國 立 交 通 大 學

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碩 士 論 文

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Analysis of a SIS model with multiple infective media on complex networks

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摘　　要

在這篇論文中我們提出與研究一個多重傳染媒介的 SIS 病毒傳播模型，在這個一般化的模型中人類之間的以異構的 scale-free 網絡作為連結方式，而人類與媒介間的連接方式我們則採用更一般化的網絡，如此一來具選擇性與不具選擇性的模型可以同時被我們討論、研究。我們的研究發現這個疾病疫情的模型可以用疾病再生指數 R_0做分類、討論，並得出以下結果。若$R_0 < 1$，則疾病疫情會消失，這表示人類與傳染媒介都痊癒。若$R_0 > 1$，則疾病疫情會爆發，穩定收斂到一個穩定的平衡態。

Analysis of a SIS model with multiple infective media in the complex networks

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ABSTRACT

In this paper, an epidemic SIS model (e.g., rabies) with multiple infective media (e.g., dogs, ferret-badgers and shrews) in complex networks is proposed and investigated. Such generalized model include a heterogeneous scale-free network between individuals and a generalized network between media and individuals. Such generalized networks is formulated in such a way so that both heterogeneous and homogeneous network are its special cases. The global dynamics of the model is studied rigorously. We compute the basic reproduction number R_0 for our model and then show that if $R_0 < 1$, then the disease-free equilibrium is globally asymptotically stable. On the contrary, if $R_0 > 1$, then there exists a unique endemic equilibrium which is globally asymptotically stable.

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在此感謝梁育豪學長費心費力的指導我完成這篇論文，與學長的討論過程中給我許多的啟發與學習，這段時間學長無私的奉獻，讓我銘感五內；感謝黃俊銘學長、謝瑞洸、黃于哲的陪伴與相互鼓勵。

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林辰燁

西元 2014 年 7 月

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1 Introduction

The study of the diseases spread is an important issue no matter in the medical practice or the academic. Heretofore, many different epidemic models are constructed and investigated to describe how the infectious transmission in one area (network) is and why some diseases eventually break out but some eventually extinguish, such as tuberculosis, malaria, and rabies or etc. Classically, these models divide involved nodes (individuals) into several compartments such as susceptible (S), infected (I), exposed (E) and recovered (R) compartments, and then are classified as the susceptible-infected-susceptible (SIS), susceptible-infected-recovered (SIR), susceptible-infected-died (SID) or susceptible-exposed-infected-susceptible (SEIR) models according to the period of immunity of nodes.

Recent researches [1–5] about the epidemic models have demonstrated that the structure of the network plays a significant role in determining the outbreak or the extinction of an epidemic. As a result, the heterogeneity of contacts for nodes in the network should be taken into consideration. Specifically, one should further separate each compartment, e.g., S, into several smaller parts S_i, $i = 1, \ldots, n$, where nodes in each different part have the different levels of influence to the epidemic. Specifically, the network of disease transmission inside the individuals could be considered as the scale-free(SF) one, an heterogeneous network with power-law degree distributions.

The network model with an infective vector is considered in [6–8]. They consider an epidemic model where the disease spread not only through the contacts between individuals themselves but also through the contacts between individuals and one kind of infective media.

It should also be noted that in [6], both individuals and the infective vector are considered as the same nodes in the network, i.e. both are scale-free nodes. However, the model under consideration in [7,8] assumes that the infective vector may contact a person without any selectivity. However, it may happens that some infectious diseases spread

with more than one infective media. For instance, it was reported, see e.g., [9] that the animals tested positive for rabies in Taiwan from January 1–October 3, 2013 include not only dog but also ferret-badgers and shrews. In fact, 159 of 512(31.1%) ferret-badgers and one of 138(0.7%) shrews tested positive for rabies. Motivated by the incidence occurred in Taiwan recently, we generalize the model so that our model consists of multiple infective media. Moreover, our model assume that the contact between vectors and individuals is satisfied by a general formulation, which include both scenarios considered in [6] and [7,8], respectively.

The rest of this paper is organized as follows. In Section 2, we build the epidemic model considered in this paper. In Section 3, we first summarize the work of Driessche and Watmough in [10] where a general method to determine whether epidemic will breakout or extinguish was given. It was shown that when the *basic reproduction number* R_0 is less than 1, the disease free equilibrium (DFE) is locally asymptotically stable; whereas when R_0 is greater than 1, the DFE is unstable. Then we show that this method can be well applied to our model. In Section 4, we present a global analysis of our model in both cases $R_0 < 1$ and $R_0 > 1$. In Section 5, we do some numerical simulations to verify the correction of our results and discuss the relationship between the basic reproduction number R_0 and the epidemic parameters in the model. We finally conclude our results in Section 6.

2 Model formulation

In this section, we introduce our epidemic model, a SIS model with multiple infective media within the diseases spread not only through the contacts between individuals themselves, but also through the contacts between individuals and multiple infective vectors.

To simulate the process of interactions, a complex network is established and nodes in the network are assumed spatially distributed. Here each node represents either an

individual (human) or a vector. In the process of disease spread, the state of each node belongs to either one of the following states: susceptible (healthy), infected. A susceptible node could become an infected one if it has a contact with infected nodes. Moreover, an infected node could become a susceptible one if one accepts a successful cure. Precisely, we assume that, at each time step, the transmission rate that susceptible individuals become infected by contacts with infected individuals is α, and an infected individual is cured and becomes susceptible again with probability γ. For the consideration of the heterogeneity in the individuals' contacts, we divide the individuals into n subgroups where each individual in the k's group, $k = 1, \ldots, n$, has the same contact degree k. We shall denote the number of susceptible, infected individuals of degree k at time t by $S_k(t)$, $I_k(t)$, respectively. Furthermore, we assume that there is no natural death or disease-related death for the individuals. Hence the total population N_k of each kth group is constant. That is, $N_k\,(= N_k(t)) \equiv S_k(t) + I_k(t)$, $k = 1, \ldots, n$, are constant.

We further assume that there are m kinds of medias involving the disease transmission in our model. In the epidemic process, it is assumed that no infection exists between any two vectors and an infected vector of the l-th kind can recover to a susceptible one with the probability $\bar{\mu}_l$. Denote the numbers of susceptible, infected media of the l-th kind at time t by $S_l^m(t)$, $I_l^m(t)$, respectively. Similarly, we will not consider the possibility of vector removal due to birth and death. Hence the total population N_l^m of each media of the l-th kind is constant. That is, $N_l^m\,(= N_l^m(t)) \equiv S_k^m(t) + I_k^m(t)$, $l = 1, \ldots, m$, are constant.

Now we are in the position to describe the interactions between the individuals and media. We assume that a susceptible individual with degree k, $k = 1, \ldots, n$, may be attacked by an infected vector with probability $\bar{q}_k$ $(\sum_{k=1}^{n} \bar{q}_k = 1)$. And at each time step, the transmission rate that susceptible individuals become infected by contacts with infected media of the l-th kind is $\bar{\beta}_l$. Meanwhile, the transmission rate that susceptible

Table 1. The description of parameters

Parameter	Description
$S_k(t), I_k(t)$	the number of susceptible, infected individuals with degree k at time t
N_k	the total population of individuals with degree k
$S_l^m(t), I_k^m(t)$	the number of susceptible, infected medium of the l-th kind at time t
N_k^m	the total population of medium of the l-th kind
α	the transmission rate that susceptible individuals become infected by contacts with infected individuals
γ	the probability that an infected individual is cured and become susceptible
$\bar{\mu}_l$	the probability that an infected vector of the l-th kind recover and become susceptible
$\bar{q}_k$	the probability that a susceptible individual with degree k is attacked by an infected vector
$\bar{\beta}_l$	the transmission rate that susceptible individuals become infected by contacts with infected media of the l-th kind
$\bar{r}_l$	the transmission rate that susceptible media of the l-th kind become infected by contacts with infected individuals

media of the l-th kind become contagious (infected) by contacts with infected individuals is $\bar{r}_l$.

For clarity, we list the parameters and variables on our model in Table 1 and the transmission sketch is shown in Fig. 1.

