} \mu_{2}^{T}(l,n)R_{4}\mu_{2}(l,n) + \sum_{\theta=-\theta_{\max}+\theta_{\min}}^{-1} \sum_{l=m-\theta_{\min}+\theta}^{-1} \mu_{2}^{T}(l,n)R_{4}\mu_{2}(l,n) + \sum_{\theta=-\theta_{\max}+\theta_{\max}+\theta_{\max}}^{-1} \sum_{l=m-\theta_{\min}+\theta}^{-1} \mu_{2}^{T}(l,n)R_{4}\mu_{2}(l,n) + \sum_{\theta=-\theta_{\max}+\theta_{\max}+\theta_{\max}}^{-1} \sum_{l=m-\theta_{\min}+\theta_{\max}+\theta_{\max}}^{-1} \sum_{l=m-\theta_{\max}+\theta_{\max}+\theta_{\max}}^{-1} \sum_{l=m-\theta_{\max}+\theta_{\max}+\theta_{\max}}^{-1} \sum_{l=m-\theta_{\max}+\theta_{\max}+\theta_{\max}}^{-1} \sum_{l=m-\theta_{\max}+\theta_{\max}+\theta_{\max}+\theta_{\max}}^{-1} \sum_{l=m-\theta_{\max}+\theta_{\max}+\theta_{\max}+\theta_{\max}}^{-1} \sum_{l=m-\theta_{\max}+\theta$$

$$V_{5}(m,n) = \sum_{l=m-\theta(m)}^{m-1} f^{T}(y(l,n)) T_{1}f(y(l,n))$$
(22).

Define $\Delta V(m,n) = V(m+1,n) - V(m,n)$, then

$$\varepsilon\left\{\Delta V(m,n)\right\} = \varepsilon\left\{\sum_{i=1}^{5} \Delta V_i(m,n)\right\}$$
(23),

Where

$$\varepsilon \{ \Delta V_{1}(k,i) \} = \varepsilon \left(x^{T}(m+1,n)P_{1}x(m+1,n) - x^{T}(m,n)P_{1}x(m,n) + y^{T}(m+1,n)P_{2}y(m+1,n) - y^{T}(m,n)P_{2}y(m,n) \right)$$

$$(24)$$

$$\varepsilon \{ \Delta V_{2}(m,n) \} = \varepsilon \left(x^{T}(m,n)P_{3}x(m,n) - x^{T}(m-\vartheta(m),n)P_{3}x(m-\vartheta(m),n) + y^{T}(m,n)P_{4}y(m,n) - y^{T}(m-\vartheta(m),n)P_{4}y(m-\vartheta(m),n) \right)$$

$$(25)$$

$$\varepsilon \{\Delta V_3(m,n)\} = \varepsilon \{x^T(m,n)Q_1x(m,n) + x^T(m - \vartheta_{\min},n)(Q_2 - Q_1)x(m - \vartheta_{\min},n) - x^T(m - \vartheta_{\max},n)Q_2x(m - \vartheta_{\max},n) + y^T(m,n)Q_3y(m,n) + y^T(m - \theta_{\min},n)(Q_4 - Q_3)y(m - \theta_{\min},n) - y^T(m - \theta_{\max},n)Q_4y(m - \theta_{\max},n))$$

(26),

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$$\varepsilon \left\{ \Delta V_{4}(m,n) \right\} = \varepsilon \left\{ \vartheta_{\min} \mu_{1}^{T}(m,n) R_{1} \mu_{1}(m,n) - \sum_{l=m-\vartheta_{\min}}^{m-1} \mu_{1}^{T}(l,n) R_{1} \mu_{1}(l,n) + (\vartheta_{\max} - \vartheta_{\min}) \mu_{1}^{T}(m,n) R_{2} \mu_{1}(m,n) - \sum_{l=m-\vartheta_{\min}}^{m-\vartheta_{\min}-1} \mu_{1}^{T}(l,n) R_{2} \mu_{1}(l,n) + (\vartheta_{\max} - \vartheta_{\min}) R_{3} \mu_{2}(m,n) - \sum_{l=m-\vartheta_{\min}}^{m-1} \mu_{2}^{T}(l,n) R_{3} \mu_{2}(l,n) + (\vartheta_{\max} - \vartheta_{\min}) + \mu_{2}^{T}(m,n) R_{4} \mu_{2}(k,n) - \sum_{l=m-\vartheta_{\max}}^{m-\vartheta_{\max}-1} \mu_{2}^{T}(l,n) R_{4} \mu_{2}(l,n) \right\}$$

$$(27),$$

$$\varepsilon \left\{ \Delta V_5(m,n) \right\} = \varepsilon \left\{ f^T(y(m,n)T_1f(y(m,n)) - f^T(y(m-\theta(m),n)T_1f(y(m-\theta(m),n))) \right\}$$
(28).

