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Istvan Lauko
University of Wisconsin - Milwaukee

Gabriella Pinter
University of Wisconsin - Milwaukee

Rachel Elizabeth TeWinkel
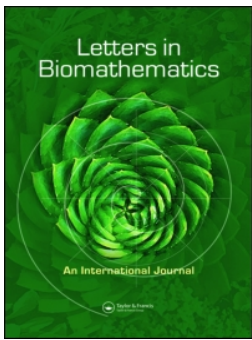*University of Wisconsin-Milwaukee,* tewinke2@uwm.edu

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Equilibrium analysis for an epidemic model with a reservoir for infection

Istvan Lauko, Gabriella Pinter and Rachel Elizabeth TeWinkel

University of Wisconsin-Milwaukee, Milwaukee, WI, USA

ABSTRACT

We consider a system of non-linear differential equations describing the spread of an epidemic in two interacting populations. The model assumes that the epidemic spreads within the first population, which in turn acts as a reservoir of infection for the second population. We explore the conditions under which the epidemic is endemic in both populations and discuss the global asymptotic stability of the endemic equilibrium using a Lyapunov function and results established for asymptotically autonomous systems. We discuss monkeypox as an example of an emerging disease that can be modelled in this way and present some numerical results representing the model and its extensions.

1. Introduction

In this paper we consider an epidemic model motivated by monkeypox, an emerging disease that has become more prevalent recently in several areas of Africa (Bhunu & Mushayabasa, 2011; Bhunu, Mushayabasa, & Hyman, 2012; Damon, 2011; Hammarlund et al., 2005; Hutin et al., 2001; Kantele, Chickering, Vapalahti, & Rimoin, 2016; Levine, Townsend, Carroll, Damon, & Reynolds, 2007; McCollum & Damon, 2014; The Center for Food Security and Public Health, 2013). It is believed that the noticeable increase in monkeypox (Nolen et al., 2016) is linked to the decrease in herd immunity to smallpox (Hutin et al., 2001; Levine et al., 2007; Lloyd-Smith et al., 2009; McCollum & Damon, 2014) due to the phasing out of smallpox vaccinations (Nolen et al., 2016; Rimoin & Graham, 2011; Rimoin et al., 2007, 2010). Hosts of the monkeypox virus include prairie dogs, tree squirrels, chimpanzees, and baboons, but the complete list of pathogen hosts is not known (Centers for Disease Control and Prevention, 2015; Reynolds et al., 2013; The Center for Food Security and Public Health, 2013; World Health Organization, 2016). Monkeypox infects both humans and animals, and is generally considered impossible to eradicate (Damon, 2011; Kantele et al., 2016; McCollum & Damon, 2014; Reynolds et al., 2013; Rimoin & Graham, 2011). Humans become infected with the monkeypox virus when they come into direct contact with infected animals or other humans (Centers for Disease Control and Prevention, 2015; Hammarlund et al., 2005; Jezek, Arita,

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CONTACT Rachel Elizabeth TeWinkel ✉ tewinke2@uwm.edu ▢ University of Wisconsin-Milwaukee, P.O. Box 413, Milwaukee, WI 53201-0413, USA

Mutombo, & Szczeniowski, 1986; Jezek, Grab, Szczeniowski, Paluku, & Mutombo, 1988; The Center for Food Security and Public Health, 2013; Weaver & Isaacs, 2009; World Health Organization, 2016). Since human-animal cross-infection usually occurs when humans hunt and eat animals, we can assume that animals do not become infected via contact with the human population, but that animals can infect humans (Reynolds et al., 2013). This creates an asymmetric disease transmission between the animal and human populations, and we can effectively treat the animal population as a reservoir for the disease within which disease dynamics are independent from the disease's course in the human population. Monkeypox was explicitly modelled by Bhunu and Mushayabasa and Bhunu, Mushayabasa and Hyman with traditional SIR models in both the animal and human population, and with standard incidence for disease transmission (Bhunu & Mushayabasa, 2011; Bhunu et al., 2012). However, the analysis presented in Bhunu and Mushayabasa (2011) and Bhunu et al. (2012) is not complete, and here we present an alternative full equilibrium analysis for the first model by Bhunu and Mushayabasa, and establish global stability of the endemic equilibrium in both populations under suitable conditions on the parameters (Bhunu & Mushayabasa, 2011). We utilize the theory developed by Markus (1956) and later by Thieme and Castillo-Chavez (Castillo-Chavez & Thieme, 1994; Thieme, 1992) for asymptotically autonomous systems together with the techniques of identifying suitable Lyapunov functions for SIR models with standard incidence described by Vargas-De-León (2011).

We note that these ideas can be readily generalized for multiple reservoir (and human) populations, and are more widely applicable than the special case of monkeypox. In particular, birds can harbour avian flu viruses that can adapt to and spread in human populations (Centers for Disease Control and Prevention, 2017a), bats are a reservoir for rabies (Gilbert et al., 2015), and ebola viruses are also thought to have a natural animal reservoir (Centers for Disease Control and Prevention, 2017b). The model considered in this paper would suggest that once the disease becomes endemic in the reservoir population, endemic disease in the human population is inevitable. Thus it could be suggested that an effective control measure would be the mass culling of animals that harbour the disease causing pathogens to prevent the establishment of an endemic disease in the animal population. While this strategy is widely used for controlling avian flu within domestic bird populations (Centers for Disease Control and Prevention, 2017a), it is not practical or even possible for the cases of monkeypox, rabies, or ebola within wild populations. The prediction of endemic levels of the disease in the human population (while it may be a good approximation at times) are not wholly realistic, due to fluctuations in incidence of monkeypox in the human population (Nolen et al., 2016).

2. Description of the model

We consider two populations, denoted by A and H, in which a disease spreads. Both populations are divided into susceptible, infectious and recovered individuals, denoted by S_a, I_a and R_a, and S_h, I_h and R_h, respectively. The total number of individuals in each population is given as $N_a(t) = S_a(t) + I_a(t) + R_a(t)$ and $N_h(t) = S_h(t) + I_h(t) + R_h(t)$. Susceptible individuals in A are recruited through migration and birth at the rate Λ_a and susceptible individuals in H are recruited at a rate of Λ_h (Bhunu & Mushayabasa, 2011). Let d_a, d_h be the death rates by the disease for A and H, respectively, μ_a, μ_h be the natural death

rates for A and H, respectively, and ρ_a, ρ_h be the recovery rates with permanent immunity for A and H, respectively. It is assumed that no one in population H can infect any individual in population A, while individuals in A can infect those in H on suitable contact. Although this model can be used to describe epidemics of different diseases, in the case of monkeypox population A is the animal population and H represents the human population. Disease transmission is modelled using standard incidence, assuming a constant (density-independent) contact rate both within and across the two populations resulting in infection rates

$$f_a(S_a, I_a, R_a) = \frac{\beta_{a_1} I_a}{N_a} S_a, \quad \text{and} \quad f_h(S_a, I_a, R_a, S_h, I_h, R_h) = \left(\frac{\beta_{a_2} I_a}{N_a} + \frac{\beta_h I_h}{N_h} \right) S_h,$$

where β_{a_1}, β_{a_2} and β_h are the effective contact rates in population A, between populations A and H, and in population H, respectively. We assume that $\Lambda_a, \Lambda_h, \mu_a, \mu_h, \rho_a, \rho_h$ are positive, while $d_a, d_h, \beta_{a_1}, \beta_{a_2}$ and β_h are non-negative parameters. Thus we have the following system of non-linear differential equations (1a)–(1f) (Bhunu & Mushayabasa, 2011)

$$\frac{dS_a}{dt} = \Lambda_a - \mu_a S_a - \frac{\beta_{a_1} I_a}{N_a} S_a, \tag{1a}$$

$$\frac{dI_a}{dt} = \frac{\beta_{a_1} I_a}{N_a} S_a - (\mu_a + \rho_a + d_a) I_a, \tag{1b}$$

$$\frac{dR_a}{dt} = \rho_a I_a - \mu_a R_a, \tag{1c}$$

$$\frac{dS_h}{dt} = \Lambda_h - \mu_h S_h - \left(\frac{\beta_{a_2} I_a}{N_a} + \frac{\beta_h I_h}{N_h} \right) S_h, \tag{1d}$$

$$\frac{dI_h}{dt} = \left(\frac{\beta_{a_2} I_a}{N_a} + \frac{\beta_h I_h}{N_h} \right) S_h - (\mu_h + \rho_h + d_h) I_h, \tag{1e}$$

$$\frac{dR_h}{dt} = \rho_h I_h - \mu_h R_h. \tag{1f}$$

Since

$$N_a' = \Lambda_a - \mu_a N_a - d_a I_a \quad \text{and} \quad N_h' = \Lambda_h - \mu_h N_h - d_h I_h,$$

the set $\Omega = \Omega_a \times \Omega_h$, where

$$\Omega_a = \left\{ (S_a, I_a, R_a) \in \mathbb{R}^3_+ : S_a \geq 0, \ I_a \geq 0, \ R_a \geq 0, \ S_a + I_a + R_a \leq \frac{\Lambda_a}{\mu_a} \right\}$$

and

$$\Omega_h = \left\{ (S_h, I_h, R_h) \in \mathbb{R}^3_+ : S_h \geq 0, \ I_h \geq 0, \ R_h \geq 0, \ S_h + I_h + R_h \leq \frac{\Lambda_h}{\mu_h} \right\},$$

is positively invariant under the dynamics of (1a)–(1f), and solutions with initial conditions in Ω exist globally.

