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LINKING POPULATION DYNAMICS AND DISEASE MODELS FOR MULTI-HOST PATHOGEN SYSTEMS: IMPLICATIONS FOR PATHOGEN AND SPECIES INVASION

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We consider models for the spread of disease in one or two species where density-dependent population dynamics can range from affecting primarily reproduction and juvenile survival to affecting death rates of adults. We show that disease and competition (both intra- and inter-specific) can interact to change the dynamics of a system, resulting in changes in species density, disease invasion and prevalence. Additionally, we show that the mechanism of competition between and within species can affect the ability of a disease to spread and persist. If density dependence acts only on reproduction and juvenile survival rates, disease is more likely to persist, while for the same system if competition acts solely on the survival rate of adults the disease is less likely to successfully invade. This has implications both for conservation and public health, especially as climate change and invasive species change community structure and as zoonotic diseases become more important.

Keywords: Lotka–Volterra Competition; Multi-Host SIS Disease Model; Basic Reproduction Number; Infected Coexistence; Standard Incidence.

1. Introduction

Understanding the mechanisms that drive the coexistence of competing species is an important goal in community ecology.¹ Theoretical and empirical investigations have shown that generalist pathogens or parasites infecting multiple host species can influence species diversity and community structure.^{2–7} In Refs. 2 and 8, nonspatial, and spatial models, respectively, the spread of Barley/Cereal Yellow Dwarf Viruses among multiple grass hosts were analyzed, suggesting that this class of multi-host

pathogens can mediate the outcome of inter-specific competition, facilitating and maintaining invasion by novel species. In Ref. 9, using a competition and disease model, the authors argue that it is likely that a shared disease, parapoxvirus, in addition to competition for space and food, is the impetus for the continued decline of the native red squirrel in the United Kingdom in the presence of the introduced gray squirrel. A review of empirical studies in Ref. 10 finds strong evidence for parasite-induced extinction of one species (usually a native species replaced by an introduced exotic) induced by reservoir effects and apparent competition.

Experimental research also shows that the composition of the host community can affect pathogen dynamics via dilution or amplification affects.^{5,7} Thus, the interaction between community and disease ecology can help us understand the structure of a biological system and the reasons why species coexist with each other and why pathogens persist.¹ Although often difficult to quantify empirically, host-pathogen interactions can be studied through mathematical models that combine elements of population dynamics and epidemiology.^{2,11-13} Such models can give important qualitative insight into the effects of pathogens on plant and animal populations and the factors that influence species coexistence or exclusion in communities.¹⁴⁻¹⁶

Two-species models in which one or both species share a common pathogen and do not interact competitively have been discussed in several pioneering papers.¹⁴⁻¹⁹ In Ref. 20, the authors considered an SIRS epidemic model of two competing species using standard incidence or frequency-dependent disease incidence. Their model assumes that inter-specific competition affects mortality alone and that there is no death due to disease. Under these conditions, the authors in Ref. 20 derived stability conditions for all possible equilibria. In Ref. 19, the authors considered several models with frequency-dependent disease transmission and two competing species. The authors analyzed the stability for all equilibria when density dependence affected adult mortality alone and did a partial analysis when density dependence affects only birth. However, the general model with density dependence acting on both adult mortality and reproduction was not analyzed. The authors of Ref. 21 consider a model with Lotka-Volterra competition between two species which share a common pathogen. Density-dependent disease transmission is used in the model, which in its complete generality is intractable. Both intra- and inter-specific density-dependent and disease-related death rates are considered; however, the birth rates are unaffected by inter-specific competition. The authors derive conditions that guarantee the persistence of hosts, the pathogen, or both and complex behaviors of the model are demonstrated.

In Ref. 22, the authors consider a two-species model with density-dependent disease transmission in which both species compete via density-dependent reproduction, while death rates are density independent. They analyzed the model from an ecological perspective, using the notions of forces of infection and invasion criteria to determine whether resident populations allow small invasions of other species to prosper or cause them to decay. As with previous models, the infected coexistence case proved impossible to be fully analyzed. A similar model is used for the red/gray

squirrel system discussed in Refs. 23 and 9. In Ref. 9, both intra-specific crowding and inter-specific competition were modeled causing density-dependent effects on reproduction but not on adult mortality. The authors point to two different sources as justification of this choice; documented negative correlations between squirrel density and squirrel productivity (but not adult survival) for both species, and documented reduced red squirrel recruitment (but no effect on adult mortality) in the presence of gray squirrels.

In this paper, we analyze a general one (see Sec. 2) and two (see Sec. 3) species model incorporating both competitive dynamics and standard incidence disease spread. In Ref. 24, stochastic models based on continuous time Markov chains (CTMC) and stochastic differential equations were constructed based on similar deterministic models that we consider in this paper. Branching process theory for the CTMC model is applied to estimate the probability of pathogen invasion when the population is near the disease-free state. Here we aim to understand the full spectrum of interactions of competitive dynamics between species with disease spread among species and the effect that this interaction has on pathogen invasion, persistence and the ultimate fate of populations.

When considering two competing populations without disease, competition can be thought of as having a general effect on the intrinsic growth rate, and differentiating between relative competitive effects on birth rates versus death rates is not necessary. However, when coupling a competition model (including the subcase of one species logistic growth) to a disease model, modelers must choose between competition acting solely on the death term solely on the birth term or a combination of the two. Since this choice has a direct effect on the basic reproduction number, care must be taken in incorporating competition in birth and death rates for the system being modeled, as the model structure could create artificial dependence on the sensitivity of the basic reproduction number to either the birth or the death rate. In many cases, this choice can significantly alter not only the basic reproduction number, \mathcal{R}_0 (see Sec. 4), but also can change the dynamics and outcome of the model, resulting in insights and predictions that may or may not be representative of the system being considered. We present results of stability analysis (see Sec. 5) and numerical simulations for model equilibria in terms of several simple ecologically relevant parameters. Throughout the paper, we illustrate the differences in dynamics between models that include competition in reproduction or competition in mortality with both analytical and numerical results.

2. One-Host Susceptible–Infected–Susceptible (SIS) Model

We start by considering a one species model which incorporates density-dependent species birth and death dynamics and standard incidence (also known as frequency dependent incidence) disease transmission. The variables S, I denote the density of susceptible and infected individuals, respectively, and $N = S + I$ is the total population density. The birth and death rates of each species are density dependent.

The model equations for the S and I variables are given as

$$\frac{dS}{dt} = bN \left(1 - \frac{\epsilon N}{\theta}\right) - dS \left(1 + \frac{(1-\epsilon)N}{\psi}\right) - \left(\frac{\beta SI}{N}\right) + \gamma I, \quad (2.1a)$$

$$\frac{dI}{dt} = \left(\frac{\beta SI}{N}\right) - dI \left(1 + \frac{(1-\epsilon)N}{\psi}\right) - (\gamma + \delta)I. \quad (2.1b)$$

Model (2.1) is for a directly transmitted disease. We assume that there is no vertical transmission of the pathogen and the disease does not impact reproduction. Thus, all individuals are born into the susceptible class. The parameter $\epsilon \in [0, 1]$ is the proportion of intra-specific competition that affects the birth and juvenile survival rate while $(1 - \epsilon)$ is the proportion that affects the death rate of the species. If $\epsilon = 0$, then density dependence affects only the death rate of adults. On the other hand, if $\epsilon = 1$, then density dependence decreases the reproduction rate, while the death rate is density independent.

We define parameters $\theta := \frac{Kb}{r}$ and $\psi := \frac{Kd}{r}$ so that the carrying capacity for the species is, $K = \frac{r\theta}{b} = \frac{r\psi}{d}$. Here, $r := b - d$ is the intrinsic *per capita* growth rate for the species, with b and d the intrinsic *per capita* birth and natural death rates, respectively, when no density dependence is incorporated. We assume that $b > d > 0$ and hence $r > 0$. The disease may shorten the life span of those infected, via the parameter $\delta \geq 0$; the disease-induced mortality rate. We will assume that the intrinsic growth rate is larger than the mortality rate due to disease, i.e., $r - \delta > 0$, so that the host cannot be driven extinct by the disease. The disease does not confer immunity, so individuals may recover and become infected again via the parameter $\gamma \geq 0$; the rate of recovery of infected individuals. Thus, the model is of type SIS. Finally, the parameter $\beta > 0$ is the transmission rate of the disease for standard incidence. The transmission term β is the product of the number of contacts per individual per unit time and the probability of contact with an infectious individual resulting in successful transmission of the disease.

Define $i := I/N$ to be the infected proportion for the species. Using the chain rule, the differential equation for i is computed as

$$\frac{di}{dt} = \frac{d}{dt} \left(\frac{I}{N} \right) = \frac{1}{N} \frac{dI}{dt} - \frac{I}{N^2} \frac{dN}{dt}.$$

Substituting (2.1a) and (2.1b) in the above, we can rewrite system (2.1) in the variables i (infected proportion) and N (total population size) as

$$\frac{dN}{dt} = \left[r \left(1 - \frac{N}{K}\right) - \delta i \right] N, \quad (2.2a)$$

$$\frac{di}{dt} = (1 - i)i(\beta - \delta) - i \left(r \left(1 - \frac{\epsilon N}{\theta}\right) + d + \gamma \right). \quad (2.2b)$$

In Ref. 19, the authors analyze model (2.2) with the additional assumption that the birth rate can be reduced due to infections, so that $b(1 - f)$ is a *per capita* birth

rate for infectives at very low population sizes. In our models (2.1) and (2.2), $f = 0$. In the rest of this section, we analyze model (2.2) from a different perspective than that in Ref. 19, by focusing on how varying the parameter $\epsilon \in [0, 1]$, and hence varying the distribution of density dependence between the birth and death rates, can significantly alter the long-term dynamics of the system.

2.1. The basic reproduction number and equilibria

We will assume that all parameters, except ϵ , of model (2.2) are fixed, and allow $\epsilon \in [0, 1]$ to vary. Using the next generation method²⁵ we can compute the basic reproduction number for model (2.2) as a function of the parameter ϵ as

$$\mathcal{R}_0(\epsilon) = \frac{\beta}{\delta + \gamma + b - r\epsilon} = \frac{\beta}{\delta + \gamma + b(1 - \epsilon) + d\epsilon}. \quad (2.3)$$

We note that the denominator of $\mathcal{R}_0(\epsilon)$, $\delta + \gamma + b - r\epsilon = \delta + \gamma + b(1 - \epsilon) + d\epsilon$ is positive and represents the length of the infectious period of the disease. For the special cases, $\epsilon = 1$ (density dependence in birth only), and $\epsilon = 0$ (density dependence affects death only), the basic reproduction number is

$$\mathcal{R}_0(\epsilon = 1) = \frac{\beta}{d + \delta + \gamma}, \quad (2.4a)$$

$$\mathcal{R}_0(\epsilon = 0) = \frac{\beta}{b + \delta + \gamma}. \quad (2.4b)$$

We observe from (2.3) that \mathcal{R}_0 is a strictly increasing function of ϵ , since

$$\frac{d\mathcal{R}_0}{d\epsilon} = \frac{\beta r}{(\delta + \gamma + b - r\epsilon)^2} > 0, \quad (2.5)$$

since all the parameters of the model are strictly positive or non-negative. In particular, from the assumption $r > 0$, we have from (2.4a), (2.4b) and (2.5) that for $\hat{\epsilon} \in (0, 1)$

$$\mathcal{R}_0(0) < \mathcal{R}_0(\hat{\epsilon}) < \mathcal{R}_0(1). \quad (2.6)$$

There are three possible cases to examine.

Case 1. $\mathcal{R}_0(0) < 1 < \mathcal{R}_0(1)$. Here $\mathcal{R}_0(\epsilon)$ for $\epsilon \in [0, 1]$ can be either less than, greater than or equal to 1 depending on the value of ϵ chosen.

Case 2. $\mathcal{R}_0(0) \geq 1$. In this case, $\mathcal{R}_0(\epsilon) > 1, \forall \epsilon \in (0, 1]$.

Case 3. $\mathcal{R}_0(1) \leq 1$. In this case, $\mathcal{R}_0(\epsilon) < 1, \forall \epsilon \in [0, 1)$.

For Cases 2 and 3, choice of ϵ will not change long-term disease persistence, although it may change transient dynamics and relative densities. In Case 1, choice of ϵ can significantly alter the disease dynamics of the system. This is the case that we will concentrate on in this paper. To analyze model (2.2) for the three cases

above, we introduce a critical threshold parameter ϵ^* defined as

$$\epsilon^* := \frac{\delta + \gamma + b - \beta}{r},$$

and allow ϵ^* to vary in the different cases.

Case 1. $\epsilon^* := \frac{\delta + \gamma + b - \beta}{r} \in (0, 1)$.

In this case, $\mathcal{R}_0(\epsilon = \epsilon^*) = 1$. If $\epsilon < \epsilon^*$, then $\mathcal{R}_0(\epsilon) < 1$, and if $\epsilon > \epsilon^*$, then $\mathcal{R}_0(\epsilon) > 1$. We note that $0 < \epsilon^* < 1$ implies that $0 < d + \gamma < \beta - \delta < b + \gamma$. In particular $\beta > \delta$. There are three possible equilibria (\bar{i}, \bar{N}) for model (2.2). These are

$$E_0 := (0, 0), \quad \text{trivial equilibrium,} \quad (2.7)$$

$$E_1 := (0, K), \quad \text{disease-free equilibrium (DFE),} \quad (2.8)$$

$$E_2 := \left(i^* = \frac{(\epsilon - \epsilon^*)r}{\beta - \delta + \delta\epsilon}, N^* = K \left(1 - \frac{\delta i^*}{r} \right) \right), \quad \text{endemic equilibrium.} \quad (2.9)$$

The equilibria E_0 and E_1 are always feasible. In this case, we have $\beta - \delta + \delta\epsilon > 0$, and we can show that $i^* < 1$ for all values of $\epsilon \in [0, 1]$. Thus, the only feasibility condition for E_2 is the condition $\epsilon > \epsilon^*$, which guarantees that $i^* > 0$.

The Jacobian of system (2.2) at E_0 is

$$J(E_0) = \begin{bmatrix} \beta - (\delta + \gamma + b) & 0 \\ 0 & r \end{bmatrix}. \quad (2.10)$$

The eigenvalues of $J(E_0)$ are $r > 0$ and $\beta - (\delta + \gamma + b) < 0$, since $\epsilon^* > 0$. Thus, the trivial equilibrium is a saddle and hence unstable.

The Jacobian of system (2.2) at E_1 is

$$J(E_1) = \begin{bmatrix} \beta - (\delta + \gamma + b) + r\epsilon & 0 \\ -\delta K & -r \end{bmatrix}. \quad (2.11)$$

The eigenvalues of $J(E_1)$ are $-r < 0$ and $\beta - (\delta + \gamma + b) + r\epsilon$. If $\epsilon < \epsilon^*$ (i.e., $\mathcal{R}_0(\epsilon) < 1$), the second eigenvalue $\beta - (\delta + \gamma + b) + r\epsilon < 0$ and the DFE E_1 is stable. On the other if $\epsilon > \epsilon^*$ (i.e., $\mathcal{R}_0(\epsilon) > 1$) then $\beta - (\delta + \gamma + b) + r\epsilon > 0$ and the DFE E_1 is a saddle and unstable.

Finally, we consider the local stability of the endemic equilibrium E_2 . The Jacobian of system (2.2) at E_2 is

$$J(E_2) = \begin{bmatrix} -i^*(\beta - \delta) & \frac{\epsilon r i^*}{N^*} \\ -\delta N^* & \delta i^* - r \end{bmatrix}. \quad (2.12)$$

The trace (Tr) and determinant (det) of $J(E_2)$ can be computed as

$$\text{Tr}(J(E_2)) = -(\beta - \delta)(i^*) + \delta i^* - r = -(\beta - \delta)(i^*) - \frac{rN^*}{K}, \quad (2.13)$$

$$\det(J(E_2)) = \frac{r^2 N^*(\epsilon - \epsilon^*)}{K}. \quad (2.14)$$

The condition $\beta > \delta$, the feasibility condition $\epsilon > \epsilon^*$ for E_2 (which implies $0 < i^* < 1$), and $0 < N^* < K$, guarantee that the trace, $\text{Tr}(J(E_2))$, is negative and the determinant is positive. Thus, if $\epsilon > \epsilon^*$ (i.e., $\mathcal{R}_0(\epsilon) > 1$) then E_2 is feasible and locally stable.

In Fig. 1, we illustrate our results for Case 1 numerically and we summarize our conclusions in the following Lemma.