Considering Ineq. (12), it follows that for diagonal matrices $\Lambda_1 > 0$, $\Lambda_2 > 0$, there exist

$$2y^{T}(m,n)K\Lambda_{1}f(y(m,n)) - 2f^{T}(y(m,n))\Lambda_{1}f(y(m,n)) \ge 0 \quad (29)$$

$$2y^{T}(m-\theta(m),n)K\Lambda_{2}f(y(m-\theta(m),n)) -2f^{T}(y(m-\theta(m),n))\Lambda_{2}f(y(m-\theta(m),n)) \ge 0$$
(30).

Utilizing Lemma 1, we ascertain

$$-\sum_{l=m-\vartheta_{\min}}^{m-1} \mu_{l}^{T}(l,n)R_{l}\mu_{l}(l,n) \leq -\frac{1}{\vartheta_{\min}} \left[x(m,n) - x(m-\vartheta_{\min},n)\right]^{T} R_{l} \left[x(m,n) - x(m-\vartheta_{\min},n)\right]$$
(31)

$$-\sum_{l=m-\vartheta_{\max}}^{m-\vartheta_{\min}-1} \mu_{l}^{T}(l,n) R_{2} \mu_{l}(l,n) \leq -\frac{1}{\vartheta_{\max}-\vartheta_{\min}} \Big[x(m-\vartheta_{\min},n) -x(m-\vartheta_{\min},n) \Big]^{T} R_{2} \Big[x(m-\vartheta_{\max},n) -x(m-\vartheta_{\max},n) \Big]$$
(32),

$$-\sum_{l=m-\theta_{\min}}^{m-1} \mu_{2}^{T}(l,n)R_{3}\mu_{2}(l,n) \leq -\frac{1}{\theta_{\min}} [y(m,n)$$
(33)

$$-x(m-\theta_{\min},n)]^{T} R_{3} [y(m,n) - y(m-\theta_{\min},n)]$$

$$-\sum_{l=m-\theta_{\max}}^{m-\theta_{\min}-1} \mu_{2}^{T}(l,n) R_{4} \mu_{2}(l,n) \leq -\frac{1}{\theta_{\max}-\theta_{\min}} [y(m-\theta_{\min},n) - x(m-\theta_{\max},n)]^{T} R_{4} [y(m-\theta_{\min},n) - y(m-\theta_{\max},n)]$$
(34).

Considering the spatial continuity and limitary of GRNs, we can obtain

$$\begin{cases} x^{T}(m,n+1)S_{1}x(m,n+1) \leq \lambda_{1}x^{T}(m,n)S_{1}x(m,n) \\ x^{T}(m,n-1)S_{1}x(m,n-1) \leq \lambda_{1}x^{T}(m,n)S_{2}x(m,n) \end{cases}$$
(35),

$$\begin{cases} y^{T}(m,n+1)S_{2}y(m,n+1) \leq \lambda_{2}y^{T}(m,n)S_{2}y(m,n) \\ x \end{cases}$$
(36),

 $\int y^{T}(m, n-1)S_{2}y(m, n-1) \leq \lambda_{2}y^{T}(m, n)S_{2}y(m, n)$

where

$$\begin{cases} \lambda_1 = \max \left\{ x^2(m,n) / x^2(m,n-1) \right\} \\ \lambda_2 = \max \left\{ y^2(m,n) / y^2(m,n-1) \right\}, \end{cases}$$

Then, combing (17)-(36), we can obtain $\varepsilon \{\Delta V(m,n)\} \le \varepsilon \{\zeta^T \Xi \zeta\}$

