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Innovation diffusion on time-varying activity driven networks

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Abstract. Since its introduction in the 1960s, the theory of innovation diffusion has contributed to the advancement of several research fields, such as marketing management and consumer behavior. The 1969 seminal paper by Bass [F.M. Bass, Manag. Sci. **15**, 215 (1969)] introduced a model of product growth for consumer durables, which has been extensively used to predict innovation diffusion across a range of applications. Here, we propose a novel approach to study innovation diffusion, where interactions among individuals are mediated by the dynamics of a time-varying network. Our approach is based on the Bass' model, and overcomes key limitations of previous studies, which assumed timescale separation between the individual dynamics and the evolution of the connectivity patterns. Thus, we do not hypothesize homogeneous mixing among individuals or the existence of a fixed interaction network. We formulate our approach in the framework of activity driven networks to enable the analysis of the concurrent evolution of the interaction and individual dynamics. Numerical simulations offer a systematic analysis of the model behavior and highlight the role of individual activity on market penetration when targeted advertisement campaigns are designed, or a competition between two different products takes place.

1 Introduction

Innovation diffusion models aim at describing the diffusion of products or ideas through communication channels, established among members of a social system [1]. The theory of innovation diffusion has opened new research avenues across a number of fields, such as the study of consumers' behavior, the development of marketing strategies, and the design of improved modeling techniques [2]. One of the prominent paradigms for the description of innovation diffusion is the Bass' model [3], in which innovation (or the adoption of a new product) spreads through two distinct mechanisms: via word of mouth (WM), arising from the interaction between peers, or via an external marketing source (EM). The adopters of an innovation or of a product can be further subdivided in two groups: those who adopt the product due to the effect of EM, called innovators, and those who do it because of WM, called imitators.

The adoption mechanism was originally described through a macroscopic hazard model, where the hazard of adoption in a population is regulated by two parameters, corresponding to the EM and WM effect, respectively. Even though the Bass model is considered one of the most influential theories for innovation diffusion modeling, the majority of the technical literature has relied on simplifying assumptions that are likely to hamper its use in a range of practical applications [2,4–12].

Among these assumptions, timescale separation has often been debated in the study of social and technological networks [13,14]. Therein, individuals generally interact over a time-varying interaction network, in which links may be generated or deleted over time. The validity of a timescale separation rests upon the individual dynamics evolving on a timescale that is either much slower or much faster than the timescale of the generation or deletion of links in the network. This assumption has been extensively adopted in the application of the Bass' model, leading to two different limit conditions: an all-to-all network, resulting from homogeneous mixing [3–5,15], or a network quenched on the definition of static connectivity patterns [16–24]. Recent efforts in the field of network science have highlighted the need of explicitly considering the concurrent co-evolution of individual dynamics and interaction networks, towards the synthesis of more realistic models of social and technological networks [13,14].

In this regard, activity driven networks (ADNs) have been introduced to model contact and diffusion processes over time-varying networks, overcoming the timescale separation assumption and explicitly accounting for the concurrent evolution of the interaction network and of the dynamic process evolving on it. The approach is based on an activity potential, which is the probability per unit time that a node will establish contacts with other nodes in the network. The probability distribution of such potential is

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of fundamental importance to shape the dynamics of the system. It has been posited to follow a power-law pattern in several socio-technological applications [13,14,25–30], like in modeling epidemic spreading and interaction dynamics on large, time-resolved databases, like those containing Twitter interactions, Physical Review Letters coautorships, and actor interactions on the Internet Movie Data Base [14,29,30].

The ADN paradigm enables the simultaneous treatment of the dynamics of interactions and the dynamic processes evolving on the network structure, overcoming assumptions on timescale separation. Through a heterogeneous mean-field approach [13,28] or numerically [31], it is possible to characterize important aspects of the system dynamics, such as the threshold for the occurrence of an outbreak in epidemic models [29,30]. Many system properties have been found to be related to the activity parameters of ADN-based models, often leading to results that are different from those observed for static networks [14,29–31].

In this paper, we propose a novel innovation diffusion model, based on the original Bass' formulation [3], where the hypotheses of homogeneous mixing and time-invariance of the communication network are relaxed in favor of the more realistic interaction paradigm offered by ADNs [14,29,30]. After preliminary considerations about the relationship between the original Bass' model and its adaptation to networks, our model is introduced. Then, numerical results highlighting the role of individual activity and connectivity on shaping the adoption curve are provided. Finally, the role of individual activity is elucidated by analyzing two different processes: a targeted marketing scheme, and the competition between two different products.

