

AN ABSTRACT OF THE THESIS OF

Carrie Anna Manore for the degree of Doctor of Philosophy in Mathematics presented on May 31, 2011.

Title: Non-Spatial and Spatial Models for Multi-Host Pathogen Spread in Competing Species: Applications to Barley Yellow Dwarf Virus and Rinderpest.

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Vrushali A. Bokil

Modeling and analyzing the combined effects of disease and population dynamics is important in understanding the effects of mechanisms such as pathogen transmission and direct competition between host species on the distribution and abundance of different species in an ecological community. Mathematical analysis of such models in a spatially explicit environment gives additional important insight into these systems. Motivated by our participation in the IGERT Ecosystem Informatics program, we explore the interactions between and among disease, competition, and spatial heterogeneity from a mathematical modeling perspective. In particular, we formulate a model in which two species compete directly via Lotka-Volterra competition and share a directly transmitted pathogen via both mass action (density-dependent) and frequency-dependent incidence. We determine conditions under which the pathogen is endemic as well as conditions for long-term coexistence of the two species and the pathogen. As the interior equilibria are intractable, we examine a special case for which full stability analysis is possible. We show that in this case, mass action and frequency incidence behave qualitatively the same. We prove existence, uniqueness, and stability for the full model with frequency incidence under the assumption of no death due to disease using theory of asymptotically autonomous equations. Using persistence theory, we show that for the full model with mass action, if all boundary equilibria are unstable, then both species and the pathogen persist uniformly

strongly. We extend the multi-host competition-disease model to include multiple patches in order to model Barley Yellow Dwarf Virus in native grasslands. Our results suggest that connectivity can interact with arrival time and host infection tolerance to determine the success or failure of an invasion. Lastly, we simulate the spread of the multi-host virus rinderpest in livestock across the United States, finding that the outcome varies greatly with the starting location of the epidemic.

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Non-Spatial and Spatial Models for Multi-Host Pathogen Spread in Competing Species:
Applications to Barley Yellow Dwarf Virus and Rinderpest

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Carrie Anna Manore

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APPROVED:

Major Professor, representing Mathematics

Chair of the Department of Mathematics

Dean of the Graduate School

I understand that my thesis will become part of the permanent collection of Oregon State University libraries. My signature below authorizes release of my thesis to any reader upon request.

Carrie Anna Manore, Author

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Academic

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Personal

I wish to thank my family and my dear friends—you are so important to me and I love you all. Thanks for keeping me (relatively) sane.

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**NON-SPATIAL AND SPATIAL MODELS FOR MULTI-HOST
PATHOGEN SPREAD IN COMPETING SPECIES: APPLICATIONS
TO BARLEY YELLOW DWARF VIRUS AND RINDERPEST**

1 INTRODUCTION

Modeling and analyzing the combined effects of disease and population dynamics is important in understanding the effects of mechanisms such as pathogen transmission and direct competition between host species on the distribution and abundance of different species in an ecological community. Although mathematical advances have been made in this area, analysis of equilibria of basic models that combine the dynamics of disease and two interacting species is difficult and can often be intractable. Mathematical analysis of such models in a spatially explicit environment gives additional insight into the role that spatial heterogeneity can have on the dynamics of communities of different species. Motivated by my participation in the IGERT Ecosystem Informatics program and collaboration with several faculty and Researchers in mathematics and ecology, I explore the interactions between and among disease, competition, and spatial heterogeneity using mathematical modeling and analysis.

Theoretical and empirical investigations have shown that generalist pathogens or parasites infecting multiple host species can influence species diversity and community structure [118, 81, 24, 34, 63, 84]. Empirical studies have also demonstrated the importance of the combined effects of inter- and intra-specific competition between species and the effects of pathogens (apparent competition) on the population dynamics of multi-host systems [59]. 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 [39]. In addition, understanding the population biology of diseases is important in conservation biology [48]. Mathematical models that include competition between multiple species in addition to a shared pathogen are difficult to analyze for the case of infected coexistence and several important cases remain open. This thesis considers models in which two species compete directly via Lotka-Volterra competition and share a directly transmitted pathogen.

Humans are converting and fragmenting landscapes on every continent, changing connectivity of habitats through effects including reduced patch size, creation of novel habitats, and altered movement rates among patches that affect a diversity of species. Pathogen movement and epidemics can depend intimately upon landscape connectivity patterns [136, 104], which, in turn, control epidemic propagation or fadeout [78, 129]. Importantly, models including spatial heterogeneity can make qualitatively different predictions compared to models assuming homogeneous mixing [70, 66, 79]. In addition, many emerging pathogens infect multiple hosts, but most multi-host theory developed to date has focused on non-spatial models [49, 81, 102, 118, 73, 17, 26, 71]. Thus, in spite of the importance of landscape connectivity for understanding spatial spread and persistence of disease in real communities, the body of spatially-explicit theory dealing with multi-host pathogens remains quite small [110], [48]. As a result, the spatial dynamics of multispecies host-parasite assemblages are gaining increasing attention in both mathematics and ecology.

There are many ways to incorporate space into a model of ecological systems, including multi-patch, metapopulation, interacting particle and reaction diffusion models. In particular, metapopulation and patch models of disease are gaining impetus with the recognition that species live in increasingly fragmented landscapes [62, 10, 12, 11, 58, 100, 101], and that the heterogeneity of the landscape, as well as the demography and the epidemiology of multiple interacting species, determine spatial spread and persistence of the disease [113]. Multi-patch models can be thought of as graphs with systems of differential equations at each vertex. They involve explicit movement of individuals between distinct locations [10]. It has been shown that even a simple two-patch competition model can yield behavior different from the non-spatial model. Thus, we also focus on multi-patch models, for dispersal of organisms.

In this thesis, we utilize tools from dynamical systems, in particular the qualitative theory of autonomous differential equations [112], asymptotically autonomous systems, and persistence theory [137]. We also draw upon concepts from mathematical ecology and

epidemiology such as models for competition between species and for the transmission of infection in populations as well as spatial heterogeneity. At times, direct analysis of these complex models, especially with multiple species and habitat patches is very difficult. So we also make use of numerical analysis, bifurcation analysis and sensitivity analysis in order to understand the qualitative behavior of a system. An outline for the remainder of the thesis is now presented.

1.1 Outline of Thesis

In Chapter 2, background for dynamical systems is described along with a presentation of basic population dynamics and epidemiological models. Here, we also present a framework for multi-patch disease models.

In Chapter 3, a model of two competing species that share a directly transmitted pathogen is presented. We consider two different types of disease transmission mechanisms; mass action (density dependent) and frequency dependent transmission. All boundary equilibria for this model are computed and a local stability analysis is performed. We prove existence, uniqueness, and stability of the endemic coexistence equilibrium, for the case of frequency incidence disease transmission, when death due to disease is negligible. We use the theory of asymptotically autonomous differential equations to analyze this model. The analytic form for the endemic coexistence equilibrium for both models remained intractable, so a simplified model is analyzed in which all the equilibria are tractable

In Chapter 4, the full two species competition-disease model with mass action is analyzed using persistence theory, which can be helpful when the endemic coexistence equilibria are intractable. This follows the approach of Han and Pugliese [61] who show persistence results for a similar model.

In Chapters 5 and 6, two multi-host pathogen systems are considered in a spatially explicit context. In Chapter 5, we model the transmission of a generalist pathogen within a patch framework that incorporates the movement of vectors between discrete host patches to investigate the effects of local host community composition and vector movement rates on disease dynamics. We use barley and cereal yellow dwarf viruses (B/CYDV), a suite of generalist, aphid-vectored pathogens of grasses, and their interactions with a range of host species as our case study. We examine whether B/CYDV can persist locally or in a patch framework across a range of host community configurations. We then determine how pathogen-mediated interactions between perennial and annual competitors are altered at the local and regional scale when the host populations are spatially structured.

In Chapter 6, we consider the spread of rinderpest in livestock in the United States. Because of the potential severity of a rinderpest epidemic, it is prudent to prepare for an unexpected outbreak in animal populations. There is no immunity to the disease among the livestock or wildlife in the United States (US). If rinderpest were to emerge in the US, the loss in livestock could be devastating. We predict the potential spread of rinderpest using a two-stage model for the spread of a multi-host infectious disease among agricultural animals in the US. The model incorporates large-scale interactions among US counties and the small-scale dynamics of disease spread within a county.

Finally, in Chapter 7, conclusions and future directions are presented.

1.2 Resulting Publications

This thesis resulted in the following accepted and submitted publications.

1. V. A. Bokil and C. A. Manore, *Coexistence of competing species with a directly transmitted pathogen*, Submitted, 2011

Also published online as Tech. Report ORST-MATH 10-05, Oregon State University,

<http://hdl.handle.net/1957/18639>, 2010.

2. C. Manore, B. McMahon, J. Fair, J. M. Hyman, M. Brown, and M. LaBute, *Disease properties, geography, and mitigation strategies in a simulation spread of rinderpest across the united states*, Vet. Res. 42 (2011), no. 1, 55.
3. S. M. Moore, C. A. Manore, V. A. Bokil, E. T. Borer, and P. R. Hosseini, *Spatiotemporal model of barley and cereal yellow dwarf virus transmission dynamics with seasonality and plant competition*, Published online, Bull. Math. Biol., DOI 10.1007/s11538-011-9654-4.

2 MODELS IN ECOLOGY AND EPIDEMIOLOGY: A DYNAMICAL SYSTEMS APPROACH

In this chapter, background for differential equations, dynamical systems, competition models, disease models, and multi-patch models is presented.

2.1 Ordinary Differential Equations and Dynamical Systems

Let $x' = f(x)$ be a system of autonomous ordinary differential equations with initial condition $x(0) = x_0$, where $f : X \rightarrow \mathbb{R}^n$ and X is an open subset of $\mathbb{R}^n$. We have the following results:

Theorem 2.1.0.1 *The **Fundamental Existence-Uniqueness Theorem** [112] For $f \in C^1(X)$, the system $x' = f(x)$ has a unique solution on a time interval $[-a, a]$ with $a > 0$.*

Additionally, under these conditions, the solution is continuously dependent on initial conditions and parameters ([112], Chapter 2).

Definition 2.1.0.1 *A point x^* in X is an **equilibrium** of a system of ordinary differential equations if $f(x^*) = 0$. So, if $x(0) = x^*$ then $x(t) = x^*$ for all $t \geq 0$.*

Definition 2.1.0.2 *An equilibrium x^* is **locally asymptotically stable** if for every $\epsilon > 0$ there exists a $\delta > 0$ such that if $\|x(0) - x^*\| < \delta$ then $\|x(t) - x^*\| < \epsilon$ for $t \geq 0$ and if there exists a $\delta > 0$ such that for $\|x(0) - x^*\| < \delta$, $\lim_{t \rightarrow \infty} x(t) = x^*$.*

A semiflow is a triple (X, T, Φ) where X is called the *state space*, T is a time set, and Φ is the semiflow map. A *semiflow* (or *dynamical system*) map induced by the

differential equations, $\Phi : T \times X \rightarrow X$ has the property that $\Phi(0, x) = x$. If $x \in X$ is the initial state of the system then $\Phi(t, x) = \Phi_t(x)$ is the state at time t . Here, X is a metric space and T is a subset of $\mathbb{R}^+ = [0, \infty)$. The map Φ also has the semiflow property $\Phi(t + s, x) = \Phi(s, \Phi(t, x))$ for $x \in X$ and $t, s \in T \subset \mathbb{R}^+$. For ordinary differential equations, $\Phi(t, x)$ is the solution at time t for initial condition x . The systems examined in Chapters 3 and 4 are also *dissipative*, meaning that there exists a bounded subset U of X such that for any $u \in X$, $\Phi_t(u) \in U$ for sufficiently large t , i.e., U is a bounded attractor of X .

Definition 2.1.0.3 The *orbit* of Φ through a point $x \in X$ is $\gamma(x) = \{\Phi(t, x) : t_-(x) \leq t \leq t_+(x)\}$ where the solution $\Phi(t, x)$ exists for all time in the open interval $(t_-(x), t_+(x))$. The positive orbit is $\gamma_+(x) = \{\Phi(t, x) : 0 \leq t_+(x)\}$.

Definition 2.1.0.4 The *omega-limit set* of a point $x \in X$ is defined as

$$\omega(x) = \bigcap_{t \geq 0} \overline{\bigcup_{s \geq t} \{\Phi(r, x) : r \geq s\}} \quad (2.1.1)$$

and consists of the limits of all sequences $\{\Phi(t_n, x)\}$ where $t_n \rightarrow \infty$ as $n \rightarrow \infty$ and the *alpha limit set* as

$$\alpha(x) = \bigcap_{t < 0} \overline{\Phi((-\infty, t], x)}.$$

Definition 2.1.0.5 For $M \subset X$, M is *forward invariant* if and only if $\Phi_t(M) \subset M$ $\forall t > 0$. M is *invariant* if all solutions with $\Phi_0(x) \in M$ are defined for all time $t \in \mathbb{R}$ and $\Phi_t(M) = M$ $\forall t \in \mathbb{R}$.

Definition 2.1.0.6 A set is *pre-compact* in a finite-dimensional normed space if it is bounded. More generally, a set P is pre-compact if any sequence of points in P has a convergent subsequence [31].

Definition 2.1.0.7 The **stable subspace**, E^S , of a linear system $x' = Ax$ is $\text{Span}\{\mathbf{u}_j, \mathbf{v}_j | a_j < 0\}$ where $\lambda_j = a_j + ib_j$ is an eigenvalue of A and $\mathbf{w}_j = \mathbf{u}_j + i\mathbf{v}_j$ it's generalized eigenvector. The **unstable subspace**, E^U is $\text{Span}\{\mathbf{u}_j, \mathbf{v}_j | a_j > 0\}$.

Theorem 2.1.0.2 Stable Manifold Theorem [112] Under the same assumptions as for Theorem 2.1.0.1 with X containing the origin, suppose that $f(0) = 0$ and that the Jacobian evaluated at that equilibrium, $Df(0)$, has k eigenvalues with negative real part and $n-k$ eigenvalues with positive real part. Then there exists a k -dimensional differentiable manifold W^S tangent to the stable subspace E^S of the linear system $x' = Df(x_0)x$ at 0 such that for all $t \geq 0$, $\Phi_t(S) \subset S$ and for all $x_0 \in W^S$, $\lim_{t \rightarrow \infty} \Phi_t(x_0) = 0$. Also, there exists an $n-k$ dimensional differential manifold W^U tangent to the unstable subspace E^U of the linear system at 0 such that for all $t \leq 0$ then $\Phi_t(U) \subset W^U$ and for all $x_0 \in U$, $\lim_{t \rightarrow -\infty} \Phi_t(x_0) = 0$.

Theorem 2.1.0.3 Poincare-Bendixson Theorem [6] Let $\gamma_+(x)$ be a positive orbit of the autonomous ODE $x' = f(x)$ with $x \in X \subset \mathbb{R}^2$ that remains in a closed and bounded region U of the plane. Suppose that U contains only a finite number of equilibria. The ω -limit set takes on only one of the following:

1. $\omega(x_0)$ is an equilibrium, or
2. $\omega(x_0)$ is a periodic orbit, or
3. $\omega(x_0)$ contains a finite number of equilibria and a set of trajectories γ_i whose α - and ω -limit sets consist of one of the equilibria for each trajectory γ_i .

2.2 Mathematical Models for Competition between Species

Populations can be represented mathematically as either the total population or the density of the population in a fixed area. Models look very similar from either perspective,

only differing by a scaling of parameters and variables [86, 56]. We start initially by assuming that populations are only affected by the per capita birth rate a , the number of births per individual per unit time, and the per capita death rate b , the number of deaths per individual per unit time. The *intrinsic rate of growth*, $r = a - b$, is the difference between the birth and death rates. In this case a population is modeled by the differential equation

$$\frac{dN}{dt} = rN. \quad (2.2.1)$$

This model assumes there is no immigration or emigration. It predicts exponential growth or decay for all time, which implies it may not be including important factors such as resource limitation that affect the growth rate of a population.

One way to deal with this problem is to add density-dependence to the model, assuming that the presence of other individuals of the same species in the habitat either decreases the birth rate, increases the death rate, or both. The mechanisms for this decrease in the growth rate can be explained by many factors, including resource limitation and direct interference [56]. The growth rate decreasing linearly with the population results in logistic growth

$$\frac{dN}{dt} = rN \left(1 - \frac{N}{K} \right) \quad (2.2.2)$$

where K is the carrying capacity of the population. This model is well-posed and forward invariant in the region $X_L = \{N \in \mathbb{R} | 0 \leq N \leq K\}$.

Multiple species often live in the same habitat and it is expected that they may interact with each other. A classic model for species interaction is the Lotka-Volterra model which, depending on parameter values, can represent predator-prey, mutualistic, or competitive interactions between species. The model is

$$\frac{dN_i}{dt} = r_i N_i \left(1 + \sum_{k=1}^n \frac{N_j}{K_{ij}} \right), \quad (2.2.3)$$

where r_i is the intrinsic growth rate of species i and where $1/K_{ij}$ represents the effect of species j on the growth rate of species i . In this thesis, we will concentrate on competitive interactions, for which the competition coefficients, $1/K_{ij}$ are negative. Notice that in

the absence of any other species, each species is governed by the logistic equation (2.2.2). Lotka-Volterra competition for 2 or 3 species is well known and fully analyzed. The two species Lotka-Volterra competition model,

$$\frac{dN_1}{dt} = r_1 N_1 \left(1 - \frac{N_1}{K_{11}} - \frac{N_2}{K_{12}} \right) \quad (2.2.4)$$

$$\frac{dN_2}{dt} = r_2 N_2 \left(1 - \frac{N_1}{K_{21}} - \frac{N_2}{K_{22}} \right), \quad (2.2.5)$$

is well-posed and forward invariant in the region $X_{LV} = \{(N_1, N_2) \in \mathbb{R}^2 | 0 \leq N_i \leq K_{ii}, i = 1, 2\}$. Although individually quite tractable, the combination of competition and disease quickly becomes complicated.

2.3 Mathematical Epidemiology

The types of disease models we consider here are compartmental Susceptible Infectious Recovered (SIR) ordinary differential equations which assume each individual in a population resides in one and only one disease state, namely susceptible, infectious, and removed (or recovered). Individuals of a population move between these compartments at certain transition rates. An organism in the susceptible class, denoted by S, is not infected and is capable of contracting the disease. A member of the infectious class, I, is infected with the disease and is able to transmit the disease to others. A member of the removed class, R, has recovered from the disease and is immune, has permanent immunity from some other source (e.g. vaccination), or is dead from the disease. In all cases, the recovered class cannot transmit or contract the pathogen. Additional compartments such as latent or vaccinated can be added as necessary.

The standard SIR disease model was developed by Ronald Ross (1915) [122] and proposed in its current form by Kermack and McKendrick (1927) [83]. Because of this, analysis of disease dynamics alone in one or multiple hosts is complete for the most commonly used modes of transmission, mass action (density dependence) and frequency

incidence. Note that most well analyzed models assume a small enough time scale that the considered populations are assumed constant (no birth or natural death included). Some work has been done on disease models for one or multiple species with basic population dynamics such as exponential growth and logistic growth.

The two most common mathematical representations of disease transmission are mass action (density-dependent) and frequency incidence. The transmission rate of a disease is (usually) proportional to infectivity, susceptibility of non-infected individuals, the contact rate between all individuals, the proportion of infected individuals, and the number of susceptible individuals. Mass action assumes that the contact rate, and thus the transmission rate, increases linearly with the number of individuals in a population while frequency incidence assumes that the contact rate is constant. Appropriate use of disease incidence depends upon the system one is considering [98, 16, 68].

Definition 2.3.0.8 *The **incidence of disease** is the rate of new infections in susceptibles resulting from contact with infectious individuals.*

For $C(N, t)$ the local contact rate, r the probability that the contact is with an infected individual (often $r = \frac{I}{N}$), p the probability that the contact is sufficient for transmission, S the number (or density) of susceptible organisms, I the number of infectious, and N the total population, then the disease incidence is $CrpS(t) = Cp\frac{I}{N}S$. There are many forms used for disease incidence, but the two most common are mass action or density dependent incidence and frequency dependent incidence. Mass action assumes that the contact rate is proportional to the global density so $C(N, t) = k(N/A)$, so incidence is $kpS\frac{I}{A} = \nu SI$. Frequency dependent incidence assumes that the contact rate is constant, so $C(N, t) = c$ incidence is $cp\frac{I}{N}S = \beta\frac{I}{N}S$

Definition 2.3.0.9 *The **basic reproduction number**, $\mathcal{R}_0$, is the expected number of secondary cases that occur after the introduction of one infected individual into a fully susceptible population. If $\mathcal{R}_0 \leq 1$ then the disease will die out.*

We use the next generation method [144, 27] to compute $\mathcal{R}_0$. For infected compartments x_i and uninfected compartments y_i , then $x'_i = \mathcal{F}_i(x, y) - \mathcal{V}_i(x, y)$ and $y'_j = g_j(x, y)$ where $\mathcal{F}_i(x, y)$ represents new infections and $\mathcal{V}_i(x, y)$ is the net outflow of infectious compartment. We assume that

- $\mathcal{F}_i(0, y) = 0$ and $\mathcal{V}_i(0, y) = 0$
- $\mathcal{F}_i(x, y) \geq 0$ for nonnegative x, y ;
- $\mathcal{V}_i(x, y) \leq 0$ for $x_i = 0$;
- $\sum_{i=1}^n \mathcal{V}_i(x, y) \geq 0$ for nonnegative x, y
- $y' = g(0, y)$ has a unique asymptotically stable equilibrium (disease-free equilibrium)

Now, linearize about the disease-free equilibrium. x is decoupled from the rest of the equations since $\frac{\partial \mathcal{F}_i}{\partial y_j}(0, y_0) = \frac{\partial \mathcal{V}_i}{\partial y_j}(0, y_0) = 0$. So, we can approximate x by $x' = (F - V)x$ where F is the Jacobian of $\mathcal{F}$ and V is the Jacobian of $\mathcal{V}$.

Let $\Phi(t, x_0)$ be the solution to $x' = (F - V)x$ for $x_0 > 0$ where $F = 0$, so there are no new secondary infections. The i th component of $\Phi(t, x_0)$ is the probability that the initial case introduced at time $t = 0$ is in disease compartment i at time t . Then, we see that $\int_0^\infty \phi(t, x_0) dt$ is the expected time the initial case spends in the disease compartments. Since when $F = 0$ then $x' = -Vx$, we know $\Phi(t, x_0) = e^{-Vt}x_0$. Then, $\int_0^\infty \Phi(t, x_0) dt = V^{-1}x_0$ where the (i, j) entry of V^{-1} represents the expected time an individual initially introduced into disease compartment j spends in disease compartment i . The (i, j) entry of F is the rate at which new infections are produced in compartment i from an index case in compartment j . Therefore, the expected number of secondary infections produced by the initial case is

$$\int_0^\infty F e^{-Vt} x_0 dt = F V^{-1} x_0.$$

This is the time spent in a disease compartment times the rate at which a member of that compartment creates a new infection. The matrix FV^{-1} is referred to as the *next*

generation matrix. The next generation matrix is nonnegative, so has a nonnegative eigenvalue with greatest modulus, which has a nonnegative eigenvector. We call this eigenvalue, $\rho(FV^{-1})$, or the spectral radius of FV^{-1} , the basic reproduction number ($\mathcal{R}_0$) of the system, [144, 27].

The following theorem proves that the stability of the disease free equilibrium can be determined solely by $\mathcal{R}_0$.

Theorem 2.3.0.4 (*Theorem 2, [144]*) *Consider a disease transmission model as described above with the accompanying five assumptions. If x_0 is a disease free equilibrium (DFE) of the model, then x_0 is locally asymptotically stable if $\mathcal{R}_0 < 1$ and is unstable if $\mathcal{R}_0 > 1$.*

2.4 Multi-patch Disease Models

The dynamics of multispecies host-parasite assemblages have recently received a lot of attention [49, 81, 102, 118, 73, 17, 26, 71]. For the most part, these studies have closely analyzed particular models of host-parasite dynamics. Metapopulation models of disease are also gaining impetus as natural and human-made landscape features such as forests, rivers, roads and crops cause many endangered species to live in fragmented landscapes [62, 10, 12, 11, 58, 100, 101]. The heterogeneity of the landscape as well as the demography and the epidemiology of multiple interacting species determine spatial spread and persistence of the disease.

There are many ways to incorporate space into a model of ecological systems, including multi-patch, metapopulation, interacting particle and reaction diffusion models. Which model to use depends upon the biology and dispersal mechanisms of the organism(s), the structure of the environment, time and spatial scales, the data available, and the question one is trying to answer [31]. We focus here on multi-patch, or network models, for dispersal of organisms. Multi-patch models are graphs with systems of differential

equations at each vertex. They involve explicit movement of individuals between distinct locations [10]. It has been shown that even a simple two-patch competition model can yield behavior different from the non-spatial model. Two species which could not coexist in one patch can coexist in a two-patch system with moderate movement rates [33]. For the case of spatio-temporal dynamics of disease spread, a multi-patch model would consist of an SIR model on each vertex of a graph with connection between some or all of the vertices. Multi-patch models can be viewed as a discrete approximation of diffusion or as a model for discrete, or patchy, environments.

In a patchy environment, motivation for using a patch model is obvious. However, a patch model can also be seen as discrete diffusion, an approximation to the continuous reaction-diffusion model as described in [5]. Allen [5] analyzes a Lotka-Volterra two patch model for competition between species. Consider the reaction-diffusion model

$$u_t = f(u) + \eta u_{xx}, \quad x \in [0, L] \quad (2.4.1)$$

where η is the diffusion coefficient. The boundary conditions are either Dirichlet ($u(0, t) = 0 = u(L, t)$), Neumann ($u_x(0, t) = 0 = u_x(L, t)$), or Robin ($u_x(0, t) = -\beta_1 u(0, t)$, $u_x(L, t) = \beta_2 u(L, t)$). Dirichlet boundary conditions result from a population that avoids the boundary but can enter or leave the region. Neumann boundary conditions mean that the individuals cannot move across the boundary. Robin boundary conditions imply the movement across the boundary is proportional to the population density.

Let's use finite differences to approximate partial derivatives so

$$u_{xx}(x, t) \approx \frac{u(x+h, t) - 2u(x, t) + u(x-h, t)}{h^2}. \quad (2.4.2)$$

Let the population in patch 1 be $u_1(t) = u(x, t)$ and the population in patch 2 be $u_2(t) = u(x+h, t)$. Then, $u'_1 = f_1(u_1) + \frac{D}{h^2}(u_2 - 2u_1 + u(x-h, t))$ and $u'_2 = f_2(u_2) + \frac{D}{h^2}(u_1 - 2u_2 + u(x+2h, t))$ where $u(x-h, t)$ and $u(x+2h, t)$ are determined by the boundary conditions.

- For Dirichlet, $u(x-h, t) = 0 = u(x+2h, t)$;

- for Neumann, $\frac{u(x,t)-u(x-h,t)}{h} = 0 = \frac{u(x+2h,t)-u(x+h,t)}{h}$;
- and for Robin, $\frac{u(x,t)-u(x-h,t)}{h} = -\beta_1 u(x,t)$ and $\frac{u(x+2h,t)-u(x+h,t)}{h} = \beta_2 u(x+h,t)$.

So we end up with three different versions of the general two patch model $u'_j = f_j(u_j) + D_j(u_k - \alpha_j u_j)$ for $j = 1, 2$, $j \neq k$ depending on boundary conditions. See [5] for a full analysis of this system.

The question of how disease affects patchy populations, including whether or not a disease might drive a population to extinction, is an important one to biologists today. Although opening “corridors” between habitat patches may be important for preserving a species, if one does not examine the possible changes that this might make in disease dynamics, the result may be increased chance of epidemics or even local extinction [64, 100]. In addition, competition is an important structuring factor in animal and plant communities. Classical competition theory predicts competitive exclusion of species with similar requirements; however recent ideas stress that species diversity may be explained by a multitude of processes acting at different scales, and that similarities in competitive abilities often may facilitate coexistence [19, 2].

Multi-patch models can be generalized to apply to any system with a generalist pathogen infecting multiple hosts where spatial heterogeneity is important. They are designed for disease transmission in multiple species in multiple patches, which can be interpreted as regions, cities, meadows, etc. We assume that each individual patch is homogeneous, but that different patches may have different parameters. For each of the n patches and s species, the patch population is split into compartments labeled S_{ip}, E_{ip}, I_{ip} and R_{ip} , for $p = 1, 2, \dots, n$ and $i = 1, 2, \dots, s$. The total number of species i in patch p is represented by

$$N_{ip} = S_{ip} + E_{ip} + I_{ip} + R_{ip}.$$

Movement between the patches will be represented by the constants $m_{ipq}^S, m_{ipq}^E, m_{ipq}^I, m_{ipq}^R$ for movement of species i from patch q to patch p when in a given S, E, I or R compartment, respectively. This model assumes that movement between patches may change

with infection, but that individuals do not move into different disease compartments while traveling. We also assume that $m_{ipp} = 0 \forall i, p$.

Each species in each patch has a given birth and death rate. The birth rate is $b_{ip}(N_{ip})$ and the natural death rate (independent of disease) is $d_{ip}(N_{ip})$. We assume that the birth and the death rates are nonnegative functions. The disease transmission rate from species j to species i in patch p , $\beta_{ijp}(N_{jp})$, is assumed to be a nonnegative non-increasing function and disease is transmitted horizontally according to either mass action or frequency incidence. Once an individual is infected, it moves into the exposed, or latent compartment in which it has the pathogen but is unable to transmit it to others. After a period of time, the individual moves into the infective compartment where it is then able to transmit the disease to other individuals. Then, depending on the disease, the individual may move into a recovered compartment where the individual is either immune to the disease permanently, or is temporarily immune and then moves back into the susceptible compartment. The average rate of movement between the exposed, infective, and recovered compartments is ϵ_{ip} , γ_{ip} , and δ_{ip} respectively, with $1/\epsilon_{ip}$, $1/\gamma_{ip}$, and $1/\delta_{ip}$ being the average period of time spent in each compartment. Most epidemic models assume that the infection periods (e.g., latent, infectious, isolation periods) are either exponentially distributed or have fixed durations [67]. In some cases, the disease may cause death and the death rate will be represented as α_{ip} .

This general model can of course be adapted to various cases, such as when the latent period is so short, it can be ignored, creating an SIR model, or when the recovered period is either very short or nonexistent resulting in an SEI or SEIS model.

In the following section, I adapt the model analyzed by [12, 10, 11] so that some or all of the included species are competing with each other within a patch via the basic Lotka-Volterra competition model. We then compute the basic reproduction number for this adapted model. Competition will be represented as $\eta_{ip}(S_{ip}, E_{ip}, I_{ip}, R_{ip}) > 1$, a function of S_{ip} , E_{ip} , I_{ip} , and R_{ip} or possibly just N_{ip} , for $i = 1, 2, \dots, s$. This leads to the following systems of ordinary differential equations:

$$\frac{dS_{ip}}{dt} = b_{ip}(N_{ip})\eta_{ip} - d_{ip}S_{ip} - \sum_{j=1}^s \beta_{ijp}S_{ip}\frac{I_{ip}}{N_{jp}} + \delta_{ip}R_{ip} + \sum_{q=1}^n m_{ipq}^S S_{iq} - \sum_{q=1}^n m_{iqp}^S S_{ip} \quad (2.4.3)$$

$$\frac{dE_{ip}}{dt} = -d_{ip}E_{ip} + \sum_{j=1}^s \beta_{ijp}S_{ip}\frac{I_{ip}}{N_{jp}} + \sum_{q=1}^n m_{ipq}^E E_{iq} - \sum_{q=1}^n m_{iqp}^E E_{ip} - \epsilon_{ip}E_{ip} \quad (2.4.4)$$

$$\frac{dI_{ip}}{dt} = \epsilon_{ip}E_{ip} - d_{ip}I_{ip} - (\gamma_{ip} + \alpha_{ip})I_{ip} + \sum_{q=1}^n m_{ipq}^I I_{iq} - \sum_{q=1}^n m_{iqp}^I I_{ip} \quad (2.4.5)$$

$$\frac{dR_{ip}}{dt} = \gamma_{ip}I_{ip} - d_{ip}R_{ip} - \delta_{ip}R_{ip} + \sum_{q=1}^n m_{ipq}^R R_{iq} - \sum_{q=1}^n m_{iqp}^R R_{ip} \quad (2.4.6)$$

with the initial conditions $S_{ip}(0)$, and $E_{ip}(0), I_{ip}(0), R_{ip}(0) \geq 0$, as well as $\sum_{p=1}^n (E_{ip}(0) + I_{ip}(0)) > 0$ for some species i .

The population of species i in each patch p changes with the sum of all four equations above and since the solutions for all of the above equations are positive, the total population remains nonnegative for all $t \geq 0$. The total population of species i in the entire system is $N_i = \sum_{p=1}^n N_{ip}$ and the change in the total population of species i can be represented by

$$\frac{dN_i}{dt} = \sum_{p=1}^n b_{ip}(N_{ip})\eta_{ip}(S_{ip}, E_{ip}, I_{ip}, R_{ip}) - d_{ip}N_{ip} - \alpha_{ip}I_{ip} \quad (2.4.7)$$

We know that the population of patch p is at equilibrium if $\frac{dS_{ip}}{dt}, \frac{dE_{ip}}{dt}, \frac{dI_{ip}}{dt}, \frac{dR_{ip}}{dt} = 0$ for each species i and is at a disease-free equilibrium (DFE) if $E_{ip} + I_{ip} = 0$ for each species i . Similarly, species i is at a DFE if $E_{ip} + I_{ip} = 0$ for each patch p . Then, the whole system is at a DFE if $E_{ip} + I_{ip} = 0$ for all species i and for all patches p , implying that each patch is at an equilibrium, hence satisfying for each patch p

$$\frac{dN_{ip}}{dt} = b_{ip}(N_{ip})\eta_{ip}(N_{ip}) - d_{ip}N_{ip} + \sum_{q=1}^n m_{ipq}^S N_{iq} - \sum_{q=1}^n m_{iqp}^S N_{ip} = 0 \quad (2.4.8)$$

We want to determine if (2.4.8) has a solution, $S_{ip}^* = N_{ip}^*$ that will give us the DFE and whether or not this solution is unique. The uniqueness of the solution depends upon

the birth, death and the competition rates. We will assume that η_{ip} has Lotka-Volterra form

$$\eta_{ip} = 1 + \sum_{j=1}^s \sigma_{ijp}(S_{jp} + E_{jp} + \zeta_{jp}I_{jp} + R_{jp})$$

where σ_{ijp} is the effect of competition with species j and species i in patch p and where ζ_{jp} is the reduction in biomass or fitness of infectious individuals of species j in patch p , which decreases their ability to compete. Then (2.4.7) can be rewritten as

$$\frac{dN_i}{dt} = \sum_{p=1}^n b_{ip}(N_{ip}) \left(1 + \sum_{j=1}^s \sigma_{ijp}(S_{jp} + E_{jp} + \zeta_{jp}I_{jp} + R_{jp}) \right) - \alpha_{ip}I_{ip} - d_{ip}N_{ip}$$

Finding the disease-free equilibria (DFEs) for the full models with multiple patches and species is often intractable. We will now analyze a system of two patches each with two species that compete with each other and are susceptible in some form to a common disease. In order to further simplify, we will first consider an SI model. We will explore this using the following set of ordinary differential equations for species i in patch k :

$$\frac{dS_{ik}}{dt} = b_{ik}N_{ik} \left(1 - \sum_{j=1}^2 c_{ijk}N_{jk} \right) - \sum_{j=1}^2 \beta_{ijk}S_{ik}I_{jk} - d_{ik}S_{ik} - m \left(\frac{S_{ik}}{K_{ik}} - \sum_{q \neq k} \frac{S_{iq}}{K_{iq}} \right) \quad (2.4.9)$$

$$\frac{dI_{ik}}{dt} = \sum_{j=1}^2 \beta_{ijk}S_{ik}I_{jk} - d_{ik}I_{ik} - \gamma_{ik}I_{ik} - \alpha_{ik}I_{ik} - m \left(\frac{I_{ik}}{K_{ik}} - \sum_{q \neq k} \frac{I_{iq}}{K_{iq}} \right) \quad (2.4.10)$$

with the initial conditions $S_{iq}(0), I_{iq}(0) \geq 0$, as well as $\sum_{p=1}^n (I_{ip}(0)) \geq 0$ for some species i . For this system, b_{ik} is the constant birth rate, d_{ik} is the natural constant death rate and K_{ik} is the carrying capacity. For mass action, $\beta_{ijk}(N_{jk}) = \beta_{ijk}N_{jk}$ to result in the above disease transmission term where β_{ijk} is the transmission rate from species j to species i in patch k . Lastly, α_{ik} is the death rate due to infection. In this case, we will assume that migration is density dependent and that m , the migration rate, is assumed to be constant and strictly positive for simplifying purposes. Also, we are assuming that competition is constant and affects only the birth rate, with c_{ijk} being the competition exerted upon species i by species j in patch k . We will assume that the growth rate $r = b - d$ is positive for each species.

