Dynamics of Continuous, Discrete and Impulsive Systems
Series **B:** *Applications & Algorithms* **13 (2006)** 429-439

STABILITY OF A MODEL FOR A DELAYED GENETIC REGULATORY NETWORK

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Abstract. We introduce a model for a genetic regulatory network with delays and analyse its stability. Based on the theory of linear time-varying delayed differential equations, a sufficient condition on local asymptotical stability is provided. This improves the conditions that Chen and Aihara [11] presented and has the advantage of dramatically reducing the computational complexity. At the same time, using the Lyapunov stability theory, a sufficient condition on global exponential stability is derived. Both conditions are delay-independent. Finally, a simple model is used for illustration. Numerical simulations show the effectiveness and feasibility of the proposed stability conditions.

Keywords. genetic regulatory network; protein; gene; Lyapunov stability; time delay; functional differential equation.

AMS(MOS) subject classification: 65L20, 65L07

1 Introduction

With the development of the Human Genome project, genome sequencing and gene recognition have been accumulating a wealth of experimental data. It is the major goal for us to analyse and explore the biological meaning of the vast volumes of such biological data. Genetic regulatory networks reflect how genes and proteins interact with one another to form systems or networks that perform sophisticated biological functions. Since genetic regulatory networks with time delays are high-dimensional and nonlinear, it is indispensable to consider the network dynamics from the viewpoint of nonlinear dynamical systems. It is also expected that such theoretical studies on genetic networks may lead to engineering developments of circuits and devices such as biotechnological design principles of synthetic genetic regulatory networks [1], [2], and new kinds of integrated circuits like neurochips inspired by biological neural networks. From a dynamic behavior viewpoint, however, how to appropriately represent real genetic regulatory systems mathematically in terms of gene functions, expression mechanisms, and signal-transduction pathways remains unclear. There are two basic models for genetic networks [3-7]: 1) Boolean or logical models, and 2) differential equation or dynamic system models. There also exist hybrid models which combine discrete and continuous system models [8-10].