2 Network-based Bass' models

According to the original Bass' model for the diffusion of innovation [3], the adoption rate of an innovation or a new product introduced at time $t = 0$ in a population of M individuals is given by:

$$\frac{dn(t)}{dt} = [M - n(t)] \left[p + \frac{q}{M}\right], \quad n(0) = 0, \qquad (1)$$

where $n(t)$ is the number of individuals who have adopted the product by time t, and p and q are two model parameters that quantify the effect on the adoption dynamics of EM and WM, respectively. Equation (1) can be explicitly solved [3], yielding a skewed bell-shaped curve for the adoption rate $dn(t)/dt$ and a sigmoidal-shaped curve for the cumulative adoptions $n(t)$.

Several methods have been proposed to identify parameters p and q from marketing data, such as ordinary and nonlinear least squares, maximum likelihood, and genetic algorithms [32]. In reference [33], multiple datasets on diffusion of innovation and products have been studied, yielding average parameter values of the order of $p = 0.003$ and $q = 0.38$. Figure 1 illustrates the cumulative density of adoption $\rho = n(t)/M$ obtained by integrating equation (1) with parameters $M = 10^5$, $p = 0.003$, and $q = 0.38$. According to references [1,3], different portions of the sigmoidal-shaped curve of adoption can be associated with different cohorts of adopters who adopt the product with different timing. In particular, Rogers [1] relates the first 2.5% of adopters to innovators, who usually adopt the product irrespective of the influence of the WM, followed by early adopters (following 13.5%), early majority (following 34%), late majority (following 34%), and laggards (last 16%). Bass [3] has grouped the latter four categories in a comprehensive group of imitators, who are individuals that are progressively led to adoption by WM rather than EM. Diamond-shaped markers in Figure 1 indicate the end of each cohort and the inception of the following one.

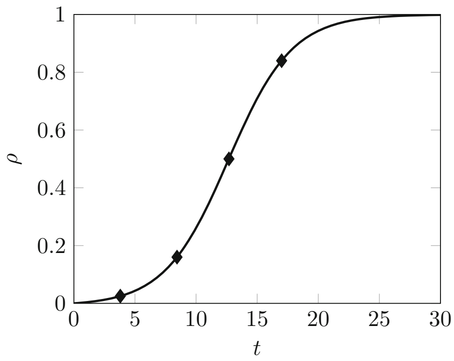

Fig. 1. Cumulative density of adoptions versus time obtained by integrating equation (1) with parameters $M = 10^5$, $p = 0.003$, and $q = 0.38$. Diamond-shaped markers indicate the end of each cohort of adopters and the inception of the following one, according to reference [1].

The original formulation of the Bass' model, based upon a nonlinear ordinary differential equation, describes the adoption process at the aggregate population level, implicitly assuming that each individual can interact with any other member in the population. Several research efforts have been conducted to develop agent- and network-based models to describe the adoption process at the microscopic, individual level. In particular, network-based Bass' models aim at releasing the assumption of all-to-all communication of the original Bass formulation, by describing interaction among individuals through a graph with a prescribed topology [32].

The implementation of microscopic models for the diffusion of innovation requires the reinterpretation at the individual level of the two macroscopic parameters p and q in equation (1), often called "forces" or "influences" [34]. Thus, global parameters must be replaced by individual probabilities of adoption that allow consistent comparisons with the original Bass' model [34,35]. Only in this perspective, and with a slight abuse of language, we will refer to these models as "equivalent" [34] to the original Bass' model.

To this aim, we consider a network of M individuals labeled with index $i = 1, \ldots, M$, and we assume all-to-all communication, i.e., individuals are connected through a complete graph. In this case, a discrete-time diffusion model that is equivalent to the Bass' model in equation (1) is obtained by setting the probability of adoption of each individual in the time interval $[t, t+\Delta t[$ as:

$$\mathrm{Pr}_i = p\Delta t + q\Delta t\frac{n(t)}{M} - pq\Delta t^2\frac{n(t)}{M}, \quad (2)$$

where Δt is the discrete-time step size. We define the per-time-step adoption probability γ as the probability that an individual adopts the product via EM in a time-step of duration Δt and the per-time-step, per-contact probability λ as the probability that an individual adopts the product via WM upon exchanging information with a single individual with which it is connected. In the case of a complete graph, comparing equation (1) with equation (2) and neglecting second order terms in Δt, we find that $\gamma_{\mathrm{C}} = p$ and $\lambda_{\mathrm{C}} = q/M$.

