The implementation of Impulsive Gene Regulatory Networks Applying the Message Passing Interface

M. Kostadinova - Gocheva

***Abstract*—This paper introduces a parallel implementation of Impulsive Gene Regulatory Networks (GRNs) using the Message Passing Interface (MPI), with a focus on enhancing system robustness through *h*-manifolds analysis. Impulsive GRNs model sudden, discrete changes in gene expression that occur due to environmental or internal factors, posing challenges for accurate and scalable simulation. To address this, we develop an MPI-based framework that partitions the network into subsystems processed concurrently, enabling real-time synchronization of impulsive events. In addition to improving computational efficiency, we incorporate stability criteria to ensure the robustness of the system under uncertainty and external disturbances. This technique allows evaluation and design of gene regulatory networks that can be scalable and quick in simulation, as well as robust against changes. Simulation results demonstrate both performance gains and enhanced system stability, making this method suitable for large-scale biological modeling in high-performance computing environments.**

***Keywords*—gene regulatory networks, impulses, mathematical model, parallel programming**

I. INTRODUCTION

To understand how complicated dynamical behavior of gene regulatory network (GRN) systems, it is logical to employ neural networks (NNs) as dynamical systems characterized by the interconnections among genes (mRNA), proteins, and small molecules. The defined structure established by these models helps practitioners in addressing a significant challenge in estimating network connectivity from experiments: the limitation that only certain representative subsets of neurons can be recorded concurrently. This modeling approach has been extensively used by many researchers [1]-[5].

According to their extensive applications delayed GRNs have attracted much interest from various researchers [6]-[10], including several recent articles. Delay effects are often seen in neural network modeling applications [11], [12]. Delay effects are often seen in neural network modeling applications. Additionally, with the limited transmission speed of information in everyday situations, time delays are inevitable in the spreading of signals within biological networks [13].

Stability is the most extensively explored dynamical characteristic of gene regulatory network models. It is complexly associated with synchronization and regulation. Even so, the current findings on the stability of Gene Regulatory Network (GRN) models have mostly been based on Lyapunov-type ideas of asymptotic and exponential stability. The global asymptotic stability criteria for gene regulatory networks with time-varying delays are established in [9]. Global exponential stability criteria for Gene Regulatory Networks with constant and spreading delays have been proposed in [12], [13]. An investigation of asymptotic stability has been conducted, and effective criteria for the asymptotic stability of gene regulatory network states under impulsive influences have been established in [14]-[16].

Even so, for models with several equilibrium points, the notion of stability for integral manifolds of states is more significant [8], [9], [12]-[16]. However, for models with many equilibrium points, the principle of stability for integral manifolds of states becomes more significant [17]. Integral manifolds are specifically defined by a function *h*. The extended concept of stability for *h*-manifolds is employed to examine the stability characteristics of various probable manifolds of trajectories known as *h*-manifolds. The concepts of stability in *h*-manifolds are notably adaptable as they encompass the stability of an individual state. [18]-[23]. The stability notions of *h* manifolds provide significant practical advantages and applications, and their previous absence in the study of GRNs stimulates our attention.

The Lyapunov direct approach is widely recognized for its extensive application in analyzing the qualitative behavior of many systems, particularly in problems with stability [24]-[26].

The above described factors were the impetus for our practical analysis of a delayed impulsive GRN using a Lyapunov-based *h*-manifold approach. The fundamental contributions of our research are:

a) In opposition to the findings in [6]-[12], we incorporate impulsive effects, rendering the model more comprehensive and facilitating the utilization of impulsive control methodologies;
b) As opposed to the impulsive Gene Regulatory Networks examined in [14], [16], [27], [28], the model described here incorporates time-varying transcriptional and translational delays, hence enhancing its realism.
c) The extended hybrid idea of practical stability for the *h*-manifold is incorporated into the delayed impulsive GRN model. This enables us to extend several established stability conclusions for delayed impulsive GRNs [14]-[16], [28], [29], [30] to the *h*-manifold scenario, taking into account the realistic stability extension;
d) The Lyapunov function approach is utilized, providing practical stability conditions for *h*-manifolds in relation to the model.
e) Robust stability analysis is conducted, and innovative criteria are developed to ensure the

robust practical stability of *h*-manifolds associated with the impulsive GRN.

In this paper, we demonstrate a practical realized model and explore the effectiveness of a parallel system.

Parallel programming is essential for analyzing impulsive genomic networks for several key reasons:

- High computational complexity

Stochasticity: Impulsive networks are frequently represented using stochastic differential equations (SDEs) or algorithms that replicate random jumps (impulses). A simulation is highly time-consuming, as it necessitates a limited number of time steps for precision.

Replicates: The stochastic characteristics of the simulations necessitate that, for the results (means, variances, probability distributions) to have statistical significance, hundreds, thousands, or even millions of independent simulations must be performed under identical beginning settings. This task is well-suited for parallelization.

- Parametric exploration

Monitoring the network's activity includes traversing a large parameter space (constant speed, impulse values, thresholds, cutoffs).

Parallel programming enables simultaneous execution of simulations with varying parameter settings, significantly expediting the process of detailing the system's behavior.

