



Contents lists available at ScienceDirect

Annual Reviews in Control

journal homepage: www.elsevier.com/locate/arcontrol

Review article

On the dynamics of deterministic epidemic propagation over networks[☆]Wenjun Mei^{a,*}, Shadi Mohagheghi^b, Sandro Zampieri^c, Francesco Bullo^a^a Mechanical Engineering and Center for Control, Dynamical-Systems and Computation, University of California at Santa Barbara, USA^b Department of Electrical and Computer Engineering, University of California at Santa Barbara, USA^c Department of Information Engineering, University of Padova, Italy

ARTICLE INFO

Article history:

Received 6 May 2017

Revised 9 September 2017

Accepted 17 September 2017

Available online xxx

Keywords:

Network propagation model

Nonlinear dynamical system

Phase transition

Mathematical epidemiology

ABSTRACT

In this work we review a class of deterministic nonlinear models for the propagation of infectious diseases over contact networks with strongly-connected topologies. We consider network models for Susceptible-Infected (SI), Susceptible-Infected-Susceptible (SIS), and Susceptible-Infected-Recovered (SIR) settings. In each setting, we provide a comprehensive nonlinear analysis of equilibria, stability properties, convergence, monotonicity, positivity, and threshold conditions. For the network SI setting, specific contributions include establishing its equilibria, stability, and positivity properties. For the network SIS setting, we review a well-known deterministic model, provide novel results on the computation and characterization of the endemic state (when the system is above the epidemic threshold), and present alternative proofs for some of its properties. Finally, for the network SIR setting, we propose novel results for transient behavior, threshold conditions, stability properties, and asymptotic convergence. These results are analogous to those well-known for the scalar case. In addition, we provide a novel iterative algorithm to compute the asymptotic state of the network SIR system.

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[☆] This material is based upon work supported by, or in part by, the [U.S. Army Research Laboratory](http://www.army.mil) and the U.S. Army Research Office under grant no. [W911NF-15-1-0577](http://www.army.mil).

* Corresponding author.

E-mail addresses: wenjun_mei@umail.ucsb.edu (W. Mei), shadi.mohagheghi@gmail.com (S. Mohagheghi), zampi@dei.unipd.it (S. Zampieri), bullo@engineering.ucsb.edu (F. Bullo).

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1. Introduction

1.1. Problem motivation and description

Propagation phenomena appear in numerous disciplines. Examples include the spread of infectious diseases in contact networks, the transmission of information in communication networks, the diffusion of innovations in competitive economic networks, cascading failures in power grids, and the spreading of wild-fires in forests.

One important class of models of propagation phenomena are scalar deterministic models. These models have been widely studied, e.g., see the survey by Hethcote (2000). These models qualitatively capture some dynamic features, including phase transitions and asymptotic states. However, shortcomings of scalar models are also prominent: for example, scalar models are typically based on the assumption that individuals in the population have the same chances of interacting with each other. This assumption overlooks the internal structure of the network over which the propagation occurs, as well as the heterogeneity of individuals in the network. Both these aspects play critical roles in shaping the dynamical behavior of the propagation processes.

In a general formulation, propagation is a dynamical process on a complex network. Each network node has a state taking value in a discrete set and state changes are influenced by the nodes' neighbors in the network. Many relevant research questions arise naturally, including: how to model the local dynamics at each node, how to identify model parameters, how to estimate the state of such a dynamical system, and how to analyze the system transient and asymptotic properties.

Various types of models have been proposed to describe propagation processes over complex networks; one key distinguishing feature of these models is whether the propagation dynamics is assumed to be stochastic or deterministic. Deterministic network epidemic models were originally proposed in the late 1970s in the seminal works (Hethcote, 1978; Lajmanovich & Yorke, 1976). These models are of great research value, as attested by the large literature focusing on them (see below). Moreover, they can be considered as approximations of certain Markov-chain models, e.g., see Sahneh, Scoglio, and Mieghem (2013).