Considering a generic connection scheme [36], where individual i communicates with $k_i < M$ neighbors and assuming that $n_i(t) \leq k_i$ individuals within the neighborhood of i have already adopted the product by time t, we obtain an equivalent expression to equation (2)

$$\mathrm{Pr}_i = p\Delta t + q\Delta t\frac{n_i(t)}{k_i} - pq\Delta t^2\frac{n_i(t)}{k_i}. \quad (3)$$

Comparing with equation (2), the per-time-step, per-contact probabilities are $\gamma = p$ and $\lambda = q/k_i$. In particular, for a k-regular graph, the probabilities are $\gamma_{\mathrm{kREG}} = p$ and $\lambda_{\mathrm{kREG}} = q/k$.

Several studies have been conducted to study the dynamics of diffusion of innovation over static networks, i.e., network with a time-invariant link set [32,34,35,37–40]. These efforts have demonstrated that the diffusion of innovation is strongly influenced by the topology of the underlying graph. Fibich and Gibori have conjectured that, given a population of M individuals, the adoption curve of the diffusion of innovation over any topology is always slower than the adoption curve of the original Bass' model and faster than the adoption curve obtained over a ring topology [35]. In the next section, we propose our new approach to describe the dynamics of innovation diffusion over an activity driven, time-varying network.

3 Model of innovation diffusion over ADNs

We consider a network of M nodes, each associated with an individual and a set of N products that may be adopted by the individuals. Each individual can be in either of the $N+1$ states, i.e., Susceptible (S) or Adopter of product $j = 1, \ldots, N$, (A_j). The topology of the interaction network at time t is described by a graph that varies in time. Each individual i, ($i = 1, \ldots, M$), is characterized by its activity potential x_i. Variables x_i do not change in time and are independent and identically distributed realizations of a random variable x, with a probability density function $F(x)$. Following [14,29,30], we consider a power-law density function of the form $F(x) \propto x^{-\alpha}$, with $2 \leq \alpha \leq 3$. Realizations x_i of the random variable x are constrained as $\epsilon \leq x_i \leq 1$, where ϵ is a cutoff value that is suitably chosen to avoid the singularity of $F(x)$ for x close to zero.

The interaction network is initiated from a disconnected network with N nodes and, in a time increment Δt, the innovation diffusion model evolves according to the following rules [14,29,30]:

1. network formation: node $i = 1, \ldots, M$ becomes active with probability $x_i\Delta t$. An active node contacts m other nodes drawn at random from a uniform distribution, creating undirected edges. In case the node is not active, no connections are generated. At the end of this step, we obtain an undirected graph, possibly not connected;
2. WM: if a node is in the S state, it may adopt product j via WM from its current neighbors in state A_j with a per-time-step, per-contact probability λ_j. The adoption of product j is exclusive and permanent, i.e., an individual in the S state who has neighboring adopters of different products can either adopt only one of those products, or not adopt any of them. We randomize the order of the products so that none of them is preferentially chosen over the others. Once the product is adopted it will never be abandoned;
3. EM: each node in the S state is influenced by external advertisement to adopt product j via EM with per-time-step probability γ_j. Also in this case, the adoption is exclusive and permanent, and the constraint $\sum_{j=1}^{N}\gamma_j < 1$ holds; and
4. network reset: at the next time $t+\Delta t$, all the edges in the network are removed and the process resumes.

If one limits the adoption mechanism only to WM, the process is analogous to an epidemic Susceptible-Infected model [29,30]. Similar to the original Bass' model, our model does not bias a preference in adopting a product via WM or EM at a given time. Specifically, our implementation randomizes the adoption mechanism between WM (step 2) and EM (step 3) and between different products, should such adoptions occur during the same time step.

All the simulations in this paper are obtained for a network of $M = 10^5$ nodes, with an activity distribution following a power-law $F(x) \propto x^{-\alpha}$, with $\alpha = 2.1$, and a lower cutoff $\epsilon = 10^{-3}$. The time step size is set to $\Delta t = 1$ and the initial number of adopters to $n(0) = 0$. Simulation results are averaged over 100 independent trials.

4 Adoption of a single product

Here, we analyze the dynamics of adoption of a single product in an ADN and compare it with the dynamics of adoption in a static k-regular network. To simplify the notation, we drop subscript j used to differentiate products.