Lemma 2.1. *For fixed positive parameter values $b, d, \theta, \psi, \beta$ and fixed non-negative parameter values δ, γ , under the assumption $\epsilon^* \in (0, 1)$, and the condition $0 \leq \epsilon \leq 1$, we have that*

- (1) *The basic reproduction number $\mathcal{R}_0(\epsilon)$ satisfies $\mathcal{R}_0(\epsilon^*) = 1$ where $\epsilon^* = (\delta + \gamma + b - \beta)/r$ and the inequality*

$$\mathcal{R}_0(0) = \frac{\beta}{b + \delta + \gamma} < \mathcal{R}_0(\epsilon) < \mathcal{R}_0(1) = \frac{\beta}{d + \delta + \gamma} \quad (2.15)$$

holds for $\epsilon \in (0, 1)$.

- (2) *The trivial equilibrium E_0 is a saddle.*
- (3) *The DFE $E_1 = (0, K)$ is unstable for $\epsilon > \epsilon^*$ when $\mathcal{R}_0(\epsilon) > 1$, but stable for $\epsilon < \epsilon^*$ when $\mathcal{R}_0(\epsilon) < 1$, i.e., the DFE undergoes a bifurcation at the critical value $\epsilon = \epsilon^*$.*

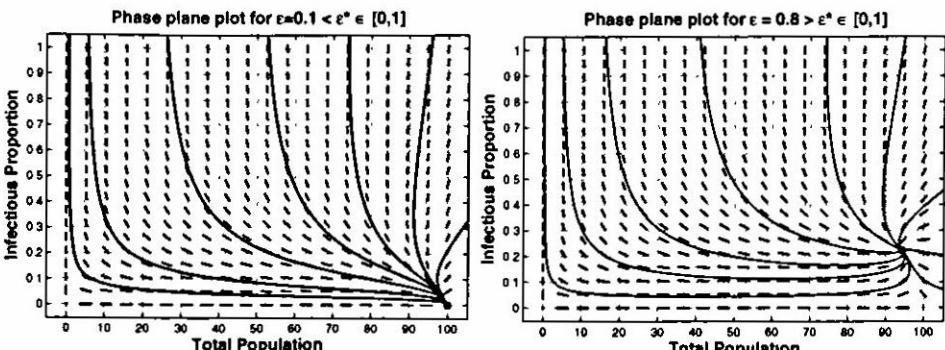


Fig. 1. Disease persistence depends on choice of ϵ . Left: Phase plane for $\epsilon^* \in [0, 1]$ and $\epsilon = 0.1 < \epsilon^*$. Competition affects death more than birth and the disease dies out. Right: Phase plane for $\epsilon^* \in [0, 1]$ and $\epsilon = 0.8 > \epsilon^*$. Competition affects birth more than death and the disease persists. For both figures, parameters are $\beta = 1, b = 0.8, d = 0.4, r = b - d = 0.4, K = 100, \delta = 0.1, \gamma = 0.2$ and $\epsilon^* = 0.25$.

- (4) The endemic equilibrium $E_2 = (i^*, N^*)$ is infeasible for $\epsilon < \epsilon^* (\mathcal{R}_0(\epsilon) < 1)$, but feasible and stable for $\epsilon > \epsilon^* (\mathcal{R}_0(\epsilon) > 1)$, i.e., the EE undergoes a bifurcation at the critical value $\epsilon = \epsilon^*$.

Next, we consider the second case in which $\mathcal{R}_0(0) \geq 1$. In this case, values of ϵ^* are restricted to

Case 2. $\epsilon^* := \frac{\delta + \gamma + b - \beta}{r} \leq 0$.

The basic reproduction number $\mathcal{R}_0(\epsilon) > 1$ for any $\epsilon \in (0, 1]$ since $\mathcal{R}_0(\epsilon)$ is an increasing function of ϵ . From the local stability analysis this implies that for all values of ϵ , the trivial equilibrium is unstable, the DFE is a saddle and the EE is always feasible and stable. When $\epsilon^* < 0$, there is an additional boundary equilibrium $E_3 := (i^+ = -\frac{r\epsilon^*}{\beta - \delta}, N^+ = 0)$ that exists and is feasible for this case. However, under the assumption $r > \delta$, E_3 is unstable. Figure 2 illustrates this case numerically.

Finally, the last case assumes that $\mathcal{R}_0(1) \leq 1$. In this case, values of ϵ^* are restricted to

Case 3. $\epsilon^* := \frac{\delta + \gamma + b - \beta}{r} \geq 1$.

The basic reproduction number $\mathcal{R}_0(\epsilon) < 1$ for any $\epsilon \in [0, 1)$ since $\mathcal{R}_0(\epsilon)$ is an increasing function of ϵ . From the local stability analysis this implies that for all values of ϵ , the trivial equilibrium is a saddle, the DFE is stable and the EE is always infeasible and unstable. Figure 3 illustrates this case numerically.

2.2. Biological significance

We now examine the value of ϵ^* biologically for the three different cases considered above.

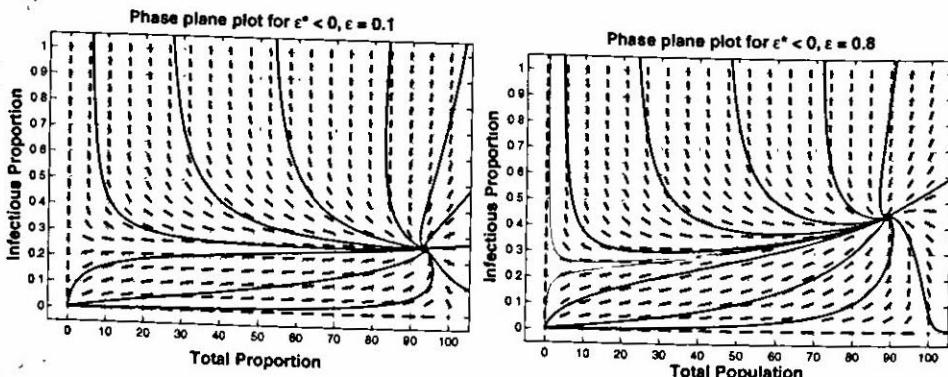


Fig. 2. The disease persists regardless of choice of ϵ . Left: Phase plane for $\epsilon^* < 0$ and $\epsilon = 0.1$ so competition affects mostly the death rate. Right: Phase plane for $\epsilon^* < 0$ and $\epsilon = 0.8$. Competition affects mostly the birth rate and the endemic disease level increases. For both figures, parameters are $\beta = 1.4$, $b = 0.8$, $d = 0.4$, $r = b - d = 0.4$, $K = 100$, $\delta = 0.1$, $\gamma = 0.2$ and $\epsilon^* = -0.75$.

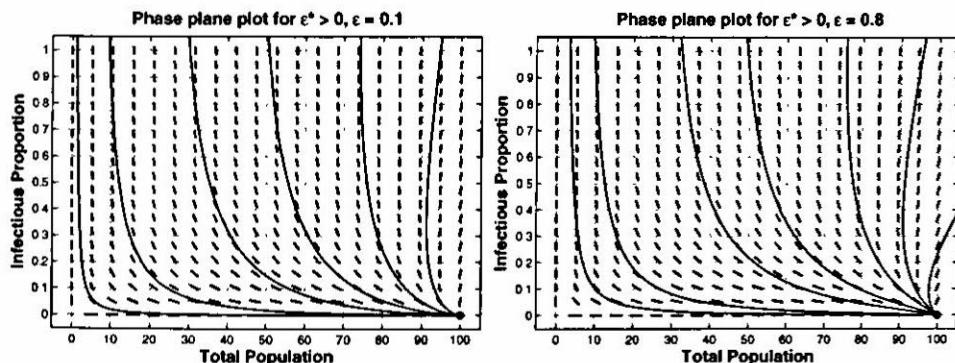


Fig. 3. The disease dies out regardless of choice of ϵ . Left: Phase plane for $\epsilon^* > 0$ and $\epsilon = 0.1$ so competition affects mostly the death rate. Right: Phase plane for $\epsilon^* > 0$ and $\epsilon = 0.8$. Competition affects mostly the birth rate. For both figures, parameters are $\beta = 0.5$, $b = 0.8$, $d = 0.4$, $r = b - d = 0.4$, $K = 100$, $\delta = 0.1$, $\gamma = 0.2$ and $\epsilon^* = 1.5$.

Case 1. $\epsilon^* \in (0, 1)$. If $\epsilon = 1$, i.e., if we have density-dependent birth and density-independent mortality in model (2.2), then $\epsilon > \epsilon^*$, the basic reproduction number $\mathcal{R}_0(\epsilon = 1) > 1$ and the pathogen will always invade. While, in the case of density-dependent mortality and density-independent birth, i.e., for $\epsilon = 0$, $\epsilon < \epsilon^*$, the basic reproduction number $\mathcal{R}_0(\epsilon = 0) < 1$ and the pathogen will not invade. For $\epsilon \in (0, 1)$, the pathogen may invade or not depending on how density dependence is distributed between the birth and the death rates. Thus, the critical threshold $\epsilon = \epsilon^*$, determines the ability of the pathogen to invade or not.

It is easy to show that when $0 < \epsilon^* < 1$ we have the condition

$$0 < \beta - (\delta + \gamma + d) < r.$$

Thus, if the transmission rate is larger than the adjusted loss (natural mortality plus disease-induced mortality plus recovery rate) of infected individuals, and if the difference between the two is bounded by the intrinsic growth rate r , then disease persistence is sensitive to choice of ϵ . The pathogen will invade if $\epsilon > \epsilon^*$, and the pathogen will not invade if $\epsilon < \epsilon^*$.

Case 2. $\epsilon^* \leq 0$. Here, the transmission rate is larger than (or equal to) the adjusted loss (natural mortality plus disease-induced mortality plus recovery rate) of infected individuals plus the intrinsic growth rate r , and the pathogen will always invade for any $\epsilon \in [0, 1]$, i.e., irrespective of how density dependence is distributed across the birth and death rates.

Case 3. $\epsilon^* \geq 1$. Here, the transmission rate is smaller than (or equal to) the adjusted loss (natural mortality plus disease-induced mortality plus recovery rates) of infected individuals, and the pathogen cannot invade for any $\epsilon \in [0, 1]$, i.e., irrespective of how density dependence is distributed across the birth and death rates.

Thus, the particular way in which density dependence is distributed across birth and death rates can change disease and population dynamics.

3. Two-Species Models Combining Population Dynamics and Disease Transmission

We now extend the one species case to consider two-species models which incorporate density-dependent species birth and death dynamics with competitive effects and standard incidence disease transmission. For $i = 1, 2$, let the variables S_i denote the density of susceptible individuals in the population of species i , I_i represent the density of infected individuals in the population of species i , and $N_i = S_i + I_i$ the total population density of species i . Our two-species model is

$$\begin{aligned} \frac{dS_1}{dt} &= b_1 N_1 \left(1 - \frac{\epsilon_{11} N_1}{\theta_{11}} - \frac{\epsilon_{12} N_2}{\theta_{12}} \right) - d_1 S_1 \left(1 + \frac{(1 - \epsilon_{11}) N_1}{\psi_{11}} + \frac{(1 - \epsilon_{12}) N_2}{\psi_{12}} \right) \\ &\quad - S_1 \left(\frac{\beta_{11} I_1}{N_1} + \frac{\beta_{12} I_2}{N_2} \right) + \gamma_1 I_1, \end{aligned} \quad (3.1a)$$

$$\begin{aligned} \frac{dI_1}{dt} &= S_1 \left(\frac{\beta_{11} I_1}{N_1} + \frac{\beta_{12} I_2}{N_2} \right) - d_1 I_1 \left(1 + \frac{(1 - \epsilon_{11}) N_1}{\psi_{11}} + \frac{(1 - \epsilon_{12}) N_2}{\psi_{12}} \right) \\ &\quad - (\gamma_1 + \delta_1) I_1, \end{aligned} \quad (3.1b)$$

$$\begin{aligned} \frac{dS_2}{dt} &= b_2 N_2 \left(1 - \frac{\epsilon_{22} N_2}{\theta_{22}} - \frac{\epsilon_{21} N_1}{\theta_{21}} \right) - d_2 S_2 \left(1 + \frac{(1 - \epsilon_{22}) N_2}{\psi_{22}} + \frac{(1 - \epsilon_{21}) N_1}{\psi_{21}} \right) \\ &\quad - S_2 \left(\frac{\beta_{22} I_2}{N_2} + \frac{\beta_{21} I_1}{N_1} \right) + \gamma_2 I_2, \end{aligned} \quad (3.1c)$$

$$\begin{aligned} \frac{dI_2}{dt} &= S_2 \left(\frac{\beta_{22} I_2}{N_2} + \frac{\beta_{21} I_1}{N_1} \right) - d_2 I_2 \left(1 + \frac{(1 - \epsilon_{22}) N_2}{\psi_{22}} + \frac{(1 - \epsilon_{21}) N_1}{\psi_{21}} \right) \\ &\quad - (\gamma_2 + \delta_2) I_2. \end{aligned} \quad (3.1d)$$

Figure 4 is a transfer diagram for model (3.1).

The parameters of the model are described in Table 1. The density-dependent birth and death rates assume a Lotka-Volterra form with intra-specific and inter-specific competitive terms. The coefficient ϵ_{ii} is the proportion of intra-specific competition that affects the birth and juvenile survival rate of species i while $(1 - \epsilon_{ii})$ is the proportion that affects the death rate of species i . For $i, j = 1, 2, i \neq j$, ϵ_{ij} is the proportion of inter-specific competition from species j that affects the reproduction rate of species i and $(1 - \epsilon_{ij})$ is the proportion of inter-specific competition from species j that affects the death rate of species i . For $i, j = 1, 2, i \neq j$, we define $\theta_{ij} := \frac{K_{ij} b_i}{r_i}$ and $\psi_{ij} := \frac{K_{ij} d_i}{r_i}$ so that $K_{ij} = \frac{r_i \theta_{ij}}{b_i} = \frac{r_i \psi_{ij}}{d_i}$. The carrying capacity for species i alone is K_{ii} and the terms K_{ij}^{-1} (via θ_{ij}^{-1} and ψ_{ij}^{-1} for $i \neq j$) are inter-specific competition coefficients. Here, $r_i := b_i - d_i$ is the intrinsic *per capita*

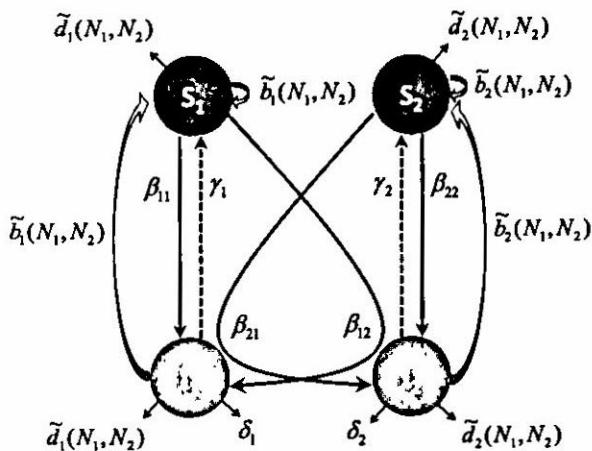


Fig. 4. Transfer diagram for the two-species model (3.1). For $i = 1, 2$, the birth rates are defined as $\tilde{b}_i(N_1, N_2) = b_i(1 - \frac{\epsilon_{i1}N_1}{\theta_{i1}} - \frac{\epsilon_{i2}N_2}{\theta_{i2}})$. The death rates are defined as $\tilde{d}_i(N_1, N_2) = d_i(1 + \frac{(1-\epsilon_{i1})N_1}{\psi_{i1}} + \frac{(1-\epsilon_{i2})N_2}{\psi_{i2}})$.

Table 1. Parameters for the model (3.1a)–(3.1d) and (3.2c) and (3.2d) followed by their units.

Parameter	Description	Unit
b_i :	Per capita birth rate of species i	Time $^{-1}$
d_i :	Per capita adult death rate of species i	Time $^{-1}$
r_i :	Per capita natural growth rate of species i	Time $^{-1}$
K_i :	Carrying capacity of species i	Individuals
K_{ij} :	Relative effect of species j on the carrying capacity of species i	Individuals
θ_{ij} :	Competition term affecting reproduction	Individuals
ψ_{ij} :	Competition term affecting adult death	Individuals
ϵ_{ij} :	Proportion of competition from species j that affects the birth and juvenile survival rate of species i , while $(1 - \epsilon_{ij})$ is the proportion of competition affecting adult mortality	Dimensionless
β_{ij} :	Product of the rate of contact between species j and species i and the probability that, given a contact, an infectious individual of species j will infect a susceptible species i	Time $^{-1}$
γ_i :	Per capita rate of recovery for species i	Time $^{-1}$
δ_i :	Per capita rate of death due to disease (proportion of infectious individuals that die from disease divided by the average time spent infectious)	Time $^{-1}$

growth rate for species i , with b_i and d_i the per capita birth and natural death rates, respectively, for species i in isolation and with no density-dependent effects. We assume that $b_i > d_i > 0$ and hence $r_i > 0$ for $i = 1, 2$.