3. Equilibrium analysis

System (1a)–(1f) has several different types of potential equilibria: disease-free, endemic disease in only one of the populations and endemic disease in both populations. Using the method of van der Driessche and Watmough (Bhunu & Mushayabasa, 2011; Castillo-Chavez, Feng, & Huang, 2001; van den Driessche & Watmough, 2002), the basic reproduction numbers of the model are $\mathcal{R}_{0_a}$ and $\mathcal{R}_{0_h}$, where

$$\mathcal{R}_{0_a} = \frac{\beta_{a_1}}{\mu_a + \rho_a + d_a} \quad \text{and} \quad \mathcal{R}_{0_h} = \frac{\beta_h}{\mu_h + \rho_h + d_h}.$$

In the following we address the feasibility and stability properties of each of the different equilibria of the system (1a)–(1f). Our analysis relies heavily on the results of Vargas-De-León given below (Vargas-De-León, 2011).

Consider the dynamics of the disease in the reservoir population A given by (1a)–(1c). The system has a disease-free equilibrium $E_{0_a} = (\Lambda_a/\mu_a, 0, 0)$ and a unique endemic equilibrium E_a^* with coordinates

$$S_a^* = \frac{\Lambda_a(\rho_a + \mu_a)}{\mu_a(\rho_a + \mu_a)\mathcal{R}_{0_a} + d_a\mu_a(\mathcal{R}_{0_a} - 1)} = \frac{\Lambda_a}{\mu_a} - \frac{\mu_a + \rho_a + d_a}{\mu_a}I_a^*, \qquad (2a)$$

$$I_a^* = \frac{\Lambda_a\mu_a(\mathcal{R}_{0_a} - 1)}{\mu_a(\rho_a + \mu_a)\mathcal{R}_{0_a} + d_a\mu_a(\mathcal{R}_{0_a} - 1)} = \frac{\Lambda_a(\beta_{a_1} - (\mu_a + \rho_a + d_a))}{(\beta_{a_1} - d_a)(\mu_a + \rho_a + d_a)}, \qquad (2b)$$

$$R_a^* = \frac{\Lambda_a\rho_a(\mathcal{R}_{0_a} - 1)}{\mu_a(\rho_a + \mu_a)\mathcal{R}_{0_a} + d_a\mu_a(\mathcal{R}_{0_a} - 1)} = \frac{\rho_a}{\mu_a}I_a^*. \qquad (2c)$$

We note that $I_a^* > 0$ whenever $\mathcal{R}_{0_a} > 1$ or $\beta_{a_1} < d_a$, but in the latter case the resulting S_a^* is negative. Thus the endemic equilibrium is feasible, that is, $E_a^* \in \Omega_a$, if and only if $\mathcal{R}_{0_a} > 1$. The following theorems are proved by Vargas-De-León by the construction of appropriate Lyapunov functions (Vargas-De-León, 2011).

Theorem 3.1: *If $\mathcal{R}_{0_a} \leq 1$, then the disease-free equilibrium E_{0_a} of (1a)–(1c) is globally asymptotically stable in Ω_a.*

Theorem 3.2: *Assume that $\mu_a > d_a$ and $\mathcal{R}_{0_a} > 1$, then the unique endemic equilibrium E_a^* of (1a)–(1c) is globally asymptotically stable in the interior of Ω_a.*

Once we know the dynamics of the disease in population A from the theorems above, we can consider how this affects disease propagation in population H. Here our analysis diverges from what was done previously in Bhunu and Mushayabasa (2011). Individuals in H can get infected by contact with infectious individuals in population A or H. However, we know that if $\mathcal{R}_{0_a} \leq 1$, then $I_a(t) \to 0$, $N_a(t) \to \Lambda_a/\mu_a$ as $t \to \infty$, while if $\mathcal{R}_{0_a} > 1$ and $\mu_a > d_a$, then $I_a(t) \to I_a^* > 0$, $N_a(t) \to N_a^* = S_a^* + I_a^* + R_a^*$ as $t \to \infty$. Thus we can

think of (1d)–(1f) as a non-autonomous system

$$\frac{dS_h}{dt} = \Lambda_h - \mu_h S_h - \left(\beta_{a_2} g(t) + \frac{\beta_h I_h}{N_h} \right) S_h, \tag{3a}$$

$$\frac{dI_h}{dt} = \left(\beta_{a_2} g(t) + \frac{\beta_h I_h}{N_h} \right) S_h - (\mu_h + \rho_h + d_h) I_h, \tag{3b}$$

$$\frac{dR_h}{dt} = \rho_h I_h - \mu_h R_h, \tag{3c}$$

where $g(t) := I_a(t)/N_a(t)$. By Theorems 3.1 and 3.2, we have that

$$\lim_{t \to \infty} g(t) = \frac{\lim_{t \to \infty} I_a(t)}{\lim_{t \to \infty} N_a(t)} = \frac{I_a^e}{N_a^e},$$

where the limits I_a^e and N_a^e depend on $\mathcal{R}_{0_a}$ and the corresponding parameters. That is, $I_a^e = 0$ when $\mathcal{R}_{0_a} \leq 1$ and $I_a^e = I_a^*$ when $\mathcal{R}_{0_a} > 1$. This makes (1d)–(1f) an asymptotically autonomous system with limit system

$$\frac{dS_h}{dt} = \Lambda_h - \mu_h S_h - \left(\beta_{a_2} \frac{I_a^e}{N_a^e} + \frac{\beta_h I_h}{N_h} \right) S_h, \tag{4a}$$

$$\frac{dI_h}{dt} = \left(\beta_{a_2} \frac{I_a^e}{N_a^e} + \frac{\beta_h I_h}{N_h} \right) S_h - (\mu_h + \rho_h + d_h) I_h, \tag{4b}$$

$$\frac{dR_h}{dt} = \rho_h I_h - \mu_h R_h, \tag{4c}$$

and we can use the theory developed for such systems (Castillo-Chavez & Thieme, 1994; Thieme, 1992) to address the stability properties of our model in all possible cases. In particular, we repeatedly make use of the following corollary (Thieme, 1992) applied to our systems:

Corollary 3.3: *If solutions of the system* (3a)–(3c) *are bounded, and the equilibrium E of the limit system* (4a)–(4c) *is globally asymptotically stable, then any solution* $(S_h(t), I_h(t), R_h(t))$ *of the system* (3a)–(3c) *satisfies* $(S_h(t), I_h(t), R_h(t)) \to E$ *as* $t \to \infty$.

3.1. Endemic equilibrium in both populations

We start with the following claim:

Proposition 3.4: *Assume that* $\mathcal{R}_{0_a} > 1$, $\beta_{a_2} > 0$ *and* $\mu_a > d_a$, *so the disease in the reservoir population tends to the endemic equilibrium* E_a^*. *Then* (1d)–(1f) *has a unique endemic equilibrium* $E_h^* \in \Omega_h$, *and* $\mathcal{E}_1 = (E_a^*, E_h^*)$ *is the unique endemic equilibrium of* (1a)–(1f) *in* Ω.

Proof: To calculate $E_h^* = (S_h^*, I_h^*, R_h^*)$, we follow the steps in (Bhunu & Mushayabasa, 2011), and set the right sides of Equations (1d)–(1f) equal to zero to obtain

$$\Lambda_h = \left(\mu_h + \frac{\beta_{a_2} I_a^*}{N_a^*} + \frac{\beta_h I_h^*}{N_h^*} \right) S_h^*, \tag{5}$$

$$\left(\frac{\beta_{a_2} I_a^*}{N_a^*} + \frac{\beta_h I_h^*}{N_h^*} \right) S_h^* = (\mu_h + \rho_h + d_h) I_h^*, \tag{6}$$

$$\rho_h I_h^* = \mu_h R_h^*. \tag{7}$$

In Bhunu and Mushayabasa (2011), the unique endemic equilibrium was found subject to $\beta_h > d_h(1 + \beta_{a_2} I_a^*/\mu_h N_a^*)$. Instead, we show the existence of the unique endemic equilibrium using a method similar to Afassinou, Chirove, and Govinder (2017) that holds regardless of the stated inequality.