Under above assumptions, the dynamics of the epidemic model is governed by in the following nonlinear differential equations:

$$\begin{cases} \dfrac{dS_k(t)}{dt} = -\alpha k S_k(t)\bar{\Theta}(\boldsymbol{I}(t)) - \bar{q}_k S_k(t)\sum\limits_{l=1}^{m}\bar{\beta}_l\frac{I_l^m(t)}{N_l^m} + \gamma I_k(t), \\ \dfrac{dI_k(t)}{dt} = \alpha k S_k(t)\bar{\Theta}(\boldsymbol{I}(t)) + \bar{q}_k S_k(t)\sum\limits_{l=1}^{m}\bar{\beta}_l\frac{I_l^m(t)}{N_l^m} - \gamma I_k(t), \qquad k = 1,\ldots,n, \\ \dfrac{dS_l^m(t)}{dt} = -\bar{r}_l S_l^m(t)\bar{\Phi}(\boldsymbol{I}(t)) + \bar{\mu}_l I_l^m(t), \\ \dfrac{dI_l^m(t)}{dt} = \bar{r}_l S_l^m(t)\bar{\Phi}(\boldsymbol{I}(t)) - \bar{\mu}_l I_l^m(t), \qquad l = 1,\ldots,m, \end{cases} \tag{1}$$

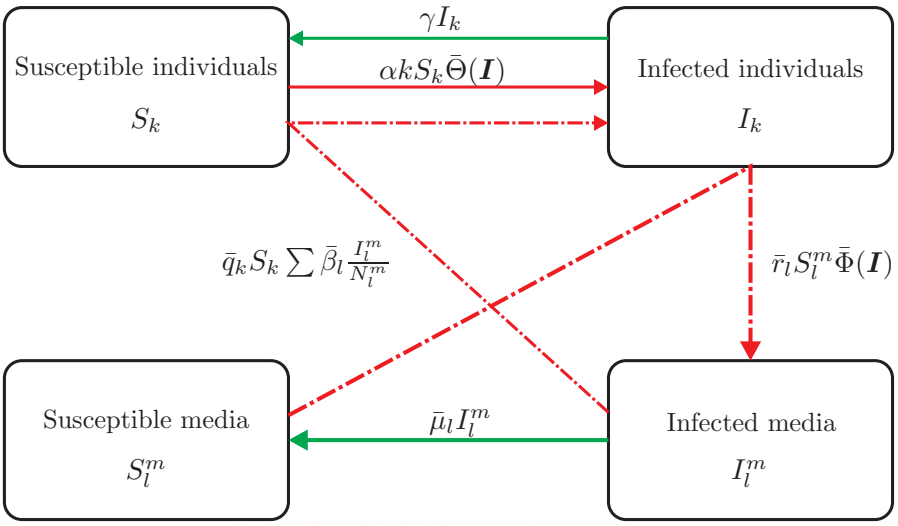


Figure 1. Flowchart of disease transmission between individuals and medias.

where $\boldsymbol{I}(t) := (I_1(t), I_2(t), \ldots, I_n(t))^T$ (T takes the notation of the transpose) is the collection of all infected individuals with different degrees at time t,

$$\bar{\Theta}(\boldsymbol{I}(t)) := \frac{\sum_{k=1}^{n} k I_k(t)}{\sum_{k=1}^{n} k N_k}$$

represents the probability of a link from an individual pointing to an infected individual and

$$\bar{\Phi}(\boldsymbol{I}(t)) := \sum_{k=1}^{n} \bar{q}_k \frac{I_k(t)}{N_k}$$

represents the probability of a link from a vector pointing to an infected individual. We remark that the specific setting of function $\bar{\Theta}$ is based on the consideration of the wide range distribution of the contact degrees between individuals. On the other hand, the setting of function $\bar{\Phi}$ is quite free since there is no assumption made on the contact degrees from a vector to individuals.

Let $x_k(t) := \frac{I_k(t)}{N_k}$ ($y_k(t) := \frac{S_k(t)}{N_k}$), $k = 1, \ldots, n$, and $v_l(t) := \frac{I_l^m(t)}{N_l^m}$ ($u_l(t) := \frac{S_l^m(t)}{N_l^m}$), $l = 1, \ldots, m$, be the relative densities of infected (susceptible) individuals of degree k and media of the l-th kind at time t, respectively. Then by the fact that $x_k + y_k = 1$ and

$v_l + u_l = 1$ for all k, l, we can rewrite equation (1) as the following density-related form.

$$\begin{cases} \dfrac{dx_k(t)}{dt} = \alpha k[1 - x_k(t)]\Theta(\boldsymbol{x}_1(t)) + \bar{q}_k[1 - x_k(t)] \sum\limits_{l=1}^{m} \bar{\beta}_l v_l(t) - \gamma x_k(t), & k = 1, \ldots, n, \\ \dfrac{dv_l(t)}{dt} = \bar{r}_l[1 - v_l(t)]\Phi(\boldsymbol{x}_1(t)) - \bar{\mu}_l v_l(t), & l = 1, \ldots, m, \\ \dfrac{dy_k(t)}{dt} = -\alpha k[1 - x_k(t)]\Theta(\boldsymbol{x}_1(t)) - \bar{q}_k[1 - x_k(t)] \sum\limits_{l=1}^{m} \bar{\beta}_l v_l(t) + \gamma[1 - y_k(t)], & k = 1, \ldots, n, \\ \dfrac{du_l(t)}{dt} = -\bar{r}_l[1 - v_l(t)]\Phi(\boldsymbol{x}_1(t)) + \bar{\mu}_l[1 - u_l(t)], & l = 1, \ldots, m, \end{cases}$$

where

$$\boldsymbol{x}_1(t) := (x_1(t), x_2(t), \cdots, x_n(t))^T \tag{2}$$

is the collection of all relative densities of infected individuals with different degrees at time t,

$$\Theta(\boldsymbol{x}_1(t)) := \frac{\sum\limits_{k=1}^{n} kI_k(t)}{\sum\limits_{k=1}^{n} kN_k} = \frac{\sum\limits_{k=1}^{n} k\frac{I_k(t)}{N_k}\frac{N_k}{N}}{\sum\limits_{k=1}^{n} k\frac{N_k}{N}} \equiv \frac{\sum\limits_{k=1}^{n} kp_k x_k(t)}{\sum\limits_{k=1}^{n} kp_k} \equiv \frac{\sum\limits_{k=1}^{n} kp_k x_k(t)}{< k >}, \tag{3}$$

$p_k := \frac{N_k}{N}$ is the density of individuals of the degree k, $< k >:= \sum_{k=1}^{n} kp_k$, and

$$\Phi(\boldsymbol{x}_1(t)) := \sum_{k=1}^{n} \bar{q}_k x_k(t). \tag{4}$$

For the simplification of notations, we define x_k for $k = n+1, \ldots, 2n+2m$, by

$$x_k = \begin{cases} v_{k-n}, & \text{if } k = n+1, \ldots, n+m, \\ y_{k-(n+m)}, & \text{if } k = n+m+1, \ldots, 2n+m, \\ u_{k-(2n+m)}, & \text{if } k = 2n+m+1, \ldots, 2n+2m, \end{cases}$$

and

$$q_k = \begin{cases} \bar{q}_k, & \text{if } k = 1, \ldots, n, \\ \bar{q}_{k-(n+m)}, & \text{if } k = n+m+1, \ldots, 2n+m, \end{cases}$$

$$\beta_k = \bar{\beta}_{k-n}, k = n+1, \ldots, n+m,$$

$$r_k = \begin{cases} \bar{r}_{k-n}, & \text{if } k = n+1, \ldots, n+m, \\ \bar{r}_{k-(2n+m)}, & \text{if } k = 2n+m+1, \ldots, 2n+2m, \end{cases}$$

$$\mu_k = \begin{cases} \bar{\mu}_{k-n}, & \text{if } k = n+1, \ldots, n+m, \\ \bar{\mu}_{k-(2n+m)}, & \text{if } k = 2n+m+1, \ldots, 2n+2m. \end{cases}$$

Then above density-related differential equations become:

$$\frac{dx_k(t)}{dt} = \begin{cases} \alpha k[1-x_k(t)]\Theta(\boldsymbol{x}_1(t)) + q_k[1-x_k(t)]\sum_{j=n+1}^{n+m}\beta_j x_j(t) - \gamma x_k(t), & k = 1, \ldots, n, \\ r_k[1-x_k(t)]\Phi(\boldsymbol{x}_1(t)) - \mu_k x_k(t), & k = n+1, ..., n+m, \\ -\alpha k x_k(t)\Theta(\boldsymbol{x}_1(t)) - q_k x_k(t)\sum_{j=n+1}^{n+m}\beta_j x_j(t) + \gamma[1-x_k(t)], & \\ \qquad k = n+m+1, \ldots, 2n+m, & \\ -r_k x_k(t)\Phi(\boldsymbol{x}_1(t)) + \mu_k[1-x_k(t)], & \\ \qquad k = 2n+m+1, \ldots, 2n+2m, & \end{cases} \tag{5}$$

where $\boldsymbol{x}_1 = (x_1(t), x_2(t), \cdots, x_n(t))^T$, Θ and Φ are defined as in (2), (3), and (4), respectively.