2.4.1 Basic Reproduction Number

Theorem 2.4.1.1 *Assuming $m > 0$, if the system is at equilibrium and a species is absent in one patch, then that species is also absent in all other patches.*

Proof. Sketch of proof. If, for example, $S_{11} = 0$ then by substituting S_{11} into the above equation (1.9), we have that $0 = \frac{mS_{12}}{K_{12}}$ which implies that either $S_{12} = 0$ or $m = 0$ and assuming strong connection, or $m > 0$, this implies that $S_{12} = 0$. Similarly, if $S_{21} = 0$ this implies using equation (1.11) that $S_{22} = 0$ and vice versa. Thus, for the DFEs, if one species in one patch is at an equilibrium of population zero, then the other patch also has a population zero of the same species at equilibrium. ■

We use the next generation matrix method to compute $\mathcal{R}_0$ for this system. Let $X = (S_{11}, S_{12}, S_{21}, S_{22}, I_{11}, I_{12}, I_{21}, I_{22})$ and let $\frac{dX}{dt} = \mathcal{F}(X) - \mathcal{V}(X)$. Then for the infected compartments,

$$\mathcal{F}(X) = \begin{bmatrix} \beta_{111}S_{11}I_{11} + \beta_{121}S_{11}I_{21} \\ \beta_{112}S_{12}I_{12} + \beta_{122}S_{12}I_{22} \\ \beta_{221}S_{21}I_{21} + \beta_{211}S_{21}I_{11} \\ \beta_{222}S_{22}I_{22} + \beta_{212}S_{22}I_{12} \end{bmatrix}$$

and

$$\mathcal{V}(X) = \begin{bmatrix} d_{11}I_{11} + \gamma_{11}I_{11} + \alpha_{11}I_{11} + m(\frac{I_{11}}{K_{11}} - \frac{I_{12}}{K_{12}}) \\ d_{12}I_{12} + \gamma_{12}I_{12} + \alpha_{12}I_{12} + m(\frac{I_{12}}{K_{12}} - \frac{I_{11}}{K_{11}}) \\ d_{21}I_{21} + \gamma_{21}I_{21} + \alpha_{21}I_{21} + m(\frac{I_{21}}{K_{21}} - \frac{I_{22}}{K_{22}}) \\ d_{22}I_{22} + \gamma_{22}I_{22} + \alpha_{22}I_{22} + m(\frac{I_{22}}{K_{22}} - \frac{I_{21}}{K_{21}}) \end{bmatrix}$$

Now we will linearize $\mathcal{F}(X)$ to get

$$F = \begin{bmatrix} \beta_{111}S_{11} & 0 & \beta_{121}S_{11} & 0 \\ 0 & \beta_{112}S_{12} & 0 & \beta_{122}S_{12} \\ \beta_{211}S_{21} & 0 & \beta_{221}S_{21} & 0 \\ 0 & \beta_{212}S_{22} & 0 & \beta_{222}S_{22} \end{bmatrix}.$$

Next, we linearize $\mathcal{V}(X)$ around the DFE to get $V = \begin{bmatrix} A & 0 \\ 0 & B \end{bmatrix}$ where

$$A = \begin{bmatrix} d_{11} + \gamma_{11} + \alpha_{11} + \frac{m}{K_{11}} & -\frac{m}{K_{12}} \\ -\frac{m}{K_{11}} & d_{12} + \gamma_{12} + \alpha_{12} + \frac{m}{K_{12}} \end{bmatrix},$$

$$B = \begin{bmatrix} d_{21} + \gamma_{21} + \alpha_{21} + \frac{m}{K_{21}} & -\frac{m}{K_{22}} \\ -\frac{m}{K_{21}} & d_{22} + \gamma_{22} + \alpha_{22} + \frac{m}{K_{22}} \end{bmatrix},$$

and where 0 denotes a 2×2 zero matrix.

Now we are ready to compute $\mathcal{R}_0$ by finding the spectral radius of FV^{-1} . Let $\Gamma_{ij} = d_{ij} + \gamma_{ij} + \alpha_{ij}$. Then let

$$V_1 = \begin{bmatrix} \Gamma_{11} + \frac{m}{K_{11}} & -\frac{m}{K_{12}} \\ -\frac{m}{K_{11}} & \Gamma_{12} + \frac{m}{K_{12}} \end{bmatrix} \text{ and } V_2 = \begin{bmatrix} \Gamma_{21} + \frac{m}{K_{21}} & -\frac{m}{K_{22}} \\ -\frac{m}{K_{21}} & \Gamma_{22} + \frac{m}{K_{22}} \end{bmatrix}$$

so that $V = \begin{bmatrix} V_1 & 0 \\ 0 & V_2 \end{bmatrix}$ and $V^{-1} = \begin{bmatrix} V_1^{-1} & 0 \\ 0 & V_2^{-1} \end{bmatrix}$. Also, let $F_{ij} = \begin{bmatrix} \beta_{ij1}S_{i1} & 0 \\ 0 & \beta_{ij2}S_{i2} \end{bmatrix}$ so that $F = \begin{bmatrix} F_{11} & F_{12} \\ F_{21} & F_{22} \end{bmatrix}$. So, we have that

$$FV^{-1} = \begin{bmatrix} F_{11}V_1^{-1} & F_{12}V_2^{-1} \\ F_{21}V_1^{-1} & F_{22}V_2^{-1} \end{bmatrix}$$

where

$$V_1^{-1} = \frac{1}{\theta_1} \begin{bmatrix} \Gamma_{12} + \frac{m}{K_{12}} & \frac{m}{K_{12}} \\ \frac{m}{K_{11}} & \Gamma_{11} + \frac{m}{K_{11}} \end{bmatrix} \text{ and } V_2^{-1} = \frac{1}{\theta_2} \begin{bmatrix} \Gamma_{22} + \frac{m}{K_{22}} & \frac{m}{K_{22}} \\ \frac{m}{K_{21}} & \Gamma_{21} + \frac{m}{K_{21}} \end{bmatrix}$$

for $\theta_1 = \det V_1 = \Gamma_{11}\Gamma_{12} + \Gamma_{11}\frac{m}{K_{12}} + \Gamma_{12}\frac{m}{K_{11}}$ and $\theta_2 = \det V_2 = \Gamma_{21}\Gamma_{22} + \Gamma_{21}\frac{m}{K_{22}} + \Gamma_{22}\frac{m}{K_{21}}$. Now, finding the basic reproduction number is equivalent to finding the spectral radius of the following matrix evaluated at the DFE:

$$FV^{-1} = \begin{bmatrix} C & D \\ E & F \end{bmatrix} \quad (2.4.11)$$

where

$$\begin{aligned} C &= \begin{bmatrix} \frac{1}{\theta_1} \beta_{111} S_{11} \left(\Gamma_{12} + \frac{m}{K_{12}} \right) & \frac{1}{\theta_1} \beta_{111} S_{11} \frac{m}{K_{12}} \\ \frac{1}{\theta_1} \beta_{112} S_{12} \frac{m}{K_{11}} & \frac{1}{\theta_1} \beta_{112} S_{12} \left(\Gamma_{11} + \frac{m}{K_{11}} \right) \end{bmatrix}, \\ D &= \begin{bmatrix} \frac{1}{\theta_2} \beta_{121} S_{11} \left(\Gamma_{22} + \frac{m}{K_{22}} \right) & \frac{1}{\theta_2} \beta_{121} S_{11} \frac{m}{K_{22}} \\ \frac{1}{\theta_2} \beta_{122} S_{12} \frac{m}{K_{21}} & \frac{1}{\theta_2} \beta_{122} S_{12} \left(\Gamma_{21} + \frac{m}{K_{21}} \right) \end{bmatrix}, \\ E &= \begin{bmatrix} \frac{1}{\theta_1} \beta_{211} S_{21} \left(\Gamma_{12} + \frac{m}{K_{12}} \right) & \frac{1}{\theta_1} \beta_{211} S_{21} \frac{m}{K_{12}} \\ \frac{1}{\theta_1} \beta_{212} S_{22} \frac{m}{K_{11}} & \frac{1}{\theta_1} \beta_{212} S_{22} \left(\Gamma_{11} + \frac{m}{K_{11}} \right) \end{bmatrix}, \end{aligned}$$

and where

$$F = \begin{bmatrix} \frac{1}{\theta_2} \beta_{221} S_{21} \left(\Gamma_{22} + \frac{m}{K_{22}} \right) & \frac{1}{\theta_2} \beta_{221} S_{21} \frac{m}{K_{22}} \\ \frac{1}{\theta_2} \beta_{222} S_{22} \frac{m}{K_{21}} & \frac{1}{\theta_2} \beta_{222} S_{22} \left(\Gamma_{21} + \frac{m}{K_{21}} \right) \end{bmatrix}.$$

In order to generalize to multiple species (n species) and patches (p patches), let $\Gamma_{ip} = d_{ip} + \gamma_{ip} + \alpha_{ip}$, then V has the form $\text{diag}(M_1, \dots, M_n)$ where

$$[M_{l_{ij}}] = \begin{cases} \Gamma_{lp} + \frac{m}{K_{lp}} & \text{for } i = j \\ \frac{m}{K_{lp}} & \text{for } i \neq j. \end{cases}$$

Assuming β_{ij} is the same for each patch, F has the form $[\beta_{ij} K_i]_{i,j=1\dots n}$ where $[K_l] = \text{diag}(S_{ik})_{k=1\dots p}$. So, finally we see that, in general, $FV^{-1} = [\beta_{ij} K_i M_j^{-1}]_{i,j=1\dots n}$, where K_i depends on the DFE. For our specific case with two species and two patches, then

$$\mathcal{R}_0 = \rho([\beta_{ij} K_i M_j^{-1}])$$

where

$$[\beta_{ij} K_i M_j^{-1}] = \begin{bmatrix} \beta_{11} K_1 M_1^{-1} & \beta_{12} K_1 M_2^{-1} \\ \beta_{21} K_2 M_1^{-1} & \beta_{22} K_2 M_2^{-1} \end{bmatrix}.$$

Although this can be difficult to compute for large models, we will compute $\mathcal{R}_0$ for the BYDV patch model during the growing season in Chapter 5.

3 COEXISTENCE OF COMPETING SPECIES WITH A DIRECTLY TRANSMITTED PATHOGEN

3.1 Introduction

Competitive interactions, as well as predator prey dynamics, have dominated investigations of species interactions in ecology and influence community structure via the distribution, abundance and resource use of species in natural communities [130, 41, 54]. Classical competition theory predicts competitive exclusion of species with similar requirements. Understanding the mechanisms that drive the coexistence of competing species is an important goal in community ecology [39].

Theoretical and empirical investigations have shown that generalist pathogens or parasites infecting multiple host species can influence species diversity and community structure [118, 81, 24, 34, 63, 84]. For example, in [48] the author argues that for most of the 20th century, the wildebeest and buffalo herds in the Serengeti were in fact being regulated not exclusively by predator prey interactions, but primarily by a virus called rinderpest. Once rinderpest was controlled through vaccination, both predator and prey populations in the area changed dramatically. In [24] and [106] a non-spatial and spatial model, respectively, for the spread of Barley/Cereal Yellow Dwarf Viruses among multiple grass hosts was analyzed, which suggests that this class of multi-host pathogens can mediate the outcome of inter-specific competition, facilitating and maintaining invasion by novel species. In [142], using a generic 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 grey squirrel.

Empirical studies have demonstrated the importance of the combined effects of inter- and intra-specific competition between species and the effects of pathogens (apparent com-

petition) on the population dynamics of multi-host systems [59]. A review of empirical studies in [43] 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 control pathogen dynamics [118]. 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 [39]. In addition, understanding the population biology of diseases is important in conservation biology [48].

Although often difficult to quantify empirically, host-pathogen interactions can be studied through mathematical models that combine elements of population dynamics and epidemiology [24, 37, 38, 49]. 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 [17, 73, 57]. The correct choice of the type of incidence (for example, mass action or frequency incidence transmission) that should be used in a model depends on many factors [68, 16, 98]. These include the species that is infected, the transmission routes of infection, and population sizes, among other things. In [18], the authors considered the cowpox virus in coexisting populations of bank voles and wood mice. Their analysis indicates that for each species in isolation frequency dependent transmission is a superior descriptor. In [124, 142] the authors argue for the use of mass action disease transmission in a SIR/SI type model to study the effects of a parapoxvirus in competing grey/red squirrel species in the United Kingdom. Therefore, we investigate both mass action and frequency incidence transmission in our models.

Two species models in which one or both species share a common pathogen and do not interact competitively have been discussed in several papers [8, 73, 17, 57, 68, 35]. In many of these studies, finding conditions for the stability of the coexistence equilibria proved to be difficult. As an alternative, numerical simulations are performed to understand the behavior of the models. In particular, it was found that two host SIS models with mass action incidence can have complicated behaviors including several infected co-

existence equilibria and multiple attractive periodic solutions [57]. In [9, 146, 145] the authors consider a two species model in which both species compete directly and one is subject to a pathogen. The models assume mass action transmission of disease and in [146] the existence of limit cycles is shown. In [145] it was found that if in the absence of disease there is competitive exclusion between the two species, the presence of disease can lead to stable or oscillatory coexistence of both species.

Mathematical models that include competition between multiple species in addition to a shared pathogen are difficult to analyze for the case of infected coexistence. In [26], the authors consider a two species model in which both species compete directly (Lotka-Volterra competition) and both species share a common pathogen. They analyzed their model 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 coexistence equilibria proved impossible to fully analyze. In [61] a model with Lotka-Volterra competition between two species which share a common pathogen is considered. Mass action disease transmission is used in the model, which in its complete generality is intractable. Both density-dependent and disease related death rates are considered; however, unlike in [26], the birth rates are unaffected by competition. The authors concentrate on deriving conditions that guarantee the persistence of either hosts or the pathogen. Using Hopf bifurcation theory and numerical simulations, complex behaviors of the model are demonstrated.

In [60] the authors considered an SIRS epidemic model of two competitive species using frequency dependent incidence and no disease related deaths. Under these conditions, the authors in [60] were able to show stability conditions for all possible equilibria. In [68] the authors considered many different models with frequency incidence disease transmission. The models were shown to have the classic endemic model behavior; the disease dies out below a threshold and approaches an endemic equilibrium above the threshold. However, the behavior of the interior equilibrium remained intractable for the case with density-independent death rates and density-dependent birth rates with both intra- and

inter-specific competition.

In this paper we consider models in which two species compete directly via Lotka-Volterra competition and share a directly transmitted pathogen (Sections 3.3 and 3.3.2). Our models differ from other similar two species models analyzed in [68, 61, 60, 26] in the following aspects. We consider both mass action and frequency incidence type transmission and compute basic reproduction numbers (Section 3.4.1). Similar to the mass action model in [26], the natural mortality rates for the two species are density-independent, while the birth rates are density-dependent with both intra- and inter-specific competition. The motivation for our choice comes from the case of the red/grey squirrel system discussed in [124, 142]. In [142] both intraspecific crowding and interspecific competition were modeled as 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 grey squirrels. As opposed to the models in [26, 61] we also consider frequency incidence disease transmission, and investigate the stability of the infected coexistence equilibrium (Section 3.5.4). In [73, 26, 17] a conjecture was made, based on numerical simulations, that the conditions under which the infected coexistence equilibrium is stable cause all the other equilibria to be unstable. However, [57] provide counterexamples to this conjecture in the most general case. The infected coexistence equilibrium for the most general mass action model has proved to be, in fact, intractable. We are able to prove this conjecture for an ecologically relevant special case in which the infected coexistence equilibrium is tractable (Section 3.4.4). In addition, we show (Section 3.5.8) that for this special case the qualitative behavior of the model with mass action disease transmission is identical to one with frequency incidence disease transmission.

3.2 Background

In this section, we present the SI disease model for one species with mass action transmission (see for e.g., [17, 61]). We also present the two-species Lotka-Volterra (pure) competition model (see for e.g., [61]). We rewrite the equilibria for these two models in a non-standard way, in order to stress the role of the basic reproduction number $\mathcal{R}_0$, and the role of two parameters, ξ_1 , and ξ_2 , whose values govern the relative importance between intra- and inter-specific competition.

3.2.1 The Logistic Growth and Mass Action Disease Model for a Single Species

As background, we present the SI disease model for one species with mass action transmission. Consider the single species SI model with logistic growth,

$$\frac{dS}{dt} = a \left(1 - \frac{N}{\theta}\right) N - bS - \beta SI, \quad (3.2.1)$$

$$\frac{dI}{dt} = \beta SI - \Gamma I, \quad (3.2.2)$$

where the variable S denotes the density of susceptible individuals in the population, I represents the density of infected individuals in the population, and $N = S + I$ is the total population density. The parameter $r := a - b$ is the intrinsic per capita growth rate, with $a(1 - N/\theta)$, and b , the per capita birth and natural death rates, respectively. We assume that $a > b > 0$ and hence $r > 0$. The parameter $\Gamma = \alpha + b$ is a per capita net rate of loss of infected individuals incorporating death due to disease $\alpha \geq 0$, and natural mortality b .

The model (3.2.1)-(3.2.2) is well-posed on the domain $\Omega^D = \{(S, I)^T | S, I \geq 0, 0 \leq N \leq K\}$. The carrying capacity of the species is $K = \frac{r\theta}{a}$. The equilibria for model (3.2.1)-(3.2.2) can be written in the form $E_0^D = (0, 0)$, $E_1^D = (K, 0)$, and

$$E_2^D = \left(\frac{\Gamma}{\beta}, \frac{\Gamma}{\beta} \left[- \left(1 - \frac{\mathcal{R}_0 \lambda}{2} \right) + \sqrt{\left(1 - \frac{\mathcal{R}_0 \lambda}{2} \right)^2 + (\mathcal{R}_0 - 1)} \right] \right), \quad (3.2.3)$$

where $\lambda = \frac{r - \alpha}{r} = 1 - \frac{\alpha}{r}$ and $\mathcal{R}_0 = \frac{\beta K}{\Gamma}$ is the basic reproduction number for the model. The stability of the *disease free equilibrium* (DFE), E_1^D , depends on $\mathcal{R}_0$. The basic reproduction number (BRN) is defined as the average number of secondary infections that occur when an infected individual is introduced into a completely susceptible population. If $\mathcal{R}_0 > 1$, then the disease may emerge in the population, whereas if $\mathcal{R}_0 < 1$, then the DFE is locally asymptotically stable [144].

3.2.2 The Logistic Growth and Frequency Incidence Disease Model for a Single Species

We present the SI disease model for one species with frequency incidence transmission (see for e.g., [17]),

$$\frac{dS}{dt} = a \left(1 - \frac{N}{\theta} \right) N - bS - \beta \frac{I}{N} S, \quad (3.2.4)$$

$$\frac{dI}{dt} = \beta \frac{I}{N} S - \Gamma I, \quad (3.2.5)$$

where the variable S denotes the density of susceptible individuals in the population, I represents the density of infected individuals in the population, and $N = S + I$ is the total population density. The model (3.2.4)-(3.2.5) is well-posed on the domain $\Omega^F = \{(S, I) \in \mathbb{R}^2 | S, I \geq 0, 0 < N \leq K\}$. The carrying capacity of the species is $K = \frac{r\theta}{a}$. The equilibria for model (3.2.4)-(3.2.5) are $E_0^F = (0, 0)$, $E_1^F = (K, 0)$, and

$$E_2^F = (S_2^F, (\mathcal{R}_0 - 1)S_2^F), \quad (3.2.6)$$

where $S_2^F = \frac{\theta}{\mathcal{R}_0^2} \left[\mathcal{R}_0 + \frac{\alpha - \beta}{a} \right]$, and $\mathcal{R}_0 := \frac{\beta}{\Gamma}$ is the basic reproduction number for the model. Thus, $\mathcal{R}_0 > 1$ is a feasibility condition for the equilibrium E_2^F .

We have the following lemma [126].

Lemma 3.2.2.1 *For the model (3.2.4)-(3.2.5), the trivial equilibrium E_0^F is always unstable. If $\mathcal{R}_0 < 1$ then the disease-free equilibrium E_1^F is globally asymptotically stable in the domain Ω^D . If $\mathcal{R}_0 > 1$ then the infected equilibrium E_2^F is globally asymptotically stable in the domain Ω^F .*

3.2.3 The Pure Competition Model for Two Species

Consider the two species model with Lotka-Volterra competition,

$$\frac{dN_i}{dt} = r_i \left(1 - \frac{N_1}{K_{i1}} - \frac{N_2}{K_{i2}} \right) N_i, \quad i = 1, 2, \quad (3.2.7)$$

where N_i is the total population density of species i , for $i = 1, 2$. The terms K_{11}, K_{22} are carrying capacities of species 1, and 2, respectively, and the terms K_{12}, K_{21} are competition parameters.

The model (3.2.7) is well-posed on the domain $\Omega^C = \{(N_1, N_2)^T | 0 \leq N_i \leq K_{ii}, i = 1, 2\}$. The equilibria for model (3.2.7) are $E_0^C = (0, 0)$, $E_1^C = (K_{11}, 0)$, $E_2^C = (0, K_{22})$, and the coexistence equilibrium $E_3^C = (N_1^C, N_2^C)$, where

$$N_1^C = \frac{K_{11}K_{12}}{K_{12} + K_{11}(\xi_1/\xi_2)}, \quad N_2^C = \frac{\xi_1}{\xi_2} N_1^C. \quad (3.2.8)$$

The parameters ξ_1 , and ξ_2 are defined as

$$\xi_1 := \frac{1}{K_{11}} - \frac{1}{K_{21}}, \quad \xi_2 := \frac{1}{K_{22}} - \frac{1}{K_{12}}. \quad (3.2.9)$$

For this pure competition model, the existence (feasibility) and stability of equilibria depend on the positivity or negativity of the parameters ξ_1 and ξ_2 . We can interpret the term $1/K_{ij}$ as the inhibition strength of species j on species i [126]. Hence, the parameters ξ_1 and ξ_2 are a measure of the relative strengths of intra- versus inter-specific competition. Also, note that the sign of ξ_1 is determined by the growth rate of species 2 linearized around the species 1 equilibrium E_1^C . Similarly, the sign of ξ_2 is determined by growth rate of species 1 linearized around the equilibrium E_2^C .

Lemma 3.2.3.1 *For the pure competition model (3.2.7), the trivial equilibrium E_0^C is always unstable. In addition, we have the following cases:*

1. $\xi_1 > 0, \xi_2 > 0$: *Intra-specific competition is stronger than inter-specific competition for both species. The equilibria E_1^C, E_2^C are unstable while E_3^C is globally asymptotically stable in the domain Ω^C .*

2. $\xi_1 < 0, \xi_2 > 0$: Intra-specific competition is stronger for species 1 and inter-specific competition is stronger for species 2. E_3^C is not feasible. E_1^C is globally asymptotically stable, while E_2^C is unstable.
3. $\xi_1 > 0, \xi_2 < 0$: Intra-specific competition is stronger for species 2 and inter-specific competition is stronger for species 1. E_3^C is not feasible. E_2^C is globally asymptotically stable, while E_1^C is unstable.
4. $\xi_1 < 0, \xi_2 < 0$: Inter-specific competition is stronger than intra-specific competition for both species. The coexistence equilibrium E_3^C is a saddle. There is a separatrix that separates the domain Ω^C into two regions. We have bistability of E_1^C and E_2^C with stability (or instability) determined by the location of the initial conditions in two regions of Ω^C . If the initial conditions lie on the separatrix, then the solution tends to E_3^C .

3.2.4 Asymptotically Autonomous Equations

The theory of asymptotically autonomous equations allows us to predict the eventual behavior of non-autonomous differential equations under certain conditions. These properties will be used to analyze the endemic coexistence equilibrium for the frequency-dependent incidence case in Section 3.3.2. We begin with background and theory for asymptotically autonomous equations. Assume that $f(t, x)$ and $g(x)$ are continuous and locally Lipschitz in x and that solutions exist for all forward time for (3.2.10) - (3.2.11). This is true for all models considered in this chapter.

Definition 3.2.4.1 *Let*

$$\frac{dx}{dt} = f(t, x) \tag{3.2.10}$$

$$\frac{dy}{dt} = g(y) \tag{3.2.11}$$

*be ordinary differential equations in $\mathbb{R}^n$. Then equation (3.2.10) is **asymptotically autonomous** with limit equation (3.2.11) if $f(t, x) \rightarrow g(x)$ as $t \rightarrow \infty$ locally uniformly for*

x in any compact subset of $\mathbb{R}^n$.

Let Φ be an asymptotically autonomous continuous semiflow on the metric space $\mathcal{X}$ and Θ its continuous limit-semiflow.

Theorem 3.2.4.1 ([138] Theorem 2.5): $\omega - \Phi$ -limit sets of points (s, x) with pre-compact (forward) orbits are non-empty, compact, and connected. Further they attract the orbits, i.e.

$$d(\Phi(t, s, x), \omega_\Phi(s, x)) \rightarrow 0, \quad t \rightarrow \infty.$$

They are also invariant under the limit-semiflow Θ so that any point y of $\omega_\Phi(s, x)$ lies on an entire Θ -orbit in $\omega_\Phi(s, x)$. (Here s is the time for the initial condition and is usually 0.)

Lemma 3.2.4.1 ([138] Lemma 3.1): Assume that the point (s, x) with $s \geq t_0$ and $x \in \mathcal{X}$ has a pre-compact Φ -orbit and that ω is its ω -limit set. Also, let M be a Θ -invariant set such that $M \cap \omega \neq \emptyset$ but $\omega \not\subseteq M$ and assume $M \cap \omega$ is an isolated compact Θ -invariant subset of ω . Then M has a non-empty stable and a non-empty unstable manifold in ω . i.e. There exists a $u \in \omega \setminus M$ with $\omega_\Theta(u) \subseteq M$ and a $w \in \omega \setminus M$ with a full Θ -orbit in ω whose $\alpha - \Theta$ -limit set is contained in M . So, u can be chosen with its forward orbit arbitrarily close to M and w can be chosen with its backward orbit arbitrarily close to M .

This lemma is essential in the proof for Theorem 4.1 from [138].

Theorem 3.2.4.2 ([138] Theorem 4.1): Let e be a locally asymptotically stable equilibrium of Θ and $\mathcal{W}_s(e) = \{x \in \mathcal{X} : \Theta(t, x) \rightarrow e, t \rightarrow \infty\}$ its basin of attraction or stable set. Then every pre-compact Φ -orbit whose $\omega - \Phi$ -limit set intersects $\mathcal{W}_s(e)$ converges to e .

Proof. Let ω be an $\omega - \Phi$ -limit set which has a point x in common with $\mathcal{W}_s(e)$. By Theorem 3.2.4.1, $\omega_\Theta(x)$ is contained in ω . However, we know $\omega_\Theta(x)$ is just e so $e \in \omega$.

Since e is locally asymptotically stable, $\{e\}$ is an isolated compact Θ -invariant set. If ω does contain elements different from e then by Lemma 3.2.4.1, ω contains a full orbit through a different point from e whose $\alpha - \Theta$ -limit set is $\{e\}$. This contradicts the local stability of e and the conjecture is proved. ■

3.3 Two Species Models with Competition and Disease Dynamics

We consider two species models which incorporate species birth functions, g_i , and disease incidence functions, $\mathcal{I}_i, i = 1, 2$, in the form

$$\frac{dS_i}{dt} = g_i(N_1, N_2)N_i - b_i S_i - \mathcal{I}_i(I_1, I_2)S_i, \quad (3.3.1a)$$

$$\frac{dI_i}{dt} = \mathcal{I}_i(I_1, I_2)S_i - \Gamma_i I_i, \quad (3.3.1b)$$

for $i = 1, 2$. The variable S_i denotes the density of susceptible individuals in the population of species i , I_i represents the density of infected individuals in the population of species i , and $N_i = S_i + I_i$ is the total population density of species i . We assume that the birth terms are density-dependent, including both intra-specific and inter-specific competition. Assuming Lotka-Volterra competition, the birth functions for the two species are given as

$$g_i(N_1, N_2) = a_i \left(1 - \frac{N_1}{\theta_{i1}} - \frac{N_2}{\theta_{i2}} \right), \quad i = 1, 2. \quad (3.3.2)$$

where $r_i := a_i - b_i$ is the intrinsic per capita growth rate for species i , with $a_i(1 - N_i/\theta_{ii})$, and b_i , the per capita birth and natural death rates, respectively, for species i in isolation. We assume that $a_i > b_i > 0$ and hence $r_i > 0$ for $i = 1, 2$. The terms $\Gamma_i := \alpha_i + b_i$, for species i , are per capita net rates of loss of infected individuals incorporating death due to disease, $\alpha_i \geq 0$, and natural mortality b_i . We define $K_{ij} := \frac{r_i \theta_{ij}}{a_i}$ for $i, j = 1, 2$. The carrying capacity for species i alone is K_{ii} and the terms θ_{ij}^{-1} for $i \neq j$ are competition coefficients.

The disease transmission term, given here by the disease incidence functions $\mathcal{I}_i$ for species i , describes the rate at which susceptible hosts are converted into infected

hosts by their contact with infectious material. Transmission is the driving force in the dynamics of any infectious disease and hence the functions $\mathcal{I}_i$ are a very important part of epidemiological models.

3.3.1 Mass Action (Density Dependent) Incidence

The disease incidence functions for mass action transmission are given to be

$$\mathcal{I}_i(I_1, I_2) = \beta_{i1}I_1 + \beta_{i2}I_2, \quad (3.3.3)$$

for $i = 1, 2$. The model (3.3.1a)-(3.3.1b) can be written as

$$\frac{dS_1}{dt} = a_1 \left(1 - \frac{N_1}{\theta_{11}} - \frac{N_2}{\theta_{12}} \right) N_1 - b_1 S_1 - (\beta_{11}I_1 + \beta_{12}I_2)S_1, \quad (3.3.4)$$

$$\frac{dS_2}{dt} = a_2 \left(1 - \frac{N_2}{\theta_{22}} - \frac{N_1}{\theta_{21}} \right) N_2 - b_2 S_2 - (\beta_{22}I_2 + \beta_{21}I_1)S_2, \quad (3.3.5)$$

$$\frac{dI_1}{dt} = (\beta_{11}I_1 + \beta_{12}I_2)S_1 - \Gamma_1 I_1, \quad (3.3.6)$$

$$\frac{dI_2}{dt} = (\beta_{22}I_2 + \beta_{21}I_1)S_2 - \Gamma_2 I_2. \quad (3.3.7)$$

and makes ecological sense and is mathematically well-posed in the domain $\mathcal{D}^1 = \{(S_1, S_2, I_1, I_2) \in \mathbb{R}^4 | S_1, S_2, I_1, I_2 \geq 0, 0 \leq N_i \leq K_{ii}, i = 1, 2\}$.

Theorem 3.3.1.1 *Assuming that the initial conditions are in $\mathcal{D}^1$ the system (3.3.4)-(3.3.7) has a unique solution that remains in $\mathcal{D}^1$ for all time $t \geq 0$.*

Proof. The right hand side of system (3.3.4)-(3.3.7) is continuous and continuously differentiable so we know that a solution exists and is unique. Next we show that the system is invariant in $\mathcal{D}^1$ for all positive time. First, if $I_1 = 0$ then $I_1' \geq 0$ and similarly if $I_2 = 0$ then $I_2' \geq 0$. If $N_1 = S_1 + I_1 > K_{11}$ then $N_1' = (S_1 + I_1)' < 0$ and if $N_2 = S_2 + I_2 > K_{22}$ then $N_2' = (S_2 + I_2)' < 0$. Lastly if $S_1 = 0$, assuming $I_1 \leq K_{11}$ then $S_1' \geq 0$ and if $S_2 = 0$ assuming that $I_2 \leq K_{22}$ then $S_2' \geq 0$. So, $\mathcal{D}^1$ is forward invariant and no orbits beginning in $\mathcal{D}^1$ leave $\mathcal{D}^1$. Therefore a solution with initial conditions in $\mathcal{D}^1$ exists, is unique, and remains in $\mathcal{D}^1$ for all time. ■

3.3.2 Frequency Dependent Incidence

We also consider a two species model in which the transmission dynamics follows the frequency incidence approach. In this approach the intra-species and inter-species transmission rates $\beta_{ij} > 0$ are constant terms for $i, j = 1, 2$. This means that the contact rate between individuals of the two species is constant. Often this is the case when populations are very large, for example. Frequency incidence is also often used to model transmission through vectors. We can write the disease incidence functions as

$$\mathcal{I}_1(I_1, I_2) = \left(\beta_{11} \frac{I_1}{N_1} + \beta_{12} \frac{I_2}{N_2} \right), \quad (3.3.8)$$

$$\mathcal{I}_2(I_1, I_2) = \left(\beta_{22} \frac{I_2}{N_2} + \beta_{21} \frac{I_1}{N_1} \right). \quad (3.3.9)$$

The disease incidence is undefined when $N_i = S_i + I_i = 0$ for at least one $i = 1, 2$. However, the function $h(S_i, I_i) = S_i I_i / (S_i + I_i)$ is a Lipschitz continuous function of S_i and I_i in the region $S_i, I_i > 0$. In order to address the cases where one species die out, we extend the function as in [7] to the space $S_i, I_i \geq 0$ by defining $h(S_i, I_i) = 0$ when either S_i, I_i , or both are zero.

With these assumptions, the two-species competition model with frequency incidence disease transmission is:

$$\frac{dS_1}{dt} = a_1 \left(1 - \frac{N_1}{\theta_{11}} - \frac{N_2}{\theta_{12}} \right) N_1 - b_1 S_1 - \left(\beta_{11} \frac{I_1}{N_1} + \beta_{12} \frac{I_2}{N_2} \right) S_1, \quad (3.3.10a)$$

$$\frac{dS_2}{dt} = a_2 \left(1 - \frac{N_2}{\theta_{22}} - \frac{N_1}{\theta_{21}} \right) N_2 - b_2 S_2 - \left(\beta_{22} \frac{I_2}{N_2} + \beta_{21} \frac{I_1}{N_1} \right) S_2, \quad (3.3.10b)$$

$$\frac{dI_1}{dt} = \left(\beta_{11} \frac{I_1}{N_1} + \beta_{12} \frac{I_2}{N_2} \right) S_1 - \Gamma_1 I_1, \quad (3.3.10c)$$

$$\frac{dI_2}{dt} = \left(\beta_{22} \frac{I_2}{N_2} + \beta_{21} \frac{I_1}{N_1} \right) S_2 - \Gamma_2 I_2. \quad (3.3.10d)$$

The model (3.3.10a)-(3.3.10d) makes ecological sense and is mathematically well-posed in the domain $\mathcal{D}^1 = \{(S_1, S_2, I_1, I_2) \in \mathbb{R}^4 | S_1, S_2, I_1, I_2 \geq 0, 0 \leq N_i \leq K_{ii}, i = 1, 2\}$. The total

population size $N_i = S_i + I_i$ of species i satisfy the differential equations,

$$\frac{dN_1}{dt} = r_1 \left(1 - \frac{N_1}{K_{11}} - \frac{N_2}{K_{12}} \right) N_1 - \alpha_1 I_1, \quad (3.3.11a)$$

$$\frac{dN_2}{dt} = r_2 \left(1 - \frac{N_2}{K_{22}} - \frac{N_1}{K_{21}} \right) N_2 - \alpha_2 I_2, \quad (3.3.11b)$$

Theorem 3.3.2.1 *Assuming that the initial conditions are in $\mathcal{D}^1$ the system (3.3.10a)-(3.3.10d) has a unique solution that remains in $\mathcal{D}^1$ for all time $t \geq 0$.*

Proof. Similar to the proof of Theorem 3.3.1.1 since the difference between the two models is only in disease incidence. ■

3.4 Computation of Equilibria and Linear Stability Analysis for Mass Action

We will denote equilibrial susceptible densities for species i by $\hat{S}_i$ and similarly $\hat{I}_i$ for the infected equilibrial densities of species i , for $i = 1, 2$. Below we present the equilibria for model (3.3.1a)-(3.3.1b), and their linear stability analysis. An equilibrium E_e is represented using the notation $E_e = (\hat{S}_1^e, \hat{S}_2^e, \hat{I}_1^e, \hat{I}_2^e)$.

The trivial equilibrium E_0 of model (3.3.1a)-(3.3.1b) is

$$E_0 = (\hat{S}_1^0 = 0, \hat{S}_2^0 = 0, \hat{I}_1^0 = 0, \hat{I}_2^0 = 0). \quad (3.4.1)$$

The eigenvalues of the Jacobian of this model evaluated at E_0 , i.e., $\mathcal{J}(E_0)$, are r_i and $-\Gamma_i$ for $i = 1, 2$. Thus, by assumption at least two of the eigenvalues are always positive, and hence the equilibrium E_0 is always unstable.

There are three disease free equilibria E_1, E_2 and E_3 . These are given as $E_1 = (\hat{S}_1^1 = K_{11}, \hat{S}_2^1 = 0, \hat{I}_1^1 = 0, \hat{I}_2^1 = 0)$, $E_2 = (\hat{S}_1^2 = 0, \hat{S}_2^2 = K_{22}, \hat{I}_1^2 = 0, \hat{I}_2^2 = 0)$, and

$E_3 = (\hat{S}_1^3, \hat{S}_2^3, \hat{I}_1^3 = 0, \hat{I}_2^3 = 0)$, with

$$\hat{S}_1^3 = \frac{K_{11}K_{12}}{K_{12} + K_{11}(\xi_1/\xi_2)}, \quad \hat{S}_2^3 = \frac{\xi_1}{\xi_2} \hat{S}_1^3, \quad (3.4.2)$$

and the parameters ξ_1 and ξ_2 are defined in (3.2.9). We will refer to E_1, E_2 as the *disease free one-host equilibria*, since one of the species survives in an uninfected state reaching carrying capacity, while the other species dies out. The equilibrium E_3 is called the *disease free coexistence equilibrium* (DFE).

3.4.1 The Coexistence DFE

As a DFE, the coexistence equilibrium is biologically feasible when $\frac{\xi_1}{\xi_2} > 0$.

