Probabilistic Boolean Networks

Design of Probabilistic Boolean Networks Based on Network Structure and Steady-State Probabilities

The goal is to find a PBN based on network structure and desired steady-state properties. In systems biology and synthetic biology, such problems are important as an inverse problem. Using a matrix-based representation of PBNs, a solution method for this problem is proposed. In the problem of finding a PBN, we must calculate not only Boolean functions, but also the probabilities of selecting a Boolean function and the number of candidates of Boolean functions. Hence, the problem of finding a PBN is more difficult than that of finding a BN. The paper also contains some numerical examples.

Function perturbation impact on stability in distribution of probabilistic Boolean networks

In practical gene regulatory networks, function perturbation often occurs due to gene mutation. This paper studies the function perturbation impact on the stability and set stability in distribution of PBNs by using the semi-tensor product of matrices. Firstly, the stability and set stability in distribution of PBNs is recalled and the function perturbation problem is formulated. Secondly, when a given PBN is stable at an equilibrium (or a set) in distribution, based on the transition probability matrix and reachable set with positive probability, some necessary and sufficient conditions are presented to guarantee that the PBN is still stable at an equilibrium (or a set) in distribution after function perturbation.

Stability and Set Stability in Distribution of Probabilistic Boolean Networks

Stability in the distribution (SD) of a PBN determines whether the probability distribution converges to the distribution of the target state. The SD is easily generalized to subset stability; that is, to set stability in distribution (SSD). Paper shows that the transition probability from any state to an invariant subset (or to a fixed point) is nondecreasing in time. This monotonicity is an important property in establishing stability criteria and in estimating the transient period. After calculating the largest invariant subset of a Markov chain in a given set by the algorithm, a necessary and sufficient condition for SSDs of Markov chains is proposed.

On detectability of probabilistic Boolean networks

This paper devotes to introducing and investigating the detectability of PBNs. Two types of detectability, weak detectability and strong detectability, are proposed to deal with different situations. Firstly, by resorting to the semitensor product (STP) of matrices, the equivalent algebraic expression of the PBN is converted into another kind of expression, which is called the data form. This data form can estimate the current state distribution from the corresponding output sequence. Then, using this data form constructs the detection form, based on which, two necessary and sufficient conditions are derived for checking weak detectability and strong detectability. Secondly, combining the STP and this detection form, a nice algorithm is established for checking whether a PBN is weak detectability.

Optimization-Based Approaches to Control of Probabilistic Boolean Networks

the outline of PBNs is explained. An optimal control method using polynomial optimization is explained. The finite-time optimal control problem is reduced to a polynomial optimization problem. Furthermore, another finite-time optimal control problem, which can be reduced to an integer programming problem, is also explained.

How Is Probability Assigned?

- Literature-based modeling is definitely a first approach, as existing knowledge needs to be included in the model.
- A unique function doesn't always describe a specific interaction. In this case the investigator can try different options and choose the best representing the final behavior of the real biological system. Also, in the case that independent possible functions are identified, a probabilistic updating scheme is suggested.
- It has been shown that the respective selection probabilities are varying for different biological conditions, e.g., after interferon treatment or after viral infection on macrophage, while the structure of the constituent network, i.e., predictor functions, remains stable