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Evolving networks with multispecies nodes and spread in the number of initial links

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We consider models for growing networks incorporating two effects not previously considered: (i) different species of nodes, with each species having different properties (such as different attachment probabilities to other node species) and (ii) when a new node is created, its number of links to old nodes is random with a given probability distribution. Our numerical simulations show good agreement with analytic solutions. As an application of our model, we investigate the movie-actor network with movies considered as nodes and actors as links.

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I. INTRODUCTION

It is known that many evolving network systems, including the World Wide Web, as well as social, biological, and communication systems, show power-law distributions. In particular, the number of nodes with k links is often observed to be $n_k \sim k^{-\nu}$, where ν typically varies from 2.0 to 3.1 [1]. The mechanism for power-law network scaling was addressed in a seminal paper by Barabási and Albert (BA) who proposed [2] a simple growing network model in which the probability of a new node forming a link with an old node (the "attachment probability") is proportional to the number of links of the old node. This model yields a power-law distribution of links with exponent $\nu = 3$. Many other works have been done extending this model. For example Krapivsky and Redner [3] provide a comprehensive description for a model with a more general dependence of the attachment probability on the number k of old node links. For attachment probability proportional to $A_k = ak + b$, they found that, depending on b/a, the exponent ν can vary from 2 to ∞. Furthermore, for $A_k \sim k^{\alpha}$, when $\alpha < 1$, n_k decays faster than a power law, while when $\alpha > 1$, there emerges a single node that connects to nearly all other nodes. Other modifications of the model are the introduction of aging of nodes [4], initial attractiveness of nodes [5], the addition or rewiring of links [6], the assignment of weights to links [7], etc.

We have attempted to construct more general growing network models featuring two effects that have not been considered previously: (i) multiple species of nodes; in real network systems, there may be different species of nodes with each species having different properties (e.g., each species may have different probabilities for adding new nodes and may also have different attachment probabilities to the same node species and to other node species, etc.) and (ii) initial link distributions; i.e., when a new node is created, its number of links to old nodes is not necessarily a constant number, but, rather, is characterized by a given probability distribution p_k of new links.

As an application of our model, we investigate the movie-actor network with movies considered as nodes and actors as links (i.e., if the same actor appears in two movies, there is a link between the two movies [8]). Moreover, we consider theatrical movies and made-for-television movies to constitute two different species.

II. MODEL

We construct a growing network model that incorporates multiple species and initial link probabilities. Given an initial network, we create new nodes at a constant rate. We let the new node belong to species j with probability $Q^{(j)}$ $(\Sigma_j Q^{(j)} = 1)$. We decide how many links l the new node establishes with the already existing nodes by randomly choosing l from a probability distribution $p_l^{(j)}$. Then, we randomly attach the new node to l existing nodes with a preferential attachment probability proportional to a factor $A_k^{(j,i)}$, where k is the number of links of the target node of species i to which the new node of species j may connect. That is, the connection probability between an existing node and a new node is determined by the number of links of the existing node and the species of the new node and the target node.

As for the single-species case [3], the evolution of this model can be described by rate equations. In our case the rate equations give the evolution of $N_k^{(i)}$, the number of species-i nodes that have k links,

$$\frac{dN_k^{(i)}}{dt} = \sum_{j=1}^{S} Q^{(j)} \overline{k^{(j)}} \frac{[A_{k-1}^{(j,i)} N_{k-1}^{(i)} - A_k^{(j,i)} N_k^{(i)}]}{\displaystyle\sum_m \sum_k A_k^{(j,m)} N_k^{(m)}} + Q^{(i)} p_k^{(i)}, \tag{1}$$

where S is the total number of species, $\overline{k^{(j)}} = \Sigma_l l p_l^{(j)}$ is the average number of new links to a new node of species j, and t is normalized so that the rate of creation of new nodes is 1 per unit time. The term proportional to $A_{k-1}^{(j,i)} N_{k-1}^{(i)}$ accounts for the increase of $N_k^{(i)}$ due to the addition of a new node of species j, which links to a species i node with $k-1$ connections. The term proportional to $A_k^{(j,i)} N_k^{(i)}$ accounts for the decrease of $N_k^{(i)}$ due to linking of a new species-j node with

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an existing species i node with k connections. The denominator, $\Sigma_m \Sigma_k A_k^{(j,m)} N_k^{(m)}$, is a normalization factor. If we add a new node with l initial links, we have l chances of increasing/decreasing $N_k^{(i)}$. This is accounted for by the factor $\overline{k^{(j)}} = \Sigma_l l p_l^{(j)}$ appearing in the summand of Eq. (1). The last term $Q^{(i)} p_k^{(i)}$ accounts for the introduction of new nodes of species i. Since all nodes have at least one link, $N_0^{(i)} = 0$.

