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GLOBAL ANALYSIS OF A MULTI-GROUP ANIMAL EPIDEMIC MODEL WITH INDIRECT INFECTION AND TIME DELAY*

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Abstract The transmission mechanism of some animal diseases is complex because of the multiple transmission pathways and multiple-group interactions, which lead to the limited understanding of the dynamics of these diseases transmission. In this paper, a delay multi-group dynamic model is proposed in which time delay is caused by the latency of infection. Under the biologically motivated assumptions, the basic reproduction number R_0 is derived and then the global stability of the disease-free equilibrium and the endemic equilibrium is analyzed by Lyapunov functionals and a graph-theoretic approach as for time delay. The results show the global properties of equilibria only depend on the basic reproductive number R_0: the disease-free equilibrium is globally asymptotically stable if $R_0 \leq 1$; if $R_0 > 1$, the endemic equilibrium exists and is globally asymptotically stable, which implies time delay span has no effect on the stability of equilibria. Finally, some specific examples are taken to illustrate the utilization of the results and then numerical simulations are used for further discussion. The numerical results show time delay model may experience periodic oscillation behaviors, implying that the spread of animal diseases depends largely on the prevention and control strategies of all sub-populations.

Keywords Multi-group model, delay, indirect infection, global stability, Lyapunov functional.

MSC(2010) 34D20, 37N25.

1. Introduction

Many animal diseases such as brucellosis and tuberculosis, not only cause huge economic losses, but also affect human public health in the world. Particularly in developing countries, many animal diseases represent a significant public health burden and continue receiving worldwide attention. For example, there are more than 500,000 new cases of brucellosis that are reported annually around the world and the disease remains endemic in many areas of the world, including Latin America, the Middle East, parts of Africa, and Asia including China [20]. Therefore, the prevention and control of animal diseases is one of the issues to which the health authorities pay close attention.

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There is an incubation period when some animal diseases have no clinical features and infectious force and the infected animals can not be detected by a serological test for the majority of animal disease, such as bovine brucellosis. Therefore, the impact of latency is one of the key research contents. In the study of infectious diseases with the dynamic model, the latent period is expressed by an extra class which is defined as E if time delay is exponentially distributed. However, the reality appears that an assumption of a constant delay is more reasonable, which will result in a delay differential equation (see [5,10,15,22]). For the prevention and control of animal diseases, no matter how the incubation period is presented, it is important to investigate the global dynamics of mathematical models to describe infectious animal diseases.

For farms in many regions of the world, there exists the mixed feeding in the cattle, sheep and other species. In many areas of China, even for the same species, different populations may be raised in a pasture [16]. In other words, there is the exist mixed cross infection between species or populations as well as the infection in internal species or population. It is an important risk factor for the prevention and control of animal diseases. Therefore, the main objective is to develop a multi-group dynamic model and investigate how preferential mixing may influence the effectiveness of animal disease control measures.

Many mathematical models are used to characterize the transmission mechanism of some animal diseases (see [1,6,12,18,26]), and some theoretical results have been used to guide the prevention and control of specific animal disease (see [13,24,27]). However, there is few researches by now studying the influence of cross infection and latency and no particular dynamical model investigating the role of culling measures. Thus the present work aims to understand the transmission dynamics of some animal diseases in a general mathematical model which has a potential to incorporate the above-mentioned risk factors. The study tends to be crucial for the effective prevention and intervention against animal diseases outbreak.

A multi-group dynamic model with indirect transmission for the spread of some animal diseases is proposed to study the influence of these risk factors on the dynamics of disease transmission. In fact, based on the common characteristic of the spread of some animal diseases, animal population is classified into three compartments: the susceptible compartment $S(t)$, the exposed compartment $E(t)$ (that is, the latent period is represented by an extra class E) and the infectious compartment $I(t)$. In addition, infectious animal can shed pathogen into the environment through the abortion or animal secretions, and pathogen can be harvested by susceptible individuals that become infected individuals. Let $B(t)$ denote pathogens in the environment. The indirect transmission occurs mainly through the ingestion of fecal pathogens in the habitat, ignoring pathogen infection to other sub-population. The following model with cross-infection among populations is proposed:

$$\begin{aligned}
\frac{dS_k}{dt} &= m_k(S_k) - n_k(S_k)\sum_{j=1}^{n}\beta_{kj}f_j(I_j) - n_k(S_k)g_k(B_k),\\
\frac{dE_k}{dt} &= n_k(S_k)\sum_{j=1}^{n}\beta_{kj}f_j(I_j) + n_k(S_k)g_k(B_k) - (\sigma_k+\mu_k)E_k,\\
\frac{dI_k}{dt} &= \sigma_k E_k - \varphi_k(I_k),\\
\frac{dB_k}{dt} &= h_k(I_k) - \theta_k(B_k).
\end{aligned} \tag{1.1}$$

The intrinsic growth rate of the susceptible class is given by $m_k(S_k)$ with all the newly produced animals assumed to be susceptible. $n_k(S_k)$ is a contact function. The elimination rate of the infectious animals, including the disease induced death rate, is denoted by $\varphi_k(I_k)$. $h_k(I_k)$ is defined as the pathogen shedding rate of the infectious animals. $\theta_k(B_k)$ represents the disinfection rate and decaying rate of pathogen in the environment. If a constant delay is used to express the latency of animal diseases, the following delay differential equation can be obtained:

$$\begin{aligned}
\frac{dS_k}{dt} &= m_k(S_k) - n_k(S_k)\sum_{j=1}^{n}\beta_{kj}f_j(I_j(t-\tau)) - n_k(S_k)g_k(B_k),\\
\frac{dI_k}{dt} &= n_k(S_k)\sum_{j=1}^{n}\beta_{kj}f_j(I_j(t-\tau)) + n_k(S_k)g_k(B_k) - \varphi_k(I_k),\\
\frac{dB_k}{dt} &= h_k(I_k(t-\tau)) - \theta_k(B_k).
\end{aligned} \tag{1.2}$$

The initial condition of system (1.2) is given as

$$\begin{aligned}
&S_k(x) = \phi_{k1}(x), I_k(x) = \phi_{k2}(x), B_k(x) = \phi_{k3}(x), k = 1, 2, \cdots, n,\\
&\phi_{ki}(x) \geq 0, x \in [-\tau, 0], \phi_{ki}(0) > 0, i = 1, 2, 3,
\end{aligned} \tag{1.3}$$

where $(\phi_{k1}, \phi_{k2}, \phi_{k3}) \in \mathcal{C}_k([-\tau, 0], \mathbb{R}^3_{+0})$ be the Banach space of continuous functions from $[-\tau, 0]$ to $\mathbb{R}^3_{+0}$ equipped with the sup-norm, where $\mathbb{R}^3_{+0} = \{(x_1, x_2, x_3) : x_i \geq 0, i = 1, 2, 3\}$.

In this paper, the dynamic properties of system (1.2) with the initial condition (1.3) are investigated. On very general and biologically plausible assumptions, the global stability of equilibria is analyzed by means of a graph-theoretical approach to the method of global Lyapunov functionals, which are determined by the basic reproduction number R_0: the disease-free equilibrium of system (1.2) is globally asymptotically stable if $R_0 \leq 1$; if $R_0 > 1$, there exists a unique endemic equilibrium which is globally asymptotically stable. In addition, if the assumptions are not satisfied, other dynamic properties of system (1.2) are analyzed by numerical simulation.

The paper is organized as follows. Some assumptions are given in Section 2. In Section 3, the global stability of equilibria of system (1.2) is established. Some examples and numerical simulations are shown in Section 4. A brief summary is given in Section 5.

2. The assumptions and basic reproduction number

Throughout the paper, we assume that the transmission matrix $B = (\beta_{kj})$ is irreducible, which is equivalent to assuming that individuals in I_j can infect those in S_k directly for any two distinct groups k and j. The functions $m_k, n_k, f_k, g_k, \varphi_k, h_k$ and θ_k are assumed to be sufficiently smooth such that solutions of system (1.2) with nonnegative initial conditions exist and are unique. Based on the biological significance, the following assumptions are made:

(H_1) There exists $S_k^0 > 0$ such that the equation $m(S_k^0) = 0$ and $m_k'(S) < 0$ for $S \geq 0$.