Furthermore, since $x_k + x_{k+(n+m)} (= x_k + y_k) = 1$ for $k = 1, \ldots, n$, and $x_k + x_{k+(n+m)} (= v_{k-n} + v_{k-n}) = 1$ for $k = n+1, \ldots, n+m$, to analyze the dynamics of equation (5) is equivalent to analyze the dynamics of equations (just) related to variables x_k, $k =$

$1, \ldots, n+m$. Then the equivalent dynamical equation reads as the following:

$$\frac{dx_k(t)}{dt} = \begin{cases} \alpha k[1-x_k(t)]\Theta(\boldsymbol{x}_1(t)) + q_k[1-x_k(t)]\sum_{j=n+1}^{n+m}\beta_j x_j(t) - \gamma x_k(t), & k = 1, \ldots, n, \\ r_k[1-x_k(t)]\Phi(\boldsymbol{x}_1(t)) - \mu_k x_k(t), & k = n+1, ..., n+m. \end{cases} \tag{6}$$

3 Local stability analysis

In this section, we are to analyze the local stability of the disease free equilibrium (DFE)

$$\boldsymbol{\xi}_0 := (\underbrace{0, \cdots, 0}_{n+m}, \underbrace{1, \cdots, 1}_{n+m})^T \tag{7}$$

for equation (5) (equivalently, $\boldsymbol{x}_0 = \mathbf{0} \in \mathbb{R}^{n+m}$ for (6)) by using the general method proposed by Driessche and Watmough in [10]. We first use a subsection to introduce their work and then we show how this method can be applied to our model (5).

3.1 Definition of the basic reproduction number R_0

Let $\boldsymbol{\xi} = (\xi_1, \cdots, \xi_{\bar{n}})^T$ denote the collection of all numbers of compartments in the epidemic model (network) and the first $\bar{m}$ components of $\boldsymbol{\xi}$ correspond to all the infected compartments. Suppose that the dynamics of the epidemic model is governed by the following equation.

$$\begin{aligned} \frac{d\boldsymbol{\xi}}{dt} &= \boldsymbol{f}(\boldsymbol{\xi}) \\ &:= \boldsymbol{\mathcal{F}}(\boldsymbol{\xi}) - \boldsymbol{\mathcal{V}}(\boldsymbol{\xi}) \\ &:= \boldsymbol{\mathcal{F}}(\boldsymbol{\xi}) - [\boldsymbol{\mathcal{V}}^-(\boldsymbol{\xi}) - \boldsymbol{\mathcal{V}}^+(\boldsymbol{\xi})], \end{aligned} \tag{8}$$

where $\boldsymbol{f}(\boldsymbol{\xi}) = (f_1(\boldsymbol{\xi}), \cdots, f_{\bar{n}}(\boldsymbol{\xi}))^T$, $\boldsymbol{\mathcal{F}}(\boldsymbol{\xi}) = (\mathcal{F}_1(\boldsymbol{\xi}), \cdots, \mathcal{F}_{\bar{n}}(\boldsymbol{\xi}))^T$, $\boldsymbol{\mathcal{V}}(\boldsymbol{\xi}) = (\mathcal{V}_1(\boldsymbol{\xi}), \cdots, \mathcal{V}_{\bar{n}}(\boldsymbol{\xi}))^T$ and $\boldsymbol{\mathcal{V}}^{\pm}(\boldsymbol{\xi}) = (\mathcal{V}_1^{\pm}(\boldsymbol{\xi}), \cdots, \mathcal{V}_{\bar{n}}^{\pm}(\boldsymbol{\xi}))^T$. Here each function takes the meaning as follows: $\mathcal{F}_i(\boldsymbol{\xi})$ is the rate of appearance of new infections in compartment i, $\mathcal{V}_i^+(\boldsymbol{\xi})$ is the rate of transfer of nodes into compartment i by all other means, and $\mathcal{V}_i^-(\boldsymbol{\xi})$ is the rate of transfer of nodes out of compartment i. Moreover, these functions are assumed to satisfy the following assumptions (A1) – (A5) described below.

Since each function represents a directed transfer of nodes, they are all nonnegative. Thus,

(A1) If $\boldsymbol{\xi} \geq 0$, then $\boldsymbol{\mathcal{F}}(\boldsymbol{\xi})$, $\boldsymbol{\mathcal{V}}^+(\boldsymbol{\xi})$, $\boldsymbol{\mathcal{V}}^-(\boldsymbol{\xi}) \geq 0$. Here a vector $\boldsymbol{v} \geq 0$ means that all components of $\boldsymbol{v}$ are nonegative.

If a compartment is empty, then there can be no transfer of nodes out of the compartment by death, infection, nor any other means. Thus,

(A2) If $\boldsymbol{\xi}$ has some component $\xi_i = 0$, then $V_i^-(\boldsymbol{\xi}) = 0$.

Notice that (A1) and (A2) imply that the nonnegative cone $\{\boldsymbol{\xi} : \boldsymbol{\xi} \geq 0\}$ is positive invariant since $f_i(\boldsymbol{\xi}) \geq 0$ whenever $\xi_i = 0$.

The next condition arises from the simple fact that the incidence of infection for uninfected compartments is zero.

(A3) $\mathcal{F}_i(\boldsymbol{\xi}) = 0$ for $i > \bar{m}$.

Define X_s be the set of all disease free states, i.e.,

$$X_s := \{\boldsymbol{\xi} \geq 0 : \xi_i = 0,\ i = 1, \ldots, \bar{m}\}. \tag{9}$$

Then to ensure that the disease free subspace X_s is invariant, we assume that if the population is free of disease, then the population will remain free of disease. That is, there is no (density independent) immigration of infection. This condition is stated as follows:

(A4) If $\boldsymbol{\xi} \in X_s$, then $F_i(\boldsymbol{\xi}) = 0$ and $V_i^+(\boldsymbol{\xi}) = 0$ for $i = 1, \ldots, \bar{m}$.

The remaining condition is based on the derivatives of $\boldsymbol{f}$ near a DFE. For our purposes, we restrict a DFE of (8) to be locally asymptotically stable equilibrium for the disease free model, i.e., (8) restricted to X_s. Note that we need not assume that the model has a unique DFE. Consider a population near the $\boldsymbol{\xi}_0 \in X_s$. If the population remains near

the DFE (i.e., the introduction of a few infective nodes does not result in an epidemic), then the population will return to the DFE according to the linearized system

$$\dot{\boldsymbol{\xi}} = D\boldsymbol{f}(\boldsymbol{\xi}_0)(\boldsymbol{\xi} - \boldsymbol{\xi}_0), \tag{10}$$

where $D\boldsymbol{f}(\boldsymbol{\xi}_0)$ is the derivative $[\partial f_i/\partial \xi_j]$ evaluated at the DFE $\boldsymbol{\xi}_0$ (i.e., the Jacobian matrix). Here the derivative is one sided since $\boldsymbol{\xi}_0$ is on the domain boundary. We restrict our attention to systems in which the DFE is stable in the absence of new infection. That is,

(A5) If $\boldsymbol{\mathcal{F}}(\boldsymbol{\xi})$ is set zero, then all eigenvalues of $D\boldsymbol{f}(\boldsymbol{\xi}_0)$ have negative real parts.

Lemma 1. *([10]) Let $\boldsymbol{\xi}_0$ be a disease free equilibrium of (8) and suppose assumptions (A1)–(A5) hold true. Then the derivatives $D\boldsymbol{\mathcal{F}}(\boldsymbol{\xi}_0)$ and $D\boldsymbol{\mathcal{V}}(\boldsymbol{\xi}_0)$ are partitioned as*

$$D\boldsymbol{\mathcal{F}} = \begin{pmatrix} \boldsymbol{F} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{0} \end{pmatrix}, \qquad D\boldsymbol{\mathcal{V}}(\boldsymbol{\xi}_0) = \begin{pmatrix} \boldsymbol{V} & \boldsymbol{0} \\ \boldsymbol{J}_3 & \boldsymbol{J}_4 \end{pmatrix},$$

where $\boldsymbol{F}$ and $\boldsymbol{V}$ are the $\bar{m} \times \bar{m}$ matrices defined by

$$\boldsymbol{F} = \left[\frac{\partial \mathcal{F}_i}{\partial \xi_j}(\boldsymbol{\xi}_0)\right] \quad \text{and} \quad \boldsymbol{V} = \left[\frac{\partial \mathcal{V}_i}{\partial \xi_j}(\boldsymbol{\xi}_0)\right] \quad \text{with } 1 \le i, j \le \bar{m}. \tag{11}$$

Furthermore, $\boldsymbol{F}$ is nonnegative, $\boldsymbol{V}$ is a nonsingular M-matrix and all eigenvalues of $\boldsymbol{J}_4$ have positive real part.

Define the basic reproduction number R_0 by

$$R_0 := \rho(\boldsymbol{F}\boldsymbol{V}^{-1}), \tag{12}$$

where $\rho(A)$ denotes the spectral radius of a matrix A. Then it describes "the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual". Precisely, if $R_0 < 1$, then on average an infected individual produces less than one new infected individual over the course of its infectious period, and the infection cannot grow. Conversely, if $R_0 > 1$, then each infected individual produces, on

average, more than one new infection, and the disease can invade the population. We conclude the result in the following theorem.

Theorem 1. *([10]) Let $\boldsymbol{\xi}_0$ be a disease free equilibrium of (8) and suppose assumptions (A1)–(A5) hold true. Then the following assertions hold.*

(i) If $R_0 < 1$, then $\boldsymbol{\xi}_0$ is locally asymptotically stable.