Theorem 3.4.1.1 *The basic reproduction number (BRN) for model (3.3.1a)-(3.3.1b) with coexisting species is*

$$\mathcal{R}_0^C = \frac{\mathcal{R}_{11} + \mathcal{R}_{22}}{2} + \frac{\sqrt{(\mathcal{R}_{11} - \mathcal{R}_{22})^2 + 4\mathcal{R}_{12}\mathcal{R}_{21}}}{2}, \quad (3.4.3)$$

where, for $i, j = 1, 2$

$$\mathcal{R}_{ij} = \frac{\beta_{ij}\hat{S}_i^1}{\Gamma_j}; \quad (3.4.4)$$

The basic reproduction number for species j in isolation is $\mathcal{R}_0^j = \mathcal{R}_{jj}$, for $j = 1, 2$. The condition $\mathcal{R}_0^C < 1$ leads to the inequality

$$\mathcal{R}_{11} + \mathcal{R}_{22} + \mathcal{R}_{12}\mathcal{R}_{21} - \mathcal{R}_{11}\mathcal{R}_{22} < 1. \quad (3.4.5)$$

Proof. We will use the next generation matrix method [144], which has become a standard tool to determine the stability of the coexistence DFE, E_3 . Let $X = (S_1, S_2, I_1, I_2)^T$. Then we can rewrite system (3.3.1a)-(3.3.1b) in the form

$$\frac{dX}{dt} = \mathcal{F}(X) - \mathcal{V}(X), \quad (3.4.6)$$

where $\mathcal{F}(X)$ represents the vector function that includes the new infectious cases and $\mathcal{V}(X)$ contains all other dynamics due to death and recovery. We compute the Jacobian

of $\mathcal{F}$ and $\mathcal{V}$ and evaluate these at the coexistence DFE, $E_3 = (\hat{S}_1^3, \hat{S}_2^3, 0, 0)$. Let F and V be the matrices defined by

$$F = \left[\frac{\partial \mathcal{F}_i}{\partial x_j}(E_3) \right]; \quad V = \left[\frac{\partial \mathcal{V}_i}{\partial x_j}(E_3) \right], \quad (3.4.7)$$

where $3 \leq i, j \leq 4$ and x_j is the j th component of the vector X defined in (5.5.3). Computing these matrices we have

$$F = \begin{bmatrix} \beta_{11}\hat{S}_1^3 & \beta_{12}\hat{S}_1^3 \\ \beta_{21}\hat{S}_2^3 & \beta_{22}\hat{S}_2^3 \end{bmatrix}, \quad (3.4.8)$$

and $V = \text{diag}(\Gamma_i)$. The BRN $\mathcal{R}_0^C$ for model (3.3.1a)-(3.3.1b) with coexisting species is given as

$$\mathcal{R}_0^C = \rho(FV^{-1}), \quad (3.4.9)$$

where $\rho(A)$ is the spectral radius of the matrix A . We have

$$FV^{-1} = \begin{bmatrix} \frac{\beta_{11}\hat{S}_1^3}{\Gamma_1} & \frac{\beta_{12}\hat{S}_1^3}{\Gamma_2} \\ \frac{\beta_{21}\hat{S}_2^3}{\Gamma_1} & \frac{\beta_{22}\hat{S}_2^3}{\Gamma_2} \end{bmatrix}. \quad (3.4.10)$$

Thus, using the definition (3.4.4) it is easily shown that the spectral radius of the matrix FV^{-1} is given by the formula (3.4.3).

Assuming $\mathcal{R}_0^C < 1$ in (3.4.3) we can now easily derive

$$\frac{\beta_{11}}{\Gamma_1}\hat{S}_1^3 + \frac{\beta_{22}}{\Gamma_2}\hat{S}_2^3 + \left(\frac{\beta_{12}\beta_{21}}{\Gamma_1\Gamma_2} - \frac{\beta_{11}\beta_{22}}{\Gamma_1\Gamma_2} \right) \hat{S}_1^3\hat{S}_2^3 < 1, \quad (3.4.11)$$

which is equivalent to the inequality (3.4.5).

■

Theorem 3.4.1.2 *The coexistence DFE, E_3 is feasible and stable if and only if the conditions $\xi_1 > 0$, $\xi_2 > 0$ and $\mathcal{R}_0^C < 1$ are satisfied.*

Proof. The Jacobian of the system (3.3.1a)-(3.3.1b) evaluated at the DFE $E_3 = (\hat{S}_1^3, \hat{S}_2^3, \hat{I}_1^3 = 0, \hat{I}_2^3 = 0)$ is the block triangular matrix

$$\mathcal{J}(E_3) = \begin{bmatrix} \mathcal{A} & * \\ \mathbf{0} & F - V \end{bmatrix}, \quad (3.4.12)$$

where the matrix $\mathcal{A}$ is the Jacobian matrix of the system (3.2.7) evaluated at $E_3^C = (N_1^C, N_2^C) = (\hat{S}_1^3, \hat{S}_2^3)$ (see section 3.2.3), and the matrices F and V are as defined in (3.4.7) (the $*$ indicates a nonzero entry). Since the Jacobian $\mathcal{J}(E_3)$ is block triangular, its eigenvalues are the eigenvalues of the matrices $\mathcal{A}$ and $F - V$.

From [21], $E_3^C = (N_1^C, N_2^C)$ is globally asymptotically stable if and only if $\xi_1 > 0$ and $\xi_2 > 0$. Thus, the eigenvalues of the matrix $\mathcal{A}$ are negative if and only if $\xi_1 > 0$ and $\xi_2 > 0$, which are also feasibility conditions for E_3 . From the next generation approach, the eigenvalues of the matrix $F - V$ are negative if and only if $\mathcal{R}_0^C = \rho(FV^{-1}) < 1$ [144].

■

3.4.2 The Disease Free One-Host Equilibrium

When $\xi_1/\xi_2 < 0$ the coexistence DFE is infeasible. We have the following two cases.

1. Assume $\xi_1 < 0$ and $\xi_2 > 0$. In this case the disease free one-host equilibrium $E_1 = (K_{11}, 0, 0, 0)$ is feasible and stable if in addition the condition

$$\mathcal{R}_0^1 = \frac{K_{11}\beta_{11}}{\Gamma_1} < 1 \quad (3.4.13)$$

is satisfied, where $\mathcal{R}_0^1$ is the basic reproduction number for species 1 alone. This result follows from conditions on stability of E_1^C (see Section 3.2.3) and conditions on stability of E_1^D (see Section 3.2.1).

2. Assume $\xi_1 > 0$ and $\xi_2 < 0$. In this case the one-host DFE $E_2 = (0, K_{22}, 0, 0)$ is feasible and stable if in addition the condition

$$\mathcal{R}_0^2 = \frac{K_{22}\beta_{22}}{\Gamma_2} < 1 \quad (3.4.14)$$

is satisfied, where $\mathcal{R}_0^2$ is the basic reproduction number for species 1 alone. As in case 1, this result follows from conditions on stability of E_2^C and E_1^D .

3.4.3 Infected One-Host Equilibria

There are two types of *infected one-host equilibria*. In these one of the species survives while the other species dies out. The first type of infected one-host equilibria are given as

$$E_{4a,4b} = \left(\hat{S}_1^4 = \frac{\Gamma_1}{\beta_{11}}, \hat{S}_2^4 = 0, \hat{I}_1^{4a,4b} = \frac{I_{4a,4b}^*}{\beta_{11}}, \hat{I}_2^4 = 0 \right), \quad (3.4.15)$$

where $I_{4a,4b}^*$ are roots of the quadratic polynomial $P_4(x) = x^2 + 2\Gamma_1 \left(1 - \frac{\mathcal{R}_0^1 \lambda_1}{2}\right) x + \Gamma_1^2 (1 - \mathcal{R}_0^1)$, with the parameter λ_1 defined as $\lambda_1 := \frac{r_1 - \alpha_1}{r_1}$. Solving for the roots, the infected component of species 1 in the one-host equilibria $E_{4a,4b}$ is

$$\hat{I}_1^{4a,4b} = \hat{S}_1^4 \chi_{4a,4b}, \quad (3.4.16)$$

where ,

$$\chi_{4a,4b} = - \left(1 - \frac{\mathcal{R}_0^1 \lambda_1}{2}\right) \pm \sqrt{\left(1 - \frac{\mathcal{R}_0^1 \lambda_1}{2}\right)^2 + (\mathcal{R}_0^1 - 1)}. \quad (3.4.17)$$

Lemma 3.4.3.1 *The infected one-host equilibrium E_{4a} with $\hat{I}_1^{4a}$ is biologically feasible if and only if $\mathcal{R}_0^1 > 1$, whereas the equilibrium E_{4b} with $\hat{I}_1^{4b}$ is always infeasible.*

Proof. Case 1: Let $\mathcal{R}_0^1 > 1$, then $\chi_{4a} > 0$, and $\chi_{4b} < 0$. Thus, E_{4a} is feasible and E_{4b} is biologically infeasible.

Case 2: Let $0 < \mathcal{R}_0^1 \leq 1$. In this case we note that the first term of $\chi_{4a,4b}$ in (3.4.17) can be rewritten as

$$- \left(1 - \frac{\mathcal{R}_0^1 \lambda_1}{2}\right) = - \left(1 - \frac{\mathcal{R}_0^1}{2}\right) - \frac{\alpha_1 \mathcal{R}_0^1}{2r_1} < 0, \quad (3.4.18)$$

as the rates α_1 and r_1 are both positive. Thus, in this case as well $\chi_{4b} < 0$, and E_{4b} is biologically infeasible. If $\mathcal{R}_0^1 = 1$, then $\chi_{4a} = 0$, and the equilibrium E_{4a} reduces to the

disease free one-host equilibrium E_1 , whereas, if $0 < \mathcal{R}_0^1 < 1$ then $\chi_{4a} < 0$ and E_{4a} is also biologically infeasible. ■

We will now refer to the equilibrium E_{4a} as simply E_4 .

Lemma 3.4.3.2 *Let $\mathcal{R}_0^1 > 1$. If $\alpha_1 > 0$, then $\hat{N}_1^4 = \hat{S}_1^4(1 + \chi_{4a}) < K_{11}$. If $\alpha_1 = 0$ then $\hat{N}_1^4 = K_{11}$.*

Proof. The condition $\mathcal{R}_0^1 > 1$ guarantees the feasibility of the equilibrium E_4 . By assumption $\alpha_1 > 0$, and hence $\lambda_1 < 1$. We then have

$$1 - \lambda_1 < \mathcal{R}_0^1(1 - \lambda_1) < \mathcal{R}_0^1 \left(1 - \frac{\lambda_1}{2}\right)^2 - \mathcal{R}_0^1 \frac{\lambda_1^2}{4} \quad (3.4.19)$$

$$1 - \mathcal{R}_0^1 \lambda_1 + \frac{(\mathcal{R}_0^1)^2 \lambda_1^2}{4} + \mathcal{R}_0^1 - 1 < (\mathcal{R}_0^1)^2 \left(1 - \lambda_1 + \frac{\lambda_1^2}{4}\right) \quad (3.4.20)$$

$$\implies \left(1 - \frac{\mathcal{R}_0^1 \lambda_1}{2}\right)^2 + (\mathcal{R}_0^1 - 1) < \left(\mathcal{R}_0^1 - \frac{\mathcal{R}_0^1 \lambda_1}{2}\right)^2 \quad (3.4.21)$$

$$\implies \sqrt{\left(1 - \frac{\mathcal{R}_0^1 \lambda_1}{2}\right)^2 + (\mathcal{R}_0^1 - 1)} < \mathcal{R}_0^1 - \frac{\mathcal{R}_0^1 \lambda_1}{2} \quad (3.4.22)$$

$$\implies \frac{\Gamma_1}{\beta_{11}} \left\{ \left(\frac{\mathcal{R}_0^1 \lambda_1}{2}\right) + \sqrt{\left(1 - \frac{\mathcal{R}_0^1 \lambda_1}{2}\right)^2 + (\mathcal{R}_0^1 - 1)} \right\} < K_{11}, \quad (3.4.23)$$

since from (3.4.13) $\mathcal{R}_0^1 = (K_{11}\beta_{11})/\Gamma_1$. From (3.4.15) and (3.4.16) we finally have

$$\hat{N}_1^4 = \hat{S}_1^4(1 + \chi_{4a}) < K_{11}. \quad (3.4.24)$$

If $\alpha_1 = 0$ (as in Section 3.4.4), then $\lambda_1 = 1$ and $\hat{N}_1^4 = K_{11}$. Hence, we can see that the total population of the infected one-host equilibrium is less than (or equal to) the carrying capacity for species 1 in the case that the disease related mortality $\alpha_1 > 0$ ($\alpha_1 = 0$). ■

Theorem 3.4.3.1 *Assume $\alpha_1 > 0$. If $\mathcal{R}_0^1 > 1$ and $K_{21} < \hat{N}_1^4$, then the infected one-host equilibrium for species 1, E_4 , is feasible and stable.*

Proof. From Lemma 3.4.3.2 we know that the condition $\mathcal{R}_0^1 > 1$ guarantees the feasibility of E_4 .

The Jacobian for the (species 1) infected one-host equilibrium E_4 , with the order changed to $E_4 = (\hat{S}_1^4, \hat{I}_1^4, \hat{S}_2^4, \hat{I}_2^4)$ for convenience, is

$$\mathcal{J}(E_4) = \begin{bmatrix} P & * \\ 0 & Q \end{bmatrix}, \quad (3.4.25)$$

where

$$P = \begin{bmatrix} a_1 \left(1 - \frac{2\hat{N}_1^4}{\theta_{11}}\right) - b_1 - \beta_{11}\hat{I}_1^4 & a_1 \left(1 - \frac{2\hat{N}_1^4}{\theta_{11}}\right) - \beta_{11}\hat{S}_1^4 \\ \beta_{11}\hat{I}_1^4 & \beta_{11}\hat{S}_1^4 - \Gamma_1 \end{bmatrix},$$

$$Q = \begin{bmatrix} a_2 \left(1 - \frac{\hat{N}_1^4}{\theta_{21}}\right) - b_2 - \beta_{21}\hat{I}_1^4 & a_2 \left(1 - \frac{\hat{N}_1^4}{\theta_{21}}\right) \\ \beta_{21}\hat{I}_1^4 & -\Gamma_2 \end{bmatrix}.$$

Since $\mathcal{J}(E_4)$ is block triangular we need only consider the eigenvalues of P and Q . We notice that the upper left block matrix, P , is the same as the Jacobian for species 1 alone with the disease, i.e., the Jacobian of the system (3.2.1)-(3.2.2) evaluated at the equilibrium E_2^D (with the parameters and variables appropriately defined); see Section 3.2.1. Based on stability results of model (3.2.1)-(3.2.2) (see [21]), the eigenvalues of P are negative if and only if $\mathcal{R}_0^1 > 1$.

We next consider the bottom right block matrix, Q , and use the trace determinant theorem to arrive at conditions for stability. With some algebraic manipulations the trace and determinant of the matrix Q can be written as

$$\text{Tr}[Q] = r_2 \left(1 - \frac{\hat{N}_1^4}{K_{21}}\right) - (\beta_{21}\hat{I}_1^4 + \Gamma_2), \quad (3.4.26)$$

$$\det[Q] = -r_2 \left(1 - \frac{\hat{N}_1^4}{K_{21}}\right) (\beta_{21}\hat{I}_1^4 + \Gamma_2) + \beta_{21}\hat{I}_1^4\alpha_2. \quad (3.4.27)$$

If $K_{21} < \hat{N}_1^4$, then $\left(1 - \frac{\hat{N}_1^4}{K_{21}}\right) < 0$ and hence $\text{Tr}(Q) < 0$ and $\det(Q) > 0$, as all the parameters are positive. Thus, if $\mathcal{R}_0^1 > 1$ and $K_{21} < \hat{N}_1^4$ then the infected one host equilibrium E_4 is stable. ■

Remark 3.4.3.1 *The condition $K_{21} < \hat{N}_1^4$ is not necessary for the stability of E_4 . Necessary conditions for stability of E_4 are obtained by the application of the Trace-determinant theorem. From (3.4.27), $\det(Q) > 0$ gives us the condition*

$$r_2 \left(1 - \frac{\hat{N}_1^4}{K_{21}} \right) (\beta_{21} \hat{I}_1^4 + \Gamma_2) - \beta_{21} \hat{I}_1^4 \alpha_2 < 0. \quad (3.4.28)$$

We can similarly define

$$E_{5a,5b} = \left(\hat{S}_1^5 = 0, \hat{S}_2^5 = \frac{\Gamma_2}{\beta_{22}}, \hat{I}_1^5 = 0, \hat{I}_2^{5a,5b} = \frac{I_{5a,5b}^*}{\beta_{22}} \right), \quad (3.4.29)$$

where $I_{5a,5b}^*$ are roots of the quadratic polynomial $P_5(x) = x^2 + 2\Gamma_2 \left(1 - \frac{\mathcal{R}_0^2 \lambda_2}{2} \right) x + \Gamma_2^2 (1 - \mathcal{R}_0^2)$, with $\lambda_2 := \frac{r_2 - \alpha_2}{r_2}$. The infected component of species 2 in the one-host equilibria $E_{5a,5b}$, is $\hat{I}_2^{5a,5b} = \hat{S}_2^5 \chi_{5a,5b}$, with $\chi_{5a,5b}$ defined similarly to (3.4.17) as

$$\left[- \left(1 - \frac{\mathcal{R}_0^2 \lambda_2}{2} \right) \pm \sqrt{\left(1 - \frac{\mathcal{R}_0^2 \lambda_2}{2} \right)^2 + (\mathcal{R}_0^2 - 1)} \right], \quad (3.4.30)$$

As for the case with species 1, only the root I_{5a}^* is positive and the equilibrium E_{5a} is conditionally feasible, whereas the root I_{5b}^* is always negative and thus the equilibrium E_{5b} is always infeasible. We will refer to E_{5a} as simply E_5 in the future.

By similar arguments we can prove

Theorem 3.4.3.2 *Assume $\alpha_2 > 0$. If $\mathcal{R}_0^2 > 1$ and $K_{12} < \hat{N}_2^5$ then the infected one-host equilibrium $E_{5a} = E_5$ is biologically feasible and stable. The equilibrium E_{5b} is always infeasible.*

Proof. The proof is similar to the proof of Theorem 3.4.3.1 ■

3.4.4 Analysis of the Infected Coexistence Equilibrium of the Competition and Disease Model Under Additional Assumptions

As discussed in [26] the infected coexistence equilibria are difficult to analyze. It is possible to have multiple such equilibria present in the model with mass action disease

transmission. We will consider a special case in which the infected coexistence equilibrium is given by an analytical formula making analysis possible.

In this section, we derive an analytical expression for the infected coexistence equilibrium of the two species model (3.3.1a)-(3.3.1b) under additional assumptions. Consequently we are able to perform a full stability analysis. This allows us to prove the conjecture made in [73] and [17] based on numerical simulations about the behavior of the infected coexistence equilibrium of population models that are combined with mass action disease models. This conjecture states that if all other equilibria are unstable then the infected coexistence equilibrium is stable and, conversely, that if any of the other equilibria are stable then the infected coexistence equilibrium is unstable.

Here we make the following additional assumptions on the model (3.3.1a)-(3.3.1b) described in Section 3.3.

- (A1) $\alpha_i = 0$, so that there is no increased death rate as a result of the disease.
- (A2) $a = a_1 = a_2$, $b = b_1 = b_2$, $\theta = \theta_{11} = \theta_{22}$, and $\beta = \beta_{ij}$ for all $i, j = 1, 2$. As before, let $r := a - b$ be the intrinsic growth rate for both the species. Also, $K = K_{11} = K_{22} = \frac{r\theta}{a}$, so the carrying capacity is the same for both species.
- (A3) $\theta_{12} \neq \theta_{21}$ (in order to retain a difference between the species).

As before, we define $K_{ij} := \frac{r\theta_{ij}}{a}$. These simplifications are not only didactic but result in a model that can represent actual ecological systems. For example, if two species are limited by different resources then they may have very similar intra-specific competition but quite different inter-specific competition while still being susceptible to a generalist pathogen or parasite [25].

First, we compute the possible equilibria, in the form $E_e = (\hat{S}_1^e, \hat{S}_2^e, \hat{I}_1^e, \hat{I}_2^e)$, for the competing two species SI model with mass action disease transmission, (3.3.1a)-(3.3.1b)

under the additional assumptions (A1), (A2) and (A3). We then use the Jacobian of our simplified model to establish stability conditions for all the equilibria. Finally we prove that the conjecture of [73] and of [17] holds.

The Jacobian for this simplified system computed at an equilibrium $E_e = (\hat{S}_1^e, \hat{S}_2^e, \hat{I}_1^e, \hat{I}_2^e)$ is

$$\mathcal{J}(E_e) = \begin{bmatrix} \mathcal{A}(E_e) & \mathcal{B}(E_e) \\ \mathcal{C}(E_e) & \mathcal{D}(E_e) \end{bmatrix}, \quad (3.4.31)$$

where, the 2×2 matrices $\mathcal{A}$, $\mathcal{B}$, $\mathcal{C}$, and $\mathcal{D}$ evaluated at an equilibrium E_e are defined as

$$\mathcal{A}(E_e) = \begin{bmatrix} A(E_e) - b - \mathcal{I}(E_e) & A_{12}(E_e) \\ B_{21}(E_e) & B(E_e) - b - \mathcal{I}(E_e) \end{bmatrix}, \quad (3.4.32)$$

$$\mathcal{B}(E_e) = \begin{bmatrix} A(E_e) - \beta \hat{S}_1^e & A_{12}(E_e) - \beta \hat{S}_1^e \\ B_{21}(E_e) - \beta \hat{S}_2^e & B(E_e) - \beta \hat{S}_2^e \end{bmatrix}, \quad (3.4.33)$$

$$\mathcal{C}(E_e) = \begin{bmatrix} \mathcal{I}(E_e) & 0 \\ 0 & \mathcal{I}(E_e) \end{bmatrix}, \quad (3.4.34)$$

and

$$\mathcal{D}(E_e) = \begin{bmatrix} \beta \hat{S}_1^e - b & \beta \hat{S}_1^e \\ \beta \hat{S}_2^e & \beta \hat{S}_2^e - b \end{bmatrix}. \quad (3.4.35)$$

with the definitions

$$A(E_e) := \frac{-a\hat{N}_1^e}{\theta} + g_1(\hat{N}_1^e, \hat{N}_2^e), \quad (3.4.36)$$

$$A_{12}(E_e) := \frac{-a\hat{N}_1^e}{\theta_{12}}, \quad (3.4.37)$$

$$B(E_e) := \frac{-a\hat{N}_2^e}{\theta} + g_2(\hat{N}_1^e, \hat{N}_2^e), \quad (3.4.38)$$

$$B_{21}(E_e) := \frac{-a\hat{N}_2^e}{\theta_{21}}. \quad (3.4.39)$$

For $i = 1, 2$, we have $\hat{N}_i = \hat{S}_i + \hat{I}_i$. From (3.3.3) we have the disease incidence function,

$$\mathcal{I}(E_e) = \beta(\hat{I}_1^e + \hat{I}_2^e), \quad (3.4.40)$$

$(\mathcal{I}_1 = \mathcal{I}_2)$, and for $i = 1, 2$, the birth functions g_i as defined in (3.3.2) (with $\theta = \theta_{11} = \theta_{22}$) evaluated at E_e are given as

$$g_1(E_e) = a \left(1 - \frac{\hat{N}_1^e}{\theta} - \frac{\hat{N}_2^e}{\theta_{12}} \right), \quad (3.4.41a)$$

$$g_2(E_e) = a \left(1 - \frac{\hat{N}_2^e}{\theta} - \frac{\hat{N}_1^e}{\theta_{21}} \right). \quad (3.4.41b)$$

3.4.5 Trivial and Disease Free Equilibria

As in the non simplified model, the trivial equilibrium $E_0 = (0, 0, 0, 0)$ is always unstable for positive parameters.

The disease free one-host equilibria $E_1 = (K, 0, 0, 0)$ is stable if conditions

$$(C1) \quad \mathcal{R}_0 = \frac{K\beta}{b} < 1, \text{ and}$$

$$(C2) \quad \xi_1 < 0,$$

hold. In the symmetric case, the other disease free one-host equilibrium $E_2 = (0, 0, K, 0)$ is stable if condition (C1) holds and if the condition

$$(C3) \quad \xi_2 < 0,$$

holds.

The disease free coexistence equilibrium for the simplified model is $E_3 = (\hat{S}_1^3, \hat{S}_2^3, 0, 0)$ with

$$\hat{S}_1^3 = \frac{KK_{12}}{K_{12} + K(\xi_1/\xi_2)}, \quad \hat{S}_2^3 = \frac{\xi_1}{\xi_2} \hat{S}_1^3, \quad (3.4.42)$$

where the parameters ξ_1 and ξ_2 defined in (3.2.9) reduce to

$$\xi_1 = \frac{1}{K} - \frac{1}{K_{21}}, \quad \xi_2 = \frac{1}{K} - \frac{1}{K_{12}}. \quad (3.4.43)$$

The DFE E_3 is feasible when $\xi_1/\xi_2 > 0$. The Jacobian (3.4.31) evaluated at E_3 is of the form

$$\mathcal{J}(E_3) = \begin{bmatrix} \mathcal{A}(E_3) & \mathcal{B}(E_3) \\ 0 & \mathcal{D}(E_3) \end{bmatrix}, \quad (3.4.44)$$

where the 2×2 matrices $\mathcal{A}$, $\mathcal{B}$, and $\mathcal{D}$ defined in (3.4.32), (3.4.33), and (3.4.35), respectively are all evaluated at the equilibrium E_3 .

Lemma 3.4.5.1 *Assume that $\xi_1/\xi_2 > 0$, so that the disease free coexistence equilibrium E_3 is feasible. In this case*

$$\det [\mathcal{A}](E_3) = r^2 \hat{S}_1^3 \xi_1, \quad (3.4.45)$$

$$\text{Tr}[\mathcal{A}](E_3) = -\frac{r\hat{S}_1^3}{K} \left(1 + \frac{\xi_1}{\xi_2} \right). \quad (3.4.46)$$

Thus, $\text{Tr}[\mathcal{A}](E_3)$ is always negative, whereas $\det [\mathcal{A}](E_3) > 0$ if and only if $\xi_1 > 0$ and (by assumption) $\xi_2 > 0$.

Proof. Evaluating (3.4.32), and (3.4.36)-(3.4.41b) at E_3 we have

$$\text{Tr}[\mathcal{A}](E_3) = 2r - 2a \left(\frac{\hat{S}_1^3 + \hat{S}_2^3}{\theta} \right) - a \left(\frac{\hat{S}_2^3}{\theta_{12}} + \frac{\hat{S}_1^3}{\theta_{21}} \right). \quad (3.4.47)$$

Substituting (3.4.42) in the above we get

$$\text{Tr}[\mathcal{A}](E_3) = r\hat{S}_1^3 \left(\frac{2}{\hat{S}_1^3} - \left(\frac{2}{K} + \frac{1}{K_{21}} \right) - \frac{\xi_1}{\xi_2} \left(\frac{2}{K} + \frac{1}{K_{12}} \right) \right), \quad (3.4.48)$$

which can be simplified as

$$\begin{aligned} \text{Tr}[\mathcal{A}](E_3) = r\hat{S}_1^3 & \left(\frac{2K_{21}(\xi_2 K_{12} + \xi_1 K) - \xi_2 K_{12}(2K_{21} + K)}{\xi_2 K K_{12} K_{21}} \right) \\ & - \left(\frac{\xi_1 K_{21}(2K_{12} + K)}{\xi_2 K K_{12} K_{21}} \right). \end{aligned} \quad (3.4.49)$$

This can be rewritten in the form

$$\text{Tr}[\mathcal{A}](E_3) = \frac{r\hat{S}_1^3}{\xi_2 K} \left\{ \xi_1 \left(\frac{K}{K_{12}} - 2 \right) - \xi_2 \frac{K}{K_{21}} \right\}. \quad (3.4.50)$$

Using the definitions of ξ_1 , and ξ_2 , from (3.4.43), we obtain

$$\text{Tr}[\mathcal{A}](E_3) = -\frac{r\hat{S}_1^3}{K\xi_2}(\xi_1 + \xi_2). \quad (3.4.51)$$

Next, consider the determinant of $\mathcal{A}$ evaluated at the equilibrium E_3 ,

$$\det[\mathcal{A}](E_3) = AB - A_{12}B_{21} - b(A + B) + b^2 \quad (3.4.52)$$

$$= (AB - A_{12}B_{21} - b^2) - b(A + B - 2b) \quad (3.4.53)$$

$$= \Theta - b(\text{Tr}[\mathcal{A}](E_3)), \quad (3.4.54)$$

where the terms A, A_{12}, B, B_{21} defined in (3.4.36)-(3.4.39), are all evaluated at E_3 . The term Θ can be simplified as

$$\Theta = AB - A_{12}B_{21} - b^2 \quad (3.4.55)$$

$$\begin{aligned} &= (a^2 - b^2) - a^2 \left[\frac{2(\hat{S}_1^3 + \hat{S}_2^3)}{\theta} + \frac{\hat{S}_1^3}{\theta_{21}} + \frac{\hat{S}_2^3}{\theta_{12}} \right] \\ &\quad + a^2 \left[\frac{2(\hat{S}_1^3)^2}{\theta\theta_{21}} + \frac{2(\hat{S}_2^3)^2}{\theta\theta_{12}} + \frac{4\hat{S}_1^3\hat{S}_2^3}{\theta^2} \right]. \end{aligned} \quad (3.4.56)$$

Since $\hat{S}_2^3 = (\xi_1/\xi_2)\hat{S}_1^3$, we have

$$\Theta = a(\text{Tr}[\mathcal{A}](E_3)) - r^2 + 2a^2(\hat{S}_1^3)^2 \left[\frac{1}{\theta\theta_{21}} + \left(\frac{\xi_1}{\xi_2} \right)^2 \frac{1}{\theta\theta_{12}} + 2\frac{\xi_1}{\xi_2} \frac{1}{\theta} \right]. \quad (3.4.57)$$

Substituting (3.4.57) in (3.4.54), using the definitions of ξ_1 , ξ_2 , from (3.4.43), and (??), respectively, and simplifying we have

$$\det[\mathcal{A}](E_3) = r^2(\hat{S}_1^3)^2 \left(\frac{\xi_1^2}{\xi_2 K_{12}} + \frac{\xi_1}{K} \right) \quad (3.4.58)$$

$$= r^2(\hat{S}_1^3)^2 \xi_1 \left(\frac{\xi_1 K + \xi_2 K_{12}}{K K_{12} \xi_2} \right) \quad (3.4.59)$$

$$= r^2 \hat{S}_1^3 \xi_1, \quad (3.4.60)$$

by using (3.4.42). ■

Since the Jacobian $\mathcal{J}(E_3)$ is block upper triangular, its eigenvalues are the same as those of matrices $\mathcal{A}(E_3)$ and $\mathcal{D}(E_3)$. The matrix $\mathcal{A}(E_3)$ is the Jacobian of the two species model with pure competition, (3.2.7) evaluated at (N_1^C, N_2^C) (see Section 3.2.3) under the assumptions (A2) and (A3). From Lemma 3.4.5.1, the eigenvalues of $\mathcal{A}(E_3)$ are negative if and only if the conditions

$$(C4) \quad \xi_1 > 0, \text{ and}$$

$$(C5) \quad \xi_2 > 0,$$

hold. The matrix $\mathcal{D}(E_3)$ on the other hand is related to the disease parameters and its eigenvalues are $\lambda_1^3 = -b$ and $\lambda_2^3 = \beta(\hat{S}_1^3 + \hat{S}_2^3) - b$. The eigenvalue λ_1^3 is always negative and λ_2^3 is negative under the condition

$$(C6) \quad \mathcal{R}_0^C = \frac{\beta(\hat{S}_1^3 + \hat{S}_2^3)}{b} < 1.$$

So, the DFE E_3 is feasible and stable if and only if the conditions (C4), (C5) and (C6) hold.

We note that this result is a special case of Theorem 3.4.1.2 derived from the stability results of the pure competition model [21]. The condition (C6) is the analogue of the inequality (3.4.5) for this special case.

3.4.6 The Infected One-Host Equilibrium

There are two infected one-host equilibria. These are $E_4 = (\hat{S}_1^4, 0, \hat{I}_1^4, 0)$ and $E_5 = (0, \hat{S}_2^5, 0, \hat{I}_2^5)$, where for $i = 1, 2$

$$\hat{S}_1^4 = \hat{S}_2^5 = \frac{b}{\beta}, \tag{3.4.61}$$

$$\hat{I}_1^4 = \frac{r\theta}{a} - \frac{b}{\beta} = (\mathcal{R}_0 - 1)\hat{S}_1^4, \tag{3.4.62}$$

$$\hat{I}_2^5 = \frac{r\theta}{a} - \frac{b}{\beta} = (\mathcal{R}_0 - 1)\hat{S}_1^5. \tag{3.4.63}$$

and $\mathcal{R}_0 = \mathcal{R}_0^1 = \mathcal{R}_0^2 = \frac{K\beta}{b}$ is the same for both species. The Jacobian (3.4.31) evaluated at E_4 ,

$$\mathcal{J}(E_4) = \begin{bmatrix} a\left(1 - \frac{2K}{\theta}\right) - \beta K & \frac{-aK}{\theta_{12}} & a\left(1 - \frac{2K}{\theta}\right) - b & \frac{-aK}{\theta_{12}} - b \\ 0 & a\left(1 - \frac{K}{\theta_{21}}\right) - \beta K & 0 & a\left(1 - \frac{K}{\theta_{21}}\right) \\ \beta K - b & 0 & 0 & b \\ 0 & \beta K - b & 0 & -b \end{bmatrix}.$$

has eigenvalues $\lambda_1^4 = -K\beta$, $\lambda_2^4 = b(1 - \mathcal{R}_0)$, $\lambda_3^4 = -r$, and $\lambda_4^4 = rK\xi_1$. We can see that λ_1 and λ_3 are always negative. Thus, the stability (and feasibility) conditions for E_4 are

$$(C7) \quad \mathcal{R}_0 = \frac{K\beta}{b} > 1,$$

which guarantees that $\lambda_2^4 < 0$ and condition (C2) which guarantees that $\lambda_4^4 < 0$. For the symmetric case, E_5 is feasible and stable if conditions (C7) and (C3) hold.

3.4.7 The Infected Coexistence Equilibrium

Lastly, we consider the infected coexistence equilibrium E_6 . We can prove algebraically or by using a software like MAPLE that $E_6 = (\hat{S}_1^6, \hat{S}_2^6, \hat{I}_1^6, \hat{I}_2^6)$, with

$$\hat{S}_1^6 = \frac{b}{\beta\left(1 + \frac{\xi_1}{\xi_2}\right)}, \quad (3.4.64)$$

$$\hat{S}_2^6 = \frac{\xi_1}{\xi_2} \hat{S}_1^6, \quad (3.4.65)$$

$$\hat{I}_1^6 = \frac{\beta\left(1 + \frac{\xi_1}{\xi_2}\right) - b\left(\frac{1}{K} + \frac{\xi_1}{K_{12}\xi_2}\right)}{\beta\left(1 + \frac{\xi_1}{\xi_2}\right)\left(\frac{1}{K} + \frac{\xi_1}{K_{12}\xi_2}\right)}, \quad (3.4.66)$$

$$\hat{I}_2^6 = \frac{\xi_1}{\xi_2} \hat{I}_1^6. \quad (3.4.67)$$

Before we look at local stability for E_6 we prove two results.