Where

$$\begin{aligned} \zeta^{T} &= \left[x^{T}(m,n), x^{T}\left(m-\vartheta(m),n\right), x^{T}(m-\vartheta_{\min},n), x^{T}(m-\vartheta_{\max},n) \\ , y^{T}(m,n), y^{T}\left(m-\theta(m),n\right), y^{T}(m-\theta_{\min},n), y^{T}(m-\theta_{\max},n) \\ f^{T}\left(y(m,n)\right), f^{T}\left(\left(m-\theta(m)\right)\right), x^{T}(m,n+1), x^{T}(m,n-1), \\ y^{T}(m,n+1), y^{T}(m,n-1) \right]^{T} \end{aligned}$$

The analysis above implies that Eq. (9), in the absence of Brownian motion, demonstrates mean square asymptotic stability, thereby completing the proof. **Theorem 2** For given scalars θ_{\min} , θ_{\max} , θ_{\max} , θ_{\min} and θ_{\max} satisfying Ineq. (2), the trivial solution of Eq. (9) is stability if there exist scalars $\rho > 0$, matrices $\Lambda_h^T = \Lambda_h > 0$ (h = 1, 2), $P_{h'}^T = P_{h'} > 0$, $R_{h'}^T = R_{h'} > 0$ and $Q_{h'}^T = Q_{h'} > 0$ $(h' = 1, \dots, 4)$, $T_1^T = T_1 > 0$, $S_1^T = S_1 > 0$ and $S_2^T = S_2 > 0$, such that the following LMIs hold:

$$\begin{split} & P_{1} + \mathcal{G}_{\min}R_{1} + (\mathcal{G}_{\max} - \mathcal{G}_{\min})R_{2} \leq \rho I \quad (38), \\ & \Theta_{1} = \begin{bmatrix} \Phi_{11} & 0 & \frac{R_{1}}{\mathcal{G}_{\min}} & 0 & \Phi_{15} & \Phi_{16} & \Phi_{17} \\ * & \Phi_{22} & 0 & 0 & 0 & 0 & 0 \\ * & * & \Phi_{33} & \frac{R_{2}}{\mathcal{G}_{\max} - \mathcal{G}_{\min}} & 0 & 0 & 0 \\ * & * & * & \Phi_{44} & 0 & 0 & 0 \\ * & * & * & * & \Phi_{55} & \Phi_{56} & \Phi_{57} \\ * & * & * & * & * & \Phi_{66} & \Phi_{67} \\ * & * & * & * & * & * & \Phi_{77} \end{bmatrix} < 0 \quad (39), \\ & \Theta_{2} = \begin{bmatrix} \Pi_{11} & 0 & \Pi_{13} & 0 & \Pi_{15} & \Pi_{16} & \Pi_{17} \\ * & \Pi_{22} & 0 & 0 & 0 & 0 \\ * & * & R_{33} & \Pi_{34} & 0 & 0 & 0 \\ * & * & R_{33} & \Pi_{34} & 0 & 0 & 0 \\ * & * & * & R_{166} & \Pi_{67} \\ * & * & * & * & R_{166} & \Pi_{67} \\ * & * & * & * & * & R_{166} & \Pi_{77} \end{bmatrix} < 0 \quad (40), \end{split}$$

Where ~

$$\begin{split} \Phi_{11} &= \tilde{A}^T P_1 \tilde{A} + \mathcal{G}_{\min} \left(\tilde{A} - I \right)^T R_1 (\tilde{A} - I) \\ &+ \left(\mathcal{G}_{\max} - \mathcal{G}_{\min} \right) \left(\tilde{A} - I \right)^T R_2 (\tilde{A} - I) \\ &- P_1 + P_3 + Q_1 - R_1 / \mathcal{G}_{\min} + \lambda_1 S_1 \\ \end{split} \\ \Phi_{15} &= \tilde{A}^T P_1 \tilde{B} + \mathcal{G}_{\min} \left(\tilde{A} - I \right)^T R_1 \tilde{B} + \left(\mathcal{G}_{\max} - \mathcal{G}_{\min} \right) \left(\tilde{A} - I \right)^T R_2 \tilde{B} , \\ \Phi_{16} &= \tilde{A}^T P_1 \xi_1 + \mathcal{G}_{\min} \left(\tilde{A} - I \right)^T R_1 \xi_1 + \left(\mathcal{G}_{\max} - \mathcal{G}_{\min} \right) \left(\tilde{A} - I \right)^T R_2 \xi_1 , \\ \Phi_{17} &= \tilde{A}^T P_1 \xi_1 + \mathcal{G}_{\min} \left(\tilde{A} - I \right)^T R_1 \xi_1 + \left(\mathcal{G}_{\max} - \mathcal{G}_{\min} \right) \left(\tilde{A} - I \right)^T R_2 \xi_1 , \\ \Phi_{22} &= 3 \tilde{D}^T P_2 \tilde{D} - P_3 + 3 \mathcal{G}_{\min} \tilde{D}^T R_3 \tilde{D} + 3 \left(\mathcal{G}_{\max} - \mathcal{G}_{\min} \right) \tilde{D}^T R_4 \tilde{D} , \\ \Phi_{33} &= Q_2 - Q_1 - \frac{R_1}{\mathcal{G}_{\min}} - \frac{R_2}{\mathcal{G}_{\max} - \mathcal{G}_{\min}} , \end{split}$$