(ii) If $R_0 > 1$, then $\boldsymbol{\xi}_0$ is unstable.

Here R_0 is the basic reproduction number defined as in (12).

3.2 The basic reproduction number R_0 in our model

In this subsection, the local stability of DFE $\boldsymbol{\xi}_0$ defined in (7) for model (5) is to be analyzed by applying Theorem 1 given in the above subsection. For it, the first step is to find the basic reproduction number R_0 for model (5).

Notice that by letting $\boldsymbol{\xi} := (x_1, \cdots, x_{2n+2m})^T$ and $\boldsymbol{x}_1 := (x_1, \cdots, x_n)^T$, we can write (5) into the (componentwise) form given in (8):

$$\frac{d\xi_k}{dt} = \mathcal{F}_k(\boldsymbol{\xi}) - [\mathcal{V}_k^-(\boldsymbol{\xi}) - \mathcal{V}_k^+(\boldsymbol{\xi})],$$

for $k = 1, \ldots, 2(n+m)$, where

$$\mathcal{F}_k(\boldsymbol{\xi}) = \begin{cases} \alpha k[1-\xi_k]\Theta(\boldsymbol{x}_1) + q_k[1-\xi_k]\sum_{j=n+1}^{n+m}\beta_j\xi_j, & k = 1, \ldots, n, \\ r_k[1-\xi_k]\Phi(\boldsymbol{x}_1), & k = n+1, \ldots, n+m, \\ 0, & k = n+m+1, \ldots, 2n+m, \\ 0, & k = 2n+m+1, \ldots, 2n+2m, \end{cases} \tag{13}$$

$$\mathcal{V}_k^-(\boldsymbol{\xi}) = \begin{cases} \gamma\xi_k, & k = 1, \ldots, n, \\ \mu_k\xi_k, & k = n+1, \ldots, n+m, \\ \alpha k\xi_k\Theta(\boldsymbol{x}_1) + q_k\xi_k \sum\limits_{j=n+1}^{n+m} \beta_j\xi_j, & k = n+m+1, \ldots, 2n+m, \\ r_k\xi_k\Phi(\boldsymbol{x}_1), & k = 2n+m+1, \ldots, 2n+2m, \end{cases} \tag{14}$$

$$\mathcal{V}_k^+(\boldsymbol{\xi}) = \begin{cases} 0, & k = 1, \ldots, n, \\ 0, & k = n+1, \ldots, n+m, \\ \gamma[1-\xi_k], & k = n+m+1, \ldots, 2n+m, \\ \mu_k[1-\xi_k], & k = 2n+m+1, \ldots, 2n+2m. \end{cases} \tag{15}$$

Then it is clear that the disease free subspace $X_s = \{\boldsymbol{\xi}_0\}$, $\boldsymbol{\xi}_0$ is the unique DFE and assumptions (A1)–(A4) hold. Furthermore, note that when $\mathcal{F}_k(\boldsymbol{\xi})$, $k = 1, \ldots, 2(n+m)$, are set zero, we have that

$$D\boldsymbol{f}(\boldsymbol{\xi}_0) = \begin{pmatrix} \boldsymbol{C}_1 & \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{C}_2 & \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{C}_1 & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{C}_2 \end{pmatrix},$$

where $\boldsymbol{C}_1 = -\gamma\boldsymbol{I}_n$ and $\boldsymbol{C}_2 = -\mathrm{diag}([\mu_1, \cdots, \mu_m])$. Here $\boldsymbol{I}_n$ is the $n \times n$ identity matrix. Consequently, eigenvalues of $D\boldsymbol{f}(\boldsymbol{\xi}_0)$ are $-\gamma, -\mu_1, \cdots, -\mu_m$, which are all negative. Hence assumption (A5) holds.

Since all assumptions (A1)–(A5) in Theorem 1 hold true, we can apply it to our model. By direct computation, we have that matrices $\boldsymbol{F}$ and $\boldsymbol{V}$ defined in (11) are:

$$\boldsymbol{F} = \begin{pmatrix} \frac{(1\cdot 1)\alpha p_1}{< k >} & \frac{(1\cdot 2)\alpha p_2}{< k >} & \cdots & \frac{(1\cdot n)\alpha p_n}{< k >} & q_1\beta_{n+1} & q_1\beta_{n+2} & \cdots & q_1\beta_{n+m} \\ \frac{(2\cdot 1)\alpha p_1}{< k >} & \frac{(2\cdot 2)\alpha p_2}{< k >} & \cdots & \frac{(2\cdot n)\alpha p_n}{< k >} & q_2\beta_{n+1} & q_2\beta_{n+2} & \cdots & q_2\beta_{n+m} \\ \vdots & \vdots & & \vdots & \vdots & \vdots & & \vdots \\ \frac{(n\cdot 1)\alpha p_1}{< k >} & \frac{(n\cdot 2)\alpha p_2}{< k >} & \cdots & \frac{(n\cdot n)\alpha p_n}{< k >} & q_n\beta_{n+1} & q_n\beta_{n+2} & \cdots & q_n\beta_{n+m} \\ r_{n+1}q_1 & r_{n+1}q_2 & \cdots & r_{n+1}q_n & 0 & 0 & \cdots & 0 \\ r_{n+2}q_1 & r_{n+2}q_2 & \cdots & r_{n+2}q_n & 0 & 0 & \cdots & 0 \\ \vdots & \vdots & & \vdots & \vdots & \vdots & & \vdots \\ r_{n+m}q_1 & r_{n+m}q_2 & \cdots & r_{n+m}q_n & 0 & 0 & \cdots & 0 \end{pmatrix},$$

and

$$\boldsymbol{V} = \begin{pmatrix} \gamma & & & & & & \\ & \gamma & & & & & \\ & & \ddots & & & & \\ & & & \gamma & & & \\ & & & & \mu_{n+1} & & \\ & & & & & \mu_{n+2} & \\ & & & & & & \ddots \\ & & & & & & & \mu_{n+m} \end{pmatrix}.$$

Then the reproduction number is given by $R_0 = \rho(\boldsymbol{F}\boldsymbol{V}^{-1})$, the spectral radius of matrix

$\boldsymbol{FV}^{-1}$. We compute that

$$\boldsymbol{FV}^{-1} = \begin{pmatrix} \frac{(1\cdot 1)\alpha p_1}{\gamma < k >} & \frac{(1\cdot 2)\alpha p_2}{\gamma < k >} & \cdots & \frac{(1\cdot n)\alpha p_n}{\gamma < k >} & q_1\frac{\beta_{n+1}}{\mu_{n+1}} & q_1\frac{\beta_{n+2}}{\mu_{n+2}} & \cdots & q_1\frac{\beta_{n+m}}{\mu_{n+m}} \\ \frac{(2\cdot 1)\alpha p_1}{\gamma < k >} & \frac{(2\cdot 2)\alpha p_2}{\gamma < k >} & \cdots & \frac{(2\cdot n)\alpha p_n}{\gamma < k >} & q_2\frac{\beta_{n+1}}{\mu_{n+1}} & q_2\frac{\beta_{n+2}}{\mu_{n+2}} & \cdots & q_2\frac{\beta_{n+m}}{\mu_{n+m}} \\ \vdots & \vdots & & \vdots & \vdots & \vdots & & \vdots \\ \frac{(n\cdot 1)\alpha p_1}{\gamma < k >} & \frac{(n\cdot 2)\alpha p_2}{\gamma < k >} & \cdots & \frac{(n\cdot n)\alpha p_n}{\gamma < k >} & q_n\frac{\beta_{n+1}}{\mu_{n+1}} & q_n\frac{\beta_{n+2}}{\mu_{n+2}} & \cdots & q_n\frac{\beta_{n+m}}{\mu_{n+m}} \\ \frac{r_{n+1}q_1}{\gamma} & \frac{r_{n+1}q_2}{\gamma} & \cdots & \frac{r_{n+1}q_n}{\gamma} & 0 & 0 & \cdots & 0 \\ \frac{r_{n+2}q_1}{\gamma} & \frac{r_{n+2}q_2}{\gamma} & \cdots & \frac{r_{n+2}q_n}{\gamma} & 0 & 0 & \cdots & 0 \\ \vdots & \vdots & & \vdots & \vdots & \vdots & & \vdots \\ \frac{r_{n+m}q_1}{\gamma} & \frac{r_{n+m}q_2}{\gamma} & \cdots & \frac{r_{n+m}q_n}{\gamma} & 0 & 0 & \cdots & 0 \end{pmatrix}$$

$$= \left(\begin{array}{c|c} \frac{\alpha}{\gamma<k>}\boldsymbol{\eta}\boldsymbol{\chi}^T & \boldsymbol{q}\boldsymbol{\beta}^T \\ \hline \frac{1}{\gamma}\boldsymbol{r}\boldsymbol{q}^T & \boldsymbol{0} \end{array}\right),$$

where $\boldsymbol{\eta} = (1, \cdots, n)^T$, $\boldsymbol{\chi} = (1p_1, \cdots, np_n)^T$, $\boldsymbol{q} = (q_1, \cdots, q_n)^T$, $\boldsymbol{\beta} = (\beta_{n+1}, \cdots, \beta_{n+m})^T$ and $\boldsymbol{r} = (r_{n+1}, \cdots, r_{n+m})^T$. Thus, we obtain that the basic reproduction number R_0 is the largest modulus of the roots of the cubic polynomial described below:

$$\lambda^3 + a_2\lambda^2 + a_1\lambda + a_0 = 0,$$

where

$$a_2 = -\frac{\alpha}{\gamma < k >}\sum_{k=1}^{n} k^2 p_k, \tag{16}$$

$$a_1 = \left(\sum_{k=1}^{n} q_k^2\right)\left(\sum_{j=n+1}^{n+m}\frac{r_j\beta_j}{\mu_j}\right), \tag{17}$$

$$a_0 = \frac{\alpha}{\gamma < k >}\left(\sum_{k=1}^{n} k^2 p_k \sum_{k=1}^{n} q_k^2 - \sum_{k=1}^{n} kq_k \sum_{k=1}^{n} kp_k q_k\right)\left(\sum_{j=n+1}^{n+m}\frac{r_j\beta_j}{\mu_j}\right). \tag{18}$$