Lemma 3.4.7.1 *The equilibrium value $\hat{I}_i^6$ can be rewritten as*

$$\hat{I}_i^6 = (\mathcal{R}_0^C - 1)\hat{S}_i^6, \quad (3.4.68)$$

for $i = 1, 2$, with

$$\mathcal{R}_0^C = \frac{\beta}{b} (\hat{S}_1^3 + \hat{S}_2^3). \quad (3.4.69)$$

Proof. From equations (3.4.64), (3.4.66) and (3.4.42), we have

$$\hat{I}_1^6 = \hat{S}_1^6 \left\{ \frac{\beta}{b} \left(1 + \frac{\xi_1}{\xi_2} \right) \hat{S}_1^3 - 1 \right\} \quad (3.4.70)$$

$$= \hat{S}_1^6 \left\{ \frac{\beta}{b} (\hat{S}_1^3 + \hat{S}_2^3) - 1 \right\} \quad (3.4.71)$$

$$= \hat{S}_1^6 (\mathcal{R}_0^C - 1). \quad (3.4.72)$$

Similarly, we can show that $\hat{I}_2^6 = (\mathcal{R}_0^C - 1)\hat{S}_2^6$. ■

Lemma 3.4.7.2 *The total population size $\hat{N}_i^6 = \hat{S}_i^3$, for $i = 1, 2$.*

Proof. From Lemma 3.4.7.1 and equations (3.4.69), (3.4.64), and (3.4.42), we have

$$\hat{N}_1^6 = \hat{S}_1^6 + \hat{I}_1^6 = \hat{S}_1^6 \mathcal{R}_0^C \quad (3.4.73)$$

$$= \frac{b}{\beta(1 + \frac{\xi_1}{\xi_2})} \frac{\beta}{b} \hat{S}_1^3 \left(1 + \frac{\xi_1}{\xi_2} \right) = \hat{S}_1^3 \quad (3.4.74)$$

Similarly, we can show that $\hat{N}_2^6 = \hat{S}_2^3$. ■

The characteristic polynomial of $\mathcal{J}(E_6)$ is given as

$$P_6(x) = (x + \eta)(x + \epsilon)(x^2 + \delta_1 x + \delta_2), \quad (3.4.75)$$

where

$$\eta = b + \beta(\hat{I}_1^6 + \hat{I}_2^6), \quad (3.4.76)$$

$$\epsilon = b + \beta(\hat{I}_1^6 + \hat{I}_2^6) - \beta(\hat{S}_1^6 + \hat{S}_2^6), \quad (3.4.77)$$

$$\delta_1 = -(A(E_6) + B(E_6)) + 2b, \quad (3.4.78)$$

$$\delta_2 = -A_{12}(E_6)B_{21}(E_6) + A(E_6)B(E_6) - b(A(E_6) + B(E_6)) + b^2, \quad (3.4.79)$$

where for $i = 1, 2$, $\hat{N}_i^6 = \hat{S}_i^6 + \hat{I}_i^6$. The terms A, B, A_{12} and B_{21} as defined in (3.4.36)-(3.4.39) are all evaluated at the infected coexistence equilibria E_6 . Then, the eigenvalues of the Jacobian $\mathcal{J}(E_6)$ are

$$\lambda_1^6 = -\eta = -b - \beta(\hat{I}_1^6 + \hat{I}_2^6), \quad (3.4.80)$$

$$\lambda_2^6 = -\epsilon = -b - \beta(\hat{I}_1^6 + \hat{I}_2^6) + \beta(\hat{S}_1^6 + \hat{S}_2^6), \quad (3.4.81)$$

$$\lambda_{3,4}^6 = \frac{1}{2} \left(-\delta_1 \pm \sqrt{\delta_1^2 - 4\delta_2} \right). \quad (3.4.82)$$

Lemma 3.4.7.3 *The condition that $\lambda_2^6 < 0$ is equivalent to $\mathcal{R}_0^C > 1$*

Proof. From (3.4.65), (3.4.67) and Lemma 3.4.7.1 we have

$$\begin{aligned} \lambda_2^6 < 0 \\ \iff -b - \beta(\hat{I}_1^6 + \hat{I}_2^6) + \beta(\hat{S}_1^6 + \hat{S}_2^6) < 0 \\ \iff \hat{S}_1^6 - \hat{I}_1^6 + \hat{S}_2^6 - \hat{I}_2^6 < \frac{b}{\beta} \\ \iff \left(1 + \frac{\xi_1}{\xi_2}\right)(\hat{S}_1^6 - \hat{I}_1^6) < \frac{b}{\beta} \\ \iff (2 - \mathcal{R}_0^C)\left(1 + \frac{\xi_1}{\xi_2}\right) \frac{b}{\beta(1 + \frac{\xi_1}{\xi_2})} < \frac{b}{\beta} \\ \iff \mathcal{R}_0^C > 1. \end{aligned}$$

Thus, $\mathcal{R}_0^C > 1$ is both a feasibility and stability condition for the infected coexistence equilibrium E_6 . ■

Lemma 3.4.7.4 *The eigenvalues λ_3^6 and λ_4^6 are roots of the polynomial equation*

$$x^2 - \text{Tr}[\mathcal{A}](E_3)x + \det[\mathcal{A}](E_3) = 0. \quad (3.4.83)$$

Proof. From Lemma 3.4.7.2, we have $\hat{N}_i^6 = \hat{S}_i^3 = \hat{N}_i^3$ (as $\hat{I}_i^3 = 0$ for E_3), for $i = 1, 2$. Thus, from (3.4.78) and (3.4.79) and the definitions of the functions A, B, A_{12} , and B_{21}

in (3.4.36)-(3.4.39), we have

$$\delta_1 = -(A(E_3) + B(E_3)) + 2b, \quad (3.4.84)$$

$$\delta_2 = -A_{12}(E_3)B_{21}(E_3) + A(E_3)B(E_3) - b(A(E_3) + B(E_3)) + b^2. \quad (3.4.85)$$

From the definition of the matrix $\mathcal{A}$ in (3.4.32), we observe that

$$\delta_1 = -\text{Tr}[\mathcal{A}](E_3) \quad (3.4.86)$$

$$\delta_2 = \det[\mathcal{A}](E_3) \quad (3.4.87)$$

From equation (3.4.82), it is clear that the eigenvalues λ_3^6 and λ_4^6 are roots of the polynomial equation (3.4.83). ■

Theorem 3.4.7.1 *Assume that $\xi_1/\xi_2 > 0$ so that the infected coexistence equilibrium E_6 is feasible. Then E_6 is stable if and only if $\xi_1 > 0, \xi_2 > 0$, and $\mathcal{R}_0^C > 1$. In this case all the other equilibria, i.e., E_0, E_1, E_2, E_3, E_4 and E_5 are either infeasible and/or unstable.*

Proof. It is easy to see that λ_1^6 given in (3.4.80) is negative for all $I_{1,e} + I_{2,e} \geq 0$. Thus, since the infected coexistence equilibrium E_6 is feasible by assumption ($\xi_1/\xi_2 > 0$) we have $\lambda_1^6 < 0$. As a result of Lemma 3.4.7.3, the first condition for stability of E_6 is

$$(C8) \quad \mathcal{R}_0^C > 1$$

Since $\hat{I}_1^6 = (\mathcal{R}_0^C - 1)\hat{S}_1^6$, the condition (C8) is also a feasibility condition for E_6 . From Lemma 3.4.5.1, Lemma 3.4.7.4, and the Trace-Determinant theorem [6], we see that the eigenvalues λ_3^6 and λ_4^6 are negative if and only if the conditions (C4) and (C5) are satisfied.

When conditions (C4), (C5) and (C8) are satisfied, all the other equilibria, i.e., E_0 - E_5 are either infeasible or unstable based on the linear stability analysis presented above for each of these equilibria. ■

3.4.8 Bifurcations

Considering the parameters ξ_1 , and ξ_2 , defined in (3.4.43), as bifurcation parameters we can make the following observations. If $\xi_1 = 0$ and/or $\xi_2 = 0$ then $\mathcal{R}_0^C = \frac{K\beta}{b} = \mathcal{R}_0$. If $\xi_1 = 0$ and $\xi_2 > 0$ then $E_3 = E_1$ and $E_6 = E_4$. Similarly, if $\xi_1 > 0$ and $\xi_2 = 0$ then $E_3 = E_2$ and $E_6 = E_5$. If both $\xi_1 = 0$ and $\xi_2 = 0$ then the sum of the state variables

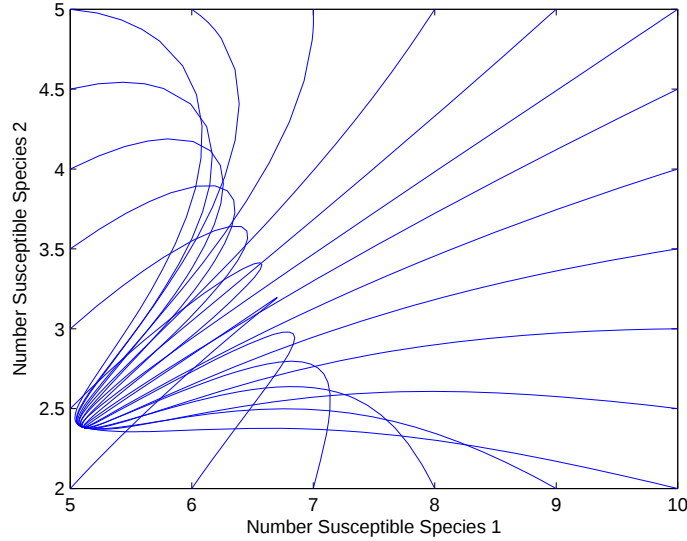


FIGURE 3.1: Phase planes for susceptible compartment when $\xi_1 > 0$ and $\xi_2 > 0$.

behaves as one species with logistic growth. In this case, the equilibrium E_3 is any solution $(\hat{S}_1, \hat{S}_2, 0, 0)$ on the line $\hat{S}_1 + \hat{S}_2 = K$. Similarly, E_6 becomes any solution $(\hat{S}_1, \hat{S}_2, \hat{I}_1, \hat{I}_2)$ on the plane $\hat{S}_1 + \hat{S}_2 = \frac{b}{\beta}$, $\hat{I}_1 + \hat{I}_2 = \frac{b}{\beta}(\mathcal{R}_0 - 1)$. Notice that in both cases, since there is no additional death due to disease, $\hat{N}_1 + \hat{N}_2 = K$. Based on these observations, we have the following results:

Corollary 3.4.8.1 *Assume $\xi_1 = 0$ and $\xi_2 > 0$. Then,*

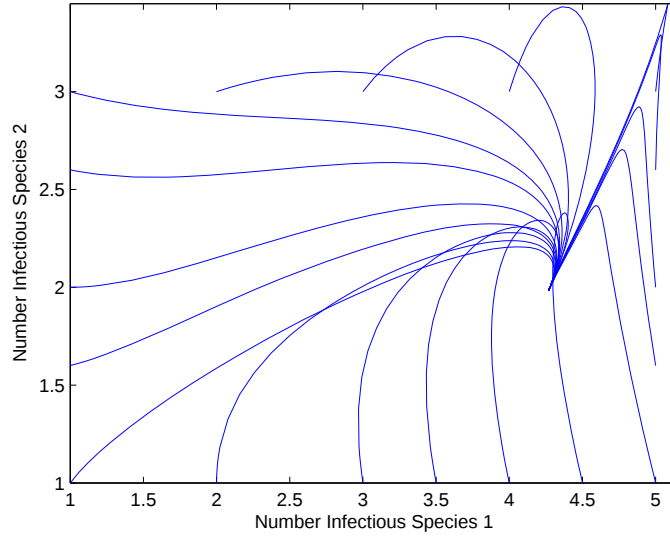


FIGURE 3.2: Phase planes for infected compartment when $\xi_1 > 0$ and $\xi_2 > 0$.

1. If $\mathcal{R}_0^C = \mathcal{R}_0 < 1$, the equilibrium $E_3 = E_1$ exists in a neutral state.
2. If $\mathcal{R}_0^C = \mathcal{R}_0 > 1$, the equilibrium $E_6 = E_4$ exists in a neutral state.

Proof. In the first case, the eigenvalues for E_3 are $\lambda_1^3 = -r$, $\lambda_{2,3}^3 = 0$, and $\lambda_4^3 = \beta K - b = b(\mathcal{R}_0 - 1)$. We can see that if $\mathcal{R}_0^C = \mathcal{R}_0 < 1$ then $\lambda_4^3 < 0$ and E_3 is neutral. In fact, E_3 exchanges stability with E_1 as it moves through the half plane $\xi_1 = 0$, $\xi_2 > 0$ when $\mathcal{R}_0 < 1$.

In the second case, the eigenvalues for E_6 are $\lambda_1^6 = -r$, $\lambda_2^6 = 0$, $\lambda_3^6 = -K\beta$, and $\lambda_4^6 = b(1 - \mathcal{R}_0)$. We can see that if $\mathcal{R}_0^C = \mathcal{R}_0 > 1$ then $\lambda_3^6 < 0$, hence E_6 is neutral. In fact, E_6 exchanges stability with E_4 as it moves through the half plane $\xi_1 = 0$, $\xi_2 > 0$ when $\mathcal{R}_0 > 1$. See Figures 3.1 - 3.6. ■

Corollary 3.4.8.2 Assume $\xi_1 > 0$ and $\xi_2 = 0$. Then,

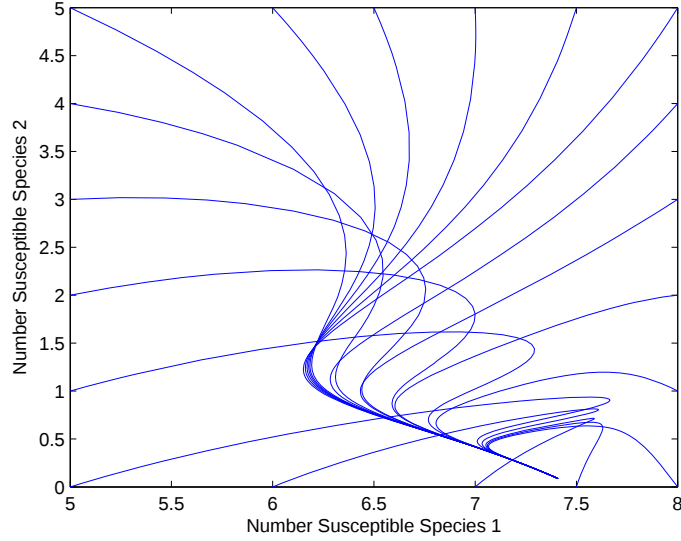


FIGURE 3.3: Phase planes for susceptible compartment when $\xi_1 = 0$ and $\xi_2 > 0$.

1. If $\mathcal{R}_0^C = \mathcal{R}_0 < 1$, the equilibrium $E_3 = E_2$ exists in a neutral state.
2. If $\mathcal{R}_0^C = \mathcal{R}_0 > 1$, the equilibrium $E_6 = E_5$ exists in a neutral state.

Proof. The proof omitted as it is similar to the proof of Corollary 1. ■

Corollary 3.4.8.3 Assume $\xi_1 = 0$ and $\xi_2 = 0$. Then,

1. If $\mathcal{R}_0^C = \mathcal{R}_0 < 1$, the equilibrium E_3 exists in a neutral state.
2. If $\mathcal{R}_0^C = \mathcal{R}_0 > 1$, the equilibrium E_6 exists in a neutral state.

Proof. In the first case the eigenvalues of E_3 are $\lambda_1^3 = -r$, $\lambda_2^3 = 0$, $\lambda_3^3 = -b$, and $\lambda_4^3 = b(\mathcal{R}_0 - 1)$. We can see if $\mathcal{R}_0^C = \mathcal{R}_0 < 1$ then E_3 is neutral. In fact, as E_3 moves along the line $\xi_1 = \xi_2$ from $\xi_1, \xi_2 > 0$ through $\xi_1, \xi_2 = 0$ into $\xi_1, \xi_2 < 0$, it progresses from stable to neutral to stable.

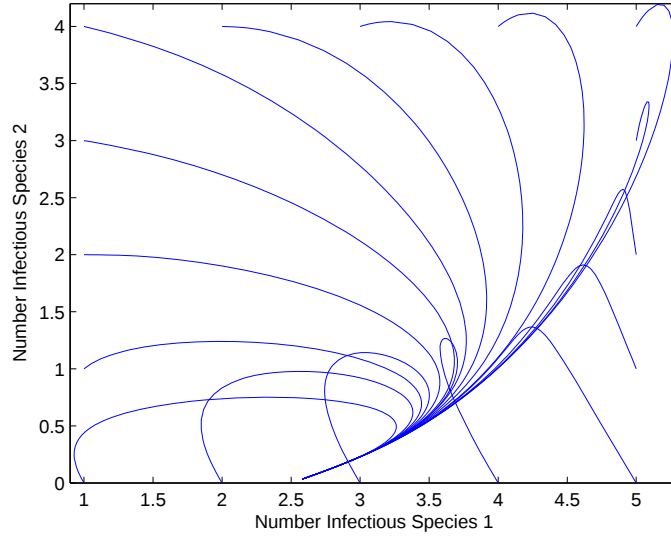


FIGURE 3.4: Phase planes for infected compartment when $\xi_1 = 0$ and $\xi_2 > 0$.

In the second case the eigenvalues of E_6 are $\lambda_1^6 = -r$, $\lambda_2^6 = 0$, $\lambda_3^6 = -\beta K$, and $\lambda_4^6 = b(1 - \mathcal{R}_0)$. We can see if $\mathcal{R}_0^C = \mathcal{R}_0 > 1$ then E_6 is neutral. Similarly to E_3 , as E_6 moves along the line $\xi_1 = \xi_2$ through $\xi_1, \xi_2 = 0$ it also progresses from stable to neutral to stable. ■

3.4.9 Hopf Bifurcations

Another simplified case, similar to the one in Section 3.4.4, except that $\beta_{11} = \beta_{22} = \beta$, $\beta_{12} = \beta_{21} = \beta_2$, and $\alpha_1 = \alpha_2 = \alpha$, for which we did not compute the interior equilibria, displays interesting behavior. We present here a bifurcation diagram for the interior equilibria of this special case using MatCont software [47]. We find complicated behavior, including two Hopf bifurcations (H), two saddle-node bifurcations (LP), and a branching point bifurcation (BP) point for the simplified model with inter-species transmission different from intra-species transmission and the addition of death due to disease. See

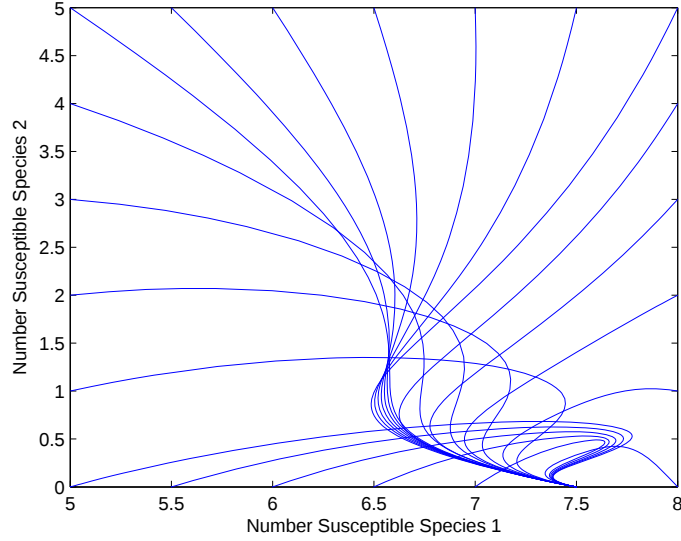


FIGURE 3.5: Phase planes for susceptible compartment when $\xi_1 < 0$ and $\xi_2 > 0$.

Figures 3.7-3.10 for the bifurcation diagrams. This shows that even a relatively simple version of the full model displays complicated behavior. In fact, when $.98 < \theta_{12} < 1.01$ there are three internal equilibria for the model.

3.5 Computation of Equilibria and Linear Stability Analysis for Frequency Incidence

Below we present the equilibria for model (3.3.10a)-(3.3.10d), and their linear stability analysis. We will denote equilibrial susceptible densities for species i by $\hat{S}_i$ and similarly $\hat{I}_i$ for the infected equilibrial densities of species i , for $i = 1, 2$. An equilibrium E_e is represented using the notation $E_e = (\hat{S}_1^e, \hat{S}_2^e, \hat{I}_1^e, \hat{I}_2^e)$.

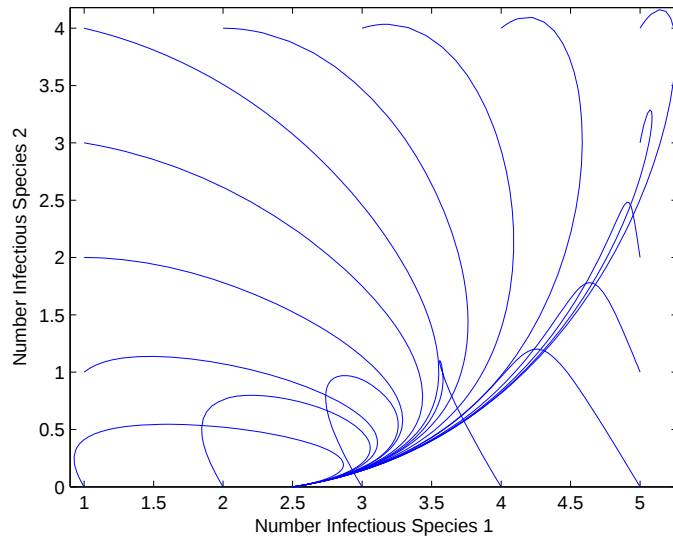


FIGURE 3.6: Phase planes for infected compartment when $\xi_1 < 0$ and $\xi_2 > 0$.

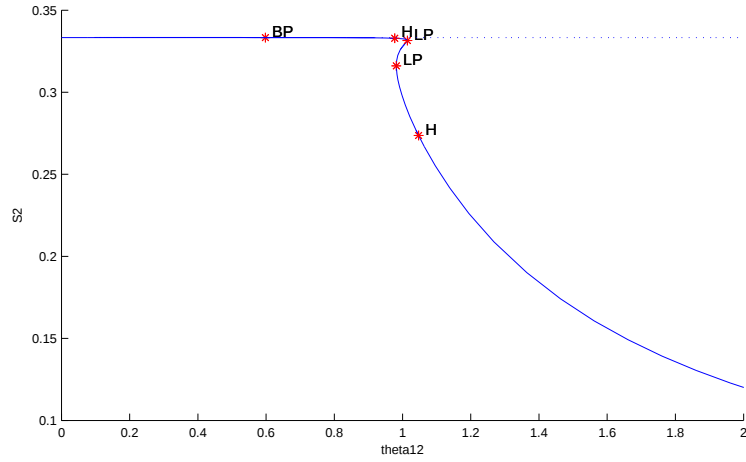


FIGURE 3.7: Bifurcation diagram for S_2 with bifurcation parameter θ_{12} and with parameters $a = 2$, $b = 1$, $\theta = 0.25$, $\theta_{21} = 1$, $\alpha = 1$, $\beta = 6$, and $\beta_2 = 0.1$.

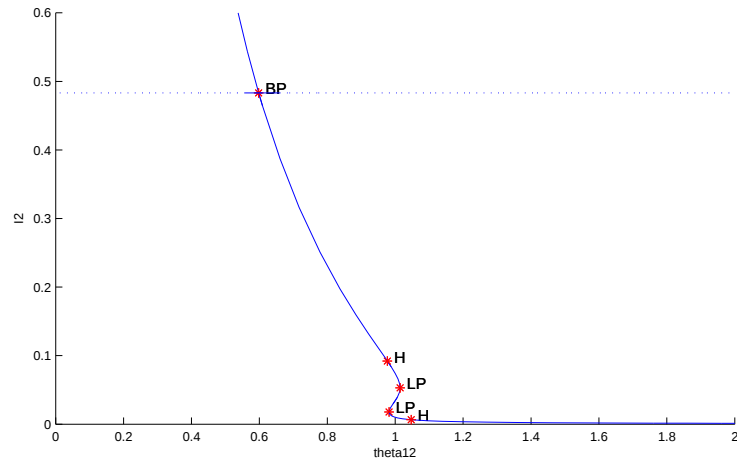


FIGURE 3.8: Bifurcation diagram for I_2 with bifurcation parameter θ_{12} and with parameters $a = 2$, $b = 1$, $\theta = 0.25$, $\theta_{21} = 1$, $\alpha = 1$, $\beta = 6$, and $\beta_2 = 0.1$.

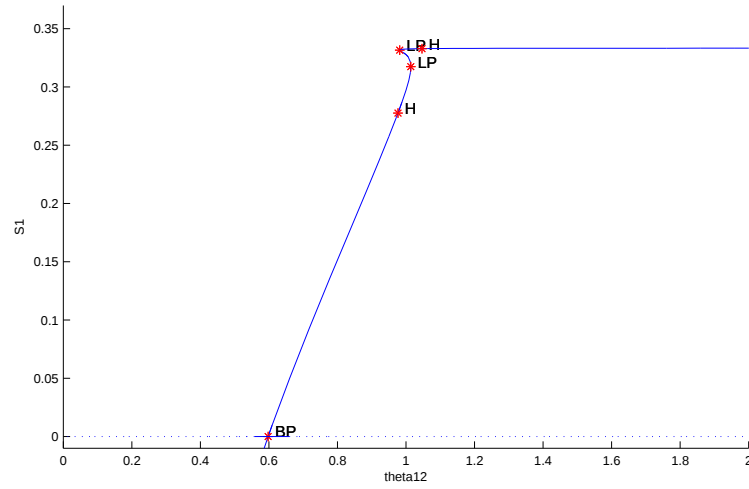


FIGURE 3.9: Bifurcation diagram for S_1 with bifurcation parameter θ_{12} and with parameters $a = 2$, $b = 1$, $\theta = 0.25$, $\theta_{21} = 1$, $\alpha = 1$, $\beta = 6$, and $\beta_2 = 0.1$.

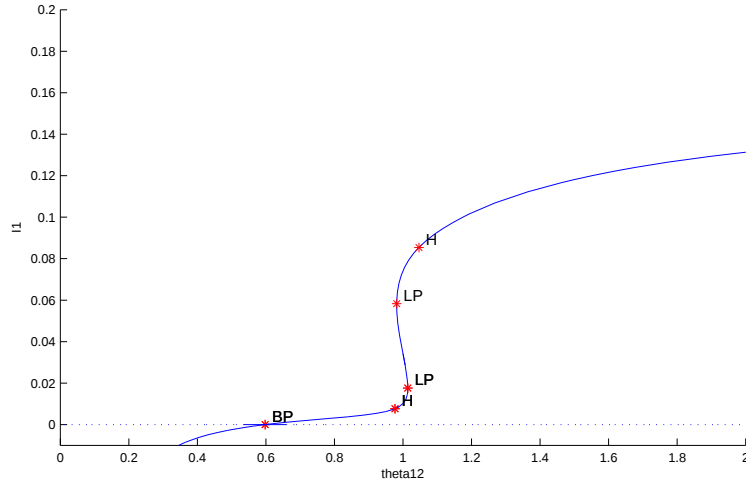


FIGURE 3.10: Bifurcation diagram for I_1 with bifurcation parameter θ_{12} and with parameters $a = 2$, $b = 1$, $\theta = 0.25$, $\theta_{21} = 1$, $\alpha = 1$, $\beta = 6$, and $\beta_2 = 0.1$.

3.5.1 Disease Free Coexistence Equilibrium

The disease free equilibrium (DFE) is $E_3 = (\hat{S}_1^3, \hat{S}_2^3, \hat{I}_1^3 = 0, \hat{I}_2^3 = 0)$, defined as in equation 3.4.2. The expressions for the susceptible components emphasize the dependence of the DFE on the parameters ξ_1 and ξ_2 .

Theorem 3.5.1.1 *The basic reproduction number (BRN) for model (3.3.1a)-(3.3.1b) with coexisting species and frequency incidence is*

$$\mathcal{R}_0^C = \frac{\mathcal{R}_{11} + \mathcal{R}_{22}}{2} + \frac{\sqrt{(\mathcal{R}_{11} - \mathcal{R}_{22})^2 + 4\mathcal{R}_{12}\mathcal{R}_{21}}}{2}, \quad (3.5.1)$$

where, for $i, j = 1, 2$

$$\mathcal{R}_{ij} = \frac{\beta_{ij}\hat{S}_i^1}{\Gamma_j\hat{S}_j^1}; \quad (3.5.2)$$

The basic reproduction number for species j in isolation is $\mathcal{R}_0^j = \mathcal{R}_{jj}$, for $j = 1, 2$. The coexistence DFE, E_1 , is feasible and stable if and only if the conditions $\xi_1 > 0$, $\xi_2 > 0$ and $\mathcal{R}_0^C < 1$ are satisfied.

Proof. A very similar analysis to that in Theorem 3.4.1.1 will result in the value of $\mathcal{R}_0^C$ for the frequency incidence case. The Jacobians of $\mathcal{F}$ and $\mathcal{V}$, called F and V , respectively, for frequency incidence are evaluated at the coexistence DFE, $E_3 = (\hat{S}_1^3, \hat{S}_2^3, 0, 0)$. We then have

$$F(E_3) = \begin{bmatrix} \beta_{11} & \beta_{12} \frac{\hat{S}_1^3}{\hat{S}_2^3} \\ \beta_{21} \frac{\hat{S}_2^3}{\hat{S}_1^3} & \beta_{22} \end{bmatrix}, V(E_3) = \text{diag}(\Gamma_i) \quad (3.5.3)$$

The BRN $\mathcal{R}_0^C$ for model (3.3.10a)-(3.3.10d) with coexisting species is given as

$$\mathcal{R}_0^C = \rho(FV^{-1}), \quad (3.5.4)$$

where $\rho(A)$ is the spectral radius of the matrix A . ■

Theorem 3.5.1.2 *The coexistence DFE, E_3 , is feasible and stable if and only if the conditions $\xi_1 > 0$, $\xi_2 > 0$ and $\mathcal{R}_0^C < 1$ are satisfied with $\mathcal{R}_0^C$ as defined in Theorem 3.4.1.1.*

Proof. The Jacobian of the system (3.3.10a)-(3.3.10d) evaluated at the DFE $E_3 = (\hat{S}_1^3, \hat{S}_2^3, \hat{I}_1^3 = 0, \hat{I}_2^3 = 0)$ is the block triangular matrix

$$\mathcal{J}(E_3) = \begin{bmatrix} \mathcal{A}(E_3) & * \\ \mathbf{0} & F(E_3) - V(E_3) \end{bmatrix}, \quad (3.5.5)$$

where the matrix $\mathcal{A}(E_3)$ is the Jacobian matrix of the system (3.2.7) evaluated at $E_3^C = (N_1^C, N_2^C) = (\hat{S}_1^3, \hat{S}_2^3)$ (see section 3.2.3), and the matrices F and V are as defined in (3.5.3) (the $*$ indicates a nonzero entry). Since the Jacobian $\mathcal{J}(E_3)$ is block triangular, its eigenvalues are the eigenvalues of the matrices $\mathcal{A}(E_3)$ and $F(E_3) - V(E_3)$.

From Section 3.2.3, $E_3^C = (N_1^C, N_2^C)$ is globally asymptotically stable if and only if $\xi_1 > 0$ and $\xi_2 > 0$. Thus, the eigenvalues of the matrix $\mathcal{A}$ are negative if and only if $\xi_1 > 0$ and $\xi_2 > 0$, which are also feasibility conditions for E_3 . From the next generation approach, the eigenvalues of the matrix $F(E_3) - V(E_3)$ are negative if and only if $\mathcal{R}_0^C = \rho(FV^{-1}) < 1$ [144]. ■

3.5.2 The Disease Free One-Host Equilibria

When $\xi_1/\xi_2 < 0$ the coexistence DFE is infeasible. We have the following two cases.

1. Assume $\xi_1 < 0$ and $\xi_2 > 0$. In this case the disease free one-host equilibrium $E_2 = (\hat{S}_1^2 = K_{11}, \hat{S}_2^2 = 0, \hat{I}_1^2 = 0, \hat{I}_2^2 = 0)$ is feasible and stable if in addition the condition

$$\mathcal{R}_0^1 = \frac{\beta_{11}}{\Gamma_1} < 1 \quad (3.5.6)$$

is satisfied, where $\mathcal{R}_0^1$ is the basic reproduction number for species 1 alone. This result follows from conditions on stability of E_1^C (see Section 3.2.3) and conditions on stability of E_1^F (see Section 3.2.1).

2. Assume $\xi_1 > 0$ and $\xi_2 < 0$. In this case the one-host DFE $E_2 = (\hat{S}_1^2 = 0, \hat{S}_2^2 = K_{22}, \hat{I}_1^2 = 0, \hat{I}_2^2 = 0)$ is feasible and stable if in addition the condition $\mathcal{R}_0^2 = \frac{\beta_{22}}{\Gamma_2} < 1$ is satisfied, where $\mathcal{R}_0^2$ is the basic reproduction number for species 2 alone. As in case 1, this result follows from conditions on stability of E_2^C and E_2^F .

3.5.3 Infected One-Host Equilibria

There are two *infected one-host equilibria* in which one of the species survives while the other species dies out. See the note in Section 3.3.2 about using Lipschitz continuity to extend the transmission functions to incorporate the extinction of one or more species. The first infected one-host equilibrium is

$$E_4 = (\hat{S}_1^4 = \frac{K_{11}}{\mathcal{R}_0^1} \left(1 - \frac{\alpha_1(\mathcal{R}_0^1 - 1)}{r_1 \mathcal{R}_0^1}\right), \hat{S}_2^4 = 0, \hat{I}_1^4 = (\mathcal{R}_0^1 - 1)\hat{S}_1^4, \hat{I}_2^4 = 0), \quad (3.5.7)$$

We can similarly define

$$E_5 = (\hat{S}_1^5 = 0, \hat{S}_2^5 = \frac{K_{22}}{\mathcal{R}_0^2} \left(1 - \frac{\alpha_2(\mathcal{R}_0^2 - 1)}{r_2 \mathcal{R}_0^2}\right), \hat{I}_1^5 = 0, \hat{I}_2^5 = (\mathcal{R}_0^2 - 1)\hat{S}_2^5), \quad (3.5.8)$$

Theorem 3.5.3.1 *Assume $\alpha_1 > 0$, then $\hat{N}_1^4 = K_{11} \left(1 - \frac{\alpha_1(\mathcal{R}_0^1 - 1)}{r_1 \mathcal{R}_0^1}\right) < K_{11}$. If $\alpha_1 = 0$ then $\hat{N}_1^4 = K_{11}$. If $\mathcal{R}_0^1 > 1$ and $K_{21} < \hat{N}_1^4$, then the infected one-host equilibrium for species 1, E_4 , is feasible and stable.*

Proof. The condition $\mathcal{R}_0^1 > 1$ guarantees the feasibility of the equilibrium E_4 . In addition, it can be seen by inspection that if $\alpha_1 = 0$ then $\hat{N}_1^4 = K_{11}$ and that if $\alpha_1 > 0$ then $\hat{N}_1^4 < K_{11}$.

The Jacobian for the (species 1) infected one-host equilibrium E_4 , with the order changed to $E_4 = (\hat{S}_1^4, \hat{I}_1^4, \hat{S}_2^4, \hat{I}_2^4)$ for convenience, is

$$\mathcal{J}(E_4) = \begin{bmatrix} P & * \\ 0 & Q \end{bmatrix}, \quad (3.5.9)$$

where * indicates a non-zero entry and

$$P = \begin{bmatrix} a_1 \left(1 - \frac{2\hat{N}_1^4}{\theta_{11}}\right) - b_1 - \beta_{11} \frac{\hat{I}_1^4}{\hat{N}_1^4} + \frac{\beta_{11} \hat{S}_1^4 \hat{I}_1^4}{(\hat{N}_1^4)^2} & a_1 \left(1 - \frac{2\hat{N}_1^4}{\theta_{11}}\right) - \beta_{11} \frac{\hat{S}_1^4}{\hat{N}_1^4} + \frac{\beta_{11} \hat{S}_1^4 \hat{I}_1^4}{(\hat{N}_1^4)^2} \\ \beta_{11} \frac{\hat{I}_1^4}{\hat{N}_1^4} - \frac{\beta_{11} \hat{S}_1^4 \hat{I}_1^4}{(\hat{N}_1^4)^2} & \beta_{11} \frac{\hat{S}_1^4}{\hat{N}_1^4} - \Gamma_1 - \frac{\beta_{11} \hat{S}_1^4 \hat{I}_1^4}{(\hat{N}_1^4)^2} \end{bmatrix},$$

$$Q = \begin{bmatrix} a_2 \left(1 - \frac{\hat{N}_1^4}{\theta_{21}}\right) - b_2 - \beta_{21} \frac{\hat{I}_1^4}{\hat{N}_1^4} & a_2 \left(1 - \frac{\hat{N}_1^4}{\theta_{21}}\right) \\ \beta_{21} \frac{\hat{I}_1^4}{\hat{N}_1^4} & -\Gamma_2 \end{bmatrix}.$$

Since $\mathcal{J}(E_4)$ is block triangular we need only consider the eigenvalues of P and Q . We notice that the upper left block matrix, P , is the same as the Jacobian for species 1 alone with the disease, i.e., the Jacobian of the system (3.2.4)-(3.2.5) evaluated at the equilibrium E_2^F (with the parameters and variables appropriately defined); see Section 3.2.2. Based on stability results of model (3.2.4)-(3.2.5) (see [21]), the eigenvalues of P are negative if and only if $\mathcal{R}_0^1 > 1$.

We next consider the bottom right block matrix, Q , and use the trace determinant theorem to arrive at conditions for stability. With some algebraic manipulations the trace

and determinant of the matrix Q can be written as

$$\text{Tr}[Q] = r_2 \left(1 - \frac{\hat{N}_1^4}{K_{21}} \right) - \left(\beta_{21} \frac{\hat{I}_1^4}{\hat{N}_1^4} + \Gamma_2 \right), \quad (3.5.10)$$

$$\det[Q] = -r_2 \left(1 - \frac{\hat{N}_1^4}{K_{21}} \right) \left(\beta_{21} \frac{\hat{I}_1^4}{\hat{N}_1^4} + \Gamma_2 \right) + \beta_{21} \frac{\hat{I}_1^4}{\hat{N}_1^4} \alpha_2. \quad (3.5.11)$$

If $K_{21} < \hat{N}_1^4$, then $\left(1 - \frac{\hat{N}_1^4}{K_{21}} \right) < 0$ and hence $\text{Tr}(Q) < 0$ and $\det(Q) > 0$, as all the parameters are positive. Thus, if $\mathcal{R}_0^1 > 1$ and $K_{21} < \hat{N}_1^4$ then the infected one host equilibrium E_4 is stable. ■

Remark 3.5.3.1 *The condition $K_{21} < \hat{N}_1^4$ is not necessary for the stability of E_4 . Necessary conditions for stability of E_4 are obtained by the application of the Trace-determinant theorem. From (3.5.11), $\det(Q) > 0$ gives us the condition*

$$r_2 \left(1 - \frac{\hat{N}_1^4}{K_{21}} \right) \left(\beta_{21} \frac{\hat{I}_1^4}{\hat{N}_1^4} + \Gamma_2 \right) - \beta_{21} \frac{\hat{I}_1^4}{\hat{N}_1^4} \alpha_2 < 0. \quad (3.5.12)$$

In fact, simulations indicate that there are situations for which $K_{21} > \hat{N}_1^4$ and E_4 appears to be stable regardless.

By similar arguments we can prove

Theorem 3.5.3.2 *Assume $\alpha_2 > 0$. If $\mathcal{R}_0^2 > 1$ and $K_{12} < \hat{N}_2^5$ then the infected one-host equilibrium E_5 is biologically feasible and stable.*

3.5.4 Infected Coexistence Equilibrium for Frequency Incidence

In this section we examine the infected coexistence (endemic) equilibrium of the system (3.3.10a)-(3.3.10d) with frequency incidence disease transmission in (3.3.8)-(3.3.9). We assume that feasibility conditions are met and both species are present (see Theorem 3.5.5.1 and Theorem 3.5.5.2). Although the actual value of this equilibrium is algebraically

intractable, we use methods similar to [102] to analyze the existence and stability of the endemic equilibrium. However, unlike the simpler case in [102], the complete analysis of this equilibrium requires results from the theory of asymptotically autonomous systems [138].

