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Epidemic spreading in multiplex networks with Markov and memory based inter-layer dynamics

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Abstract—Many spreading processes of information and diseases take place over complex networks that are composed of multiple interconnection layers. The relationship between network structure, nodes' activity and spreading dynamics impose a threshold above which an epidemic endures. The network structure of individual layers can take different forms, such as scale-free or random, which significantly impacts the epidemic threshold. Similarly, the nodes' inter-layer transition dynamics largely influences the threshold as well. In this study we consider an inter-layer dynamics following: a Markov process, and a memory based activity creating inter-event times with a heavytail distribution, which are typically observed in human behavior. It is shown that by introducing a layer of inactivity the epidemic threshold can be closely predicted with our previously derived expression for multiplex networks.

I. INTRODUCTION

Epidemic spreading in complex networks is a widely studied topic [1], [2] with diverse faces in different disciplines, such as virus and information spreading [3], [4] and competitive acceptance of ideas and influences. Different approaches exist for studying these processes, such as the heterogeneous meanfield approach [5], or the more detailed microscopic approach representing nodes individually [6], and both allow us to express a certain threshold characterizing the epidemic onset.

The underlying network structure can be complex and it can often involve multiple layers of connectivity [7]. Epidemic spreading has been studied in multiplex networks with various approaches [8]–[15] that we have described in [16], as well as many others reviewed in [17]. In [16] we demonstrated how epidemic spreading can be modeled in multiplex networks, where the nodes' move across layers according to a random walk, while the spreading was represented as a susceptibleinfected-susceptible (SIS) process. We also derived a threshold for the critical value of the infection rate below which an epidemic dies out, based on the derivation for single layer networks in [6].

Many of the spreading models assume that the activity patterns follow a Poisson process, which yields exponential inter-event times. However, it has been observed that the human behavior very often have activity patterns with interevent times following a heavy-tail distribution, which can considerably influence the spreading dynamics [18]–[20]. There

This work was partially financed by the Faculty of Computer Science and Engineering at the Ss. Cyril and Methodius University in Skopje. are different theories [21] of the reasons behind these patterns and various approaches how they can be simulated, like [22].

In this paper, we expand our analyses from [16] by showing that the epidemic threshold derived for Markov dynamics approximately holds for inter-layer dynamics with heavy-tailed inter-event times distribution. For generating such activity patterns we use a memory based approach [22] providing binary activity patterns and adapt it to multiplex networks. Moreover, we demonstrate that the spreading properties with this type of dynamics could be approximated with an appropriate Markov process, which makes the model applicable for more accurate predictions when fitted to real data.

The paper is organized as follows. In Section II we describe and characterize two processes depicting the inter-layer dynamics, a standard Markov process and a memory based approach. The spreading dynamics is represented and analyzed in Section III, including an examination of the epidemic threshold, while in Section IV we provide some conclusions.

II. INTERLAYER NODES' DYNAMICS IN MULTIPLEX NETWORKS

We define a multiplex network as N nodes interconnected in D different layers. The connectivity at each layer d can be represented by an adjacency matrix \mathbf{A}^d , where the elements $a_{ij}^d = 1$ indicate that nodes i and j are connected at layer d, and $a_{ij}^d = 0$ otherwise. Each node at each step can be present only in one layer and its state is represented by a vector $\mathbf{v}_i(t) = \left[v_i^d(t) \right]_{1 \times D}$ having a single 1 at the position representing the current layer and 0 at all other positions. We also introduce an OFF layer where the nodes are completely disconnected, which represents a type of inactivity. For the transition among the layers we consider two random processes: a Markov process defined with a constant transition matrix, and a process based on a memory of the past M time steps. In the following two subsections we present these processes and their main properties and differences.