$$\begin{split} \Phi_{44} &= -Q_2 - \frac{R_2}{g_{\max} - g_{\min}} \,, \\ \Phi_{55} &= \tilde{B}^T P_1 \tilde{B} + g_{\min} \tilde{B}^T R_1 \tilde{B} + (g_{\max} - g_{\min}) \tilde{B}^T R_2 \tilde{B} - T_1 + \Lambda_2 \,, \\ \Phi_{56} &= \tilde{B}^T P_5 \zeta_1 + g_{\min} \tilde{B}^T R_1 \zeta_1 + (g_{\max} - g_{\min}) \tilde{B}^T R_2 \zeta_1 \,, \\ \Phi_{57} &= \tilde{B}^T P_5 \zeta_1 + g_{\min} \tilde{B}^T R_1 \zeta_1 + (g_{\max} - g_{\min}) \tilde{B}^T R_2 \zeta_1 \,, \\ \Phi_{66} &= g_1^T P_1 \zeta_1 + g_{\min} g_1^T R_1 \zeta_1 + (g_{\max} - g_{\min}) g_1^T R_2 \zeta_1 - S_1 \,, \\ \Phi_{67} &= \xi_1^T P_1 \zeta_1 + g_{\min} \xi_1^T R_1 \zeta_1 + (g_{\max} - g_{\min}) \xi_1^T R_2 \zeta_1 - S_1 \,, \\ \Phi_{77} &= \xi_1^T P_1 \zeta_1 + g_{\min} \xi_1^T R_1 \zeta_1 + (g_{\max} - g_{\min}) \xi_1^T R_2 \zeta_1 - S_1 \,, \\ \Pi_{11} &= 2\tilde{C}^T P_2 \tilde{C} - P_2 + P_4 + Q_3 + \\ &= 2\theta_{\min} (\tilde{C} - I)^T R_3 (\tilde{C} - I) - R_3 / \theta_{\min} \,, \\ &+ 2(\theta_{\max} - \theta_{\min}) (\tilde{C} - I)^T R_4 (\tilde{C} - I) + \rho H_1 + \lambda_2 S_2 \,, \\ \Pi_{13} &= R_3 / \theta_{\min} \,, \\ \Pi_{16} &= \tilde{C}^T P_2 \zeta_2 + \theta_{\min} (\tilde{C} - I)^T R_3 \zeta_2 + (\theta_{\max} - \theta_{\min}) (\tilde{C} - I)^T R_4 \zeta_2 \,, \\ \Pi_{17} &= \tilde{C}^T P_2 \zeta_2 + \theta_{\min} (\tilde{C} - I)^T R_3 \zeta_2 + (\theta_{\max} - \theta_{\min}) (\tilde{C} - I)^T R_4 \zeta_2 \,, \end{split}$$

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 $\Pi_{22} = -P_4 + K^T \Lambda_2 K + \rho H_2,$