Then we give a formula to compute to the roots of a cubic polynomial.

Lemma 2. *[11] Consider the general cubic polynomial*

$$x^3 + ax^2 + bx + c = 0. \tag{19}$$

Let $\triangle := \left(\frac{2a^3-9ab+27c}{54}\right)^2 + \left(\frac{3b-a^2}{9}\right)^3$. *Then the following assertions hold:*

Case 1: *When* $\triangle > 0$, (19) *has one real root and one pair of conjugate virtual roots;*

Case 2: *When* $\triangle = 0$, (19) *has three real roots, at least two of which are repeated roots;*

Case 3: *When* $\triangle < 0$, (19) *has three different real roots.*

Moreover, the roots of (19) *are*

$$z_1 = \sqrt[3]{\rho_1} + \sqrt[3]{\rho_2} + \frac{a}{3},$$
$$z_2 = \psi\sqrt[3]{\rho_1} + \bar{\psi}\sqrt[3]{\rho_2} + \frac{a}{3},$$
$$z_3 = \bar{\psi}\sqrt[3]{\rho_1} + \psi\sqrt[3]{\rho_2} + \frac{a}{3},$$

where $\rho_1 = -\frac{2a^3 - 9ab + 27c}{54} + \sqrt{\triangle}$, $\rho_2 = -\frac{2a^3 - 9ab + 27c}{54} - \sqrt{\triangle}$, $\psi = -\frac{1}{2} + i\frac{\sqrt{3}}{2}$ *and* $i^2 = -1$.

By Lemma 2, if $\triangle \leq 0$, the basic reproduction number $R_0 = \max\{|z_1|, |z_2|, |z_3|\}$; if $\triangle > 0$, we obtain the reproduction number $R_0 = z_1$. We conclude our local stability in the following theorem.

Theorem 2. *For the disease transmission model* (5) *(equivalently,* (6)*), if* $R_0 < 1$, *then the disease-free equilibrium* $\boldsymbol{\xi}_0$ *(*$\boldsymbol{x}_0$*) is locally asymptotically stable. On the other hand, if* $R_0 > 1$, *then* $\boldsymbol{\xi}_0$ *(*$\boldsymbol{x}_0$*) is unstable.*

4 Global stability analysis

In this section, the qualitatively global analysis of model (6) (equivalently, (5)) is presented. We first show that set $\triangle_{n+m} := [0, 1]^{n+m}$ is positive invariant.

Lemma 3. *Set $\triangle_{n+m}$ is positively invariant under the flow determined by equation (6). That is, $\boldsymbol{x}(t) \in \triangle_{n+m}$ for all $t > 0$ and $\boldsymbol{x}(0) \in \triangle_{n+m}$.*

Proof. Denote the boundaries of set $\triangle_{n+m}$ by $\partial\triangle_{n+m}$. Then it consists of the two parts $\partial\triangle^1_{n+m}$ and $\partial\triangle^2_{n+m}$, where

$$\partial\triangle^1_{n+m} := \{\boldsymbol{x} \in \triangle_{n+m} : x_k = 0 \text{ for some } k\}, \text{ and}$$

$$\partial\triangle^2_{n+m} := \{\boldsymbol{x} \in \triangle_{n+m} : x_k = 1 \text{ for some } k\}.$$

Then to prove that $\triangle_{n+m}$ is positively invariant, it suffices to prove that the assignment vector at any boundary point of the vector field yielded by equation (6) is tangent or pointing into the set $\triangle_{n+m}$. Since $\triangle_{n+m}$ is a rectangle in $\mathbb{R}^{n+m}$, the "outer normals" at boundaries $\partial\triangle^1_{n+m}$ and $\partial\triangle^2_{n+m}$ are $\vec{\boldsymbol{n}}^1_k := -\boldsymbol{e}_k$ and $\vec{\boldsymbol{n}}^2_k := \boldsymbol{e}_k$, respectively, where $\boldsymbol{e}_k$ denotes the standard unit vector in $\mathbb{R}^{n+m}$. Moreover, we compute that

(I). For $\boldsymbol{x} \in \partial\triangle^1_{n+m}$ with $x_k = 0$ for some $k = 1, \ldots, n+m$:

$$\dot{\boldsymbol{x}} \cdot \vec{\boldsymbol{n}}^1_k = \begin{cases} -\left[\alpha k \Theta(\boldsymbol{x}_1) + q_k \sum_{j=n+1}^{n+m} \beta_j x_j\right], & \text{for } k = 1, \cdots, n, \\ -r_k \sum_{j=1}^{n} \Phi(\boldsymbol{x}_1), & \text{for } k = n+1, 2, \cdots, n+m. \end{cases}$$

Thus, $\dot{\boldsymbol{x}} \cdot \vec{\boldsymbol{n}}^1_k \leq 0$ for all $k = 1, \ldots, n+m$.

(II). For $\boldsymbol{x} \in \partial\triangle^2_{n+m}$ with $x_k = 1$ for some $k = 1, \ldots, n+m$:

$$\dot{\boldsymbol{x}} \cdot \vec{\boldsymbol{n}}^2_k = \begin{cases} -\gamma, & \text{for } k = 1, \cdots, n, \\ -\mu_k, & \text{for } k = n+1, 2, \cdots, n+m. \end{cases}$$

Thus, $\dot{\boldsymbol{x}} \cdot \vec{\boldsymbol{n}}^2_k < 0$ for all $k = 1, \ldots, n+m$.

By (I) and (II), we have that the assignment vector at any boundary point of the vector field yielded by equation (6) is tangent or pointing into the set $\triangle_{n+m}$. Hence, the proof of Lemma 3 is complete. □

Next, we show that DFE $\boldsymbol{\xi}_0$ defined in (7) is globally asymptotically stable in model (5) if $R_0 < 1$. Equivalently, equilibrium $\boldsymbol{x}_0 = \boldsymbol{0} \in \mathbb{R}^{n+m}$ is globally asymptotically stable

in model (6) if $R_0 < 1$. (For simplification, we also call $\boldsymbol{x}_0$ to be a DEF for model (6).) Before it, we first show that no equilibrium lies in $\triangle_{n+m}$ expect $\boldsymbol{x}_0$ and recall a general qualitative analytic result in the differential equations proposed by Lajmanovich and Yorke [12].

Lemma 4. *The only equilibrium for (6) in $\partial\triangle_{n+m}$, the boundary of $\triangle_{n+m}$, is DFE $\boldsymbol{x}_0$.*

Proof. Suppose the statement of Lemma 4 is false. Then there exists an equilibrium $\bar{\boldsymbol{x}} := (\bar{x}_1, \cdots, \bar{x}_{n+m})$ for (6) in $\partial \triangle_{n+m} - \{\boldsymbol{x}_0\}$. Then by definition, $\bar{x}_k = 0$ for some $k \in \{1, \cdots, n+m\}$.

(I). If $k \in \{1, \cdots, n\}$, then by (6), since $\frac{dx_k}{dt} = 0$, we have that $\alpha k \Theta(\bar{\boldsymbol{x}}_1) + q_k \sum_{j=n+1}^{n+m} \beta_j \bar{x}_j = 0$. Hence $\Theta(\bar{\boldsymbol{x}}_1), \sum_{j=n+1}^{n+m} \beta_j \bar{x}_j = 0$. Consequently, $\bar{x}_j = 0$ for all $j = 1, \ldots, n+m$, i.e., $\bar{\boldsymbol{x}} = \boldsymbol{x}_0 (= \mathbf{0})$, a contradiction.