4.1 Analysis through a mean-field approximation

Through a heterogeneous mean-field approximation along the lines of [14,29,30], one can show that the proposed model does not exhibit a threshold for the parameters λ and γ that trigger the inception of the diffusion. The lack of a critical threshold implies that once a product is adopted by some individual, it will ultimately be adopted by the whole population, even for very small values of these parameters. For large M, let us define n_x^t and M_x as the cumulative number of adopters with activity potential x at time t and the number of individuals with activity potential x, respectively. The number of individuals with activity potential x who have not adopted the product at time t is $M_x - n_x^t$. In analogy with the epidemic modeling terminology, we will refer to such individuals as susceptible. In a mean-field approximation, the number of adopters with activity potential x at time $t + \Delta t$ is given by:

$$n_x^{t+\Delta t} = M_x^t + m\lambda(M_x - n_x^t)x\Delta t\int dx' \frac{n_{x'}^t}{M} + m\lambda(M_x - n_x^t) \times \int dx' \frac{n_{x'}^t x' \Delta t}{M} + (M_x - n_x^t)\gamma\Delta t. \quad (4)$$

In the right-hand side of equation (4), the second term represents the number of active and susceptible individuals with activity potential x who adopt the product through contacting any other adopter; the third term represents the number of susceptible individuals with activity potential x who adopt the product (irrespective of their activity state) through contacting any other active adopter; and the fourth term represents the number of susceptible individuals with activity potential x who adopt the product by way of EM. Differently from [14,29,30] where the mean-field equations are representative of autonomous dynamical systems, here the forcing term $(M_x - n_x^t)\gamma\Delta t$ describes the effect of EM on the whole population. A discrete-time mean-field model is obtained by introducing $\theta^t = \int dx' n_{x'}^t x'$ and obtaining an ancillary equation by multiplying both sides of equation (4) by x.

Then, both equations are integrated with respect to x. For the computation of the diffusion threshold, we hypothesize that the initial number of adopters is close to zero and, therefore, neglect the second order terms in n and θ. Hence, dividing both sides by M, the following linear discrete-time system describing the dynamics of the densities $\rho^t = n^t/M$ and $\vartheta^t = \theta^t/M$ in proximity of the origin is obtained:

$$\begin{aligned}\rho^{t+\Delta t} &= \rho^t + \Delta t(\lambda m\langle x\rangle - \gamma)\rho^t + \Delta t\lambda m\vartheta^t + \Delta t\gamma\\ \theta^{t+\Delta t} &= \vartheta^t + \Delta t\lambda m\langle x^2\rangle\rho^t + \Delta t(\lambda m\langle x\rangle - \gamma)\vartheta^t\\ &\quad + \Delta t\langle x\rangle\gamma.\end{aligned} \quad (5)$$

The eigenvalues of the state matrix of system (5) are $1 + \Delta t\lambda m\langle x\rangle - \Delta t\gamma \pm \jmath\lambda m\Delta t\sqrt{\langle x^2\rangle}$, where $\jmath$ is the imaginary unit. Thus, for $\gamma = 0$, (i.e., in absence of EM) the origin of the state space of system (5) is unstable for any value of the system parameters and $\lambda > 0$, since the magnitude of the eigenvalues is greater than the unity. This implies that, even in the absence of EM, the product adoption will propagate through the population for any value of the WM probability $\lambda > 0$ and for any $n(0) > 0$. For $\gamma > 0$,

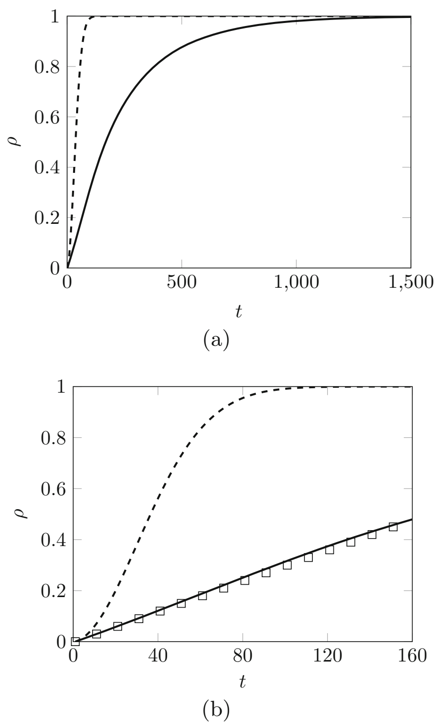

Fig. 2. Cumulative density of adoptions versus time for a k-regular network (dashed line) and an ADN (continuous line) with $m = k = 5$. In (a), the ADN curve is illustrated up to an adoption density $\rho = 99.7\%$. In (b), the time axis is restricted to the instant of complete adoption for the k-regular model, $t = 160$. Squares illustrate the hypothetical effect of EM only.

the origin of system (5) may become stable, even though this is seldom verified, since $\gamma \ll \lambda$. However, the constant exogenous inputs $\Delta t\gamma$ and $\Delta t\langle x\rangle\gamma$ will cause the density of adopters to increase in time even for $n(0) = 0$.