For simplification, define

$$\lambda_a^* = \frac{\beta_{a_2} I_a^*}{N_a^*}, \quad m_h = \mu_h + \rho_h + d_h, \quad \lambda_h^* = \frac{\beta_h I_h^*}{N_h^*},$$

$$a = \frac{\Lambda_h \lambda_a^*}{m_h}, \quad b = \frac{\Lambda_h}{m_h}, \quad c = \frac{\rho_h a}{\mu_h}, \quad d = \frac{\rho_h b}{\mu_h}, \quad e = \Lambda_h + a + c, \quad f = b + d.$$

Using (5),

$$S_h^* = \frac{\Lambda_h}{\mu_h + \lambda_a^* + \lambda_h^*}. \tag{8}$$

From (6) and using (8),

$$I_h^* = \frac{S_h^* \left(\lambda_a^* + \lambda_h^* \right)}{m_h} = \left(\frac{\Lambda_h}{\mu_h + \lambda_a^* + \lambda_h^*} \right) \left(\frac{\lambda_a^* + \lambda_h^*}{m_h} \right) = \frac{a + b\lambda_h^*}{\mu_h + \lambda_a^* + \lambda_h^*}. \tag{9}$$

Clearly, by (7) and (9),

$$R_h^* = \frac{\rho_h}{\mu_h} I_h^* = \left(\frac{a + b\lambda_h^*}{\mu_h + \lambda_a^* + \lambda_h^*} \right) \left(\frac{\rho_h}{\mu_h} \right) = \frac{c + d\lambda_h^*}{\mu_h + \lambda_a^* + \lambda_h^*}. \tag{10}$$

Then it follows that

$$\frac{I_h^*}{N_h^*} = \left(\frac{a + b\lambda_h^*}{\mu_h + \lambda_a^* + \lambda_h^*} \right) \left(\frac{\mu_h + \lambda_a^* + \lambda_h^*}{\Lambda_h + a + b\lambda_h^* + c + d\lambda_h^*} \right) = \frac{a + b\lambda_h^*}{e + f\lambda_h^*}$$

so that

$$\lambda_h^* = \frac{\beta_h \left(a + b\lambda_h^* \right)}{e + f\lambda_h^*}. \tag{11}$$

Rearranging (11), we obtain

$$f\lambda_h^{*2} + \lambda_h^* \left(e - \beta_h b \right) - \beta_h a = 0. \tag{12}$$

The above quadratic equation in λ_h^* has one positive root. Now (8), (9) and (10) imply that the corresponding $E_h^* = (S_h^*, I_h^*, R_h^*)$ is feasible. ∎

Consider now the endemic equilibrium $\mathcal{E}_1 = (E_a^*, E_h^*) \in \Omega$. We prove the following theorem.

Theorem 3.5: *If $\mathcal{R}_{0_a} > 1$, $\mu_a > d_a$, $\beta_{a_2} > 0$ and $\mu_h > d_h$ then the unique endemic equilibrium $\mathcal{E}_1 = (E_a^*, E_h^*)$ of* (1a)–(1f) *is globally asymptotically stable in the interior of Ω.*

Proof: Since $\mathcal{R}_{0_a} > 1$ and $\mu_a > d_a$ Theorem 3.2 implies that E_a^* is a globally asymptotically stable equilibrium of (1a)–(1c) in the interior of Ω_a. Using this result, and the assumption that $\beta_{a_2} > 0$ we have that the system

$$\frac{dS_h}{dt} = \Lambda_h - \mu_h S_h - \left(\beta_{a_2} \frac{I_a^*}{N_a^*} + \frac{\beta_h I_h}{N_h} \right) S_h,$$

$$\frac{dI_h}{dt} = \left(\beta_{a_2} \frac{I_a^*}{N_a^*} + \frac{\beta_h I_h}{N_h} \right) S_h - (\mu_h + \rho_h + d_h) I_h,$$

$$\frac{dR_h}{dt} = \rho_h I_h - \mu_h R_h$$

is the asymptotic limit of system (1d)–(1f), and E_h^* is its unique equilibrium. We claim that E_h^* is a globally asymptotically stable equilibrium of (4a)–(4c).

Consider the function $L : \{(S_h, I_h, R_h) \in \Omega_h : S_h > 0,\ I_h > 0,\ R_h > 0\} \to \mathbb{R}$

$$L = N_h - N_h^* - N_h^* \ln \left(\frac{N_h}{N_h^*} \right) + \frac{N_h^* (d_h + 2\mu_h)}{\beta_h \left(I_h^* + R_h^* \right)} \left[I_h - I_h^* - I_h^* \ln \left(\frac{I_h}{I_h^*} \right) \right]$$

$$+ \frac{(d_h + 2\mu_h)}{2\rho_h} \left(1 + \frac{S_h^*}{I_h^* + R_h^*} \right) \left(\frac{(R_h - R_h^*)^2}{N_h} \right) + D \left(N_h - N_h^* \right)^2 + E \left(R_h - R_h^* \right)^2,$$

where $D, E > 0$ are yet to be determined. $L \in C^1(\Omega_h)$, $L(S_h^*, I_h^*, R_h^*) = 0$ and L is positive semi-definite. Calculating the derivative of L along solutions of (4a)–(4c) and using the relationships

$$\Lambda_h = \left(\mu_h + \frac{\beta_{a_2} I_a^*}{N_a^*} + \frac{\beta_h I_h^*}{N_h^*} \right) S_h^*, \quad \frac{\beta_{a_2} I_a^*}{N_a^*} + \frac{\beta_h I_h^*}{N_h^*} S_h^* = (\mu_h + \rho_h + d_h) I_h^*,$$

$$\rho_h I_h^* = \mu_h R_h^*,$$

we obtain

$$L' = \left(\mu_h \left(S_h^* + I_h^* + R_h^* \right) + d_h I_h^* - \mu_h \left(S_h + I_h + R_h \right) - d_h I_h \right) \left(\frac{N_h - N_h^*}{N_h} \right)$$

$$+ \frac{N_h^* (d_h + 2\mu_h)}{\beta_h \left(I_h^* + R_h^* \right)} \left[\frac{\beta_{a_2} I_a^* S_h I_h^* \left(I_h - I_h^* \right)}{N_a^* I_h I_h^*} - \frac{\beta_{a_2} I_a^* S_h^* I_h \left(I_h - I_h^* \right)}{N_a^* I_h I_h^*} \right.$$

$$\left. + \frac{\beta_h S_h N_h^* \left(I_h - I_h^* \right)}{N_h^* N_h} - \frac{\beta_h S_h^* N_h \left(I_h - I_h^* \right)}{N_h^* N_h} \right]$$

$$+ \frac{(d_h + 2\mu_h)}{2\rho_h}\left(1 + \frac{S_h^*}{I_h^* + R_h^*}\right)\left(\frac{2\left(\rho_h(I_h - I_h^*) - \mu_h(R_h - R_h^*)\right)\left(R_h - R_h^*\right)}{N_h}\right.$$

$$\left. - \frac{N_h'\left(R_h - R_h^*\right)^2}{N_h^2}\right) + 2DN_h'\left(N_h - N_h^*\right)$$

$$+ 2E\left(\rho_h I_h - \mu_h R_h - \rho_h I_h^* + \mu_h R_h^*\right)\left(R_h - R_h^*\right).$$

Since

$$\beta_h S_h N_h^*\left(I_h - I_h^*\right) - \beta_h S_h^* N_h\left(I_h - I_h^*\right) = \beta_h\left(I_h - I_h^*\right)\left(S_h N_h^* - S_h^* N_h\right)$$
$$= \beta_h\left(I_h - I_h^*\right)\left(\left(S_h - S_h^*\right)\left(I_h^* + R_h^*\right) - S_h^*\left(I_h - I_h^*\right) - S_h^*\left(R_h - R_h^*\right)\right)$$

and

$$\beta_{a_2} I_a^* S_h I_h^*\left(I_h - I_h^*\right) - \beta_{a_2} I_a^* S_h^* I_h\left(I_h - I_h^*\right) = \beta_{a_2} I_a^*\left(I_h - I_h^*\right)\left(I_h\left(S_h - S_h^*\right) - S_h\left(I_h - I_h^*\right)\right),$$

we have

$$L' = \left(\mu_h\left(S_h^* + I_h^* + R_h^*\right) + d_h I_h^* - \mu_h\left(S_h + I_h + R_h\right) - d_h I_h\right)\left(\frac{N_h - N_h^*}{N_h}\right)$$