(37),

$$\begin{aligned} \Pi_{33} &= Q_{3} - Q_{4} - R_{3} / \theta_{\min} - R_{4} / (\theta_{\max} - \theta_{\min}), \\ \Pi_{34} &= R_{4} / (\theta_{\max} - \theta_{\max}), \\ \Pi_{44} &= -Q_{4} - R_{4} / (\theta_{\max} - \theta_{\min}), \\ \Pi_{55} &= -2\Lambda_{1} + T_{1}, \\ \Pi_{66} &= \xi_{2}^{T} P_{2} \xi_{2} + \theta_{\min} \xi_{2}^{T} R_{3} \xi_{2} + (\theta_{\max} - \theta_{\min}) \xi_{2}^{T} R_{4} \xi_{2} - S_{2}, \\ \Pi_{77} &= \xi_{2}^{T} P_{2} \xi_{2} + \theta_{\min} \xi_{2}^{T} R_{3} \xi_{2} + (\theta_{\max} - \theta_{\min}) \xi_{2}^{T} R_{4} \xi_{2} - S_{2}. \\ \text{Proof} \\ \text{Employing Lemma 2, we ascertain} \\ &2y^{T} (m, n) \tilde{C}^{T} P_{2} \tilde{D} x (m - \theta(m), n) \leq y^{T} (m, n) \tilde{C}^{T} P_{2} \tilde{C} y (m, n) \\ &+ x^{T} (m - \theta(m), n) \tilde{D}^{T} P_{2} \tilde{D} x (m - \theta(m), n) \\ &2 \theta_{\min} y^{T} (m, n) (\tilde{C} - I)^{T} R_{3} \tilde{D} x (m - \theta(m), n) \leq \\ &\theta_{\min} y^{T} (m, n) (\tilde{C} - I)^{T} R_{3} \tilde{D} x (m - \theta(m), n) \\ &2 (\theta_{\max} - \theta_{\min}) y^{T} (m, n) (\tilde{C} - I)^{T} R_{4} \tilde{D} x (m - \theta(m), n) \\ &2 (\theta_{\max} - \theta_{\min}) y^{T} (m, n) (\tilde{C} - I)^{T} R_{4} \tilde{D} x (m - \theta(m), n) \\ &2 (\theta_{\max} - \theta_{\min}) y^{T} (m, n) (\tilde{C} - I)^{T} R_{4} \tilde{D} x (m - \theta(m), n) \\ &2 y^{T} (m - \theta(m), n) K \Lambda_{2} f ((y(m - \theta(m), n)) \\ &2 y^{T} (m - \theta(m), n) K^{T} \Lambda_{2} K y (m - \theta(m), n)), \\ &0 \\ \text{Observing Ineq. (10), it is evident that} \\ &\sigma^{T} (y(m, n), y(m - \theta(m), n) \\ &\leq \rho y^{T} (m, n) H_{1} y(m, n) + \rho y^{T} (m - \theta(m), n) H_{2} y (m - \theta(m), n) \\ &\leq \rho y^{T} (m, n) H_{1} y(m, n) + \rho y^{T} (m - \theta(m), n) H_{2} y (m - \theta(m), n) \\ \end{aligned}$$

Subsequently, by consolidating Eqs. (17)-(36) and Eqs. (41)-(44), we obtain

$$\varepsilon \left\{ \Delta V(m,n) \right\} \le \varepsilon \left\{ \Psi_1^{\mathsf{T}} \Theta_1 \Psi_1 + \Psi_2^{\mathsf{T}} \Theta_2 \Psi_2 \right\}$$
(46)

Where

$$\begin{aligned} \Psi_1^T &= \left[x^T(m,n), x^T\left(m - \mathcal{G}(m), n\right), x^T(m - \mathcal{G}_{\min}, n), x^T\left(m - \mathcal{G}_{\max}, n\right), \\ f^T\left(y\left(m - \theta(m), n\right)\right), x^T(m, n+1), x^T(m, n-1)\right]^T \end{aligned} \\ \Psi_2^T &= \left[y^T(m,n), y^T\left(m - \theta(m), n\right), y^T(m - \theta_{\min}, n), y^T(m - \theta_{\max}, n), \\ f^T\left(y(m, n)\right), y^T(m, n+1), y^T(m, n-1)\right]^T \end{aligned}$$

This is complete the proof.

IV. SIMULATION EXAMPLES

In this section, we present two examples to demonstrate the validity of Theorems 1 and 2. Specifically, Example 1 highlights the passivity properties of the proposed GRNs model without Brownian motion, while Example 2 exhibits the passivity characteristics of the same model when Brownian motion is taken into account.