4.2 Comparison with k-regular networks

We now compare the dynamics of adoption on a k-regular network with an ADN that has an instantaneous number of link per active node $m = k$. As stated in Section 2, a suitable choice of the simulation parameters is required to draw consistent comparisons among different implementations of the Bass' model on a network. We consider a baseline Bass' model with influence parameters $p = 0.003$ and $q = 0.38$ [33]. For comparison purposes, we select a k-regular graph with $k = 5$ and, following the discussion in Section 2, we consistently set the per-time-step, per-contact probabilities as $\gamma_{5\text{REG}} = p = 0.003$ and $\lambda_{5\text{REG}} = q/k = 0.076$ and compare the results with an ADN with the same per-time-step, per-contact probabilities, i.e., $\gamma_{\text{ADN}} = \gamma_{5\text{REG}}$ and $\lambda_{\text{ADN}} = \lambda_{5\text{REG}}$. Figure 2 illustrates the cumulative densities of adoption for the 5-regular network and the ADN.

The time for a complete adoption of the product in the population is much longer when the ADN model is adopted. Complete adoption occurs at $t = 160$ for the 5-regular network, and at $t = 2690$ for the ADN (to enhance readability, in Figure 2a we plot the adoption curve for the ADN up to $t = 1500$, where an adoption density $\rho = 99.7\%$ is reached). Figure 2b provides a detailed view of the two curves, for $0 \leq t \leq 160$, showing that while the adoption curve obtained on the 5-regular network has the typical sigmoidal shape of Bass' model, the trend of the adoption curve in the ADN is almost linear. The reason for this behavior is that the average degree per unit time in the ADN-based model is too low to support the spread of the product via WM, causing EM to be the only mechanism to support the spread.

To further elaborate on this claim, we compute the average degree per unit time in an ADN, $\langle k_{\mathrm{ADN}} \rangle$. Following [14], we can relate $\langle k_{\mathrm{ADN}} \rangle$ to the activity potential and to the number m of links an active node establishes in a time step through $\langle k_{\mathrm{ADN}} \rangle = 2m\langle x \rangle$, where $\langle x \rangle$ is the average value of the activity potentials. For power-law distributions with $2 \leq \alpha \leq 3$, the first statistical moment is finite and the first moment estimators converge for finite realizations, whereas the second and higher central moments are infinite and their estimators do not converge for finite realizations [41]. In our case, with a finite number $M = 10^5$ of realizations of variable x and an exponent $\alpha = 2.1$ for the power-law, we robustly estimate $\langle x \rangle \approx 0.055$. Thus, $\langle k_{\mathrm{ADN}} \rangle = 2m\langle x \rangle \approx 0.05$, which is two orders of magnitudes lower than the considered 5-regular network. In Figure 2b we plot (with square markers) the linear trend $\gamma_{\mathrm{ADN}} \cdot t = 0.003 \cdot t$, which represents the effect of the EM alone and almost exactly matches the adoption curve obtained in the ADN.

As an additional study, we compare a k-regular network with an ADN that has an average instantaneous degree $\langle k_{\mathrm{ADN}} \rangle = k$. We consider again the case $k = 5$ and we set the instantaneous degree per active node m in the ADN as $m = k/(2\langle x \rangle) \approx 454$. As illustrated in Figure 3, the complete adoption of the product is still achieved faster in the k-regular model than in the ADN ($t = 160$ versus $t = 2079$), which is faster than its previous realization with $m = 5$. However, the detailed view illustrated in Figure 3b reveals that in the early phases, the ADN model exhibits a faster rate of adoption, followed by an adoption rate that is dominated by EM (compare the slope of the adoption curve with the squares illustrating the hypothetical effect of EM alone, i.e., $\gamma_{\mathrm{ADN}} \cdot t = 0.003 \cdot t$). By resorting to the nomenclature of the five cohorts of adopters [1], we find that the innovation phase has a comparable duration in the two models, the early adoption phase is faster in the ADN than in the k-regular network, whereas the inception of the remaining three cohorts occurs later in the ADN than in the k-regular network. Table 1 details this observation by reporting the times at which cohorts follow one another.

Our simulations reveal that an increase in the instantaneous number of links per active node m shapes the dynamics of adoption, yet substantial changes can be observed only in the early phase. Figure 4 compares the adoption curves on two ADNs with different number of links per active nodes per unit time, i.e., $m_1 = 454$ and $m_2 = 5000$, for $0 \leq t \leq 160$. The ADN with the higher number of nodes favors the adoption of the product in the initial phase of the adoption. Subsequently, the adoption curves tend to coincide. An extensive simulation campaign targeting variations of m revealed a saturation effect, i.e., no clear advantage can be appreciated by indefinitely increasing the value of parameter m.