III. ANALYSIS OF THE MODEL

Equation (1) implies that total number of nodes and total number of links increase at fixed rates. The total number of nodes of species i increases at the rate $Q^{(i)}$. Thus

$$\sum_k N_k^{(i)} = Q^{(i)} t. \tag{2}$$

The link summation over all species $\Sigma_i \Sigma_k k N_k^{(i)}$ is twice the total number of links in the network. Thus

$$\sum_i^S \sum_k k N_k^{(i)} = 2\langle \dot{k} \rangle t, \tag{3}$$

where $\langle \dot{k} \rangle = \Sigma_i \Sigma_k Q^{(i)} k p_k^{(i)} = \Sigma_i Q^{(i)} \overline{k^{(i)}}$. Solutions of Eq. (1) occur in the form (cf., Ref. [3] for the case of single-species nodes),

$$N_k^{(i)} = n_k^{(i)} t, \tag{4}$$

where $n_k^{(i)}$ is independent of t. Equation (1) yields

$$n_k^{(i)} = \frac{B_{k-1}^{(i)} n_{k-1}^{(i)} + Q^{(i)} p_k^{(i)}}{(B_k^{(i)} + 1)}, \tag{5}$$

where $B_k^{(i)}$ is

$$B_k^{(i)} = \sum_{j=1}^{S} Q^{(j)} \overline{k^{(j)}} \frac{A_k^{(j,i)}}{\displaystyle\sum_m \sum_k A_k^{(j,m)} n_k^{(m)}}. \tag{6}$$

To most simply illustrate the effect of spread in the initial number of links, we first consider the case of a network with a single species of node and with a simple form for the attachment $A_k = A_k^{(1,1)}$. In particular, we choose [3] $A_k = k + c$. [Note that by Eq. (1), this is equivalent to $A_k = ak + b$ with $c = b/a$.] Inserting this A_k into Eq. (6), we obtain $\Sigma_k (k+c) n_k = 2\langle \dot{k} \rangle + cQ$ and $B_k = (k+c)/\eta$, where $\eta = (2\langle \dot{k} \rangle + cQ)/(Q\overline{k}) = 2 + c/\overline{k} \geqslant 2$. (Note that $\langle \dot{k} \rangle = Q\overline{k}$ for the single-species case.) Thus Eq. (5) yields

$$[(k+c)n_k - (k+c-1)n_{k-1}] + \eta n_k = \eta Q p_k. \tag{7}$$

Setting $p_k = p_1 (k+c)^{-\beta}$, we can solve Eq. (7) for large k by approximating the discrete variable k as continuous, so that

$$(k+c)n_k - (k+c-1)n_{k-1} \cong \frac{d}{dk}[(k+c)n_k]. \tag{8}$$

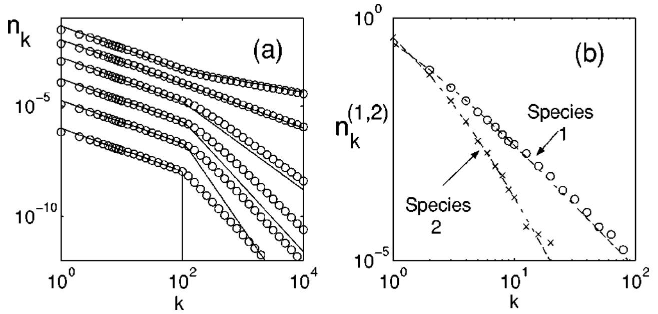

FIG. 1. (a) n_k and p_k versus k for the single-species network model. Solid lines are the initial link probability p_k and circles are the n_k obtained from Eq. (7). (b) $n_k^{(1)}$ and $n_k^{(2)}$ versus k for the two-species network model. Circles (species 1) and crosses (species 2) are log-binned data from our numerical simulation. The total number of nodes in our numerical network system is 10^6. The dashed lines are solutions obtained from Eqs. (5) and (13).