A. Markov process dynamics

In a Markov process the inter-layer transitions of each node are represented by a time-invariant stochastic state-transition matrix $\mathbf{L}_i = [l_{jk}^i]_{D \times D}$ with l_{jk}^i representing the probability that node *i* will move from layer *j* to layer *k* at each step, while the elements on the main diagonal l_{jj}^i are the probabilities that the node will remain in layer j. We can then define a time dependent transition probability vector for each node i as

$$\mathbf{w}_i(t+1) = \mathbf{v}_i(t)\mathbf{L}_i,\tag{1}$$

and

$$\mathbf{v}_i(t+1) = \text{MultiRealize}[\mathbf{w}_i(t+1)], \quad (2)$$

where $MultiRealize[\cdot]$ is a function making a random realization of the probabilities.

By definition a Markov process has no memory effects and the inter-layer transitions are based solely on the previous state. If the Markov process starts from $\mathbf{v}_i(0)$, the expected value of the status vector at time t can be expressed as

$$E(\mathbf{v}_i(t)) = \pi_i^T, t \to \infty \tag{3}$$

where π_i^T is the left eigenvector of the largest eigenvalue of \mathbf{L}_i . For more details the reader can consult [16].

In Fig. 1a we show the inter-event times distribution P_{τ} for the first two layers of a single node *i* moving across four layers following a Markov process with a transition matrix

$$\mathbf{L}_{i} = \begin{bmatrix} 0.5 & 1/6 & 1/6 & 1/6 \\ 0.5 & 0.3 & 0.1 & 0.1 \\ 0.5 & 0.1 & 0.3 & 0.1 \\ 0.5 & 0.1 & 0.1 & 0.3 \end{bmatrix},$$
(4)

which gives an expected value of the status vector for this process $\pi_i^T = (1/2, 1/6, 1/6, 1/6)$. An *inter-event time* is a period between two node appearances in the same layer. We have performed $T = 10^8$ transition steps and as it can be seen the inter-event times distribution is exponential and drops more rapidly for layers with higher expectation probability. We can choose an appropriate \mathbf{L}_i according to some observed data and represent various patterns of nodes' activities, like a node transitioning to certain levels with a higher probability than to others. Similarly, in Fig. 1b we show the average distribution P_{τ} for an entire network of N = 500 nodes with the same π_i^T run over $T = 10^4$ steps.

B. Memory based dynamics

In order to achieve heavy-tail distributed inter-event times we adapt the procedure proposed in [22] to multiplex networks. Each node at each moment can be only in one of the D layers and it has an age based memory of the layers it has visited in the past M time steps. We denote by $c_i^d(t)$ how many time steps from the past M, node i has been in layer d as $c_i^d(t) = \sum_{m=1}^M v_i^d(t-m)$. Then the probability that a node will visit layer d at the next step is

$$w_i^d(t) = \frac{c_i^d(t) + b_d}{M + \sum_{d=1}^D b_d},$$
(5)

where we have introduced boost parameters $b_d > 0, \forall d$. The boosts b_d ensure that none of the probabilities $w_i^d(t)$ converges toward zero, hence, the systems does not have an absorbing state. The next states are then drawn according to Eq. 2.

In Fig. 1c we show the inter-event time distribution P_{τ} for the first two layers of a single node *i* moving across four layers



(c) Memory based - single node (d) Memory based - entire network

Fig. 1. The distribution P_{τ} of the inter-event times τ for the first two out of four layers, where blue is for Layer 1, and red for Layer 2: a) a dynamics of a single node following a Markov process with expected values of the status vector $\pi_i^T = (1/2, 1/6, 1/6, 1/6)$ run over $T = 10^8$ steps; b) an average Markov dynamics for a network of N = 500 nodes with the same π_i^T run over $T = 10^4$ steps; c) a memory based dynamics of a single node with $\mathbf{b} = (1, 1/3, 1/3)$ and M = 1000, run over $T = 10^8$ steps; and d) an average memory based dynamics of a network of N = 500 nodes with the same M = 100, run over $T = 10^8$ steps; and d) an average memory based dynamics of a network of N = 500 nodes with the same b and M = 100, run over $T = 10^4$ steps. In all cases the inter-event times distribution of the other two layers is same as for Layer 2.