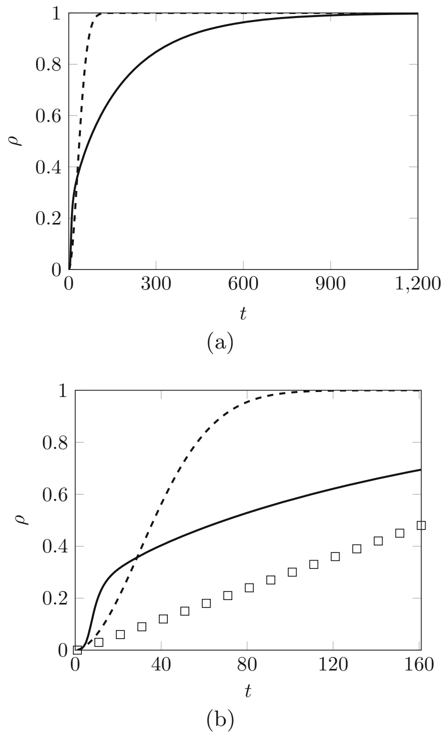

Fig. 3. Cumulative density of adoptions versus time for a k-regular network (dashed line) and an ADN (continuous line) with $k = 5$, $m = 454$. In (a), both curves are illustrated up to an adoption density $\rho = 99.7\%$ for the ADN. In (b), the time axis is restricted to the instant of complete adoption for the k-regular model, $t = 160$. Squares illustrate the hypothetical effect of EM only.

Table 1. Comparison of ending times of cohort of adopters between ADN and k-regular networks, relatively to the simulations illustrated in Figure 3.

Cohort	ADN	k-regular
Innovators	5	6
Early adopters	10	18
Early majority	70	37
Late majority	289	61
Laggards	2079	160

The distribution of the activity potentials, describing the probability of individuals to become active and contact other individuals in the population, also contributes to shaping the dynamics of adoption. To elucidate the role of such a distribution, in Figure 5 we compare the adoption curves for two ADNs where the probability density function $F(x)$ is described by two power-laws with different exponents, i.e., $\alpha_1 = 2.1$, and $\alpha_2 = 2.5$. The average values of the activies potential distributions for the two networks are $\langle x \rangle_1 = 0.0055$ and $\langle x \rangle_2 = 0.0029$. For both

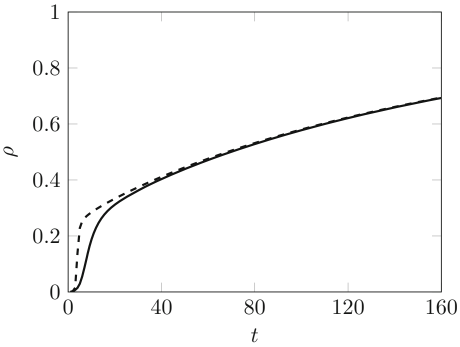

Fig. 4. Cumulative density of adoptions versus time for two ADNs with $m_1 = 454$ (continuous line) and $m_2 = 5000$ (dashed line) links per active node per unit time, and $0 \leq t \leq 160$.

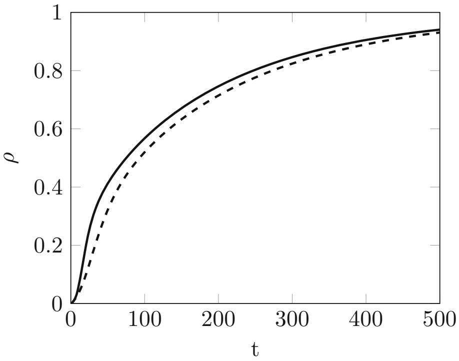

Fig. 5. Cumulative density of adoptions versus time for two ADNs with two different exponents for the power-law distribution of the activity potential, $\alpha_1 = 2.1$ (continuous line), and $\alpha_2 = 2.5$ (dashed line), and a fixed number of links per active node per unit time, $m_1 = m_2 = 100$. Results are plotted for $0 \leq t \leq 500$.

networks, we fix the same number of links per active node per unit time, i.e., $m_1 = m_2 = 100$. Consequently, the two instantaneous average degrees of the two networks are $\langle k_{\mathrm{ADN}1} \rangle = 1.1$ and $\langle k_{\mathrm{ADN}2} \rangle = 0.58$. As expected, a faster adoption is obtained with the network that has a larger instantaneous degree. Also in this case, the advantage is more evident in the early phase of adoption.