$$+ \frac{N_h^*\left(d_h + 2\mu_h\right)}{\beta_h\left(I_h^* + R_h^*\right)}\left[\frac{\beta_{a_2} I_a^*\left(I_h - I_h^*\right)\left(S_h - S_h^*\right)}{N_a^* I_h^*} - \frac{\beta_{a_2} I_a^* S_h\left(I_h - I_h^*\right)^2}{N_a^* I_h I_h^*}\right.$$

$$+ \frac{\beta_h\left(I_h - I_h^*\right)\left(S_h - S_h^*\right)\left(I_h^* + R_h^*\right)}{N_h^* N_h} - \frac{\beta_h S_h^*\left(I_h - I_h^*\right)^2}{N_h^* N_h}$$

$$\left. - \frac{\beta_h S_h^*\left(I_h - I_h^*\right)\left(R_h - R_h^*\right)}{N_h^* N_h}\right]$$

$$+ \frac{(d_h + 2\mu_h)}{2\rho_h}\left(1 + \frac{S_h^*}{I_h^* + R_h^*}\right)\left(\frac{2\rho_h\left(I_h - I_h^*\right)\left(R_h - R_h^*\right)}{N_h}\right.$$

$$\left. - \frac{2\mu_h\left(R_h - R_h^*\right)^2}{N_h} - \frac{N_h'\left(R_h - R_h^*\right)^2}{N_h^2}\right)$$

$$+ 2DN_h'\left(N_h - N_h^*\right) + 2E\rho_h\left(I_h - I_h^*\right)\left(R_h - R_h^*\right) - 2E\mu_h\left(R_h - R_h^*\right)^2.$$

Notice that the first term in L' can be written as

$$\left(\frac{\left(S_h - S_h^*\right) + \left(I_h - I_h^*\right) + \left(R_h - R_h^*\right)}{N_h}\right)\left(-\mu_h\left(S_h - S_h^* + I_h - I_h^* + R_h - R_h^*\right)\right.$$

$$\left. - d_h\left(I_h - I_h^*\right)\right)$$

$$
\begin{aligned}
= & -\frac{\mu_h \left((S_h - S_h^*) - (R_h - R_h^*) \right)^2}{N_h} - \frac{(d_h + \mu_h)(I_h - I_h^*)^2}{N_h} \\
& - \frac{(d_h + 2\mu_h)(S_h - S_h^*)(I_h - I_h^*)}{N_h} \\
& - \frac{(d_h + 2\mu_h)(I_h - I_h^*)(R_h - R_h^*)}{N_h},
\end{aligned}
\tag{13}
$$

so we can write

$$
\begin{aligned}
L' = & -\frac{\mu_h \left((S_h - S_h^*) - (R_h - R_h^*) \right)^2}{N_h} - \frac{(d_h + \mu_h)(I_h - I_h^*)^2}{N_h} \\
& + \frac{N_h^*(d_h + 2\mu_h)}{\beta_h(I_h^* + R_h^*)} \left(\frac{\beta_{a_2} I_a^*(I_h - I_h^*)(S_h - S_h^*)}{N_a^* I_h^*} \right) \\
& - \left(\frac{N_h^*(d_h + 2\mu_h)}{\beta_h(I_h^* + R_h^*)} \right) \left(\frac{\beta_{a_2} I_a^* S_h (I_h - I_h^*)^2}{N_a^* I_h I_h^*} + \frac{\beta_h S_h^* (I_h - I_h^*)^2}{N_h^* N_h} \right) \\
& - \frac{(d_h + 2\mu_h)}{2\rho_h} \left(1 + \frac{S_h^*}{I_h^* + R_h^*} \right) \left(\frac{2\mu_h (R_h - R_h^*)^2}{N_h} + \frac{N_h'(R_h - R_h^*)^2}{N_h^2} \right) \\
& + 2DN_h'(N_h - N_h^*) + 2E\rho_h (I_h - I_h^*)(R_h - R_h^*) - 2E\mu_h (R_h - R_h^*)^2.
\end{aligned}
$$

Now rearranging the terms as in (13), we obtain

$$
\begin{aligned}
L' = & -\frac{\mu_h \left((S_h - S_h^*) - (R_h - R_h^*) \right)^2}{N_h} - \frac{(d_h + \mu_h)(I_h - I_h^*)^2}{N_h} \\
& + \frac{N_h^*(d_h + 2\mu_h)}{\beta_h(I_h^* + R_h^*)} \left(\frac{\beta_{a_2} I_a^*(I_h - I_h^*)(S_h - S_h^*)}{N_a^* I_h^*} \right) \\
& - \left(\frac{N_h^*(d_h + 2\mu_h)}{\beta_h(I_h^* + R_h^*)} \right) \left(\frac{\beta_{a_2} I_a^* S_h (I_h - I_h^*)^2}{N_a^* I_h I_h^*} + \frac{\beta_h S_h^* (I_h - I_h^*)^2}{N_h^* N_h} \right) \\
& - \frac{(d_h + 2\mu_h)}{2\rho_h} \left(1 + \frac{S_h^*}{I_h^* + R_h^*} \right) \left(\frac{2\mu_h (R_h - R_h^*)^2}{N_h} + \frac{N_h'(R_h - R_h^*)^2}{N_h^2} \right) \\
& - 2D\mu_h \left((S_h - S_h^*) - (R_h - R_h^*) \right)^2 - 2D(d_h + 2\mu_h)(I_h - I_h^*)^2 \\
& - 2D(d_h + 2\mu_h)(S_h - S_h^*)(I_h - I_h^*) - 2D(d_h + 2\mu_h)(I_h - I_h^*)(R_h - R_h^*) \\
& + 2E\rho_h (I_h - I_h^*)(R_h - R_h^*) - 2E\mu_h (R_h - R_h^*)^2.
\end{aligned}
$$

At this point we can see that most terms of L' are negative semi-definite in Ω_h, except for the third term, some of the ones involving parameters D and E, and potentially the fifth term involving N_h'. To deal with this term we utilize the assumption that $\mu_h > d_h$, and

obtain

$$\frac{2\mu_h \left(R_h - R_h^*\right)^2}{N_h} + \frac{N_h' \left(R_h - R_h^*\right)^2}{N_h^2} = \frac{\left(2\mu_h N_h + N_h'\right)\left(R_h - R_h^*\right)^2}{N_h^2}$$

$$= \frac{\left(2\mu_h (S_h + I_h + R_h) + \Lambda_h - \mu_h (S_h + I_h + R_h) - d_h I_h\right)\left(R_h - R_h^*\right)^2}{N_h^2}$$

$$= \frac{\left(\mu_h (S_h + R_h) + \Lambda_h + (\mu_h - d_h) I_h\right)\left(R_h - R_h^*\right)^2}{N_h^2} \geq 0.$$

Now we can choose the values of D and E in such a way that all the remaining terms that may not be negative semi-definite cancel out. In particular, let

$$\frac{N_h^* (d_h + 2\mu_h)}{\beta_h \left(I_h^* + R_h^*\right)} \left(\frac{\beta_{a_2} I_a^*}{N_a^* I_h^*}\right) - 2D(d_h + 2\mu_h) = 0 \quad \text{and}$$

$$- 2D\left(d_h + 2\mu_h\right) + 2E\rho_h = 0.$$

This implies

$$D = \frac{N_h^* \beta_{a_2} I_a^*}{2\beta_h N_a^* I_h^* \left(I_h^* + R_h^*\right)} > 0 \quad \text{and}$$

$$E = \frac{N_h^* \beta_{a_2} I_a^* (d_h + 2\mu_h)}{2\rho_h \beta_h N_a^* I_h^* \left(I_h^* + R_h^*\right)} > 0,$$

and with these parameters L' is negative semi-definite in Ω_h, with $L' = 0$ if and only if $S_h = S_h^*, I_h = I_h^*, R_h = R_h^*$. Thus the largest compact invariant set in $\{(S_h, I_h, R_h) \in \Omega_h : L' = 0\}$ is $\{E_h^*\}$, therefore, by the LaSalle invariance principle $\{E_h^*\}$ is globally asymptotically stable in Ω_h (LaSalle, 1976; LaSalle & Lefschetz, 1961). Now Corollary 3.3 implies that $\mathcal{E}_2$ is a globally asymptotically stable equilibrium of (1a)–(1f). ∎

Note that our theorem shows that if the disease is endemic in the reservoir population, and $\beta_{a_2} > 0$, then irrespective of the reproductive number $\mathcal{R}_{0_h}$ the disease becomes endemic in the human population (if $\mu_h > d_h$).

3.2. Disease-free equilibrium in the reservoir population

The other equilibrium of the reservoir system (1a)–(1c) is the disease-free equilibrium given by $E_a = (S_a^0, I_a^0, R_a^0) = (\Lambda_a/\mu_a, 0, 0)$. By Theorem 3.1 we know that this equilibrium is globally asymptotically stable if $\mathcal{R}_{0_a} \leq 1$. In this case, $I_a(t) \to 0$ as $t \to \infty$, so in the limit there is no infection in population H coming from the reservoir population A. Thus, in the limit, dynamics in population H become exactly the same as the general dynamics in the reservoir population, and Corollary 3.3 applies. Thus we have the following results.