A. Robust stability of proposed discrete-time RGNs without molecular Brownian motion

In this section, we consider a GRNs (9) with 5 nodes, where L=100. The parameters are assumed to be [17]

$$\begin{split} \tilde{A} &= \tilde{C} = \begin{bmatrix} 0.1 & 0 & 0 & 0 & 0 \\ 0 & 0.1 & 0 & 0 & 0 \\ 0 & 0 & 0.1 & 0 & 0 \\ 0 & 0 & 0 & 0.1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}, \\ \tilde{D} &= \begin{bmatrix} 0.08 & 0 & 0 & 0 & 0 \\ 0 & 0.08 & 0 & 0 & 0 \\ 0 & 0 & 0.08 & 0 & 0 \\ 0 & 0 & 0 & 0.08 & 0 \\ 0 & 0 & 0 & 0.08 & 0 \\ 0 & 0 & 0 & 0.08 & 0 \\ 0 & 0 & 0 & 0.08 & 0 \\ 0 & 0 & 0 & 0.08 & 0 \\ 0 & 0 & 0 & 0.5 & 0.5 \\ 0 & 0.5 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0.5 & 0.5 \\ 0 & 0.5 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0.5 & 0 \end{bmatrix}, \\ \tilde{K} &= \begin{bmatrix} 0.65 & 0 & 0 & 0 & 0 \\ 0 & 0.65 & 0 & 0 & 0 \\ 0 & 0 & 0.65 & 0 & 0 \\ 0 & 0 & 0 & 0.65 & 0 \\ 0 & 0 & 0 & 0 & 0.65 \end{bmatrix}, \end{split}$$

where $f(x') = {x'}^2 / (1 + {x'}^2)$, $\lambda_1 = \lambda_2 = 2$, the time delays $\Re(m) = 4 + 2\sin(m\pi/2)$ and $\Re(m) = 4 + \sin(m\pi/2)$, so that $\Re_{\min} = 2$, $\Re_{\max} = 6$, $\Re_{\min} = 3$, $\Re_{\max} = 5$, coupling coefficient $\xi_1 = \xi_2 = 0.2$. The simulation results for the trajectories of mRNA and protein concentrations in Example 1 are presented in Figs. 1-5.



Fig. 1 The trajectory of $x_1(m,n)$ and $y_1(m,n)$, (a) $x_1(m,n)$, (b) $y_1(m,n)$



Fig. 2 The trajectory of $x_2(m,n)$ and $y_2(m,n)$, (a) $x_2(m,n)$, (b) $y_2(m,n)$



Fig. 3 The trajectory of $x_3(m,n)$ and $y_3(m,n)$, (a) $x_3(m,n)$, (b) $y_3(m,n)$



Fig. 4 The trajectory of $x_4(m,n)$ and $y_4(m,n)$, (a) $x_4(m,n)$, (b) $y_4(m,n)$



Fig. 5 The trajectory of $x_5(m,n)$ and $y_5(m,n)$, (a) $x_5(m,n)$, (b) $y_5(m,n)$

Based on the references [15, Theorem 1], [18, Remark 2], [19, Theorem 1], and Theorem 1 of this paper, the maximum delay $\theta_{\max} = \theta_{\max}$ is derived when $\tau_1 = \tau_2 = \tau \in \{0.1, 0.3, 0.5, 0.7, 0.9, 1.0\}$ and $\mu_1 = \mu_2 = \mu > 1$. The following illustrations are provided for Tab. 1:

Tab 1. Upper bounds on $\theta_{\text{max}} = \vartheta_{\text{max}}$ with different τ

Case	0.1	0.3	0.5	0.7	0.9	1.0
[15, Theorem 1]	∞	∞	8	8	∞	3.9616
[18, Remark 2]	∞	∞	∞	∞	00	5.4571
[19, Theorem 1]	∞	∞	∞	∞	2.8994	\
Theorem 1	∞	∞	00	∞	00	∞

(1) If $\mu \le 0.7$, it is deemed achievable to satisfy the LMI conditions outlined in the aforementioned references and Theorem 1.

(2) When $\mu = 0.9$, the LMIs conditions specified in [19, Theorem 1] are feasible, whereas the LMI conditions presented in [15, Theorem 1], [18, Remark 2], and Theorem 1 of this paper are infinite.

(3) When $\mu = 1$, the LMIs conditions discussed in [15, Theorem 1] and [18, Remark 2] are feasible, while the LMI conditions in [19, Theorem 1] are not. Only the LMI conditions from Theorem 1 of this paper remain infinite.