In this paper, we review three key continuous-time deterministic models for epidemic propagation over networks. Depending upon the nodal dynamics, i.e., the disease propagation behavior, deterministic epidemic propagation models are classified as: the *Susceptible-Infected* (SI) model, the *Susceptible-Infected-Susceptible* (SIS) model and the *Susceptible-Infected-Recovered* (SIR) model; basic representations of these models are illustrated in Fig. 1. In this work we focus on transient and asymptotic behavior of these three continuous-time dynamical models over networks. It is our key objective to relate the structure of the network to the function of the network (i.e., the transient and asymptotic behavior of the propagation phenomenon).

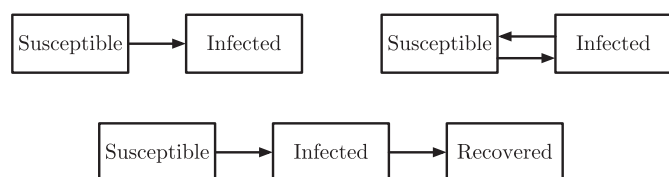


Fig. 1. Three basic models of infectious diseases: SI, SIS and SIR.

1.2. Literature review on deterministic epidemic models over networks

The literature on epidemic propagation is exceedingly vast. This paper focuses on deterministic models over networks and on their dynamical behavior. Accordingly, this subsection reviews the literature on deterministic epidemic models. Unless specified, the works and results reviewed in what follows are all for the deterministic models. For readers interested in Markov-chain models and in the mean-field approximation method, we refer to Nowzari, Preciado, and Pappas (2016); Pastor-Satorras, Castellano, Van Mieghem, and Vespignani (2015); Ruhi and Hassibi (2015); Sahneh et al. (2013), Bullo (2017, Chapter 17). (Note that Markov-chain network epidemic models and their deterministic approximating models are different in some of the dynamical properties, such as the epidemic threshold and the asymptotic behavior.)

The dynamics of several classic scalar epidemic models, i.e., the population models without network structure, are surveyed in detail by Hethcote (2000). Among the different metrics discussed, identifying the *effective reproduction number* R is of particular interest to researchers; R is the expected number of individuals that a randomly infected individual can infect during its infection period. In these scalar models, whether an epidemic outbreak occurs or the disease dies down depends upon whether $R > 1$ or $R < 1$, i.e., upon whether the system is above or below the so-called *epidemic threshold*. Here by epidemic outbreak we mean an exponential growth of the fraction of the infected population for small time. The *basic reproduction number* R_0 is the effective reproduction number in a fully-healthy susceptible population. In what follows we focus our review on deterministic network models.

The earliest work on the (continuous-time heterogeneous) SIS model on networks is Lajmanovich and Yorke (1976). This work proposes an n -dimensional model on a contact network and analyzes the system's asymptotic behavior. This article proposes a rigorous analysis of the threshold for the epidemic outbreak, which depends on both the disease parameters and the spectral radius of the contact network. For the case when the basic reproduction number is above the epidemic threshold, this paper establishes the existence and uniqueness of a nonzero steady-state infection probability, called the endemic state. In what follows we refer to the model by Lajmanovich and Yorke (1976) as the *network SIS model*; it is also known as the multi-group or multi-population SIS model.

Allen (1994) proposes and analyzes a discrete-time network SIS model. This work appears to be the first to revisit and formally reproduce, for the discrete-time case, the earlier results by Lajmanovich and Yorke (1976); see also the later work by Wang, Chakrabarti, Wang, and Faloutsos (2003). This work confirms the existence of an epidemic threshold, as a function of the spectral radius of the contact network. Further recent results on the discrete-time model are obtained by Ahn and Hassibi (2013) and by Ruhi and Hassibi (2015).

Mieghem, Omic, and Kooij (2009) argue that the (continuous-time) network SIS model is in fact the mean-field approximation of the original Markov-chain SIS model of exponential dimension; this claim is rigorously proven by Sahneh et al. (2013). Mieghem et al. (2009) refer to this model as the intertwined SIS model and write the endemic state as a continued fraction.

The works of Fall, Iggidr, Sallet, and Tewa (2007) and Khanafer, Baçsar, and Ghahesifard (2016) discuss the continuous-time network SIS model in a more modern language. Fall et al. (2007) refer to this model as the n -group SIS model and

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