Proposition 3.6: *Assume that $\mathcal{R}_{0_a} \leq 1$, so the disease dies out in the reservoir population. Additionally, let $\mathcal{R}_{0_h} \leq 1$. Then the disease-free equilibrium $\mathcal{E}_0 = (\Lambda_a/\mu_a, 0, 0, \Lambda_h/\mu_h, 0, 0)$ of (1a)–(1f) is globally asymptotically stable in Ω.*

Proposition 3.7: *Assume that $\mathcal{R}_{0_a} \leq 1$, $\mathcal{R}_{0_h} > 1$ and $\mu_h > d_h$. Then the equilibrium $\mathcal{E}_2 = (\Lambda_a/\mu_a, 0, 0, S_h^*, I_h^*, R_h^*)$ of (1a)–(1f) is globally asymptotically stable in Ω. (Note that (S_h^*, I_h^*, R_h^*) are given by the same expressions as (2a)–(2c) with the parameters corresponding to population H.)*

4. Numerical results and possible modifications to the model

In this section we present some numerical results related to the model (1a)–(1f) with animals as the reservoir population A and humans represented as population H. Figure 1 shows the results of a numerical simulation of (1a)–(1f) using MATLAB's `ode45` and the parameters $\Lambda_a = 152500/3$, $\mu_a = 1/8$, $\rho_a = 1/20$, $d_a = 1/30$, $\Lambda_h = 2900/6$, $\mu_h = $
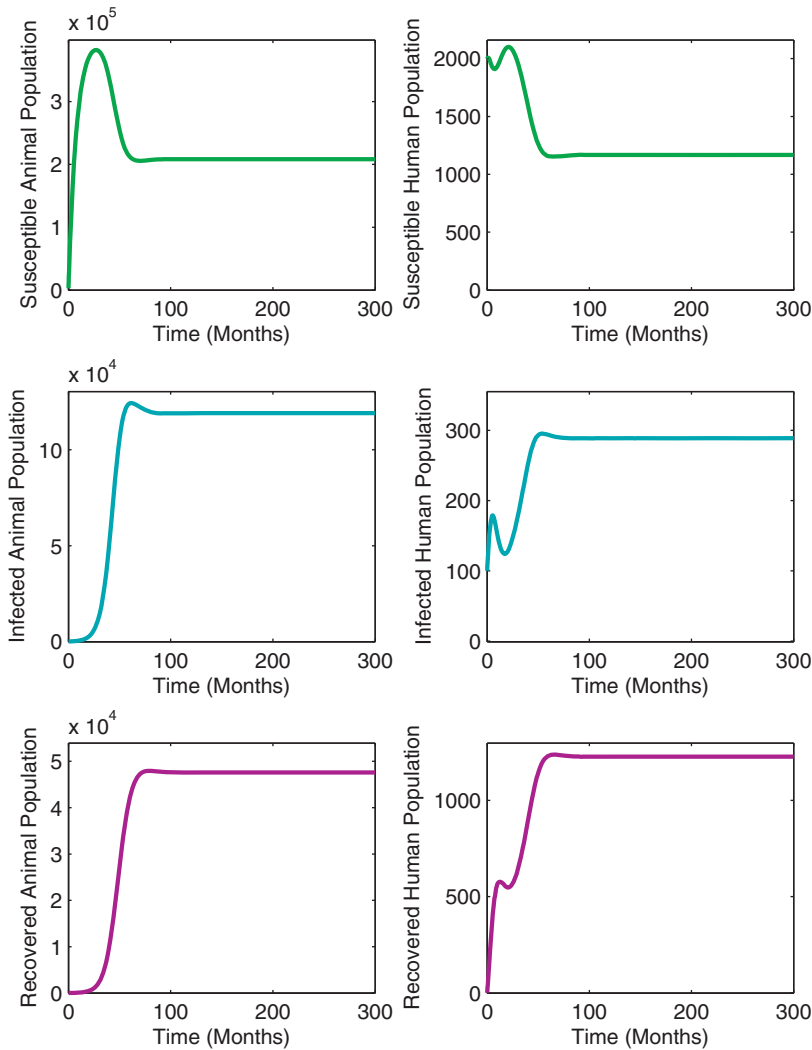

Figure 1. The above shows the results for a simulation with all parameters constant and the criteria for Theorem 3.5 met.

$1/6$, $\rho_h = 17/24$, $d_h = 1/8$ individuals per month and $\beta_h = 31/24$, $\beta_{a_1} = 3/8$ and $\beta_{a_2} = 41/120$ as the contact rates. The initial values used were $S_h^0 = 2000$, $I_h^0 = R_h^h = R_a^0 = 0$, $S_a^0 = 30000$ and $I_a^0 = 1000$. These are artificial values and are used only for illustration purposes. Under these conditions, the endemic equilibrium of (1a)–(1f) is globally asymptotically stable.

We used monkeypox as a motivating example for our next simulation. Since there is no longer any vaccination against smallpox and this vaccine provided some immunity against monkeypox, there is waning herd immunity against monkeypox (Hutin et al., 2001; Levine et al., 2007; Lloyd-Smith et al., 2009; McCollum & Damon, 2014; Nolen et al., 2016; Rimoin & Graham, 2011; Rimoin et al., 2007, 2010). Thus, for the next simulation, we assume that as time goes on there is an increasing likelihood that a human will get infected when they come into contact with an infected animal. For this simulation, we use $\beta_{a_2}(t) = 1/(1 + 9\,e^{-t})$. Figure 2 shows the results of a numerical simulation with this
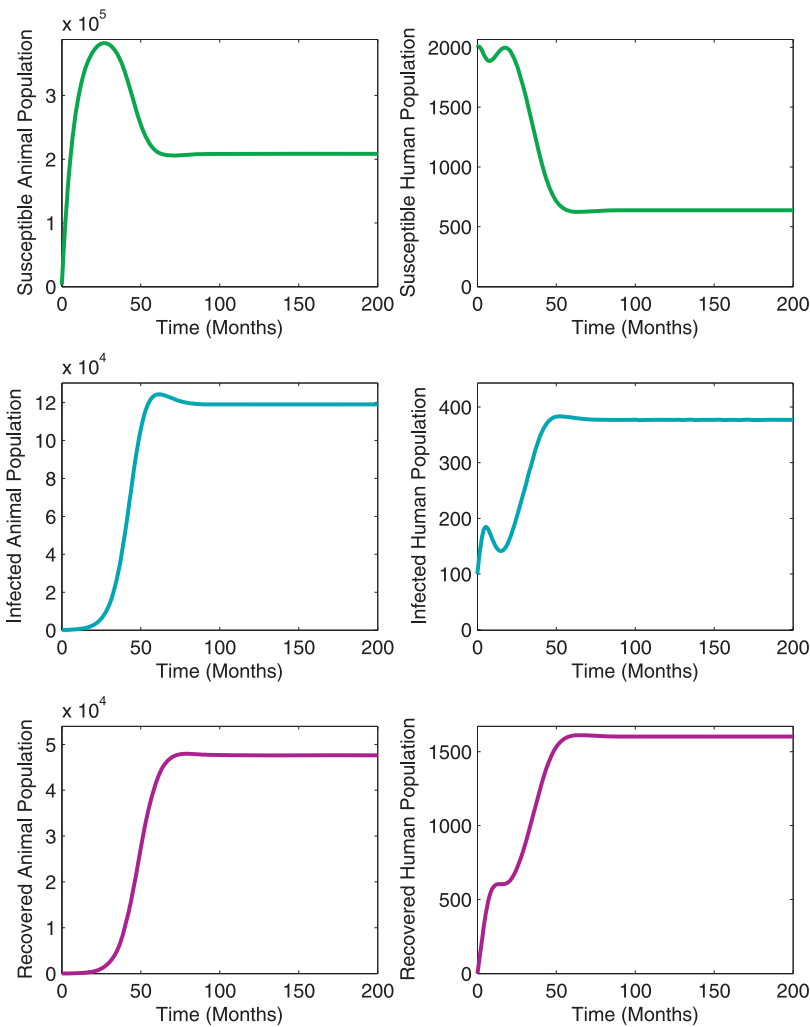

Figure 2. The results for a simulation with all parameters constant except $\beta_{a_2}(t)$ which is an increasing function of time.