(H_2) $n_k(0) = 0$, and $n_k(S) > 0, n_k'(S) > 0$ for $S > 0$.

(H_3) $f_k(0) = g_k(0) = 0$, and $f_k(I), g_k(B) > 0$, $f'_k(I) \geq 0$, $g'_k(B) \geq 0$ for $I, B > 0$.
(H_4) $h_k(0) = 0$, $h_k(I) > 0, h'_k(I) > 0$ for $I > 0$.
(H_5) $\varphi_k(0) = 0$, and $\varphi'_k(I) > 0$ for $I \geq 0$; there exists constant $\mu_k > 0$ such that $\varphi_k(I) \geq \mu_k I$.
(H_6) $\theta_k(0) = 0$, and $\theta'_k(B) > 0$ for $B \geq 0$.

The assumption (H_1) implies that the possible form of $m_k(S_k)$ is $A_k - \mu_k S_k$ and system (1.2) always has a disease-free equilibrium $E_0 = (S_1^0, 0, 0, S_2^0, 0, 0, \cdots, S_n^0, 0, 0)$, and the host population has carried capacity $S_k^0 > 0, k = 1, 2, \cdots, n$ when there is no disease. With biological considerations, we are interested in solutions that are nonnegative and bounded. From the first equation of system (1.2), it concludes that $S'_k \leq m_k(S_k)$, which means that $\limsup_{t\to\infty} S_k(t) \leq S_k^0$. Adding the first two equations of (1.2) yields that

$$(S_k + I_k)' = m_k(S_k) - \varphi_k(I_k) \leq m_k(S_k) - \mu_k I_k.$$

Choose Π_k sufficiently large such that $\Pi_k \geq \mu_k S_k^0 + \max\{m_k(S_k)\}$. If t is sufficiently large,

$$(S_k + I_k)' \leq m_k(S_k) - \mu_k I_k \leq \Pi_k - \mu_k(S_k + I_k),$$

and it follows that

$$\lim_{t\to+\infty} \sup(S_k + I_k) \leq \frac{\Pi_k}{\mu_k}, \qquad \lim_{t\to+\infty} \sup B_k \leq \theta^{-1}(h_k(\frac{\Pi_k}{\mu_k})).$$

Therefore, the set

$$\begin{aligned} X = &\{(S_k, I_k, B_k) \in \mathcal{C}_k : \\ &\|S_k\| \leq S_k^0, \|S_k + I_k\| \leq \frac{\Pi_k}{\mu_k}, \|B_k\| \leq \theta^{-1}(h_k(\frac{\Pi_k}{\mu_k})), k = 1, 2, \cdots, n\} \end{aligned}$$

is the positively invariant set for system (1.2).

The next generation matrix for system (1.2) is

$$M_0 = (m_{ij})_{n\times n} = \left(\frac{n_k(S_k^0)\beta_{kj} f'_{j_{I_j}}(0)}{\varphi'_{j_{I_j}}(0)} \right)_{n\times n} + \frac{n_k(S_k^0) g'_{k_{B_k}}(0) h'_{k_{I_k}}(0)}{\varphi'_{k_{I_k}}(0)\theta'_{k_{I_k}}(0)}.$$

According to the next generation matrix formulated in Diekmann et al and van den Driessche and Watmough [4,21], the basic reproduction number of system (1.2) is defined as

$$R_0 = \rho(M_0).$$

3. The properties of equilibria of system (1.2)

In this section, the global stability of the disease-free equilibrium and the endemic equilibrium of system (1.2) is studied. It is important for us to understand the extinction and persistence of infectious animal diseases.

3.1. The stability of the disease-free equilibrium and the permanence of system (1.2)

This subsection shows that the disease will be eliminated if the basic reproduction number $R_0 \leq 1$, otherwise, the disease persists. In order to prove the global asymptotic stability of the equilibria, the following assumption is made:

(H_7) $\frac{f_k}{\varphi_k}$, $\frac{g_k}{\theta_k}$ and $\frac{h_k}{\varphi_k}$ are non-increasing on $(0,+\infty)$. Furthermore, $\lim_{I_k\to 0^+}\frac{f_k(I_k)}{\varphi_k(I_k)} = \frac{f_k'(0)}{\varphi_k'(0)} > 0$, $\lim_{I_k\to 0^+}\frac{h_k(I_k)}{\varphi_k(I_k)} = \frac{h_k'(0)}{\varphi_k'(0)} > 0$ and $\lim_{B_k\to 0^+}\frac{g_k(B_k)}{\theta_k(B_k)} = \frac{g_k'(0)}{\theta_k'(0)} > 0$.

Theorem 3.1. *Assume that $B = (\beta_{kj})$ is irreducible and conditions (H_1)-(H_7) are satisfied. If $R_0 \leq 1$, the disease-free equilibrium E_0 of system (1.2) is globally asymptotically stable.*

Proof. Since the function $\frac{f_k}{\varphi_k}$, $\frac{g_k}{\theta_k}$, and $\frac{h_k}{\varphi_k}$ are nonincreasing, we obtain

$$\begin{aligned}
&\frac{n_k(S_k)f_k(I_k)}{\varphi_k(I_k)} \leq \lim_{I_k\to 0^+}\frac{n_k(S_k^0)f_k(I_k)}{\varphi_k(I_k)} = \frac{n_k(S_k^0)f_k'(0)}{\varphi_k'(0)},\\
&\frac{n_k(S_k)g_k(B_k)}{\theta_k(B_k)} \leq \lim_{B_k\to 0^+}\frac{n_k(S_k^0)g_k(B_k)}{\theta_k(B_k)} = \frac{n_k(S_k^0)g_k'(0)}{\theta_k'(0)},\\
&\frac{h_k(I_k)}{\varphi_k(I_k)} \leq \lim_{I_k\to 0^+}\frac{h_k(I_k)}{\varphi_k(I_k)} = \frac{h_k'(0)}{\varphi_k'(0)}.
\end{aligned} \tag{3.1}$$

Define

$$\begin{aligned}
\mathcal{F}_0 &= \begin{pmatrix} \Big(\frac{n_k(S_k^0)\beta_{kj}f_j'(0)}{\varphi_j'(0)}\Big)_{n\times n} & \Big(\frac{n_k(S_k^0)g_k'(0)}{\theta_k'(0)}\Big)_{n\times n} \end{pmatrix},\\
\mathcal{V}_0 &= \begin{pmatrix} \Big(U\Big)_{n\times n} & \boldsymbol{0} \\ \Big(-\frac{h_k'(0)}{\varphi_k'(0)}\Big)_{n\times n} & \Big(U\Big)_{n\times n} \end{pmatrix},
\end{aligned}$$

and it follows that

$$\mathcal{F}_0\mathcal{V}_0^- = \begin{pmatrix} M_0 & M_1 \end{pmatrix}, \tag{3.2}$$

where

$$M_1 = \Big(\frac{n_k(S_k^0)g_k'(0)}{\theta_k'(0)}\Big)_{n\times n} = \begin{pmatrix} \frac{n_1(S_1^0)g_1'(0)}{\theta_1'(0)} & 0 & \cdots & 0 \\ 0 & \frac{n_2(S_2^0)g_2'(0)}{\theta_2'(0)} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \frac{n_n(S_n^0)g_n'(0)}{\theta_n'(0)} \end{pmatrix}.$$