We make the same assumptions about disease transmission as those for the one-host model in Sec. 2. The intra-species disease transmission coefficient β_{ii} is the product of the contact rate between individuals of species i and the probability of successful transmission within species i for $i = 1, 2$; the inter-species disease

transmission coefficient β_{ij} is the product of the contact rates between species i and j and the probability that an individual of species i will contract the pathogen given a contact with an infectious individual from species j , $j = 1, 2, i \neq j$.

For computation and analysis of equilibria, we express the model (3.1a)–(3.1d) in terms of the proportion of infected individuals $i_k := \frac{I_k}{N_k}$ of species k , and the total population size $N_k = S_k + I_k$ of species k , $k = 1, 2$. Then, model (3.1a)–(3.1d) can be rewritten as

$$\begin{aligned} \frac{di_1}{dt} &= (1 - i_1)(\beta_{11}i_1 + \beta_{12}i_2 - \delta_1 i_1) \\ &\quad - \left(r_1 \left(1 - \frac{\epsilon_{11}N_1}{K_{11}} - \frac{\epsilon_{12}N_2}{K_{12}} \right) + d_1 + \gamma_1 \right) i_1, \end{aligned} \quad (3.2a)$$

$$\begin{aligned} \frac{di_2}{dt} &= (1 - i_2)(\beta_{22}i_2 + \beta_{21}i_1 - \delta_2 i_2) \\ &\quad - \left(r_2 \left(1 - \frac{\epsilon_{22}N_2}{K_{22}} - \frac{\epsilon_{21}N_1}{K_{21}} \right) + d_2 + \gamma_2 \right) i_2, \end{aligned} \quad (3.2b)$$

$$\frac{dN_1}{dt} = \left(r_1 \left(1 - \frac{N_1}{K_{11}} - \frac{N_2}{K_{12}} \right) - \delta_1 i_1 \right) N_1, \quad (3.2c)$$

$$\frac{dN_2}{dt} = \left(r_2 \left(1 - \frac{N_2}{K_{22}} - \frac{N_1}{K_{21}} \right) - \delta_2 i_2 \right) N_2. \quad (3.2d)$$

The model (3.2a)–(3.2d) makes ecological sense and is mathematically well posed in the domain $\mathcal{D}^2 = \{(i_1, i_2, N_1, N_2) \in \mathbb{R}^4 \mid 0 \leq i_1, i_2 \leq 1, 0 \leq N_i \leq K_{ii}, i = 1, 2\}$.

Equations (3.2a) and (3.2b) for infected proportions do not decouple from the equations for the total population sizes (3.2c) and (3.2d) in the most general case of nonzero ϵ_{ij} , $i, j = 1, 2$. However, in the special case in which $\epsilon_{ij} = 0$ for $i, j = 1, 2$, and density dependence affects only death rates, the system (3.2a) and (3.2b) decouples from (3.2c) and (3.2d). The authors of Ref. 19 consider this special subcase in their paper and fully analyze existence and local stability of all equilibria. They also considered the second special case in which $\epsilon_{ij} = 1, \forall i, j$ and density dependence affects only reproduction. They obtained conditions of local stability for the DFE, and deduced conditions for existence of the infected equilibria. However, they did not prove stability of the infected equilibrium and the most general case of $\epsilon_{ij} \in [0, 1]$ is not analyzed.

In Ref. 21, the authors analyzed a two-species SIS host-pathogen model in which birth rates have a logistic form and competitive effects are incorporated in the death rates alone. Their model assumes a directly transmitted disease with density-dependent (mass action) disease transmission. The authors in Ref. 21 numerically demonstrate the existence of multiple endemic equilibria for their model, which does not occur in the standard incidence disease transmission model that we consider here. In this paper, we consider the most general case of nonzero ϵ_{ij} , $i, j = 1, 2$ and partially analyze existence and stability conditions for all equilibria.

4. Threshold Quantities and Pathogen Invasion

In this section, we compute the basic reproduction numbers and type reproduction number for the two-species model (3.2a)–(3.2d). We also consider how the choice of the parameters ϵ_{ij} , $i, j = 1, 2$, affects the basic reproduction numbers leading to pathogen invasion.

4.1. The basic reproduction number

The basic reproduction number \mathcal{R}_0^C for model (3.2a)–(3.2d) is computed as the spectral radius of the next generation matrix K .²⁵ We define a quantity D_k , $k = 1, 2$ that incorporates loss of diseased individuals due to natural death, death due to disease and recovery, as a function of the total population sizes N_1, N_2 . For $i, j = 1, 2, i \neq j$ define

$$D_i(N_i, N_j) = \delta_i + \gamma_i + b_i - r_i \left(\epsilon_{ii} \frac{N_i}{K_{ii}} + \epsilon_{ij} \frac{N_j}{K_{ij}} \right). \quad (4.1)$$

Consider the 2×2 matrices

$$A = \begin{bmatrix} \beta_{11} & \beta_{12} \\ \beta_{21} & \beta_{22} \end{bmatrix}; \quad B(N_1, N_2) = \text{diag}(D_1(N_1, N_2), D_2(N_1, N_2)). \quad (4.2)$$

Let $E_j = (i_1^j, i_2^j, N_1^j, N_2^j)$ denote an equilibrium solution for Eqs. (3.2a)–(3.2d). The coexistence DFE for model (3.2a)–(3.2d) is $E_3 = (0, 0, K_1^*, K_2^*)$ where

$$K_1^* = \frac{K_{11}K_{12}}{K_{12} + K_{11}(\xi_{21}/\xi_{12})}, \quad K_2^* = \frac{\xi_{21}}{\xi_{12}} K_1^*, \quad (4.3)$$

defined via the parameters

$$\xi_{21} = 1/K_{11} - 1/K_{21}, \quad (4.4a)$$

$$\xi_{12} = 1/K_{22} - 1/K_{12}. \quad (4.4b)$$

The next generation matrix K is defined as

$$K = A[B(K_1^*, K_2^*)]^{-1} = \begin{bmatrix} \mathcal{R}_{11} & \mathcal{R}_{12} \\ \mathcal{R}_{21} & \mathcal{R}_{22} \end{bmatrix}, \quad (4.5)$$

where, for $i, j = 1, 2$, $\mathcal{R}_{ij} := \frac{\beta_{ij}}{D_j(K_1^*, K_2^*)}$. We note that the quantity $D_i(K_1^*, K_2^*) > 0$ for $i = 1, 2$. This is because for $i, j = 1, 2, i \neq j$, $\frac{K_1^*}{K_{ii}} + \frac{K_2^*}{K_{jj}} = 1$, and we have $D_i(K_1^*, K_2^*) > \delta_i + \gamma_i + b_i - r_i(\frac{K_1^*}{K_{ii}} + \frac{K_2^*}{K_{jj}}) = \delta_i + \gamma_i + b_i - r_i = \delta_i + \gamma_i + d_i > 0$.

The basic reproduction number, $\mathcal{R}_0^C = \rho(K)$, the spectral radius of K , is computed to be

$$\mathcal{R}_0^C = \frac{1}{2}(\mathcal{R}_{11} + \mathcal{R}_{22} + \sqrt{(\mathcal{R}_{11} - \mathcal{R}_{22})^2 + 4\mathcal{R}_{12}\mathcal{R}_{21}}). \quad (4.6)$$

The single species basic reproduction numbers, $\mathcal{R}_{0,1}$ for species 1, and $\mathcal{R}_{0,2}$ for species 2, are defined as

$$\mathcal{R}_{0,1} := \frac{\beta_{11}}{D_1(K_{11}, 0)} = \frac{\beta_{11}}{\delta_1 + \gamma_1 + b_1 - r_1 \epsilon_{11}}; \quad (4.7)$$

$$\mathcal{R}_{0,2} := \frac{\beta_{22}}{D_2(0, K_{22})} = \frac{\beta_{22}}{\delta_2 + \gamma_2 + b_2 - r_2 \epsilon_{22}}. \quad (4.8)$$

As observed for the one-host case in Sec. 2 the denominators $D_1(K_{11}, 0) > 0$ and $D_2(0, K_{22}) > 0$.

4.2. Pathogen invasion and extinction

Since the basic reproduction number for the two-species system can vary with choice of ϵ_{ij} , changing the balance of density-dependent population dynamics can change the stability of the DFE leading to pathogen invasion or extinction. Figure 5 illustrates this concept, showing a case where disease persists when competition is incorporated in the birth rate alone but the disease dies out for competition incorporated in the death rate only.

In the single species model, a single critical parameter ϵ^* allowed us to explore how changing the balance of density-dependent population dynamics can change the stability of the DFE. For the two-species model a complete bifurcation analysis of \mathcal{R}_0^C will depend on analogous critical parameters ϵ_{ij}^* defined in an implicit manner.

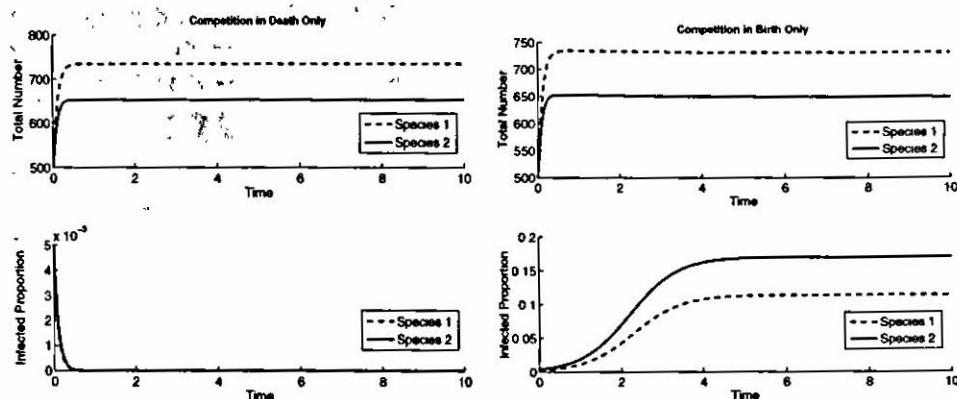


Fig. 5. An illustration of how choice of competition via parameter ϵ_{ij} determines whether or not the disease will persist for two competing species. The top row depicts N_1 and N_2 , the total number of species 1 and species 2, respectively. The bottom row depicts i_1 and i_2 , the infected proportion of species 1 and species 2, respectively. Left column: Case of density-independent reproduction and density-dependent mortality ($\epsilon_{ij} = 0 \forall i, j$): disease dies out. Parameters and initial conditions are $b_1 = b_2 = 19, d_1 = d_2 = 8, K_{11} = K_{22} = 800, K_{12} = K_{11} * 10, K_{21} = K_{22} * 5, \beta_{11} = 5, \beta_{22} = 6, \beta_{12} = 3, \beta_{21} = 4, \delta_1 = 0.4, \delta_2 = 0.2, \gamma_1 = \gamma_2 = 0, N_1(0) = 500, N_2(0) = 500$ and $i_k = I_k/N_k = 0.005$ for $k = 1, 2$. Right column: Case of density-dependent reproduction and density-independent mortality: disease persists. Parameters and initial conditions are the same except that $\epsilon_{ij} = 1 \forall i, j$.

For the special case $\epsilon_{11} = \epsilon_{12} = \epsilon_1$ and $\epsilon_{22} = \epsilon_{21} = \epsilon_2$, we have $D_i = b_i(1 - \epsilon_i) + d_i\epsilon_i + \delta_i + \gamma_i$ and

$$\mathcal{R}_0^C = \frac{1}{2} \left(\mathcal{R}_{0,1} + \mathcal{R}_{0,2} + \sqrt{(\mathcal{R}_{0,1} - \mathcal{R}_{0,2})^2 + 4\mathcal{R}_{12}\mathcal{R}_{21}} \right). \quad (4.9)$$

In the special case that $\beta_{ii} = \beta_{ij}, i = 1, 2, i \neq j$, then

$$\mathcal{R}_0^C(\epsilon_1, \epsilon_2) = \mathcal{R}_{0,1}(\epsilon_1) + \mathcal{R}_{0,2}(\epsilon_2). \quad (4.10)$$

Since the single species basic reproduction number $\mathcal{R}_{0,i}$ is an increasing function of ϵ_i , \mathcal{R}_0^C is also an increasing function of ϵ_i . The curve $\mathcal{R}_0^C(\epsilon_1, \epsilon_2) = 1$ can be characterized further. We define parameters $\epsilon_i^*, i = 1, 2$ similar to the single species case, i.e.,

$$\epsilon_i^* = \frac{\delta_i + \gamma_i + b_i - \beta_{ii}}{r_i}. \quad (4.11)$$

Using the definitions of ϵ_i^* , the curve $\mathcal{R}_0^C(\epsilon_1, \epsilon_2) = 1$ given by $\mathcal{R}_{0,1}(\epsilon_1) + \mathcal{R}_{0,2}(\epsilon_2) = 1$, can be rewritten as

$$(\epsilon_1 - \epsilon_1^*)(\epsilon_2 - \epsilon_2^*) = \frac{\beta_{11}\beta_{22}}{r_1 r_2}. \quad (4.12)$$

Thus, values of $(\epsilon_1, \epsilon_2) \in [0, 1] \times [0, 1]$ that lie on this curve divide the unit square into regions of stability or instability of the endemic equilibrium.

In the most general case of nonzero $\epsilon_{ij}, i, j = 1, 2$, when $\beta_{11}\beta_{22} > \beta_{12}\beta_{21}$, which can happen when intra-specific disease transmission is greater than inter-specific disease transmission, we can show that \mathcal{R}_0^C is a strictly increasing function of ϵ_{ij} . The basic reproduction number for the disease is lowest when most of the competition occurs in the death rate while the basic reproduction number is higher when competition affects mostly the birth rate. This means that if the disease-free coexistence equilibrium is stable when $\epsilon_{ij} = 0, \forall i, j$ and competition acts on mortality alone, then there is a possibility that the disease-free coexistence equilibrium will in fact be unstable for the same system if competition is chosen to act on reproduction (so $\epsilon_{ij} > 0$ for some i, j). As the disease-free coexistence equilibrium becomes unstable, a bifurcation results, and the one-host infected or infected coexistence equilibria could become stable (depending on the other parameter values).

Figure 6 (Right) shows how \mathcal{R}_0^C changes as ϵ_1 and ϵ_2 vary. For this case, there is no death due to disease but there is recovery from the disease. Once recovered, an individual is susceptible again. Both species produce about 20 offsprings during their two-year lifespan, so they have a relatively high intrinsic growth rate. Figure 6 (Left) shows how \mathcal{R}_0^C varies for a scenario where once acquired, the disease is chronic and death due to disease is not negligible. The rest of the characteristics of both populations are the same. For both cases we have $\beta_{11}\beta_{22} > \beta_{12}\beta_{21}$. We can see that with no recovery and relatively low death due to disease, \mathcal{R}_0^C increases significantly as ϵ_1 and ϵ_2 approach 1. The black line, where $\mathcal{R}_0^C = 1$, represents

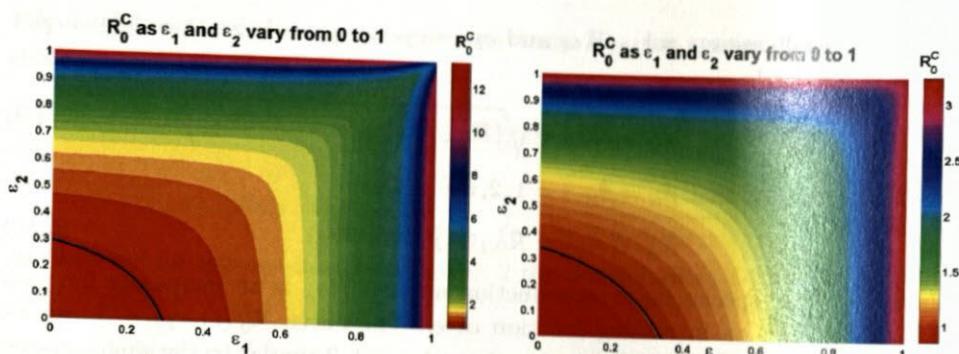


Fig. 6. Change in \mathcal{R}_0^C as ϵ_1 and ϵ_2 vary from 0 to 1. The black line is $\mathcal{R}_0^C = 1$. Left: A case of chronic disease (i.e., no recovery). Here \mathcal{R}_0^C moves from less than 1 to greater than 12 as values of ϵ_1 and ϵ_2 change, resulting in a bifurcation as the DFE moves from stable (below black line) to unstable (above the black line). Parameters (in 1/year) are $b_1 = b_2 = 10, d_1 = d_2 = 0.5, \beta_{11} = \beta_{22} = 6, \beta_{12} = \beta_{21} = 3, \delta_1 = \delta_2 = 0.8$, and $\gamma_1 = \gamma_2 = 0$. Right: A case of recovery from disease but with no immunity conferred. Parameters (in 1/year) are $b_1 = b_2 = 10, d_1 = d_2 = 0.5, \beta_{11} = \beta_{22} = 7, \beta_{12} = \beta_{21} = 4, \delta_1 = \delta_2 = 0$, and $\gamma_1 = \gamma_2 = 3$ where time is years. \mathcal{R}_0^C varies from less than 1 to over 3.

bifurcation points below which the coexistence DFE is stable and above which it is unstable.

