

Meeting: 1006, Lubbock, Texas, SS 11A, Special Session on Future Directions in Mathematical Systems and Control Theory

1006-93-37 **Xiuxia Du** (duxiuxia@netra.wustl.edu), Campus Box 1127, Washington University, One Brookings Drive, St. Louis, MO 63130, and **Bijoy Ghosh*** (ghosh@netra.wustl.edu), Campus Box 1127, Washington University, One Brookings Drive, St. Louis, MO 63130. *Systems Modeling in Computational Biology.*

The mechanisms that govern gene expressions and protein-protein interactions are of significant values for us to understand and ultimately to engineer the the cellular processes. The advent and wide-spread use of high-throughput microarray technology open the door for researchers to explore the complexity of gene regulations and protein-protein interactions. However, the mathematical tools which can be used for this purpose are still very preliminary. In this talk, we will use smoothing spline theory to build a dynamic system. This system is able to reproduce the observed temporal gene expression profile and also sheds light on the interaction patterns among the gene clusters. Pearson correlation coefficients are employed as a metric to quantify the similarity of gene expression profiles. (Received January 18, 2005)