Bifurcation analysis of the Microscopic Markov Chain Approach to contact-based epidemic spreading in networks

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ABSTRACT

The dynamics of many epidemic compartmental models for infectious diseases that spread in a single host population present a second-order phase transition. This transition occurs as a function of the infectivity parameter, from the absence of infected individuals to an endemic state. Here, we study this transition, from the perspective of dynamical systems, for a discrete-time compartmental epidemic model known as Microscopic Markov Chain Approach, whose applicability for forecasting future scenarios of epidemic spreading has been proved very useful during the COVID-19 pandemic. We show that there is an endemic state which is stable and a global attractor and that its existence is a consequence of a transcritical bifurcation. This mathematical analysis grounds the results of the model in practical applications.

1. Introduction and main results

The problem of modelling the spread of a contagious disease among individuals has been studied in deep over many years [1–4]. The development of compartmental models, i.e., models that divide the individuals among a set of possible states, has given rise to a new collection of techniques that enable, for instance, the analysis of the onset of epidemics [5–15], the study of epidemics in structured networks [16–21], or the study of the impact of a vaccination campaign [22–27]. All previous works heavily rely on the mathematical approach to the study of epidemic spreading [28] and here we follow the same spirit.

In this paper we consider a connected undirected network $\mathcal{N}_n$ made up of n nodes, whose weights $r_{ij} \in [0, 1]$ represent the contact probability between nodes i and j. Since the network is undirected and connected, the $n \times n$ contacts matrix $R = (r_{ij})$ is symmetric and irreductible. We also assume the absence of self-loops, thus $r_{ii} = 0$ for all i. The non-zero entries of matrix R represent the existing links in the network that are used to transmit the infection, while $r_{ij} = r_{ji} = 0$ is used to indicate that nodes i and j are not connected. In the special case that all non-zero contact probabilities are one, $r_{ij} = r_{ji} = 1$, matrix R becomes the adjacency matrix of the network. Note that, for a non-connected network, we can apply our results separately to every connected component of the network.

We now define a discrete dynamical system based on the infection process on the network [10], called the *Microscopic Markov Chain Approach* (MMCA), that is a mathematical model for the well-known susceptible–infected–susceptible (SIS) epidemic spreading model. In the

SIS model on networks, each node may be in one of two different states: susceptible (healthy) or infected. The discrete-time dynamic of the SIS makes that, at each time step, susceptible nodes may get infected (with probability $\beta \in [0, 1]$) by contacts with their infected neighbours, while infected nodes may recover spontaneously (with probability $\mu \in [0, 1]$). We consider that, at each time step, all nodes contact to all their neighbours, known as a *reactive* process. Other options are also possible, like contacting only a maximum number of neighbours, or even just one neighbour per time step; this last option is known as a *contact* process. From now on, we will restrict our analysis to the reactive process, which is the most common choice in the literature of the SIS model.

Following [10], we also add to the SIS dynamic the possibility of one-step reinfections, which means that an infected node that has recovered, may become infected by its neighbours within the same time step. The rationale is that the recovery of a node cannot last too long if it has many infected neighbours, thus it should effectively be equivalent to a non-recovery. An example could be computer viruses and other kinds of malware: to get rid of the virus, you cannot just remove it from one computer, since the neighbours would infect it again almost immediately.

The MMCA model provides a mathematical description of the SIS spreading process based on the use of the probabilities of the nodes of being infected. Denoting p_i^k the probability that node i is infected at the time step k, its evolution is given by the MMCA equation

$$p_i^{k+1} = (1 - q_i^k)(1 - p_i^k) + (1 - \mu)p_i^k + \mu(1 - q_i^k)p_i^k, \tag{1}$$

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