Therefore, within the specified range $\tau \le 1$, Theorem 1 of this paper exhibits a reduced level of conservativeness compared to the other theorems mentioned.

B. Robust stability of proposed discrete-time RGNs with molecular Brownian motion

Considering the Brownian motion for Eq. (9), $H_1 = H_2 = 1$, by using the Toolbox YALMIP in MATLAB to solve the Eqs. (38)-(40), we can obtain the following feasible solution:

	123.7624	-3.6860	30.4576	-24.3507	1.2589]
	-3.6860	100.0948	4.3267	26.7041	-30.3114	
$P_1 =$	30.4576	4.3267	160.8677	31.5952	-0.9129	,
	-24.3507	26.7041	31.5952	128.1865	-6.2252	
	1.2589	-30.3114	-0.9129	-6.2252	153.6969	
	213.5355	-11.7444	0.2031	-14.9690	-15.0062	2]
	-11.7444	223.8458	-14.5358	0.6587	-6.3989	
$P_{2} =$	0.2031	-14.5358	204.9699	2.9470	-0.1778	
	-14.9690	0.6587	2.9470	216.3033	14.7650	
	-15.0062	-6.3989	-0.1778	14.7650	201.8289	
	[12.8719	-0.7229	3.2591	-2.2803	0.0723	
	-0.7229	10.9296	0.6907	2.6611	-3.3137	
$P_3 =$	= 3.2591	0.6907	17.4109	3.5905	-0.2864	,
	-2.2803	2.6611	3.5905	13.7605	-0.9807	
	0.0723	-3.3137	-0.2864	-0.9807	15.9501	
	√ 48.9448	-8.2973	-1.9276	-8.5427	-10.5340]
	-8.2973	58.4982	-10.3107	-1.6811	-2.2717	
$P_{4} =$	-1.9276	-10.3107	40.6860	-0.0330	-0.0792	,
	-8.5427	-1.6811	-0.0330	50.8505	10.4751	
	-10.5340	-2.2717	-0.0792	10.4751	38.5927	