- Model complexity

Realistic genetic networks include lots of elements (genes, mRNAs, proteins) and complex nonlinear interactions among them. Simulations of extensive models are extremely demanding for an individual CPU. Parallel methods (especially with data partitioning) can distribute the computations to different parts of the network or to different equations within a single simulation (although this is more difficult for impulsive systems).

- Big data analysis

Many simulations provide huge amounts of data. Post-processing, including statistical analysis, visualization, and pattern recognition, can also optimize performance using parallel processing.

- Time constraints

Researchers often need fast results for hypothesis testing, model validation, or interaction with experimental data. Parallel execution on a multi-core computer or computing cluster could reduce the processing time from days or weeks to hours or minutes [31]-[35].

The Message Passing Interface MPI is a portable message passing standard that facilitates the development of parallel applications and libraries.

The standard defines the syntax and semantics of a core of library routines useful to a wide range of users writing portable message passing programs in Fortran or C. MPI is used to specify the communication among a set of processes forming a concurrent program. The message passing paradigm is attractive be cause of its wide portability and scalability. [36]

OpenMP (OpenMP 2009), the Open standard for shared memory Multi Processing, was designed to facilitate the creation of programs that are able to exploit the features of parallel computers where memory is shared by the individual processor cores. OpenMP is intended to facilitate the construction of portable parallel programs by enabling the application developer to specify the parallelism in a code at a high level, via an approach that moreover permits the incremental insertion of its constructs.

However, it also permits a low-level programming style, where the programmer explicitly assigns work to individual threads [37].

II. MATHEMATICAL MODEL

Let $\mathbb{R}^n$ be the n - dimensional Euclidean space,

$$||x|| = \sum_{i=1}^{n} |x_i|$$

represent the norm of a vector $x = (x_1, x_2, \dots, x_n)^T \in \mathbb{R}^n$, $\mathbb{R}_+ = [0, \infty)$ and $\mathbb{R}_+^n = \mathbb{R}_+ \times \dots \mathbb{R}_+$.

Ren and Cao examined in [9] a delayed genetic regulation network defined by a system of delayed differential equations.

$$\begin{cases} \dot{M}_i(t) = -a_i M_i(t) + \sum_{j=1}^{n} w_{ij} f_j\left(P_j\left(t-\sigma(t)\right)\right) + B_{i,} \\ \dot{P}_i(t) = -c_i p_i(t) + d_i M_i\left(t-\tau(t)\right), \qquad i = 1, \dots, n, \end{cases} \tag{1}$$

that regulates the concentrations of mRNA $M_i(t)$ and protein $P_i(t)$ of the *i*th node, respectively, at time *t*, where $i, i = 1, 2, \dots, n$ is the number of the node, the positive constants a_i and c_i represent the decay rates of mRNA and protein, respectively, d_i are the translation rates, f_j are the regulatory functions defined as

$$f_i(x) = \frac{\left(x/\beta_j\right)^{H_j}}{1 + \left(x/\beta_j\right)^{H_j}}$$

where H_i are the Hill coefficients and β_j are positive constants, $B_i(t) = \sum_{j \in I_i} b^{ij}$, b_{ij} represents a constant that shows the dimensionless transcriptional rate of a transcription-regulating factor *j* to *i*, I_i is the set of all the *j* which is a repressor of gene *i*, and the coupling coefficients w_{ij} are defined as

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

$\sigma(t)$ is a transcriptional delay and $\tau(t)$ is a translational delay.

The term $\sum_{j=1}^{n} w_{ij} f_j\left(P_j\left(t-\sigma(t)\right)\right)$ is called the sum input function (SUM) logic as in [8] and the cited references. The regulatory function f_j is monotonically growing for each $j = 1, 2, \dots, n$, i.e., there exist constants l_j such that

$$0 \le \frac{f_j(\xi_1) - f_j(\xi_2)}{\xi_1 - \xi_2} \le l_j, \tag{2}$$

for all $\xi_1, \xi_2 \in \mathbb{R}$, $\xi_1 \neq \xi_2$.

This research is to apply the delayed GRN model (1) to an impulsive setting. Analyze a series of discrete times $\{t_k\}$, $t_k \in \mathbb{R}_+$, $k = 1,2, \dots$ are such that

$$t_1 < t_2 < \cdots < t_k < \cdots, \lim_{k\to\infty} t_k = \infty$$

To implement the concept of impulsive control, we provide a delayed impulsive Gene Regulatory Network (GRN) model defined as

$$\begin{cases} \dot{M}_i(t) = -a_i M_i(t) + \sum_{j=1}^{n} w_{ij}(t) f_j\left(P_j\left(t-\sigma_j(t)\right)\right) + B_i(t), t \neq t_k, \\ \dot{P}_i(t) = -c_i p_i(t) + d_i(t) M_i\left(t-\tau_i(t)\right), t \neq t_k, \\ M_i(t_k^+) = M_i(t_k) + \Theta_{ik}\left(M_i(t_k)\right), \\ P_i(t_k^+) = P_i(t_k) + \Omega_{ik}\left(P_i(t_k)\right), \end{cases} \quad (3)$$