$\beta_{a_2}(t)$ and all other parameters the same as for Figure 1. The analysis for our asymptotically autonomous system is still valid because $\beta_{a_2}(t) \to 1$ as $t \to \infty$ and so if we define $g(t) := \beta_{a_2}(t)I_a(t)/N_a(t)$, then $g(t) \to I_a^e/N_a^e$ as $t \to \infty$. Since $\beta_{a_2} \to 1$, it makes sense that Figure 2 shows the system approaching a higher I_h^* value than in Figure 1.

In the proof of the global asymptotic stability for the co-existence equilibrium, we assumed that $\mu_a > d_a$ and $\mu_h > d_h$. However, even if we break both of those conditions, the numerical results still seem to indicate that the co-existence endemic equilibrium of (1a)–(1f) is globally asymptotically stable. Figure 3 shows the results of a simulation of this kind, with $\Lambda_a = 152500/3$, $\mu_a = 1/25$, $\rho_a = 1/20$, $d_a = 1/10$, $\Lambda_h = 2900/6$, $\mu_h = 1/9$, $\rho_h = 17/24$, $d_h = 1/6$ individuals per month and $\beta_h = 31/24$, $\beta_{a_1} = 3/8$ and $\beta_{a_2} =$
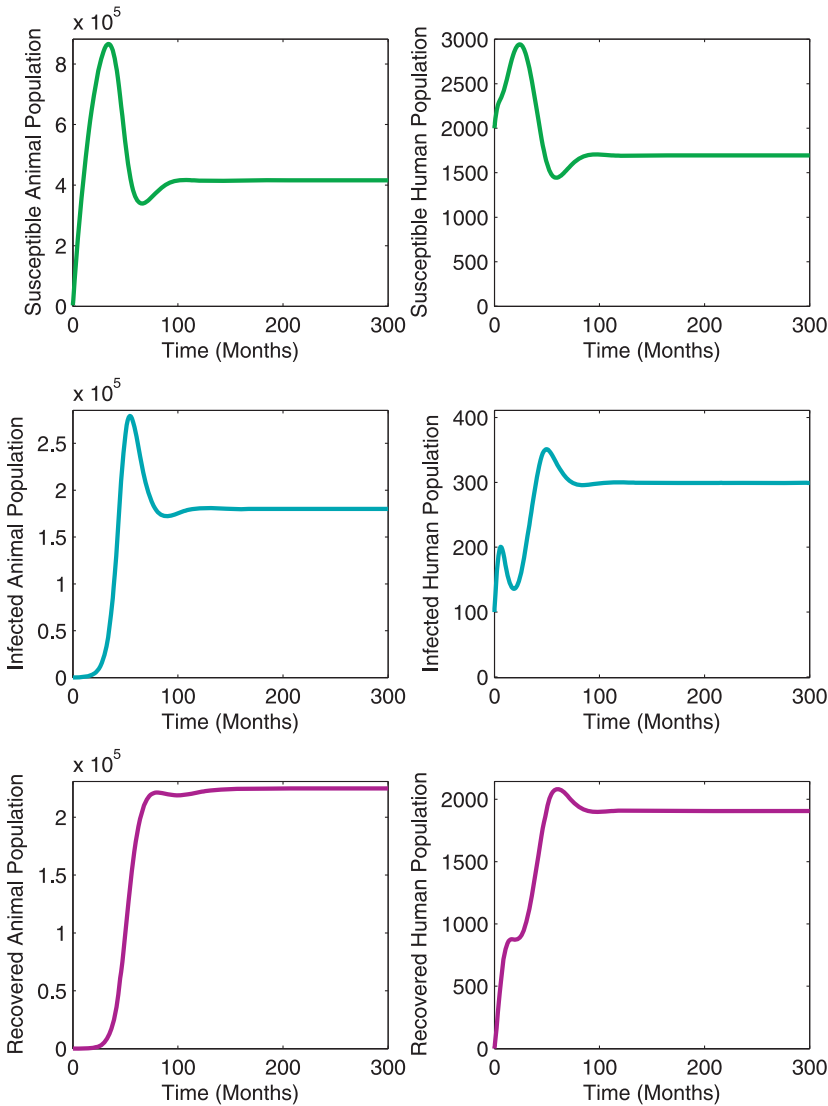

Figure 3. The results of a simulation with all parameters constant, but with $\mu_a < d_a$ and $\mu_h < d_h$.

41/120 as the contact rates. The initial values used are the same as those in the previous two sets of results.

We also simulate a more complicated scenario where there are multiple reservoir populations. Suppose there are n such reservoir populations, $A_1, A_2, \ldots, A_n$ and one population H as in the previous model. S_h, I_h, R_h and N_h are defined as before with S_{a_i}, I_{a_i} and R_{a_i} representing the susceptible, infected and recovered individuals in population A_i, for $i = 1, 2, \ldots, n$, with the total number of individuals in population A_i being given as N_{a_i}. Susceptible individuals in A_i are recruited through migration and birth at the rate Λ_{a_i} and susceptible individuals in H are recruited at a rate of Λ_h. We represent the death rates from disease in population A_i by d_{a_i} and the death rate by disease in population H as d_h. Further, we assume μ_{a_i}, μ_h are the natural death rates for A_i and H, respectively, and ρ_{a_i}, ρ_h be the recovery rates with permanent immunity for A_i and H, respectively. It is assumed that no one in population H can infect any individual in any A_i population, while individuals in any A_i population can infect those in H on suitable contact. We assume there is no cross-infection between A_i and A_j when $i \neq j$. Disease transmission is modelled using standard incidence, assuming a constant (density-independent) contact rate both within and across the two populations resulting in infection rates

$$f_{a_i}(S_{a_i}, I_{a_i}, R_{a_i}) = \frac{\beta_{a_{i1}} I_{a_i}}{N_{a_i}} S_{a_i}, \quad \text{for } i = 1, 2, \ldots, n, \text{ and}$$

$$f_h(S_{a_1}, I_{a_1}, R_{a_1}, \ldots, S_{a_n}, I_{a_n}, R_{a_n}, S_h, I_h, R_h) = \left(\left(\sum_{i=1}^{n} \frac{\beta_{a_{i2}} I_{a_i}}{N_{a_i}} \right) + \frac{\beta_h I_h}{N_h} \right) S_h,$$

where $\beta_{a_{i1}}$ is the effective contact rate within population A_i, $\beta_{a_{i2}}$ is the effective contact rate between populations A_i and H and β_h is the effective contact rate within population H. We assume that, for $i = 1, 2, \ldots, n$, $\Lambda_{a_i}, \Lambda_h, \mu_{a_i}, \mu_h, \rho_{a_i}, \rho_h$ are positive parameters and $d_{a_i}, d_h, \beta_{a_{1i}}, \beta_{a_{2i}}$ and β_h are non-negative parameters. Specifically, this leads to the following model. For $i = 1, 2, \ldots, n$,

$$\frac{dS_{a_i}}{dt} = \Lambda_{a_i} - \mu_{a_i} S_{a_i} - \frac{\beta_{a_{i1}} I_{a_i}}{N_{a_i}} S_{a_i}, \tag{14a}$$

$$\frac{dI_{a_i}}{dt} = \frac{\beta_{a_{1i}} I_{a_i}}{N_{a_i}} S_{a_i} - (\mu_{a_i} + \rho_{a_i} + d_{a_i}) I_{a_i}, \tag{14b}$$

$$\frac{dR_{a_i}}{dt} = \rho_{a_i} I_{a_i} - \mu_{a_i} R_{a_i}, \tag{14c}$$

$$\frac{dS_h}{dt} = \Lambda_h - \mu_h S_h - \left(\left(\sum_{i=1}^{n} \frac{\beta_{a_{i2}} I_{a_i}}{N_{a_i}} \right) + \frac{\beta_h I_h}{N_h} \right) S_h, \tag{14d}$$

$$\frac{dI_h}{dt} = \left(\left(\sum_{i=1}^{n} \frac{\beta_{a_{i2}} I_{a_i}}{N_{a_i}} \right) + \frac{\beta_h I_h}{N_h} \right) S_h - (\mu_h + \rho_h + d_h) I_h, \tag{14e}$$

$$\frac{\mathrm{d}R_h}{\mathrm{d}t} = \rho_h I_h - \mu_h R_h. \tag{14f}$$

Let

$$\Omega_{a_i} = \left\{ (S_{a_i}, I_{a_i}, R_{a_i}) \in \mathbb{R}^3_+ : S_{a_i} \geq 0, \ I_{a_i} \geq 0, \ R_{a_i} \geq 0, \ S_{a_i} + I_{a_i} + R_{a_i} \leq \frac{\Lambda_{a_i}}{\mu_{a_i}} \right\}$$

and

$$\Omega_h = \left\{ (S_h, I_h, R_h) \in \mathbb{R}^3_+ : S_h \geq 0, \ I_h \geq 0, \ R_h \geq 0, \ S_h + I_h + R_h \leq \frac{\Lambda_h}{\mu_h} \right\}.$$

Then for $i = 1, 2, \ldots, n$, the set $\tilde{\Omega} = \Omega_{a_1} \times \Omega_{a_2} \times \cdots \times \Omega_{a_n} \times \Omega_h$ is positively invariant under the dynamics of (14a)–(14f) and solutions with initial conditions in $\tilde{\Omega}$ exist globally.

