

Analysis and Design of Gene Switches Composed of Positive Feedback Loops

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ABSTRACT

The design and construction of synthetic gene-regulatory networks have recently been attracting much attention, and actually some simple synthetic gene-regulatory networks such as a genetic toggle switch and a gene oscillator have been constructed in *E. coli*[2, 1]. These studies used mathematical models not only to predict the behaviors of the gene networks but also to compare with experimental data. However, the mathematical models of these gene networks were very simple, obtained by ignoring possible components and interactions, i.e. time delays, transportation factors which could significantly change the dynamical properties of model for large or complicated networks.

Although these simple models worked very well for the simple gene networks in these works, it is still an open problem to explore whether such simple models are also useful for analyzing and designing more complicated and high dimensional artificial gene networks.

In this poster, by using the theory of dynamical systems, especially monotone dynamical systems[4, 3], we propose a gene network with only positive feedback loops as a gene switch and show that this gene network has the following desirable properties:

1. It is automatically guaranteed that almost all orbits of a gene network model with only positive feedback loops converge to stable equilibrium points. Thus, it is unnecessary to check if or not a gene switch has only equilibrium points as attractors.
2. Even if all the time delays of the model are ignored, by replacing all the delays with 0, the equilibrium points and their stabilities are invariant. Thus, it is no problem for designing a gene switch to use ordinary differential equations rather than functional differential equations that are more troublesome to analyze.
3. The dimension of the model can be reduced by chang-

ing some differential equations (ODEs) into algebraic equations, keeping the equilibrium points and their stabilities invariant. This property makes analysis of the model more tractable.

Furthermore, we show that we can design a gene switch starting from minimal ODEs model which satisfies functional requirements, and then add some components to make the model more suitable for experimental implementation.

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