where $\sigma_j(t)$ and $\tau_i(t)$ are time delays for mRNAs j and protein i, respectively, $0 \le \sigma_j(t) \le \sigma$, $0 \le \tau_i(t) \le \tau$, $i, j = 1, 2, \dots, n$, the coupling parameters $w_{ij}(t)$, the translation rates $d_i(t)$ and $B_i(t)$ are continuous functions, the quantities $M_i(t_k) = M_i(t_k^-)$ and $P_i(t_k) = P_i(t_k^-)$ represent the concentration of the ith mRNA and ith protein at time t_k (before an impulsive perturbation), respectively, $M_i(t_k^+)$ and $P_i(t_k^+)$ are the concentration of the ith mRNA and ith protein after an impulsive jump at the moment t_k, respectively, the functions Θ_{ik} and Ω_{ik} are the impulsive controllers that represent the level of abrupt changes of $M_i(t)$ and $P_i(t)$ at the impulsive moments t_k, i.e. $\Delta M_i(t_k) = M_i(t_k^+) - M_i(t_k) = \Theta_{ik}\left(M_i(t_k)\right)$ and $\Delta P_i(t_k) = P_i(t_k^+) - P_i(t_k) = \Omega_{ik}\left(P_i(t_k)\right)$, $i = 1, 2, \dots, n$, $k = 1, 2, \dots$.

Remark 1. The proposed model (5) extends the delayed model (1) and similar designs examined [6]-[8], [11], [12] in the impulsive situation. The impulsive model (5) employs impulsive discrete times and the impulsive functions Θ_{ik} and Ω_{ik} to regulate the qualitative behavior of the GRN (1). So, the impulsive control system (5) can be defined as a closed-loop system of (1) managed by the impulsive controllers that relate to these functions Θ_{ik} and Ω_{ik}.

The impulsive controllers will be considered to be in the form

$$\begin{cases} \Delta M_i(t_k) = \Theta_{ik}\left(M_i(t_k)\right) = \alpha_{ik}\left(M_i(t_k)\right) \\ \Delta P_i(t_k) = \Omega_{ik}\left(P_i(t_k)\right) = \gamma_{ik}\left(P_i(t_k)\right) \end{cases} \quad (4)$$

$i = 1, 2, \dots, n, \quad k = 1, 2, \dots$

Then, we can be rewrite the model (3) as

$$\begin{cases} \dot{M}_i(t) = -a_i M_i(t) + \sum_{j=1}^{n} w_{ij}(t) f_j\left(P_j\left(t-\sigma_j(t)\right)\right) + B_i(t), t \neq t_k, \\ \dot{P}_i(t) = -c_i p_i(t) + d_i(t) M_i\left(t-\tau_i(t)\right), t \neq t_k, \\ \Delta M_i(t_k) = \alpha_{ik}\left(M_i(t_k)\right), \\ \Delta P_i(t_k) = \gamma_{ik}\left(P_i(t_k)\right), \end{cases} \quad (5)$$

where $i = 1, 2, \dots, n$, $k = 1, 2, \dots$, the constant sequences $\{\alpha_{ik}\}, \{\gamma_{ik}\} \in \mathbb{R}$ define the level of intensity (magnitude) of sudden changes of $M_i(t)$ and $P_i(t)$ at the impulsive moments t_k and can be applied as controls.

Let $\eta = \max\{\sigma, \tau\}$. We introduce the class $PCB_\eta = PCB\left[[-\eta, 0], \mathbb{R}_+^{2n}\right]$, of functions $\psi : [-\eta, 0] \to \mathbb{R}_+^{2n}$ that are bounded, piecewise continuous on $[-\eta, 0]$ with points of jump discontinuities at which the one-sided limits exist and the functions are continuous from the left. The norm of a function $\psi \in PCB\left[[-\eta, 0], \mathbb{R}_+^{2n}\right]$ that corresponds to the norm $\|.\|$ will be denoted by

$$\|\psi\|_\eta = \sup_{\upsilon \in [-\eta, 0]} \|\psi(\upsilon)\|$$

Let $\phi \in PCB\left[[-\tau, 0], \mathbb{R}_+^{2n}\right]$, $\phi = (\phi_1, \phi_2, \dots, \phi_n,)^T$ and $\varphi \in PCB\left[[-\sigma, 0], \mathbb{R}_+^{n}\right]$, $\varphi = (\varphi_1, \varphi_2, \dots, \varphi_n,)^T$. We consider initial conditions for the model (5) of the type

$$\begin{cases} M_i(\upsilon; 0, \phi) = \phi_i(\upsilon), -\tau \le \upsilon \le 0, \\ P_i(\upsilon; 0, \varphi) = \varphi_i(\upsilon), -\sigma \le \upsilon \le 0 \\ M_i(0^+; 0, \phi) = \phi_i(0),\ P_i(0^+; 0, \varphi) = \varphi_i(0), \end{cases} \quad (6)$$

$i = 1, 2, \dots, n$, where $M_i(0^+; 0, \phi)$ and $P_i(0^+; 0, \varphi)$ are the right-hand side limits at $t = 0$

