

Modeling and Finding Gene Regulatory Network by Combining Generalized Logical Network with Probability Description for State Transition and Time Delay

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2004

Abstract

We are investigating a method to extend the generalized logical network for improved gene regulatory network representation based on microarray gene expression data and possibly other protein and DNA interaction data. We incorporate expression delay and transition probability between states. We have three major efforts: obtaining states of the gene expression levels; estimate state transition probabilities and transition time distribution; obtaining the regulatory network by finding logical functions that best fit the graph of pathways. We are testing our ideas using microarray data of yeast gene expression.