Solution of the resulting differential equation,

$$\frac{d}{dk}[(k+c)n_k] + \eta n_k = \eta Q p_1 (k+c)^{-\beta}, \tag{9}$$

for n_k with $\beta \neq \eta + 1$ consists of a homogeneous solution proportional to $(k+c)^{-(\eta+1)}$ plus the particular solution, $[\eta Q p_1/(\eta + 1 - \beta)](k+c)^{-\beta}$. For $\beta = \eta + 1$, the solution is $n_k = \eta Q p_1 (k+c)^{-(\eta+1)} \ln[d(k+c)]$, where d is an arbitrary constant. Hence, for *sufficiently large* k we have $n_k \sim k^{-(\eta+1)}$ if $\beta > \eta + 1$, and $n_k \sim k^{-\beta}$ if $\beta < \eta + 1$. Thus the result for $\beta > \eta + 1$ is independent of β and, for $c = 0$, coincides with that given in Ref. [2] ($\eta + 1 = 3$ when $c = 0$). Solutions of Eq. (7) for n_k versus k in the range $1 \leqslant k \leqslant 10^4$ are shown as open circles in Fig. 1(a) for initial link probabilities of the form

$$p_k = \begin{cases} p_1 k^{-1} & \text{for } 1 \leqslant k \leqslant 10^2 \\ p_1 10^{2(\bar{\beta}-1)} k^{-\bar{\beta}} & \text{for } k \geqslant 10^2, \end{cases} \tag{10}$$

which are plotted as solid lines in Fig. 1(a). The values of $\bar{\beta}$ used for the figure are $\bar{\beta} = 0.5$, 1, 2, 3, 4, and ∞ ($\bar{\beta} = \infty$ corresponds to $p_k \equiv 0$ for $k > 10^2$). For clarity n_k has been shifted by a constant factor so that n_1 coincides with the corresponding value of p_1. Also, to separate the graphs for easier visual inspection, the value of p_1 for successive $\bar{\beta}$ values is changed by a constant factor [since Eq. (7) is linear, the form of the solution is not effected]. We note from Fig. 1(a) that n_k follows p_k for $k < 10^2$ in all cases. This is as expected, since p_k decreases slower than k^{-3} in this range. Furthermore, n_k very closely follows p_k for $k > 10^2$ for $\bar{\beta} = 0.5, 1.0, 2.0$. As $\bar{\beta}$ increases deviations of n_k from p_k in $k > 10^2$ become more evident, and the large k asymptotic k^{-3} dependence is observed. Thus, if p_k decreases sufficiently rapidly, then the behavior of n_k is determined by the growing network dynamics, while, if p_k decreases slowly, then the behavior of n_k is determined by p_k.

To simply illustrate the effect of multiple species we now consider a growing two-species network with $p_k = \delta_{1,k}$ (i.e., $p_k = 0$ for $k \geqslant 2$). Then, Eq. (6) becomes

$$B_k^{(1)} = \frac{Q^{(1)} A_k^{(1,1)}}{\sum_m \sum_k A_k^{(1,m)} n_k^{(m)}} + \frac{Q^{(2)} A_k^{(2,1)}}{\sum_m \sum_k A_k^{(2,m)} n_k^{(m)}}, \tag{11a}$$

$$B_k^{(2)} = \frac{Q^{(1)} A_k^{(1,2)}}{\sum_m \sum_k A_k^{(1,m)} n_k^{(m)}} + \frac{Q^{(2)} A_k^{(2,2)}}{\sum_m \sum_k A_k^{(2,m)} n_k^{(m)}}, \tag{11b}$$

where Σ_m represents summation of species-1 and species-2 nodes.