Define $E_{a_i}^{(t)} := (S_{a_i}^{(t)}, I_{a_i}^{(t)}, R_{a_i}^{(t)})$ and $E_{a_i}^e := (S_{a_i}^e, I_{a_i}^e, R_{a_i}^e)$ for $i = 1, 2, \ldots, n$. Depending on the parameters, $E_{a_i}^e$ is either the disease-free equilibrium or the endemic equilibrium. By the structure of the model in (14a)–(14f) – with animals uninfected by humans and each animal population independent, that is, unable to infect any other animal population – we have that $E_{a_i}^{(t)} \to E_{a_i}^e$ for $i = 1, 2, \ldots, n$, and each $E_{a_i}^e$ is globally asymptotically stable by Theorems 3.1 and 3.2 under appropriate conditions. Thus, it is straightforward to extend the results of the equilibrium analysis for (1a)–(1f) and we have the following corollary.

Corollary 4.1: *If there exists an $i \in 1, 2, \ldots, n$ such that $\mathcal{R}_{0_{a_i}} > 1$, $\mu_{a_i} > d_{a_i}$ and $\beta_{a_{i2}} > 0$, and $\mu_h > d_h$, then the unique endemic equilibrium $\tilde{\mathcal{E}} = (E_{a_1}^e, \ldots, E_{a_n}^e, E_h^*)$ of (14a)–(14f) is globally asymptotically stable in the interior of $\tilde{\Omega}$.*

In the simplest scenario for this model, we assume $i = 2$. Figure 4 shows the results of an epidemic simulation with two animal populations and one human population. The initial values used for this simulation are $S_{a_1}^0 = 3000$, $I_{a_1}^0 = 100$, $S_{a_2}^0 = 2500$, $I_{a_2}^0 = 40$, $S_h^0 = 2000$, $I_h^0 = 100$ and $R_{a_1}^0 = R_{a_2}^0 = R_h^0 = 0$. The contact rates are $\beta_{a_{11}} = 1/4$, $\beta_{a_{21}} = 1/9$, $\beta_{a_{12}} = 1/8$, $\beta_{a_{22}} = 1/11$ and $\beta_h = 31/24$. The parameter values, with units of individuals per month, are $\Lambda_h = 2900/6$, $\mu_h = 1/6$, $\rho_h = 17/24$, $d_h = 1/8$, $\Lambda_{a_1} = 152500/2$, $\mu_{a_1} = 1/8$, $\rho_{a_1} = 1/20$, $d_{a_1} = 1/30$, $\Lambda_{a_2} = 500$, $\mu_{a_2} = 1/25$, $\rho_{a_2} = 1/10$ and $d_{a_2} = 1/30$.

Looking at the system (1a)–(1f) and revisiting our assumptions, the infection in the human population depends on infection in both populations. In Figure 5 we see the change in I_h^*/N_h^* as $\mathcal{R}_{0_a}$ changes. The values used for this figure were $\Lambda_a = 152500/3$, $\mu_a = 1/25$, $\rho_a = 1/20$, $d_a = 1/10$, $\Lambda_h = 2900/6$, $\mu_h = 1/9$, $\rho_h = 17/24$, $d_h = 1/6$ individuals per month and $\beta_{a_2} = 0.3$. In order to get the change in $\mathcal{R}_{0_a}$, we use a range of β_{a_1} values, namely $0 \leq \beta_{a_1} \leq 1.9$. The initial values used were $S_h^0 = 2000$, $I_h^0 = R_h^h = R_a^0 = 0$, $S_a^0 = 3000$ and $I_a^0 = 1000$. (These values are simply for illustration purposes.) We notice that I_h^*/N_h^* increases after $\mathcal{R}_{0_a} = 1$. When $\beta_h = 1/3$ we have $\mathcal{R}_{0_h} \approx 0.338$ and when $\beta_h = 1/9$ we have $\mathcal{R}_{0_h} \approx 0.113$. Even if $\beta_h = 0$, when $\mathcal{R}_{0_a} \geq 1$, we see there is infection in the human population so limiting infection from humans to humans is not enough to fully mitigate this disease in humans. In all three curves there is a sharp increase in I_h^*/N_h^* for $1 \leq \mathcal{R}_{0_a} \leq 2$ so that the differences between the different I_h^*/N_h^* curves are nearly indistinguishable the closer $\mathcal{R}_{0_a}$ is to 1. While we do not know what β_{a_1} is in reality, this shows
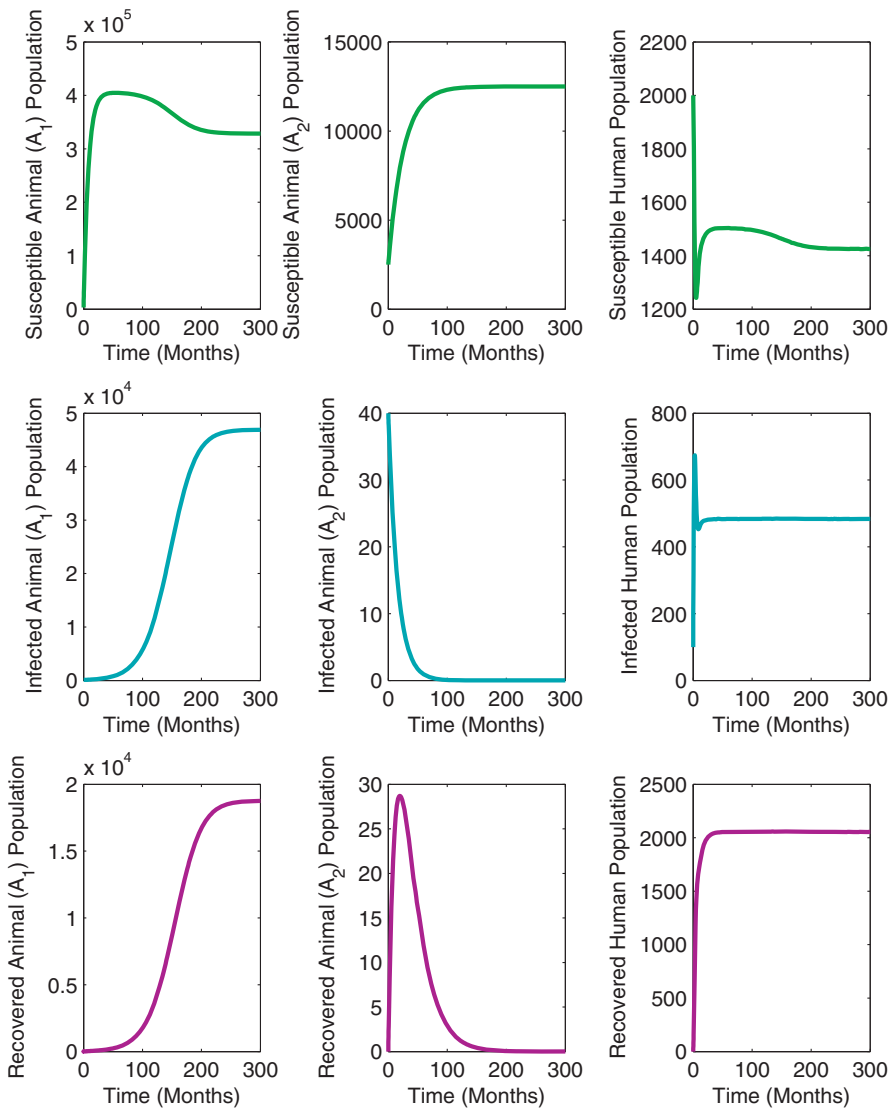
Figure 4. The results of a simulation with two animal populations as in (14a)–(14f) for $i = 2$. The first two columns show the results for populations A_1 and A_2, respectively. The last column shows the results for the human population.

that if it is high enough for there to be endemic infection in the animal population, there will be some level of infection in the human population. Figure 6 uses the same parameters as in 5, but with $\beta_h \geq 1$. Specifically, $\beta_h = 1$ where $\mathcal{R}_{0_h} \approx 1.014$, $\beta_h = 1.5$ when we have $\mathcal{R}_{0_h} \approx 1.521$ and $\beta_h = 2$ when $\mathcal{R}_{0_h} \approx 2.028$. As expected, the increase in β_h results in higher values for I_h^*/N_h^* than in Figure 5. While difficult, it is important to continue studying monkeypox in both human and animal populations since infection in the animal population has a substantial impact on infection in the human population.