Because $B = (\beta_{kj})$ is irreducible, M_0 is also irreducible. There exist $w_k > 0, k = 1, 2, \cdots, n$ such that

$$(w_1, w_2, \cdots, w_n)\rho(M_0) = (w_1, w_2, \cdots, w_n)M_0.$$

The Lyapunov functional is defined as

$$L = \sum_{k=1}^{n}\{\sum_{i=1}^{n} w_i m_{ik}(I_k + n_k(S_k)\sum_{j=1}^{n}\int_{t-\tau}^{t}\beta_{kj}f_j(I_j(x))dx) + w_k\frac{n_k(S_k^0)g_k'(0)}{\theta_k'(0)}(B_k + \int_{t-\tau}^{t}h_k(I_k(x))dx)\},$$

the derivative of L along positive solutions of system (1.2) is

$$\begin{aligned} L' =& \sum_{k=1}^{n}\{\sum_{i=1}^{n} w_i m_{ik}(n_k(S_k)\sum_{j=1}^{n}\beta_{kj}f_j(I_j) + n_k(S_k)g_k(B_k) - \varphi_k(I_k)) \\ &+ w_k\frac{n_k(S_k^0)g_k'(0)}{\theta_k'(0)}(-\theta_k(B_k) + h_k(I_k))\} \\ =&(w_1, w_2, \cdots, w_n)M_0\left(\left(\frac{n_k\beta_{kj}f_j}{\varphi_j}\right)_{n\times n}\left(\frac{n_k g_k}{\theta_k}\right)_{n\times n}\right)\Psi \\ &-(w_1, w_2, \cdots, w_n)\begin{pmatrix} M_0 & M_1 \end{pmatrix}\begin{pmatrix} (U)_{n\times n} & \boldsymbol{0} \\ \left(-\frac{h_k}{\varphi_k}\right)_{n\times n} & (U)_{n\times n} \end{pmatrix}\Psi, \end{aligned} \tag{3.3}$$

where $(U)_n$ is a unit matrix, $\Psi = (\varphi_1, \varphi_2, \cdots, \varphi_n, \theta_1, \theta_2, \cdots, \theta_n)^T$, and

$$\left(\frac{n_k g_k}{\theta_k}\right)_{n\times n} = \begin{pmatrix} \frac{n_1 g_1}{\theta_1} & 0 & \cdots & 0 \\ 0 & \frac{n_2 g_2}{\theta_2} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \frac{n_n g_n}{\theta_n} \end{pmatrix},$$

$$\left(\frac{-h_k}{\varphi_k}\right)_{n\times n} = \begin{pmatrix} -\frac{h_1}{\varphi_1} & 0 & \cdots & 0 \\ 0 & -\frac{h_2}{\varphi_2} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & -\frac{h_n}{\varphi_n} \end{pmatrix}.$$

If (3.1) and (3.2) is used, it follows from (3.3) that

$$\begin{aligned} L' \le&(w_1, w_2, \cdots, w_n)M_0\left(\left(\frac{n_k(S_k^0)\beta_{kj}f_j'(0)}{\varphi_j'(0)}\right)_{n\times n}\left(\frac{n_k(S_k^0)g_k'(0)}{\theta_k'(0)}\right)_{n\times n}\right)\Psi \\ &-(w_1, w_2, \cdots, w_n)\begin{pmatrix} M_0 & M_1 \end{pmatrix}\begin{pmatrix} (U)_{n\times n} & \boldsymbol{0} \\ \left(-\frac{h_k'(0)}{\varphi_k'(0)}\right)_{n\times n} & (U)_{n\times n} \end{pmatrix}\Psi \\ =&(w_1, w_2, \cdots, w_n)(M_0 - 1)\mathcal{F}_0\Psi \\ =&(w_1, w_2, \cdots, w_n)(\rho(M_0) - 1)\mathcal{F}_0\Psi \\ \le&0. \end{aligned}$$

With a similar argument as the proof of Theorem 3.1 of [23], $L' = 0$ if and only if $S_k = S_k^0$ and either $R_0 = 1$ or $I_k = B_k = 0$. Hence the only compact invariant

subset of the set $\{(S_k, I_k, B_k) \in X \mid L' = 0\}$ is the singleton E_0. By LaSalle's Invariance Principle, E_0 is globally asymptotically stable in X if $R_0 \leq 1$. □

Next, let $\Phi_t(x) = \Phi(t, x(t))$ be the continuous flow on X generated by the solution $x(t)$ of system (1.2) with initial condition (1.3). The positive orbit $\gamma^+(x)$ through x is defined as $\gamma^+(x) = \bigcup_{t\geq 0}\{\Phi(t)x\}$. The ω-limit set $\omega(x)$ of x consists of $y \in X$ if and only if there is a sequence $t_n \to \infty$ as $n \to \infty$ such that $\Phi(t_n)x \to y$ as $n \to \infty$. As for any bounded subset U of X, the semigroup $\Phi(t)$ is said to be asymptotically smooth if there exists a compact set $\mathscr{M}$ such that $d(\Phi(t)U, \mathscr{M}) \to 0$ as $t \to \infty$ in which $\Phi(U) \subset U, t \geq 0$. The following result is established from [9, Theorem 4.2]:

Lemma 3.1. *Suppose that the following conditions are satisfied:*

(i) X^0 *is open and dense in* X *with* $X^0 \bigcup X_0 = X$ *and* $X^0 \bigcap X_0 = \emptyset$*;*

(ii) the solution operators $\Phi(t)$ *satisfy:*

$$\Phi(t) : X^0 \to X^0, X_0 \to X_0;$$

(iii) $\Phi(t)$ *is point dissipative in* X*;*

(iv) $\gamma^+(U)$ *is bounded in* X *if* U *is bounded in* X*;*

(v) $\Phi(t)$ *is asymptotically smooth;*

(vi) $\mathscr{A} = \bigcup_{x\in A_\partial} \omega(x)$ *is isolated and has an acyclic covering* N*, where* A_∂ *is the global attractor of* $\Phi(t)$ *restricted to* X_0 *and* $N = \bigcup_{i=1}^{k} N_i$*;*

(vii) for each $N_i \in N$*,*

$$W^s(N_i) \bigcap X^0 = \emptyset,$$

where W^s *refers to the stable set.*

Then $\Phi(t)$ *is a uniform repeller with respect to* X^0*, i.e. there is an* $\eta > 0$ *such that for any* $x \in X^0$*,* $\liminf_{t\to\infty} d(\Phi(t)x, X_0) \geq \eta$*.*

Theorem 3.2. *If* $R_0 > 1$*, the system (1.2) is uniformly persistent. More precisely, there exists an* $\eta > 0$ *such that*

$$\liminf_{t\to\infty} I(t) \geq \eta.$$

Proof. Let

$$X^0 = \{(S_k, \phi_{k2}(s), B_k) : \phi_{k2}(s) > 0, k = 1, 2, \cdots, n \text{ for some s} \in [\tau, 0)\},$$
$$X_0 = \{(S_k, \phi_{k2}(s), B_k) : \phi_{k2}(s) = 0, k = 1, 2, \cdots, n \text{ for all s} \in [\tau, 0]\}.$$

We verify all the conditions of the above Lemma. It is straightforward to see that (i), (ii) and (iii) are satisfied. According to the method of Theorem 6.1 in [19], (iv) and (v) is verified.

As for (vi), $\mathscr{A} = \{E_0\}$ is isolated. Hence the covering is simply $N = \{E_0\}$, which is acyclic (there is no orbit which connects E_0 to itself in X_0).

