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The sensitivity analysis of a SBNP with three genes

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Abstract: In this work, a perturbation analysis of stochastic boolean network with perturbation has been realized, by using power series expansions. More specifically, we have considered the sensitivity analysis of a SBNP with three genes, where we have perturbed the perturbation probability.

keywords: Power series expansions; Stochastic boolean network; Markov chains.

MSC2010: 30E; 37N; 65C.

1 Introduction

Stochastic boolean network with perturbation (SBNP) have received much attention in modeling genetic regulatory networks. A SBNP can be regarded as a Markov chain process and is characterised by a transition probability matrix. In this study, we propose efficient algorithms for constructing a SBNP when its transition probability matrix is given. Thus an important issue is developing computational methods from the perturbation point of view.

In this work, we estimate the steady-state probability distribution of a PBNs with gene perturbations. We establish an approximate expression for computing the steady-state probability distribution based on a power series approach.

2 Results and discussion

Let us consider a Markov chain X on the denombrable state space $S = \{1, 2, \dots\}$, P denote the transition kernel of a Markov chain in S having unique stationary distribution π . Indeed, P must be a stochastic matrix; that is, $p_{ij} \geq 0$, and $\sum_{j \geq 0} p_{ij} = 1$, for all $i \geq 0$.

Consider a PBNs with gene perturbation [2]. This network is modeled by a homogeneous Markov chain with discrete time of transition probability matrix \tilde{A} (the nominal matrix) defined by [4]:

$$\tilde{A} = (1 - p)^n A + \tilde{P}_n$$

Let \tilde{P}_n be the $2^n \times 2^n$ perturbation matrix of a PBN with n genes, then we have for $n=1,2,\dots$

$$\tilde{P}_n = Q_n - (1-p)^n I_{2^n} = \underbrace{Q_1 \otimes Q_1 \otimes \dots \otimes Q_1}_{n \text{ terms}} - (1-p)^n I_{2^n}, \quad (1)$$

where

$$Q_1 = \begin{pmatrix} 1-p & p \\ p & 1-p \end{pmatrix}.$$

Suppose this Markov chain is ergodic with a unique stationary distribution π . Note the fundamental matrix associated with this chain by [1]:

$$Z = (I - \tilde{A} + \Pi)^{-1}. \quad (2)$$

We note the matrix of transition probabilities of the perturbed model which is of the same structure as the original model, by: $\bar{A} = (1-p)^n A + \bar{P}_n$,

where

$$\bar{P}_n = \underbrace{I_2 \otimes I_2 \otimes \dots \otimes I_2}_r \otimes Q_1 \otimes Q_1 \otimes \dots \otimes Q_1 - (1-p)^n I_{2^n}, \quad n > r. \quad (3)$$

Similarly, we assume that the Markov chain describing the state of the perturbed model is ergodic with a unique stationary distribution $\bar{\pi}$.

We analyze the effect of the perturbation (change in value) of the probability p on the stationary distribution π .

For our numerical experiment, suppose we are given a SBNP consisting of three genes [3], we apply another method of Power Series Expansions (PSE).

The following algorithm will allow us to have absolute relative errors when calculating the stationary distribution $\tilde{\pi}$ by N-order constrained polynomials.

Algorithm Absolute relative errors of the calculation of the stationary distribution by the method PSE

Begin

Inputs: The precision ϵ ;

Outputs: The order N of the PSE polynomial, the value of the remainder ER ;

1. Calculate the matrix :

$$\tilde{A}(i, j) = (1-p)^n A(i, j) + \tilde{P}_n;$$

2. Calculate the matrix :

$$\bar{A}(i, j) = (1-p)^n A(i, j) + \bar{P}_n;$$

3. Calculate the matrix Z :

$$Z = (I - \tilde{A} + \Pi)^{-1};$$

4. Calculate the stationary distribution :

$$\pi = \pi \tilde{A};$$

5. Calculate the stationary distribution :

$$\bar{\pi} = \pi \sum_{k=0}^N [(\bar{P} - \tilde{P}) Z]^k;$$

end.

where the relative error committed on the computation of the stationary distributions by PSE is defined by:

$$ER = \left| \frac{\bar{\pi} - \pi}{\pi} \right|. \quad (4)$$

The graphical representation of the relative error made on the computation of the stationary distributions is given in the following figure.

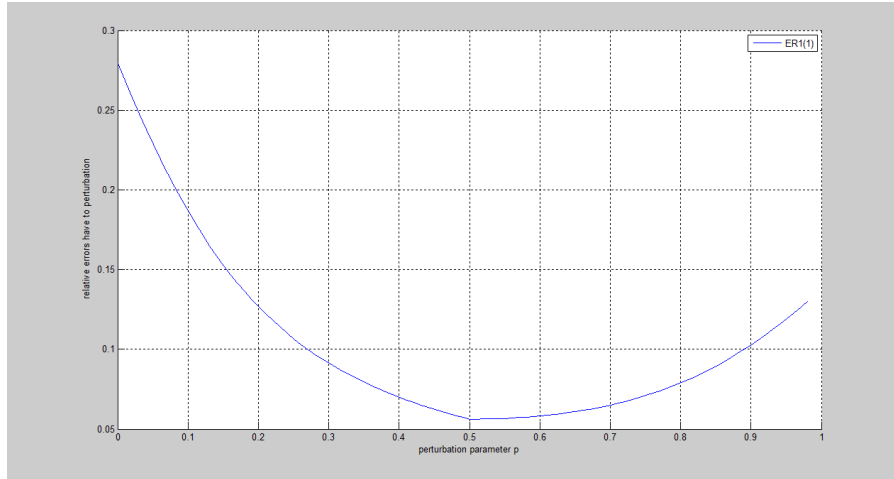


Figure 1: Graphical representation of the relative error.

3 Conclusions and Future work

In this work, we have been able to illustrate numerically the effect of changing the values of the probability of perturbation 'p' on the calculation of the stationary distribution of a stochastic Boolean network with perturbation of three genes. This sensitivity analysis is carried out using the power series expansions method.

Analyzing of more complex networks in the presence of parametric uncertainties will also be the topic of ongoing research.

References

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