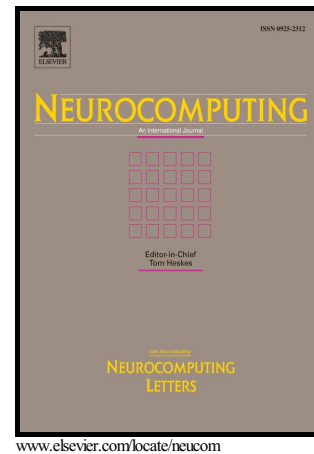


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Delay-dependent asymptotic stability criteria for genetic regulatory networks with impulsive perturbations

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Abstract

This paper considers the problem for asymptotic stability of genetic regulatory networks with impulse control using the delay partitioning approach. By using the direct Lyapunov method, a new Lyapunov-Krasovskii functional is introduced based on the decomposition approach. Time delays here are assumed to be time-varying and belong to the given intervals. When dealing with the time derivative of Lyapunov functional, a new tight integral inequality is adopted for bounding the cross terms. Then, a new less conservative delay-dependent stability criterion is formulated in terms of linear matrix inequalities (LMIs), which can be easily solved by the Matlab LMI toolbox. Finally, the proposed method is validated through the numerical simulation, which shows the effectiveness of the presented stability criteria.

Keywords. *Asymptotic stability; genetic regulatory network; impulse; Lyapunov-Krasovskii functional; linear matrix inequality.*

1 Introduction

Since the genetic regulatory networks have been introduced by MacDonald in 1989, various aspects of genetic networks such as boolean networks, Bayesian networks, differential equation models, stochastic master equation models have received a great deal of interest in areas of biology, engineering and other research fields. A great number of genes and proteins either directly or indirectly interact with one another in living cells. Such interaction make up a dynamic GRNs which acts as a complex dynamic system for controlling cellular functions. GRNs, structured by networks of regulatory interactions among DNA, RNA, and proteins, have received increasing attention within the past few decades. 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.

The study of GRN has got the interest of many researchers, many notable researches have proposed different kinds of mathematical models to describe GRN. Basically, there are two types of genetic network models, i.e. Boolean method and dynamical system method using ordinary differential [1, 2]. In Boolean models, the expression of each gene in the network is assumed to be either ON or OFF, no intermediate activity levels are ever taken into consideration, and the state of a gene is determined by the Boolean function of the states of other related genes [1]. While in the differential equation model, variables which describe the change rates of the concentration of gene products, such as mRNAs and proteins, are continuous values. The differential equation model outstand the Boolean model for its more secured accuracy. Also, from many experiment results, it is understood that time delays are inevitable due to the transcription, translation, diffusion, and translocation processes of genes, which will affect the entire dynamics of the biochemical systems [3, 4]. Hence, time delays should be taken into account when modeling the biochemical systems.

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