Next, $W^s(E_0) \bigcap X^0 = \emptyset$. Suppose this is not true, and then there exists a solution $(S_k, I_k, B_k) \in X^0$ such that

$$\lim_{t\to\infty} S_k(t) = S_k^0, \qquad \lim_{t\to\infty} I_k(t) = 0, \qquad \lim_{t\to\infty} B_k(t) = 0.$$

For any sufficiently small constant $\varepsilon > 0$, there exists a $t_0 = t_0(\varepsilon) > 0$; for all $t > t_0$,

$$\begin{aligned} &n_k(S_k(t)) > n_k(S_k^0) - \varepsilon, \ \frac{f_k(I(t))}{\varphi_k(I(t))} > \frac{f_k'(0)}{\varphi_k'(0)} - \varepsilon, \\ &\frac{h_k(I(t))}{\varphi_k(I(t))} > \frac{h_k'(0)}{\varphi_k'(0)} - \varepsilon, \quad \frac{g_k(I(t))}{\theta_k(I(t))} > \frac{g_k'(0)}{\theta_k'(0)} - \varepsilon. \end{aligned} \tag{3.4}$$

From (3.4), it can be obtained

$$\begin{aligned} L' =& \sum_{k=1}^{n}\{\sum_{i=1}^{n} w_i m_{ik}(n_k(S_k)\sum_{j=1}^{n}\beta_{kj} f_j(I_j) + n_k(S_k)g_k(B_k) - \varphi_k(I_k)) \\ &+ w_k \frac{n_k(S_k^0)g_k'(0)}{\theta_k'(0)}(-\theta_k(B_k) + h_k(I_k))\} \\ =&(w_1, w_2, \cdots, w_n)M_0 \left(\left(\tfrac{n_k\beta_{kj} f_j}{\varphi_j} \right)_{n\times n} \left(\tfrac{n_k g_k}{\theta_k} \right)_{n\times n} \right) \\ &- (w_1, w_2, \cdots, w_n) \begin{pmatrix} M_0 & M_1 \end{pmatrix} \begin{pmatrix} \left(U\right)_{n\times n} & \boldsymbol{0} \\ \left(-\tfrac{h_k}{\varphi_k}\right)_{n\times n} & \left(U\right)_{n\times n} \end{pmatrix} \Psi \\ >&(w_1, w_2, \cdots, w_n)M_0 \\ &\times \left(\left((n_k(S_k^0) - \varepsilon)\beta_{kj}(\tfrac{f_j'(0)}{\varphi_j'(0)} - \varepsilon) \right)_{n\times n} \left((n_k(S_k^0) - \varepsilon)(\tfrac{g_k'(0)}{\theta_k'(0)} - \varepsilon) \right)_{n\times n} \right)\Psi \\ &- (w_1, w_2, \cdots, w_n) \begin{pmatrix} M_0 & M_1 \end{pmatrix} \begin{pmatrix} \left(U\right)_{n\times n} & \boldsymbol{0} \\ \left((-\tfrac{h_k'(0)}{\varphi_k'(0)} + \varepsilon)\right)_{n\times n} & \left(U\right)_{n\times n} \end{pmatrix} \Psi \\ =&(w_1, w_2, \cdots, w_n)(M_0 - 1)\mathcal{F}_0\Psi + H(\varepsilon) \\ >&0, R_0 > 1, \end{aligned}$$

where

$$\begin{aligned} &H(\varepsilon) \\ =&(w_1, w_2, \cdots, w_n)M_0 \\ &\times \left(\left(\beta_{kj}(\varepsilon^2 - (\tfrac{f_j'(0)}{\varphi_j'(0)} + n_k(S_k^0))\varepsilon) \right)_{n\times n} \left((\varepsilon^2 - (n_k(S_k^0) + \tfrac{g_k'(0)}{\theta_k'(0)})\varepsilon) \right)_{n\times n} \right)\Psi \\ &- (w_1, w_2, \cdots, w_n) \begin{pmatrix} M_0 & M_1 \end{pmatrix} \begin{pmatrix} \boldsymbol{0} & \boldsymbol{0} \\ \left(\varepsilon\right)_{n\times n} & \boldsymbol{0} \end{pmatrix} \Psi. \end{aligned}$$

This implies that $L(t)$ tends to infinity or approaches a positive constant as $t \to \infty$. On the other hand, according to the definition of L, $\lim_{t\to\infty} I(t) = 0$ implies $\lim_{t\to\infty} B(t) = 0$ and $\lim_{t\to\infty} L(t) = 0$, which is a contradiction. Thus $W^s(E_0)\bigcap X^0 = \emptyset$ and it can conclude that $\liminf_{t\to\infty} I(t) \geq \eta$. □

Remark 3.1. Theorem 2 implies that the extinction of infectious diseases is independent of initial sizes of the populations and the disease will be eliminated if $R_0 \leq 1$. If $R_0 > 1$, the disease persists and it has at least one positive equilibrium through a well known result in persistence theory [11, 25].

3.2. The global stability of the endemic equilibrium

In this subsection, it is shown that the endemic equilibrium is globally asymptotically stable in the interior of the feasible region X. Biologically, it implies that the disease always becomes endemic and persists at a unique endemic equilibrium, no matter how small the size of the initial outbreak is. By Theorem 1 and Remark, an endemic equilibrium E^* exists and satisfies the equilibrium equations:

$$\begin{aligned} m_k(S_k^*) &= n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j^*) + n_k(S_k^*)g_k(B_k^*), \\ \varphi_k(I_k^*) &= n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j^*) + n_k(S_k^*)g_k(B_k^*), \\ h_k(I_k^*) &= \theta_k(B_k^*). \end{aligned} \tag{3.5}$$

Theorem 3.3. *Assume that $B = (\beta_{kj})$ is irreducible and conditions $(H_1) - (H_7)$ are satisfied. If $R_0 > 1$, the endemic equilibrium $E^* = (S_k^*, I_k^*, B_k^*), k = 1, 2, \cdots, n$ of system (1.2) is globally asymptotically stable and thus is the unique one.*

Proof. Let

$$\overline{\beta}_{kj} = \beta_{kj}n_k(S_k^*)f_j(I_j^*), k, j = 1, 2, \cdots, n, \tag{3.6}$$

and

$$\overline{B} = \begin{pmatrix} \sum\limits_{l\neq 1}\overline{\beta}_{1l} & -\overline{\beta}_{21} & \cdots & -\overline{\beta}_{n1} \\ -\overline{\beta}_{12} & \sum\limits_{l\neq 2}\overline{\beta}_{2l} & \cdots & -\overline{\beta}_{n2} \\ \vdots & \vdots & \ddots & \vdots \\ -\overline{\beta}_{1n} & -\overline{\beta}_{2n} & \cdots & \sum\limits_{l\neq n}\overline{\beta}_{nl} \end{pmatrix}.$$

Note that $\overline{B}$ is the Laplacian form of the matrix $(\overline{\beta}_{kj})$. Since (β_{kj}) is irreducible, matrices $(\overline{\beta}_{kj})$ and $\overline{B}$ are also irreducible.

By Lemma 2.1 in [7], the linear system

$$\overline{B}v = 0,$$

has a positive solution

$$v = (v_1, v_2, \cdots, v_n) = (c_{11}, c_{22}, \cdots, c_{nn}), \tag{3.7}$$

where c_{kk} denotes the cofactor of the kth diagonal entry of $\overline{B}$ and $v_k = c_{kk} > 0$ for $k = 1, 2, \cdots, n$.

Define the functional L_k as

$$\begin{aligned}L_k =& \int_{S_k^*}^{S_k} \frac{n_k(x)-n_k(S^*)}{n_k(x)}dx + \int_{I_k^*}^{I_k} \frac{\varphi_k(x)-\varphi_k(I^*)}{\varphi_k(x)}dx\\ &+ \frac{n_k(S_k^*)g_k(B_k^*)}{h_k(I_k^*)}\int_{B_k^*}^{B_k}\frac{\theta_k(x)-\theta_k(B^*)}{\theta_k(x)}dx\\ &+ n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j^*)\int_{t-\tau}^{t}(\frac{f_j(I_j(x))}{f_j(I_j^*)}-\ln\frac{f_j(I_j(x))}{f_j(I_j^*)})dx\\ &+ n_k(S_k^*)g_k(B_k^*)\int_{t-\tau}^{t}(\frac{h_k(I_k(x))}{h_k(I_k^*)}-\ln\frac{h_k(I_k(x))}{h_k(I_k^*)})dx.\end{aligned}$$