The solution

$$\begin{aligned} \left(M(t), P(t)\right)^T &= \left(M(t; 0, \phi), P(t; 0, \varphi)\right)^T \\ &= (M_1(t; 0, \phi), M_2(t; 0, \phi), \dots, M_n(t; 0, \phi), \\ &\quad P_1(t; 0, \varphi), P_2(t; 0, \varphi), \dots, P_n(t; 0, \varphi))^T \end{aligned}$$

of the initial value problem (5), (6) is in general, a piecewise continuous function with points of discontinuity at the moments t_k, $k = 1, 2, \dots$, and according to the theory of impulsive differential systems [38]-[42] we assume that

$$\begin{gathered} M_i(t_k^-) = M_i(t_k),\ P_i(t_k^-) = P_i(t_k), \\ M_i(t_k^+) = M_i(t_k) + \alpha_{ik} M_i(t_k),\ P_i(t_k^+) = P_i(t_k) + \gamma_{ik} P_i(t_k) \end{gathered}$$

for $i = 1, 2, \dots, n$, $k = 1, 2, \dots$

The primary objective of this study is to establish practical stability criteria for the manifolds associated with the delayed impulsive control GRN model (5). To this end, for a continuous function $h = h(t, M, P), h: [-\eta, \infty] \times \mathbb{R}_+^n \times \mathbb{R}_+^n \to \mathbb{R}^l$, $l \le 2n$, we define the next manifolds called h – manifolds [20], [23], [42].

$$\begin{gathered} \mathcal{M}_t(2n-l) = \{(M, P)^T \in \mathbb{R}_+^n \times \mathbb{R}_+^n : h(t, M, P) = 0, \quad t \in [0, \infty)\}, \\ \mathcal{M}_{t,\eta}(2n-l) = \{(M, P)^T \in \mathbb{R}_+^n \times \mathbb{R}_+^n : h(t, M, P) = 0, \\ t \in [-\eta, 0]\}, \\ \mathcal{M}_t(2n-l)(\varepsilon) = \{(M, P)^T \in \mathbb{R}_+^n \times \mathbb{R}_+^n : \|h(t, M, P)\| < \varepsilon, \\ t \in [0, \infty)\}, \varepsilon > 0, \\ \mathcal{M}_{t,\eta}(2n-l)(\varepsilon) = \left\{\psi \in PCB_\eta : \|h(t, \psi)\|_\eta < \varepsilon, \quad t \in [-\eta, 0]\right\}, \end{gathered}$$

where $\|h(t, \psi)\|_\eta = \sup_{-\eta \le \upsilon \le 0} \left\|h\left(t, \psi(\upsilon)\right)\right\|$.

If we accept that the sets $\mathcal{M}_t(2n-l)(\varepsilon), \mathcal{M}_{t,\eta}(2n-l)(\varepsilon)$ are $(2n-l)$ - dimensional manifolds in $\mathbb{R}_+^{2n}$, we present the subsequent definitions of practical stability for the delayed impulsive GRN (5) for the function h.

Definiton 1. The delayed impulsive GRN (5) is said to be:

$(a)(\lambda, A)$ - practically stable with respect to the function h, if given (λ, A) with $0 < \lambda < A$, we have $\psi = (\phi, \varphi)^T \in \mathcal{M}_{t,\eta}(2n-l)(\lambda)$ implies

$$\big(M(t;0,\phi),P(t;0,\varphi)\big)^T \in \mathcal{M}_t(2n-l)(A), t \geq 0;$$

$(b)(\lambda, A)$ - globally practically exponentially stable with respect to the function h, if given (λ, A) with $0 < \lambda < A$ and $\psi = (\phi, \varphi)^T \in \mathcal{M}_{t,\eta}(2n-l)(\lambda)$ there exist positive constants ν, μ

$$\big(M(t;0,\phi),P(t;0,\varphi)\big)^T \in \mathcal{M}_t(2n-l)\big(A + \nu\|h(0^+,\psi)\|_\eta e^{-\mu t}\big)\ t \geq 0.$$

Remark 2. The concepts of stability about a function h are very important in various applications. The h-manifolds delineated by this function could represent manifolds of trajectories constrained by the function *h*. Therefore, the concept of stability in *h*-manifolds provides a robust methodology applicable not just to individual solutions but also to cases involving manifolds of solutions. $M_t(2n-l)$ are attractors for the models. Thus, the stability with respect to *h*-manifolds extends numerous single state stability concepts studied in [14]-[16], [28]-[30] practical stability.

Remark 3. Additionally, practical stability is different from Lyapunov stability and can be used in situations where the model doesn't have Lyapunov stability, while the state behavior remains acceptable for practical needs [25]. It is also seen from part (b) of Definition 1 that for $A = 0$ the global practical exponential stability implies the global exponential stability of the *h* -manifold $\mathcal{M}_t(2n-l)$ [42].

Remark 4. Also, if $h(t,M,P) = (M,P)$, reduces to the practical stability of the zero solution of the delayed impulsive GRN model (5), which is examined in [43].