in a memory based process with M = 1000 run over $T = 10^8$ steps. The boosts are set to $\mathbf{b} = (1, 1/3, 1/3, 1/3)$, while an initial memory is drawn with a probability vector $\mathbf{b}/2$. Alternatively, instead of an initial memory of size M = 1000, we can start with M = 0, or even initially drawn M = 100, and then increment it stepwise up to M = 1000. In any case the number of steps T should be large enough compared to M for the heavy-tail distribution to be observed. In Fig. 1d we show the average distribution P_{τ} for an entire network of N = 500nodes with the same b and M = 100 run over $T = 10^4$ steps. A small discontinuity appears at $\tau = M$ in both Fig. 1c and Fig. 1d. If the process is run long enough the distribution of the layer presence is mainly determined by the relative values of the boosts and partially by the initial memory. Therefore, we draw the initial memory according to the boosts, hence, in this case we will have $E(\mathbf{v}_i(t)) = (1/2, 1/6, 1/6, 1/6)$ as $t \to \infty$.

The previous expression for $w_i^d(t)$ does not allow an explicit representation of the inter-layer transition dependence between layers. Therefore, we could modify Eq. 5 to

$$w_i^d(t) = \frac{b_d + \sum_{j=1}^D c_i^j(t) u_{jd}}{M + \sum_{d=1}^D b_d},$$
(6)

where the matrix elements u_{jd} are from a matrix U_i of a similar form as L_i , which allows a more flexible fit to observed data or perceived inter-layer dependencies, however, in this paper we focus only on using Eq. 5.

III. SIS OVER MULTIPLEX NETWORKS

The SIS model defines two node states, i.e. when a node is in a susceptible state (S) it is healthy and upon contact with infected nodes from the same layer (d) in the current time (t) it can get infected (I). At the beginning there is a finite number of nodes in state I, while all other nodes are in state S. Thus, we can represent the state of a node by a vector $\mathbf{s}_i(t) = [s_i^S(t) \ s_i^I(t)], \forall i \in \{1, ..., N\}$, having 1 for the current state and 0 for the other state. With $\mathbf{p}_i(t) = [p_i^S(t) \ p_i^I(t)]$ we denote the probabilities that a node is susceptible or infected at time t. Therefore, we can represent the reactivebased epidemic SIS spreading process, i.e. there are as many stochastic contagions per unit time as there are neighbors to a node [23]–[25], for each node i in a multiplex network with the difference equations

$$p_i^S(t+1) = s_i^S(t)(1 - q_i(t)) + s_i^I(t)\eta(1 - q_i(t)), \quad (7)$$

$$p_i^I(t+1) = s_i^S(t)q_i(t) + s_i^I((1-\eta) + \eta q_i(t)), \qquad (8)$$

where $q_i(t)$ is a probability that node *i* gets infected at *t*,

$$q_i(t) = 1 - \prod_{j=1}^{N} \left[1 - \sum_{d=1}^{D} \beta a_{ji}^d s_j^I(t) v_j^d(t) v_i^d(t) \right], \quad (9)$$

and

$$\mathbf{s}_i(t+1) = \text{MultiRealize} \left[\mathbf{p}_i(t+1) \right].$$
 (10)

In (7): $s_i^S(t)(1-q_i(t))$ is the probability that a node was susceptible and does not get infected; while $s_i^I(t)\eta(1-q_i(t))$ is a probability that a node was infected, got cured with a rate η , $0 \le \eta \le 1$, and did not get another infection. In (8): $s_i^S(t)q_i(t)$ is a probability that a node was susceptible and became infected; and $s_i^I(t)$ is the probability that the node was infected and it was not cured $1-\eta$, or it got cured and reinfected again $\eta q_i(t)$. Obviously the probability that a node will be infected $q_i(t)$ depends on its current layer, as expressed by (9), where β is an infection rate, $0 \le \beta \le 1$, and

$$o_{ji}^{d}(t) = v_{j}^{d}(t)v_{i}^{d}(t)$$
(11)

is the probability that both nodes i and j are at layer d.