4.3 Targeted advertising

Advertising is a costly activity, and its effects seldom reach the whole population. For this reason, advertisement campaigns should be targeted to specific segments of the population, in order to maximize costs and benefits [40]. Here, we analyze the scenario where only a fraction of the population is exposed to EM, so that only a fraction of the population can turn into innovators, and we evaluate the effect of two possible external marketing strategies. More precisely, we consider the adoption of a single product and modify the process as follows: (i) at the beginning of the simulation, a static set ξM of the population is selected to be exposed to EM, we call this subset the targeted population; (ii) phase 3 is modified so that only the susceptible

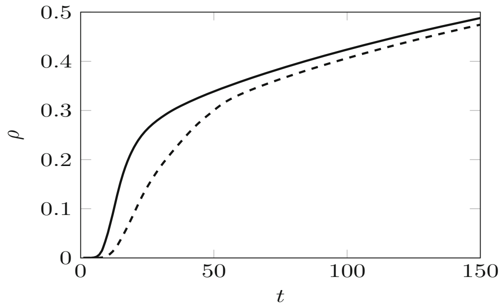

Fig. 6. Cumulative density of adoptions versus time for $0 \leq t \leq 150$, when selective marketing strategies are applied. The continuous line refers to the activity-based strategy and the dashed one refers to the random one. Model parameters are $\lambda = 0.076$, $\gamma = 0.003$, $m = 454$, and $\xi = 0.001$.

individuals of the targeted set may adopt the product with probability γ. The specific criterion to define the targeted set corresponds to different kinds of marketing strategies. Here, two different strategies are implemented: random and activity-based. In the former, the targeted set comprises ξM individuals drawn at random from the population with uniform probability. In the latter, the targeted set consists of the ξM individuals with the highest activity potentials.

Figure 6 displays the outcome of the two strategies. We find that a clear advantage is achieved with the activity-based targeting strategy, especially during the early adoption phase. The most active individuals are very likely to generate many contacts over time and to contact a large fraction of the population very early, irrespective of their adoption state. In the activity-based targeting, the most active individuals constitute the targeted set and will act as innovators very early, since they are exposed to the EM. Then, they will be able to widely spread the product due to their high activity potential. For random targeting, these highly active individuals may be involved only in a later phase, leading to the observed variation in the early stage adoption. The advantage in the application of the activity-based targeting strategy becomes less evident after the early adoption phase, where the two adoption curves tend to coincide.

5 Two competing products

Here, we consider the presence in the market of $N = 2$ competing products and we elucidate the roles of the model parameters and individual activity on the product adoption. According to the model description, two probabilities for WM and two for EM of the two products are defined, i.e., λ_1, λ_2, γ_1, and γ_2.

We study the effect of different probabilities of adoption for both the innovation and the imitation process. Figure 7 displays the trend of the adopter density versus time for different EM probabilities $\gamma_1 > \gamma_2$, and the same WM probability, $\lambda_1 = \lambda_2$ associated with the two products. As expected, a larger EM probability induces a faster growth in the adoption process and a higher steady-state

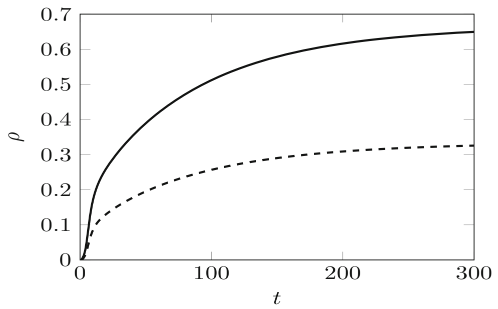

Fig. 7. Cumulative density of adoptions versus time for product 1 (continuous line) and product 2 (dashed line), for different EM probabilities and the same WM probability. Simulation parameters are set as $\lambda_1 = \lambda_2 = 0.076$, $\gamma_1 = 0.006$, $\gamma_2 = 0.003$, and $m = 454$.

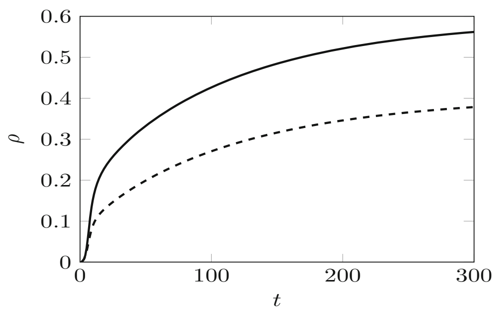

Fig. 8. Cumulative density of adoptions versus time for product 1 (continuous line) and product 2 (dashed line), for different WM probabilities and the same EM probability. Simulation parameters are set as $\lambda_1 = 0.1, \lambda_2 = 0.076$, $\gamma_1 = \gamma_2 = 0.003$, and $m = 454$.