Remark 5. The practical stability of model (5) with respect to the function h guarantees that the set $\{(t,M,P): t \in \mathbb{R}_+,\ (M,P)^T \in \mathcal{M}_t(2n-l)(A)\}$ is a positively invariant set of (5).

Next, the fundamentals of the method of piecewise continuous Lyapunov functions $\mathcal{V}$: $\mathbb{R}_+ \times \mathbb{R}^{2n} \to \mathbb{R}_+$ will be given [38], [40], [43].

Let $\mathcal{X}_k = (t_{k-1}, t_k) \times R^{2n},\ k = 1,2,\dots,\ t_0 = 0,$

$$\mathcal{X} = \bigcup_{k=1}^{\infty} \mathcal{X}.$$

Definition 2. A function $\mathcal{V}$: $R_+ \times \mathrm{R}^{2n} \to R_+$ belongs to the class $\mathcal{V}_0$ if:

1. The function $\mathcal{V}$ is continuous on $\cup_{k=1}^{\infty} \mathcal{X}_k$ and $\mathcal{V}\ (t,0,0) = 0$ for $t \geq 0$;

2. On each of the sets $\mathcal{X}_k$ the function $\mathcal{V}$ is locally Lipschitz continuous on the variables $(M,P)^T$;

3. There exist the finite limits

$$\mathcal{V}(t_k^-,M,P) = \lim_{\substack{t \to t_k \\ t<t_k}} \mathcal{V}(t,M,P), \mathcal{V}(t_k^+,M,P) = \lim_{\substack{t \to t_k \\ t<t_k}} \mathcal{V}(t,M,P)$$

and

$$\mathcal{V}(t_k^-,M,P) = \mathcal{V}(t_k,M,P)$$

for each $k = 1,2,\dots$

For a function $\mathcal{V} \in \mathcal{V}_0$ and $\psi = (\phi,\varphi)^T \in PCB\left[[-\eta,0],\mathbb{R}^{2n}\right]$, we will define the derivative with respect to the model (5) is defined by

$$D^+_{(5)}\mathcal{V}\big(t,\phi(0),\varphi(0)\big)$$

$$= \lim_{\upsilon \to 0^+} sup \frac{1}{\upsilon}\big[\mathcal{V}\big(t+\upsilon, M(t+\upsilon;0,\phi), P(t+\upsilon;0,\varphi)\big) - \mathcal{V}\big(t,\phi(0),\varphi(0)\big)\big],$$

where $\big(M(t;0,\phi),\ P(t;0,\varphi)\big)^T$ is the state of (5) with $(\phi,\varphi)^T \in PCB\big[[-\eta,0],\mathbb{R}^{2n}\big]$.

The following result from [23] will be applied in the proofs of our main results.

Lemma 1. Assume that the Lyapunov function $\mathcal{V} \in \mathcal{V}_0$ is such that for $\psi = (\phi,\varphi)^T \in PCB\big[[-\eta,0],\mathbb{R}^{2n}\big]$ *and* $t \geq 0$:

(i) $\mathcal{V}\big(t^+,\phi(0)+\Delta(\phi),\varphi(0)+\Delta(\varphi)\big) \leq \mathcal{V}\big(t,\phi(0),\varphi(0)\big),$ $t = t_k,\ k = 1,2,\dots;$

(ii) For $\mu, \rho \geq 0$, the inequality

$$D^+_{(5)}\mathcal{V}\big(t,\phi(0),\varphi(0)\big) \leq -\mu\mathcal{V}\big(t,\phi(0),\varphi(0)\big) + \rho,\ t \neq t_k$$

is satisfied whenever

$$\mathcal{V}\big(t+\upsilon,\phi(\upsilon),\varphi(\upsilon)\big) \leq \mathcal{V}\big(t,\phi(0),\varphi(0)\big),\ -\eta \leq \upsilon \leq 0.$$

Then

$$\mathcal{V}[\big(t,M(t;0,\phi),P(t;0,\varphi)\big) \leq \sup_{\substack{-\eta \leq \upsilon \leq 0 \\ t \geq 0.]}} \mathcal{V}\ \big(0,\phi(\upsilon),\varphi(\upsilon)\big)e^{-\mu t} + \frac{\rho}{\mu},$$

Remark 6. The comparison Lemma 1 and related results that involve the Lyapunov-Razumikhin condition (7) are intensively applied in the study of the stability properties of different classes of delayed differential systems.

III. MAIN RESULTS

1. STABILITY OF H -MANIFOLDS. RESULTS.

In this section, we will apply the Lyapunov-Razumiknin approach to study the practical stability properties of the delayed impulsive control GRN model (5) with respect to a function *h*.

We will begin with criteria for practical stability with respect to *h*-manifolds.