From Eq. (3.5), the time derivative of $L_k(t)$ along solutions of system (1.2) becomes

$$\begin{aligned}\frac{dL_k}{dt} =&(1-\frac{n_k(S_k^*)}{n_k(S_k)})(m_k(S_k)-n_k(S_k)(\sum_{j=1}^{n}\beta_{kj}f_j(I_j(t-\tau))+g_k(B_k)))\\ &+(1-\frac{\varphi_k(I_k^*)}{\varphi_k(I_k)})(n_k(S_k)(\sum_{j=1}^{n}\beta_{kj}f_j(I_j(t-\tau))+g_k(B_k))-\varphi_k(I_k))\\ &+n_k(S_k^*)g_k(B_k^*)(\frac{h_k(I_k(t-\tau))}{h_k(I_k^*)}-\frac{\theta_k(B_k)}{\theta_k(B_k^*)}-\frac{h_k(I_k(t-\tau))\theta_k(B_k^*)}{h_k(I_k^*)\theta_k(B_k)}+1)\\ &+n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j^*)(\frac{f_j(I_j)}{f_j(I_j^*)}-\frac{f_j(I_j(t-\tau))}{f_j(I_j^*)}+\ln\frac{f_j(I_j(t-\tau))}{f_j(I_j)})\\ &+n_k(S_k^*)g_k(B_k^*)(\frac{h_k(I_k)}{h_k(I_k^*)}-\frac{h_k(I_k(t-\tau))}{h_k(I_k^*)}+\ln\frac{h_k(I_k(t-\tau))}{h_k(I_k)})\\ =&m_k(S_k)(1-\frac{n_k(S_k^*)}{n_k(S_k)})+n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j(t-\tau))+n_k(S_k^*)g_k(B_k)\\ &-n_k(S_k)g_k(B_k)\frac{\varphi_k(I_k^*)}{\varphi_k(I_k)}-\varphi_k(I_k)+\varphi_k(I_k^*)\\ &-n_k(S_k)\frac{\varphi_k(I_k^*)}{\varphi_k(I_k)}\sum_{j=1}^{n}\beta_{kj}f_j(I_j(t-\tau))\\ &+n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j^*)(\frac{f_j(I_j)}{f_j(I_j^*)}-\frac{f_j(I_j(t-\tau))}{f_j(I_j^*)}+\ln\frac{f_j(I_j(t-\tau))}{f_j(I_j)})\\ &+n_k(S_k^*)g_k(B_k^*)(\frac{h_k(I_k)}{h_k(I_k^*)}-\frac{\theta_k(B_k)}{\theta_k(B_k^*)}-\frac{h_k(I_k)\theta_k(B_k^*)}{h_k(I_k^*)\theta_k(B_k)}+1)\\ &-n_k(S_k^*)g_k(B_k^*)(\frac{h_k(I_k(t-\tau))\theta_k(B_k^*)}{h_k(I_k^*)\theta_k(B_k)}-1-\ln\frac{h_k(I_k(t-\tau))\theta_k(B_k^*)}{h_k(I_k^*)\theta_k(B_k)})\\ &+n_k(S_k^*)g_k(B_k^*)(\frac{h_k(I_k)\theta_k(B_k^*)}{h_k(I_k^*)\theta_k(B_k)}-1-\ln\frac{h_k(I_k)\theta_k(B_k^*)}{h_k(I_k^*)\theta_k(B_k)})\\ =&(m_k(S_k)-m_k(S_k^*))(1-\frac{n_k(S_k^*)}{n_k(S_k)})+n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j(t-\tau))\end{aligned}$$

$$
\begin{aligned}
&- n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j^*)\frac{\varphi_k(I_k)}{\varphi_k(I_k^*)} + 2n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j^*)\\
&- n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j^*)\frac{n_k(S_k^*)}{n_k(S_k)} - n_k(S_k)\frac{\varphi_k(I_k^*)}{\varphi_k(I_k)}\sum_{j=1}^{n}\beta_{kj}f_j(I_j(t-\tau))\\
&+ n_k(S_k^*)g_k(B_k^*)(2+\frac{g_k(B_k)}{g_k(B_k^*)} - \frac{n_k(S_k^*)}{n_k(S_k)} - \frac{\varphi_k(I_k)}{\varphi_k(I_k^*)} - \frac{n_k(S_k)g_k(B_k)\varphi_k(I_k^*)}{n_k(S_k^*)g_k(B_k^*)\varphi_k(I_k)})\\
&+ n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j^*)(\frac{f_j(I_j)}{f_j(I_j^*)} - \frac{f_j(I_j(t-\tau))}{f_j(I_j^*)} + \ln\frac{f_j(I_j(t-\tau))}{f_j(I_j)})\\
&+ n_k(S_k^*)g_k(B_k^*)(\frac{h_k(I_k)}{h_k(I_k^*)} - \frac{\theta_k(B_k)}{\theta_k(B_k^*)} - \frac{h_k(I_k)\theta_k(B_k^*)}{h_k(I_k^*)\theta_k(B_k)} + 1)\\
&- n_k(S_k^*)g_k(B_k^*)(\frac{h_k(I_k(t-\tau))\theta_k(B_k^*)}{h_k(I_k^*)\theta_k(B_k)} - 1 - \ln\frac{h_k(I_k(t-\tau))\theta_k(B_k^*)}{h_k(I_k^*)\theta_k(B_k)})\\
&+ n_k(S_k^*)g_k(B_k^*)(\frac{h_k(I_k)\theta_k(B_k^*)}{h_k(I_k^*)\theta_k(B_k)} - 1 - \ln\frac{h_k(I_k)\theta_k(B_k^*)}{h_k(I_k^*)\theta_k(B_k)}).
\end{aligned}
\tag{3.8}
$$

We consider the function $M(x) = 1 - x + \ln x$, which is nonpositive for $x > 0$ and $M(x) = 0$ if and only if $x = 1$. Eq. (3.8) is equivalent to

$$
\begin{aligned}
\frac{dL_k}{dt} =&(m_k(S_k) - m_k(S_k^*))(1 - \frac{n(S^*)}{n(S)}) + n_k(S_k^*)g_k(B_k^*)M(\frac{g_k(B_k^*)\theta_k(B_k)}{g_k(B_k)\theta_k(B_k^*)})\\
&+ n_k(S_k^*)g_k(B_k^*)(\frac{g_k(B_k)}{g_k(B_k^*)} - 1)(1 - \frac{g_k(B_k^*)\theta_k(B_k)}{g_k(B_k)\theta_k(B_k^*)})\\
&+ n_k(S_k^*)g_k(B_k^*)(\frac{h_k(I_k)}{h_k(I_k^*)} - 1)(1 - \frac{h_k(I_k^*)\varphi_k(I_k)}{h_k(I_k)\varphi_k(I_k^*)})\\
&+ n_k(S_k^*)g_k(B_k^*)(M(\frac{n_k(S_k^*)}{n_k(S_k)}) + M(\frac{n_k(S_k)g_k(B_k)\varphi_k(I_k^*)}{n_k(S_k^*)g_k(B_k^*)\varphi_k(I_k)}))\\
&+ n_k(S_k^*)g_k(B_k^*)(M(\frac{h_k(I_k^*)\varphi_k(I_k)}{h_k(I_k)\varphi_k(I_k^*)}) + M(\frac{h_k(I_k(t-\tau))\theta_k(B_k^*)}{h_k(I_k^*)\theta_k(B_k)}))\\
&+ 2n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j^*) + n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j(t-\tau))\\
&- n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j^*)\frac{\varphi_k(I_k)}{\varphi_k(I_k^*)} - n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j^*)\frac{n_k(S_k^*)}{n_k(S_k)}\\
&- n_k(S_k)\frac{\varphi_k(I_k^*)}{\varphi_k(I_k)}\sum_{j=1}^{n}\beta_{kj}f_j(I_j(t-\tau))\\
&+ n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j^*)(\frac{f_j(I_j)}{f_j(I_j^*)} - \frac{f_j(I_j(t-\tau))}{f_j(I_j^*)} + \ln\frac{f_j(I_j(t-\tau))}{f_j(I_j)}).
\end{aligned}
\tag{3.9}
$$

It follows from (3.6) and (3.7) that

$$
\sum_{k=1}^{n}v_k n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj}f_j(I_j) = \sum_{k=1}^{n}\sum_{j=1}^{n}v_j n_j(S_j^*)\beta_{jk}f_k(I_k)
$$

$$= \sum_{k=1}^{n}\sum_{j=1}^{n} v_j n_j(S_j^*)\beta_{jk} f_k(I_k^*)\frac{f_k(I_k)}{f_k(I_k^*)} = \sum_{k=1}^{n}\sum_{j=1}^{n} v_j \overline{\beta}_{jk}\frac{f_k(I_k)}{f_k(I_k^*)}$$
$$= \sum_{k=1}^{n}\sum_{j=1}^{n} v_k \overline{\beta}_{kj}\frac{f_k(I_k)}{f_k(I_k^*)} = \sum_{k=1}^{n}\sum_{j=1}^{n} v_k \beta_{kj} n_k(S_k^*) f_j(I_j^*)\frac{f_k(I_k)}{f_k(I_k^*)}. \tag{3.10}$$

