



## Brief paper

# Stability of epidemic models over directed graphs: A positive systems approach<sup>☆</sup>



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## ABSTRACT

We study the stability properties of a susceptible–infected–susceptible (SIS) diffusion model, so-called the  $n$ -intertwined Markov model, over arbitrary directed network topologies. As in the majority of the work on infection spread dynamics, this model exhibits a threshold phenomenon. When the curing rates in the network are high, the disease-free equilibrium is the unique equilibrium over the network. Otherwise, an endemic equilibrium state emerges, where some infection remains within the network. Using notions from positive systems theory, we provide novel proofs for the global asymptotic stability of the equilibrium points in both cases over strongly connected networks based on the value of the basic reproduction number, a fundamental quantity in the study of epidemics. When the network topology is weakly connected, we provide conditions for the existence, uniqueness, and global asymptotic stability of an endemic state, and study the stability of the disease-free equilibrium. Finally, we demonstrate that the  $n$ -intertwined Markov model can be viewed as a best-response dynamical system of a concave game among the nodes. This characterization allows us to cast new infection spread dynamics; additionally, we provide a sufficient condition for global convergence to the disease-free equilibrium, which can be checked in a distributed fashion.

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## 1. Introduction

Epidemiological models for disease spread among humans constitute important classes of spread dynamics, as they can potentially provide models for many engineering related phenomena such as the spread of viruses in computer networks (Ganesh, Mas-soulié, & Towsley, 2005; Goffman & Newill, 1967; Kephart & White, 1991; Van Mieghem, Omic, & Kooij, 2009). There is a vast literature on various aspects of epidemiological models and the study of infection propagation over networks (Kephart & White, 1991; Pastor-Satorras & Vespignani, 2001; Wang, Chakrabarti, Wang, &

Faloutsos, 2003) and the references therein. Characterization of the stability properties of such diffusion dynamics is a crucial first step towards designing efficient algorithms for controlling their evolutions. Most dynamical epidemiological models, including the  $n$ -intertwined Markov model (Van Mieghem & Omic, 2013; Van Mieghem et al., 2009) studied here, can possess two equilibrium points, under certain conditions: a *disease-free* state at which the network is cured, and an *endemic* state at which the infection persists in the network (Diekmann, Heesterbeek, & Metz, 1990; Fall, Iggidr, Sallet, & Tewa, 2007; Lajmanovich & Yorke, 1976; Shuai & van den Driessche, 2013). This has also been observed in time-varying or switching models that allow for abrupt changes in their parameters (Rami, Bokharaie, Mason, & Wirth, 2014). A threshold called the basic reproduction number, whose value depends on the curing and infection rates across the network as well as the network topology, determines the equilibrium point the state of the network will converge to (Diekmann et al. (1990).

For the  $n$ -intertwined Markov model, the basic reproduction number, introduced as a critical threshold in Van Mieghem et al. (2009) and Van Mieghem and Omic (2013), characterizes this threshold phenomenon. In particular, when the basic reproduction number is less than or equal to 1, the unique equilibrium is the

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disease-free equilibrium; otherwise, the endemic state emerges. Our aim in this paper is to fully characterize the stability properties of this model over networks with directed topologies. Moreover, we use fundamental results from positive systems theory to construct proofs that could become a starting point for studying the stability of a variety of epidemiological models that share similar characteristics with  $n$ -intertwined Markov model.

A sufficient condition for the stability of the disease-free equilibrium over strongly connected digraphs has been established in Preciado, Zargham, Enyioha, Jadbabaie, and Pappas (2014). For compartmental susceptible–infected–susceptible (SIS) models, a necessary and sufficient condition for the global asymptotic stability of this equilibrium was presented in Fall et al. (2007) using a linear Lyapunov function. For the same model, the global asymptotic stability (GAS) of the endemic state over strongly connected directed graphs has been studied in Ahn and Hassibi (2013), Fall et al. (2007) and Shuai and van den Driessche (2013)—see Shuai and van den Driessche (2013) for a summary of other approaches to establish this result. The results in Ahn and Hassibi (2013) and Fall et al. (2007) rely on the assumption that the state of the model will evolve in the strictly positive quadrant when the state of the network is initialized away from the origin. The result in Shuai and van den Driessche (2013) was established using a non-quadratic Lyapunov function, and by relying on advanced combinatorial results such as Kirchhoff’s matrix tree theorem.