4.3. The type reproduction number

In order to better understand \mathcal{R}_0^C and to inform analysis of endemic equilibria, we consider the type reproduction number, which was not relevant for the one-species model. The type reproduction number is a threshold quantity developed by and Roberts Heesterbeek^{26,27} that generalizes the basic reproduction number. It isolates infections generated by a single type of species or a subset of species in a heterogeneous population of many different species, and is a helpful threshold quantity for controlling the pathogen through one or more species. For n epidemiologically distinct types of hosts, the type reproduction number of type i , denoted by T_i , is defined as the expected number of cases in individuals of type i caused by one infected individual of type i in a completely susceptible population, either directly or through chains of infection passing through any sequence of the other types.^{26,27} The type reproduction for a single species i is defined to be the quantity²⁷:

$$T_i = \mathbf{e}_i^T K [\mathbb{I} - (\mathbb{I} - P)K]^{-1} \mathbf{e}_i. \quad (4.13)$$

In (4.13), the vector \mathbf{e}_i is the i th unit column vector in \mathbb{N}^n , and \mathbf{e}_i^T denotes its transpose. The matrix P is an $n \times n$ projection matrix on type i , with the diagonal entry $P_{ii} = 1$ and all other entries are zero. The matrix \mathbb{I} is the $n \times n$ identity matrix.^{26,27}

For the two-host model (3.1) or (3.2), the next generation matrix K is defined in (4.5). From formula (4.13) we can compute the type reproduction numbers T_1

and T_2 as

$$T_1 = \mathcal{R}_{11} + \frac{\mathcal{R}_{12}\mathcal{R}_{21}}{1 - \mathcal{R}_{22}}, \quad (4.14a)$$

$$T_2 = \mathcal{R}_{22} + \frac{\mathcal{R}_{12}\mathcal{R}_{21}}{1 - \mathcal{R}_{11}}. \quad (4.14b)$$

We note the following properties of the type reproduction numbers:

- (TP1) If $\mathcal{R}_{11} > 1$ and $\mathcal{R}_{22} < 1$ then $T_1 > 1$.
- (TP2) If $\mathcal{R}_{11} < 1$ and $\mathcal{R}_{22} > 1$ then $T_2 > 1$.
- (TP3) If $\mathcal{R}_{ii} < 1$ for $i = 1, 2$, then $(1 - \mathcal{R}_{11})(1 - \mathcal{R}_{22}) < \mathcal{R}_{12}\mathcal{R}_{21}$ if and only if $T_i > 1$ for $i = 1, 2$.

5. Analysis of Equilibria

In this section, we compute equilibrial solutions for the model (3.2a)–(3.2d) and identify conditions for their existence and local stability. Let $E_j = (i_1^j, i_2^j, N_1^j, N_2^j)$ denote an equilibrium solution for model (3.2a)–(3.2d). For our model with standard incidence disease transmission, if one of the equilibrial infected proportions i_k^j is zero, for $k = 1, 2$, then the other equilibrial infected proportion must also be zero i.e., the disease either stays endemic in both species or dies out in both species. This is commonly observed in disease models with standard incidence.²⁸

As shown for the single species model in Sec. 2, in the case $\epsilon^* \in (0, 1)$, the distribution of density dependence between the birth and death rates of the species can significantly alter disease dynamics of the system. Thus, for the two-species model (3.2a)–(3.2d) we focus on the case when both $\epsilon_1^* > 0$ and $\epsilon_2^* > 0$, with the $\epsilon_k^*, k = 1, 2$ defined in (4.11). The stability analysis of equilibria is based on the important parameters and threshold quantities enumerated in Table 2. We will also make use of additional threshold parameters that will be defined below.

Table 2. Summary of important quantities and their ecological relevance for species and disease persistence.

Parameter	Description
ξ_{21}	Measure of intra- versus inter-specific effects exerted by species 1 (constant times <i>per capita</i> growth of species 2, η_{21} , invading species 1 at carrying capacity)
ξ_{12}	Measure of intra- versus inter-specific effects exerted by species 2 (constant times <i>per capita</i> growth of species 1, η_{12} , invading species 2 at carrying capacity)
κ_{21}	<i>Per capita</i> growth rate of species 2 invading at species 1 infected carrying capacity
κ_{12}	<i>Per capita</i> growth rate of species 1 invading at species 2 infected carrying capacity
$\mathcal{R}_{0,1}$	Basic reproduction number for the pathogen in species 1 alone
$\mathcal{R}_{0,2}$	Basic reproduction number for the pathogen in species 2 alone
\mathcal{R}_0^C	Basic reproduction number for the pathogen when both species are present

5.1. Disease-free equilibria

In addition to the coexistence DFE $E_3 = (0, 0, K_1^*, K_2^*)$ defined in Eqs. (4.3) and (4.4) in Sec. 4.1, model (3.2a)–(3.2d) has the DFE $E_0 = (0, 0, 0, 0)$, $E_1 = (0, 0, K_{11}, 0)$ and $E_2 = (0, 0, 0, K_{22})$.

The Jacobian of model (3.2a)–(3.2d) at equilibrium E_0 is

$$J(E_0) = \begin{bmatrix} -r_1\epsilon_1^* & \beta_{12} & 0 & 0 \\ \beta_{21} & -r_2\epsilon_2^* & 0 & 0 \\ 0 & 0 & r_1 & 0 \\ 0 & 0 & 0 & r_2 \end{bmatrix}, \quad (5.1)$$

with two of the eigenvalues being $r_1 > 0$ and $r_2 > 0$. Thus, the equilibrium E_0 is unstable.

Next, we study the stability of the DFEs E_1 , E_2 and E_3 . The term $1/K_{ij}$ can be interpreted as the inhibition strength of species j on species i .²⁸ Hence, the parameters ξ_{21} and ξ_{12} defined in (4.4) are a measure of the relative strengths of intra- versus inter-specific competition. The *per capita* growth rate of species 1 at equilibrium E_2 , denoted as $\eta_{12} := \frac{1}{N_1} \frac{dN_1}{dt}|_{E_2} = r_1 K_{22} \xi_{12}$, determines the ability of species 1 to invade species 2 at its carrying capacity. Since $r_1 K_{22} > 0$, the sign of η_{12} is determined by ξ_{12} . Similarly, the *per capita* growth rate of species 2 near the equilibrium E_1 , denoted $\eta_{21} := \frac{1}{N_2} \frac{dN_2}{dt}|_{E_1} = r_2 K_{11} \xi_{21}$, and the ability of species 2 to invade species 1 when species 1 is at its carrying capacity, is determined by the sign of ξ_{21} . Based on the signs of ξ_{12} and ξ_{21} there are four cases to consider.

Case 1. When $\xi_{12} > 0$ and $\xi_{21} < 0$, species 1 inhibits species 2 more than it inhibits itself while species 2 inhibits itself more than it inhibits species 1. In this case, species 1 wins and remains in a disease-free state under additional conditions. The function

$$Q_1(N) = \frac{\beta_{22}}{D_2(N, 0)} = \frac{\beta_{22}}{\delta_2 + \gamma_2 + b_2 - r_2 \epsilon_{21} \frac{N}{K_{21}}}, \quad (5.2)$$

is an increasing function of N . Since $\xi_{21} < 0$, we have $K_{21} < K_{11}$ and thus $0 < Q_1(K_{21}) < Q_1(K_{11})$, since the quantity $Q_1(K_{21}) = \frac{\beta_{22}}{\delta_2 + \gamma_2 + b_2 + r_2(1 - \epsilon_{21})} > 0$, for $0 \leq \epsilon_{21} \leq 1$. We define

$$\bar{R}_{0,2} := Q_1(K_{11}) = \frac{\beta_{22}}{\delta_2 + \gamma_2 + b_2 - r_2 \epsilon_{21} \frac{K_{11}}{K_{21}}}. \quad (5.3)$$

The Jacobian of model (3.2a)–(3.2d) at equilibrium E_1 is

$$J(E_1) = \begin{bmatrix} r_1(\epsilon_{11} - \epsilon_1^*) & \beta_{12} & 0 & 0 \\ \beta_{21} & r_2 \left(\epsilon_{21} \frac{K_{11}}{K_{21}} - \epsilon_2^* \right) & 0 & 0 \\ -\delta_1 K_{11} & 0 & -r_1 & -r_1 \frac{K_{11}}{K_{12}} \\ 0 & 0 & 0 & \eta_{21} \end{bmatrix}. \quad (5.4)$$

The eigenvalues of $J(E_1)$ are $-r_1 < 0, \eta_{21}$ which is negative if and only if $\xi_{21} < 0$, and the eigenvalues of the upper left 2×2 matrix of $J(E_1)$,

$$J_{11} = \begin{bmatrix} r_1(\epsilon_{11} - \epsilon_1^*) & \beta_{12} \\ \beta_{21} & r_2\left(\epsilon_{21}\frac{K_{11}}{K_{21}} - \epsilon_2^*\right) \end{bmatrix} = A - B(K_{11}, 0), \quad (5.5)$$

with matrices A and B defined in Eq. (4.2). The eigenvalues of J_{11} are negative if and only if trace of J_{11} is negative and the determinant of J_{11} is positive, i.e.,

$$r_1(\epsilon_{11} - \epsilon_1^*) + r_2\left(\epsilon_{21}\frac{K_{11}}{K_{21}} - \epsilon_2^*\right) < 0, \quad \text{and} \quad (5.6)$$

$$r_1 r_2 (\epsilon_{11} - \epsilon_1^*) \left(\epsilon_{21} \frac{K_{11}}{K_{21}} - \epsilon_2^* \right) > \beta_{12} \beta_{21}. \quad (5.7)$$

Since $\beta_{12} > 0$ and $\beta_{21} > 0$, (5.6) and (5.7) imply that $\epsilon_{11} < \epsilon_1^*$ (which is equivalent to $\mathcal{R}_{0,1} < 1$) and $\epsilon_{21} \frac{K_{11}}{K_{21}} < \epsilon_2^*$ (which is equivalent to $\bar{\mathcal{R}}_{0,2} < 1$).

Since matrix $J_{11} = A - B(K_{11}, 0)$, all the eigenvalues of matrix J_{11} have negative real parts if and only if $\rho(A[B(K_{11}, 0)]^{-1}) < 1$. Defining

$$\begin{aligned} \mathcal{R}_{K0} &:= \rho(A[B(K_{11}, 0)]^{-1}) \\ &= \frac{1}{2} \left(\mathcal{R}_{0,1} + \bar{\mathcal{R}}_{0,2} + \sqrt{(\mathcal{R}_{0,1} - \bar{\mathcal{R}}_{0,2})^2 + 4 \frac{\beta_{12} \beta_{21}}{\beta_{11} \beta_{22}} \mathcal{R}_{0,1} \bar{\mathcal{R}}_{0,2}} \right), \end{aligned} \quad (5.8)$$

conditions (5.6) and (5.7) together imply that $\mathcal{R}_{K0} < 1$. Thus, conditions for stability of E_1 are $\xi_{21} < 0$ and $\mathcal{R}_{K0} < 1$.

Case 2. When $\xi_{12} < 0$ and $\xi_{21} > 0$, species 2 can invade species 1. We define the threshold quantities

$$\bar{\mathcal{R}}_{0,1} := \frac{\beta_{11}}{D_1(0, K_{22})} = \frac{\beta_{11}}{\delta_1 + \gamma_1 + b_1 - r_1 \epsilon_{12} \frac{K_{22}}{K_{12}}}, \quad (5.9)$$

$$\begin{aligned} \mathcal{R}_{0K} &:= \rho(A[B(0, K_{22})]^{-1}) \\ &= \frac{1}{2} \left(\mathcal{R}_{0,2} + \bar{\mathcal{R}}_{0,1} + \sqrt{(\mathcal{R}_{0,2} - \bar{\mathcal{R}}_{0,1})^2 + 4 \frac{\beta_{12} \beta_{21}}{\beta_{11} \beta_{22}} \mathcal{R}_{0,2} \bar{\mathcal{R}}_{0,1}} \right). \end{aligned} \quad (5.10)$$

Since $\xi_{12} < 0$, using an argument similar to that in Case 1 we have $\bar{\mathcal{R}}_{0,1} > 0$ and $\mathcal{R}_{0K} > 0$.

In this case, the equilibrium E_2 is stable if and only if $\xi_{12} < 0, \mathcal{R}_{0,2} < 1, \bar{\mathcal{R}}_{0,1} < 1$, and $r_1 r_2 (\epsilon_{22} - \epsilon_2^*) (\epsilon_{12} \frac{K_{22}}{K_{12}} - \epsilon_1^*) > \beta_{12} \beta_{21}$. Using similar arguments as for Case 1, these conditions are equivalent to the conditions $\xi_{12} < 0$ and $\mathcal{R}_{0K} < 1$.

The coexistence DFE is biologically feasible when $\frac{\xi_{21}}{\xi_{12}} > 0$, which happens in the next two cases.

Case 3. When both $\xi_{12} > 0$ and $\xi_{21} > 0$ then intra-specific competition is stronger in both species than inter-specific competition. The equilibria E_1 and E_2 are both unstable. The Jacobian of system (3.2a)–(3.2d) at equilibrium E_3 is

$$J(E_3) = \begin{bmatrix} J_{31} & \mathbf{0} \\ J_{32} & J_{33} \end{bmatrix}. \quad (5.11)$$

The eigenvalues of $J(E_3)$ are the eigenvalues of the 2×2 matrices J_{31}

$$J_{31} = \begin{bmatrix} r_1 \left(\epsilon_{11} \frac{K_1^*}{K_{11}} + \epsilon_{12} \frac{K_2^*}{K_{12}} - \epsilon_1^* \right) & \beta_{12} \\ \beta_{21} & r_2 \left(\epsilon_{21} \frac{K_1^*}{K_{21}} + \epsilon_{22} \frac{K_2^*}{K_{22}} - \epsilon_2^* \right) \end{bmatrix}, \quad (5.12)$$

and J_{33}

$$J_{33} = \begin{bmatrix} -\frac{K_1^* r_1}{K_{11}} & -\frac{K_1^* r_1}{K_{12}} \\ -\frac{K_2^* r_2}{K_{21}} & -\frac{K_2^* r_2}{K_{22}} \end{bmatrix}. \quad (5.13)$$

The matrix $J_{32} = \text{diag}(-\delta_1 K_1^*, -\delta_2 K_2^*)$. The trace of matrix J_{33} is $-\left(\frac{K_1^* r_1}{K_{11}} + \frac{K_2^* r_2}{K_{22}}\right)$ and is negative, and the determinant of matrix J_{33} is $r_1 r_2 K_1^* K_2^* \left(\frac{1}{K_{11} K_{22}} - \frac{1}{K_{12} K_{21}}\right)$ and is positive under the assumption $\xi_{12} > 0$ and $\xi_{21} > 0$. Matrix J_{31} can be written as the difference of two matrices

$$J_{31} = A - B(K_1^*, K_2^*). \quad (5.14)$$

All eigenvalues of matrix J_{31} have negative real parts if and only if the eigenvalues of the matrix $K := A[B(K_1^*, K_2^*)]^{-1}$ are in the interior of the unit ball. The matrix K is the next generation matrix defined in (4.5), and its spectral radius is \mathcal{R}_0^C . Thus, the coexistence DFE, $E_3 = (0, 0, K_1^*, K_2^*)$, is feasible and locally stable if and only if the conditions $\xi_{21} > 0$, $\xi_{12} > 0$ and $\mathcal{R}_0^C < 1$ are satisfied.

