A general stochastic model for studying time evolution of transition networks

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HIGHLIGHTS

- A general model describing the dynamics of transition networks is derived.
- A simulation algorithm for studying the network evolutionary behavior is proposed.
- The disease propagation dynamics in different networks generally have different properties but they do share some common features.
- The model provides a good prediction of user growth in the Facebook network.

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ABSTRACT

We consider a class of complex networks whose nodes assume one of several possible states at any time and may change their states from time to time. Such networks represent practical networks of rumor spreading, disease spreading, language evolution, and so on. Here, we derive a model describing the dynamics of this kind of network and a simulation algorithm for studying the network evolutionary behavior. This model, derived at a microscopic level, can reveal the transition dynamics of every node. A numerical simulation is taken as an "experiment" or "realization" of the model. We use this model to study the disease propagation dynamics in four different prototypical networks, namely, the regular nearest-neighbor (RN) network, the classical Erdös–Renyí (ER) random graph, the Watts–Strogátz small-world (SW) network, and the Barabási–Albert (BA) scalefree network. We find that the disease propagation dynamics in these four networks generally have different properties but they do share some common features. Furthermore, we utilize the transition network model to predict user growth in the Facebook network. Simulation shows that our model agrees with the historical data. The study can provide a useful tool for a more thorough understanding of the dynamics networks.

1. Introduction

Many large-scale real-world networks, such as the Internet, the global aviation network and protein interaction networks, can be described as *complex networks* in which nodes represent individuals or organizations, and links mimic interactions among the nodes [1,2]. In many cases, each node of the network may assume several states and can change from one state

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to another. For instance, in a rumor spreading network [3], each node of the network can be regarded as being in one of three possible states, namely, *spreader*, *ignorant* and *stifler*. Other examples can be found in epidemic spreading networks described by the susceptible–infected–recovered (SIR) model [4–6], the susceptible–infected–susceptible (SIS) model [7,8], or the susceptible–infected (SI) model [9–11]. Furthermore, complex networks of language evolution [12,13], the growth of membership-based websites [14], the spread of social behavior [15,16], spatial prisoner's dilemma game [17], and so on, also fall in this category. In this paper, we refer to this important class of networks as *transition networks*, which exist in many social, biological and communication systems.

For convenience of illustration, we discuss the main idea here using the familiar SIR epidemic spreading model [18,19]. Moreover, we stress that the proposed model is generally applicable to networks with any connection mechanism, like the SEIR, SIS, language evolution, human behavior spreading and so on, and in any network setting, such as the Erdös–Renyí (ER) random graph, Watts–Strogátz (WS) small world and Barabási–Albert (BA) scalefree networks. In an SIR model, individuals are categorized as Susceptible, Infected, and Recovered. For instance, under the homogeneous mixing hypothesis assumption [20,21], a standard deterministic SIR model can be described in terms of the densities of susceptible $S(t)$, infected $I(t)$, and recovered individuals $R(t)$. The ODEs provide a crude description revealing only the density dynamics, but fail to reveal disease propagation dynamics at any specific node. The homogeneous mixing hypothesis discards possible heterogeneities in the network, and inhomogeneous dynamics cannot be captured with this standard SIR model. Furthermore, the ODEs are deterministic while disease spreading is often subject to non-deterministic processes depending on the nature of transmission. Hence, in principle, a stochastic model is more realistic than a deterministic one. In addition, stochasticity introduces variances and co-variances which influence the behavior, and helps push the system away from the deterministic attractor so that transitions may play a significant role. Also, stochasticity may cause extinction of the epidemic [22].

In this paper, a stochastic process model is established for general complex transition networks with arbitrary connectivity distribution and transition probability. In most cases, the proposed model cannot be solved analytically, as it is the case with most models using ODEs. Hence, the proposed model has to be solved numerically. In our study, a simulation algorithm, which does not involve fixed time steps, is established. Specifically, our model aims to provide analytical expressions of

1. the probability that the next transition will occur at a certain time;
2. the probability that a particular transition will occur;
3. the probability that a particular transition will occur with a specific link.

Clearly, with these expressions, this model can expose the transition dynamics of every individual in continuous time, whereas the ODE-based model describes the dynamics of "density" and the standard Monte-Carlo simulation can only capture the dynamics of each node at pre-defined discrete time-steps. It should be noted that no mathematical model can fully predict transition dynamics of a natural system. However, the proposed model offers a more realistic physical meaning of the relationship between individuals in a system and is thus able to provide a better overall picture of the transition network behavior.

In addition, our study examines the spreading network in four representative complex network models, namely, the regular nearest-neighbor (RN) network, the ER random-graph network, the WS small-world network, and the BA scale-free network. A brief overview of epidemiological characteristics shows that the epidemic dynamics of the aforementioned four types of complex networks have their own particular characteristics but they also share some common features. One of the findings is that homogeneity or heterogeneity may not be a key condition controlling the rate of epidemic spreading, while the average path length may play an important role. Also, the transition network model is used to predict user growth of Facebook during 2004 to 2013. Simulation shows the proposed model fits well with the historical data. Details of the model derivation and experimental results will be shown in the subsequent sections.

In the next section, we describe the model in detail. In Section 3, a numerical simulation algorithm is presented. Some numerical simulations of disease propagation and a summary of the results are presented in Section 4, while the study of user growth of Facebook network is shown in Section 5. Finally, the conclusion is given in Section 6.

2. Formulation of general stochastic process model for transition networks

The standard deterministic ODE-based SIR model [23] is established to describe the dynamics of "density", which is similar to the concept of "molecular concentration" in modeling a chemical reaction process. Hence, while an ODE-based model exposes the dynamics of "molecular concentration" in continuous time, our model reaches to the "molecular" level and reveals the dynamics of every "molecule" in continuous time. To facilitate discussion, a numerical simulation of disease propagation is first provided to give a sense of some differences between the standard SIR model and the proposed model applied to the SIR case. A typical numerical simulation using the proposed model generates time series $\{X(t_i), Y(t_i), Z(t_i) \mid t_i \in \Re^+, i = 1, 2, \ldots\}$, with the following properties:

1. One and only one infection or recovery occurs in the time interval $[t_{i-1}, t_i)$. Thus, we treat the infection/recovery as being completed at time t_i, i.e., at time t_i, the state of the network changes.
2. The numbers of S, I and R individuals are changing at t_i. Hence, in the time interval $[t_{i-1}, t_i)$, we can treat $\{X(t), Y(t), Z(t)\} = \{X(t_i), Y(t_i), Z(t_i)\}$.