fraction of adopters. Similar results are obtained for the imitation process, using different values of the WM probabilities, $\lambda_1 > \lambda_2$ and the same EM probability, $\gamma_1 = \gamma_2$, and are illustrated in Figure 8. We also perform simulations with the same WM and EM probabilities, i.e., $\lambda_1 = \lambda_2$ and $\gamma_1 = \gamma_2$, obtaining an even distribution of the steady-state market share (50% for each product) and the same growth rate in the adoption density ρ. These results are not reported here for brevity and are consistent with those obtained in reference [24], where the Bass' model is applied to the competition of two products. In particular, products associated with either a larger WM or EM probability result into obtaining a larger market share and a faster growth in their adoption curve, whereas equal WM and EM probabilities yield an even distribution of the market shares.

Finally, we consider the effect of individual activity on the product adoption. We assume that the probabilities of adoption are the same for the two products and for both adoption modes, i.e., $\lambda_1 = \lambda_2$ and $\gamma_1 = \gamma_2$, and we modify our model by initially assigning the two products to two distinct groups of the population. Product 1 is assigned to a fraction ξ of the population, consisting of the ξM most active individuals, whereas product 2 is assigned to a fraction ξ of the population, consisting of the ξM least active individuals. Figure 9 displays the simulation outcome and shows that the diffusion of product 1, initially distributed to the most active individuals, prevails on that of product 2, both in terms of steady-state market share and in the growth rate of the adoption process during the transient phase. As in the case of targeted marketing, the individual activity contributes to shaping the dynamics of adoption. In this case, targeting the most active individuals with a product will favor the prevalence of that product in the competition on the market.

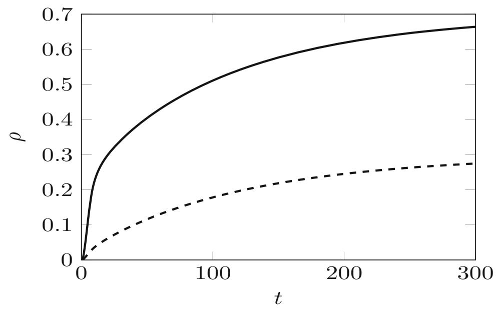

Fig. 9. Cumulative density of adoptions versus time by initially distributing product 1 (continuous line) to the most active individuals and product 2 (dashed line) to the least active ones. Results are obtained for $\lambda_1 = \lambda_2 = 0.076$, and $\gamma_1 = \gamma_2 = 0.003$, $m = 454$ and $\xi = 0.001$.

6 Conclusions

In this paper, we have proposed a novel modeling framework for innovation diffusion, where interactions among individuals are regulated by a time-varying network, whose topology is controlled by the activity of the individuals. The individual dynamics of adoption is that of the well-known Bass' model [3], while the time evolution of the individual's interaction is dictated by the dynamics of ADNs. Numerical simulations have been carried out to highlight the role of model parameters and individual activity on the innovation diffusion dynamics. Our model offers a more realistic framework to describe innovation diffusion in real-world settings, where the time scale of individual adoption is comparable with interactions among individuals.

We have found that the rate of innovation diffusion in the ADN model is regulated by the parameters describing individual activity. In particular, our results suggest that the average of the distribution of the individual activity potentials and the instantaneous number of links established by an active individual are key model parameters. Notably, in the case of diffusion of a single product, we have compared the dynamics of innovation diffusion on ADNs with k-regular networks. We have found that instances of the model with a low individual activity or a low number of links per active node do not allow the network to support the innovation diffusion via word of mouth, causing the external marketing to be the sole driver of the spread of the innovation. On the other hand, when the activity parameters are large enough, the word of mouth phenomenon takes place and reinforces the external marketing in the diffusion process. While the time for complete adoption is larger in ADNs models, there exist parameter choices that cause the early adoption phase to be completed faster in ADNs than in k-regular networks.

The role of individual activity is also evident in two further numerical experiments. The former investigated targeted marketing, where only a fraction of the population is exposed to advertisement. We have found that market penetration can be enhanced by initially assigning the product to the most active individuals in the network. This is especially evident during the early adoption phase, and fades as the system reaches steady state. The latter experiment dealt with the competition of two products. In this case, the product initially assigned to the most active individuals penetrates the market to a greater extent.

The proposed model is expected to aid in the systematic analysis of the dynamics of innovation diffusion in real-world applications. Interesting development of the proposed research may entail new approaches for the optimization of marketing strategies to improve the diffusion of innovation, while limiting the cost of the advertisement campaign.

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