

Generation of Genetic Networks from a Small Number of Gene Expression Patterns under the Boolean Network Model

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Abstract

There are lots of work for inferring genetic network architectures from state transition tables which correspond to time series of gene expression patterns, using the Boolean network model. Results of those computational experiments suggested that a small number of state transition (INPUT/OUTPUT) pairs are sufficient in order to infer the original Boolean network correctly. Tatsuya AKUTSU, Satoru MIYANO and Satoru KUHARA gave a mathematical proof for this. So there is possibility to devise an algorithm to generate all consistent genetic networks from a small number of gene expression patterns under the Boolean network model.

Index terms— Generation, consistent network.

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December inference of gene regulation mechanism from time series of gene expression patterns are getting more important especially due to the invention of DNA microarray technology. Expression profiles of several thousands of genes are now being produced for further analyses. Some methods have been proposed for the inference of gene regulation mechanism from time series of gene expression patterns.

A statistical method is proposed by Arkin, Shen and Ross. They used correlation matrices to infer chemical reaction networks from time series of measured concentration of species. Though they treated chemical reaction networks, they also suggested that their method might be applied to genetic networks. However, it seems difficult to apply their method to the inference of large scale networks.

A metabolic pathway is suggested to be inferred by DeRisi, Iyer and Brown from gene expression patterns of *Saccharomyces cerevisiae* obtained by using DNA microarrays. A network model similar to the Boolean network model is constructed by Yuh, Bolouri and Davidson from time series of expression patterns I General Terms : Gene network, gene regulatory network, Genetic network, gene expression pattern, Boolean network, microarray data, Sum of product, Boolean algebra. Keywords : Generation, consistent network. relating to a sea urchin gene. But their inference methods are not systematic or automatic. Besides, some studies have been done on the inference of genetic networks from state transition data using the Boolean network .

On the other hand, Liang, Fuhrman and Somogyi proposed an algorithm named REVEAL for inference of Boolean networks (corresponding to genetic networks) from state transition tables (corresponding to time series of gene expression patterns). REVEAL used information theoretic principles in order to reduce the search space. They made some computational experiments on REVEAL. The results suggested that only a small number of state transition pairs (100 pairs from 1015) were sufficient for inferring Boolean networks with 50 nodes (genes) whose in degree (the number of input nodes to a node) was bounded by 3.

Tatsuya AKUTSU, Satoru MIYANO and Satoru KUHARA gave a mathematical proof for their observation. We will extend their algorithm to identify genetic networks from gene expression patterns derived by gene disruptions and gene over expressions using a Boolean network-like model. They proved mathematically a lower bound and an upper bound of the number of expression patterns required to identify the network correctly. In this paper we will try to extend try to provide an algorithm to generate all the consistent genetic networks from a small number of gene expression patterns under the Boolean network model. a) Genetic network A gene



Figure 1:

$$1x_1, \dots, x_n$$

Figure 2: Table 1 (



Figure 3:



Figure 4:



Figure 5:



Figure 6: 3 .



Figure 7: ??) 3 ?2 ?? 6 = 8 ?? ?2 ?? 6

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(a) : Minterms formulation from a Boolean network

Figure 8: Table 1

.1 EXPERIMENTAL OUTCOMES a) Performance Analysis

This paper improves the previous works done by the authors worldwide.

The improvements are listed below:-1) It generates only the consistent network. So overhead of checking inconsistent networks is eliminated. 2) Huge improvement is achieved in running time.

3) As all consistent networks are generated, so counting problem is solved simultaneously. 4) The in degree/out degree have no limit. A node (gene) can be expressed by any number of nodes(genes).

IV.

.2 CONCLUSION

We have proved mathematically that to generate all consistent Boolean networks it requires $O(n^8 n)$ times. For that purpose, we proposed a simple algorithm. Of course, real biological systems are different from Boolean networks nodes in a Boolean

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