By assumption (H_7), it can be obtained that

$$\begin{aligned}
&(\frac{f_k(I_k)}{f_k(I_k^*)} - 1)(1 - \frac{f_k(I_k^*)\varphi_k(I_k)}{f_k(I_k)\varphi_k(I_k^*)}) \\
=&\frac{\varphi_k(I_k)}{f_k(I_k)f_k(I_k^*)}(f_k(I_k) - f_k(I_k^*))(\frac{f_k(I_k)}{\varphi_k(I_k)} - \frac{f_k(I_k^*)}{\varphi_k(I_k^*)}) \le 0, \\
&(\frac{g_k(B_k)}{g_k(B_k^*)} - 1)(1 - \frac{g_k(B_k^*)\theta_k(B_k)}{g_k(B_k)\theta_k(B_k^*)}) \le 0
\end{aligned}$$

and

$$(\frac{h_k(I_k)}{h_k(I_k^*)} - 1)(1 - \frac{h_k(I_k^*)\varphi_k(I_k)}{h_k(I_k)\varphi_k(I_k^*)}) \le 0. \tag{3.11}$$

Define a Lyapunov functional L as

$$L = \sum_{k=1}^{n} v_k L_k.$$

By calculating the derivative of L along positive solutions of system (1.2), it follows from (3.9), (3.10) and (3.11) that

$$\begin{aligned}
\frac{dL}{dt} =& \sum_{k=1}^{n} v_k L_k' \\
\le& 2\sum_{k=1}^{n} v_k n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj} f_j(I_j^*) - \sum_{k=1}^{n} v_k n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj} f_j(I_j^*)\frac{\varphi_k(I_k)}{\varphi_k(I_k^*)} \\
&- \sum_{k=1}^{n} v_k n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj} f_j(I_j^*)\frac{n_k(S_k^*)}{n_k(S_k)} - \sum_{k=1}^{n} v_k n_k(S_k)\frac{\varphi_k(I_k^*)}{\varphi_k(I_k)}\sum_{j=1}^{n}\beta_{kj} f_j(I_j(t-\tau)) \\
&+ \sum_{k=1}^{n} v_k n_k(S_k^*)\sum_{j=1}^{n}\beta_{kj} f_j(I_j^*)(\frac{f_j(I_j)}{f_j(I_j^*)} + \ln\frac{f_j(I_j(t-\tau))}{f_j(I_j)}) \\
=& \sum_{k=1}^{n} v_k \sum_{j=1}^{n}\overline{\beta}_{kj}(2 + \frac{f_k(I_k)}{f_k(I_k^*)} - \frac{n_k(S_k^*)}{n_k(S_k)} - \frac{\varphi_k(I_k)}{\varphi_k(I_k^*)} - \frac{n_k(S_k)f_k(I_k)\varphi_k(I_k^*)}{n_k(S_k^*)f_k(I_k^*)\varphi_k(I_k)}) \\
&+ \sum_{k=1}^{n} v_k \sum_{j=1}^{n}\overline{\beta}_{kj}(\frac{n_k(S_k)\varphi_k(I_k^*)}{n_k(S_k^*)\varphi_k(I_k)}(\frac{f_k(I_k)}{f_k(I_k^*)} - \frac{f_j(I_j(t-\tau))}{f_j(I_j^*)}) \\
&+ \sum_{k=1}^{n} v_k \sum_{j=1}^{n}\overline{\beta}_{kj}\ln\frac{f_j(I_j(t-\tau))}{f_j(I_j)} \\
=& \sum_{k=1}^{n} v_k \sum_{j=1}^{n}\overline{\beta}_{kj}(\frac{f_k(I_k)}{f_k(I_k^*)} - 1)(1 - \frac{f_k(I_k^*)\varphi_k(I_k)}{f_k(I_k)\varphi_k(I_k^*)})
\end{aligned}$$

$$
\begin{aligned}
&+\sum_{k=1}^{n} v_k \sum_{j=1}^{n} \overline{\beta}_{kj} M\Big(\frac{f_k(I_k^*)\varphi_k(I_k)}{f_k(I_k)\varphi_k(I_k^*)}\Big) + \sum_{j=1}^{n} v_k \sum_{j=1}^{n} \overline{\beta}_{kj} M\Big(\frac{n(S^*)}{n(S)}\Big) \\
&+\sum_{k=1}^{n} v_k \sum_{j=1}^{n} \overline{\beta}_{kj} M\Big(\frac{n_k(S_k)\varphi_k(I_k^*) f_j(I_j(t-\tau))}{n_k(S_k^*)\varphi_k(I_k) f_j(I_j^*)}\Big) + \sum_{k=1}^{n} v_k \sum_{j=1}^{n} \overline{\beta}_{kj} \ln \frac{f_k(I_k) f_j(I_j^*)}{f_k(I_k^*) f_j(I_j)} \\
\leq &\sum_{k=1}^{n} v_k \sum_{j=1}^{n} \overline{\beta}_{kj} \ln \frac{f_k(I_k) f_j(I_j^*)}{f_k(I_k^*) f_j(I_j)}.
\end{aligned}
$$

Let

$$
H \triangleq \sum_{k=1}^{n} v_k \sum_{j=1}^{n} \overline{\beta}_{kj} \ln \frac{f_k(I_k) f_j(I_j^*)}{f_k(I_k^*) f_j(I_j)}.
$$

According to the idea developed in [8], it can be shown that $H = 0$ for all $f_j(I_j) > 0, j = 1, 2, \cdots n$. And it can be concluded that

$$
\frac{dL}{dt} = \sum_{j=1}^{n} v_k L_k' \leq \sum_{j=1}^{n} v_k \sum_{j=1}^{n} \overline{\beta}_{kj} \ln \frac{f_k(I_k) f_j(I_j^*)}{f_k(I_k^*) f_j(I_j)} = 0.
$$

Furthermore, if $\overline{\beta}_{kj} \neq 0$, $\frac{dL}{dt} = 0$ implies that

$$
m(S_k) = m(S_k^*) \ \ or \ \ n(S_k) = n(S_k^*), f_k(I_k) = f_k(I_k^*), \ \ g_k(B_k) = g_k(B_k^*).
$$

So $\frac{dL}{dt} = 0$ holds if and only if

$$
S_k = S_k^*, \ \ I_k = I_k^*, \ \ B_k = B_k^*, \ \ , k = 1, 2, \cdots, n.
$$

Therefore, the maximum invariant set in $\{(S_k, I_k, B_k) \in X : \frac{dL}{dt} = 0\}$ is the singleton E^*. By a similar argument in [23], it concludes that E^* is globally asymptotically stable in X if $R_0 > 1$. □