Case 4. When $\xi_{12} < 0$ and $\xi_{21} < 0$ then inter-specific competition is stronger than intra-specific competition in both species. In this case, there is competitive exclusion and in general the species with the highest initial density will win assuming that the conditions $\mathcal{R}_{K0} < 1$ and $\mathcal{R}_{0K} < 1$ hold.

We summarize existence and stability conditions for all the DFE in Table 3.

Table 3. Summary of existence and stability of DFE. F = feasible, NF = not feasible, U = unstable, S = stable.

DFE	Case 1	Case 2	Case 3	Case 4
E_0	F, U	F, U	F, U	F, U
E_1	F, S if $\mathcal{R}_{K0} < 1$	F, U	F, U	F, S if $\mathcal{R}_{K0} < 1$
E_2	F, U	F, S if $\mathcal{R}_{0K} < 1$	F, U	F, S if $\mathcal{R}_{0K} < 1$
E_3	NF	NF	F, S if $\mathcal{R}_0^C < 1$	F, U

5.2. Infected one-host equilibria

When all the DFE are either infeasible or unstable then disease may remain endemic in both species. System (3.2a)–(3.2d) has infected one-species equilibria of the form $E_4 = (i_1^4, i_2^4, N_1^4, 0)$ and $E_5 = (i_1^5, i_2^5, 0, N_2^5)$ under certain conditions. In this section, we consider existence and stability of these one-host infected equilibria. As in the case of the DFE, we again assume that the critical parameters $\epsilon_k^* \in (0, 1)$, $k = 1, 2$. Under this assumption we have the condition $\beta_{kk} - \delta_k > 0$, $k = 1, 2$. We define two new parameters, κ_{12} and κ_{21} (see Table 2) as

$$\kappa_{12} = r_1(1 - N_2^5/K_{12}) - \delta_1 i_1^5, \quad (5.15a)$$

$$\kappa_{21} = r_2(1 - N_1^4/K_{21}) - \delta_2 i_2^4. \quad (5.15b)$$

As described in Table 2, κ_{12} (κ_{21}) is the *per capita* growth rate of species 1 (2) at equilibrium E_5 (E_4).

From Eqs. (3.2c) and (3.2d), the total populations for the species 1 infected one-host equilibrium E_4 are $N_2^4 = 0$ and

$$N_1^4 = K_{11} \left(1 - \frac{\delta_1}{r_1} i_1^4 \right). \quad (5.16)$$

Below, we prove sufficient conditions for existence of E_4 .

Lemma 5.1. *Assume that the critical parameters $\epsilon_k^* \in (0, 1)$, $k = 1, 2$. The one-host infected equilibrium $E_4 = (i_1^4, i_2^4, N_1^4, 0)$ is feasible and unique with (i_1^4, i_2^4) in the domain $D^* = \{(i_1, i_2) \in \mathbb{R}^2 | 0 < i_1 < 1, 0 < i_2 < \frac{\beta_{21}}{\omega}\}$, $\omega = \beta_{21} + \frac{r_2 \epsilon_{21} K_{11}}{K_{21}} \frac{\delta_1}{r_1}$, $N_1^4 > 0$ and the following conditions hold:*

- (a) $\bar{\mathcal{R}}_{0,2} < 1$ (i.e., $\epsilon_{21} < \frac{\epsilon_2^* K_{21}}{K_{11}}$) and $\mathcal{R}_{0,1} > 1$ (i.e., $\epsilon_{11} > \epsilon_1^*$)
OR
- (b) $\bar{\mathcal{R}}_{0,2} < 1$, $\mathcal{R}_{0,1} < 1$ and $\beta_{12} \beta_{21} > r_1(\epsilon_1^* - \epsilon_{11})r_2(\epsilon_2^* - \frac{\epsilon_{21} K_{11}}{K_{21}})$.

Proof. We note that conditions (a) and (b) imply that $\mathcal{R}_{K0} > 1$. The proof can be found in the Appendix. \square

Theorem 5.1. *Assume that the conditions of Lemma 5.1 hold so that the one-host infected equilibrium for species 1, E_4 , is feasible. Then E_4 is locally asymptotically stable if and only if $\kappa_{21} < 0$.*

Proof. The proof can be found in the Appendix. We note that the condition $\kappa_{21} < 0$ guarantees that the *per capita* growth rate of species 2 at E_4 is negative, so species 2 cannot invade species 1 at its infected carrying capacity. \square

We can similarly prove sufficient conditions for the existence of the infected one-host equilibrium for species 2, $E_5 = (\hat{i}_1^5, \hat{i}_2^5, 0, \hat{N}_2^5)$.

Lemma 5.2. Assume that the critical parameters $\epsilon_k^* \in (0, 1)$, $k = 1, 2$. The one-host infected equilibrium $E_5 = (i_1^*, i_2^*, 0, N_2^*)$ is feasible and unique with (i_1^*, i_2^*) in the domain $D^* = \{(i_1, i_2) \in \mathbb{R}^2 \mid 0 < i_2 < 1, 0 < i_1 < \frac{\beta_{12}}{\omega}\}$, $\omega = \beta_{12} + \frac{r_1 \epsilon_{12} K_{22} \delta_2}{K_{12} r_2}$ if $N_2^* > 0$ and the following conditions hold:

- (a) $\bar{\mathcal{R}}_{0,1} < 1$ (i.e., $\epsilon_{12} < \frac{\epsilon_1^* K_{12}}{K_{22}}$) and $\mathcal{R}_{0,2} > 1$ (i.e., $\epsilon_{22} > \epsilon_2^*$)
OR
- (b) $\bar{\mathcal{R}}_{0,1} < 1$, $\mathcal{R}_{0,2} < 1$ and $\beta_{12} \beta_{21} > r_2(\epsilon_2^* - \epsilon_{22})r_1(\epsilon_1^* - \frac{\epsilon_{12} K_{22}}{K_{12}})$. We note that conditions (a) and (b) imply that $\mathcal{R}_{0K} > 1$.

Theorem 5.2. Assume that the conditions of Lemma 5.2 hold so that the one-host infected equilibrium for species 2, E_5 , is feasible. Then E_5 is locally asymptotically stable if and only if $\kappa_{12} < 0$.

The condition $\kappa_{12} < 0$ guarantees that the *per capita* growth rate of species 1 at E_5 is negative, so species 1 cannot invade species 2 at its infected carrying capacity.

Model (3.2) can also possess additional boundary equilibria of the form $(i_1^*, i_2^*, 0, 0)$ in which the disease drives the hosts to extinction. Under the assumption $r_k > \delta_k$, $k = 1, 2$ that is made in this paper for the one species case, these boundary equilibria, if they exist, will be unstable. In Ref. 28, the authors discuss conditions for existence of such boundary equilibria when $\epsilon_{ij} = 1$, $i, j = 1, 2$.

5.3. Infected coexistence equilibrium

The endemic coexistence equilibrium is difficult to analyze, since for many parameter values, equilibrium values are intractable. We derive sufficient conditions under which both species will be bounded away from zero for all time and prove existence and uniqueness of the endemic equilibrium, which depends, as expected, on choice of values for ϵ_{ij} . We derive stability conditions for a simplified case and use numerical examples to conjecture extensions of the simplified case.

Although the infected coexistence equilibrium is algebraically intractable, we use methods similar to Ref. 29 to analyze the existence and stability of the endemic equilibrium. However, unlike the simpler case in Ref. 29, the complete analysis of this equilibrium requires results from the theory of asymptotically autonomous systems.³⁰

5.3.1. Existence and uniqueness of the endemic equilibrium

To prove existence and uniqueness of the endemic equilibrium, we assume conditions **(U1)**, **(U2)** and **(U3)** (given in Appendix) hold so that both species are present for all time. For Secs. 5.3.1–5.4, we assume that $\epsilon_{11} = \epsilon_{12} = \epsilon_1$ and that $\epsilon_{22} = \epsilon_{21} = \epsilon_2$. The assumptions **(U1)**, **(U2)** and **(U3)**, given in the Appendix, are sufficient, but not necessary, conditions for the presence of both species. Under the assumption

$\epsilon_{ii} = \epsilon_{ij} = \epsilon_i$ for $i, j = 1, 2, i \neq j$, we have $\mathcal{R}_{ii} = \mathcal{R}_{0,i}$, so $\mathcal{R}_{0,i}$ will be used instead of \mathcal{R}_{ii} for Sections 5.3.1, 5.4 and 5.5.

Theorem 5.3. *A unique endemic equilibrium exists for the SIS model with competition, (3.2a) and (3.2b), if and only if (a) $\mathcal{R}_{0,i} > 1$ for either $i = 1$ or $i = 2$ or (b) $\mathcal{R}_{0,i} < 1$ for both $i = 1, 2$ and $(1 - \mathcal{R}_{0,1})(1 - \mathcal{R}_{0,2}) < \mathcal{R}_{12}\mathcal{R}_{21}$ with $\mathcal{R}_{ij} = \beta_{ij}/D_j$. We note that (a) says that either the single species basic reproduction numbers $\mathcal{R}_{0,i}$ are both greater than one, or at least one of the type reproduction numbers T_i is greater than one. Part (b) says that in the case $\mathcal{R}_{0,i} < 1$, we must have both type reproduction numbers $T_1 > 1$ and $T_2 > 1$. Both parts (a) and (b) imply that the basic reproduction number $\mathcal{R}_0^C > 1$ for the two-host system (3.2a) and (3.2b) for \mathcal{R}_0^C defined in (4.6).*

Proof. The proof can be found in the Appendix. \square

5.4. Stability analysis for no disease related mortality

Now that we have shown existence and uniqueness of the endemic equilibrium, we will prove stability for a simplified case. As with the one species, disease-free two species, and one-host infected equilibria, competition and disease spread interact to determine existence and stability of the endemic equilibrium. Let us denote the unique endemic equilibrium as $E_6 = (\hat{i}_1, \hat{i}_2, \hat{N}_1, \hat{N}_2)$. Then, we have the following result.

Theorem 5.4. *Consider the model (A.11a) and (A.11b). If $\mathcal{R}_0^C < 1$, then the DFE ($\hat{i}_1 = 0, \hat{i}_2 = 0$) is globally asymptotically stable in the region $\mathcal{D} = [0, 1] \times [0, 1]$ and if $\mathcal{R}_0^C > 1$ then the infected coexistence (endemic) equilibrium ($\hat{i}_1 > 0, \hat{i}_2 > 0$) is globally asymptotically stable in $\mathcal{D}_+ = \mathcal{D} \setminus \{0, 0\}$.*

Proof. The proof can be found in the Appendix. \square

The stability of the infected coexistence equilibrium of the proportions model (A.11a) and (A.11b) in \mathcal{D}_+ need not guarantee the stability of the infected coexistence of the model (3.2a) and (3.2b) and (3.2c) and (3.2d) in $\mathcal{D}^2 = \{(i_1, i_2, N_1, N_2) \in \mathbb{R}^4 | 0 \leq i_1, i_2 \leq 1, 0 \leq N_i \leq K_i, i = 1, 2\}$. However, if $\delta_i = 0$ for $i = 1, 2$, then the conditions under which the coexistence equilibrium (\hat{N}_1, \hat{N}_2) for the system of equations (3.2c) and (3.2d) is globally stable in the $N_1 - N_2$ plane do not depend on i_1 and i_2 . When $\delta_i = 0$ for $i = 1, 2$, then the term κ_{ij} reduces to ξ_{ij} , so conditions on stability of N_1, N_2 equilibria are given in terms of ξ_{ij} . Therefore, if these stability conditions are met for the coexistence equilibrium (namely $\xi_{21} > 0, \xi_{12} > 0$) then we can extend Theorem 5.4 to prove global asymptotic stability of the DFE and the endemic equilibrium of the model (3.2a) and (3.2b) with (3.2c) and (3.2d) in the domain \mathcal{D}^2 using the theory of asymptotically autonomous equations.

Theorem 5.5. Assume that $\delta_i = 0$ for $i = 1, 2$ and $\xi_{21} > 0, \xi_{12} > 0$. Then, if $\mathcal{R}_0^C < 1$ the DFE $E_3 = (0, 0, K_1^*, K_2^*)$ is globally asymptotically stable in $\hat{\mathcal{D}}_+^2 = \{(i_1, i_2, N_1, N_2) \in \mathbb{R}^4 \mid 0 \leq i_1, i_2 \leq 1, 0 < N_i \leq K_{ii}, i = 1, 2\}$ and if $\mathcal{R}_0^C > 1$ the unique infected coexistence equilibrium $E_6 = (\hat{i}_1, \hat{i}_2, \hat{N}_1, \hat{N}_2)$ is globally asymptotically stable with initial conditions in the region $\mathcal{D}_+^2 = \{(i_1, i_2, N_1, N_2) \in \mathbb{R}^4 \mid 0 < i_1, i_2 \leq 1, 0 < N_i \leq K_{ii}, i = 1, 2\}$.

Proof. The proof can be found in the Appendix. \square

5.5. Simulations for nonzero disease-related mortality

Consider the case in which the two species are identical except for the effect of the disease on their mortality ($\delta_1 \neq \delta_2$). For $i, j = 1, 2$, the parameters are as follows: $\beta_{ij} = 1$, $b_i = 0.8$, $d_i = 0.4$, $\gamma_i = 0$, and $K_{ii} = 8000$, $K_{ij} = 16,000$. The intrinsic growth rates are $r_i = b_i - d_i = 0.4$.

We expect endemic coexistence when the assumptions **(U1)**, **(U2)** and **(U3)** are met. To satisfy assumption **(U1)**, we need $r_k - \delta_k > 0$, and to satisfy assumption **(U2)** and **(U3)** we need $K_{kj}(1 - \delta_k/r_k) > K_{jj}$ which together implies that $\delta_k < 0.2$. For $\delta_k \in [0, 0.2]$ we have $\epsilon_k^* \leq 0$, for $k = 1, 2$. Numerical simulations confirmed that the endemic equilibrium is indeed feasible and stable when $\delta_k < 0.2$. Since the conditions **(U1)**, **(U2)** and **(U3)** are sufficient but not necessary, we expect and observed in simulations that feasibility and stability of the endemic equilibrium extends to larger values of δ_k for which $\epsilon_k^* > 0$ and that still give $\mathcal{R}_0^C > 1$.

In the first simulation we assume that all the competitive effects (density dependence) are incorporated in the birth terms, i.e. $\epsilon_{ij} = 1$, $\forall i, j = 1, 2$. In Fig. 7 using numerical computations we plot values of \mathcal{R}_0^C on the Left plot, values of κ_{12} (or ξ_{12}), and κ_{21} (or ξ_{21}) in the Center plot, and the feasibility and stability region S_B

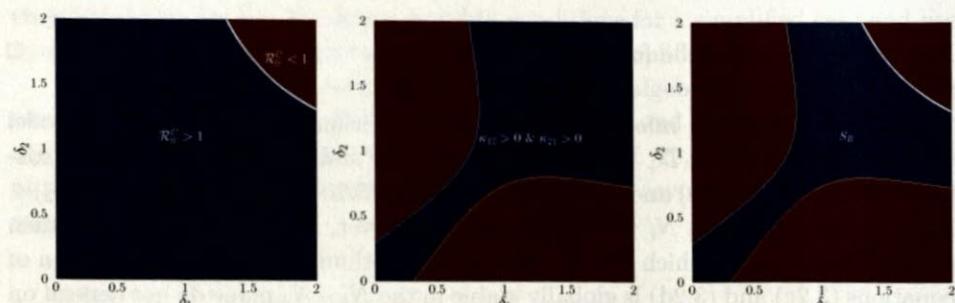


Fig. 7. Simulations for competition affecting only the birth rates, $\epsilon_{ij} = 1$; $i, j = 1, 2$. Left: In the blue region, δ_1 and δ_2 are such that $\mathcal{R}_0^C > 1$; in the red region, $\mathcal{R}_0^C < 1$ and the DFE is stable. The white curve is $\mathcal{R}_0^C = 1$. Center: The blue region represents the values of δ_1 and δ_2 for which the per capita growth rates of each species at the other species' equilibrium (infected when feasible, else uninfected), i.e., κ_{ij} , are strictly positive. Each species can invade the other in the blue region. Right: The region of feasibility and stability, S_B , of the endemic coexistence equilibrium. This region of endemic coexistence is larger than that of Figs. 8 and 9.