Theorem 1. Assume that $0 < \lambda < A$ and:

(i) There exist positive constants $K_{ij}^{(1)}$, and $K_i^{(2)}$, such that

$$\big|w_{ij}(t)\big| \leq K_{ij}^{(1)},\ \ |d_i(t)| \leq K_i^{(2)}$$

for $i,j = 1,2,\dots,n$, and $t \in \mathbb{R}_+$;

(ii) The model's parameters satisfy

$$\min_{1 \leq i \leq n}\{a_i,c_i\} \geq \max_{1 \leq i \leq n}\left\{K_i^{(2)},\ \sum_{j=1}^{n} K_{ji}^{(1)} l_i\right\};$$

(iii) $B_i(t) = 0,\ i = 1,2,\dots,n,\ t \geq 0;$

(iv) The constants α_{ik} and γ_{ik} are such that

$$-2 \leq \alpha_{ik} \leq 0, \quad -2 \leq \gamma_{ik} \leq 0,$$

$i = 1,2,\dots,n, \qquad k = 1,2,\dots;$

(v) For the function $h(t,M,P)$ the next inequalities are satisfied

$$||h(t,M,P)|| \leq ||M(t)|| + ||P(t)|| \leq \Lambda(H)||h(t,P,M)||,\ (t,P,M) \in R_+ \times R^{2n}$$

where $\Lambda(H) \geq 1, \Lambda(H)\lambda < A$ and $0 < H \leq \infty$.

Then, the delayed impulsive control GRN (5) is (λ, A) −practically stable with respect to the function h.

Then the delayed impulsive GRN (5) is robustly (λ, A) - globally practically exponentially stable with respect to the function h.

In Fig. 1 and Fig. 2, the practical realized model is shown.

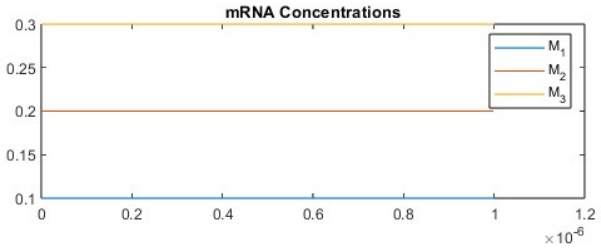

Fig 1. mRNA concentrations y(t)

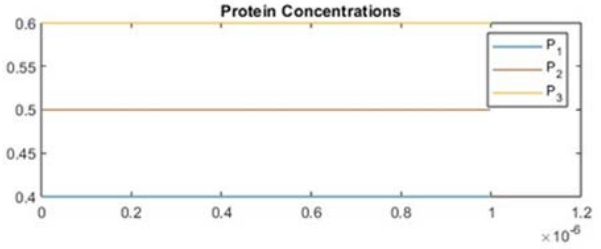

Fig 2. Protein concentrations y(t)

Fig. 1 and Fig. 2 show the delayed impulsive GRN is robustly globally practically exponentially stable.

2. HIGH PERFORMANCE PARALLEL ARCHITECTURE

The effectiveness of a parallel system is mainly influenced by the available parallel algorithms and the architecture of the system on which processing is executed. The graphical representation reflects the relationship between speedup in parallel computations and the number of processors used according to Amdahl's Law. The law defines the theoretical limit of acceleration through parallelization of program code and is formulated as follows: [45]

$$S = \frac{1}{(1-p)+\frac{p}{N}} \qquad (7)$$

S - the speedup of the system,

p - is the proportion of the execution time of the part that takes advantage of the improved resources,

$(1-p)$ - represents the sequential part, which remains unchanged regardless of the number of processors.

n - the number of cores in the system

In Fig.3. shown the graph of the function thus shown based on the verified configuration.

The evaluation of scalability will be done according to the processing time of a mRNA and protein concentrations. The present study used the IGRNs model (3).

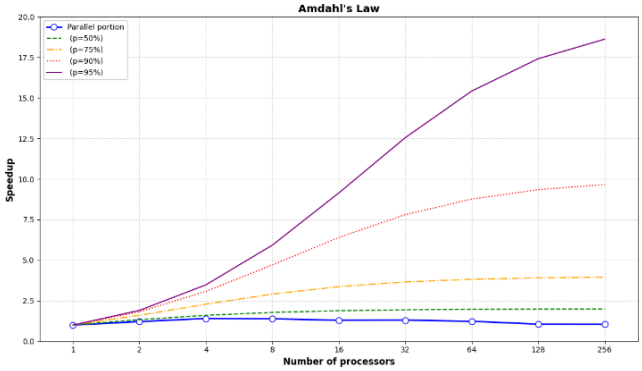

Fig. 3. Analytical assessment of the scalability of a parallel system based on an IGRNs model

The practically built parallel architecture used in the study consists of [46]:

- CPU: AMD Ryzen Threadripper 2990WX 32-Core Processor 3.00 GHz;
- RAM: 16 GB;
- Graphics card: ASUS Dual Radeon RX 580 O4G;

The algorithmization of the problem was concentrating on complexity and optimizing communication between the different processors. The results are shown in Fig. 4.

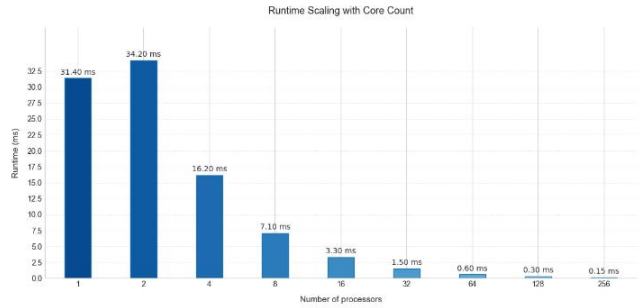

Fig 4. Time for the implementation of tasks.