4. Numerical examples

4.1. Some examples

In this subsection, some examples are given to illustrate the results and the following nonlinear system is considered:

$$
\begin{aligned}
\frac{dS_1}{dt} &= A_1 - n_1(S_1)(\beta_{11} f_1(I_1(t-\tau)) + \beta_{12} f_2(I_2(t-\tau))) - n_1(S_1) g_1(B_1) - \mu_1 S_1, \\
\frac{dI_1}{dt} &= n_1(S_1)(\beta_{11} f_1(I_1(t-\tau)) + \beta_{12} f_2(I_2(t-\tau))) + n_1(S_1) g_1(B_1) - (c_1 + \mu_1) I_1, \\
\frac{dB_1}{dt} &= h_1(I_1(t-\tau)) - d_1 B_1, \\
\frac{dS_2}{dt} &= A_2 - n_2(S_2)(\beta_{21} f_1(I_1(t-\tau)) + \beta_{22} f_2(I_2(t-\tau))) - n_2(S_2) g_2(B_2) - \mu_2 S_2, \\
\frac{dI_2}{dt} &= n_2(S_2)(\beta_{21} f_1(I_1(t-\tau)) + \beta_{22} f_2(I_2(t-\tau))) + n_2(S_2) g_2(B_2) - (\mu_2 + c_2) I_2, \\
\frac{dB_2}{dt} &= h_2(I_2(t-\tau)) - d_2 B_2,
\end{aligned}
\tag{4.1}
$$

where $A_k, \mu_k, c_k, d_k > 0$, $m_k(S_k) = A_k - \mu_k S_k$, $\theta(B_k) = d_k B_k$, $\varphi_k = c_k I_k$ and $k = 1, 2$. The possible forms of n_k, f_k are $\frac{S_k^{q_k}}{1+M_k S_k^{q_k}}$, $\frac{I_k^{p_k}}{1+M_k I_k^{p_k}}$ and $\Lambda_k \ln(1 + \frac{\lambda_k I_k}{\Lambda_k})$ with constants $q_k, \lambda_k, \Lambda_k > 0$, $0 \le p_k \le 1$ and $M_k \ge 0$ [2,14,17]. The possible forms of g_k are $\frac{\lambda_k B_k^{T_k}}{1+M_k B_k^{T_k}}$, and $\eta_k(1-e^{-\alpha_k B_k})$ with constants $\lambda_k, \eta_k, \alpha_k > 0$, $0 < T_k \le 1$ and $M_k \ge 0$ [1,3]. The possible form of h_k is $K I_k^{v_k}$ with constants $K > 0, 0 < v_k \le 1$. It is easy to see that assumptions (H_1)-(H_7) are satisfied for possible forms of f_k, g_k, h_k.

Since the functions n_k, f_k, g_k, h_k is strictly monotonously increasing on $(0, +\infty)$, the feasible region is given by

$$\Omega = \{(S_k, I_k, B_k) \in \mathcal{C}_k : \|S_k\| \le \frac{A_k}{\mu_k}, \|S_k + I_k\| \le \frac{A_k}{\mu_k}, \|B_k\| \le \frac{1}{d_k} h_k(\frac{A_k}{\mu_k})\}.$$

A direct calculation shows that

$$R_0 = \frac{R_{11} + R_{22} + \sqrt{(R_{11} - R_{22})^2 + 4R_{12}R_{21}}}{2},$$

where

$$\begin{aligned}
R_{11} &= \frac{\beta_{11} n_1(S_1^0) f_1'(0)}{c_1} + \frac{n_1(S_1^0) g_1'(0) h_1'(0)}{c_1 d_1},\\
R_{12} &= \frac{\beta_{12} n_1(S_1^0) f_2'(0)}{c_2}, \quad R_{21} = \frac{\beta_{21} n_2(S_2^0) f_1'(0)}{c_1},\\
R_{22} &= \frac{\beta_{22} n_2(S_2^0) f_2'(0)}{c_2} + \frac{n_2(S_2^0) g_2'(0) h_2'(0)}{c_2 d_2}.
\end{aligned}$$

In these cases, on the assumption that $\beta_{12}, \beta_{21} > 0$, the disease-free equilibrium is globally asymptotically stable if $R_0 \le 1$, and system (4.1) has a unique endemic equilibrium which is also globally asymptotically stable if $R_0 > 1$. In other words, time delay has no impact on the global stability of equilibria of system (4.1).

4.2. Numerical simulation

In this subsection, all the other functions are fixed except the elimination rate φ_k. The influence of time delay and the elimination rate on the dynamics properties of system (1.2) is analyzed by numerical simulation. The following two systems are considered:

$$\begin{aligned}
\frac{dS_1}{dt} &= A_1 - S_1(\beta_{11} I_1(t-\tau) + \beta_{12} I_2(t-\tau)) e^{-\mu\tau} - \lambda_1 S_1 B_1 - \mu S_1,\\
\frac{dI_1}{dt} &= S_1(\beta_{11} I_1(t-\tau) + \beta_{12} I_2(t-\tau)) e^{-\mu\tau} + \lambda_1 S_1 B_1 - \varphi_1(I_1),\\
\frac{dB_1}{dt} &= k I_1(t-\tau) e^{-\mu\tau} - d_1 B_1,\\
\frac{dS_2}{dt} &= A_2 - S_2(\beta_{21} I_1(t-\tau) + \beta_{22} I_2(t-\tau)) e^{-\mu\tau} - \lambda_2 S_2 B_2 - \mu S_2,\\
\frac{dI_2}{dt} &= S_2(\beta_{21} I_1(t-\tau) + \beta_{22} I_2(t-\tau)) e^{-\mu\tau} + \lambda_2 S_2 B_2 - \varphi_2(I_2),\\
\frac{dB_2}{dt} &= k I_2(t-\tau) e^{-\mu\tau} - d_2 B_2,
\end{aligned} \tag{4.2}$$

with the parameter values and initial values:

$$A_1 = 310, A_2 = 410, \mu = 0.1, \lambda_1 = \lambda_2 = k = d_1 = d_2 = 0,$$
$$\beta_{11} = \beta_{22} = 0.001, \beta_{12} = \beta_{21} = 0.0012,$$

and

$$S_1(0) = 2000, I_1(0) = 30, S_2(0) = 3000, I_2(0) = 40, B_1(0) = B_2(0) = 0.$$

When $\varphi_i(I_i) = (\mu + c_i)I_i, i = 1, 2$, it is easy to see that the endemic equilibrium of system (4.2) is globally asymptotically stable and the persistent level of the disease is not affected by time delay τ from Fig.1. For $\varphi_1(I_1) = \mu I_1 + \frac{c_1 I_1}{a+I_1}$, $\varphi_2(I_2) = (c_2 + \mu)I_2$, that is, the assumption (H_7) is not satisfied, it is easy to find that system (4.2) presents periodic oscillation behavior from Fig.2, implying that the endemic equilibrium of system (4.2) is not globally asymptotically stable and system (4.2) experiences the bifurcation.

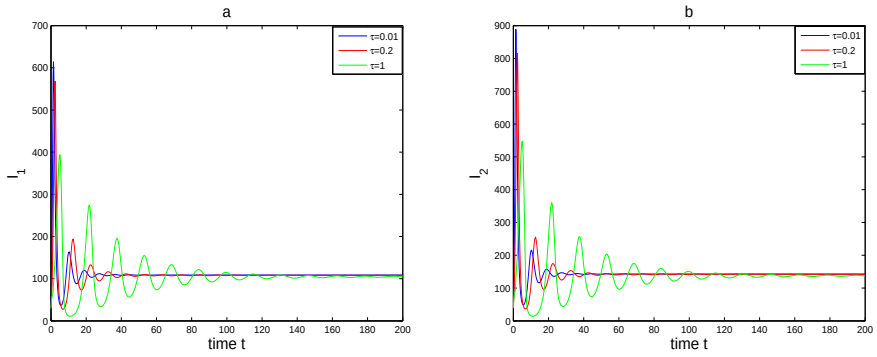

Figure 1. The simulation of the number of infected individuals on variable τ (0.01, 0.2 and 1) with $c_1 = c_2 = 2$, with all other parameters fixed except time delay τ

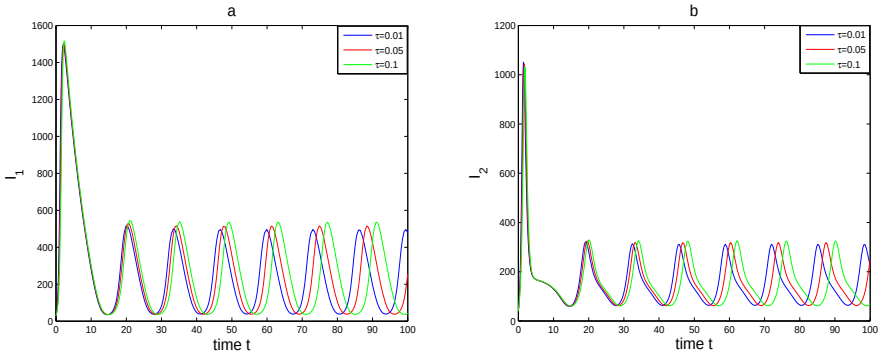

Figure 2. The simulation of the number of infected individuals on variable τ (0.01, 0.05 and 0.1) with $c_1 = 370$, $c_2 = 2$ and $a = 100$, with all other parameters fixed except time delay τ

5. Conclusions and discussions

In this paper, a delayed SIB dynamic model with group mixing and discrete delay is proposed. On very general and biologically plausible assumptions of the incidence, the birth rate of individuals, shedding rate of pathogen, and removal rate functions, the basic reproduction number R_0 is derived and then the global dynamics of system (1.2) is shown, it finds that time delay has no impact on the stability of equilibria of system (1.2). In particular, if $R_0 \leq 1$, the disease-free equilibrium is globally asymptotically stable; whereas if $R_0 > 1$, E_0 is unstable and system (1.2) is uniformly persistent. Furthermore, for $R_0 > 1$, the endemic equilibrium E^* is also globally asymptotically stable.