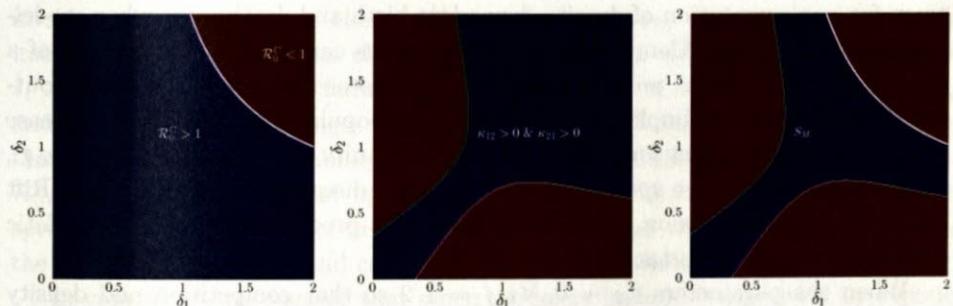


Fig. 8. Simulations for competition affecting both birth and death rates, $\epsilon_{11} = \epsilon_{12} = 0.6$ and $\epsilon_{21} = \epsilon_{12} = 0.4$. Subplots are analogous to scenarios in Fig. 7. The parameter region where the disease persists is smaller than in Fig. 7 while the species invasion (κ_{ij}) region is slightly larger.

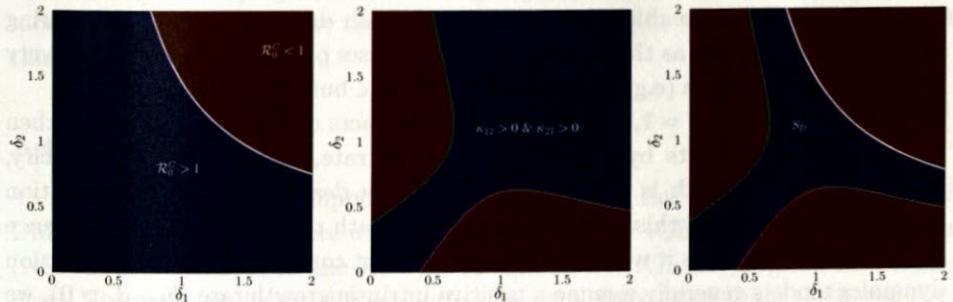


Fig. 9. Simulations for competition affecting only the death rate, $\epsilon_{ij} = 0$; $i, j = 1, 2$. Subplots are analogous to scenarios in Fig. 7. The parameter region where the disease persists is smallest of all scenarios while the species invasion region is larger. The stable region of the endemic coexistence equilibrium is smaller.

of the endemic equilibrium in the Right plot. The blue values in the Center plots indicate strictly positive per-capita rates of growth of each species at the other species only equilibria (κ_{ij} when the infected one host equilibria, E_4 and E_5 , are feasible, else ξ_{ij} when the uninfected one host equilibria, E_1 and E_2 , are feasible). We repeat the simulations for $\epsilon_{11} = \epsilon_{12} = 0.6$ and $\epsilon_{21} = \epsilon_{12} = 0.4$ in Fig. 8, and for $\epsilon_{ij} = 0$; $i, j = 1, 2$ in Fig. 9.

In all three simulations, we can see that the region of feasibility and stability of the endemic equilibrium is determined by the conditions $R_0^C > 1$, $\kappa_{21} > 0$ (or $\xi_{21} > 0$) and $\kappa_{12} > 0$ (or $\xi_{12} > 0$).

6. Discussion and Conclusion

Our analysis of two-species models incorporating standard incidence disease transmission and competition between species indicates that justification needs to be

given for implementation of density-dependent birth and death rates when modeling disease dynamics. Competition between species can change the outcome of a disease model, while the presence of a generalist disease can alter competitive outcomes. This work also implies that interaction of population dynamics and disease spread can be important for systems where community structure is changing (e.g., climate change, invasive species) and for zoonotic diseases (e.g., hanta virus, Rift Valley fever). We focus on competing species, but predator-prey and mutualistic dynamics are also important.

When the parameters $\epsilon_{ij} = 0, \forall i, j = 1, 2$ so that competition and density dependence acts only on the death rate of adult individuals, then at the carrying capacity, the density-dependent death rate is increased until it equals the birth rate, and the population reaches equilibrium. Since at carrying capacity the death rate is at a maximum (i.e., $d_i(N_i) = b_i$), then the loss of infected individuals due to natural death is greater than it would be without competition, hence \mathcal{R}_0 is lower. This is especially noticeable when recovery or death due to disease are occurring on a similar time scale as the birth or death processes or when there is no recovery or death due to disease (e.g., disease that is chronic but not fatal).

When $\epsilon_{ij} = 1, \forall i, j = 1, 2$ so that competition acts on the birth rate only, then density dependence acts by decreasing the birth rate, and at carrying capacity, density-dependent birth is decreased to equal the death rate so the population reaches equilibrium. In this case, the *per capita* death rate does not change, hence \mathcal{R}_0 remains the same as it would for a model without competition. Since population dynamics models generally assume a positive intrinsic growth rate ($b_i - d_i > 0$), we showed that $\mathcal{R}_0(\epsilon = 0) < \mathcal{R}_0(\epsilon) < \mathcal{R}_0(\epsilon = 1)$ for the single species model, so that the basic reproduction number is always larger when competition acts primarily on the birth rate. When $0 < \epsilon_{ij} < 1$, then the loss of infected individuals is a weighted average of the birth and deaths rates as well as recovery and death due to disease. Especially a telling subcase for chronic, nonfatal diseases is where $\delta_i = \gamma_i = 0$ so that the loss of infected individuals is exactly proportional to the inverse of the death and/or birth rates. The difference between \mathcal{R}_0 as competition varies between affecting birth and death is also quite pronounced when the intrinsic growth rate is high and recovery or death due to disease are on a similar time scale as either birth or death processes. For example, if an individual lives for several years but recovers from a disease in only a few days and if the intrinsic growth rate is relatively small, then the effect of chosen implementation of competition will be minimal. However, if a disease is chronic and may cause death on a similar time scale to natural death then the method chosen to implement competition could very well have a significant effect on the outcome of the model, specifically with regards to successful invasion of the disease.

Implementation of competition does not only affect the basic reproduction number. It also effects the relative densities of the species at equilibrium and affects the conditions for stability of equilibria. The special case where $\delta_i = 0$ that we considered in Sec. 5.4 suggests that for small death due to disease, the successful

invasion of the disease in the population depends very directly on \mathcal{R}_0^C , which itself depends on the values chosen for ϵ_{ij} . Numerical simulations with different $\delta_i > 0, i = 1, 2$ in Sec. 5.5 indicate that this dependence on \mathcal{R}_0^C as well as on κ_{12} and κ_{21} holds for wide ranges of parameter values. Additionally, it is easy to see that the conditions for stability of the one-host equilibria based on values of \mathcal{R}_0^1 , \mathcal{R}_0^2 , κ_{12} and κ_{21} all depend upon the choice of ϵ_{ij} . So, competition and disease spread can affect each other in nontrivial and nonlinear ways. Disease can change the competitive outcome and competition can change disease invasion potential.

In conclusion, we suggest that when modelers include competition or logistic growth dynamics in disease models, whether with one or multiple species, the choice of where to include competition has to be considered carefully. One simple way to test the robustness of results of a model with competition and disease is sensitivity analysis (for e.g., see Ref. 8), focusing on sensitivity of the model outcome to the choice of ϵ_{ij} . If varying the values of ϵ_{ij} significantly changes the outcome, then more careful thought about the mode of competition, or at least an indication of this sensitivity is warranted.

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Appendix A. Proofs

Proof of Lemma 5.1

Proof. First, substitute $N_1^* = K_{11}(1 - \frac{\delta_1}{r_1}i_1^*)$ and $N_2^* = 0$ into Eqs. (3.2a) and (3.2b) to get

$$\frac{di_1}{dt} = \beta_{12}i_2(1 - i_1) + i_1(\beta_{11} - \delta_1 + \delta_1\epsilon_{11})\left(\frac{r_1(\epsilon_{11} - \epsilon_1^*)}{\beta_{11} - \delta_1 + \delta_1\epsilon_{11}} - i_1\right), \quad (\text{A.1})$$

$$\frac{di_2}{dt} = i_1(\beta_{21} - \omega i_2) + i_2\left((1 - i_2)(\beta_{22} - \delta_2) - b_2 - \gamma_2 + \frac{r_2\epsilon_{21}K_{11}}{K_{21}}\right). \quad (\text{A.2})$$

At equilibrium, the rates of change are zero, so we set (A.1) and (A.2) equal to zero and solve to get

$$i_2 = \frac{i_1[r_1(\epsilon_1^* - \epsilon_{11}) + i_1(\beta_{11} - \delta_1 + \delta_1\epsilon_{11})]}{\beta_{12}(1 - i_1)} = f_1(i_1), \quad (\text{A.3})$$

$$i_1 = \frac{i_2[-r_2(\frac{\epsilon_{21}K_{11}}{K_{21}} - \epsilon_2^*) + i_2(\beta_{22} - \delta_2)]}{\beta_{21} - \omega i_2} = f_2(i_2), \quad (\text{A.4})$$

where $\omega = \beta_{21} + \frac{r_2\epsilon_{21}K_{11}}{K_{21}}\frac{\delta_1}{r_1}$. The function f_1 has an asymptote at $i_1 = 1$, while the function f_2 has an asymptote at $i_2 = \beta_{21}/\omega \leq 1$. When $\epsilon_{21} = 0$, the asymptote for f_2 moves to $i_2 = 1$.

When $i_1 = 0$, $di_1/dt = \beta_{12}i_2 > 0$ and when $i_2 = 0$, $di_2/dt = \beta_{21}i_1 > 0$. At $i_1 = 1$, $\frac{di_1}{dt} = -r_1(1 - \epsilon_{11}) - \delta_1\epsilon_{11} - d_1 - \gamma_1 < 0$ and at $i_2 = \beta_{21}/\omega$,

$$\frac{di_2}{dt} = \frac{\beta_{21}}{\omega}\left(r_2\left(\frac{\epsilon_{21}K_{11}}{K_{21}} - \epsilon_2^*\right) - \frac{\beta_{21}}{\omega}(\beta_{22} - \delta_2)\right) < 0, \quad (\text{A.5})$$

under the assumptions $\epsilon_2^* \in (0, 1)$ ($\beta_{22} > \delta_2$) and $\bar{R}_{0,2} < 1$. Thus, the domain $\mathcal{D}^* = \{(i_1, i_2) \in \mathbb{R}^2 | 0 < i_1 < 1, 0 < i_2 < \frac{\beta_{21}}{\omega}\}$ is invariant for the system (A.1) and (A.2). The nullclines always intersect at the origin.

Given that the region \mathcal{D}^* is invariant, we show that the one-host infected equilibrium E_4 is unique by examining the nullclines (A.3) and (A.4). First,

$$\left.\frac{df_1}{di_1}\right|_{i_1=0} = \frac{r_1(\epsilon_1^* - \epsilon_{11})}{\beta_{12}}, \quad \text{and} \quad \left.\frac{df_2}{di_2}\right|_{i_2=0} = \frac{r_2(\epsilon_2^* - \frac{\epsilon_{21}K_{11}}{K_{21}})}{\beta_{21}}. \quad (\text{A.6})$$

Also, both f_1 and f_2 are concave upon their respective axes since

$$\frac{d^2 f_1}{di_1^2} = \frac{2(b_1(1 - \epsilon_{11}) + d_1\epsilon_{11} + \gamma_1 + \delta_1\epsilon_{11})}{\beta_{12}(1 - i_1)^3} > 0,$$

$$\frac{d^2 f_2}{di_2^2} = \frac{2\beta_{21}\left(\frac{\beta_{21}}{\omega}(\beta_{22} - \delta_2) + r_2(\epsilon_2^* - \frac{\epsilon_{21}K_{11}}{K_{21}})\right)}{\omega^2(\frac{\beta_{21}}{\omega} - i_2)^3} > 0,$$

when the assumptions $\beta_{22} > \delta_2$ and $\bar{\mathcal{R}}_{0,2} < 1$ hold. Under these assumptions we now have two cases for which a unique one-host infected equilibrium is guaranteed.

First, when $\epsilon_{11} > \epsilon_1^*$ (i.e., $\mathcal{R}_{0,1} > 1$) then $\frac{df_1}{di_1}|_{i_1=0} < 0$ and the nullclines intersect only once in \mathcal{D}^* . Second, if $\epsilon_{11} < \epsilon_1^*$ then both $\frac{df_1}{di_1}|_{i_1=0} > 0$ and $\frac{df_2}{di_2}|_{i_2=0} > 0$ and in order for the nullclines to intersect only once, the condition $\beta_{21}\beta_{12} > r_1(\epsilon_1^* - \epsilon_{11})r_2(\epsilon_2^* - \frac{\epsilon_{21}K_{11}}{K_{21}})$ must hold so that

$$\left. \frac{df_1}{di_1} \right|_{i_1=0} < \frac{1}{\left. \frac{df_2}{di_2} \right|_{i_2=0}}.$$

Thus, under the conditions of Lemma 5.1, the one-host infected equilibrium E_4 exists and is unique in \mathcal{D}^* . \square

Proof of Theorem 5.1

Proof. The Jacobian of system (3.2) evaluated at $E_4 = (i_1^4, i_2^4, N_1^4, 0)$ is the 4×4 matrix

$$J(E_4) = \begin{bmatrix} J_{41} & J_{42} \\ 0 & \kappa_{21} \end{bmatrix}, \quad (\text{A.7})$$

where J_{41} is the 3×3 matrix,

$$J_{41} = \begin{bmatrix} A_1 & \beta_{12}(1 - i_1^4) & \frac{r_1\epsilon_{11}i_1^4}{K_{11}} \\ \beta_{21}(1 - i_2^4) & A_2 & \frac{r_2\epsilon_{21}i_2^4}{K_{21}} \\ -\delta_1 N_1^4 & 0 & \frac{-r_1 N_1^4}{K_{11}} \end{bmatrix}, \quad (\text{A.8})$$

with

$$A_1 = (\beta_{11} - \delta_1 - \gamma_1 - b_1(1 + \epsilon_{11}) - d_1\epsilon_{11}) - \beta_{12}i_2^4 - i_1^4(2(\beta_{11} - \delta_1) + \delta_1\epsilon_{11}),$$

$$A_2 = \left(\beta_{22} - \delta_2 - \gamma_2 - b_2 + \frac{r_2\epsilon_{21}K_{11}}{K_{21}} \right) - \omega i_1^4 - 2i_2^4(\beta_{22} - \delta_2),$$

and where $\omega = \beta_{21} + \eta$ and $\eta = \frac{r_2\epsilon_{21}K_{11}}{K_{21}}\frac{\delta_1}{r_1}$. The matrix J_{42} is a nonzero 3×1 column vector and 0 is a 1×3 row vector of zeros. The equilibrium E_4 is locally asymptotically stable if and only if $\kappa_{21} < 0$ and the eigenvalues of J_{41} are negative.

We can write the characteristic polynomial of J_{41} as $P(\lambda) = \lambda^3 + a_1\lambda^2 + a_2\lambda + a_3$ where the coefficients $a_i, i = 1, 2, 3$ are computed as

- (1) $a_1 = \zeta - A_1 - A_2$, with $\zeta = \frac{r_1 N_1^4}{K_{11}}$,
- (2) $a_2 = A_1 A_2 - \beta_{12} \beta_{21} (1 - i_1^4)(1 - i_2^4) + \zeta (\delta_1 \epsilon_{11} i_1^4 - A_1 - A_2)$,
- (3) $a_3 = \zeta [-A_2 \delta_1 \epsilon_{11} i_1^4 + \beta_{12} (1 - i_1^4) \eta i_2^4 + A_1 A_2 - \beta_{12} \beta_{21} (1 - i_1^4)(1 - i_2^4)]$.

The eigenvalues of matrix J_{41} are the roots of its characteristic polynomial $P(\lambda)$. To prove that the eigenvalues of J_{41} are negative, we will invoke the Routh-Hurwitz criteria,³¹ which states that the roots of the characteristic polynomial $P(\lambda)$ are negative or have negative real parts if and only if $a_1 > 0$, $a_3 > 0$ and $a_1 a_2 > a_3$.