Assuming that $N_1, N_2 > 0$, we will express the model (3.3.1a)-(3.3.1b) in terms of the proportion of infected individuals and the total population size $N_j = S_j + I_j, j = 1, 2$. Let $i_1 = \frac{I_1}{N_1}, i_2 = \frac{I_2}{N_2}$. Then, model (3.3.10a)-(3.3.10d) can be rewritten as

$$\frac{di_1}{dt} = (1 - i_1)(\beta_{11}i_1 + \beta_{12}i_2 - \alpha_1i_1) - a_1i_1 \left(1 - \frac{N_1}{\theta_{11}} - \frac{N_2}{\theta_{12}}\right), \quad (3.5.13a)$$

$$\frac{di_2}{dt} = (1 - i_2)(\beta_{22}i_2 + \beta_{21}i_1 - \alpha_2i_2) - a_2i_2 \left(1 - \frac{N_2}{\theta_{22}} - \frac{N_1}{\theta_{21}}\right), \quad (3.5.13b)$$

$$\frac{dN_1}{dt} = a_1N_1 \left(1 - \frac{N_1}{\theta_{11}} - \frac{N_2}{\theta_{12}}\right) - b_1N_1 - \alpha_1i_1N_1, \quad (3.5.13c)$$

$$\frac{dN_2}{dt} = a_2N_2 \left(1 - \frac{N_2}{\theta_{22}} - \frac{N_1}{\theta_{21}}\right) - b_2N_2 - \alpha_2i_2N_2. \quad (3.5.13d)$$

The model (3.5.13a)-(3.5.13d) makes ecological sense and is mathematically well-posed in the domain $\mathcal{D}^2 = \{(i_1, i_2, N_1, N_2) \in \mathbb{R}^4 | 0 \leq i_1, i_2 \leq 1, 0 \leq N_i \leq K_{ii}, i = 1, 2\}$. Unlike [102], in which density-dependent death rates (but no inter-species competition) were considered, the equations (3.5.13a)-(3.5.13d) do not decouple when rewritten in terms of proportions of infected individuals.

3.5.5 Ultimate Bounds for the Total Population Size

In this section we derive ultimate bounds for the total population size, defined by equations (3.5.13c)-(3.5.13d), under which the presence of both species is guaranteed for all time.

We can rewrite equations (3.5.13c)-(3.5.13d) as a pair of non-autonomous Lotka-

Volterra equations in the form

$$\frac{dN_1}{dt} = N_1 \left(r_1^\alpha(t) - \frac{a_1}{\theta_{11}} N_1 - \frac{a_2}{\theta_{12}} N_2 \right), \quad (3.5.14a)$$

$$\frac{dN_2}{dt} = N_2 \left(r_2^\alpha(t) - \frac{a_2}{\theta_{22}} N_2 - \frac{a_1}{\theta_{21}} N_1 \right), \quad (3.5.14b)$$

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

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

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 $r_k^\alpha(t)$ are continuous and bounded above and below with $0 \leq r_k - \alpha_k = \tilde{r}_k \leq \inf\{r_k^\alpha(t) : 0 \leq t < \infty\}$ and $0 < \sup\{r_k^\alpha(t) : 0 \leq t < \infty\} \leq r_k$ for $k = 1, 2$.

We next make the following definitions for $i, j = 1, 2$:

$$\tilde{K}_{ij} = \tilde{r}_i \frac{\theta_{ij}}{a_i} = K_{ij}(1 - \alpha_i/r_i), \quad (3.5.15a)$$

$$h_i(N_i, N_j) = \tilde{r}_i N_i \left(1 - \frac{N_i}{\tilde{K}_{ii}} - \frac{N_j}{\tilde{K}_{ij}} \right), \quad i \neq j, \quad (3.5.15b)$$

$$p_i(N_i, N_j) = r_i N_i \left(1 - \frac{N_i}{K_{ii}} - \frac{N_j}{K_{ij}} \right), \quad i \neq j. \quad (3.5.15c)$$

The functions h_i , and p_i are lower and upper bounds for the derivatives in (3.5.14a) and (3.5.14b). We also define the modified parameters $\tilde{\xi}_i = 1/\tilde{K}_{ii} - 1/\tilde{K}_{ji}$, $i \neq j$. Based on the analysis in Section 3.3.2, for $\tilde{\xi}_1, \tilde{\xi}_2 > 0$ 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 $\{(N_1, N_2) \in \mathbb{R}^2 | 0 < N_i \leq K_{ii}, i = 1, 2\}$ to the asymptotically stable equilibrium $(\hat{N}_1^l, \hat{N}_2^l)$

$$\hat{N}_1^l = \frac{\tilde{K}_{11}\tilde{K}_{12}}{\tilde{K}_{12} + \tilde{K}_{11}(\tilde{\xi}_1/\tilde{\xi}_2)}, \quad \hat{N}_2^l = \frac{\tilde{\xi}_1}{\tilde{\xi}_2} \hat{N}_1^l \quad (3.5.16)$$

Similarly, if $\xi_1, \xi_2 > 0$, 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 $\{(N_1, N_2) \in \mathbb{R}^2 | 0 < N_i \leq K_{ii}, i = 1, 2\}$ to the asymptotically stable equilibrium $(\hat{N}_1^u = \hat{N}_1^3 = \hat{S}_1^3, \hat{N}_2^u = \hat{N}_2^3 =$

$\hat{S}_2^3$), with $\hat{S}_i^3, i = 1, 2$ as defined in (3.4.2). Sufficient conditions for $\tilde{\xi}_1, \tilde{\xi}_2, \xi_1, \xi_2 > 0$ to hold are Assumption (U1) and the following additional assumptions

$$(U2) \quad \tilde{K}_{21} > K_{11},$$

$$(U3) \quad \tilde{K}_{12} > K_{22},$$

which we will now make.

Using results on nonautonomous Lotka-Volterra models in [1] we state the following two results.

Theorem 3.5.5.1 *If the assumptions (U1), (U2) and (U3) hold, then there exists a solution (N_1^*, N_2^*) of (3.5.14a) and (3.5.14b) (or equivalently (3.5.13c)-(3.5.13d)) for which the optimal bounds*

$$0 < \left(\frac{\tilde{K}_{12} - K_{22}}{\tilde{K}_{12} - \tilde{K}_{22}} \right) \hat{N}_1^l \leq N_1^*(t) \leq \left(\frac{K_{12} - \tilde{K}_{22}}{K_{12} - K_{22}} \right) \hat{N}_1^u, \quad (3.5.17)$$

$$0 < \left(\frac{\tilde{K}_{21} - K_{11}}{\tilde{K}_{21} - \tilde{K}_{11}} \right) \hat{N}_2^l \leq N_2^*(t) \leq \left(\frac{K_{21} - \tilde{K}_{11}}{K_{21} - K_{11}} \right) \hat{N}_2^u, \quad (3.5.18)$$

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

Proof. The proof follows from Theorem 2 in [1] and some algebraic manipulations. We note that the assumptions (U2) and (U3) imply

$$K_{21} > \tilde{K}_{21} > K_{11} > \tilde{K}_{11}, \quad (3.5.19)$$

$$K_{12} > \tilde{K}_{12} > K_{22} > \tilde{K}_{22}. \quad (3.5.20)$$

■

Theorem 3.5.5.2 *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 (3.5.14a) and (3.5.14b) such that $N_1^k(t^*) > 0$, and*

$N_2^k(t^*) > 0$ for some $t^* \geq 0$, $k = 1, 2$, then we have

$$N_j^1(t) - N_j^2(t) \rightarrow 0, \text{ for } j = 1, 2, \text{ as } t \rightarrow \infty. \quad (3.5.21)$$

Thus, if (N_1^{**}, N_2^{**}) is any solution of (3.5.14a) and (3.5.14b) with $N_k^{**}(t^*) > 0, k = 1, 2$ for some $t^* > 0$ and $\epsilon > 0$ is arbitrary, then, from Theorem 3.5.5.1, we have that

$$0 < \left(\frac{\tilde{K}_{12} - K_{22}}{\tilde{K}_{12} - \tilde{K}_{22}} \right) \hat{N}_1^l - \epsilon < N_1^{**}(t) < \left(\frac{K_{12} - \tilde{K}_{22}}{K_{12} - K_{22}} \right) \hat{N}_1^u + \epsilon, \quad (3.5.22)$$

$$0 < \left(\frac{\tilde{K}_{21} - K_{11}}{\tilde{K}_{21} - \tilde{K}_{11}} \right) \hat{N}_2^l - \epsilon < N_2^{**}(t) < \left(\frac{K_{21} - \tilde{K}_{11}}{K_{21} - K_{11}} \right) \hat{N}_2^u + \epsilon, \quad (3.5.23)$$

hold for sufficiently large t .

Proof. The proof follows from Theorem 1 and Theorem 2 in [1], and some algebraic manipulations. ■

3.5.6 Existence and Uniqueness of an Endemic Equilibrium

Under the assumptions (U1), (U2) and (U3), we have the following result.

Theorem 3.5.6.1 *For frequency incidence, a unique endemic equilibrium exists for the SI model with competition, (3.5.13a)-(3.5.13b), if and only if (a) $\mathcal{R}_{jj} > 1$ for either $j = 1$ or $j = 2$ or (b) $\mathcal{R}_{jj} \leq 1$ for both $j = 1, 2$ and $(1 - \mathcal{R}_{11})(1 - \mathcal{R}_{22}) < \mathcal{R}_{12}\mathcal{R}_{21}$.*

Proof. We note that conditions (a) and (b) are equivalent to $\mathcal{R}_0^C > 1$ for $\mathcal{R}_0^C$ defined in (3.4.3) and (3.4.4).

We begin by setting (3.5.13c) and (3.5.13d) 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

$$\hat{N}_1(i_1, i_2) = \hat{N}_1^u + H_1(i_1, i_2), \quad (3.5.24a)$$

$$\hat{N}_2(i_1, i_2) = \hat{N}_2^u + H_2(i_1, i_2), \quad (3.5.24b)$$

for $(i_1, i_2) \in D = [0, 1] \times [0, 1]$, and $\hat{N}_i^u = \hat{S}_i^3, i = 1, 2$ are as defined in (3.4.2). The functions H_1 and H_2 are defined as

$$H_1(i_1, i_2) = \left(\frac{\alpha_1 i_1 K_{12}}{r_1} - \frac{\alpha_2 i_2 K_{22}}{r_2} \right) \left(\frac{K_{22}}{K_{21}} - \frac{K_{12}}{K_{11}} \right)^{-1}, \quad (3.5.25a)$$

$$H_2(i_1, i_2) = \left(\frac{\alpha_2 i_2 K_{21}}{r_2} - \frac{\alpha_1 i_1 K_{11}}{r_1} \right) \left(\frac{K_{11}}{K_{12}} - \frac{K_{21}}{K_{22}} \right)^{-1}. \quad (3.5.25b)$$

We then substitute $\hat{N}_1$ and $\hat{N}_2$ into equations (3.5.13a), and (3.5.13b) resulting in the equations

$$\frac{di_1}{dt} = (1 - i_1)(\beta_{11}i_1 + \beta_{12}i_2 - \alpha_1i_1) - i_1(b_1 + \alpha_1i_1), \quad (3.5.26a)$$

$$\frac{di_2}{dt} = (1 - i_2)(\beta_{22}i_2 + \beta_{21}i_1 - \alpha_2i_2) - i_2(b_2 + \alpha_2i_2). \quad (3.5.26b)$$

The model (3.5.26a)-(3.5.26b) is different from the one that is derived in [102]; however similar techniques can be used to analyze it, which we now consider. Setting (3.5.26a) and (3.5.26b) equal to zero, we obtain the isoclines for i_1 and i_2 in the plane where N_1 and N_2 are at equilibrium as

$$i_2 = f_1(i_1) = \frac{i_1[b_1 + \alpha_1i_1 - (1 - i_1)(\beta_{11} - \alpha_1)]}{(1 - i_1)\beta_{12}}, \quad (3.5.27a)$$

$$i_1 = f_2(i_2) = \frac{i_2[b_2 + \alpha_2i_2 - (1 - i_2)(\beta_{22} - \alpha_2)]}{(1 - i_2)\beta_{21}}. \quad (3.5.27b)$$

We note that the domain $D = [0, 1] \times [0, 1]$ is invariant for the system (3.5.26a) and (3.5.26b), 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 isoclines always intersect at the origin. The function f_1 has an asymptote at $i_1 = 1$, and f_2 has an asymptote at $i_2 = 1$ and

$$\left. \frac{df_1}{di_1} \right|_{i_1=0} = \frac{b_1 + \alpha_1 - \beta_{11}}{\beta_{12}}, \quad (3.5.28)$$

and

$$\left. \frac{df_2}{di_2} \right|_{i_2=0} = \frac{b_2 + \alpha_2 - \beta_{22}}{\beta_{21}}. \quad (3.5.29)$$

Also,

$$\frac{d^2 f_k}{di_k^2} = \frac{2(b_k + \alpha_k)}{\beta_{kj}(1 - i_k)^3} > 0, \quad k, j = 1, 2, \quad k \neq j, \quad 0 \leq i_k < 1, \quad (3.5.30)$$

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 $\mathcal{R}_{11} > 1$ and $\mathcal{R}_{22} > 1$. Then, we can see from (3.4.3) and (3.4.4) that $\beta_{ii} > \Gamma_i = b_i + \alpha_i$, for $i = 1, 2$. Using this in equations (3.5.28) and (3.5.29), we find that

$$\left. \frac{df_k}{di_k} \right|_{i_k=0} < 0, \quad (3.5.31)$$

which implies that there is one point of intersection in D (see Figure 3.11).

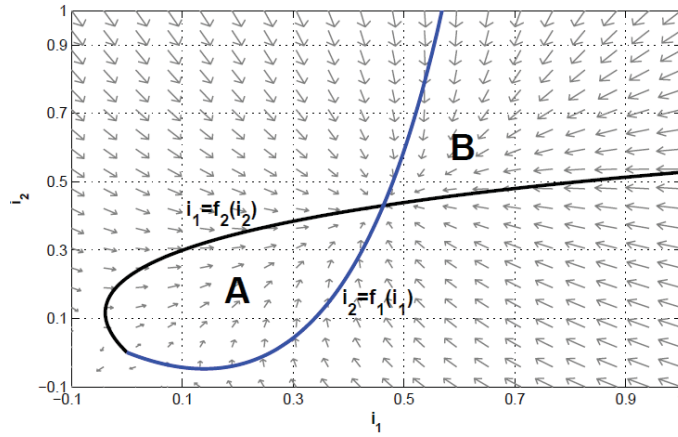


FIGURE 3.11: Isoclines for the case where both $\mathcal{R}_{11}, \mathcal{R}_{22} > 1$. Disease related parameters are $\beta_{11} = 2.7$, $\beta_{22} = 3.2$, $\beta_{12} = 1.1$, $\beta_{21} = 1.1$, $\alpha_1 = 1$, $\alpha_2 = .5$, $b_1 = 1$, and $b_2 = 2$.

Case (2): Assume $\mathcal{R}_{11} < 1$ and $\mathcal{R}_{22} > 1$. Then $\left. \frac{df_1}{di_1} \right|_{i_1=0} > 0$ and $\left. \frac{df_2}{di_2} \right|_{i_2=0} < 0$, so that f_1 and f_2 again intersect uniquely in D (see Figure 3.12).

Case (3): Assume $\mathcal{R}_{11} > 1$ and $\mathcal{R}_{22} < 1$. Changing roles in Case (2), we again have that f_1 and f_2 intersect uniquely in D .

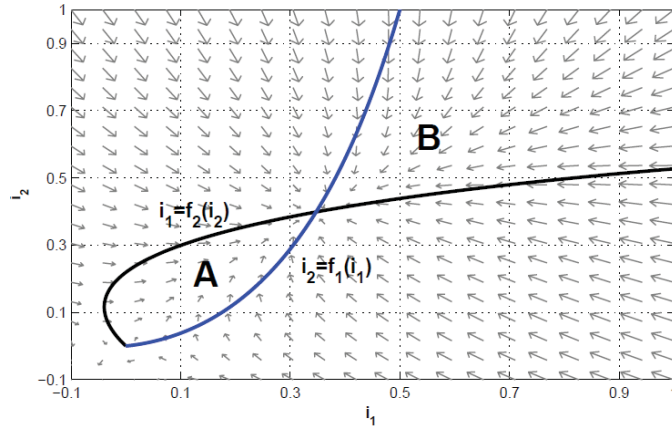


FIGURE 3.12: Isoclines for the case where $\mathcal{R}_{11} < 1$ and $\mathcal{R}_{22} > 1$. Disease related parameters are $\beta_{11} = 1.8$, $\beta_{22} = 3.2$, $\beta_{12} = 1.1$, $\beta_{21} = 1.1$, $\alpha_1 = 1$, $\alpha_2 = .5$, $b_1 = 1$, and $b_2 = 2$.

Case (4): Lastly, we consider the case where $\mathcal{R}_{11} < 1$ and $\mathcal{R}_{22} < 1$, and $(1 - \mathcal{R}_{11})(1 - \mathcal{R}_{22}) < \mathcal{R}_{12}\mathcal{R}_{21}$. This implies that $\frac{df_k}{di_k}|_{i_k=0} > 0$ for $k = 1, 2$. In order for the nullclines to cross in D , we must also have

$$\frac{df_1}{di_1}|_{i_1=0} < \frac{1}{\frac{df_2}{di_2}|_{i_2=0}}. \quad (3.5.32)$$

This is equivalent to $(1 - \mathcal{R}_{11})(1 - \mathcal{R}_{22}) < \mathcal{R}_{12}\mathcal{R}_{21}$, which holds by assumption for Case 4 (see Figure 3.13).

Necessary part of proof: Assume that there exists a unique endemic equilibrium but that conditions (a) and (b) of Theorem 3.5.6.1 do not hold. So, $\mathcal{R}_{jj} < 1$ for $j = 1, 2$ and $(1 - \mathcal{R}_{11})(1 - \mathcal{R}_{22}) \geq \mathcal{R}_{12}\mathcal{R}_{21}$. This implies that $\frac{df_k}{di_k}|_{i_k=0} > 0$ for $k = 1, 2$. However, the condition $\frac{df_1}{di_1}|_{i_1=0} < \frac{1}{\frac{df_2}{di_2}|_{i_2=0}}$ no longer holds, hence the nullclines do not intersect in the interior of D , which contradicts the assumption of existence of a unique endemic equilibrium (see Figure 3.14). ■

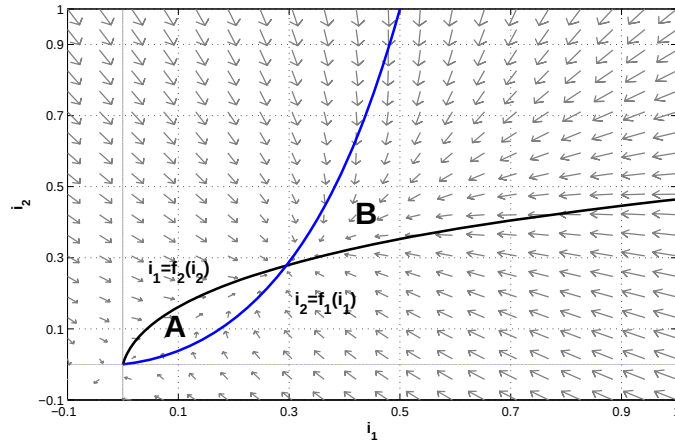


FIGURE 3.13: Isoclines for the case where $\mathcal{R}_{11}, \mathcal{R}_{22} < 1$ but $(1 - \mathcal{R}_{11})(1 - \mathcal{R}_{22}) < \mathcal{R}_{12}\mathcal{R}_{21}$. Disease related parameters are $\beta_{11} = 1.8$, $\beta_{22} = 2.3$, $\beta_{12} = 1.1$, $\beta_{21} = 1.1$, $\alpha_1 = 1$, $\alpha_2 = .5$, $b_1 = 1$, and $b_2 = 2$.

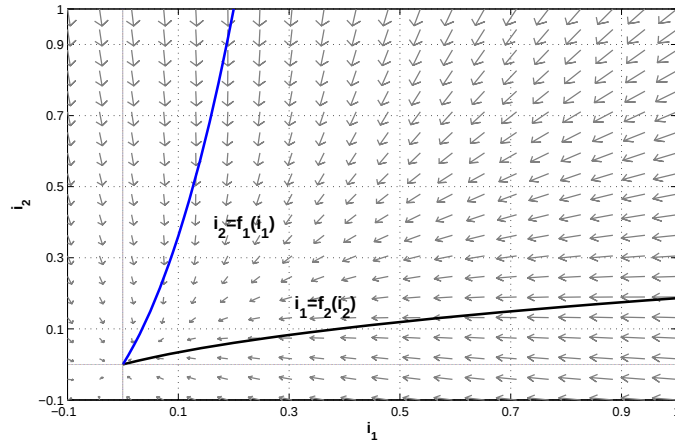


FIGURE 3.14: Isoclines for the case where neither condition (i) nor (ii) of Theorem 3.5.6.1 hold. Disease related parameters are $\beta_{11} = 1.5$, $\beta_{22} = 2$, $\beta_{12} = .2$, $\beta_{21} = .2$, $\alpha_1 = 1$, $\alpha_2 = .5$, $b_1 = 1$, and $b_2 = 2$.

3.5.7 Stability of the Endemic Equilibrium

Let us denote the unique endemic equilibrium as $E_6 = (\hat{i}_1^6, \hat{i}_2^6, \hat{N}_1(\hat{i}_1^6, \hat{i}_2^6), \hat{N}_2(\hat{i}_1^6, \hat{i}_2^6))$. Then, we have the following result.

Theorem 3.5.7.1 *Consider the frequency incidence SI model with Lotka-Volterra competition (3.5.26a)-(3.5.26b). If $\mathcal{R}_0^C < 1$ then the disease free equilibrium $(\hat{i}_1^3 = 0, \hat{i}_2^3 = 0)$ is globally asymptotically stable in the region $D = [0, 1] \times [0, 1]$ and if $\mathcal{R}_0^C > 1$ then the infected coexistence (endemic) equilibrium $(\hat{i}_1^6, \hat{i}_2^6)$ is globally asymptotically stable in $D_+ = D \setminus \{0, 0\}$.*

Proof. Suppose $\mathcal{R}_0^C < 1$. Then by Theorem 3.5.6.1 there is no infected coexistence equilibrium. The only equilibrium for (3.5.26a)-(3.5.26b) is the origin (which corresponds to the disease-free equilibrium $(0, 0, \hat{S}_1^3, \hat{S}_2^3)$ for (3.5.13a)-(3.5.13d)) and is locally asymptotically stable in D by [144]. The Poincare-Bendixson Trichotomy states that a positive orbit of the system that remains in a closed and bounded region of the plane with only a finite number of equilibria will have an omega limit set that takes on only one of three forms, namely, an equilibrium, a periodic orbit, or a finite number of equilibria, and a set of trajectories whose α - and ω - limit sets consist of one of these equilibria for each trajectory [6]. Since the solutions of our system are indeed bounded and the only equilibrium in the region $D = [0, 1] \times [0, 1]$ for (3.5.26a)-(3.5.26b) is the origin, which is stable, there are no periodic solutions in the region and the origin is globally stable for (3.5.26a)-(3.5.26b). This implies that the disease-free equilibrium $(\hat{i}_1^3 = 0, \hat{i}_2^3 = 0)$ for (3.5.26a)-(3.5.26b) is globally stable in D .

Next suppose $\mathcal{R}_0^C > 1$. Then by Theorem 3.5.6.1 there is a unique infected coexistence equilibrium, $(\hat{i}_1^6, \hat{i}_2^6)$, for (3.5.26a)-(3.5.26b). We will first show that no solution of (3.5.26a)-(3.5.26b) in the invariant region D_+ will approach the origin. The Jacobian for

(3.5.26a) and (3.5.26b) evaluated at the origin is

$$\mathcal{J}(0,0) = \begin{bmatrix} \beta_{11} - (\alpha_1 + b_1) & \beta_{12} \\ \beta_{21} & \beta_{22} - (\alpha_2 + b_2) \end{bmatrix},$$

which has eigenvalues

$$\lambda_1^6, \lambda_2^6 = \frac{1}{2}[(\beta_{11} - \Gamma_1) + (\beta_{22} - \Gamma_2) \pm \sqrt{[(\beta_{11} - \Gamma_1) - (\beta_{22} - \Gamma_2)]^2 + 4\beta_{21}\beta_{12}}], \quad (3.5.33)$$

where $\Gamma_i = \alpha_i + b_i$. Since $\mathcal{R}_0^C > 1$ then we know atleast one of $\beta_{11} - \Gamma_1$ and $\beta_{22} - \Gamma_2$ are positive or both are negative and $(\beta_{11} - \Gamma_1)(\beta_{22} - \Gamma_2) < \beta_{12}\beta_{21}$, both cases for which $\lambda_1^6 > 0$. Now, if $\lambda_2^6 > 0$ as well then the origin is a repellor. If, on the other hand, $\lambda_2^6 < 0$ then the eigenvector of λ_2^6 is

$$\begin{bmatrix} x_1 \\ x_2 \end{bmatrix} = \begin{bmatrix} \frac{1}{\beta_{21}}(\lambda_2^6 - (\beta_{22} - \Gamma_2)) \\ 1 \end{bmatrix}. \quad (3.5.34)$$

Since $\lambda_2^6 < 0$ then we can see that $x_1 < 0$ also and the stable manifold of the origin does not lie in D_+ . Hence, none of the solutions in D_+ approach the DFE.

Lastly, we need to show that no periodic solutions exist inside D_+ . We can see by examining the phase plane of the proportions system (3.5.26a) and (3.5.26b) that the region, A, 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 Poincare-Bendixson Trichotomy to deduce that all solution trajectories approach the infected coexistence equilibrium, and therefore it is globally asymptotically stable in the region D_+ . ■

We note that the stability of the infected coexistence equilibrium of the proportions model (3.5.26a)-(3.5.26b) in D_+ need not guarantee the stability of the infected coexistence

of the model (3.5.13a)-(3.5.13d) in $\mathcal{D}^2 = \{(i_1, i_2, N_1, N_2) \in \mathbb{R}^4 | 0 \leq i_1, i_2 \leq 1, 0 \leq N_i \leq K_{ii}, i = 1, 2\}$. However, if $\alpha_i = 0$ for $i = 1, 2$ then the conditions under which the coexistence equilibrium $(\hat{N}_1, \hat{N}_2)$, for the system of equations (3.5.13c) and (3.5.13d), is globally stable in the $N_1 - N_2$ plane do not depend on i_1 and i_2 . Therefore, if these stability conditions are met (namely $\xi_1 > 0, \xi_2 > 0$) then we can extend Theorem 3.5.7.1 to prove global asymptotic stability of the DFE and the endemic equilibrium of the model (3.5.13a)-(3.5.13d) in the domain $\mathcal{D}^2$ using the theory of asymptotically autonomous equations.

Theorem 3.5.7.2 *Assume that $\alpha_i = 0$ for $i = 1, 2$ and $\xi_1 > 0, \xi_2 > 0$. Then, if $\mathcal{R}_0^C < 1$ the disease free equilibrium $E_3 = (i_1^3 = 0, i_2^3 = 0, \hat{N}_1^3 = \hat{S}_1^3, \hat{N}_2^3 = \hat{S}_2^3)$ is globally asymptotically stable in $\hat{\mathcal{D}}_+^2 = \{(i_1, i_2, N_1, N_2) \in \mathbb{R}^4 | 0 \leq i_1, i_2 \leq 1, 0 < N_i \leq K_{ii}, i = 1, 2\}$ and if $\mathcal{R}_0^C > 1$ the infected coexistence equilibrium $E_6 = (\hat{i}_1^6, \hat{i}_2^6, \hat{N}_1^6, \hat{N}_2^6)$ is globally asymptotically stable with initial conditions in the region $\mathcal{D}_+^2 = \{(i_1, i_2, N_1, N_2) \in \mathbb{R}^4 | 0 < i_1, i_2 \leq 1, 0 < N_i \leq K_{ii}, i = 1, 2\}$.*

Proof. Consider the non-autonomous system with equations (3.5.13a) - (3.5.13b) rewritten as:

$$\frac{di_1}{dt} = (1 - i_1)(\beta_{11}i_1 + \beta_{12}i_2) - a_1i_1 \left(1 - \frac{N_1(t)}{\theta_{11}} - \frac{N_2(t)}{\theta_{12}}\right), \quad (3.5.35a)$$

$$\frac{di_2}{dt} = (1 - i_2)(\beta_{22}i_2 + \beta_{21}i_1) - a_2i_2 \left(1 - \frac{N_2(t)}{\theta_{22}} - \frac{N_1(t)}{\theta_{21}}\right), \quad (3.5.35b)$$

in which $N_i(t)$ is a solution of

$$\frac{dN_1}{dt} = a_1N_1 \left(1 - \frac{N_1}{\theta_{11}} - \frac{N_2}{\theta_{12}}\right) - b_1N_1, \quad (3.5.36a)$$

$$\frac{dN_2}{dt} = a_2N_2 \left(1 - \frac{N_2}{\theta_{22}} - \frac{N_1}{\theta_{21}}\right) - b_2N_2. \quad (3.5.36b)$$

We can write system (3.5.35a) - (3.5.35b) as

$$x' = f(x, t) \quad (3.5.37)$$

where x is the vector $(i_1, i_2)^T$, and the components of f are the right hand sides in (3.5.35a) - (3.5.35b). The equilibrium of system (3.5.36a) - (3.5.36b) can be found independently

of i_1 and i_2 . Under the assumption $\xi_1 > 0, \xi_2 > 0$, the coexistence equilibrium ($\hat{N}_1^6 = \hat{S}_1^3, \hat{N}_2^6 = \hat{S}_2^3$) of this system is locally (and globally) asymptotically stable independently of i_1 and i_2 in its basin of attraction, $\mathcal{D}_+^2$. Hence, $N_i(t) \rightarrow \hat{N}_i^6$ as $t \rightarrow \infty$ in $\mathcal{D}_+^2$ for $i = 1, 2$. We then substitute $\hat{N}_1^6$ into system (3.5.37) to get

$$\frac{di_1}{dt} = (1 - i_1)(\beta_{11}i_1 + \beta_{12}i_2) - a_1i_1 \left(1 - \frac{\hat{N}_1^1}{\theta_{11}} - \frac{\hat{N}_2^1}{\theta_{12}} \right), \quad (3.5.38a)$$

$$\frac{di_2}{dt} = (1 - i_2)(\beta_{22}i_2 + \beta_{21}i_1) - a_2i_2 \left(1 - \frac{\hat{N}_2^1}{\theta_{22}} - \frac{\hat{N}_1^1}{\theta_{21}} \right). \quad (3.5.38b)$$

Therefore, system (3.5.37) is an asymptotically autonomous system and has limit equations given by ((3.5.38a)-(3.5.38b)) which we can rewrite as

$$x' = h(x) \quad (3.5.39)$$

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

We now consider two cases. For the first case we assume that $\mathcal{R}_0^C < 1$. By Theorem 3.5.7.1, when $N_1 = \hat{N}_1^3$ and $N_2 = \hat{N}_2^3$ are at the (globally stable) coexistence equilibrium, the disease free equilibrium for system (3.5.38a)-(3.5.38b) is unique and globally asymptotically stable in the region D . Therefore, by Theorem 4.1 from [138], the disease free equilibrium for system (3.5.37) is also globally stable in the region $\mathcal{D}_+^2$.

For case two, assuming $\mathcal{R}_0^C > 1$ we consider the endemic equilibrium corresponding to $(\hat{i}_1^6, \hat{i}_2^6)$. Again, by Theorem 3.5.7.1 (which holds true when $\alpha_k = 0, k = 1, 2$), when N_1 and N_2 are at the (globally stable) coexistence equilibrium $\hat{N}_1^6 = \hat{S}_1^3, \hat{N}_2^6 = \hat{S}_2^3$, the endemic equilibrium for system (3.5.39) is unique and globally stable in D_+ . Therefore, by Theorem 4.1 from [138], the endemic equilibrium for system (3.5.37) is globally asymptotically stable in the region $\mathcal{D}_+^2$. ■

3.5.8 Analysis of the Infected Coexistence Equilibrium Under Additional Assumptions

We will consider a special case in which the infected coexistence equilibrium is given by an analytical formula. In this section, we derive an analytical expression for the infected coexistence equilibrium of the two species model under additional assumptions. Consequently we are able to perform a full stability analysis. We finish by comparing the results of this special case with frequency incidence transmission with the results for the special case with mass action [21].

We add the following additional assumptions to the model (3.3.10a)-(3.3.10d) described in Section 3.3.2.

- (A1) $\alpha_i = 0$, so that there is no increased death rate as a result of the disease.
- (A2) $a = a_1 = a_2$, $b = b_1 = b_2$, $\theta = \theta_{11} = \theta_{22}$, and $\beta = \beta_{ij}$ for all $i, j = 1, 2$. As before, let $r := a - b$ be the intrinsic growth rate for both the species. Also, $K = K_{11} = K_{22} = \frac{r\theta}{a}$, so the carrying capacity is the same for both species.
- (A3) $\theta_{12} \neq \theta_{21}$ (in order to retain a difference between the species).

As before, we define $K_{ij} := \frac{r\theta_{ij}}{a}$.

First, we compute the possible equilibria, in the form $E_e = (\hat{S}_1^e, \hat{S}_2^e, \hat{I}_1^e, \hat{I}_2^e)$, for the competing two species SI model with frequency incidence disease transmission, (3.3.10a)-(3.3.10d) under the additional assumptions (A1), (A2) and (A3). We then use the Jacobian of our simplified model to establish stability conditions for all the equilibria. Finally we compare our results to previous results for a mass action model.

The Jacobian for this simplified system computed at an equilibrium $E_e = (\hat{S}_1^e, \hat{S}_2^e, \hat{I}_1^e, \hat{I}_2^e)$ is

$$\mathcal{J}(E_e) = \begin{bmatrix} \mathcal{A}(E_e) & \mathcal{B}(E_e) \\ \mathcal{C}(E_e) & \mathcal{D}(E_e) \end{bmatrix}, \quad (3.5.40)$$

where, the 2×2 matrices $\mathcal{A}$, $\mathcal{B}$, $\mathcal{C}$, and $\mathcal{D}$ evaluated at an equilibrium E_e are defined as

$$\mathcal{A}(E_e) = \begin{bmatrix} A(E_e) - b - \mathcal{I}(E_e) + \frac{\beta \hat{S}_1^e \hat{I}_1^e}{\hat{N}_1^{e^2}} & A_{12}(E_e) + \frac{\beta \hat{S}_1^e \hat{I}_2^e}{\hat{N}_2^{e^2}} \\ B_{21}(E_e) + \frac{\beta \hat{S}_2^e \hat{I}_1^e}{\hat{N}_1^{e^2}} & B(E_e) - b - \mathcal{I}(E_e) + \frac{\beta \hat{S}_2^e \hat{I}_2^e}{\hat{N}_2^{e^2}} \end{bmatrix}, \quad (3.5.41)$$

$$\mathcal{B}(E_e) = \begin{bmatrix} A(E_e) - \frac{\beta \hat{S}_1^e}{\hat{N}_1^e} + \frac{\beta \hat{S}_1^e \hat{I}_1^e}{\hat{N}_1^{e^2}} & A_{12}(E_e) - \frac{\beta \hat{S}_1^e}{\hat{N}_2^e} + \frac{\beta \hat{S}_1^e \hat{I}_2^e}{\hat{N}_2^{e^2}} \\ B_{21}(E_e) - \frac{\beta \hat{S}_2^e}{\hat{N}_1^e} + \frac{\beta \hat{S}_2^e \hat{I}_1^e}{\hat{N}_1^{e^2}} & B(E_e) - \frac{\beta \hat{S}_2^e}{\hat{N}_2^e} + \frac{\beta \hat{S}_2^e \hat{I}_2^e}{\hat{N}_2^{e^2}} \end{bmatrix}, \quad (3.5.42)$$

$$\mathcal{C}(E_e) = \begin{bmatrix} \mathcal{I}(E_e) - \frac{\beta \hat{S}_1^e \hat{I}_1^e}{\hat{N}_1^{e^2}} & -\frac{\beta \hat{S}_1^e \hat{I}_2^e}{\hat{N}_2^{e^2}} \\ -\frac{\beta \hat{S}_2^e \hat{I}_1^e}{\hat{N}_1^{e^2}} & \mathcal{I}(E_e) - \frac{\beta \hat{S}_2^e \hat{I}_2^e}{\hat{N}_2^{e^2}} \end{bmatrix}, \quad (3.5.43)$$

and

$$\mathcal{D}(E_e) = \begin{bmatrix} \frac{\beta \hat{S}_1^e}{\hat{N}_1^e} - b - \frac{\beta \hat{S}_1^e \hat{I}_1^e}{\hat{N}_1^{e^2}} & \frac{\beta \hat{S}_1^e}{\hat{N}_2^e} - \frac{\beta \hat{S}_1^e \hat{I}_2^e}{\hat{N}_2^{e^2}} \\ \frac{\beta \hat{S}_2^e}{\hat{N}_1^e} - \frac{\beta \hat{S}_2^e \hat{I}_1^e}{\hat{N}_1^{e^2}} & \frac{\beta \hat{S}_2^e}{\hat{N}_2^e} - b - \frac{\beta \hat{S}_2^e \hat{I}_2^e}{\hat{N}_2^{e^2}} \end{bmatrix}. \quad (3.5.44)$$

with the definitions

$$A(E_e) := \frac{-a \hat{N}_1^e}{\theta} + g_1(\hat{N}_1^e, \hat{N}_2^e), \quad (3.5.45)$$

$$A_{12}(E_e) := \frac{-a \hat{N}_1^e}{\theta_{12}}, \quad (3.5.46)$$

$$B(E_e) := \frac{-a \hat{N}_2^e}{\theta} + g_2(\hat{N}_1^e, \hat{N}_2^e), \quad (3.5.47)$$

$$B_{21}(E_e) := \frac{-a \hat{N}_2^e}{\theta_{21}}. \quad (3.5.48)$$

For $i = 1, 2$, we have $\hat{N}_i^e = \hat{S}_i^e + \hat{I}_i^e$. We have the disease incidence function,

$$\mathcal{I}(E_e) = \beta \left(\frac{\hat{I}_1^e}{\hat{N}_1^e} + \frac{\hat{I}_2^e}{\hat{N}_2^e} \right), \quad (3.5.49)$$

($\mathcal{I}_1 = \mathcal{I}_2$), and for $i = 1, 2$, the birth functions g_i as defined in (3.3.2) (with $\theta = \theta_{11} = \theta_{22}$) evaluated at E_e are given as

$$g_1(E_e) = a \left(1 - \frac{\hat{N}_1^e}{\theta} - \frac{\hat{N}_2^e}{\theta_{12}} \right), \quad (3.5.50a)$$

$$g_2(E_e) = a \left(1 - \frac{\hat{N}_2^e}{\theta} - \frac{\hat{N}_1^e}{\theta_{21}} \right). \quad (3.5.50b)$$

The disease free coexistence equilibrium for the simplified model is $E_3 = (\hat{S}_1^3, \hat{S}_2^3, 0, 0)$, the same as in Section 3.4.4. Lemma 3.4.5.1 holds for the frequency incidence case as well.