In order to illustrate the model with our numerical simulations, we specialize to a specific case. We choose attachment coefficients $A_k^{(1,1)} = ak$, $A_k^{(1,2)} = ak$, $A_k^{(2,1)} = bk$, and $A^{(2,2)} = 0$. Thus a new species-1 node connects to existing species-1 nodes and species-2 nodes with equal probability, while a new species-2 node can connect to existing species-1 nodes only. Therefore, the first summation term in Eq. (11), $\Sigma_m \Sigma_k A_k^{(1,m)} n_k^{(m)}$, becomes $a \Sigma_k (k n_k^{(1)} + k n_k^{(2)})$, which is a times the total increase of links at each time, $2a(Q^{(1)} + Q^{(2)})$. (Recall that $Q^{(1)} + Q^{(2)} = 1$.) In order to calculate the second summation term in Eq. (11), $\Sigma_m \Sigma_k A_k^{(2,m)} n_k^{(m)} = b \Sigma_k k n_k^{(1)}$, we define a parameter γ that is the ratio of the total number of links of species 1 to the total number of links in the network. Since the probability of linking a new species-1 node to the existing species-1 nodes is determined by the total number of links of species 1, this probability is exactly the same as γ. Thus, if we add a new species-1 node, the number of links of species-1 increases by $Q^{(1)}$ due to the new node and by $\gamma Q^{(1)}$ due to the existing species-1 nodes that become connected with the new node, while the number of links of species-2 increases by $(1-\gamma) Q^{(1)}$. But, if we add a new species-2 node, the number of links increases by $Q^{(2)}$ for both species because a new species-2 node can link to the species-1 nodes only. Thus, the increase of species-1 links is $(1+\gamma) Q^{(1)} + Q^{(2)}$ and that of species-2 links is $(1-\gamma) Q^{(1)} + Q^{(2)}$. Since γ is the ratio of the number of species-1 links to the total number of links, $\gamma = [(1+\gamma) Q^{(1)} + Q^{(2)}]/2$ or

$$\gamma = \frac{1}{2 - Q^{(1)}}. \tag{12}$$

With this γ, Eq. (11) becomes

$$B_k^{(1)} = \frac{Q^{(1)}}{2} k + \frac{Q^{(2)}(2 - Q^{(1)})}{2} k = \frac{k}{\eta^{(1)}}, \tag{13a}$$

$$B_k^{(2)} = \frac{Q^{(1)}}{2} k = \frac{k}{\eta^{(2)}}. \tag{13b}$$

where $\eta^{(1)} = 2/[Q^{(1)} + Q^{(2)}(2 - Q^{(1)})]$ and $\eta^{(2)} = 2/Q^{(1)}$.

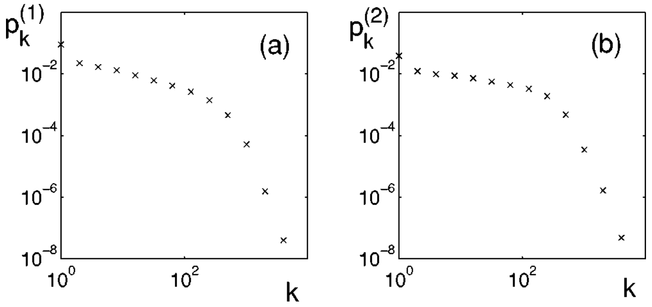

FIG. 2. The initial link probability distributions p_k of (a) theatrical movies and (b) television movies. These plots are obtained using bins of equal width in $\log_{10} k$ and dividing the number of nodes in each bin by the product of the bin width in k (which varies from bin to bin) and the total number of nodes.

Proceeding as for the single-species case, we approximate Eq. (5) by an ordinary differential equation [c.f., Eq. (9)] to obtain $n_k^{(i)} \sim k^{-(1+\eta^{(i)})}$. As an example, we set $Q^{(1)} = Q^{(2)} = 0.5$, in which case Eqs. (13) give exponents $1 + \eta^{(1)} = 2.6$ and $1 + \eta^{(2)} = 5$. In Fig. 1(b) we plot, for this case, the analytic solution obtained from Eqs. (5) and (13) as dashed lines, and the results of numerical simulations as open circles and pluses. The simulation results, obtained by histogram binning with uniform bin size in $\log_{10} k$, agree with the analytic solutions, and both show the expected large-k power-law behaviors, $n_k^{(1)} \sim k^{-2.6}$ and $n_k^{(2)} \sim k^{-5}$.

