

以時延相關條件設計時變延遲不確定性基因轉錄調控網路的整體強健狀態估測器、整體強健耗散性及外部擾動下整體隨機強健穩定度

---線性矩陣不等式法

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摘要

基因轉錄調控網路是細胞內基因之間的相互作用關係的整體表現，每一基因皆含有調控順序訊息，稱為資訊系統元素(cis element)。轉錄因子及他們間的共伴因子與其餘蛋白質能結合到此資訊系統，以增加或遞減基因表達的準位，是生命功能在基因表達層面的展現。最近利用多種生物信息學(計算分子生物學)工具和高通量實驗技術的發展，使得重建複雜的基因調控網路成為可能。由於基因轉錄調控網路中生物化學反應的時間多尺度性，如脫氧核酸 (DNA) 與蛋白質結合以及蛋白質聚合等快速反應，轉錄、翻譯和易位等人工基因轉錄調控網路之慢速反應；及電路組成的基因調控網路中電路放大器的有限交換速度，都存在時延現象，使得時延現象在生物系統中或人工基因轉錄調控網路中必需受到考慮，以便能準確預測其數學模式。於蛋白質結合中時延的存在會誘發調控產物的振盪、發散、混沌及不穩定或引起其

它基因網路的不好性能。因此為了準確預測基因轉錄調控網路，本計劃將專注於時變延遲不確定性基因轉錄調控網路之強健狀態估測器、強健耗散穩定度及強健隨機穩定度探討。參數不確定性為時變且有界。首先提出創新穩定準則保證所希望的狀態估測器之存在性，這準則與時延的上下限有關，傳統時延微分比 1 小於本計劃中不在受到此限制。接著，提出新的上邊界技巧保證強健耗散穩定度與時延的上下限有關。時變延遲一般為可微且比 1 小，本計劃中我們將使用提出改善的上邊界技巧，使得以上條件會被去除，並且使用許多的緩遲矩陣以降低準則的保守性。最後，提出適當型李亞普若夫泛函技巧，以便探討強健時延相關穩定度問題。提出此結果可以改善文獻的結果，由於估測李亞普若夫微分上邊界，不必省略一些有用項，及另外的一些項會誘發入李亞普若夫泛函內，同時時延也會受到考慮。於基因功能的瞭解與工程應用的重要意義上，如發展具有整合基因轉錄調控網路之生物技術設計原理的電路與系統，又如發展新的各種積體電路，像學習生物與神經網路的神經元晶片。最後會提出許多的範例說明驗證以上所提方法的有效性與可應用性。

關鍵字：時延範圍相關；基因轉錄調控網路；

狀態估測器；耗散性；擾動

A Robust Delay-Dependent Approach to Design Globally Robust State Estimator, Robust Passivity and Stochastic Robust Stability under External Disturbance for Uncertain Transcriptional Regulatory Networks with Time-Varying Delays---An LMI Approach

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Abstract

Transcriptional regulatory networks are the global representation of multiple interactions between genes and their products. Each gene contains some regulatory sequences, called cis elements. Transcription factors and their cofactors as well as other proteins can bind to such elements, and increase or reduce the gene expression levels, which can help us understand the cell's function at the level of gene expression. Recent research advances in multiple bioinformatics (computational molecular biology) and high-throughput experimental technologies have made the reconstruction of transcriptional regulatory networks possible. Time delays are ubiquitous in transcriptional regulatory networks, because of the vast separation of time scales between the fast reactions like DNA-binding and dimerizations, and artificial genetic networks due to slow reactions like translation transcription and degradation and the finite switching speed of amplifiers, which should be taken into account in the biological systems or artificial genetic networks in order to have more accurate models. The existence of time delay in proteins could make delayed transcriptional regulatory networks be oscillatory, divergent, chaotic and instable or have poor performance. Therefore, to have the accurate predictions, this project interests have been attracted to the robust state estimation problem, robust passivity problem and robust stochastic stability problem for uncertain transcriptional regulatory networks with time-varying delays. The parameter uncertainties are assumed to be time varying and unknown, but norm bounded. First, novel criteria are proposed to guarantee the existence of the desired state estimator. The criteria are dependent on the upper and lower bounds of the delays, and the traditional assumption that the derivatives of the delays are less than 1 is no longer required in our analysis. Then, a new bounding technique is proposed to guarantee the robust passivity and stability with dependence on the upper and lower bounds of the delay. The time-varying delays are required to be differentiable and less than 1.

In this project, we will employ a new bounding technique such that the above conditions can be removed and severable slack variables are introduced to be reduced the conservatism of the criteria. Final, an appropriate type of Lyapunov functionals is proposed to investigate the robust delay-dependent stability problem. The present results may improve the existing ones due to a method to estimate the upper bound of the derivative of Lyapunov functional without ignoring some useful terms and the introduction of additional terms into the proposed Lyapunov functional, which take into account the delay. Many examples are provided to demonstrate the effectiveness of the proposed approach in the understanding of the gene functions and potential significance on engineering applications, such as developing circuits and systems with biotechnological design principles of synthetic genetic regulatory networks and new kinds of integrated circuits like neurochips learnt from biological neural networks.

Key words: Delay-range-dependent;
Genetic transcriptional regulatory networks;
State estimator;Passivity;Disturbance