The term A_1 can be simplified by substituting Eq. (3.2a) for $\frac{di_1}{dt} = 0$ computed at E_4 into A_1 to get $A_1 = \frac{-\beta_{12} i_2^4}{i_1^4} - i_1^4 (\beta_{11} - \delta_1)$. Similarly, we substitute the Eq. (3.2b) for $\frac{di_2}{dt} = 0$ computed at E_4 into A_2 to get $A_2 = \frac{-\beta_{21} i_1^4}{i_2^4} - i_2^4 (\beta_{22} - \delta_2)$. By the assumptions of the theorem, $\beta_{11} > \delta_1$ and $\beta_{22} > \delta_2$ so that $A_1 < 0$, $A_2 < 0$. Also, $\zeta = \frac{r_1 N_1^4}{K_{11}} > 0$. Thus, the coefficient $a_1 = \zeta - A_1 - A_2 > 0$.

Next, $a_3 = \zeta [-A_2 \delta_1 \epsilon_{11} i_1^4 + \beta_{12} (1 - i_1^4) \eta i_2^4 + A_1 A_2 - \beta_{12} \beta_{21} (1 - i_1^4)(1 - i_2^4)]$. We have

$$A_1 A_2 = \beta_{12} \beta_{21} + i_1^4 (\beta_{11} - \delta_1) \beta_{21} \frac{i_1^4}{i_2^4} + i_2^4 (\beta_{22} - \delta_2) \beta_{12} \frac{i_2^4}{i_1^4}$$

$$+ i_1^4 i_2^4 (\beta_{11} - \delta_1) (\beta_{22} - \delta_2).$$

Since both $i_1^4, i_2^4 < 1$, we observe that $\beta_{12} \beta_{21} - \beta_{12} \beta_{21} (1 - i_1^4)(1 - i_2^4) > 0$, hence $C = A_1 A_2 - \beta_{12} \beta_{21} (1 - i_1^4)(1 - i_2^4) > 0$. Then, since every other term of a_3 is positive under the assumptions $\beta_{11} > \delta_1$ and $\beta_{22} > \delta_2$, we conclude that $a_3 > 0$.

Finally, we want to show that $a_1 a_2 > a_3$ where $a_2 = A_1 A_2 - \beta_{12} \beta_{21} (1 - i_1^4)(1 - i_2^4) + \zeta (\delta_1 \epsilon_{11} i_1^4 - A_1 - A_2)$. Now, $a_1 a_2$ can be written as

$$a_1 a_2 = (-A_1 - A_2) a_2 + \zeta C + \zeta^2 (\delta_1 \epsilon_{11} - A_2 - A_1). \quad (A.9)$$

We have

$$a_1 a_2 - a_3 = [(-A_1 - A_2) a_2 + \zeta C + \zeta^2 (\delta_1 \epsilon_{11} - A_2 - A_1)]$$

$$- [\zeta C - \zeta A_2 \delta_1 \epsilon_{11} i_1^4 + \zeta \beta_{12} (1 - i_1^4) \eta i_2^4]$$

$$= (-A_1 - A_2) C + \zeta (\delta_1 \epsilon_{11} i_1^4) (-A_1 - A_2) + \zeta (-A_1 - A_2)^2$$

$$+ \zeta^2 (\delta_1 \epsilon_{11} - A_2 - A_1) + \zeta A_2 \delta_1 \epsilon_{11} i_1^4 - \zeta \beta_{12} (1 - i_1^4) \eta i_2^4$$

$$= [-(A_1 + A_2) C - \zeta \delta_1 \epsilon_{11} i_1^4 A_1 + \zeta^2 (\delta_1 \epsilon_{11} - A_2 - A_1) + \zeta (A_1^2 + A_2^2)]$$

$$+ \zeta (2 A_1 A_2 - \beta_{12} (1 - i_1^4) \eta i_2^4)$$

$$= B + \zeta (2 A_1 A_2 - \beta_{12} (1 - i_1^4) \eta i_2^4),$$

where $B = [-(A_1 + A_2) C - \zeta \delta_1 \epsilon_{11} i_1^4 A_1 + \zeta^2 (\delta_1 \epsilon_{11} - A_2 - A_1) + \zeta (A_1^2 + A_2^2)]$.

From Lemma 5.1, we have $i_2^4 < \beta_{21}/(\beta_{21} + \eta)$. Hence $2A_1A_2 - \beta_{12}(1 - i_1^4)\eta i_2^4 > 2A_1A_2 - \beta_{12}\beta_{21}(1 - i_1^4)\frac{\eta}{\beta_{21} + \eta} > 0$. This can be seen by examining the first term of A_1A_2 , $\beta_{12}\beta_{21}$, which is greater than $\beta_{12}\beta_{21}(1 - i_1^4)\frac{\eta}{\beta_{21} + \eta}$ since $(1 - i_1^4)\frac{\eta}{\beta_{21} + \eta} < 1$. Thus, since B is positive and $2A_1A_2 > \zeta\beta_{12}(1 - i_1^4)\eta i_2^4$, we see that $a_1a_2 - a_3 > 0$ and hence $a_1a_2 > a_3$. Thus, the Routh-Hurwitz criteria for $P(\lambda)$ is proved, the eigenvalues of J_{41} are negative and the infected one-host equilibrium E_4 is stable. \square

Proof of Theorem 5.3

Proof. We begin by setting (3.2c) and (3.2d) equal to zero, so that we can examine i_1 and i_2 on the cross section of space where the N_i 's are at the equilibrium, (\hat{N}_1, \hat{N}_2) , or where $N'_1 = 0$ and $N'_2 = 0$, so that

$$\hat{N}_1(i_1, i_2) = K_1^* \left(\frac{K_{12}(1 - \frac{\delta_1 i_1}{r_1}) - K_{22}(1 - \frac{\delta_2 i_2}{r_2})}{K_{12} - K_{22}} \right), \quad (\text{A.10a})$$

$$\hat{N}_2(i_1, i_2) = K_2^* \left(\frac{K_{21}(1 - \frac{\delta_2 i_2}{r_2}) - K_{11}(1 - \frac{\delta_1 i_1}{r_1})}{K_{21} - K_{11}} \right), \quad (\text{A.10b})$$

for $(i_1, i_2) \in D = [0, 1] \times [0, 1]$, and $K_i^*, i = 1, 2$ as defined in (4.3). Assumptions (U1), (U2) and (U3) guarantee that $\hat{N}_1(i_1, i_2)$ and $\hat{N}_2(i_1, i_2)$ are positive. We then substitute \hat{N}_1 and \hat{N}_2 into Eqs. (3.2a) and (3.2b) resulting in the equations

$$\begin{aligned} \frac{di_1}{dt} &= (1 - i_1)(\beta_{11}i_1 + \beta_{12}i_2 - \delta_1 i_1) \\ &\quad - i_1[d_1\epsilon_1 + b_1(1 - \epsilon_1) + \gamma_1 + \epsilon_1\delta_1 i_1], \end{aligned} \quad (\text{A.11a})$$

$$\begin{aligned} \frac{di_2}{dt} &= (1 - i_2)(\beta_{22}i_2 + \beta_{21}i_1 - \delta_2 i_2) \\ &\quad - i_2[d_2\epsilon_2 + b_2(1 - \epsilon_2) + \gamma_2 + \epsilon_2\delta_2 i_2]. \end{aligned} \quad (\text{A.11b})$$

The model (A.11a) and (A.11b) is different from the one that is derived in Ref. 29; however similar techniques can be used to analyze it which we now consider. Setting (A.11a) and (A.11b) equal to zero, we obtain the nullclines for i_1 and i_2 in the plane where N_1 and N_2 are at equilibrium as

$$i_2 = f_1(i_1) = \frac{i_1[d_1\epsilon_1 + b_1(1 - \epsilon_1) + \gamma_1 + \epsilon_1\delta_1 i_1 - (1 - i_1)(\beta_{11} - \delta_1)]}{(1 - i_1)\beta_{12}}, \quad (\text{A.12a})$$

$$i_1 = f_2(i_2) = \frac{i_2[d_2\epsilon_2 + b_2(1 - \epsilon_2) + \gamma_2 + \epsilon_2\delta_2 i_2 - (1 - i_2)(\beta_{22} - \delta_2)]}{(1 - i_2)\beta_{21}}. \quad (\text{A.12b})$$

We note that the domain $D = [0, 1] \times [0, 1]$ is invariant for the system (A.11a) and (A.11b), since if $i_k = 0$ then $di_k/dt > 0$ and if $i_k = 1$ then $di_k/dt < 0$, for $k = 1, 2$, in $D_+ = D \setminus \{0, 0\}$. The nullclines always intersect at the origin. The

function f_1 has an asymptote at $i_1 = 1$, f_2 has an asymptote at $i_2 = 1$,

$$\frac{df_1}{di_1} \Big|_{i_1=0} = \frac{d_1\epsilon_1 + b_1(1 - \epsilon_1) + \gamma_1 + \delta_1 - \beta_{11}}{\beta_{12}} = \frac{r_1(\epsilon_1^* - \epsilon_1)}{\beta_{12}}, \quad (\text{A.13})$$

and

$$\frac{df_2}{di_2} \Big|_{i_2=0} = \frac{d_2\epsilon_2 + b_2(1 - \epsilon_2) + \delta_2 + \gamma_2 - \beta_{22}}{\beta_{21}} = \frac{r_2(\epsilon_2^* - \epsilon_2)}{\beta_{21}}. \quad (\text{A.14})$$

Also,

$$\frac{d^2 f_k}{di_k^2} = \frac{2(d_k\epsilon_k + b_k(1 - \epsilon_k) + \gamma_k + \epsilon_k\delta_k)}{\beta_{kj}(1 - i_k)^3} > 0, \quad k, j = 1, 2, k \neq j, 0 \leq i_k < 1, \quad (\text{A.15})$$

which implies that the nullclines $i_j = f_k(i_k)$, $k, j = 1, 2, k \neq j$ are concave up on $0 \leq i_k < 1$.

Sufficiency part of proof: We break this part up into four cases:

Case 1. Assume that $\mathcal{R}_{0,1} > 1$ and $\mathcal{R}_{0,2} > 1$ (i.e., $\epsilon_i > \epsilon_i^*$ for $i = 1, 2$). Then, we can see from (2.3) that $\beta_{ii} > b_i(1 - \epsilon_i) + d_i\epsilon_i + \delta_i + \gamma_i$, for $i = 1, 2$. Using this in Eqs. (A.13) and (A.14), we find that for $k = 1, 2$

$$\frac{df_k}{di_k} \Big|_{i_k=0} < 0, \quad (\text{A.16})$$

which implies that there is one point of intersection in \mathcal{D} (see Fig. 10).

Case 2. Assume $\mathcal{R}_{0,1} < 1$ and $\mathcal{R}_{0,2} > 1$, i.e., $T_2 > 1$. Then $\frac{df_1}{di_1}|_{i_1=0} > 0$ and $\frac{df_2}{di_2}|_{i_2=0} < 0$, so that f_1 and f_2 again intersect uniquely in \mathcal{D} (see Fig. 10).

Case 3. Assume $\mathcal{R}_{0,1} > 1$ and $\mathcal{R}_{0,2} < 1$, i.e., $T_1 > 1$. Changing roles in Case 2, we again have that f_1 and f_2 intersect uniquely in \mathcal{D} .

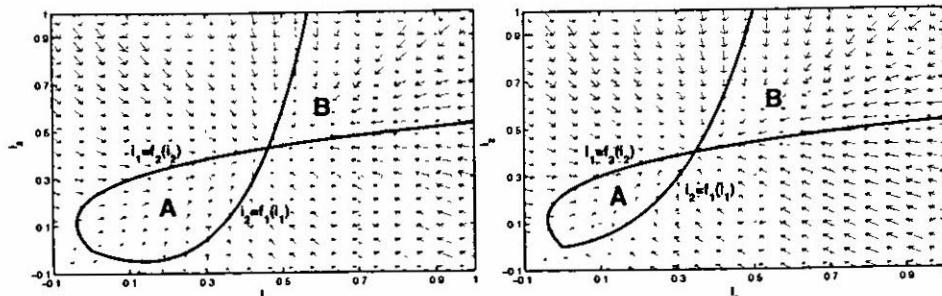


Fig. 10. (Left) Isoclines for the case where both $\mathcal{R}_{0,1}, \mathcal{R}_{0,2} > 1$. (Right) Isoclines for the case where $\mathcal{R}_{0,1} < 1$ and $\mathcal{R}_{0,2} > 1$. Disease-related parameters for both are $\beta_{11} = 1.8$, $\beta_{22} = 3.2$, $\beta_{12} = 1.1$ and $\beta_{21} = 1.1$. The parameters related to population dynamics for both are $b_1 = 1$, $b_2 = 0.5$, $d_1 = 1$, $d_2 = 2$ and $\epsilon_{ij} = 1$ for $i, j = 1, 2$.

Case 4. Lastly, we consider the case where $\mathcal{R}_{0,1} < 1$ and $\mathcal{R}_{0,2} < 1$, and $(1 - \mathcal{R}_{0,1})(1 - \mathcal{R}_{0,2}) < \mathcal{R}_{12}\mathcal{R}_{21}$, i.e., both the type reproduction numbers are greater than 1, $T_1 > 1, T_2 > 1$. This implies that $\frac{df_k}{dt_k}|_{t_k=0} > 0$ for $k = 1, 2$. In order for the nullclines to cross in \mathcal{D} , we must also have

$$\left. \frac{df_1}{dt_1} \right|_{t_1=0} < \frac{1}{\left. \frac{df_2}{dt_2} \right|_{t_2=0}}. \quad (\text{A.17})$$

This is equivalent to $(1 - \mathcal{R}_{0,1})(1 - \mathcal{R}_{0,2}) < \mathcal{R}_{12}\mathcal{R}_{21}$, which holds by assumption for Case 4 (see Fig. 11).

Necessary part of proof: Assume that there exists a unique endemic equilibrium but that conditions (a) and (b) of Theorem 5.3 do not hold. So, $\mathcal{R}_{0,i} < 1$ for $i = 1, 2$ and $(1 - \mathcal{R}_{0,1})(1 - \mathcal{R}_{0,2}) \geq \mathcal{R}_{12}\mathcal{R}_{21}$. This implies that $\frac{df_k}{dt_k}|_{t_k=0} > 0$ for $k = 1, 2$. However, the condition $\left. \frac{df_1}{dt_1} \right|_{t_1=0} < \frac{1}{\left. \frac{df_2}{dt_2} \right|_{t_2=0}}$ no longer holds, hence the nullclines do not intersect in the interior of \mathcal{D} , which contradicts the assumption of existence of a unique endemic equilibrium (see Fig. 11). \square

We note that we did not assume the condition $\epsilon_k^* \in (0, 1)$, $k = 1, 2$ to hold in the above proof. In particular, the derivatives in (A.13) and (A.14) will be negative if either $\epsilon_k > \epsilon_k^*$, when $\epsilon_k^* \in (0, 1)$, $k = 1, 2$ or $\epsilon_k^* < 0$, $k = 1, 2$.

Proof of Theorem 5.4

Proof. Suppose $\mathcal{R}_0^C < 1$. Then by Theorem 5.3 there is no infected coexistence equilibrium. The only equilibrium for (A.11a) and (A.11b) is the origin [which corresponds to the DFE $(0, 0, K_1^*, K_2^*)$ for (3.2a)-(3.2d)] and is locally asymptotically stable in \mathcal{D} by Ref. 25.

By the Poincaré–Bendixson Trichotomy,³¹ since the solutions of our system are bounded and the only equilibrium in the region $\mathcal{D} = [0, 1] \times [0, 1]$ for (A.11a) and

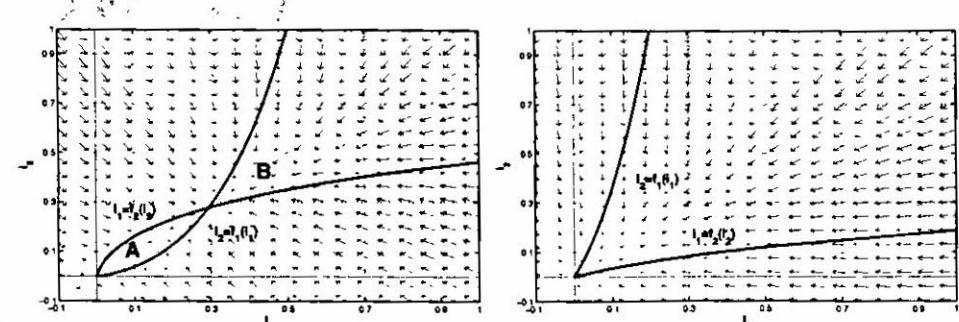


Fig. 11. (Left) Isoclines for the case where $\mathcal{R}_{0,1}, \mathcal{R}_{0,2} < 1$ but $(1 - \mathcal{R}_{0,1})(1 - \mathcal{R}_{0,2}) < \mathcal{R}_{12}\mathcal{R}_{21}$. (Right) Isoclines for the case where neither condition (i) nor (ii) of Theorem 5.3 hold and $\epsilon_{ij} = 1$. Disease-related parameters for both are $\beta_{11} = 1.5$, $\beta_{22} = 2$, $\beta_{12} = 0.2$ and $\beta_{21} = 0.2$. The parameters related to population dynamics for both are $b_1 = 1$, $b_2 = 0.5$, $d_1 = 1$, $d_2 = 2$ and $\epsilon_{ij} = 1$ for $i, j = 1, 2$.