In Figure 7, we use the same parameters as in Figure 5, but we consider I_a^*/N_a^* as a function of $\mathcal{R}_{0_a}$. Since we changed β_h to obtain three curves in Figure 5 but β_h has no
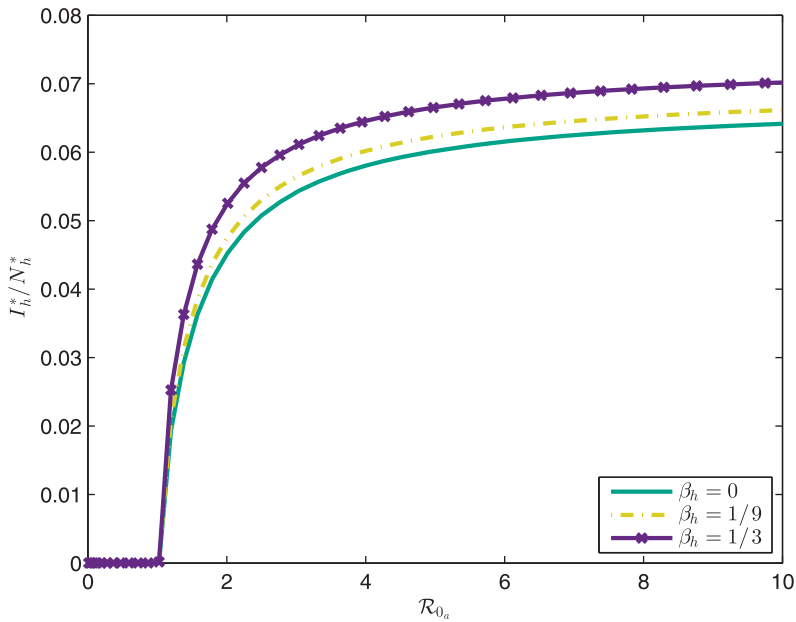
Figure 5. The above illustrates the ratio I_h^*/N_h^* as a function of $\mathcal{R}_{0_a}$. The lowest curve represents the case when $\beta_h = 0$ so we see that there is still infection in the human population as long as $\mathcal{R}_{0_a} \geq 1$.
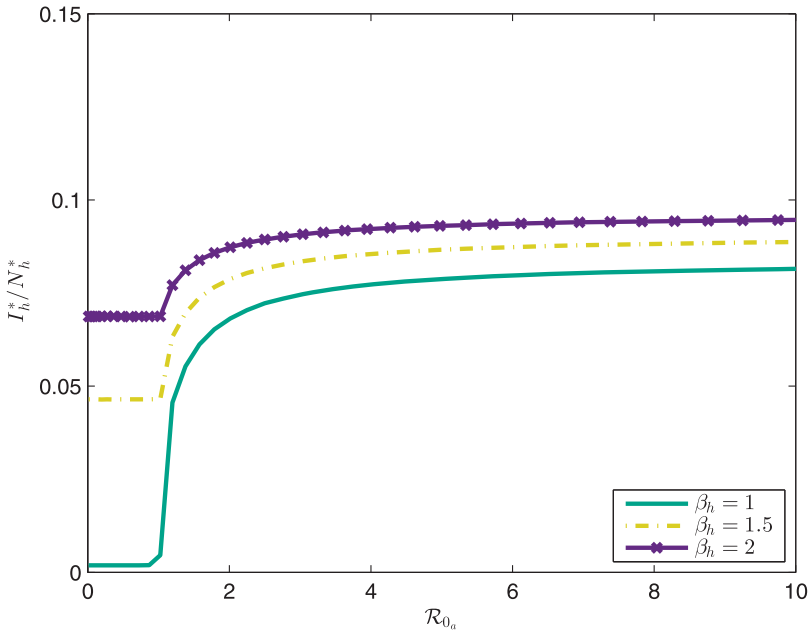

Figure 6. The above illustrates the ratio I_h^*/N_h^* as a function of $\mathcal{R}_{0_a}$ for $\mathcal{R}_{0_h} > 1$.

role in the value of I_a^*/N_a^*, the curve in Figure 7 is the same regardless of β_h. We note that, as would be expected, changing $\mathcal{R}_{0_a}$ has a greater effect on I_a^*/N_a^* than it did on I_h^*/N_h^* reflected in Figure 5.
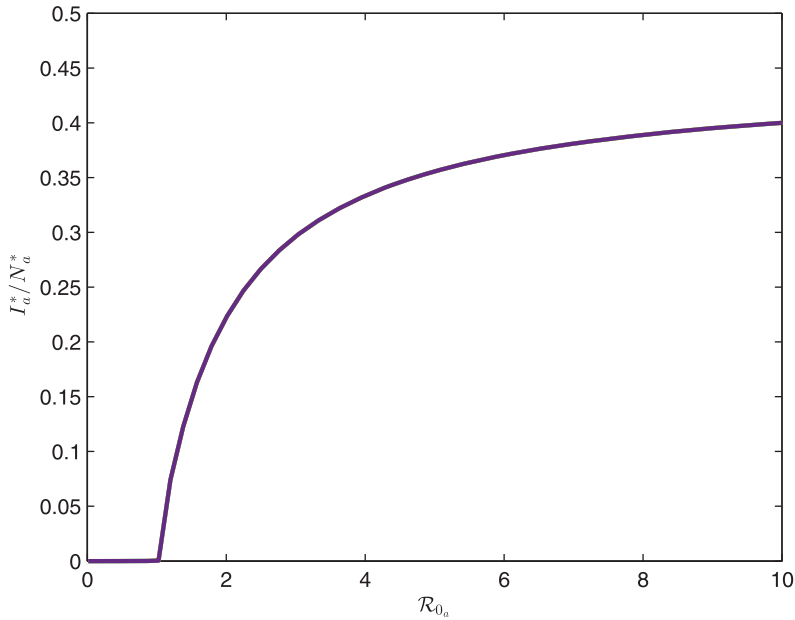
Figure 7. The above illustrates I_a^*/N_a^* as a function of $\mathcal{R}_{0_a}$.
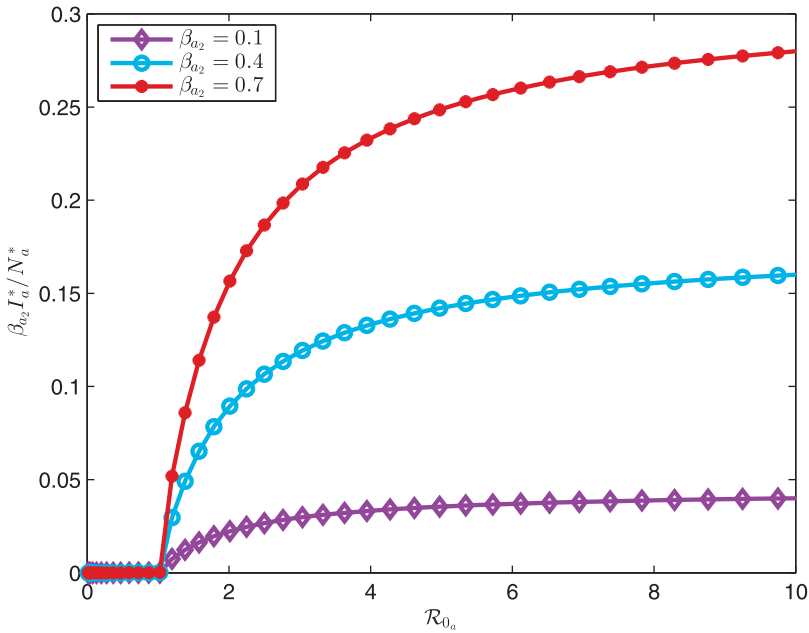

Figure 8. The above illustrates $\beta_{a_2} I_a^*/N_a^*$ as a function of $\mathcal{R}_{0_a}$ for three different values of β_{a_2} with $\beta_h = 0$.

We also know that changes in β_{a_2} impact the animal-to-human cross-infection. Figure 8 shows $\beta_{a_2} I_a^*/N_a^*$ as a function of $\mathcal{R}_{0_a}$ for the same values as in Figure 5 with $\beta_h = 0$. These results indicate that controlling the disease in the human population also depends on reducing the value of β_{a_2}, as would be expected. Continuing to educate people in areas

affected by monkeypox on recognizing the symptoms and proper handling of infected animals is crucial in limiting the spread of this disease among humans.

Future modifications to the model include possibly making the migration and birth rates functions of time, $\Lambda_a(t)$ and $\Lambda_h(t)$, in addition to experimenting with different functions for $\beta_{a_2}(t)$. These adjustments may more accurately convey seasonal influences as well as other environmental influences and trends.

Acknowledgments

Disclosure statement

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