(II). If $k \in \{n+1, \cdots, n+m\}$, then by (6), since $\frac{dx_k}{dt} = 0$, we have that $\Phi(\bar{\boldsymbol{x}}_1) = 0$ and hence $\bar{x}_j = 0$ for all $j = 1, \ldots, n$. Moreover, for $j = n+1, \ldots, n+m$, since $\frac{dx_j}{dt} = 0$, we have that $\bar{x}_j = 0$. Thus, $\bar{\boldsymbol{x}} = \boldsymbol{x}_0 (= \mathbf{0})$, a contradiction.

By (I) and (II), we conclude that the only equilibrium for (6) in $\partial\triangle_{n+m}$, is the DFE $\boldsymbol{x}_0$. It completes the proof of Lemma 4.

□

Lemma 5. *([12]) Consider the system*

$$\frac{d\boldsymbol{x}}{dt} = \boldsymbol{A}\boldsymbol{x} + \boldsymbol{H}(\boldsymbol{x}), \tag{20}$$

where $\boldsymbol{A}$ is an $\bar{m} \times \bar{m}$ matrix and $\boldsymbol{H}(\boldsymbol{x})$ is continuously differentiable in a region $D \in \mathbb{R}^{\bar{m}}$. Suppose that the following assumptions hold:

(A1) The compact convex set $C \subset D$ is positively invariant under the flow determined by equation (20).

(A2) $\lim_{\boldsymbol{x} \to \mathbf{0}} \frac{\|\boldsymbol{H}(\boldsymbol{x})\|}{\|\boldsymbol{x}\|} = 0.$

(A3) There exist some $r > 0$ *and eigenvector* $\boldsymbol{\nu} \in \mathbb{R}^{\bar{m}}$ *of* $\boldsymbol{A}^T$ *such that* $\boldsymbol{\nu} \cdot \boldsymbol{x} \geq r\|\boldsymbol{x}\|$ *for all* $\boldsymbol{x} \in C$.

(A4) $\boldsymbol{\nu} \cdot \boldsymbol{H}(\boldsymbol{x}) \leq 0$ *for all* $\boldsymbol{x} \in C$.

(A5) $\{\mathbf{0}\}$ *is the largest positively invariant set for* (20) *contained in set* $M := \{\boldsymbol{x} \in C : \boldsymbol{\nu} \cdot \boldsymbol{H}(\boldsymbol{x}) = 0\}$.

Then either (i) $\boldsymbol{x} = \mathbf{0}$ *is globally asymptotically stable in* C, *or (ii) for any initial value* $\tilde{\boldsymbol{x}}_0 \in C - \{\mathbf{0}\}$, *the solution* $\boldsymbol{\phi}(t, \tilde{\boldsymbol{x}}_0)$ *of* (20) *satisfies* $\liminf_{t\to\infty} \|\boldsymbol{\phi}(t, \tilde{\boldsymbol{x}}_0)\| \geq m$, *where* $m > 0$ *is independent of* $\tilde{\boldsymbol{x}}_0$. *Moreover, there exists a nontrivial equilibrium* $\boldsymbol{x}^*$ *of* (20) *in* C.

Theorem 3. *If* $R_0 < 1$, *then* $\boldsymbol{x}_0$ *is globally asymptotically stable in* $\triangle_{n+m}$. *On the other hand, if* $R_0 > 1$, *then there exists an epidemic equilibrium* $\boldsymbol{x}^*(> 0)$ *in* $\triangle_{n+m}$. *Moreover, for any initial value* $\tilde{\boldsymbol{x}}_0 \in \triangle_{n+m} - \{\boldsymbol{x}_0\}$, *the solution* $\boldsymbol{\phi}(t, \tilde{\boldsymbol{x}}_0)$ *of* (6) *satisfies* $\liminf_{t\to\infty} \|\boldsymbol{\phi}(t, \tilde{\boldsymbol{x}}_0)\| \geq m$, *where* $m > 0$ *is independent of* $\tilde{\boldsymbol{x}}_0$.

Proof. Notice first that equation (6) can be rewritten in the form of (20):

$$\frac{d\boldsymbol{x}}{dt} = \boldsymbol{A}\boldsymbol{x} + \boldsymbol{H}(\boldsymbol{x}), \tag{21}$$

where

$$\boldsymbol{A} = \begin{pmatrix} -\gamma + \frac{p_1}{< k >}\alpha & \frac{2p_2}{< k >}\alpha & \cdots & \frac{np_n}{< k >}\alpha & q_1\beta_{n+1} & \cdots & q_1\beta_{n+m} \\ \frac{p_1}{< k >}2\alpha & -\gamma + \frac{2p_2}{< k >}2\alpha & \cdots & \frac{np_n}{< k >}2\alpha & q_2\beta_{n+1} & \cdots & q_2\beta_{n+m} \\ \vdots & \vdots & & \vdots & \vdots & & \vdots \\ \frac{p_1}{< k >}n\alpha & \frac{2p_2}{< k >}n\alpha & \cdots & -\gamma + \frac{np_n}{< k >}n\alpha & q_n\beta_{n+1} & \cdots & q_n\beta_{n+m} \\ r_{n+1}q_1 & r_{n+1}q_2 & \cdots & r_1q_n & -\mu_{n+1} & & \\ \vdots & \vdots & & \vdots & & \ddots & \\ r_{n+m}q_1 & r_{n+m}q_2 & \cdots & r_mq_n & & & -\mu_{n+m} \end{pmatrix} \tag{22}$$

and

$$\boldsymbol{H}(\boldsymbol{x}) = \begin{pmatrix} -\alpha x_1 \Theta(\boldsymbol{x}_1) - q_1 x_1 \left(\sum_{j=n+1}^{n+m} \beta_j x_j \right) \\ \vdots \\ -\alpha n x_n \Theta(\boldsymbol{x}_1) - q_n x_n \left(\sum_{j=n+1}^{n+m} \beta_j x_j \right) \\ -r_{n+1} x_{n+1} \Phi(\boldsymbol{x}_1) \\ \vdots \\ -r_{n+m} x_{n+m} \Phi(\boldsymbol{x}_1) \end{pmatrix}. \tag{23}$$

Then (i) by Lemma 3, $\triangle_{n+m}$ is a positive invariant (compact) set for equation (6) in $\mathbb{R}^{n+m}$; (ii) Since each term of $\boldsymbol{H}(\boldsymbol{x})$ has degree equal to 2, we have that $\lim_{\boldsymbol{x}\to\boldsymbol{0}} \frac{\|\boldsymbol{H}(\boldsymbol{x})\|}{\|\boldsymbol{x}\|} = 0$. (iii) Let $\boldsymbol{A}_1 := \boldsymbol{A}^T + a\boldsymbol{I}$ where $a = \max\{\gamma, \mu_{n+1}, \cdots, \mu_{n+m}\}$. Then $\boldsymbol{A}_1$ is a nonnegative, irreducible matrix. Hence, by Perron-Frobenius theorem, there exists an eigenvalue $\lambda \in \mathbb{R}$ of $\boldsymbol{A}_1$ such that $\lambda = \rho(\boldsymbol{A}_1)(> 0)$. Moreover, it has a corresponding eigenvector $\boldsymbol{\nu} > 0$. Consequently, $\lambda - a$ is an eigenvalue of A^T and $\boldsymbol{\nu}$ is its corresponding eigenvector. Then for all $\boldsymbol{x} \in \triangle_{n+m} = [0,1]^{n+m}$, we have that $\boldsymbol{\nu} \cdot \boldsymbol{x} \geq \nu_0 \|\boldsymbol{x}\|_1 \geq \nu_0 \|\boldsymbol{x}\|_2$ where $\nu_0 > 0$ takes the minimum value of all components of $\boldsymbol{\nu}$. (iv) For $\boldsymbol{x} \in \triangle_{n+m}$, since $\boldsymbol{H}(\boldsymbol{x}) \leq 0$, we have that $\boldsymbol{\nu} \cdot \boldsymbol{H}(\boldsymbol{x}) \leq 0$. Moreover, the equality holds if and only if $\boldsymbol{H}(\boldsymbol{x}) = \boldsymbol{0}$. (v) Let $M := \{\boldsymbol{x} \in \triangle_{n+m} : \boldsymbol{\nu} \cdot \boldsymbol{H}(\boldsymbol{x}) = \boldsymbol{0}\}$. Then we have that

$$\begin{aligned} M &= \{\boldsymbol{x} \in \triangle_{n+m} : \boldsymbol{H}(\boldsymbol{x}) = \boldsymbol{0}\} \\ &= \{\boldsymbol{x} \in \triangle_{n+m} : x_k = 0,\ \forall\, k = 1, \cdots, n\}. \end{aligned}$$

