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When Markov chains meet: A continuous-time model of network evolution

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ABSTRACT

We suggest a novel approach to model continuous time processes of the interactions of independent elements. The model assumes a finite number of independent Markov chains, each representing an element. Chains move among a common space of states. Sometimes chains intersect, being in the same state at the same time. These intersections relate the chains with each other and imply many interesting processes.

In this paper, we examine our new approach in the context of network evolution. Our analytic study achieves a closed solution for the expected time until a node has any specific degree. Our numerical study demonstrates properties which are in agreement with real world networks. Thus we show the potential of our approach.

1. Introduction

Interactions among independent elements have always aroused research interest, which is even greater in the recent years due to the availability of enormous real-world data on such processes. We suggest a novel approach to model a process of interactions among independent elements. The process is represented by the dynamics of independent Markov chains, each representing an element. Chains move among a common space of states. Sometimes chains intersect, being in the same state at the same time. These intersections relate the chains with each other and generate many interesting processes, e.g. network evolution. An attractive property of the model is the description of a process over *continuous time*.

In this paper, we explore an implication of this model for a network evolution process. It is a challenge to understand the evolution of real world networks, whether they are in the realm of biology (neural network Hopfield, 1982), technology (the Internet Doyle et al., 2005), nature (ecological network Montoya and Pimm, 2006) or social relationships (Facebook Acquisti and Gross, 2006). For example, it is a challenge to understand why a network comes to have its particular degree distribution or clustering at a given time. This challenge is not new, of course. A traditional approach for modeling network evolution is inspired by the theory of random graphs, emphasizes the advantage of having a simple model, such as Erdös & Renyi's random-graph (Erdös and Renyi, 1960), which is exactly solvable for many of its properties. The new science of networks (Barabasi, 2002; Watts, 2004) approach emphasizes the topological structure of the network. Seminal examples are the small-world model of Watts and Strogatz (1998) and the scale-free model of Barabasi and Albert (1999).

We combine these approaches, demonstrating a model which is both *simple* in the aspect of analysis, and *complex* in the aspect of the topological structure of the result. In this context, the interactions among independent elements are the generation of the network links.

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The paper is organized as follows: In Section 2, we describe the model. In Section 3, we achieve a closed formula for the degree evolution. In Section 4, we present the structural features of the evolving network, which are in agreement with the real world: the diameter is small, the clustering is high and the degree distribution is highly skewed.

2. The model

We analyze a simple version of intersection model: N Markov chains are identical and independent. Each chain has only two states: M and L. The duration times in M and L are independent and exponentially distributed with parameters μ and λ, respectively. The model parameters can be normalized, so there are only two relevant parameters: N which is the number of chains, and $\rho = \frac{\lambda}{\mu}$ which is the ratio of the expected times spent in M and L.

In the context of network evolution, the model demonstrates a series of changing graphs, based on the dynamics of the Markov chains. Evolution starts with $G = (V, E)$, where $V = 1, 2, \ldots, N$ and $E = \phi$. Each node is associated with a chain. Chains move between state M and state L. M is *a meeting state*: if at any given time two chains are both in M, we say that the chains *meet*. When chain i and chain j meet for the first time, we add an undirected edge (i, j) to G and say that chain i and chain j are *acquainted*. This evolution process is an extension of the evolution process in the random graph model: when ρ goes to zero, edges are randomly added one by one. On the other hand, when ρ is high, there is a high probability that the corresponding evolving network is a series of cliques with growing sizes.

3. Analysis of the degree distribution

We derive a closed form for the expected time until the degree of an arbitrary node in the evolving network is h. One distinct chain plays the role of a *leader*. All other N chains are *non-leaders*. The meetings of the leader represent the edges incident to a specific node in the corresponding evolving network. We analyze these meetings. Specifically, we derive the expected time until the leader has met h non-leaders.

3.1. Recursion

Let $S_{i,m,l}$ denote a state of the Markov chains system during the evolution of $G = (V, E)$. It is a state where i equals 1 or 0 to indicate whether the leader (the distinct chain) is in state M or L, respectively; $m \in 0, \ldots, N-1$ is the number of non-leaders in state M which are not yet acquainted with the leader; $l \in 0, \ldots, N-m$ is the number of non-leaders in state L which are not yet acquainted with the leader. One notices that for any state where $i = 1$, the value of m (by the definition of m) is 0.

Let M_l denote the expected time until the system goes from state $S_{1,0,l}$ to state $S_{1,0,0}$. Let $L_{m,l}$ denote the expected time until the system goes from state $S_{0,m,l}$ to state $S_{1,0,0}$. M_l and $L_{m,l}$ are the expected times until the leader has been in state M with all of the non-leaders (at least once). We compute M_N and $L_{0,N}$.

When $l = 0$, $M_l = 0$. For any $l > 0$, the first transition takes the system from $S_{1,0,l}$ to $S_{0,0,l}$ with probability $\frac{\mu}{\mu+l\lambda}$ or $S_{1,0,l-1}$ with probability $\frac{l\lambda}{\mu+l\lambda}$, depending on whether it is a transition of the leader or one of the non-leaders, respectively.

Hence, each recursion equations for $l = 1, \ldots, N$ is a summation of which is the expected time to stay in $S_{1,0,l}$, and the expected time to stay in the following states:

$$M_l = \frac{1}{\mu + l\lambda} + \frac{l\lambda}{\mu + l\lambda} M_{l-1} + \frac{\mu}{\mu + l\lambda} L_{0,l}. \tag{1}$$

When $l = 0$, $L_{m,l} = 0$, for all m values. For any $l > 0$, the first transition takes the system from $S_{0,m,l}$ to $S_{0,m+1,l-1}$, $S_{0,m-1,l+1}$ or $S_{1,l}$, depending on the type of the transiting chain and the direction of this transition. Hence, for $m = 0, \ldots, N-l$ and $l = 1, \ldots, N-m$:

$$L_{m,l} = \frac{1}{m\mu + (l+1)\lambda} + \frac{l\lambda}{m\mu + (l+1)\lambda} L_{m+1,l-1} + \frac{m\mu}{m\mu + (l+1)\lambda} L_{m-1,l+1} + \frac{\lambda}{m\mu + (l+1)\lambda} M_l. \tag{2}$$

$L_{-1,l+1}$ is not defined. However, its coefficient is 0.

3.2. Recursion for an embedded process

Solving the recursion system (1) and (2) is not straightforward, since $L_{m,l}$ is not induced by lower values of m and l. To derive a closed solution, we embed the system in states $S_{1,0,l}$ and $S_{0,0,l}$, where the non-leaders who are not acquainted with the leader are in state L. Let $L_l = L_{0,l}$. When the system is in state $S_{0,0,l}$ and $l > 0$, the first transition of the leader takes the system to $S_{1,0,r}$, for some $0 \le r \le l$, depending on the number of non-leaders, that have not yet met the leader and are in state M at the time of this transition. Let T denote the time of the first transition of the leader. For $l = 1, \ldots, N$, (2) is