The system, defined by (1), (2) and (7)-(10) is a SIS *stochastic representation* over multiplex networks, which we use in our numerical simulations. On the other hand, in [16] we showed its deterministic representation using similar difference equations and we provided deeper analytical studies for the epidemic threshold. In the analysis of the epidemic dynamics in [16] we assumed that the Markov processes have already reached the stationary points, as they are independent of the spreading process. Thus, in the stationary state for the deterministic equations, (11) transforms into

$$o_{ji}^{d*} = \pi_j^d \pi_i^d, \forall i, j, \tag{12}$$

which in the stochastic representation is an expected value that nodes i and j will both be at layer d as $t \to \infty$.

For the deterministic representation in [16] we proved that for any multiplex network with a given η , we can express a critical infection rate β_c , and if $\beta > \beta_c$ eventually we will have a certain number of infected nodes, while for $\beta < \beta_c$, the infection will disappear. The critical infection rate β_c is

$$\beta_c = \frac{\eta}{\Lambda_{\max}^{\mathbf{B}}},\tag{13}$$

where $\Lambda_{\max}^{\mathbf{B}}$ is the biggest eigenvalue of a matrix

$$\mathbf{B} = \left[b_{ij}\right]_{N \times N} = \left[\sum_{l=1}^{D} a_{ji}^{d} o_{ji}^{d*}\right]$$
(14)

that is symmetric $(\mathbf{B} = \mathbf{B}^T)$ if all \mathbf{A}_d are symmetric.

When all nodes' dynamics develop according to the same \mathbf{L}_i , the matrix \mathbf{B} can be decomposed and we can rewrite (14) as $\beta_c = \eta/(\pi \pi^T \Lambda_{\max}^{\Sigma})$, where Λ_{\max}^{Σ} is the largest eigenvalue of a matrix $\boldsymbol{\Sigma} = \sum_{d=1}^{D} \mathbf{A}^d$, which is a sum of all adjacency matrices of the individual layers.

Here we study the epidemic SIS process over multiplex networks using only stochastic simulations. We examine the epidemic threshold on two different classes of multiplex networks, where the interlayer nodes' dynamics is either Markov or memory based with M = 100. The multiplex network classes are made either of Poisson random graphs, using the Erdős-Rényi (ER) model (see Fig. 2), or the heavy tailed random graphs, using the Barabási-Albert (BA) model (see Fig. 3). Similarly, for the interlayer nodes' dynamics we use both Markov and memory based dynamics, described in Section II. For each multiplex network class (ER or BA) we consider three different networks, i.e. Network I, II and III. Each of the individual layers is composed of N = 500 nodes and around E = 1500 links. The simulations are run over $T = 10^4$ steps and the parameters of the two inter-layer transition processes are chosen such that the average amount of time that nodes spend in each layer is about the same in the two processes. All parameters, such as the transition matrix L and boosts b, are assumed equal for all nodes for simplicity of the presentation.

Let us first consider **Network I** that consists of three layers, where each layer is either ER or BA network (depending on the network class) and there is no OFF layer (results are represented with black color in Figs. 2 and 3). The Markov process uses L with $l_{jj} = 0.6, \forall j$ and $l_{jk} = 0.2, \forall j \neq k$, resulting in $\pi^T = (1/3, 1/3, 1/3)$ in Eq. 3, whereas $\mathbf{b} = (2/3, 2/3, 2/3)$ for the boosts in the memory based dynamics in Eq. 5. Network II is a multiplex network consisting of four layers, where the first layer is an OFF layer and the remaining three layers are either ER or BA networks (depending on the network class). Both inter-layer nodes' dynamics types do not favorize any of the four layers in the network (results are represented with red color in Figs. 2 and 3). We use L with $l_{jj} = 1/2, \forall j$ and $l_{jk} = 1/6, \forall j \neq k$, resulting in $\pi^T = (1/4, 1/4, 1/4, 1/4)$, whereas for the memory based dynamics the boosts are equal for all four layers $\mathbf{b} = (1/2, 1/2, 1/2, 1/2)$. Network III is similar to the second network, and the only difference is that the interlayer dynamics favors the OFF layer, meaning that half of the time the nodes are not active (results are represented with blue color in Figs. 2 and 3). In this case the Markov



