Inference Structures of Gene Regulatory Networks

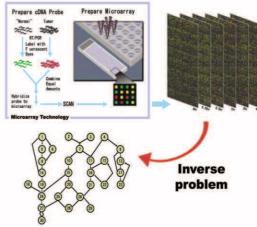
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AIST Today Vol. 3, No. 3
(2003) 12

We have developed an efficient algorithm base on the genetic algorithm (GA) for optimization of a nonlinear system where the details of gene regulatory networks.

Estimation of the interaction mechanisms among system components by using experimentally observed dynamic responses (time-courses) of some of the system components is generally referred to as "inverse problem". The S-system, which belongs to power-law formalism, is one of the best representations to solve such an inverse problem; the S-system is rich enough in structure to capture all relevant dynamics. In our research, for the purpose of solving the inverse problem, we introduce the genetic algorithm and propose an efficient procedure for the estimation of large number of parameters in the S-system formalism.



 Measure gene expression levels with DNA microarray technology in time.
 Our algorithm optimizes mathematical network models to fit to observed expression data.