Fig. 4 shows the execution time of the task based on the number of processors used. At the beginning, a limit to the increasing speedup is noticeable. As the number of processors used increases, the parallel part of the calculations is distributed over more computing units, which leads to a decrease in the total execution time. The results confirm the validity of Amdahl's law in the context of practical scalability.

IV. Conclusion

We apply the extended *h*-manifolds practical stability concept and formulate effective criteria that verify equal the practical stability and the global practical exponential stability of the model related to a manifold characterized by a continuous function *h*. Impulsive functions can be employed for the implementation of an impulsive control strategy. To improve the efficiency of parallel processing, the sequential component of the calculations must be reduced by modifying the algorithmic logic or using a more efficient parallel structure. In addition, every individual program has a suitable quantity of processors that maximizes the balance between speedup and use of resources.

References

[1] Karlebach, G., Shamir, R.: Modelling and analysis of gene regulatory networks. Nat. Rev. Mol. Cell Biol. 9, 770–780 (2008)

[2] Barbuti, R., Gori, R., Milazzo, P., Nasti, L.: A survey of gene regulatory networks modelling methods: From differential equations, to Boolean and qualitative bioinspired models. J. Membr. Comput. 2, 207–226 (2020)

[3] Guo, Y., Amir, A.: Stability of gene regulatory networks. arXiv:2006.00018 [physics.bio-ph] (2020) https://doi.org/10.48550/arXiv.2006.00018

[4] Wu, L., Liu, K., L, J., Gu, H.: Finite-time adaptive stability of gene regulatory networks stability. Neurocomputing 338, 222–232 (2019)

[5] Zhang, Q., Yu, Y., Zhang, J., Liang, H.: Using single-index ODEs to study dynamic gene regulatory network. PLoS ONE 13, e0192833 (2018)

[6] Chen, L., Aihara, K.: Stability of genetic regulatory networks with time delay. IEEE Trans. Circuits Systems I Fund. Theory Appl. 49 602–608 (2002)

[7] He, W., Cao, J.: Robust stability of genetic regulatory networks with distributed delay. Cogn Neurodyn. 2, 355–361 (2008)

[8] Li, Z., Chen, D., Liu, Y., Zhao, Y.: New delay-dependent stability criteria of genetic regulatory networks subject to time-varying delays. Neurocomputing 207, 763–771 (2016)

[9] Ren, F., Cao, J.: Asymptotic and robust stability of genetic regulatory networks with time-varying delays. Neurocomputing 71, 834-842 (2008)

[10] Zhang, X., Wang, Y., Wu, L.: Analysis and Design of Delayed Genetic Regulatory Networks. Springer, Cham (2019)

[11] Hong, H., Cortez, M.J., Cheng, Y.Y., Kim, H.J., Choi, B., Josić, K., Kim, J.K.: Inferring delays in partially observed gene regulation processes. Bioinform. 39, btad670 (2023)

[12] Zhang, L.N., Zhang, X.Y., Xue, Y., Zhang, X.: New method to global exponential stability analysis for switched genetic regulatory networks with mixed delays. IEEE Trans. Nanobiosci. 19, 308–314 (2020)

[13] Logeswari, S., Sriraman, R.: Exponential stability of gene regulatory networks with distributed delays. J. Math. Computer Sci., 38, 252–262 (2025)

[14] Arjunan, M.M., Abdeljawad, T., Anbalagan, P.: Impulsive effects on fractional order time delayed gene regulatory networks: Asymptotic stability analysis. Chaos Solitons Fract. 154, 111634 (2022)

[15] Sakthivel, R., Raja, R., Anthoni, S. M.: Asymptotic stability of delayed stochastic genetic regulatory networks with impulses. Phys. Scr. 82, 055009 (2010)

[16] Li, F., Sun, J.: Asymptotic stability of a genetic network under impulsive control. Phys. Lett. A. 374, 3177–3184 (2010)

[17] Stamova, I., Stamov, G.: Integral Manifolds for Impulsive Differential Problems with Applications. Academic Press, San Diego (2025)

[16] Stamov, G., Stamov, T., Stamova, I.: On the almost periodicity in discontinuous impulsive gene regulatory networks. Math. Methods Appl. Sci. (2021) \ https://doi.org/10.1002/mma.7828

[17] Stamov, T., Stamov, G., Stamova, I.: Fractional-order impulsive delayed reaction-diffusion gene regulatory networks: almost periodic solutions. Fractal Fract. 7, 384 (2023)

[18] Ghanmi, B.: Practical h−stability of nonlinear impulsive systems: A survey. In: A. Makhlouf, B., Hammami, M.A., Naifar, O. (eds.) State Estimation and Stabilization of Nonlinear Systems, Studies in Systems, Decision and Control, vol. 491, pp. 1-18. Springer, Cham (2023)