Fig. 2. Number of infected nodes in the ER multiplex network class, for Networks I, II and III, and different infection rates β (N = 500, $\eta = 0.5$).

process uses the transition matrix given by Eq. 4, which results in $\pi^T = (1/2, 1/6, 1/6, 1/6)$, whereas for the memory based dynamics the boost for the OFF layer is three times larger, $\mathbf{b} = (1, 1/3, 1/3, 1/3)$.

The results both in Fig. 2 and Fig. 3 show that as we increase the probability that a node is in the OFF layer β_c increases, as expected. Moreover, the epidemic thresholds obtained with the simulations in most cases are quite close to the theoretically obtained β_c with Eq. 13, which are represented with dashed vertical lines. However, we must note that a discrepancy occurs in Network III from the ER class both for Markov and memory based interlayer nodes' dynamics (compare the blue circles and crosses with the blue vertical dashed line in Fig. 2). In this case the theoretical value is $\beta_c = 0.95$, while the simulations show that the epidemic endures even for lower values of β , particularly with memory based dynamics. This phenomenon will be further analyzed in our future work, but such discrepancies have been also observed in other works. We can also conclude that there is a good match between the Markov based and memory based interlayer nodes' dynamics, compare the circles and the crosses in both Fig. 2 and Fig. 3, again except in Network III from the ER class. Thus, the simulation results show that the theoretical threshold approximately holds for inter-layer dynamics that includes processes with heavy-tailed inter-event times distribution, particularly for the SF class.

Finally, in Fig. 4 we show the epidemic dynamics over a four layer multiplex network, where as a first layer we have an OFF layer (the adjacency matrix is a zero matrix), the second layer is a BA network, the third layer is an ER network, whereas the fourth layer is a random network with small-world properties, built using the Watts-Strogatz (WS) model [26]. The results show that when the interlayer nodes' transitions are more biased toward the BA network (Network IV), the threshold is lower compared to the case when all layers, except the OFF layer, have equal probability (Network III). In **Network IV** the Markov process results in $\pi^T = (0.5, 0.3, 0.1, 0.1)$ by using L with all rows equal to π^T , while the memory process uses boosts $\mathbf{b} = (1, 0.6, 0.2, 0.2)$.



Fig. 3. Number of infected nodes in the BA multiplex network class, for Networks I, II and III, and different infection rates β (N = 500, $\eta = 0.5$).



Fig. 4. Number of infected nodes in the OFF-BA-ER-WS multiplex network, for Networks III and IV, and different infection rates β (N = 500, $\eta = 0.5$).

IV. CONCLUSION

We studied the SIS process in multiplex networks with different topologies, where one of the layers represents infective inactivity, and two different inter-layer nodes' dynamics. First, we compared the properties of the two types of transition processes and demonstrated that the memory based dynamics can be used to generate transitions across layers with heavy-tailed inter-event times. The parameters of the Markov dynamics can be fitted according to the properties of the more realistic memory based dynamics to achieve the same amount of layer presence, which could be also done with some measured data.

The analysis of the epidemic threshold showed that the analytical solution derived from the deterministic representation of the processes is approximately close to the numerical results obtained with the stochastic realizations. However, in certain random networks with weak connectivity and large amount of inactivity, where the critical infectious rate is high, the numerical results show that the epidemic can endure even for lower infection rates than the analytical threshold. Moreover, in these cases the memory based activity facilitated the spreading even more than the Markov dynamics.

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