Since the Jacobian $\mathcal{J}(E_3)$ is block upper triangular, its eigenvalues are the same as those of matrices $\mathcal{A}(E_3)$ and $\mathcal{D}(E_3)$. The matrix $\mathcal{A}(E_3)$ is the Jacobian of the two species model with pure competition, (3.2.7) evaluated at (N_1^C, N_2^C) (see Section 3.2.3) under the assumptions (A2) and (A3). From Lemma 3.2.3.1, the eigenvalues of $\mathcal{A}(E_3)$ are negative if and only if the conditions

$$(C4) \quad \xi_1 > 0, \text{ and}$$

$$(C5) \quad \xi_2 > 0,$$

hold. The matrix $\mathcal{D}(E_3)$ on the other hand is related to the disease parameters and its eigenvalues are $\lambda_1^3 = -b$ and $\lambda_2^3 = \beta \left(\frac{\hat{S}_1^3}{N_1^3} + \frac{\hat{S}_2^3}{N_2^3} \right) - b$. The eigenvalue λ_1^3 is always negative and λ_2^3 is negative under the condition

$$(C6) \quad \mathcal{R}_0^C = \frac{2\beta}{b} < 1.$$

So, the DFE E_3 is feasible and stable if and only if the conditions (C4), (C5) and (C6) hold.

We note that this result is a special case of Theorem 3.5.1.2 derived from the stability results of the pure competition model. The condition (C6) is the analogue of the inequality (3.4.5) for this special case.

3.5.9 The Infected Coexistence Equilibrium

Lastly, we consider the infected coexistence equilibrium E_6 . We only consider E_6 since the disease free one-host equilibria (E_1, E_2) and infected one-host equilibria (E_4, E_5) can be analyzed in the full system and easily extended to our simplifying assumptions.

We can prove algebraically or by using software like MAPLE that $E_6 = (\hat{S}_1^6, \hat{S}_2^6, \hat{I}_1^6, \hat{I}_2^6)$, with

$$\hat{S}_1^6 = \frac{\hat{S}_1^1}{\mathcal{R}_0^C}, \quad (3.5.51)$$

$$\hat{S}_2^6 = \frac{\xi_1}{\xi_2} \hat{S}_1^6 \quad (3.5.52)$$

$$\hat{I}_1^6 = \mathcal{R}_0^C - 1\hat{S}_1^6, \quad (3.5.53)$$

$$\hat{I}_2^6 = \frac{\xi_1}{\xi_2} \hat{I}_1^6. \quad (3.5.54)$$

Note that the total population size $\hat{N}_i^6 = \hat{S}_i^1$, for $i = 1, 2$.

The characteristic polynomial of $\mathcal{J}(E_6)$ is given as

$$P_7(x) = (x + \eta)(x + \epsilon)(x^2 + \delta_1 x + \delta_2), \quad (3.5.55)$$

where

$$\eta = b + \beta\left(\frac{\hat{I}_1^6}{\hat{N}_1^6} + \frac{\hat{I}_2^6}{\hat{N}_2^6}\right), \quad (3.5.56)$$

$$\epsilon = b + \beta\left(\frac{\hat{I}_1^6}{\hat{N}_1^6} + \frac{\hat{I}_2^6}{\hat{N}_2^6}\right) - \beta\left(\frac{\hat{S}_1^6}{\hat{N}_1^6} + \frac{\hat{S}_2^6}{\hat{N}_2^6}\right), \quad (3.5.57)$$

$$\delta_1 = -(A(E_2) + B(E_2)) + 2b, \quad (3.5.58)$$

$$\delta_2 = -A_{12}(E_2)B_{21}(E_2) + A(E_2)B(E_2) - b(A(E_2) + B(E_2)) + b^2, \quad (3.5.59)$$

where for $i = 1, 2$, $\hat{N}_i^6 = \hat{S}_i^6 + \hat{I}_i^6$. The terms A, B, A_{12} and B_{21} as defined in (3.5.45)-(3.5.48) are all evaluated at the infected coexistence equilibrium E_6 . Then, the eigenvalues of the Jacobian $\mathcal{J}(E_6)$ are

$$\lambda_1^6 = -\eta = -b - \beta\left(\frac{\hat{I}_1^6}{\hat{N}_1^6} + \frac{\hat{I}_2^6}{\hat{N}_2^6}\right), \quad (3.5.60)$$

$$\lambda_2^6 = -\epsilon = -b - \beta\left(\frac{\hat{I}_1^6}{\hat{N}_1^6} + \frac{\hat{I}_2^6}{\hat{N}_2^6}\right) + \beta\left(\frac{\hat{S}_1^6}{\hat{N}_1^6} + \frac{\hat{S}_2^6}{\hat{N}_2^6}\right), \quad (3.5.61)$$

$$\lambda_{3,4}^6 = \frac{1}{2} \left(-\delta_1 \pm \sqrt{\delta_1^2 - 4\delta_2} \right). \quad (3.5.62)$$

Lemma 3.5.9.1 *The condition that $\lambda_2^6 < 0$ is equivalent to $\mathcal{R}_0^C > 1$*

Proof. From (3.5.51), (3.5.53) and using that

$$\frac{\hat{S}_1^6}{\hat{N}_1^6} = \frac{\hat{S}_2^6}{\hat{N}_2^6} = \frac{1}{\mathcal{R}_0^C}$$

and

$$\frac{\hat{I}_1^6}{\hat{N}_1^6} = \frac{\hat{I}_2^6}{\hat{N}_2^6} = \frac{\mathcal{R}_0^C - 1}{\mathcal{R}_0^C}$$

we have

$$\begin{aligned} \lambda_2^6 < 0 \\ \iff -b - \beta\left(\frac{\hat{I}_1^6}{\hat{N}_1^6} + \frac{\hat{I}_2^6}{\hat{N}_2^6}\right) + \beta\left(\frac{\hat{S}_1^6}{\hat{N}_1^6} + \frac{\hat{S}_2^6}{\hat{N}_2^6}\right) &< 0 \\ \iff \frac{\hat{S}_1^6}{\hat{N}_1^6} - \frac{\hat{I}_1^6}{\hat{N}_1^6} + \frac{\hat{S}_2^6}{\hat{N}_2^6} - \frac{\hat{I}_2^6}{\hat{N}_2^6} &< \frac{b}{\beta} \\ \iff 2\left(\frac{1}{\mathcal{R}_0^C} - \frac{\mathcal{R}_0^C - 1}{\mathcal{R}_0^C}\right) &< \frac{2}{\mathcal{R}_0^C} \text{ from (C6)} \\ \iff \frac{2 - \mathcal{R}_0^C}{\mathcal{R}_0^C} &< \frac{1}{\mathcal{R}_0^C} \\ \iff \mathcal{R}_0^C &> 1. \end{aligned}$$

Thus, $\mathcal{R}_0^C > 1$ is both a feasibility and stability condition for the infected coexistence equilibrium E_6 . ■

Lemma 3.4.7.4 holds for the frequency incidence case as well.

Theorem 3.5.9.1 *Assume that $\xi_1/\xi_2 > 0$ so that the infected coexistence equilibrium E_6 is feasible. Then E_6 is stable if and only if $\xi_1 > 0, \xi_2 > 0$, and $\mathcal{R}_0^C > 1$.*

Proof. It is easy to see that λ_1^6 given in (3.5.60) is negative for all $\hat{I}_1^6 + \hat{I}_2^6 \geq 0$. Thus, since the infected coexistence equilibrium E_6 is feasible by assumption ($\xi_1/\xi_2 > 0$) we have $\lambda_1 < 0$. As a result of Lemma 3.5.9.1, the first condition for stability of E_6 is

$$(C8) \quad \mathcal{R}_0^C > 1$$

Since $\hat{I}_1^6 = (\mathcal{R}_0^C - 1)\hat{S}_1^6$, the condition (C8) is also a feasibility condition for E_6 . From Lemma 3.2.3.1, Lemma 3.4.7.4, and the Trace-Determinant theorem [6], we see that the eigenvalues λ_3 and λ_4 are negative if and only if the conditions (C4) and (C5) are satisfied.

■

In this case all the other equilibria, i.e. E_1, E_2, E_3, E_4 , and E_5 , are either infeasible and/or unstable.

3.6 Conclusion and Discussion

The effects of a shared disease on the outcome of competition between two species has been investigated by several authors in the ecological and mathematical ecology communities. Although many papers propose and analyze mathematical models of Lotka-Volterra competition between two species that share a common (generalist) pathogen, some important cases are difficult to analyze. In particular, it has been difficult to find existence and stability conditions of the infected coexistence equilibrium for these models. In this chapter, we consider a competition model with density independent death rates and a shared disease that spreads by either mass action or frequency incidence transmission.

For models with frequency incidence disease transmission, we prove the existence, uniqueness and global stability of the infected coexistence equilibrium under the assumption that coexistence of the species is feasible using the theory of asymptotically autonomous systems. As is the case for most models with frequency incidence disease transmission, the stability of the coexistence equilibrium depends on the basic reproduction number (BRN) being greater than one. Thus, the frequency incidence disease model exhibits the classic endemic model behavior; the disease dies out below a threshold and approaches an endemic equilibrium above the threshold.

The infected coexistence equilibrium for the model with mass action disease transmission is intractable. Hence, we simplify the model by assuming that the two species are similar enough to have the same intra-specific competition rates and to transmit the disease to each other at the same rates. We also assume that the pathogen does not cause death in its hosts, as with the common cold in humans, for example. Under these constraints, we derive all the existence and stability conditions for the equilibria of the mass action disease model. We prove that a conjecture made in [73, 26, 17] about the infected coexistence equilibrium holds for our simplified model. In particular, we show that the conditions under which infected coexistence is stable guarantee that all other equilibria are unstable and vice versa. In addition, we also show that under the simplifying assumptions, the qualitative behavior of the model with mass action disease transmission is identical to the model with frequency incidence disease transmission.

In the case of mass action disease transmission we show in [21] that, if the death rate due to disease is positive, then disease can reduce the total equilibrium density for each species in isolation [21]. This in turn affects competitive ability indirectly (apparent competition), and is another indication that in the presence of disease, the competitive outcome can change. We hypothesize that one of the driving forces behind the possible switch of competitive outcomes and the difficulty of analysis of the full model is death due to disease. This force may be magnified by differing rates of transmission between and within species. In our simplified mass action model there is negligible death due to disease and no significant difference between transmission rates. Analysis of this simplified model is tractable and we determine that the presence of disease does not change the competitive outcome of the disease free case.

4 PERSISTENCE OF DISEASE IN TWO COMPETING SPECIES

4.1 Introduction

A question often asked when analyzing models for population dynamics and/or disease spread is whether or not coexistence of multiple interacting species, or coexistence of host species along with a pathogen is possible, or whether a population will persist under certain scenarios. For some cases, this can be accomplished by analyzing the equilibria of a model and the conditions for stability of those equilibria. More generally, though, we can ask if the variables or particular subgroups of the variables of a model are bounded strictly away from zero so that even if exact equilibrial values are unknown, we can predict persistence of variables in the system with some certainty. Here, we determine conditions for the persistence of both the pathogen and the species represented in our model. The persistence of disease in multi-host systems is important because both invasivity of a pathogen, the ability to invade a new system, and endemicity of a pathogen, the ability to persist in a system, can depend upon variation in host composition and environment. Additionally, emerging diseases can play an important role in the success of invasive species and can facilitate either coexistence or competitive exclusion.

We consider the particular case of two competing species susceptible to a common generalist pathogen or parasite that is spread directly by mass action transmission. Persistence theory is useful in this case because the interior equilibria for the full model for competition and a directly transmitted pathogen is intractable. Hence, it is difficult to prove stability of any interior equilibria. We can, however, prove that particular components of the system are eventually bounded below by a number strictly greater than zero. Often, showing a population is strongly uniformly persistent involves showing that the boundary of the system, where at least one component is zero, is a repeller for the dynamical system modeling the population(s). A nice exposition of population persistence can

be found in [137]. Using this theory long term coexistence and/or pathogen persistence can be proved even if explicit formulae for equilibria are unavailable. In this chapter, we use persistence theory to obtain conditions under which a directly transmitted pathogen affecting two host species will always persist and under which both species will coexist.

The authors of [30] explore the acyclicity boundary flow approach to determining persistence in the context of dynamical systems. In [148] and [52], the Lyapunov method of determining persistence in addition to analysis of the boundary flow and acyclicity are analyzed. Thieme [139] proves several important theorems about persistence and applies the theory to an epidemic model, determining conditions for persistence of the host and the pathogen. The authors of [45] use persistence theory to analyze a model for HIV while in [46] the authors prove coexistence of vertically and horizontally transmitted pathogen strains using persistence theory. All of these papers focused on coexistence of competing species or persistence of disease in a one species model.

Han and Pugliese [61] examined a model similar to ours with competition between two species that share a common pathogen. They proved conditions under which both species and the pathogen persist. Their model has density-dependent birth terms and competition in the death terms. Our model, on the other hand, includes density-dependence and competition in the birth term while assuming a constant death rate.

4.2 Background

Let X be a metric space with metric d and let $X_1 \cup X_2 = X$, $X_1 \cap X_2 = \emptyset$. Let Φ be a continuous semiflow on X with $\Phi(t, x) = \Phi_t(x)$. Recall that $d(x, Y) = \inf_{y \in Y} d(x, y)$ where $x \in \mathbb{R}^n$ and $Y \subset \mathbb{R}^n$.

Definition 4.2.0.1 *A compact invariant set $M \subseteq Y \subseteq X$ is an **isolated** compact invariant set in Y if there exists an open subset $U \subseteq X$ such that there is no invariant set $\tilde{M}$*

with $M \subseteq \tilde{M} \subseteq U \cap Y$ except M itself. A neighborhood V of M is called an **isolating neighborhood** of M in X if every compact invariant set $K \subset V$ is a subset of M ; in this case, M is isolated.

Define

$$\Omega_2 = \bigcup_{x \in Y_2} \omega(x) \text{ with } Y_2 = \{x \in X_2 : \Phi_t(x) \in X_2, \forall t > 0\}. \quad (4.2.1)$$

If Ω_2 has a finite covering, $\Omega_2 \subseteq M = \cup_{k=1}^m M_k \subset Y$, then M is *isolated* in Y if the sets M_k are pairwise disjoint subsets which are isolated compact invariant sets in Y . Often, assumptions about an isolated covering are made to show a kind of “hyperbolicity” so that invariant sets aren’t accumulating on the boundary resulting in the possibility of cycles that begin on the interior but move arbitrarily close to the boundary with time [148]. In fact, hyperbolic equilibria are isolated [137].

Definition 4.2.0.2 A set $M \subset Y$ is **chained** in Y to a not necessarily different set $N \subset Y$ (denoted $M \mapsto N$) if there exists some $y \in Y$, $y \notin M \cup N$ and a full orbit through y in Y whose ω -limit set is contained in N and whose α -limit set is contained in M .

In this chapter, we will use the idea of chained sets in the context of equilibria for a system of ordinary differential equations (ODEs) in Y . In that context, an equilibrium $x^* \in Y$ is chained to an equilibrium $y^* \in Y$ if there exists a solution trajectory $x(t)$ defined for all $t \in \mathbb{R}$ with all its values in Y such that $x(t) \rightarrow x^*$ as $t \rightarrow -\infty$ and $x(t) \rightarrow y^*$ as $t \rightarrow \infty$ and there is some t such that $x(t) \neq y^*$, $x(t) \neq x^*$ [46].

Definition 4.2.0.3 A finite covering $M \subset Y$ with m elements is **cyclic** in Y if, after possible renumbering, $M_1 \mapsto M_2 \mapsto \dots \mapsto M_k \mapsto M_1$ for $k \in \{1, \dots, m\}$. The finite covering M is **acyclic** if it is not cyclic.

Definition 4.2.0.4 For $Y_2 \subset X_2$, Y_2 is called a **weak repeller** for X_1 if

$$\limsup_{t \rightarrow \infty} d(\Phi_t(x_1), Y_2) > 0, \forall x_1 \in X_1.$$

It is a **uniform weak repeller** if there exists $\epsilon > 0$ such that

$$\limsup_{t \rightarrow \infty} d(\Phi_t(x_1), Y_2) > \epsilon, \forall x_1 \in X_1.$$

One practical way to test whether or not a set Y_2 is a weak repeller of X_1 is to examine its stable manifold, $W^s(Y_2)$; if $W^s(Y_2) \cap X_1 = \emptyset$ then Y_2 is a weak repeller [45, 52, 127]. Alternatively, a set Y_2 is a weak repeller for X_1 if there is no $x \in X_1$ such that $\omega(x) \subset Y_2$ [52]. In the context of population dynamics and disease, in general, if the per-capita growth rate of the applicable variable linearized around Y_2 with initial conditions in X_1 is positive, then Y_2 is a weak repeller [31].

Definition 4.2.0.5 Y_2 is a **strong repeller** for X_1 if

$$\liminf_{t \rightarrow \infty} d(\Phi_t(x_1), Y_2) > 0, \forall x_1 \in X_1$$

and is a **uniform strong repeller** if there exists $\epsilon > 0$ such that

$$\liminf_{t \rightarrow \infty} d(\Phi_t(x_1), Y_2) > \epsilon, \forall x_1 \in X_1.$$

If X_2 , or the boundary with respect to a particular variable or variables, is a uniform strong repeller for X_1 as defined appropriately, then the variable (or variables) are said to be **uniformly strongly persistent**. Thieme [139] uses the following two theorems to prove strong uniform persistence under certain conditions.

Theorem 4.2.0.2 (Theorem 1.3 [139]): Let X be a locally compact metric space with metric d and let X be the union of two disjoint sets X_1 and X_2 with X_2 compact. Let Φ be a continuous semiflow on X_1 . Then if X_2 is a uniform weak repeller for X_1 it is also a uniform strong repeller for X_1 .

Theorem 4.2.0.3 (Theorem 4.4 [139]): Let X be a locally compact metric space. Let X_1 be an open set that is forward invariant under the continuous semiflow Φ on X . Assume that Ω_2 as defined in equation (4.2.1) has an isolated acyclic covering $M = \cup_{k=1}^m M_k$ with each M_k a weak repeller for X_1 . Then X_2 is a uniform weak repeller for X_1 .

The following theorem is used to show that a set is a uniform strong repeller.

Theorem 4.2.0.4 (*Theorem 4.5 [139]*): *Let X be locally compact and let X_1 be forward invariant under the continuous semiflow Φ on X and X_2 be compact in X . Assume that Ω_2 as defined in (4.2.1) has an acyclic isolated covering $M = \cup_{k=1}^m M_k$ with each M_k a weak repeller for X_1 . Then X_2 is a uniform strong repeller for X_1 .*

Proof. By Theorem 4.2.0.3, we know that X_2 is a uniform weak repeller for X_1 . Hence by Theorem 4.2.0.2, X_2 is a uniform strong repeller for X_1 . ■

The following theorem is used (by way of contradiction) to show a set is a uniform strong repeller when the assumptions of Theorem 4.2.0.4 are not met.

Theorem 4.2.0.5 (*Proposition 4.3 [139]*): *Let X be locally compact, X_2 compact in X , and X_1 forward invariant as in Theorem 4.2.0.4. Let $\{x_n\}$ be a sequence of elements in X_1 with $\limsup_{t \rightarrow \infty} d(\Phi_t(x_n), X_2) \rightarrow 0, n \rightarrow \infty$. Let $M = \cup_{k=1}^m M_k$ be an isolated covering of Ω_2 such that $\omega(x_n) \not\subseteq M_k$ for all n, k . Then M is cyclic.*

4.3 Classic Example

Consider the three species Lotka-Volterra competition model

$$\frac{dx_1}{dt} = x_1 f_1(x_1, x_2, x_3) \quad (4.3.1)$$

$$\frac{dx_2}{dt} = x_2 f_2(x_1, x_2, x_3) \quad (4.3.2)$$

$$\frac{dx_3}{dt} = x_3 f_3(x_1, x_2, x_3) \quad (4.3.3)$$

with $f_i \in C^1$. We assume that each species alone exhibits logistic type growth so that $\frac{\partial f_i}{\partial x_j} < 0$ for $i \neq j$ and there exists a carrying capacity, K_i , such that when $x_i = K_i$ and

$x_j = 0$ for $i \neq j$ then $f_i = 0$ and $\frac{\partial f_i}{\partial x_i} < 0$. This model makes ecological and mathematical sense on the domain $X = \{(x_1, x_2, x_3) : 0 \leq x_i \leq K_i, i = 1, 2, 3\}$.

Let $X_2 = \{(x_1, x_2, x_3) | x_1 = 0 \text{ or } x_2 = 0 \text{ or } x_3 = 0\}$ and let $X_1 = X \setminus X_2$. The boundary, X_2 , is forward invariant with respect to the flow, as is X_1 . We assume that x_1 out-competes x_3 , x_3 out-competes x_2 , and $f_3(x_1^*, x_2^*, 0) > 0$. Then, there are exactly five boundary equilibria in X_2 : $E_0 = (0, 0, 0)$, $E_1 = (K_1, 0, 0)$, $E_2 = (0, K_2, 0)$, $E_3 = (0, 0, K_3)$, and $E^* = (x_1^*, x_2^*, 0)$. Now suppose that all the equilibria are hyperbolic, hence isolated, i.e., one can find a neighborhood of each of the equilibria within which no other invariant set lies. The equilibrium E_0 is a weak repeller of X_1 since each species grows exponentially when close enough to zero. In the $x_1 - x_2$ plane, E^* is a global attractor. On the x_j line, E_j is an attractor for $j = 1, 2, 3$, in the $x_2 - x_3$ plane E_3 is an attractor and on the $x_1 - x_3$ plane E_1 is an attractor. So none of the boundary equilibria are chained to themselves. Since E_0 is a universal repeller there is no cycle containing E_0 . Since E^* is the global attractor in the $x_1 - x_2$ plane and both E_1 and E_2 are unstable, there is no cycle in the $x_1 - x_2$ plane nor is there a cycle containing the equilibria on the $x_1 - x_2$ plane. Hence, $M = \{E_0\} \cup \{E_1\} \cup \{E_2\} \cup \{E_3\} \cup \{E^*\}$ is acyclic.

The per-capita growth rate of x_3 near E^* , $f_3(E^*)$ is positive, hence E^* is a weak repeller for X_1 . Near E_1 , x_2 will have a positive per-capita growth rate (by global stability of E^* in $x_1 - x_2$ plane) and near E_2 , x_3 will have a positive per-capita growth rate since x_3 out-competes x_2 , so both E_1 and E_2 are weak repellers of X_1 . Near E_3 , we know that x_1 has a positive per-capita growth rate since it out-competes x_3 . Hence, the boundary equilibria form an isolated acyclic covering for Ω_2 as defined in (4.2.1) and each of them is a weak repeller for X_1 . Therefore, X_2 is a uniform strong repeller for X_1 by Theorem 4.2.0.4. This means that all three species coexist and are strongly uniformly persistent.

Now, consider the case where E^* does not exist and where x_1 out-competes x_3 , x_3 out-competes x_2 , and x_2 out-competes x_1 . For example, consider the May-Leonard model

[97]

$$\begin{aligned}\frac{dx_1}{dt} &= x_1(1 - x_1 - \alpha x_2 - \beta x_3) \\ \frac{dx_2}{dt} &= x_2(1 - \beta x_1 - x_2 - \alpha x_3) \\ \frac{dx_3}{dt} &= x_3(1 - \alpha x_1 - \beta x_2 - x_3)\end{aligned}$$

where $0 < \beta < 1 < \alpha$ and $\alpha + \beta > 2$. The only equilibria in X_2 are E_0 , E_1 , E_2 , and E_3 , all of which are still weak repellers for X_1 and are still isolated. However they do **not** form an acyclic covering because there is a heteroclinic cycle $E_1 \mapsto E_2 \mapsto E_3 \mapsto E_1$. In this case, X_2 is **not** a uniform strong repeller for X_1 . In fact, $\limsup_{t \rightarrow \infty} x_i(t) = 1$ and $\liminf_{t \rightarrow \infty} x_i(t) = 0$. The interior equilibrium is unstable in this case, so for any strictly interior initial conditions x_0 , the orbit will cycle out toward the heteroclinic cycle connecting E_1 , E_2 , and E_3 (see Figures 4.1 and 4.2). In fact the ω -limit set, $\omega(x_0)$ is $E_1 \cup E_2 \cup E_3$, [131].

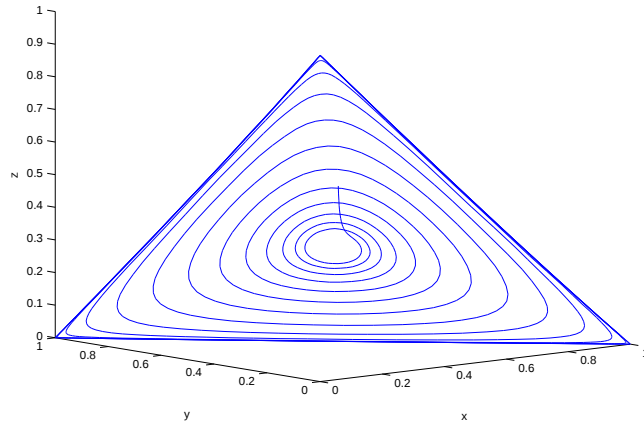


FIGURE 4.1: Orbit for May-Leonard competition with $\alpha = 0.7$, $\beta = 1.4$ and the x axis is x_1 , y -axis is x_2 and z -axis is x_3 .

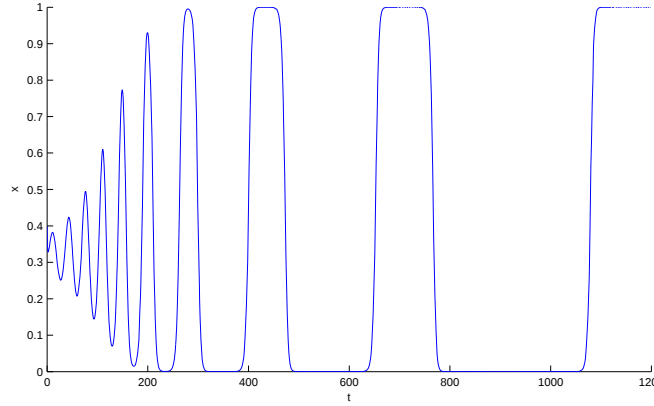


FIGURE 4.2: Time series for x_1 from Figure 4.1. Notice that the time spent very close to zero gets longer as time increases.

4.4 Competition and Disease Model with Mass Action Incidence

We will now consider the general model in Chapter 2 with Lotka-Volterra competition and mass action transmission of disease between two species in the context of strong uniform persistence. For ease of computation in the proofs, the model (3.3.4)-(3.3.7) can be re-written in terms of infected proportions i_k and total populations N_k , $k = 1, 2$, as

$$\frac{di_1}{dt} = \left(\beta_{11}(1 - i_1)N_1 - r_1 \left(1 - \frac{N_1}{K_{11}} - \frac{N_2}{K_{12}} \right) - (b_1 + \alpha_1) + \alpha_1 i_1 \right) i_1 + \beta_{12}(1 - i_1)i_2 N_2 \quad (4.4.1)$$

$$\frac{di_2}{dt} = \left(\beta_{22}(1 - i_2)N_2 - r_2 \left(1 - \frac{N_2}{K_{22}} - \frac{N_1}{K_{21}} \right) - (b_2 + \alpha_2) + \alpha_2 i_2 \right) i_2 + \beta_{21}(1 - i_2)i_1 N_1 \quad (4.4.2)$$

$$\frac{dN_1}{dt} = \left(r_1 \left(1 - \frac{N_1}{K_{11}} - \frac{N_2}{K_{12}} \right) - \alpha_1 i_1 \right) N_1 \quad (4.4.3)$$

$$\frac{dN_2}{dt} = \left(r_2 \left(1 - \frac{N_2}{K_{22}} - \frac{N_1}{K_{21}} \right) - \alpha_2 i_2 \right) N_2. \quad (4.4.4)$$

where $i_k = I_k/N_k$ for $k = 1, 2$. This system is well defined and ecologically relevant on the space $X = \{(i_1, N_1, i_2, N_2) : 0 \leq i_l \leq 1, 0 \leq N_l \leq K_l, l = 1, 2\}$.

When $i_1, i_2 = 0$, equations (4.4.3)-(4.4.4) reduce to the two species Lotka-Volterra competition model. The disease free equilibria are $E_0 = (0, 0, 0, 0)$, $E_1 = (0, K_{11}, 0, 0)$, $E_2 = (0, 0, 0, K_{22})$, and $E_3 = (0, K_1^*, 0, K_2^*)$ where $K_{ij} = r_i \theta_{ij}/a_i$ and K_i^* are defined in equation (3.2.8) as $K_1^* = \frac{K_{11}K_{12}}{K_{12} + K_{11}(\xi_1/\xi_2)}$, $K_2^* = \frac{\xi_1}{\xi_2}K_1^*$. Stability of the resulting disease free equilibria can be determined by the parameters $\xi_1 = 1/K_{11} - 1/K_{21}$ and $\xi_2 = 1/K_{22} - 1/K_{12}$ as defined in (3.2.9) and seen in Section 3.4, and by $\mathcal{R}_0^1$, $\mathcal{R}_0^2$, and $\mathcal{R}_0^C$ as in equations (3.4.13), (3.4.14), and (3.4.3). The sign of ξ_1 is determined directly by the per-capita growth rate of species 2 near (linearized around) the equilibrium E_1 and the sign of ξ_2 is determined by the per-capita growth rate of species 1 linearized around the equilibrium E_2 .

We re-frame the conditions for stability of the infected one host equilibria in terms of the proportions model (4.4.1)-(4.4.4). The infected one host equilibrium for species 2 is $E_5 = (Q_1^*, 0, i_2^*, N_2^*)$ where Q_1^* is the smallest root (only root in the interval $(0, 1)$) of

$$\alpha_1 Z^2 - \left(\beta_{12} \left(N_2^* - \frac{\Gamma_2}{\beta_{22}} \right) + r_1 \left(1 - \frac{N_2^*}{K_{12}} \right) + \Gamma_1 \right) Z + \beta_{12} \left(N_2^* - \frac{\Gamma_2}{\beta_{22}} \right) = 0, \quad (4.4.5)$$

$N_2^* = K_{22}(1 - \frac{\alpha_2 i_2^*}{r_2})$, and i_2^* is the smallest root (only root in the interval $(0, 1)$) of

$$\frac{\alpha_2}{r_2} Z^2 - (1 + \frac{\alpha_2}{r_2}) Z + \frac{\mathcal{R}_0^2 - 1}{\mathcal{R}_0^2} = 0. \quad (4.4.6)$$

Because competition affects only the birth rates in our model, equations (4.4.1)-(4.4.2), (4.4.5), and (4.4.6) are different from those in [61] for which competition affects the death rate only. Equations (4.4.1)-(4.4.2) replace the terms $-(b_i - a_i r_i N_i/K_i)$ in [61] with $-r_i(1 - N_i/K_{ii} - N_j/K_{ij})$ for $i \neq j$. Equation (4.4.5) adds the term, not present in the Han-Pugliese model [61], $r_1(1 - N_2^*/K_{12})$ to the Z coefficient. Finally, equation (4.4.6) differs by adding the term α_2/r_2 to the Z coefficient. We note that the equilibrium $E_5 = (Q_1^*, 0, i_2^*, N_2^*)$ corresponds to E_5 in (3.4.29) so $i_2^* N_2^* = I_2^* = \hat{I}_2^5$ (see Lemma 4.4.0.2).

The Jacobian of the system at equilibrium $E_5 = (Q_1^*, 0, i_2^*, N_2^*)$ is

$$\mathcal{J}(E_5) = \begin{bmatrix} A & B \\ C & D \end{bmatrix} \quad (4.4.7)$$

where

$$B = \begin{bmatrix} \beta_{12}(1 - Q_1^*)N_2^* & \frac{r_1}{K_{12}}Q_1^* + \beta_{12}(1 - Q_1^*)i_2^* \\ 0 & 0 \end{bmatrix}, \quad (4.4.8)$$

$$C = \begin{bmatrix} 0 & \frac{r_2}{K_{21}}i_2^* + \beta_{21}(1 - i_2^*)Q_1^* \\ 0 & \frac{-r_2}{K_{21}}N_2^* \end{bmatrix}, \quad (4.4.9)$$

$$A = \begin{bmatrix} -r_1(1 - \frac{N_2^*}{K_{12}}) - \Gamma_1 + 2\alpha_1Q_1^* - \beta_{12}i_2^*N_2^* & \beta_{11}(1 - Q_1^*)Q_1^* + \frac{r_1}{K_{11}}Q_1^* \\ 0 & r_1(1 - \frac{N_2^*}{K_{12}}) - \alpha_1Q_1^* \end{bmatrix}, \quad (4.4.10)$$

and where

$$D = \begin{bmatrix} \beta_{22}(1 - 2i_2^*)N_2^* - r_2(1 - \frac{N_2^*}{K_{22}}) - \Gamma_2 + 2\alpha_1i_2^* & \beta_{22}(1 - i_2^*)i_2^* + \frac{r_2}{K_{22}}i_2^* \\ -\alpha_2N_2^* & r_2(1 - \frac{N_2^*}{K_{22}}) - \alpha_2i_2^* - \frac{r_2}{K_{22}}N_2^* \end{bmatrix}. \quad (4.4.11)$$

The eigenvalues of the Jacobian of (4.4.1)-(4.4.4) evaluated at E_5 are the same as those for the matrices A and D . The eigenvalues of D are negative if $\mathcal{R}_0^2 > 1$ since it is the same as the Jacobian for species 2 alone with the pathogen. The eigenvalues of A are $\lambda_1^2 = r_1(1 - N_2^*/K_{12}) - \alpha_1Q_1^*$ and $\lambda_2^2 = -\Gamma_1 + 2\alpha_1Q_1^* - \beta_{12}i_2^*N_2^* - r_1(1 - N_2^*/K_{12})$. Using the definition of Q_1^* one can show that λ_2^2 is always negative (Lemma 4.4.0.3). Hence necessary and sufficient conditions for stability of E_5 are $\mathcal{R}_0^2 > 1$ and

$$\kappa_1 = \lambda_1^2 = r_1(1 - N_2^*/K_{12}) - \alpha_1Q_1^* < 0. \quad (4.4.12)$$

This condition guarantees that the per capita growth rate of species 1 at E_5 is negative so species 1 cannot “invade” species 2 at equilibrium.

Lemma 4.4.0.2 *The equilibrium E_5 corresponds to the one-host infected equilibrium for species 2 in the non-proportions model (3.3.4)-(3.3.7), i.e. $i_2^*N_2^* = I_2^* = \hat{I}_2^5$.*

Proof. First,

$$i_2^* = \frac{r_2}{\alpha_2} \frac{1}{2} \left(1 + \frac{\alpha_2}{r_2} - \sqrt{\left(1 + \frac{\alpha_2}{r_2} \right)^2 - 4 \frac{\alpha_2}{r_2} \left(\frac{\mathcal{R}_0^2 - 1}{\mathcal{R}_0^2} \right)} \right)$$

and

$$N_2^* = K_{22} \left(1 - \frac{\alpha_2 i_2^*}{r_2} \right) = \frac{K_{22}}{2} \left(1 - \frac{\alpha_2}{r_2} + \sqrt{\left(1 + \frac{\alpha_2}{r_2} \right)^2 - 4 \frac{\alpha_2}{r_2} \left(\frac{\mathcal{R}_0^2 - 1}{\mathcal{R}_0^2} \right)} \right).$$

Let $G = \left(1 + \frac{\alpha_2}{r_2} \right)^2 - 4 \frac{\alpha_2}{r_2} \left(\frac{\mathcal{R}_0^2 - 1}{\mathcal{R}_0^2} \right)$. Then,

$$N_2^* i_2^* = \frac{K_{22}}{2} \left(1 - \frac{\alpha_2}{r_2} + \sqrt{G} \right) \frac{r_2}{\alpha_2} \frac{1}{2} \left(1 + \frac{\alpha_2}{r_2} - \sqrt{G} \right) \quad (4.4.13)$$

$$= \frac{K_{22}}{4} \left(\frac{r_2}{\alpha_2} - \frac{\alpha_2}{r_2} + 2\sqrt{G} - \frac{r_2}{\alpha_2} \left(\left(1 + \frac{\alpha_2}{r_2} \right)^2 - 4 \frac{\alpha_2}{r_2} \left(\frac{\mathcal{R}_0^2 - 1}{\mathcal{R}_0^2} \right) \right) \right) \quad (4.4.14)$$

$$= \frac{K_{22}}{4} \left(4 \left(\frac{\mathcal{R}_0^2 - 1}{\mathcal{R}_0^2} \right) - 2 - \frac{2\alpha_2}{r_2} + 2\sqrt{G} \right) \quad (4.4.15)$$

$$= \frac{K_{22}}{2} \left(1 - \frac{\alpha_2}{r_2} - \frac{2}{\mathcal{R}_0^2} + \sqrt{G} \right) \quad (4.4.16)$$

and using that $I_2^* = \hat{I}_2^5 = \frac{I_5^*}{\beta_{22}}$ with I_5^* the largest root of the quadratic polynomial

$$P_5(Z) = Z^2 + 2\Gamma_2 \left(1 - \frac{\mathcal{R}_0^2 \lambda_2}{2} \right) Z + \Gamma_2^2 (1 - \mathcal{R}_0^2) \text{ with } \lambda_2 := \frac{r_2 - \alpha_2}{r_2},$$

$$I_2^* = \frac{-\Gamma_2}{\beta_{22}} - \frac{\Gamma_2}{\beta_{22}} \frac{\mathcal{R}_0^2}{2} \left(\frac{\alpha_2 - r_2}{r_2} \right) \quad (4.4.17)$$

$$+ \frac{1}{2\beta_{22}} \sqrt{4\Gamma_2^2 (\mathcal{R}_0^2)^2 \left(\frac{\alpha_2 - r_2}{r_2} \right) + 4\Gamma_2^2 \frac{(\mathcal{R}_0^2)^2}{4} \left(\frac{\alpha_2 - r_2}{r_2} \right)^2 + 4\Gamma_2^2 \mathcal{R}_0^2} \quad (4.4.18)$$

$$= \frac{K_{22}}{2} \left(1 - \frac{\alpha_2}{r_2} - \frac{2}{\mathcal{R}_0^2} + \sqrt{\left(1 - \frac{\alpha_2}{r_2} \right)^2 + \frac{4\alpha_2}{\mathcal{R}_0^2 r_2}} \right). \quad (4.4.19)$$

Since $\sqrt{\left(1 - \frac{\alpha_2}{r_2} \right)^2 + \frac{4\alpha_2}{\mathcal{R}_0^2 r_2}} = \sqrt{G}$, we have that $I_2^* = i_2^* N_2^*$. ■

Lemma 4.4.0.3 $\lambda_2^2 = -\Gamma_1 + 2\alpha_1 Q_1^* - \beta_{12} i_2^* N_2^* - r_1 (1 - N_2^*/K_{12})$ is always negative under the assumptions of model (4.4.1)-(4.4.4).