IV. THE MOVIE-ACTOR NETWORK

We now investigate the movie-actor network. We collected data from the Internet Movie Database website [9]. The total number of movies is 285 297 and the total number of actors/actresses is 555 907. Within this database are 226 325 theatrical movies and 24 865 made-for-television movies. The other movies in the database are made for television series, video, miniseries, and video games. In order to get good statistics, we choose only theatrical and television movies made between 1950 to 2000. Thus we have two species of movies. We also consider only actors/actresses from these movies. We consider two movies to be linked if they have an actor/actress in common [10]. We label the theatrical movies as species 1, and the made-for-television movies as species 2.

In order to apply our model, Eq. (1), we require $Q^{(j)}$, $p_k^{(j)}$, and $A_k^{(j,i)}$, as input which we obtain from the movie-actor network data. For simplicity, we assume these quantities to be time independent [11]. We take $Q^{(1)}$ and $Q^{(2)}$ to be, respectively, the fractions of theatrical and made-for-television movies in our database. We obtain $Q^{(1)} = 0.83$ and $Q^{(2)} = 0.17$. We now consider $p_k^{(j)}$. Suppose a new movie is produced casting r actors. For each actor s $(s = 1,2,\ldots,r)$, let l_s denote the number of previous movies in which that actor appeared. Then the total number of the initial links of the new movie is $\Sigma_s l_s$. From histograms of this number, we obtain (Fig. 2) the initial link probability distributions $p_k^{(j)}$.

The attachment $A_k^{(j,i)}$ can be numerically obtained from data via

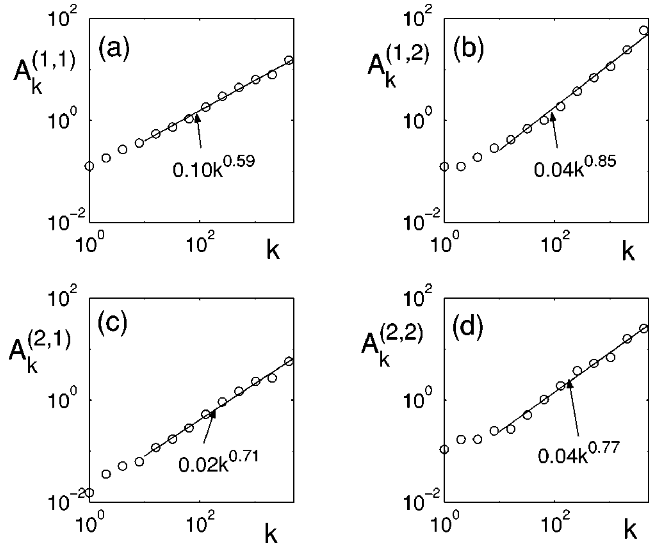

FIG. 3. Attachment coefficients for theatrical movies (a) $A_k^{(1,1)}$ and (b) $A_k^{(1,2)}$, and for television movies (c) $A_k^{(2,1)}$ and (d) $A_k^{(2,2)}$. All data are obtained using log-binning without normalization (see Fig. 2 caption).

$$A_k^{(j,i)} \sim \frac{\langle \Delta(j;i,k) \rangle}{\delta t}, \tag{14}$$

where $\Delta(j;i,k)$ is the increase during a time interval δt in the number of links between old species-i nodes that had k links and new species-j nodes, and $\langle \cdots \rangle$ is an average over all such species-i nodes [12]. In the movie network, we count all movies and links from 1950 to 1999, and measure the increments in the number of links for a δt of 1 yr. We obtain attachment coefficients $A_k^{(1,1)} \sim 0.10k^{0.59}$ and $A_k^{(1,2)} \sim 0.04k^{0.85}$ for theatrical movies, and $A_k^{(2,1)}0 \sim 0.02k^{0.71}$ and $A_k^{(2,2)} \sim 0.04k^{0.77}$ for television movies. See Fig. 3.

Incorporating these results for $Q^{(i)}$, $p_k^{(i)}$, and $A_k^{(j,i)}$ in our multispecies model, Eq. (1), we carry out numerical simulations as follows:

(i) We add a new movie at each time step. We randomly designate each new movie as a theatrical movie with probability $Q^{(1)}=0.83$ or a television movie with probability $Q^{(2)}=0.17$.

