

Control engineering approaches toward gene regulatory networks

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Traditional biology has focused on identifying individual genes, proteins and cells, and studying their specific functions. But that kind of research can yield relatively limited insights about the whole organisms, including the human body. As an analogy, if one wanted to study an airplane, and focused on identifying the engine, wings, and seat belts, and studied their specific functions, one would have no real understanding of how an airplane operates. More importantly, one would have no understanding of how to effectively service the airplane when something malfunctions. So too, a traditional approach to studying biology and human health has left us with a limited understanding of how the whole organisms operate, and how we can best predict, prevent, or remedy potential health problems. As a result, traditional biological/medical researchers have had a limited success in curing genome-related (complex) diseases such as cancer, HIV AIDS, and diabetes.

Actually, genes encode proteins, some of which in turn regulate other genes. Such interactions work in highly structured but incredibly complex ways, similar to the complex interactions among many parts of an airplane. With advances in the measurement technology for gene expression and in genome sequencing, it has become possible to measure the expression level of thousands of genes simultaneously in a cell at a series of time points over a specific biological process. Such time-course gene expression data provides a snapshot of most (if not all) of the interesting genes and may lead to a better understanding of gene regulatory networks, and thus a better understanding of life. The long-term objective of the proposed research is to develop the modeling and simulation analysis methods for studying gene regulatory network, using the principles, concepts, and methodology of complex dynamic engineering systems, while designing the control approaches for disease-alerted gene regulatory networks.