Proof. Using the definitions of Q_1^* , we know

$$\begin{aligned}
& \lambda_2^2 < 0 \\
& \Leftrightarrow -\Gamma_1 + 2\alpha_1 Q_1^* - \beta_{12} i_2^* N_2^* - r_1(1 - N_2^*/K_{12}) < 0 \\
& \Leftrightarrow 2\alpha_1 Q_1^* < \beta_{12} I_2^* + r_1(1 - N_2^*/K_{12}) + \Gamma_1 \\
& \Leftrightarrow \Gamma_1 + r_1(1 - N_2^*/K_{12}) + \beta_{12}(N_2^* - \Gamma_2/\beta_{22}) - \sqrt{B^2 - 4AC} < \beta_{12} I_2^* + r_1(1 - N_2^*/K_{12}) + \Gamma_1 \\
& \Leftrightarrow -\sqrt{B^2 - 4AC} < 0
\end{aligned}$$

where $A = \alpha_1$, $B = \beta_{12} \left(N_2^* - \frac{\Gamma_2}{\beta_{22}} \right) + r_1 \left(1 - \frac{N_2^*}{K_{12}} \right) + \Gamma_1$, and $C = \beta_{12} \left(N_2^* - \frac{\Gamma_2}{\beta_{22}} \right)$ and where $I_2^* = i_2^* N_2^* = N_2^* - \Gamma_2/\beta_{22}$. Note that $B^2 - 4AC > 0$ is easily shown with algebra.

■

Similarly, the infected one host equilibrium for species 1, $E_4 = (i_1^*, N_1^*, Q_2^*, 0)$ corresponding to E_4 in (3.4.15) is stable when $\mathcal{R}_0^1 > 1$ and a condition analogous to (4.4.12) holds, i.e.,

$$\kappa_2 = \lambda_1^1 = r_2(1 - N_1^*/K_{21}) - \alpha_2 Q_2^* < 0. \quad (4.4.20)$$

This condition guarantees that the per capita growth rate of species 2 at E_4 is negative so species 2 is cannot “invade” species 1 at equilibrium.

4.5 Strong Uniform Persistence of the Hosts and Pathogen

First we show that for this model, at least one of the species will survive, i.e. not go extinct, for all nonnegative parameters.

Theorem 4.5.0.6 *For system (4.4.1)-(4.4.4) with $N_1(0) > 0$ and $N_2(0) > 0$, at least one of N_1 or N_2 is uniformly strongly persistent, i.e. there exists $\epsilon > 0$ such that for any solution $x(t) = (i_1(t), N_1(t), i_2(t), N_2(t))$ of (4.4.1)-(4.4.4), $\liminf_{t \rightarrow \infty} \max\{N_1(t), N_2(t)\} > \epsilon$.*

Parameter	Description
ξ_1	measure of intra- versus inter-specific effects exerted by species 1
ξ_2	measure of intra- versus inter-specific effects exerted by species 2
κ_1	per capita growth rate of species 1 at species 2 infected 1-host equilibrium
κ_2	per capita growth rate of species 2 at species 1 infected 1-host equilibrium
$\mathcal{R}_0^1$	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

TABLE 4.1: Summary of important parameters and their ecological relevance.

ξ_1	ξ_2	$\mathcal{R}_0^1$	κ_2	$\mathcal{R}_0^2$	κ_1	$\mathcal{R}_0^C$	Equilibrium
−	+	< 1					$(0, N_1^*, 0, 0)$
+	−			< 1			$(0, 0, 0, N_2^*)$
+	+					< 1	$(0, N_1^*, 0, N_2^*)$
−	+	> 1	−				$(i_1^*, N_1^*, Q_2^*, 0)$
+	−			> 1	−		$(Q_1^*, 0, N_2^*, i_2^*)$

TABLE 4.2: Conditions for stability of the disease-free and one-host infected equilibria. The values listed in the Equilibrium column are the non-zero variables at equilibrium. Variables not listed are zero.

Proof. Define $X_2 = \{(i_1, N_1, i_2, N_2) : 0 \leq i_l \leq 1, N_l = 0, l = 1, 2\}$ and let $X_1 = X \setminus X_2$. Then both X_1 and X_2 are forward invariant with respect to the semiflow Φ induced by (4.4.1)-(4.4.4). Also, Ω_2 is defined in equation (4.2.1) and $M = \{(0, 0, 0, 0)\} = E_0$ is a finite covering for Ω_2 and E_0 is trivially isolated in X and acyclic in X_2 . It remains to show that E_0 is a weak repeller of X_1 . We consider the flow in X_1 near E_0 and assume that i_1, N_1, i_2 , and N_2 are close enough to zero that quadratic terms can be neglected, i.e. we linearize the flow around E_0 . Then,

$$\begin{aligned} \frac{dN_1}{dt} &= r_1 N_1 \\ \frac{dN_2}{dt} &= r_2 N_2 \end{aligned}$$

so that either N_1 or N_2 or both (depending on initial conditions) are growing exponentially when close enough to E_0 , hence E_0 is a weak repeller of X_1 . Now, since X_2 is compact in X , by Theorem 4.2.0.4 we know that X_2 is a uniform strong repeller for X_1 , which implies at least one of N_1 or N_2 is strongly uniformly persistent. ■

The next theorem gives conditions under which species 1 will persist uniformly strongly in the system. A similar theorem holds for species 2 with the indices switched.

Theorem 4.5.0.7 *If $\xi_2 > 0$ and either (1) $\mathcal{R}_0^2 \leq 1$ or (2) $\mathcal{R}_0^2 > 1$ and $\kappa_1 > 0$ (as defined in (4.4.12)), then N_1 persists uniformly strongly, i.e. there exists $\epsilon > 0$ such that $\liminf_{t \rightarrow \infty} N_1(t) > \epsilon$ with initial conditions $N_1(0) > 0$.*

Proof. Define $X_2 = \{(i_1, N_1, i_2, N_2) : 0 \leq i_l \leq 1, 0 \leq N_2 \leq K_{22}, N_1 = 0, l = 1, 2\}$ and let $X_1 = X \setminus X_2$. X_2 is compact in X and X_1 is forward invariant. Note that if initial conditions for N_1 (or N_2) are positive then the solution to equations (4.4.3)-(4.4.4) for N_1 (or N_2), respectively, will be positive for all time. Consider the following two cases:

Case 1: Let $\xi_2 > 0$ and $\mathcal{R}_0^2 \leq 1$. Then, the solutions that start in X_2 and remain in X_2 will converge to one of E_0 or $E_2 = (0, 0, 0, K_2)$ (in this case, $E_5 = (Q_1^*, 0, i_2^*, N_2^*)$ is not feasible). For $X_2 \cap \{N_2 = 0\}$, the solution $x(t)$ tends to E_0 , but for $X_2 \cap \{N_2 > 0\}$,

$x(t)$ converges to E_2 as $t \rightarrow \infty$. Because of this, neither E_0 nor E_2 is chained to itself, i.e. there is no $y \in X_2$, $y \neq E_0$ (or E_2) such that $\omega(y)$ is E_0 (or E_2) and $\alpha(y)$ is E_0 (or E_2). Also, E_0 and E_2 are not chained to each other in a cyclic way because this would require a $y \in X_2$, $y \neq E_0, y \neq E_2$ with $\omega(y) = E_0$ and $\alpha(y) = E_2$, which is clearly not possible. So, $M = \{E_0\} \cup \{E_2\}$ is an acyclic covering for Ω_2 as defined in equation (4.2.1).

We will now show that E_0 and E_2 are weak repellers for X_1 . By the same argument as in Theorem 4.5.0.6, E_0 is a weak repeller for X_1 . If we linearize the flow around E_2 assuming $N_1(0) > 0$, then

$$\frac{dN_1}{dt} = r_1 \left(1 - \frac{K_{22}}{K_{12}} \right) N_1. \quad (4.5.1)$$

Since $\xi_2 > 0$, then $K_{12} > K_{22}$ and the right hand side of equation (4.5.1) is positive. Hence, E_2 is also a weak repeller for X_1 . Also, both E_0 and E_2 are isolated since the growth rate of N_1 is positive near both of them in X_1 and since E_0 is a repeller and E_2 an attractor in X_2 . Hence, by Theorem 4.2.0.4, X_2 is a uniform strong repeller for X_1 .

Case 2: Let $\xi_2 > 0$, $\mathcal{R}_0^2 > 1$ and $\kappa_1 > 0$. Solutions that start in X_2 and remain in X_2 for all time will converge to one of E_0 , E_2 , and E_5 (which is now feasible and stable). The same analysis for E_0 holds as in Case 1. For $X_2 \cap \{i_2 = i_1 = 0, N_2 > 0\}$, $x(t)$ converges to E_2 and for $X_2 \cap \{i_2 > 0 \text{ or } i_1 > 0, N_2 > 0\}$, $x(t)$ converges to E_5 as $t \rightarrow \infty$ since $\mathcal{R}_0^2 > 1$. Thus, neither E_0 , E_2 , nor E_5 can be chained to itself in X_2 . They are also not chained to each other in a cyclic way because this would require a $y \in X_2$ with $y \neq E_0, E_2$ (or E_5) and $\omega(y) = E_0$, or would require $y \in X_2$ with $y \neq E_2, E_5$ and $\alpha(y) = E_5$ while $\omega(y) = E_2$, neither of which is not possible. So, $M = \{E_0\} \cup \{E_2\} \cup \{E_5\}$ is an acyclic covering for Ω_2 .

By similar arguments as in Case 1, both E_0 and E_2 are weak repellers for X_1 . To show E_5 is a weak repeller, linearize the flow around E_5 and consider initial conditions in X_1 to get

$$\frac{dN_1}{dt} = (r_1 \left(1 - \frac{N_2^*}{K_{12}} \right) - \alpha_1 Q_1^*) N_1 \quad (4.5.2)$$

However, $\kappa_1 > 0$ holding implies that the right hand side of equation (4.5.2) is positive, hence E_5 is a weak repeller for X_1 as well. Also, E_0 , E_2 , and E_5 are isolated since any flow close enough to one of them will either be moving away or toward it in at least one component. Therefore, by Theorem 4.2.0.4, X_2 is a uniform strong repeller for X_1 . ■

A similar theorem holds for species 2 with the indices switched.

Theorem 4.5.0.8 *If $\xi_1 > 0$ and either (1) $\mathcal{R}_0^1 \leq 1$ or (2) $\mathcal{R}_0^1 > 1$ and $\kappa_2 > 0$ (as defined in (4.4.20)), then N_2 persists uniformly strongly, i.e. there exists $\epsilon > 0$ such that $\liminf_{t \rightarrow \infty} N_2(t) > \epsilon$ with initial conditions $N_2(0) > 0$.*

Proof. The proof is analogous to Theorem 4.5.0.7. ■

Now that we have shown that at least one species will persist uniformly strongly and found conditions under which a particular species is strongly uniformly persistent, we will prove that the disease persists uniformly strongly under certain conditions. The following proofs use similar methods as those in Proposition 1.2 of [139] and Theorem 4.7 in [61].

Theorem 4.5.0.9 *If $\xi_2 < 0$, $\xi_1 > 0$, and $\mathcal{R}_0^2 > 1$ then for initial conditions $N_1(0), N_2(0) > 0$ and $i_1(0) > 0$ or $i_2(0) > 0$ the disease persists uniformly strongly, i.e. there exists $\epsilon > 0$ such that $\liminf_{t \rightarrow \infty} \min\{i_1(t), i_2(t)\} > \epsilon$.*

Proof. Let $X_2 = \{(i_1, N_1, i_2, N_2) : i_1 = 0 \text{ or } i_2 = 0, 0 \leq N_l \leq K_l, l = 1, 2\}$ and let $X_1 = X \setminus X_2$. Also, let $\tilde{X}_1 = \{(i_1, N_1, i_2, N_2) : 0 < i_l \leq 1, 0 < N_l \leq K_l, l = 1, 2\}$. Notice that both X_1 and $\tilde{X}_1$ are forward invariant. Three equilibria, E_0 , E_1 , and E_2 , form a covering for Ω_2 (defined as usual). As before, these equilibria are not chained to themselves or each other in a cyclic way in X_2 , so $M = \{E_0\} \cup \{E_1\} \cup \{E_2\}$ is in fact an acyclic covering for Ω_2 . E_0 is isolated and a weak repeller for $\tilde{X}_1$. For $X_2 \cap \{N_2 = 0, N_1 > 0; i_1 = i_2 = 0\}$, the solution $x(t)$ tends toward E_1 while for $X_2 \cap \{N_2 > 0, N_1 \geq 0; i_1 = i_2 = 0\}$, $x(t)$ tends

toward E_2 . When the flow is linearized around E_1 , N_2 grows exponentially since $\xi_1 > 0$, so E_1 is also an isolated weak repeller for $\tilde{X}_1$. Next consider the flow of i_2 linearized around E_2 ,

$$\frac{di_2}{dt} = (\beta_{22}K_{22} - (b_2 + \alpha_2))i_2.$$

Since $\mathcal{R}_0^2 = \frac{\beta_{22}K_{22}}{b_2 + \alpha_2} > 1$ then i_2 is growing exponentially near E_2 and E_2 is isolated and a weak repeller for $\tilde{X}_1$. Notice that the conditions of Theorem 4.2.0.4 are not met by our assumptions since we want X_2 to repel $\tilde{X}_1$ and $X_2 \cup \tilde{X}_1 \neq X$, so other methods must be used. For the remainder of the proof, we first show that X_2 is a uniform weak repeller for $\tilde{X}_1$. We then use this to prove that X_2 is a uniform strong repeller for $\tilde{X}_1$ by way of contradiction.

First we show that X_2 is a uniform weak repeller for $\tilde{X}_1$ so that there exists an $0 < \tilde{\epsilon}$, chosen so that $\tilde{\epsilon} < \min(Q_1^*, Q_2^*, i_1^*, i_2^*)$, such that

$$\limsup_{t \rightarrow \infty} \min\{i_1(t), i_2(t)\} > \tilde{\epsilon} \quad (4.5.3)$$

for any solution $x(t)$ with initial conditions $N_1(0), N_2(0) > 0$ and $i_1(0) > 0$ or $i_2(0) > 0$. Assume X_2 is *not* a uniform weak repeller for $\tilde{X}_1$. Then there exists a sequence $x_n = (i_{1,n}, N_{1,n}, i_{2,n}, N_{2,n}) \in \tilde{X}_1$ such that $\limsup_{t \rightarrow \infty} d(\Phi_t(x_n), X_2) \rightarrow 0$ as $n \rightarrow \infty$. Since each of E_0 , E_1 , and E_2 is a weak repeller for $\tilde{X}_1$, then we know that $\omega(x_n) \not\subset M$. Then the assumptions of Theorem 4.2.0.5 are met and M must be cyclic. This is a contradiction, hence X_2 is a uniform weak repeller for $\tilde{X}_1$.

Now we will show that X_2 is a uniform strong repeller for $\tilde{X}_1$ by way of contradiction. Suppose that X_2 is *not* a uniform strong repeller for $\tilde{X}_1$. Then, there exists no $\epsilon > 0$ such that $\liminf_{t \rightarrow \infty} \min\{i_{1,j}(t), i_{2,j}(t)\} > \epsilon$ thus there exists a sequence of initial conditions, $x_j^0 = (i_{1,j}(0), N_{1,j}(0), i_{2,j}(0), N_{2,j}(0)) \in \tilde{X}_1$, and a sequence $0 < \epsilon_j < \tilde{\epsilon}$ such that

$$\liminf_{t \rightarrow \infty} \min\{i_{1,j}(t), i_{2,j}(t)\} < \epsilon_j \text{ for } j = 1, 2, \dots \quad (4.5.4)$$

where $\lim_{j \rightarrow \infty} \epsilon_j = 0$ and where $i_{1,j}(t), N_{1,j}(t), i_{2,j}(t)$, and $N_{2,j}(t)$ are solutions with initial values $x_j^0 \in \tilde{X}_1$. By equations (4.5.3) and (4.5.4), we can also find sequences of times

$0 < r_j < s_j < t_j$ with $\lim_{t \rightarrow \infty} r_j = \infty$ and

$$\lim_{j \rightarrow \infty} \min\{i_{1,j}(s_j), i_{2,j}(s_j)\} = 0 \quad (4.5.5)$$

$$\min\{i_{1,j}(r_j), i_{2,j}(r_j)\} = \min\{i_{1,j}(t_j), i_{2,j}(t_j)\} = \tilde{\epsilon} \quad (4.5.6)$$

$$\min\{i_{1,j}(t), i_{2,j}(t)\} \leq \tilde{\epsilon} \text{ for } r_j \leq t \leq t_j \quad (4.5.7)$$

Also, r_j can be chosen large enough that

1. when $\mathcal{R}_0^1 \leq 1$ then $N_{2,j}(t) > \epsilon^* > 0$ for $t > r_j$ by Case (1) of Theorem 4.5.0.8 and
2. when $\mathcal{R}_0^1 > 1$ then $\max\{N_{1,j}(t), N_{2,j}(t)\} > \epsilon^* > 0$ for $t \geq r_j$ by Theorem 4.5.0.6.

After choosing a subsequence, the sequence $(i_{1,j}(r_j), N_{1,j}(r_j), i_{2,j}(r_j), N_{2,j}(r_j))$ is convergent in X by compactness of X . Let $x^{**}(0) = (i_{1,**}(0), N_{1,**}(0), i_{2,**}(0), N_{2,**}(0))$ be its limit as $j \rightarrow \infty$. Then by (4.5.6) we know that $\min\{i_{1,**}(0), i_{2,**}(0)\} = \tilde{\epsilon}$ so that $x^{**} \in X_1$.

There are now two more steps. First, show that $\{t_j - r_j\}$ is unbounded. Suppose not. Then, after choosing subsequences, $\{s_j - r_j\}$ is convergent and, by the semi-group property of the flow, $\lim_{j \rightarrow \infty} (s_j - r_j) = s^*$ and $\lim_{j \rightarrow \infty} (i_{1,j}(r_j + s^*), N_{1,j}(r_j + s^*), i_{2,j}(r_j + s^*), N_{2,j}(r_j + s^*)) = x^{**}(s^*)$ where $x^{**}(t)$ is the solution with initial value $x^{**}(0) \in X_1$. Since X_1 is forward invariant, $x^{**}(s^*) \in X_1$. We also can see that $\lim_{j \rightarrow \infty} (i_{1,j}(s_j), N_{1,j}(s_j), i_{2,j}(s_j), N_{2,j}(s_j)) = x^{**}(s^*)$, which implies that $x^{**}(s^*) \in X_2$ by (4.5.5) and the compactness of X_2 . This is a contradiction, hence $t_j - r_j$ is unbounded.

Second, assuming that X_2 is not a uniform strong repeller for $\tilde{X}_1$, if $x^{**}(0) \in \tilde{X}_1$ then, by (4.5.3) we know that

$$\limsup_{t \rightarrow \infty} \min\{i_{1,**}(t), i_{2,**}(t)\} > \tilde{\epsilon}. \quad (4.5.8)$$

If $x^{**}(0) \in X \setminus \tilde{X}_1$ then there are two cases. Case 1: If $\mathcal{R}_0^1 \leq 1$ we know $N_{2,j}(t) > \epsilon^*$ for $t \geq r_j$ so $N_{2,**}(0) \geq \epsilon^*$ and, by (4.5.6), $\min\{i_{1,**}(0), i_{2,**}(0)\} = \tilde{\epsilon}$. Then we must have $N_{1,**}(0) = 0$ so that $N_{1,**}(t) = 0$ and from analysis of the one-species infected

equilibrium in Section 4.4, we know that $\lim_{t \rightarrow \infty} i_{1,**}(t) = Q_1^*$ and $\lim_{t \rightarrow \infty} i_{2,**}(t) = i_2^*$ so that equation (4.5.8) holds for this case as well since $\tilde{\epsilon} < \min(Q_1^*, Q_2^*, i_1^*, i_2^*)$. Case 2: If $\mathcal{R}_0^1 > 1$ then $\max\{N_{1,j}(t), N_{2,j}(t)\} > \epsilon^*$ for $t \geq r_j$ and either $N_{1,**}(0) = 0$ and $N_{2,**}(0) \geq \epsilon^*$ or $N_{1,**}(0) \geq \epsilon^*$ and $N_{2,**}(0) = 0$. Similarly to Case 1 we can now show that equation (4.5.8) holds for Case 2 as well.

Now, since $\{t_j - r_j\}$ is unbounded, using a subsequence, we can assume that $\{t_j - r_j\}$ is increasing monotonically and that the $\lim_{j \rightarrow \infty} (t_j - r_j) = \infty$. Then, by (4.5.7) we have that for $k > j$, $\min\{i_{1,k}(r_k + r), i_{2,k}(r_k + r)\} \leq \epsilon^*$ for $0 \leq r \leq t_j - r_j$. Fix r and j and let $k \rightarrow \infty$ so that for $0 \leq r \leq t_j - r_j$, $\min\{i_{1,**}(r), i_{2,**}(r)\} = \lim_{k \rightarrow \infty} \min\{i_{1,k}(r_k + r), i_{2,k}(r_k + r)\} \leq \epsilon^*$. Now, let $j \rightarrow \infty$ and $\lim_{j \rightarrow \infty} t_j - r_j = \infty$ so that the previous inequality holds for all $r \geq 0$. This contradicts (4.5.8), hence X_2 is a uniform strong repeller for $\tilde{X}_1$. ■

An analogous theorem holds for the indices exchanged on the relevant parameters.

Theorem 4.5.0.10 *If $\xi_1 < 0$, $\xi_2 > 0$, and $\mathcal{R}_0^1 > 1$ then for initial conditions $N_1(0), N_2(0) > 0$ and $i_1(0) > 0$ or $i_2(0) > 0$ the disease persists uniformly strongly in at least one of the species, i.e. there exists $\epsilon > 0$ such that $\liminf_{t \rightarrow \infty} \min\{i_1(t), i_2(t)\} > \epsilon$.*

Proof. The proof is the same as that for Theorem 4.5.0.9 with indices reversed. ■

Now we consider conditions under which the disease will persist uniformly strongly in the system (whether in one species or both species). Notice that if inter-species disease transmission is positive then it is not possible for both species to persist but only one species has disease present.

Theorem 4.5.0.11 *If $\xi_1 > 0$, $\xi_2 > 0$, and $\mathcal{R}_0^C > 1$ then disease persists uniformly strongly, i.e. there exists $\epsilon > 0$ such that $\liminf_{t \rightarrow \infty} \min\{i_1(t), i_2(t)\} > \epsilon$ for any solution $x(t)$ with $N_1(0), N_2(0) > 0$ and $i_1(0) > 0$ or $i_2(0) > 0$.*

Proof. Define $X_2 = \{(i_1, N_1, i_2, N_2) : i_1 = 0 \text{ or } i_2 = 0, 0 \leq N_l \leq K_l, l = 1, 2\}$, $X_1 = X \setminus X_2$, and let $\tilde{X}_1 = \{(i_1, N_1, i_2, N_2) : 0 < i_l \leq 1, 0 < N_l \leq K_l, l = 1, 2\}$. Both X_1 and $\tilde{X}_1$ are forward invariant with respect to the semiflow Φ . Let Ω_2 be defined as in (4.2.1). By analyzing the semiflow in X_2 we see that Ω_2 has a finite covering of four equilibria: $E_0 = (0, 0, 0, 0)$, $E_1 = (0, K_{11}, 0, 0)$, $E_2 = (0, 0, 0, K_{22})$, and $E_3 = (0, K_1^*, 0, K_2^*)$. None of these four equilibria are chained to themselves or to each other in a cyclic way because E_0 is unstable, E_1 and E_2 are unstable for initial conditions $X_2 \cap \{N_1, N_2 > 0; i_1 = i_2 = 0\}$, while E_3 is stable. Thus, $M = \{E_0\} \cup \{E_1\} \cup \{E_2\} \cup \{E_3\}$ forms an acyclic covering for Ω_2 .

We will now show that each of the equilibria in M is isolated and a weak repeller as well. As with the previous theorems, E_0 is a stable equilibrium with initial conditions in $X_2 \cap \{N_1, N_2 = 0\}$, but if initial conditions for N_1 or N_2 are positive then N_1 or N_2 will increase exponentially and E_0 is unstable, hence E_0 is isolated and a weak repeller for $\tilde{X}_1$.

E_1 is stable with initial conditions in $X_2 \cap \{N_2 = i_2 = i_1 = 0\}$, but, since $\xi_1 > 0$, with initial conditions in $X_2 \cap \{N_2 > 0, i_2 = i_1 = 0\}$ then E_1 is unstable. With initial conditions in $X_2 \cap \{N_2 = i_2 = 0, i_1 > 0\}$ then E_1 is stable if $\mathcal{R}_0^1 \leq 1$ and is unstable if $\mathcal{R}_0^1 > 1$. Finally, with initial conditions in $\tilde{X}_1$, E_1 is unstable since N_2 will grow exponentially. Thus, E_1 is both isolated and a weak repeller for $\tilde{X}_1$. Very similar analysis (with indices exchanged) will show that E_2 is also isolated and a weak repeller.

Near E_3 with initial conditions in $X_2 \cap \{i_1 = i_2 = 0\}$, E_3 is stable since $\xi_1, \xi_2 > 0$. With initial conditions in $X_2 \cap \{N_1 = 0 \text{ or } N_2 = 0\}$ then E_3 is not an attractor (unstable). With initial conditions in $\tilde{X}_1$, E_3 is also unstable since $\mathcal{R}_0^C > 1$ so that $i_1(t)$ or $i_2(t)$ grow(s) exponentially near E_3 . This can be seen by examining the flow of i_1 and i_2 linearized around E_3 ,

$$\frac{di_1}{dt} = (\beta_{11}K_1^* - (b_1 + \alpha_1))i_1 + \beta_{12}K_2^*i_2 \quad (4.5.9)$$

$$\frac{di_2}{dt} = (\beta_{22}K_2^* - (b_2 + \alpha_2))i_2 + \beta_{21}K_1^*i_1. \quad (4.5.10)$$

This system has strictly positive real eigenvalues when $\mathcal{R}_0^C > 1$ since the Jacobian of equations (4.4.1)-(4.4.2) from which $\mathcal{R}_0^C$ is derived has the same eigenvalues as the Jacobian matrix formed by (4.5.9)-(4.5.10). Hence the solution to the above system is growing exponentially near E_3 . Therefore, in all cases, E_3 is isolated and is a weak repeller for $\tilde{X}_1$.

Next we show that X_2 is a uniform weak repeller for $\tilde{X}_1$ so that there exists an $0 < \tilde{\epsilon} < \min(Q_1^*, Q_2^*, i_1^*, i_2^*)$ such that

$$\limsup_{t \rightarrow \infty} \min\{i_1(t), i_2(t)\} > \tilde{\epsilon} \quad (4.5.11)$$

for any solution $x(t)$ with initial conditions $N_1(0), N_2(0) > 0$ and $i_1(0) > 0$ or $i_2(0) > 0$. Assume X_2 is *not* a uniform weak repeller for $\tilde{X}_1$. Then there exists a sequence $x_n = (i_{1,n}, N_{1,n}, i_{2,n}, N_{2,n}) \in \tilde{X}_1$ such that $\limsup_{t \rightarrow \infty} d(\Phi_t(x_n), X_2) \rightarrow 0$ as $n \rightarrow \infty$. Since each of E_0, E_1, E_2 , and E_3 is a weak repeller for $\tilde{X}_1$, then we know that $\omega(x_n) \not\subset M$. Then the assumptions of Theorem 4.2.0.5 are met and M must be cyclic. This is a contradiction, hence X_2 is a uniform weak repeller for $\tilde{X}_1$.

Now we will show that X_2 is a uniform strong repeller for $\tilde{X}_1$ by way of contradiction. Suppose that X_2 is *not* a uniform strong repeller for $\tilde{X}_1$. Then, there exists no $\epsilon > 0$ such that $\liminf_{t \rightarrow \infty} \min\{i_{1,j}(t), i_{2,j}(t)\} > \epsilon$ thus there exists a sequence of initial conditions, $x_j^0 = (i_{1,j}(0), N_{1,j}(0), i_{2,j}(0), N_{2,j}(0)) \in \tilde{X}_1$ and a sequence $0 < \epsilon_j < \tilde{\epsilon}$ such that

$$\liminf_{t \rightarrow \infty} \min\{i_{1,j}(t), i_{2,j}(t)\} < \epsilon_j \text{ for } j = 1, 2, \dots \quad (4.5.12)$$

where $\lim_{j \rightarrow \infty} \epsilon_j = 0$ and where $i_{1,j}(t), N_{1,j}(t), i_{2,j}(t)$, and $N_{2,j}(t)$ are solutions with initial values $x_j^0 \in \tilde{X}_1$. By equations (4.5.11) and (4.5.12), we can also find sequences of times $0 < r_j < s_j < t_j$ with $\lim_{t \rightarrow \infty} r_j = \infty$ and

$$\lim_{j \rightarrow \infty} \min\{i_{1,j}(s_j), i_{2,j}(s_j)\} = 0 \quad (4.5.13)$$

$$\min\{i_{1,j}(r_j), i_{2,j}(r_j)\} = \min\{i_{1,j}(t_j), i_{2,j}(t_j)\} = \tilde{\epsilon} \quad (4.5.14)$$

$$\min\{i_{1,j}(t), i_{2,j}(t)\} \leq \tilde{\epsilon} \text{ for } r_j \leq t \leq t_j \quad (4.5.15)$$

Also, r_j can be chosen large enough that

1. when $\mathcal{R}_0^1 \leq 1$ then $N_{2,j}(t) > \epsilon^* > 0$ for $t > r_j$ by case (1) of Theorem 4.5.0.8,
2. when $\mathcal{R}_0^2 \leq 1$ then $N_{1,j}(t) > \epsilon^* > 0$ for $t > r_j$ by case (1) of Theorem 4.5.0.7, and
3. when $\mathcal{R}_0^1 > 1$ or $\mathcal{R}_0^2 > 1$ then $\max\{N_{1,j}(t), N_{2,j}(t)\} > \epsilon^* > 0$ for $t \geq r_j$ by Theorem 4.5.0.6.

After choosing a subsequence, the sequence $(i_{1,j}(r_j), N_{1,j}(r_j), i_{2,j}(r_j), N_{2,j}(r_j))$ is convergent in X by compactness of X . Let $x^{**}(0) = (i_{1,**}(0), N_{1,**}(0), i_{2,**}(0), N_{2,**}(0))$ be its limit as $j \rightarrow \infty$. Then by (4.5.14) we know that $\min\{i_{1,**}(0), i_{2,**}(0)\} = \tilde{\epsilon}$ so that $x^{**} \in X_1$.

There are now two more steps. First, show that $\{t_j - r_j\}$ is unbounded. Suppose not. Then, after choosing subsequences, $\{s_j - r_j\}$ is convergent and, by the semi-group property of the flow, $\lim_{j \rightarrow \infty} (s_j - r_j) = s^*$ and $\lim_{j \rightarrow \infty} (i_{1,j}(r_j + s^*), N_{1,j}(r_j + s^*), i_{2,j}(r_j + s^*), N_{2,j}(r_j + s^*)) = x^{**}(s^*)$ where $x^{**}(t)$ is the solution with initial value $x^{**}(0) \in X_1$. Since X_1 is forward invariant, $x^{**}(s^*) \in X_1$. We also can see that $\lim_{j \rightarrow \infty} (i_{1,j}(s_j), N_{1,j}(s_j), i_{2,j}(s_j), N_{2,j}(s_j)) = x^{**}(s^*)$, which implies that $x^{**}(s^*) \in X_2$ by (4.5.13) and the compactness of X_2 . This is a contradiction, hence $t_j - r_j$ is unbounded.

Second, assuming that X_2 is not a uniform strong repeller for $\tilde{X}_1$, if $x^{**}(0) \in \tilde{X}_1$ then, by (4.5.11) we know that

$$\limsup_{t \rightarrow \infty} \min\{i_{1,**}(t), i_{2,**}(t)\} > \tilde{\epsilon}. \quad (4.5.16)$$

If $x^{**}(0) \in X \setminus \tilde{X}_1$ then there are three cases. Case 1: If $\mathcal{R}_0^1 \leq 1$ we know $N_{2,j}(t) > \epsilon^*$ for $t \geq r_j$ so $N_{2,**}(0) \geq \epsilon^*$ and, by (4.5.14), $\min\{i_{1,**}(0), i_{2,**}(0)\} = \tilde{\epsilon}$. Then we must have $N_{1,**}(0) = 0$ so that $N_{1,**}(t) = 0$ and from analysis of the one-species infected equilibrium in Section 4.4, we know that $\lim_{t \rightarrow \infty} i_{1,**}(t) = Q_1^*$ and $\lim_{t \rightarrow \infty} i_{2,**}(t) = i_2^*$ so that equation (4.5.16) holds for this case as well. Case 2: If $\mathcal{R}_0^2 \leq 1$ we know $N_{1,j}(t) > \epsilon^*$ for $t \geq r_j$ so $N_{1,**}(0) \geq \epsilon^*$ and, by (4.5.14), $\min\{i_{1,**}(0), i_{2,**}(0)\} = \tilde{\epsilon}$. Then we must have $N_{2,**}(0) = 0$ so that $N_{2,**}(t) = 0$ and from analysis of the one-species infected equilibrium in Section 4.4, we know that $\lim_{t \rightarrow \infty} i_{2,**}(t) = Q_2^*$ and $\lim_{t \rightarrow \infty} i_{1,**}(t) = i_1^*$ so that equation (4.5.16)

holds for this case as well. Case 3: If $\mathcal{R}_0^1 > 1$ or $\mathcal{R}_0^2 > 1$ then $\max\{N_{1,j}(t), N_{2,j}(t)\} > \epsilon^*$ for $t \geq r_j$ and either $N_{1,**}(0) = 0$ and $N_{2,**}(0) \geq \epsilon^*$ or vice versa. Similarly to Cases 1 and 2 we can now show that equation (4.5.16) holds for Case 3 as well.

Now, since $\{t_j - r_j\}$ is unbounded, using a subsequence, we can assume that $\{t_j - r_j\}$ is increasing monotonically and that $\lim_{j \rightarrow \infty} (t_j - r_j) = \infty$. Then, by (4.5.15) we have that for $k > j$, $\min\{i_{1,k}(r_k + r), i_{2,k}(r_k + r)\} \leq \epsilon^*$. Fix r and j and let $k \rightarrow \infty$ so that for $0 \leq r \leq t_j - r_j$, $\min\{i_{1,**}(r), i_{2,**}(r)\} = \lim_{k \rightarrow \infty} \min\{i_{1,k}(r_k + r), i_{2,k}(r_k + r)\} \leq \epsilon^*$. Now, let $j \rightarrow \infty$ and $\lim_{j \rightarrow \infty} t_j - r_j = \infty$ so that the previous inequality holds for all $r \geq 0$. This contradicts (4.5.16), hence X_2 is a uniform strong repeller for $\tilde{X}_1$. ■

Theorem 4.5.0.12 *If $\xi_1 < 0$, $\xi_2 < 0$, $\mathcal{R}_0^1 > 1$, $\mathcal{R}_0^2 > 1$, and $\mathcal{R}_0^C > 1$ then disease persists uniformly strongly, i.e. there exists $\epsilon > 0$ such that $\liminf_{t \rightarrow \infty} \min\{i_1(t), i_2(t)\} > \epsilon$ for any solution $x(t)$ with $N_1(0), N_2(0) > 0$ and $i_1(0) > 0$ or $i_2(0) > 0$.*

Proof. The proof is similar to that of Theorem 4.5.0.11 except in the following aspects: First, that in $X_2 \cap \{i_1 = i_2 = 0\}$, E_3 is unstable and E_1 and E_2 are bistable, with stability determined by initial conditions. With initial conditions in $\tilde{X}_1$, near E_1 , i_1 has a positive growth rate since $\mathcal{R}_0^1 > 1$; near E_2 , i_2 grows since $\mathcal{R}_0^2 > 1$; and near E_3 , the same analysis holds as for Theorem 4.5.0.11. So, each of E_0 , E_1 , E_2 , and E_3 are weak repellers for $\tilde{X}_1$.