(ii) With initial link probability $p_k^{(j)}$, we randomly choose the number of connections to make to old movies.

(iii) We then use the attachment $A_k^{(j,i)}$ to randomly choose connections of new species-j movie to old species-i movies.

(iv) We repeat points (i)–(iii) adding 100 000 new movies, and finally calculate the probability distributions of movies with k links.

Figure 4 shows $n_k^{(i)}$ versus k obtained from our movie-actor network database (dots) and from numerical simulations using Eq. (1) (open circles) with our empirically obtained results for $Q^{(j)}$, $p_k^{(j)}$, and $A_k^{(j,i)}$. The results are roughly consistent with the existence of two scaling regions [13]. For small k ($k \lesssim 10^2$) the two species exhibit slow power-law decay with different exponents, $n_k^{(1)} \sim k^{-0.5}$, $n_k^{(2)} \sim k^{-0.2}$, while for large k the probabilities decay much more rapidly. Indeed, the results of Ref. [3] suggest that the decay should be exponential for large k since the attachment $A_k^{(j,i)}$ grows sublinearly with k. We showed in Sec. III, for the single-species model with a linear attachment $A_k \sim k$, that n_k follows p_k when p_k decays slowly, while n_k is independent of p_k when p_k decays sufficiently quickly. As we will show later, this feature is also applicable to multispecies networks with nonlinear attachments. As seen in Figs. 5(a) and 5(b), $n_k^{(i)}$ follows $p_k^{(i)}$ in the small-k region. However, it is not clear whether $n_k^{(i)}$ follows $p_k^{(i)}$ in the large k region. In order to check the behavior of $n_k^{(i)}$ in this region, we carried out another numerical simulation using an initial link probability $\overline{p_k^{(i)}}$ which is cut off at $k=50$. That is, $\overline{p_k^{(i)}} = p_k^{(i)}/\Sigma \overline{p_k^{(i)}}$ when $k \leqslant 50$ and $\overline{p_k^{(i)}}=0$ when $k>50$. Using $\overline{p_k^{(i)}}$

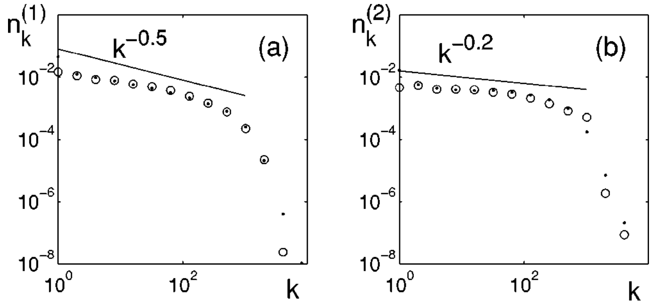

FIG. 4. The probability distributions $n_k^{(i)}$ of movies that have k links; (a) theatrical movies $n_k^{(1)}$ and (b) television movies $n_k^{(2)}$. Dots are $n_k^{(i)}$ obtained from the movie network while circles are from numerical simulation using $Q^{(j)}$ obtained from our database, $p_k^{(j)}$ in Fig. 2 and $A_k^{(j,i)}$ in Fig. 3. All data are obtained using log binning (see Fig. 2 caption).