Let $\boldsymbol{x} \in M - \{\boldsymbol{0}\}$. Then $\boldsymbol{A}\boldsymbol{x} + \boldsymbol{H}(\boldsymbol{x}) = \boldsymbol{A}\boldsymbol{x}$ has its first n components being positive by (22). This means that initial value starting at point $\boldsymbol{x}$ will leave M immediately under the flow determined by (21). Hence, we conclude that the largest invariant set for (21) contained in M is $\{\boldsymbol{0}\}$. Thus, all assumptions in Lemma 5 hold and hence either one of the following cases hold: *Case 1:* Equilibrium $\boldsymbol{x}_0(= \boldsymbol{0})$ is globally asymptotically stable

in $\triangle_{n+m}$. *Case 2:* For any initial value $\tilde{\boldsymbol{x}}_0 \in \triangle_{n+m} - \{\boldsymbol{x}_0\}$, the solution $\boldsymbol{\phi}(t, \tilde{\boldsymbol{x}}_0)$ of (6) satisfies $\liminf_{t\to\infty} \|\boldsymbol{\phi}(t, \tilde{\boldsymbol{x}}_0)\| \geq m$, where $m > 0$ is independent of $\tilde{\boldsymbol{x}}_0$. Moreover, there exists a nontrivial equilibrium $\boldsymbol{x}^*$ of (6) in $\triangle_{n+m}$. In fact, by Lemma 4, $\boldsymbol{x}^*(> 0)$ is an epidemic equilibrium. By Theorem 2, Case 1 occurs iff $R_0 < 1$ and Case 2 occurs iff $R_0 > 1$. This completes the proof of Theorem 3. □

Theorem 4. *If $R_0 > 1$, then there exists a unique endemic equilibrium $\boldsymbol{x}^*(> 0)$ of (6) such that $\boldsymbol{x}^*$ is globally asymptotically stable in $\triangle_{n+m} - \{\boldsymbol{x}_0\}$.*

Proof. Note that the existence of the endemic equilibrium $\boldsymbol{x}^*(> 0)$ is guaranteed by Theorem 3. Then we aim to show that such endemic equilibrium is unique and globally asymptotically stable.

(I). We show that the existence of the endemic equilibrium $\boldsymbol{x}^*$ is unique. Suppose that $\boldsymbol{x}^* = (x_1^*, \cdots, x_{n+m}^*)^T$ and $\boldsymbol{z}^* = (z_1^*, \cdots, z_{n+m}^*)^T$ are two distinct endemic equilibria of (6). Then there exists at least one k_0 such that $x_{k_0}^* \neq z_{k_0}^*$. Without loss of generality, we assume that $x_{k_0}^* > z_{k_0}^*$ and $\frac{x_{k_0}^*}{z_{k_0}^*} \geq \frac{x_k^*}{z_k^*}$ (or $z_k^* \geq \frac{z_{k_0}^*}{x_{k_0}^*} x_k^*$) for all $k = 1, \ldots, n+m$. Since $\boldsymbol{x}^*$ and $\boldsymbol{z}^*$ are two equilibria of (6), we have that:

(i) If $k_0 \in \{1, \cdots, n\}$, then

$$
\begin{aligned}
&-\gamma x_{k_0}^* + \alpha k_0 (1 - x_{k_0}^*)\Theta(\boldsymbol{x}_1^*) + q_{k_0}(1 - x_{k_0}^*) \sum_{j=n+1}^{n+m} \beta_j x_j^* \\
&= -\gamma z_{k_0}^* + \alpha k_0 (1 - z_{k_0}^*)\Theta(\boldsymbol{z}_1^*) + q_{k_0}(1 - z_{k_0}^*) \sum_{j=n+1}^{n+m} \beta_j z_j^* = 0, \\
\Rightarrow \quad &-\gamma z_{k_0}^* + (1 - x_{k_0}^*) \left[\alpha k_0 \Theta(\boldsymbol{x}_1^*) \frac{z_{k_0}^*}{x_{k_0}^*} + q_{k_0} \sum_{j=n+1}^{n+m} \beta_j x_j^* \frac{z_{k_0}^*}{x_{k_0}^*} \right] \\
&= -\gamma z_{k_0}^* + (1 - z_{k_0}^*) \left[\alpha k_0 \Theta(\boldsymbol{z}_1^*) + q_{k_0} \sum_{j=n+1}^{n+m} \beta_j z_j^* \right] = 0,
\end{aligned}
$$

by timing $\frac{z_{k_0}^*}{x_{k_0}^*}$ on the left-hand side of the first equality. Hence,

$$
(1 - x_{k_0}^*) \left[\alpha k_0 \Theta(\frac{z_{k_0}^*}{x_{k_0}^*} \boldsymbol{x}_1^*) + q_{k_0} \sum_{j=n+1}^{n+m} \beta_j \left(\frac{z_{k_0}^*}{x_{k_0}^*} x_j^* \right) \right] = (1 - z_{k_0}^*) \left[\alpha k_0 \Theta(\boldsymbol{z}_1^*) + q_{k_0} \sum_{j=n+1}^{n+m} \beta_j z_j^* \right]
$$

But this make a contradiction with $x_{k_0}^* > z_{k_0}^*$ and $z_k^* \geq \frac{z_{k_0}^*}{x_{k_0}^*} x_k^*$ for all $k = 1, \ldots, n+m$.

(ii) If $k_0 \in \{n+1, \cdots, n+m\}$, then

$$-\mu_{k_0} x^*_{k_0} + r_{k_0}(1 - x^*_{k_0})\Phi(\boldsymbol{x}^*_1) = -\mu_{k_0} z^*_{k_0} + r_{k_0}(1 - z^*_{k_0})\Phi(\boldsymbol{z}^*_1) = 0.$$

By timing $\frac{z^*_{k_0}}{x^*_{k_0}}$ on the left-hand side of the above first equality, we have that, after some simple reduction,

$$(1 - x^*_{k_0})\Phi(\frac{z^*_{k_0}}{x^*_{k_0}}\boldsymbol{x}^*_1) = (1 - z^*_{k_0})\Phi(\boldsymbol{z}^*_1).$$

But this make a contradiction with $x^*_{k_0} > z^*_{k_0}$ and $z^*_k \geq \dfrac{z^*_{k_0}}{x^*_{k_0}}\, x^*_k$ for all $k = 1, \ldots, n+m$.

By (i) and (ii), we have the result that model (6) has a unique endemic equilibrium.

(II). We show that the endemic equilibrium $\boldsymbol{x}^*$ is globally asymptotically stable in $\triangle_{n+m} - \{\boldsymbol{x}_0\}$. Define G and g be two real-valued functions in $\triangle_{n+m}$ by

$$G(\boldsymbol{x}) = \max_{1 \leq k \leq n+m} \left\{ \frac{x_k}{x^*_k} \right\} \quad \text{and} \quad g(\boldsymbol{x}) = \min_{1 \leq k \leq n+m} \left\{ \frac{x_k}{x^*_k} \right\}. \tag{24}$$

Then $G(\boldsymbol{x})$ and $g(\boldsymbol{x})$ are continuous and their right-hand derivatives exist along solutions of (6).

Let $\boldsymbol{x}(t)$ be a solution of (6). Then for any given $t_0 \geq 0$, there is some sufficiently small $\epsilon > 0$ such that $G(\boldsymbol{x}(t)) = \frac{x_{k_0}(t)}{x^*_{k_0}}$, for some $k_0 \in \{1, \ldots, n+m\}$ in $t \in [t_0, t_0 + \epsilon]$, and hence

$$G'|_{(6)}(\boldsymbol{x}(t_0)) = \frac{x'_{k_0}(t_0)}{x^*_{k_0}},$$

where $G'|_{(6)}$ is define as

$$G'|_{(6)} = \limsup_{h \to 0^+} \frac{G(\boldsymbol{x}(t+h)) - G(\boldsymbol{x}(t))}{h}.$$

Note that by the definition of G, we have that for $t \in [t_0, t_0 + \epsilon]$,

$$\frac{x_{k_0}(t_0)}{x^*_{k_0}} \geq \frac{x_k(t_0)}{x^*_k} \quad (\text{or } x^*_k \geq \frac{x^*_{k_0}}{x_{k_0}(t_0)} x_k(t_0)), \quad k = 1, \ldots, n+m. \tag{25}$$

In the following, we will show that if $G(\boldsymbol{x}(t_0)) > 1$ (i.e., $x_{k_0}(t_0) > x^*_{k_0}$), then $G'|_{(6)}(\boldsymbol{x}(t_0)) < 0$. Indeed,

(i) If $k_0 \in \{1, \cdots, n\}$, then

$$\begin{aligned} x^*_{k_0}\frac{x'_{k_0}(t_0)}{x_{k_0}(t_0)} &= \left\{-\gamma x_{k_0}(t_0) + [1 - x_{k_0}(t_0)]\left[\alpha k_0 \Theta(\boldsymbol{x}_1(t_0)) + q_{k_0}\sum_{j=n+1}^{n+m}\beta_j x_j(t_0)\right]\right\}\frac{x^*_{k_0}}{x_{k_0}(t_0)} \\ &= -\gamma x^*_{k_0} + [1 - x_{k_0}(t_0)]\left[\alpha k_0 \Theta(\frac{x^*_{k_0}}{x_{k_0}(t_0)}\boldsymbol{x}_1(t_0)) + q_{k_0}\sum_{j=n+1}^{n+m}\beta_j\left(\frac{x^*_{k_0}}{x_{k_0}(t_0)}x_j(t_0)\right)\right] \\ &< -\gamma x^*_{k_0} + [1 - x^*_{k_0}]\left[\alpha k_0 \Theta(\boldsymbol{x}^*_1) + q_{k_0}\sum_{j=n+1}^{n+m}\beta_j x^*_j\right] \\ &\quad \text{(by (25), } \boldsymbol{x}^* > 0 \text{ and } x_{k_0}(t_0) > x^*_{k_0}\text{)} \\ &= 0, \end{aligned}$$

since $\boldsymbol{x}^*$ is an equilibrium. Hence, we have that $G'|_{(6)}(\boldsymbol{x}(t_0)) < 0$.