On the other hand, the stability of equilibria depends on the properties of the function $\frac{f_k}{\varphi_k}$, $\frac{g_k}{\theta_k}$ and $\frac{h_k}{\varphi_k}$. If these functions are non-increasing, the dynamical properties of system (1.2) are completely determined by R_0. The removal rate $\varphi_k(I_k)$ is influenced by the resource which is used to monitor and cull infected animals, and the incidence $g_k(B_k)$ and the disinfection $\theta_k(B_k)$ are determined by animal breeding environment. That is, in some animal breeding environment, $\frac{f_k}{\varphi_k}$, $\frac{g_k}{\theta_k}$ and $\frac{h_k}{\varphi_k}$ may be monotonically increasing function, such as $f_k(I_k) = \beta I_k$ and $\varphi_k(I_k) = \mu I_k + \frac{cI_k}{a+I_k}$ with constants $\beta, \mu, c, a > 0$, among which c represents the maximal supply of resources for monitoring and culling per unit time, and a is half-saturation constant, measuring the efficiency of the resource supply in the sense. Therefore, assumption (H_7) may not be satisfied and other complex dynamics properties of system (1.2) may occur, such as oscillations. In other words, the spread of animal diseases depends largely on the development of the prevention and control strategies. As is shown in Fig.2, animal diseases transmission in a sub-population can be affected by other sub-population control measures, which implies that the disease may not be eliminated if control measures are carried out in a region. In addition, as is shown in the numerical simulation, the impact of time delay on the bifurcation of system (1.2) is still unclear. We leave these for further research.

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References

[1] R. Breban, J.M. Drake, D.E. Stallknecht and P. Rohani, *The role of environmental transmission in recurrent avian influenza epidemics,* PLoS Comput. Biol., 5(2009)(10), e1000346. doi:10.1371/journal.pcbi.1000346.

[2] C.J. Briggs and H.C.J. Godfray, *The dynamics of insect-pathogen interactions in stage-structured populations,* Am. Nat., 145(1995), 845–887.

[3] C.T. Codeço, *Endemic and epidemic dynamics of cholera: the role of the aquatic reservoir,* BMC Infect. Dis., 1(2001)(1), doi:10.1186/1471-2334-1-1.

[4] O. Diekmann , J.A.P. Heesterbeek and J.A.J. Metz, *On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations,* J. Math. Biol., 28(1990), 365–382.

[5] Y. Enatsu, Y. Nakata and Y. Muroya, *Lyapunov functional techniques for the global stability analysis of a delayed SIRS epidemic model,* Nonlinear Anal. RWA., 13(2012), 2120–2133.

[6] N.M. Ferguson, C.A. Donnelly and R.M. Anderson, *The foot-and-mouth epidemic in great Britain: pattern of spread and impact of interventions,* Science, 292(2001), 1155–1160.

[7] H. Guo, M.Y. Li and Z.S Shuai, *Global stability of the endemic equilibrium of multi-group SIR epidemic models,* Canad. Appl. Math. Quart., 14(2006)(3), 259–284.

[8] H. Guo, M.Y. Li and Z.S. Shuai, *A graph-theoretic approach to the method of global Lyapunov functions,* Proc. Amer. Math. Soc., 136 (2008), 2793–2802.

[9] J.K. Hale, P. Waltman, *Persistence in infinite-dimensional systems,* SIAM J. Math. Anal., 20(1989), 388–395.

[10] G. Huang and Y. Takeuchi, *Global analysis on delay epidemiological dynamic models with nonlinear incidence,* J. Math. Biol., 63(2011), 125–139.

[11] V. Hutson and K. Schmitt, *Permanence and the dynamics of biological systems,* Math. Biosci., 111(1992), 1–71.

[12] M.J. Keeling and C.A. Gilligan, *Meta-population dynamics of bubonic plague,* Nature, 407(2000), 903-905.

[13] M.J. Keeling, M.E.J. Woolhouse, R.M. May, G. Davies and B.T. Grenfell, *Modeling vaccination strategies against foot-and-mouth disease,* Nature, 421(2003)(9), 136–142.

[14] R.J. Knell, M. Begon and D.J. Thompson, *Transmission dynamics of Bacillus thuringiensis infecting Plodia interpunctella: a test of the mass action assumption with an insect pathogen,* Proc. R. Soc. London B Biol. Sci., 263(1996), 75–81.

[15] M.Y. Li, Z.S. Shuai and C.C. Wang, *Global stability of multi-group epidemic models with distributed delays,* J. Math. Anal. Appl., 361(2010), 38–47.

[16] M.T. Li, G.Q. Sun, Y.F. Wu, J. Zhang and Z. Jin, *Transmission dynamics of a multi-group brucellosis model with mixed cross infection in public farm,* Appl. Math. Comput., 237(2014), 582–594.

[17] W.M. Liu and S.A.Levin, *Influence of nonlinear incidence rates upon the behavior of SIRS epidemiological models,* J. Math. Biol., 23(1986), 187–204.

[18] S. Roy, T.F. McElwain and Y. Wan, *A network control theory approach to modeling and optimal control of zoonoses: case study of brucellosis transmission in sub-saharan Africa,* PLoS Negl. Trop. Dis., 5(2011)(10), e1259. doi:10.1371/journal.pntd. 0001259.

[19] G. Röst, J.H. Wu, *SEIR epidemiological model with varying infectivity and infinite delay,* Math. Biosci. Eng., 5(2008), 389–402.

[20] G. Pappas, P. Papadimitriou, N. Akritidis, L. Christou and E.V. Tsianos, *The new global map of human brucellosis,* Lancet Infect. Dis., 6(2006), 91–99.

[21] P. van den Driessche and J. Watmough, *Reproduction numbers and subthreshold endemic equilibria for compartmental models of disease transmission,* Math. Biosci., 180(2002), 29–48.

[22] R. Xu and Z.E. Ma, *Global stability of a SIR epidemic model with nonlinear incidence rate and time delay,* Nonlinear Anal. RWA., 10(2009), 3175–3189.

[23] Z. Yuan and L. Wang, *Global stability of epidemiological models with group mixing and nonlinear incidence rates,* Nonlinear Anal. RWA., 11(2010), 995–1004.

[24] J. Zhang, Z. Jin, G.Q. Sun, T. Zhou and S.G. Ruan, *Analysis of rabies in China: transmission dynamics and control,* PLoS ONE, 6(2011)(7), e20891. doi:10.1371/journal. pone.0020891.

[25] X. Zhao, *Dynamical Systems in Population Biology,* Springer, New York, 2003.

[26] J. Zinsstag, S. Dürra, M. Penny, R. Mindekem, F. Roth, S. Menendez Gonzalez, S. Naissengar and J. Hattendorf, *Transmission dynamics and economics of rabies control in dogs and humans in an African city,* Proc. Natl. Acad. USA., 106(2009), 14996–15001.

[27] J. Zinsstag, F. Roth, D. Orkhon, G. Chimed-Ochir, M. Nansalmaa, J. Kolar and P. Vounatsou, *A model of animal-human brucellosis transmission in Mongolia,* Prev. Vet. Med., 69(2005), 77–95.