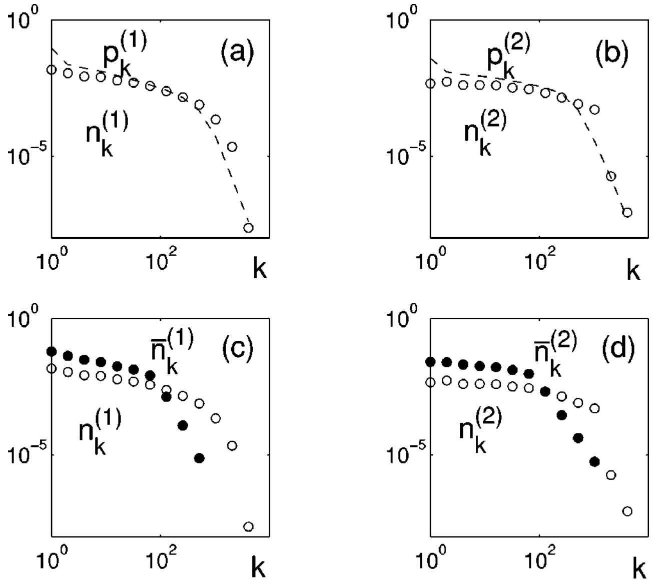

FIG. 5. (a) and (b) are $n_k^{(i)}$ (circles) obtained from numerical simulations using $p_k^{(i)}$ (dashed lines), while (c) and (d) show $n_k^{(i)}$ from (a) and (b) (open circles) plotted with the results denoted by $\overline{n_k^{(i)}}$ (filled circles) from simulation using a cutoff initial link probability $\overline{p_k^{(i)}}$ (where $\overline{p_k^{(i)}} = p_k^{(i)}/\Sigma \overline{p_k^{(i)}}$ when $k \leqslant 50$ and $\overline{p_k^{(i)}}=0$ when $k>50$). All data are obtained using log binning (see Fig. 2 caption).

in place of $p_k^{(i)}$, we obtain from our simulation corresponding to the data, $\overline{n_k^{(i)}}$ versus k, which are shown in Figs. 5(c) and 5(d) as filled-in circles. For comparison, the data for $n_k^{(i)}$ from Figs. 5(a) and 5(b) are plotted in Figs. 5(c) and 5(d) as open circles. It is seen that the cutoff at $k=50$ induces a substantial change in the distribution of the number of links for $k>50$. Thus it appears that, in the range tested, the large-k behavior of the movie-actor network is determined by the initial link probability $p_k^{(i)}$ rather than by the dynamics of the growing network.

V. CONCLUSION

In this paper we propose a model for the evolution of the distribution $n_k^{(i)}$ of links k per node of i species, i.e., a growing multispecies network with variable initial link probabilities $p_k^{(i)}$. We have analyzed our model in two extreme cases. In the case of a network with a single species of nodes, we found that the behavior of n_k is determined by the growing network dynamics if p_k decreases sufficiently rapidly, while the behavior of n_k is determined by p_k if p_k decreases slowly. In the case of a network with two species of nodes with $p_k=\delta_{1,k}$, we found that the attachment coefficients determine the behavior of $n_k^{(i)}$. In particular, each species may show different power-law behaviors. We have also investigated the movie-actor network as an example. We believe that the effect of multiple species nodes may be important for modeling other complicated networks (e.g., the World Wide Web can be divided into commercial sites and educational or personal sites). We also conjecture that the initial link probability distribution is a key feature of many growing networks.

ACKNOWLEDGMENTS

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[1] S.N. Dorogovtsev and J.F.F. Mendes, e-print cond-mat/0106144. They summarize values of γ for several network systems in Table I.

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[8] Barabási and Albert also investigated the movie-actor network. However, they consider actors as nodes that are linked if they are cast in the same movie. See Refs. [2] and [6].

[9] The Internet Movie Database, http://www.imdb.com

[10] This scenario could be more accurately modeled by tracking the connectivity of actors/actresses as well as movies. In particular, actors/actresses who appear in many movies cause correlations between movie links that are not present in our model.

[11] The *a priori* degree distribution of the movie network is time dependent since it depends on the personal history of all actors. In a more complete growth dynamics, this fact should be taken into account.

[12] The technique we use for obtaining $A_k^{(j,i)}$ is similar to that used by H. Jeong *et al.* who presume single-species situations (in which case the superscripts j and i do not apply). [H. Jeong, Z. Néda, and A.-L. Barabási, cond-mat/0104131].

[13] Similar observations suggesting two scaling regions have also been recently observed in other cases of growing networks. Barabási *et al.* investigated the scientific collaboration network [A.-L. Barabási, *et al.* cond-mat/0104162]. They argue that a model in which links are continuously created between the existing nodes explains the existence of two scaling regions in their data. Vazquez investigated the citation network of papers (nodes) and authors (links) for Phys. Rev. D and found two scalings in its in-degree distribution. See A. Vazquez, e-print cond-mat/0105031.