In all the aforementioned results, the underlying graphs were assumed to be strongly connected (or connected when the graph is undirected). Nonetheless, weakly connected directed graphs are common in practice, and characterizing the equilibrium points as well as their stability over these graphs presents new challenges in epidemiological networks.

The main contributions of this paper are as follows. First, using tools from the theory of positive systems, we characterize the stability properties of the endemic state equilibrium of the  $n$ -intertwined Markov model over strongly connected digraphs. In particular, we show that when the basic reproduction number is greater than 1, the endemic state is locally exponentially stable, and when the network is not initialized at the disease-free equilibrium, the endemic state is GAS. The proofs we present here do not make any assumption on the evolution of the state, and unlike (Shuai & van den Driessche, 2013), the stability properties are established using a quadratic Lyapunov function that allows us to avoid relying on advanced combinatorial and graph-theoretic notions. Moreover, we provide a game-theoretic framework that subsumes more general classes of infection dynamics. Using this model, we show that the  $n$ -intertwined Markov model prescribes the best-response dynamics of a concave game. This allows us to provide a new condition for the stability of the disease-free equilibrium, which can be checked in a distributed way. Finally, using our key construction for strongly connected digraphs, our next contribution is to study the existence, uniqueness, and stability properties of the disease-free and endemic states over weakly connected digraphs. By studying the input-to-state stability of the network, we provide conditions for a GAS endemic state to emerge over weakly connected digraphs. Unlike endemic states over strongly connected digraphs, we show that at the endemic states emerging over weakly connected graphs a subset of the nodes could be healthy while the remaining nodes become infected.

## 2. Mathematical preliminaries

All the matrices and vectors in this paper are real valued. For a set of  $n \in \mathbb{Z}_{\geq 1}$  elements, we use the combinatorial notation  $[n]$  to denote  $\{1, \dots, n\}$ . The  $(i, j)$ th entry of a matrix  $X \in \mathbb{R}^{n \times m}$ ,  $n, m \in \mathbb{Z}_{\geq 1}$  is denoted by  $x_{ij}$ . For two real vectors  $x, y \in \mathbb{R}^n$ ,  $n \in \mathbb{Z}_{\geq 1}$ , we

write  $x \gg y$  if  $x_i > y_i$  for all  $i \in [n]$ ,  $x \succ y$  if  $x_i \geq y_i$  for all  $i \in [n]$  but  $x \neq y$ , and  $x \succeq y$  if  $x_i \geq y_i$  for all  $i \in [n]$ . We say a vector  $x \in \mathbb{R}^n$  is strictly positive if  $x \gg 0$ . For any vector  $x \in \mathbb{R}^n$ , we define  $x_{\min} := \min_{i \in [n]} x_i$  and  $x_{\max} := \max_{i \in [n]} x_i$ . The absolute value of a scalar variable is denoted by  $|\cdot|$ . We also denote the cardinality of a finite set by  $|\cdot|$ . For a square matrix  $X$ , its set of eigenvalues is denoted by  $\sigma(X)$ , its spectral radius by  $\rho(X) = \max_{\lambda \in \sigma(X)} |\lambda|$ , and its abscissa is given by  $\mu(X) = \max_{\lambda \in \sigma(X)} \text{Re}(\lambda)$ . When the eigenvalues of a matrix  $X$  are real, we denote the largest eigenvalue by  $\lambda_1(X)$  and the smallest eigenvalue by  $\lambda_n(X)$ . The Euclidean norm of a vector is denoted by  $\|\cdot\|_2$ . The induced 2-norm of a matrix  $X \in \mathbb{R}^{n \times n}$  is given by

$$\|X\|_2 = \max_{\substack{y \in \mathbb{R}^n \\ \|y\|_2=1}} \|Xy\|_2 = \sqrt{\lambda_1(X^T X)}.$$

We use the operator  $\text{diag}(\cdot)$  for two purposes. When applied to a square matrix  $X \in \mathbb{R}^{n \times n}$ ,  $\text{diag}(X)$  returns a column vector that contains the diagonal entries of  $X$ . For a vector  $x \in \mathbb{R}^n$ ,  $X = \text{diag}(x)$ , or  $X = \text{diag}(x_1, \dots, x_n)$ , is a diagonal matrix with  $X_{ii} = x_i$ ,  $i \in [n]$ . When a diagonal matrix has positive diagonal entries, we call it a positive diagonal matrix. The identity matrix is denoted by  $I$ , and the all-ones vector is denoted by  $\mathbf{1}$ . We assume both  $I$  and  $\mathbf{1}$  have the appropriate dimensions whenever used.