[20] Bohner, M., Stamov, G., Stamova, I., Spirova, C.: On *h*-manifolds stability for impulsive delayed SIR epidemic models. Appl. Math. Model. 118, 853–862 (2023)

[21] Perrone, D.: Stability of the Reeb vector field of *H*-contact manifolds. Math. Z. 263, 125–147 (2009)

[22] Rosenberg, H., Souam, R., Toubiana, E.: General curvature estimates for stable *H*-surfaces in *3*-manifolds applications. J. Differential Geom. 84, 623–648 (2010)

[23] Stamov, G., Gospodinova, E., Stamova, I. Practical exponential stability with respect to *h*-manifolds of discontinuous delayed Cohen–Grossberg neural networks with variable impulsive perturbations. Math. Model. Control 1, 26–34 (2021)

[24] Lasalle, J., Lefschetz, S.: Stability by Lyapunov Direct Method and Application. Academic Press, New York (1961)

[25] Lakshmikantham, V., Leela, S., Martynyuk, A.A.: Practical Stability of Nonlinear Systems. World Scientific, Teaneck (1990)

[26] Martynyuk, A.A.: Stability and control: theory, methods and applications. In: Advances in Stability Theory at the End of the 20th Century, vol. 13. Taylor and Francis, London (2003)

[27] Stamov, G., Stamov, T., Stamova, I.: On the almost periodicity in discontinuous impulsive gene regulatory networks. Math. Methods Appl. Sci. (2021) , https://doi.org/10.1002/mma.7828

[28] Stamov, T., Stamova, I.: Design of impulsive controllers and impulsive control strategy for the Mittag-Leffler stability behavior of fractional gene regulatory networks. Neurocomputing 424, 54-62 (2021)

[29] Qiu, J., Sun, K., Yang, C., Chen, X., Chen, X., Zhang, A.: Finite-time stability of genetic regulatory networks with impulsive effects. Neurocomputing 219, 9–14 (2017)

[30] Xue, Y., Zhang, Y., Li, J.: Stabilization of genetic regulatory networks with time-varying delays via event-triggered impulsive control. Math. Methods Appl. Sci. 47, 4970–4988 (2024)

[31] Gillespie, D. T. (2001). Approximate accelerated stochastic simulation of chemically reacting systems. The Journal of Chemical Physics, 115(4), 1716–1733.

[32] Zhou, Y., Liepe, J., Sheng, X., Stumpf, M. P., & Barnes, C. (2011). GPU accelerated biochemical network simulation. Bioinformatics, 27(6), 874–876.

[33] Nobile, M. S., Cazzaniga, P., Besozzi, D., & Mauri, G. (2014). GPU accelerated simulations of mass-action kinetics models with cupSODA. Journal of Supercomputing, 69(1), 17–24.

[34] Liu, X., & Chen, L. (2009). Impulsive control for stochastic nonlinear systems. Automatica, 45(3), 683-689.

[35] Zeiser, S., Franz, U., Wittlich, J., & Liebscher, V. (2010). Simulation of genetic networks modelled by piecewise deterministic Markov processes. I ET Systems Biology, 4(2), 113-123.

[36] Dongarra, J. J., Otto, S. W., Snir, M., & Walker, D. (1994, October). An introduction to the MPI standard. University of Tennessee and Oak Ridge National Laboratory; Oregon Graduate Institute of Science & Technology; IBM T.J. Watson Research Center.

[36] Message Passing Interface Forum, *MPI: A Message-Passing Interface Standard (Version 3.1)*. Jun. 4, 2015., https://www.mpi-forum.org/docs/mpi-3.1/mpi31report.pdf

[37] OpenMP Architecture Review Board, OpenMP Application Programming Interface (Version 5.2). Nov. 2023. https://www.openmp.org/spec-html/5.2/openmp.html

[38] Benchohra, M., Henderson, J., Ntouyas, J.: Impulsive Differential Equations and Inclusions. Hindawi, New York (2006)

[39] Haddad, W.M., Chellaboina, V.S., Nersesov, S.G.: Impulsive and Hybrid Dynamical Systems, Stability, Dissipativity, and Control. Princeton University Press, Princeton (2006)

[40] Li, X., Song, S.: Impulsive Systems with Delays: Stability and Control. Science Press & Springer, Singapore (2022)

[42] Stamova, I., Stamov, G.: Integral Manifolds for Impulsive Differential Problems with Applications. Academic Press, San Diego (2025)

[43] Stamova, I.M., Stamov, G.T.: Applied Impulsive Mathematical Models. Springer, Cham (2016)

[44] Cao, J., Stamov, T., Stamov, G., Stamova, I.: Impulsive controllers design for the practical stability analysis of gene regulatory networks with distributed delays. Fractal Fract. 7, 847 (2023)

[45] Amdahl, G. M. (1967). *Validity of the Single Processor Approach to Achieving Large-Scale Computing Capabilities.* AFIPS Conference Proceedings, 30: 483–485. doi:10.1145/1465482.1465560

[46] AMD, "AMD Ryzen Threadripper 2990WX 32-Core Processor – Product Specifications", AMD, [Online]. Available: https://www.amd.com. [Accessed: July 22, 2025].