	2.7042	-0.1259	0.9816	-0.5557	0.0805]	
	-0.1259	2.1523	0.3358	0.8485	-0.9746	
$R_{1} =$	0.9816	0.3358	4.2993	1.1904	-0.2049	,
	-0.5557	0.8485	1.1904	3.0357	-0.4269	
	0.0805	-0.9746	-0.2049	-0.4269	3.6748	
	∟ [1 7331	-0.0651	0 6060	-0 3321	0.0501	
	-0.0651	1 4070	0.0007	0.5381	-0.6028	
$R_2 =$	-0.0051	0.2164	0.2104	0.5501	0.1512	
		0.5381	0.7606	1 9/89	-0.2752	,
	0.0501	-0.6028	-0.1512	-0.2752	2 3320	
		-0.0020	-0.1312	-0.2752	2.3320	
	5.7483	-0.0526	0.1349	-0.1986	-0.0597	
P	-0.0526	5.6706	-0.0627	0.1248	-0.1449	
$R_3 =$	= 0.1349	-0.0627	5.8235	0.1382	0.0078	,
	-0.1986	0.1248	0.1382	5.7519	0.0637	
	0.0597	-0.1449	0.0078	0.0637	5.8304	
	5.7039	0.0074	0.2253	-0.2084	0.0196	
	0.0074	5.4746	0.0183	0.2110	-0.2036	
$R_{4} =$	= 0.2253	0.0183	5.9165	0.2123	0.0106	,
	-0.2084	0.2110	0.2123	5.6941	-0.0178	
	0.0196	-0.2036	0.0106	-0.0178	5.9395	
	[16.5609	-0.8663	5.1341	-3.5436	0.3629	
	-0.8663	12.9783	1.2278	4.2080	-5.0871	
$Q_1 =$	5.1341	1.2278	23.4792	5.4297	-0.2733	,
	-3.5436	4.2080	5.4297	17.7222	-1.6074	
	0.3629	-5.0871	-0.2733	-1.6074	21.6668	
	[10.9880	-0.5090	3.1548	-2.2462	0.1975	
	-0.5090	8.7228	0.7094	2.6094	-3.1257	
$Q_2 =$	3.1548	0.7094	15.1520	3.3182	-0.1488	,
	-2.2462	2.6094	3.3182	11.6579	-0.9199	
	0.1975	-3.1257	-0.1488	-0.9199	14.1244	
	[12.3794]	0.1271	0.2321	-0.0822	0.1614	
	0.1271	12.0238	0.1539	0.2238	-0.1548	
$O_2 =$	0.2321	0.1539	12.6806	0.1934	0.0127	
~,	-0.0822	0.2238	0.1934	12.3398	-0.1533	ĺ
	0.1614	-0.1548	0.0127	-0.1533	12.7364	
	L □ 33 5527	0.0635	0.0271	0.0465	0 0775]	
	0.0635	33,4630	0.0747	0.0279	0.0044	
0.=	0.0271	0 0747	33 6230	0.0122	0.0020	
\mathbf{z}_4	0.0465	0.0279	0.0122	33,5365	-0.0748	,
	0.0775	0.0044	0.0020	-0.0748	33.6417	
	L [28.2705	-1.0388	-0 6300	0 6731	_1 6035]	1
	-1 0388	-1.0500	-0.0377	-0.0751	-0.5944	
۸ –	-0.6300	-1 3030	-1.3039	-0.2000	-0.3944	
· •1 -	-0 6731	-0 2060	-0 1083	28 7993	1 3151	'
	-1 6035	-0.2000	-0.1003	1 3151	26 5794	
ſ		12 0501	3 0640	12 5407	17 0107	י 7
	12 9591	-13.8381	-5.9049	-13.342/	-1/.910/	1
	-13.8381	17 2242	-11.2343	-3.1103	-3./813	
1 1 ₂ =	-3.9049	-11.2040	.0 1811	56 8761	-0.4444	
	-13.3427	-3.1103	-0.4811	17 5052	35 3414	
	-1/.710/	-2.1013	-0.4444	17.3032	55.5414	

```
25.9074 -1.9785 -1.3087 -1.1906 -3.1202
     -1.9785 27.9776 -2.4724 -0.3971 -1.1587
T_1 =
     -1.3087 -2.4724 24.5675 -0.2367 -0.6299
     -1.1906 -0.3971 -0.2367 26.9743
                                      2.4963
     -3.1202
            -1.1587
                     -0.6299
                              2.4963
                                     22.5941
                      3.8109 -3.6727
                                      0.0575
     18.7595 -0.3106
     -0.3106 15.1752 0.0214
                             3.4803 -3.7849
     3.8109
             0.0214 22.3917
                              3.5736
                                      0.2704
S_1 =
     -3.6727
             3.4803
                      3.5736
                             18.7794
                                      -0.1615
     0.0575
            -3.7849
                      0.2704 -0.1615 22.5104
     25.4054 -0.7231
                      0.3288 -1.2286 -0.9016
     -0.7231 25.7523 -0.8859
                              0.3244 -0.6595
     0.3288 -0.8859
                     25.1405
                              0.4728
                                      0.0106
S_{2} =
                      0.4728 25.5519
                                      0.8999
     -1.2286
             0.3244
     -0.9016 -0.6595
                     0.0106 0.8999 25.0024
```

 $\rho = 2.0809$.

From Fig. 6, it can be observed that when the values of ξ_1 and ξ_2 fall within the range of region I, the system is robustly stable. Nevertheless, should the values of ξ_1 and ξ_2 reside within the confines of region II, the proposed GRN model ceases to exhibit stability.



Fig. 6 Determining the stability of Eq. (9) under different coupling coefficients.

V. CONCLUSION

In this seminal investigation, we introduce an innovative methodology aimed at integrating reaction-diffusion mechanisms into discrete-time GRNs. Our principal objective revolves around scrutinizing the robust stability of these networks in the presence of time-varying delays and Dirichlet boundary conditions, leveraging advanced Lyapunov-Krasovskii functions. Furthermore, we undertake a comprehensive analysis of asymptotic stability concerning GRNs incorporating reaction-diffusion terms alongside Brownian motion. This unprecedented inquiry marks the initial attempt to incorporate reaction-diffusion phenomena into discrete-time GRNs. To substantiate the efficacy and validity of our novel approach, we furnish detailed numerical examples and simulation outcomes. These findings serve to corroborate the accuracy and efficacy of our methodology, thus emphasizing its potential to significantly impact the realm of gene regulatory network modeling and analysis.

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