(A.11b) is the origin, which is stable, there are no periodic solutions in the region and the origin is globally stable for (A.11a) and (A.11b).

Next suppose $\mathcal{R}_0^C > 1$. Then by Theorem 5.3 there is a unique infected coexistence equilibrium, (\hat{i}_1, \hat{i}_2) , for (A.11a) and (A.11b). We will first show that no solution of (A.11a) and (A.11b) in the invariant region \mathcal{D}_+ will approach the origin. The Jacobian for (A.11a) and (A.11b) evaluated at the origin is

$$\begin{aligned}\mathcal{J}(0,0) &= \begin{bmatrix} \beta_{11} - (d_1\epsilon_1 + b_1(1-\epsilon_1) + \delta_1 + \gamma_1) & \beta_{12} \\ \beta_{21} & \beta_{22} - (d_2\epsilon_2 + b_2(1-\epsilon_2) + \delta_2 + \gamma_2) \end{bmatrix}, \\ &= \begin{bmatrix} r_1(\epsilon_1 - \epsilon_1^*) & \beta_{12} \\ \beta_{21} & r_2(\epsilon_2 - \epsilon_2^*) \end{bmatrix}\end{aligned}$$

which has eigenvalues

$$\lambda_1, \lambda_2 = \frac{1}{2}[(\beta_{11} - D_1^*) + (\beta_{22} - D_2^*) \pm \sqrt{[(\beta_{11} - D_1^*) - (\beta_{22} - D_2^*)]^2 + 4\beta_{21}\beta_{12}}], \quad (\text{A.18})$$

where $D_i^* = \delta_i + \gamma_i + d_i\epsilon_i + b_i(1-\epsilon_i)$ is $D_i(K_1^*, K_2^*)$ for the case $\epsilon_{ii} = \epsilon_{ij} = \epsilon_i$ for $i = 1, 2$. Since $\mathcal{R}_0^C > 1$ then we know at least one of $\beta_{11} - D_1^*$ and $\beta_{22} - D_2^*$ are positive or both are negative and $(\beta_{11} - D_1^*)(\beta_{22} - D_2^*) < \beta_{12}\beta_{21}$, both cases for which $\lambda_1 > 0$. Now, if $\lambda_2 > 0$ as well then the origin is a repeller. If, on the other hand, $\lambda_2 < 0$ then the eigenvector of λ_2 is

$$\begin{bmatrix} x_1 \\ x_2 \end{bmatrix} = \begin{bmatrix} \frac{1}{\beta_{21}}(\lambda_2 - (\beta_{22} - D_2^*)) \\ 1 \end{bmatrix}. \quad (\text{A.19})$$

Since $\lambda_2 < 0$ then we can see that $x_1 < 0$ also and the stable manifold of the origin does not lie in \mathcal{D}_+ . Hence, none of the solutions in \mathcal{D}_+ approach the DFE.

Lastly, we need to show that no periodic solutions exist inside \mathcal{D}_+ . We can see by examining the phase plane of the proportions system (A.11a) and (A.11b) that the region, A (see Figs. 10 and 11), enclosed by the nullclines of i_1 and i_2 but to the left of and below the endemic equilibrium is invariant. Along the i_1 nullcline in A, $di_2/dt > 0$ and along the i_2 nullcline in A, $di_1/dt > 0$, which proves that the region A is invariant. The region to the right of and above the endemic equilibrium, B, enclosed by the nullclines is also invariant with $di_2/dt < 0$ along the i_1 nullcline and $di_1/dt < 0$ along the i_2 nullcline. So, any solution trajectory that tries to orbit around the endemic equilibrium will be “trapped” in either region A or region B and will approach the endemic equilibrium. Thus, no periodic solutions exist. Since the solutions are bounded, we can use the Poincaré–Bendixson Trichotomy to deduce that all solution trajectories approach the infected coexistence equilibrium, and therefore it is globally asymptotically stable in the region \mathcal{D}_+ . \square

Proof of Theorem 5.5

Proof. Consider the nonautonomous system with Eqs. (3.2a) and (3.2b) rewritten as:

$$\begin{aligned}\frac{di_1}{dt} &= (1 - i_1)(\beta_{11}i_1 + \beta_{12}i_2) \\ &\quad - \left(r_1 \left(1 - \frac{\epsilon_1 N_1(t)}{K_{11}} - \frac{\epsilon_1 N_2(t)}{K_{12}} \right) + d_1 + \gamma_1 \right) i_1,\end{aligned}\quad (\text{A.20a})$$

$$\begin{aligned}\frac{di_2}{dt} &= (1 - i_2)(\beta_{22}i_2 + \beta_{21}i_1) \\ &\quad - \left(r_2 \left(1 - \frac{\epsilon_2 N_2(t)}{K_{22}} - \frac{\epsilon_2 N_1(t)}{K_{21}} \right) + d_2 + \gamma_2 \right) i_2,\end{aligned}\quad (\text{A.20b})$$

in which N_i is a solution of

$$\frac{dN_1}{dt} = r_1 \left(1 - \frac{N_1}{K_{11}} - \frac{N_2}{K_{12}} \right) N_1, \quad (\text{A.21a})$$

$$\frac{dN_2}{dt} = r_2 \left(1 - \frac{N_2}{K_{22}} - \frac{N_1}{K_{21}} \right) N_2. \quad (\text{A.21b})$$

We can write system (A.20a) and (A.20b) as

$$x' = f(x, t) \quad (\text{A.22})$$

where x is the vector $(i_1, i_2)^T$, and the components of f are the right-hand sides in (A.20a) and (A.20b). The equilibrium of system (A.21a) and (A.21b) can be found independently of i_1 and i_2 . Under the assumption $\xi_{21} > 0, \xi_{12} > 0$, the coexistence equilibrium (K_1^*, K_2^*) of this system is locally (and globally) asymptotically stable independently of i_1 and i_2 in its basin of attraction. Hence, $N_i(t) \rightarrow K_i^*$ as $t \rightarrow \infty$ in $\hat{\mathcal{D}}_+^2$ for $i = 1, 2$. We then substitute \hat{N}_i into system (A.22) to get

$$\begin{aligned}\frac{di_1}{dt} &= (1 - i_1)(\beta_{11}i_1 + \beta_{12}i_2) \\ &\quad - \left(r_1 i_1 \left(1 - \frac{\epsilon_1 K_1^*}{K_{11}} - \frac{\epsilon_1 K_2^*}{K_{12}} \right) + d_1 + \gamma_1 \right) i_1,\end{aligned}\quad (\text{A.23a})$$

$$\begin{aligned}\frac{di_2}{dt} &= (1 - i_2)(\beta_{22}i_2 + \beta_{21}i_1) \\ &\quad - \left(r_2 i_2 \left(1 - \frac{\epsilon_2 K_2^*}{K_{22}} - \frac{\epsilon_2 K_1^*}{K_{21}} \right) + d_2 + \gamma_2 \right) i_2.\end{aligned}\quad (\text{A.23b})$$

Therefore, system (A.22) is an asymptotically autonomous system and has limit equations given by (A.23a) and (A.23b) which we can rewrite as

$$x' = h(x) \quad (\text{A.24})$$

in the region $\hat{\mathcal{D}}_+^2$.

We now consider two cases. For the first case, we assume that $\mathcal{R}_0^G < 1$. By Theorem 5.4, when $N_1 = K_1^*$ and $N_2 = K_2^*$ are at the (globally stable) coexistence equilibrium, the DFE for system (A.23a) and (A.23b) is unique and globally

asymptotically stable in the region \mathcal{D} . Therefore, by Theorem 4.1 from Ref. 30, the DFE for system (A.22) is also globally stable in the region $\hat{\mathcal{D}}_+^2$.

For case two, assuming $\mathcal{R}_0^C > 1$ we consider the endemic equilibrium corresponding to (\hat{i}_1, \hat{i}_2) . Again, by Theorem 5.4 (which holds true when $\delta_k = 0, k = 1, 2$), when N_1 and N_2 are at the (globally stable) coexistence equilibrium $\hat{N}_1 = K_1^*, \hat{N}_2 = K_2^*$, the endemic equilibrium for system (A.24) is unique and globally stable in \mathcal{D}_+ . Therefore, by Theorem 4.1 from Ref. 30, the endemic equilibrium for system (A.22) is globally asymptotically stable in the region \mathcal{D}_+^2 . \square

Ultimate bounds for the total population size

Here we derive ultimate bounds for the total population size, defined by equations (3.2c) and (3.2d), under which the presence of both species is guaranteed for all time. We can rewrite equations (3.2c) and (3.2d) as a pair of nonautonomous Lotka-Volterra equations in the form

$$\frac{dN_1}{dt} = N_1 \left(r_1^\delta(t) - \frac{r_1}{K_{11}} N_1 - \frac{r_1}{K_{12}} N_2 \right), \quad (\text{A.25a})$$

$$\frac{dN_2}{dt} = N_2 \left(r_2^\delta(t) - \frac{r_2}{K_{22}} N_2 - \frac{r_2}{K_{21}} N_1 \right), \quad (\text{A.25b})$$

where the functions $r_k^\delta(t) = r_k - \delta_k i_k(t)$, $k = 1, 2$. We make the assumption

(U1) $\tilde{r}_k = r_k - \delta_k > 0$, $k = 1, 2$.

The functions $i_k(t)$, $k = 1, 2$ are continuous and bounded above and below on $0 \leq t < \infty$, with $\inf\{i_k(t) : 0 \leq t < \infty\} \geq 0$ and $\sup\{i_k(t) : 0 \leq t < \infty\} \leq 1$ for $k = 1, 2$. Thus, the functions $r_k^\delta(t)$ are continuous and bounded above and below with $0 < \tilde{r}_k \leq \inf\{r_k^\delta(t) : 0 \leq t < \infty\}$ and $0 < \sup\{r_k^\delta(t) : 0 \leq t < \infty\} \leq r_k$ for $k = 1, 2$.

We define for $i, j = 1, 2$:

$$\tilde{K}_{ij} = \tilde{r}_i \frac{\theta_{ij}}{b_i} = K_{ij}(1 - \delta_i/r_i), \quad (\text{A.26a})$$

$$h_i(N_i, N_j) = \tilde{r}_i N_i \left(1 - \frac{N_i}{\tilde{K}_{ii}} - \frac{N_j}{\tilde{K}_{ij}} \right), \quad i \neq j, \quad (\text{A.26b})$$

$$p_i(N_i, N_j) = r_i N_i \left(1 - \frac{N_i}{K_{ii}} - \frac{N_j}{K_{ij}} \right), \quad i \neq j. \quad (\text{A.26c})$$

The functions h_i , and p_i are lower and upper bounds for the derivatives in (A.25a) and (A.25b). We also define the modified parameters $\tilde{\xi}_{ji} = 1/\tilde{K}_{ii} - 1/\tilde{K}_{ji}$, $i \neq j$. For $\tilde{\xi}_{21}, \tilde{\xi}_{12} > 0$ the solution to $\frac{dN_i}{dt} = h_i(N_i, N_j)$, $i, j = 1, 2, i \neq j$ with positive initial conditions stays positive for all time and converges globally

in $\{(N_1, N_2) \in \mathbb{R}^2 \mid 0 < N_i \leq K_{ii}, i = 1, 2\}$ to the asymptotically stable equilibrium $(\hat{N}_1^l, \hat{N}_2^l)$

$$\hat{N}_1^l = \frac{\tilde{K}_{11}\tilde{K}_{12}}{\tilde{K}_{12} + \tilde{K}_{11}(\tilde{\xi}_{12}/\tilde{\xi}_{21})}, \quad \hat{N}_2^l = \frac{\tilde{\xi}_{12}}{\tilde{\xi}_{21}}\hat{N}_1^l. \quad (\text{A.27})$$

Similarly, if $\xi_{21}, \xi_{12} > 0$, the solution to $\frac{dN_i}{dt} = p_i(N_i, N_j), i, j = 1, 2, i \neq j$ with positive initial conditions remains positive for all time and converges globally in $\{(N_1, N_2) \in \mathbb{R}^2 \mid 0 < N_i \leq K_{ii}, i = 1, 2\}$ to the asymptotically stable equilibrium $(\hat{N}_1^u = K_1^*, \hat{N}_2^u = K_2^*)$. Sufficient conditions for $\tilde{\xi}_{21}, \tilde{\xi}_{12}, \xi_{21}, \xi_{12} > 0$ to hold are Assumption (U1) and the following additional assumptions

- (U2) $\tilde{K}_{21} > K_{11}$,
- (U3) $\tilde{K}_{12} > K_{22}$,

which we will now make.

Using results on nonautonomous Lotka–Volterra models in Ref. 32 we state the following two results.

Theorem A.1. *If the assumptions (U1), (U2) and (U3) hold, then there exists a solution (N_1^*, N_2^*) of (A.25a) and (A.25b) [or equivalently (3.2c) and (3.2d)] for which the optimal bounds*

$$0 < \left(\frac{\tilde{K}_{12} - K_{22}}{\tilde{K}_{12} - \tilde{K}_{22}} \right) \hat{N}_1^l \leq N_1^*(t) \leq \left(\frac{K_{12} - \tilde{K}_{22}}{K_{12} - \tilde{K}_{22}} \right) \hat{N}_1^u, \quad (\text{A.28})$$

$$0 < \left(\frac{\tilde{K}_{21} - K_{11}}{\tilde{K}_{21} - \tilde{K}_{11}} \right) \hat{N}_2^l \leq N_2^*(t) \leq \left(\frac{K_{21} - \tilde{K}_{11}}{K_{21} - \tilde{K}_{11}} \right) \hat{N}_2^u, \quad (\text{A.29})$$

hold for all $0 \leq t < \infty$.

Proof. The proof follows from Theorem 2 in Ref. 32 and some algebraic manipulations. We note that the assumptions (U2) and (U3) imply

$$K_{21} > \tilde{K}_{21} > K_{11} > \tilde{K}_{11}, \quad (\text{A.30})$$

$$K_{12} > \tilde{K}_{12} > K_{22} > \tilde{K}_{22}. \quad (\text{A.31})$$

□

Theorem A.2. *If the assumptions (U1), (U2) and (U3) hold, and if (N_1^1, N_2^1) , and (N_1^2, N_2^2) are any two solutions of (A.25a) and (A.25b) such that $N_1^k(t^*) > 0$, and $N_2^k(t^*) > 0$ for some $t^* \geq 0$, $k = 1, 2$, then we have*

$$N_j^1(t) - N_j^2(t) \rightarrow 0, \quad \text{for } j = 1, 2, \text{ as } t \rightarrow \infty. \quad (\text{A.32})$$

Thus, if (N_1^{**}, N_2^{**}) is any solution of (A.25a) and (A.25b) with $N_k^{**}(t^*) > 0, k = 1, 2$ then, for some $t^* > 0$ and arbitrary $\epsilon > 0$, from Theorem A.1 we have that

$$0 < \left(\frac{\tilde{K}_{12} - K_{22}}{\tilde{K}_{12} - \tilde{K}_{22}} \right) \hat{N}_1^l - \epsilon < N_1^{**}(t) < \left(\frac{K_{12} - \tilde{K}_{22}}{K_{12} - K_{22}} \right) \hat{N}_1^u + \epsilon, \quad (\text{A.33})$$

$$0 < \left(\frac{\tilde{K}_{21} - K_{11}}{\tilde{K}_{21} - \tilde{K}_{11}} \right) \hat{N}_2^l - \epsilon < N_2^{**}(t) < \left(\frac{K_{21} - \tilde{K}_{11}}{K_{21} - K_{11}} \right) \hat{N}_2^u + \epsilon, \quad (\text{A.34})$$

hold for sufficiently large t .

Proof. The proof follows from Theorem 1 and Theorem 2 in Ref. 32, and some algebraic manipulations. \square