NEW RESULTS ON ASYMPTOTIC AND ROBUST STABILITY OF GENETIC REGULATORY NETWORKS WITH TIME-VARYING DELAYS

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Abstract. The robust asymptotic stability problem of genetic regulatory networks with time-varying delays is investigated. Based on a piecewise analysis method, the variation interval of the time delay is firstly divided into two subintervals, and then the convexity property of the matrix inequality and the free weighting matrix method are fully used in this paper. By using a Lyapunov functional approach and linear matrix inequality techniques, the stability criteria for the delayed genetic regulatory networks are expressed as a set of linear matrix inequalities (LMIs), which can lead to much less conservative analysis results. A genetic network example is given to illustrate that the results in this paper are more effective and less conservative than some existing ones.

Keywords: Genetic regulatory networks, Piecewise analysis method, Time-varying delays, Linear matrix inequality (LMI)

1. Introduction. During the past decades, genetic regulatory networks have drawn increasing attention in the biological and biomedical sciences [1, 2], but few results have been carried out in this area [3, 4, 5, 6, 7, 8]. Nowadays, one of the main challenges in systems biology is to understand the genetic regulatory networks, for example, how genes and proteins interact to form a complex network that performs complicated biological functions. Recent mathematical modeling of genetic networks as dynamical system models provides a powerful tool for studying gene regulation processes in living organisms, and genetic network models in literature can be roughly classified into two types, i.e., the Boolean model (or discrete model) and the differential equation model (or continuous model) [9, 10]. In Boolean models, the activity of each gene is functioned in one of two states: ON or OFF, and the state of a gene is interacted by a Boolean function of the states of other related genes. In the differential equation models, the variables describe the concentrations of gene products, such as mRNAs and proteins, as continuous values of the gene regulation systems. Using continuous values, the second approach is viewed more accurate, and being able to provide more detailed understanding and insights of the dynamic behavior demonstrated by biological systems.

Recently, studies on genetic regulatory networks are considerable, and many important results have been obtained in the literature [11, 12, 13, 14]. These results make significant