Let  $f : \mathbb{R}^n \rightarrow \mathbb{R}^n$  be a continuously differentiable function that defines a dynamical system  $\dot{x} = f(x)$ , and let  $\bar{x}$  be an equilibrium point of this system, i.e.,  $f(\bar{x}) = 0$ . The Jacobian matrix of  $f$ ,  $J(x) \in \mathbb{R}^{n \times n}$ , is given by  $J(x) = \frac{\partial}{\partial x} f(x)$ . Let  $D \subset \mathbb{R}^{n \times n}$  be a compact domain where the trajectories of the dynamical system  $\dot{x} = f(x)$  lie. A continuously differentiable function  $V : D \rightarrow \mathbb{R}$  is a Lyapunov function if,  $V(\bar{x}) = 0$  and  $V(x) > 0$  for all  $x \in D \setminus \{\bar{x}\}$ . The Lie derivative of  $V$  along  $f$  is given by  $\mathcal{L}_f V(x) := \frac{d}{dx} V(x)^T f(x)$ .

Some of our results rely on properties of Metzler and irreducible matrices. A real square matrix  $X$  is called Metzler if its off-diagonal entries are nonnegative. We say that a matrix  $X \in \mathbb{R}^{n \times n}$  is reducible if there exists a permutation matrix  $T$  such that  $T^{-1}XT = \begin{pmatrix} Y & Z \\ 0 & W \end{pmatrix}$ , where  $Y$  and  $W$  are square matrices, or if  $n = 1$  and  $X = 0$  (Berman & Plemmons, 1979). A real square matrix is called irreducible if it is not reducible. A survey on Metzler matrices and their stability properties can be found in Berman and Plemmons (1979) and Farina and Rinaldi (2011). Hurwitz Metzler matrices have the following equivalent characterizations, see Berman and Plemmons (1979) and Rantzer (2011).

**Proposition 1.** For a Metzler matrix  $X \in \mathbb{R}^{n \times n}$ , the following statements are equivalent:

- (i) The matrix  $X$  is Hurwitz.
- (ii) There exists a vector  $\xi \gg 0$  such that  $X\xi \ll 0$ .
- (iii) There exists a vector  $v \gg 0$  such that  $v^T X \ll 0$ .
- (iv) There exists a positive diagonal matrix  $Q$  such that  $X^T Q + QX = -K$ , where  $K$  is positive definite.

### Graph theory

A directed graph, or digraph, is a pair  $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ , where  $\mathcal{V}$  is the set of nodes and  $\mathcal{E} \subseteq \mathcal{V} \times \mathcal{V}$  is the set of edges. Given  $\mathcal{G}$ , we denote an edge from node  $i \in \mathcal{V}$  to node  $j \in \mathcal{V}$  by  $(i, j)$ . We say node  $i \in \mathcal{V}$  is a neighbor of node  $j \in \mathcal{V}$  if and only if  $(i, j) \in \mathcal{E}$ . When  $(i, j) \in \mathcal{E}$  if and only if  $(j, i) \in \mathcal{E}$ , we call the graph undirected. For a graph with  $n \in \mathbb{Z}_{\geq 1}$  nodes, we associate an adjacency matrix  $A \in \mathbb{R}^{n \times n}$  with entries  $a_{ij} \in \mathbb{R}_{\geq 0}$ , where  $a_{ij} = 0$  if and only if  $(i, j) \notin \mathcal{E}$ . For undirected graphs, the adjacency matrix is symmetric.

In a digraph, a directed path is a collection of nodes  $\{i_1, \dots, i_\ell\} \subseteq \mathcal{V}$ ,  $\ell \in \mathbb{Z}_{> 1}$ , such that  $(i_k, i_{k+1}) \in \mathcal{E}$  for all  $k \in [\ell - 1]$ . A digraph is strongly connected if there exists a directed path between any two nodes in  $\mathcal{V}$ . A strongly connected component

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