(ii) If $k_0 \in \{n+1, \cdots, n+m\}$, then

$$\begin{aligned} x^*_{k_0}\frac{x'_{k_0}(t_0)}{x_{k_0}(t_0)} &= \{-\mu_{k_0}x_{k_0}(t_0) + r_{k_0}[1 - x_{k_0}(t_0)]\Phi(\boldsymbol{x}_1(t_0))\}\frac{x^*_{k_0}}{x_{k_0}(t_0)} \\ &= -\mu_{k_0}x^*_{k_0} + r_{k_0}[1 - x_{k_0}(t_0)]\Phi(\frac{x^*_{k_0}}{x_{k_0}(t_0)}\boldsymbol{x}_1(t_0)) \\ &< -\mu_{k_0}x^*_{k_0} + r_{k_0}[1 - x^*_{k_0}]\Phi(\boldsymbol{x}^*_1) \\ &\quad \text{(by (25), } \boldsymbol{x}^* > 0 \text{ and } x_{k_0}(t_0) > x^*_{k_0}\text{)} \\ &= 0, \end{aligned}$$

since $\boldsymbol{x}^*$ is an equilibrium. Hence, we have that $G'|_{(6)}(\boldsymbol{x}(t_0)) < 0$.

By (i) and (ii), we showed that if $G(\boldsymbol{x}(t_0)) > 1$, then $G'|_{(6)}(\boldsymbol{x}(t_0)) < 0$. By the similar argument, it can be showed that if $g(\boldsymbol{x}(t_0)) < 1$, then $g'|_{(6)}(\boldsymbol{x}(t_0)) > 0$. Moreover, if $G(\boldsymbol{x}(t_0)) = 1$, then $G'|_{(6)}(\boldsymbol{x}(t_0)) \leq 0$, and if $g(\boldsymbol{x}(t_0)) = 1$, then $g'|_{(6)}(\boldsymbol{x}(t_0)) \geq 0$. The proof of these assertions are omitted here since the similarity.

Define the Lyapunov candidate functions U and V in $\triangle_{n+m}$ by

$$U(\boldsymbol{x}) = \max\{G(\boldsymbol{x}) - 1, 0\},$$

$$V(\boldsymbol{x}) = \max\{1 - g(\boldsymbol{x}), 0\}.$$

Then U and V are continuous and nonnegative functions in $\triangle_{n+m}$. Moreover,

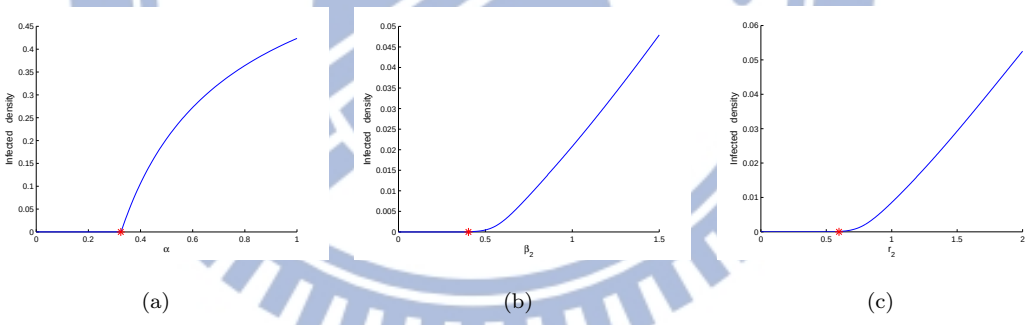
$$U' \mid_{(6)} (\boldsymbol{x}(t)) \leq 0,$$

$$V' \mid_{(6)} (\boldsymbol{x}(t)) \leq 0.$$

Let $S_U := \{\boldsymbol{x} \in \triangle_{n+m} : U' \mid_{(6)} (\boldsymbol{x}(t)) = 0\}$ and $S_V := \{\boldsymbol{x} \in \triangle_{n+m} : V' \mid_{(6)} (\boldsymbol{x}(t)) = 0\}$. Then we have that $S_U = \{\boldsymbol{x} \in \triangle_{n+m} : 0 \leq x_k \leq x_k^*, k = 1, \ldots n+m\}$ and $S_V = \{\boldsymbol{x} \in \triangle_{n+m} : x_k^* \leq x_k \leq 1\} \cup \{\boldsymbol{x}_0\}$. By LaSalle invariance principle, any solution of (6) starting in $\triangle_{n+m}$ will eventually approach to $S_U \cap S_V = \{\boldsymbol{x}^*, \boldsymbol{x}_0\}$. However, by Theorem 3, since there exists some $m > 0$ such that for any initial value $\tilde{\boldsymbol{x}}_0 \in \triangle_{n+m} - \{\boldsymbol{x}_0\}$, the solution $\boldsymbol{\phi}(t, \tilde{\boldsymbol{x}}_0)$ of (6) satisfies $\liminf_{t\to\infty} \|\boldsymbol{\phi}(t, \tilde{\boldsymbol{x}}_0)\| \geq m$, we conclude that $\boldsymbol{x}^*$ is globally asymptotically stable in $\triangle_{n+m} - \{\boldsymbol{x}_0\}$.

By (I) and (II), the proof of Theorem 4 is complete. □

5 Numerical simulation



(a) (b) (c)

Figure 2. The stable densities of infected nodes with parameters α, β_2, r_2.

In this section, we show some numerical simulations to verify the analytic results obtained in above sections. First, we show that the relationship between the stable densities of infected nodes and the model parameters α, β_2, r_2 in Fig. 2. There, we see that for each parameter, there exists a threshold such that the epidemic extinguishes when the parameter value less than it, and the epidemic breaks out when the parameter value greater than it. Moreover, the stable densities increase as parameter value increases.

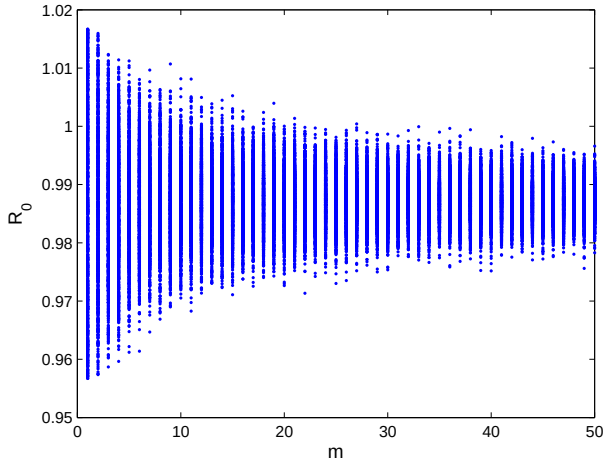


Figure 3. The basic reproduction number R_0 with m.

Fig. 3 shows the basic reproduction number R_0 in term of m, the number of kinds of media, with fixed $n = 20$, $\gamma = 0.8$, $\alpha = 0.056$, $p_k = q_k = 0.05$ for $k = 1, \ldots, 20$ and $\mu_1 = \ldots = \mu_m = 0.8$, but parameters β, r are set free where r satisfying $\sum_{l=1}^{m} r_l = 1$. In the figure, we see that the distribution of values of R_0 shrinks as m increases. Moreover, the range of values of R_0 contains 1, the epidemic threshold when $m < 10$, but is a subset of $(0, 1)$ when $m > 40$.

6 Conclusion

We have discussed an epidemic SIS model with multiple infective media in complex networks. In the model, we assume that diseases spread not only through the contacts between individuals themselves but also through the contacts of individuals and different kinds of infective media. This epidemic SIS model is particularly suited for disease such as rabies where the disease can spread through the infective dogs, ferret badgers or other animals. Moreover, for the reality, the heterogeneity of the individuals' contacts is taken into consideration. Through the rigorous mathematical analysis, the global dynamics of the model is derived. We first compute the basic reproduction number R_0 and then show that if $R_0 < 1$, then the disease-free equilibrium is globally asymptotically stable. On

the contrary, if $R_0 > 1$, then there exists a unique endemic equilibrium which is globally asymptotically stable.

In spite that the epidemic model under consideration is quite general, there is still some limitations. For instance, in our model, the disease transmission between vectors and the disease-related death is ignored. It is an interesting and important issue for the future investigation.

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