Second, if $x^{**}(0) \in X \setminus \tilde{X}_1$, there are two cases. By Theorem 4.5.0.6, we know that $\max\{N_{1,j}(t), N_{2,j}(t)\} > \epsilon^*$. Case 1: $N_{1,**}(0) = 0$ and $N_{2,**}(0) \geq \epsilon^*$ so that $\lim_{t \rightarrow \infty} i_{1,**}(t) = i_1^*$ and $\lim_{t \rightarrow \infty} i_{2,**}(t) = Q_2^*$ so that equation (4.5.16) holds for this theorem. Case 2: $N_{2,**}(0) = 0$ and $N_{1,**}(0) \geq \epsilon^*$ so that $\lim_{t \rightarrow \infty} i_{2,**}(t) = i_2^*$ and $\lim_{t \rightarrow \infty} i_{1,**}(t) = Q_1^*$ so that equation (4.5.16) holds. ■

Theorem 4.5.0.13 *Let $\xi_2 < 0$, $\mathcal{R}_0^2 > 1$, and $\kappa_1 > 0$. Let either (1) $\xi_1 > 0$ or (2) $\xi_1 < 0$ and $\mathcal{R}_0^1 > 1$. Then, species 1 persists uniformly strongly, i.e. there exists $\epsilon > 0$ such that $\liminf_{t \rightarrow \infty} N_1(t) > \epsilon$ with initial conditions $N_1(0), N_2(0) > 0$ and $i_1(0) > 0$ or $i_2(0) > 0$.*

Proof. Define $X_2 = \{(i_1, N_1, i_2, N_2) : 0 \leq i_l \leq 1, N_1 = 0, 0 \leq N_2 \leq K_{22}, l = 1, 2\}$, $X_1 = X \setminus X_2$, and let $\tilde{X}_1 = \{(i_1, N_1, i_2, N_2) : 0 < i_l \leq 1, 0 < N_l \leq K_{ll}, l = 1, 2\}$. Both X_1 and $\tilde{X}_1$ are forward invariant with respect to the semiflow Φ . Let Ω_2 be defined as in (4.2.1). By analyzing the semiflow in X_2 we see that Ω_2 has a finite covering of three equilibria: $E_0 = (0, 0, 0, 0)$, $E_2 = (0, 0, 0, K_{22})$, and $E_5 = (Q_1^*, 0, i_2^*, N_2^*)$.

We will now show that each of the equilibria in M is isolated and a weak repeller. As with the previous theorems, E_0 is a stable equilibrium with initial conditions in $X_2 \cap \{N_1, N_2 = 0\}$, but if initial conditions for N_1 or N_2 are positive then N_1 or N_2 will increase exponentially and E_0 is unstable, hence E_0 is isolated and a weak repeller for $\tilde{X}_1$. Also, E_0 is not chained to itself and is not part of a cycle.

E_2 is stable with initial conditions in $X_2 \cap \{N_2 > 0, i_1 = i_2 = 0\}$, but, since $\mathcal{R}_0^2 > 1$, with initial conditions in $X_2 \cap \{N_2 > 0, i_2 > 0 \text{ or } i_1 > 0\}$ then E_2 is unstable. Finally, with initial conditions in $\tilde{X}_1$, E_2 is a weak repeller since the flow linearized around E_2 with initial conditions in $\tilde{X}_1$ is

$$\frac{di_2}{dt} = (\beta_{22}K_{22} - (b_2 + \alpha_2))i_2 \quad (4.5.17)$$

which will grow exponentially since $\mathcal{R}_0^2 > 1$. Thus, E_2 is both isolated and a weak repeller for $\tilde{X}_1$.

E_5 is not an attractor with initial conditions in $X_2 \cap \{i_1 = i_2 = 0\}$ or $X_2 \cap \{N_2 = 0\}$ but is an attractor for $X_2 \cap \{N_2 > 0, i_2 > 0 \text{ or } i_1 > 0\}$. With initial conditions in $\tilde{X}_1$, E_5 is also a weak repeller since $\kappa_1 > 0$ so that N_1 grows exponentially near E_5 . This can be seen by examining the flow of N_1 linearized around E_5 ,

$$\frac{dN_1}{dt} = (r_1(1 - K_{22}/K_{12}) - \alpha_1 Q_1^*)N_1 \quad (4.5.18)$$

which is positive since $\kappa_1 > 0$. Therefore, E_5 is isolated and is a weak repeller for $\tilde{X}_1$.

None of these three equilibria are chained to themselves or to each other in a cyclic way in X_2 because E_0 is unstable, E_2 is stable only for initial conditions $X_2 \cap \{N_2 >$

$0; i_1 = i_2 = 0\}$, while E_5 is stable for $X_2 \cap \{N_2 > 0; i_1 > 0 \text{ or } i_2 > 0\}$. Thus, $M = \{E_0\} \cup \{E_2\} \cup \{E_5\}$ forms an acyclic covering for Ω_2 .

Next we show that X_2 is a uniform weak repeller for $\tilde{X}_1$ so that there exists an $0 < \tilde{\epsilon} < \min(K_{11}, N_1^*)$ such that

$$\limsup_{t \rightarrow \infty} N_1(t) > \tilde{\epsilon} \quad (4.5.19)$$

for any solution $x(t)$ with initial conditions $N_1(0), N_2(0) > 0$ and $i_1(0) > 0$ or $i_2(0) > 0$. Assume X_2 is *not* a uniform weak repeller for $\tilde{X}_1$. Then there exists a sequence $x_n = (i_{1,n}, N_{1,n}, i_{2,n}, N_{2,n}) \in \tilde{X}_1$ such that $\limsup_{t \rightarrow \infty} d(\Phi_t(x_n), X_2) \rightarrow 0$ as $n \rightarrow \infty$. Since each of E_0 , E_2 , and E_5 is a weak repeller for $\tilde{X}_1$, then we know that $\omega(x_n) \not\subset M$. Then the assumptions of Theorem 4.2.0.5 are met and M must be cyclic. This is a contradiction, hence X_2 is a uniform weak repeller for $\tilde{X}_1$.

Now we will show that X_2 is a uniform strong repeller for $\tilde{X}_1$ by way of contradiction. Suppose that X_2 is *not* a uniform strong repeller for $\tilde{X}_1$. Then, there exists no $\epsilon > 0$ such that $\liminf_{t \rightarrow \infty} N_{1,j}(t) > \epsilon$ thus there exists a sequence of initial conditions $x_j^0 = (i_{1,j}(0), N_{1,j}(0), i_{2,j}(0), N_{2,j}(0)) \in \tilde{X}_1$ and a sequence $0 < \epsilon_j < \tilde{\epsilon}$ such that

$$\liminf_{t \rightarrow \infty} N_{1,j}(t) < \epsilon_j \text{ for } j = 1, 2, \dots \quad (4.5.20)$$

where $\lim_{j \rightarrow \infty} \epsilon_j = 0$ and where $i_{1,j}(t), N_{1,j}(t), i_{2,j}(t)$, and $N_{2,j}(t)$ are solutions with initial values $x_j^0 \in \tilde{X}_1$. By equations (4.5.19) and (4.5.20), we can also find sequences of times $0 < r_j < s_j < t_j$ with $\lim_{t \rightarrow \infty} r_j = \infty$ and

$$\lim_{j \rightarrow \infty} N_{1,j}(s_j) = 0 \quad (4.5.21)$$

$$N_{1,j}(r_j) = N_{1,j}(t_j) = \tilde{\epsilon} \quad (4.5.22)$$

$$N_{1,j}(t) \leq \tilde{\epsilon} \text{ for } r_j \leq t \leq t_j \quad (4.5.23)$$

After choosing a subsequence, the sequence $(i_{1,j}(r_j), N_{1,j}(r_j), i_{2,j}(r_j), N_{2,j}(r_j))$ is convergent in X by compactness of X . Let $x^{**}(0) = (i_{1,**}(0), N_{1,**}(0), i_{2,**}(0), N_{2,**}(0))$ be its limit as $j \rightarrow \infty$. Then by (4.5.22) we know that $N_{1,**}(0) = \tilde{\epsilon}$ so that $x^{**} \in X_1$.

There are now two more steps. First, show that $\{t_j - r_j\}$ is unbounded. Suppose not. Then, after choosing subsequences, $\{s_j - r_j\}$ is convergent and, by the semi-group property of the flow, $\lim_{j \rightarrow \infty} (s_j - r_j) = s^*$ and $\lim_{j \rightarrow \infty} (i_{1,j}(r_j + s^*), N_{1,j}(r_j + s^*), i_{2,j}(r_j + s^*), N_{2,j}(r_j + s^*)) = x^{**}(s^*)$ where $x^{**}(t)$ is the solution with initial value $x^{**}(0) \in X_1$. Since X_1 is forward invariant, $x^{**}(s^*) \in X_1$. We also can see that $\lim_{j \rightarrow \infty} (i_{1,j}(s_j), N_{1,j}(s_j), i_{2,j}(s_j), N_{2,j}(s_j)) = x^{**}(s^*)$, which implies that $x^{**}(s^*) \in X_2$ by (4.5.13) and the compactness of X_2 . This is a contradiction, hence $t_j - r_j$ is unbounded.

Second, assuming that X_2 is not a uniform strong repeller for $\tilde{X}_1$, if $x^{**}(0) \in \tilde{X}_1$ then, by (4.5.19) we know that

$$\limsup_{t \rightarrow \infty} \min\{i_{1,**}(t), i_{2,**}(t)\} > \tilde{\epsilon}. \quad (4.5.24)$$

If $x^{**}(0) \in X \setminus \tilde{X}_1$ then we know by Theorems 4.5.0.9 and 4.5.0.12 that disease is uniformly strongly persistent in this case. Since $\kappa_1 > 0$, E_5 is unstable with initial conditions in $\tilde{X}_1$. So the only possibility is if $\mathcal{R}_0^1 > 1$ and $\kappa_2 < 0$ so that E_4 exists and is globally stable for initial conditions in $\tilde{X}_1$. Then, from analysis of the one-species infected equilibrium in Section 4.4, we know that $\lim_{t \rightarrow \infty} N_{1,**}(t) = N_1^* > \epsilon^*$ so there exists a r_j large enough so we know $N_{1,j}(t) > \epsilon^*$ for $t \geq r_j$ and equation (4.5.24) holds for this case as well.

Now, since $t_j - r_j$ is unbounded, using a subsequence, we can assume that $t_j - r_j$ is increasing monotonically and that the $\lim_{j \rightarrow \infty} (t_j - r_j) = \infty$. Then, by (4.5.15) we have that for $k > j$, $N_{1,k}(r_k + r) \leq \epsilon^*$ for $0 \leq r \leq t_j - r_j$. Fix r and j and let $k \rightarrow \infty$ so that for $0 \leq r \leq t_j - r_j$, $N_{1,**}(r) = \lim_{k \rightarrow \infty} N_{1,k}(r_k + r) \leq \epsilon^*$. Now, let $j \rightarrow \infty$ and $\lim_{j \rightarrow \infty} t_j - r_j = \infty$ so that the previous inequality holds for all $r \geq 0$. This contradicts (4.5.24), hence X_2 is a uniform strong repeller for $\tilde{X}_1$. ■

An analogous theorem holds for species 2.

Theorem 4.5.0.14 *Let $\xi_1 < 0$, $\mathcal{R}_0^1 > 1$, and $\kappa_2 > 0$. Let either (1) $\xi_2 > 0$ or (2) $\xi_2 < 0$ and $\mathcal{R}_0^2$ (and hence $\mathcal{R}_0^C$) > 1 . Then, species 2 persists uniformly strongly, i.e. there exists $\epsilon > 0$ such that $\liminf_{t \rightarrow \infty} N_2(t) > \epsilon$ with initial conditions $N_1(0), N_2(0) > 0$ and $i_1(0) > 0$*

or $i_2(0) > 0$.

Proof. The proof is analogous to that for Theorem 4.5.0.13. ■

The following theorems are direct results of combining the conditions of Theorems 4.5.0.6-4.5.0.14.

Theorem 4.5.0.15 *If $\xi_1 > 0$, $\xi_2 < 0$, $\mathcal{R}_0^2 > 1$, and $\kappa_1 > 0$ and if either (1) $\mathcal{R}_0^1 < 1$ or (2) $\mathcal{R}_0^1 > 1$ and $\kappa_2 > 0$, then both species and the disease persist uniformly strongly, i.e. there exists an $\epsilon > 0$ such that $\liminf_{t \rightarrow \infty} \min\{N_1(t), i_1(t), N_2(t), i_2(t)\} > \epsilon$ for initial conditions $i_k(0), N_k(0) > 0$ with $k = 1, 2$.*

A similar result holds when exchanging the indices.

Theorem 4.5.0.16 *If $\xi_2 > 0$, $\xi_1 < 0$, $\mathcal{R}_0^1 > 1$, and $\kappa_2 > 0$ and if either (1) $\mathcal{R}_0^2 < 1$ or (2) $\mathcal{R}_0^2 > 1$ and $\kappa_1 > 0$, then both species and the disease persist uniformly strongly, i.e. there exists an $\epsilon > 0$ such that $\liminf_{t \rightarrow \infty} \min\{N_1(t), i_1(t), N_2(t), i_2(t)\} > \epsilon$ for initial conditions $i_k(0), N_k(0) > 0$ with $k = 1, 2$.*

Theorem 4.5.0.17 *If $\xi_1, \xi_2 > 0$ and $\mathcal{R}_0^C > 1$ and any one of the conditions (1) $\mathcal{R}_0^1, \mathcal{R}_0^2 < 1$, (2) $\mathcal{R}_0^1 > 1$, $\mathcal{R}_0^2 < 1$ and $\kappa_2 > 0$, (3) $\mathcal{R}_0^2 > 1$, $\mathcal{R}_0^1 < 1$ and $\kappa_1 > 0$, or (4) $\mathcal{R}_0^1 > 1$, $\mathcal{R}_0^2 > 1$, $\kappa_2 > 0$ and $\kappa_1 > 0$, then both species and the disease persist uniformly strongly.*

Theorem 4.5.0.18 *If $\xi_1 < 0, \xi_2 < 0$, $\mathcal{R}_0^C > 1$, $\mathcal{R}_0^1 > 1$, $\mathcal{R}_0^2 > 1$, $\kappa_2 > 0$ and $\kappa_1 > 0$, then both species and the disease persist uniformly strongly.*

Note that, as in Corollary 4.15 of [61], if conditions are met such that any one of Theorems 4.5.0.15-4.5.0.18 hold, then there exists at least one internal equilibrium of the full system by [91] Remark 3.10 and Theorem 4.7, and by [69] pp. 160-166. See Table 4.3 for a summary of our results.

ξ_1	ξ_2	$\mathcal{R}_0^1$	κ_2	$\mathcal{R}_0^2$	κ_1	$\mathcal{R}_0^C$	SUP
	+			< 1			N_1
	+			> 1	+		N_1
+	-			> 1	+		N_1
-	-	> 1		> 1	+		N_1
+		< 1					N_2
+		> 1	+				N_2
-	+	> 1	+				N_2
-	-	> 1	+	> 1			N_2
-	+	> 1					i_1, i_2
+	-			> 1			i_1, i_2
+	+					> 1	i_1, i_2
-	-	> 1		> 1		> 1	i_1, i_2
+	-	< 1		> 1	+		All
+	-	> 1	+	> 1	+		All
+	+	< 1		< 1		> 1	All
+	+	> 1	+	< 1		> 1	All
+	+	< 1		> 1	+	> 1	All
+	+	> 1	+	> 1	+	> 1	All
-	+	> 1	+	< 1			All
-	+	> 1	+	> 1	+		All
-	-	> 1	+	> 1	+	> 1	All

TABLE 4.3: Conditions for strong uniform persistence (SUP). + denotes strictly positive, - denotes strictly negative. For the column SUP, the variable listed is the one guaranteed strong uniform persistence; ‘All’ means that every variable is SUP.

4.6 Discussion and Conclusion

We make two main observations. Han and Pugliese [61] found conditions for strong uniform persistence of disease and for one or both species for the case of density-dependent birth with competition in the death term. We find that adding competition to the birth term and removing density dependence from death affects the actual equilibrium densities of the computed boundary equilibria but does not qualitatively change the conditions under which the species and/or the disease persist uniformly strongly. This suggests that the particular way in which competition acts on the growth rate of the species does not change the qualitative outcome of our model in the context of strong uniform persistence of both species and the pathogen. We frame our persistence results in the context of the ecologically relevant terms ξ_1 , ξ_2 , $\mathcal{R}_0^C$, $\mathcal{R}_0^1$, $\mathcal{R}_0^2$, κ_1 , and κ_2 , all of which have intuitive ecological significance (see Table 4.1) and can be used exclusively to show feasibility and stability of the boundary equilibria (Section 3.3 and Table 4.2).

The second observation is that, in the case where both species and the disease persist uniformly strongly, we obtain a modified version of the conjecture in Chapter 2 (Theorem 3.4.7.1) that when all other feasible equilibria are unstable the endemic coexistence equilibrium is stable. The modified theorem is as follows:

Theorem 4.6.0.19 *When all feasible boundary equilibria are unstable, both species and the pathogen are strongly uniformly persistent for all initial conditions with $N_1(0), N_2(0) > 0$ and $i_1(0) > 0$ or $i_2(0) > 0$. Thus, under these conditions, there is endemic coexistence.*

This can be seen from Tables 4.2 and 4.3 since conditions for strong uniform persistence of all species and the pathogen can be derived from situations in which the feasible boundary equilibria (including the one-host infected equilibria) are unstable (see Figure 4.3). These persistence results are verified for the simplified system in Section 3.4.4, for which all dynamics are known. For the simplified case, $\kappa_1 = \xi_2$, $\kappa_2 = \xi_1$, and $\mathcal{R}_0^1 = \mathcal{R}_0^2 = \mathcal{R}_0$,

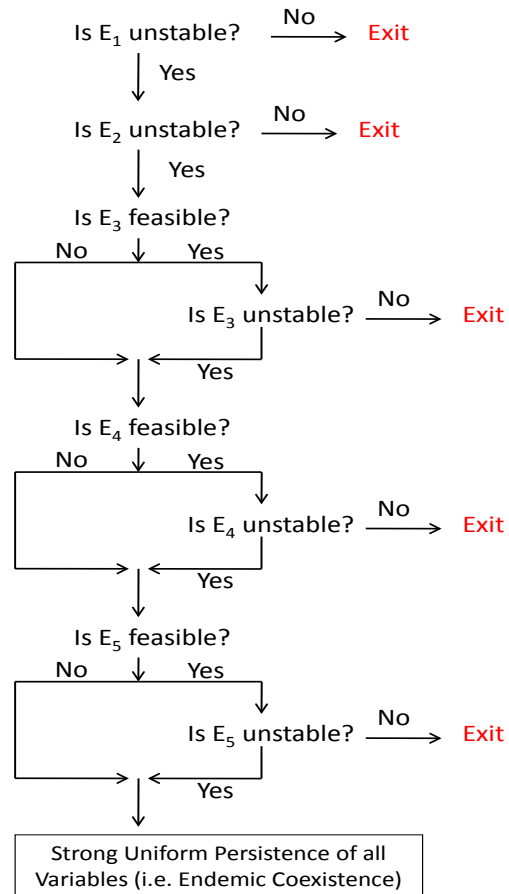


FIGURE 4.3: Flow chart for determining strong uniform persistence of both species and the pathogen.

so persistence can be determined by the parameters ξ_1 , ξ_2 , $\mathcal{R}_0$, and $\mathcal{R}_0^C$. When $\xi_1 > 0$, $\xi_2 > 0$, and $\mathcal{R}_0^C > 1$ then both species and the pathogen persist. In this case, conditions for strong uniform persistence are the same as those for global stability of the unique endemic coexistence equilibrium.

Although stability of particular interior equilibria and/or limit cycles is not proved, the strong uniform persistence of the system is proved. This is an important result from an ecological perspective, since it guarantees that all variables stay bounded strictly away from zero, thus will not go extinct. In summary, we use persistence theory to complete the analysis of the full model for competition and disease with mass action incidence, showing that persistence of both species and the disease is determined by a few ecologically relevant parameters.

5 A SPATIOTEMPORAL MODEL FOR THE SPREAD OF BARLEY YELLOW DWARF VIRUS IN GRASSLANDS

5.1 Introduction

In Chapters 3 and 4, it is shown that competition between species and inter-specific disease transmission can interact to determine persistence of the hosts and/or pathogen under conditions different from those derived for the single host model or a model with multiple hosts that do not directly compete for resources. For example, even if the basic reproduction number for one species alone with the pathogen is below one, the presence of a nearby competent host can cause the pathogen to persist. On the other hand, two species exhibiting competitive exclusion without a pathogen present can coexist in the presence of a multi-host pathogen (see Sections 3.4, 3.5, and 4.4). The question of how disease affects populations, including whether or not a disease might drive a population to extinction, is an important one to biologists today. The results from Chapters 3 and 4 have important implications for the successful invasion of exotic species in the presence of a generalist pathogen. A pathogen can mitigate exclusion or coexistence of host species, while, conversely, the presence of multiple hosts can cause a disease to either persist or die out, all depending on properties of the system.

These results assume that the pathogen and host species are mixing in a single homogeneous environment. However, space can often play an important role in invasion of pathogens and exotic species, and spatial models of disease are gaining impetus as natural and human-made landscape features such as forests, rivers, roads and crops cause many endangered species to live in fragmented landscapes [62, 10, 12, 11, 58, 100, 101]. The heterogeneity of the landscape as well as the demography and the epidemiology of multiple interacting species determine spatial spread and persistence of the disease. Although opening “corridors” between habitat patches may be important for preserving a species, if

one does not examine the possible changes that this might make in disease dynamics, the result may be increased chance of epidemics or even local extinction [64, 100]. Therefore, in Chapters 5 and 6, we couple multi-host disease models such as those discussed in Chapters 2-4 with a multi-patch model in order to determine the effects of spatial heterogeneity on single patch results. See Section 2.4 for an introduction to multi-patch epidemic models.

This chapter is the interdisciplinary chapter resulting from my participation in the Ecosystem Informatics IGERT program at Oregon State University. It is the result of work by teams from multiple disciplines and institutions. We apply mathematical methods to model and analyze the spread of Barley/Cereal Yellow Dwarf Virus (BYDV) in native California grasslands.

5.1.1 Spatial Dynamics of Host-Pathogen Systems

Humans are converting and fragmenting landscapes on every continent, changing connectivity of habitats through effects including reduced patch size, creation of novel habitats, and altered movement rates among patches that affect a diversity of species. Pathogen movement and epidemics can depend intimately upon landscape connectivity patterns [136, 104], which, in turn, control epidemic propagation or fadeout [78, 129]. Importantly, models including spatial heterogeneity can make qualitatively different predictions compared to models assuming homogeneous mixing [70, 66, 79]. In addition, many emerging pathogens infect multiple hosts, but most multi-host theory developed to date has focused on non-spatial models [49, 81, 102, 118, 73, 17, 26, 71]. Thus, in spite of the importance of landscape connectivity for understanding spatial spread and persistence of disease in real communities, the body of spatially-explicit theory dealing with multi-host pathogens remains quite small [110] (chapter 5), [47]. As a result, the spatial dynamics of multispecies host-parasite assemblages are gaining increasing attention in both mathematics and ecology. In particular, metapopulation and patch models of disease are gaining impetus with the recognition that species live in increasingly fragmented landscapes [62, 10, 12, 11, 58, 100, 101], and that the heterogeneity of the landscape, as

well as the demography and the epidemiology of multiple interacting species, determine spatial spread and persistence of the disease [113].

The dynamics of generalist pathogens depend on many factors that influence their persistence and determine the manner in which disease spreads. Among these factors spatial dynamics are particularly important for plant pathogens because natural plant communities exist in spatially heterogeneous landscapes. The different host species, affected by a common generalist pathogen, are often distributed in patches [113]. Another factor is cross-species transmission dynamics. Host species differ in their susceptibility to a disease and their competency in transmitting the disease to other hosts. Hence, the diversity and composition of a community can influence the pathogen load at both population and community levels [84, 105, 118]. The mere presence of a host that is highly susceptible to a disease can lead to a local epidemic, while the presence of a host with a low reservoir competency can lead to a dilution effect where the overall disease prevalence is reduced [81]. Finally, if a generalist pathogen is vector-transmitted then host populations may also differ in their contact with and effect on the vector population [118].

Pathogens that are host generalists can also mediate the outcome of interspecific competition between host species. If the pathogen has differential effects on the fitness of the competing species, relative competitive strengths and hence population outcomes can be altered [24]. Theoretical and empirical investigations have shown that a generalist pathogen infecting multiple (competing) host species can influence species diversity and community structure [118, 81, 24, 34, 63, 84]. Consequently, generalist pathogens can have a significant impact on endangered species, particularly in the presence of a species that acts as a reservoir for the pathogen [44].

In this paper we use barley and cereal yellow dwarf viruses (B/CYDV), a suite of aphid-vectored pathogens, and their interactions with a range of host species as our case study. Our goal is to construct and analyze a model that helps in determining the possibility of invasion of native species by exotic (i.e., non-native) species due to the presence of disease (B/CYDV) among the (competing) multiple species in a patch

framework.

Here we develop a multi-patch framework to examine the influence of spatial heterogeneity, seasonality, and competition on disease dynamics and pathogen-mediated plant invasion. We begin by investigating the effects of local host community composition and vector movement on B/CYDV dynamics in which the landscape is divided into a system of discrete patches containing smaller local populations, with disease transmission occurring via vector movement between patches (Section 5.3). We then analyze a simplified two patch model in order to derive the B/CYDV system's basic reproduction number, which serves as a threshold for invasion into a susceptible host community. We also use the basic reproduction number to examine the sensitivity of spatial transmission dynamics to key epidemiological and biological parameters (Section 5.5). We then examine whether B/CYDV can persist locally or in a patch framework across a range of host community configurations. First we adjust the number of patches connected by aphid migration and vary aphid migration rates between patches. We also modify community configurations to examine whether pathogen-mediated interactions and competitive outcome between perennial and annual competitors are altered at the local and regional scale when the host populations are spatially structured (Section 5.6).

5.2 The B/CYDV Empirical System

B/CYDV is one of the most economically important diseases of grain crops worldwide and infects over 100 grass species in both agricultural and natural systems [75]. Because it can be a devastating crop pathogen, the vast majority of the theoretical and empirical studies of B/CYDV have been focused on crop settings. Thus, the history of modeling of this pathogen is strongly focused on epidemiology in single host species [82, 50, 88, 149]. However, B/CYDV also infects many non-crop grass species. Exotic (i.e., non-native) annual grasses have been invading and displacing native perennial grasses in

much of the western United States [24, 94, 93]. Recent theoretical and empirical work has demonstrated that B/CYDV may also play a critically important role in facilitating and maintaining natural grassland invasion [94, 24]. Borer et al. [24] analyzed a non-spatial model of B/CYDV, which suggested that the virus could reverse the competitive outcome between perennial and annual host grasses, leading to the successful invasion by the competitively inferior annuals. However, continued existence of B/CYDV requires the persistence of the perennial grass in the community due to its role as a reservoir for infection between growing seasons. Hence we incorporate patch structure in the nonspatial model considered in [24] to examine the effect of spatial heterogeneity of the host species on disease dynamics and the possibility of invasion by exotic species.

The virus has a short latency period in both its host plants and the aphid vector; however, once infected, a vector is potentially infective for life and individual hosts typically do not recover from a B/CYDV infection. Host susceptibility to B/CYDV varies, with some species suffering increased mortality and reduced fecundity when infected and other species experiencing little change in their overall fitness [75]. Studies have also shown that the presence of highly competent reservoir species can increase the prevalence of B/CYDV in local host communities [118, 24, 94, 93]. Host-aphid interactions also vary by host, with aphids showing preference for and experiencing higher fitness on certain host species [89, 103]. The various host species often compete for resources and the presence of B/CYDV may alter their relative competitive abilities, leading to shifts in host community composition [24]. Annual grasses may act to amplify the prevalence of B/CYDV because aphids feed preferentially on annuals and have higher growth rates when feeding on annuals [23]. The transmission rates to and from aphids may also be higher for annual grasses [42]. While the effect of these host community differences have been investigated at the local level, their importance for regional patterns of B/CYDV spread and persistence have not been fully explored. Both local, within-field movements and long-distance dispersal by aphids are important for B/CYDV transmission [76], and host-vector interactions at multiple spatial scales may influence local and regional disease dynamics.

5.3 Model formulation

In California grasslands, the wet winter and spring growing seasons alternate with hot, dry summers, during which perennial grasses remain dormant and annuals persist only as seeds. We use a differential-difference modeling approach [24] to describe the punctuated seasonality of this system. During the growing season (of length τ), differential equations are the effective model, and the dormant summer season is described by difference equations $[(t_n + \tau) \text{ to } (t_{n+1} = t_n + 1)]$ where $t_n = n$ is time in years. Since time units are in years, $\tau < 1$. We use the following susceptible-infected model structure to summarize the multihost-pathogen dynamics of the California grassland community.

Each of the vector and host subpopulations consists of susceptible (S) and infected (I) individuals. Vector population dynamics are modeled explicitly in order to represent infection dynamics within the aphid population as well as aphid migration between patches. Vector population dynamics and epidemiology during the growing (rainy) season are represented by a pair of differential equations for each subpopulation in a patch model. We use a simplified, reduced parameter Lotka-Volterra competition formulation [32], with a reduced competitive pressure from infected individuals (parameterized as ϵ), as described in [24]. Fecundity and biomass reduction are represented by the same parameter ϵ , because plant fecundity is largely a function of plant biomass and the empirical estimates were identical. We explicitly track susceptible perennial seedlings (p_S), infected perennial seedlings (p_I), susceptible perennial adults (P_S), infected perennial adults (P_I), susceptible annuals (a_S), and infected annuals (a_I). We also explicitly track the susceptible vectors (V_S), and infected vectors (V_I). Figure 5.1 shows the competitive structure between the susceptible and infected host compartments, while Figure 5.2 shows the transmission of infection from vectors to hosts. Figure 5.3 depicts the movement of vectors between patches. Aphid population growth depends on the relative densities of annual and perennial hosts, because aphids show both a preference for annual grasses and higher performance (fecundity) on annual hosts [23].

Host and vector growing season/continuous time equations for $t_n < t \leq t_n + \tau$:

(a = annuals, p = 1st year perennials, P = adult perennials, V = vector)

$$\frac{dp_{S,j}}{dt} = -(\mu_p \eta_p + \beta_{vp} V_{I,j}) p_{S,j}, \quad (5.3.1a)$$

$$\frac{dp_{I,j}}{dt} = -\mu_p \eta_p \epsilon_p p_{I,j} + \beta_{vp} V_{I,j} p_{S,j}, \quad (5.3.1b)$$

$$\frac{dP_{S,j}}{dt} = -\beta_{vp} V_{I,j} P_{S,j}, \quad (5.3.1c)$$

$$\frac{dP_{I,j}}{dt} = \beta_{vp} V_{I,j} P_{S,j}, \quad (5.3.1d)$$

$$\frac{da_{S,j}}{dt} = -(\mu_a \eta_a + \beta_{va} V_{I,j}) a_{S,j}, \quad (5.3.1e)$$

$$\frac{da_{I,j}}{dt} = -\mu_a \eta_a \epsilon_a a_{I,j} + \beta_{va} V_{I,j} a_{S,j}, \quad (5.3.1f)$$

$$\frac{dV_{S,j}}{dt} = r(t) - (\beta_{av} a_{I,j} + \beta_{pv} (p_{I,j} + P_{I,j})) V_{S,j} - \mu_V V_{S,j} + M_{S,j}, \quad (5.3.1g)$$

$$\frac{dV_{I,j}}{dt} = (\beta_{av} a_{I,j} + \beta_{pv} (p_{I,j} + P_{I,j})) V_{S,j} - \mu_V V_{I,j} + M_{I,j}. \quad (5.3.1h)$$

Dry season/discrete time for each patch, j , and for $t_n + \tau \rightarrow t_{n+1}$:

$$p_{S,j}(t_{n+1}) = b_P (P_{S,j}(t_n + \tau) + \epsilon_p P_{I,j}(t_n + \tau)), \quad (5.3.2a)$$

$$p_{I,j}(t_{n+1}) = 0, \quad (5.3.2b)$$

$$P_{S,j}(t_{n+1}) = \sigma_{P_S} (p_{S,j}(t_n + \tau) + P_{S,j}(t_n + \tau)), \quad (5.3.2c)$$

$$P_{I,j}(t_{n+1}) = \sigma_{P_I} (p_{I,j}(t_n + \tau) + P_{I,j}(t_n + \tau)), \quad (5.3.2d)$$

$$a_{S,j}(t_{n+1}) = b_A (a_{S,j}(t_n + \tau) + \epsilon_a a_{I,j}(t_n + \tau)), \quad (5.3.2e)$$

$$a_{I,j}(t_{n+1}) = 0, \quad (5.3.2f)$$

$$V_{S,j}(t_{n+1}) = C, \quad (5.3.2g)$$

$$V_{I,j}(t_{n+1}) = 0. \quad (5.3.2h)$$

Plant competition terms:

$$\eta_a = 1 + \alpha_{aa} (a_{S,j} + \epsilon_a a_{I,j}) + \alpha_{ap} (p_{S,j} + \epsilon_p p_{I,j}) + \alpha_{aP} (P_{S,j} + \epsilon_p P_{I,j}), \quad (5.3.3a)$$

$$\eta_p = 1 + \alpha_{pp} (p_{S,j} + \epsilon_p p_{I,j}) + \alpha_{pa} (a_{S,j} + \epsilon_a a_{I,j}) + \alpha_{pP} (P_{S,j} + \epsilon_p P_{I,j}). \quad (5.3.3b)$$

Vector growth term:

$$r(t) = d_V(\lambda(a_{S,j} + a_{I,j}) + (p_{S,j} + p_{I,j}) + (P_{S,j} + P_{I,j})). \quad (5.3.4)$$

Vector migration terms where $Y \in \{S, I\}$:

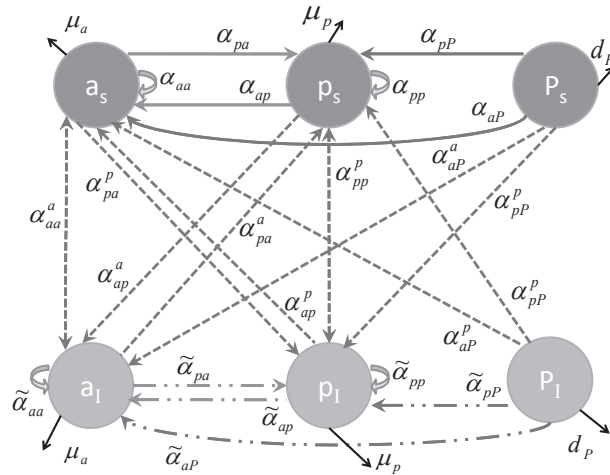
$$M_{Y,j} = - \sum_{k=1, k \neq j}^N m_{jk} V_{Y,j} + \sum_{k=1, k \neq j}^N m_{kj} V_{Y,k}, \quad (5.3.5)$$

where N is the total number of patches. We remark here that the parameter m_{jk} denotes the migration rate from patch j to patch k and not from patch k to j , as is assumed in some other papers.

During the dry season it is assumed that all infected aphids die, while the uninfected aphids may either survive as a function of their density at the end of the growing season or they may recolonize from outside the patch system. These two possibilities correspond to different life history strategies employed by aphids; some species remain within the grassland at low abundances between growing seasons with uninfected offspring emerging at the beginning of the growing season, while others migrate to an alternate host, typically in another habitat (e.g., *Rhopalosiphum padi* switches from grasses to a species of *Prunus* during the dry season).

The model considers age structure in the perennial grasses. Perennial adults are qualitatively different from annual grasses; they are competitively superior and less palatable to aphids [23]. In contrast, first-year perennials are more similar to annuals in these characteristics. The model also examines both reduced fecundity and disease-induced dormant season mortality. See Table 1 for a description of model parameters. The subscript S represents susceptible and I represents infected individuals of a species and/or age class. The subscript j indicates the patch in which the individuals reside.

We note that B/CYDV requires an aphid vector for transmission from plant to plant and cannot be spread via seeds. We use a Lotka-Volterra competition framework



5.4 Estimation of Model Parameter Values from Field Data

A great deal of information about aphid reproductive rates, host composition of grasslands, transmission competence of hosts for certain B/CYDV serotypes, and population dynamic effects of infection on different host species is available for model parameterization [24]. We have amassed data on 20 different native and exotic, annual, and perennial grass US West Coast species ([42, 23]; Welsh, Borer, and Mitchell, unpubl. data). The

Symbol	Description	Value	Reference
b_P	Perennial birth rate	45.0	[24]
b_A	Annual birth rate	200	[133]
σ_{P_S}	Healthy perennial (adult) survival rate	0.88	[93]
σ_{P_I}	Infected perennial (adult) survival rate	0.77	[93]
ϵ_p	Fractional reduction in biomass and fecundity of infected perennials	0.5	[93]
ϵ_a	Fractional reduction in biomass and fecundity of infected annuals	0.11	[93]
τ	Growing season length	20 wks	[24]
C	Number of aphids at beginning of growing season	100	
β_{vp}	Aphid to perennial transmission rate	0.2	
β_{va}	Aphid to annual transmission rate	0.4	
β_{pv}	Perennial to aphid transmission rate	0.02	[24]
β_{av}	Annual to aphid transmission rate	0.04	[24]
λ	Vector preference and performance (aphids per annual/aphids per perennial)	1.5	[94]
μ_a	Annual death rate	1	[24]
μ_p	Seedling perennial death rate	0.5	[24]
μ_V	Aphid death rate	10	
d_V	Aphid fecundity rate	13.2	
m_{jk}	Aphid migration rate from patch j to patch k	1×10^{-5}	see text
α_{pp}	Competition between first-year perennials	1.3×10^{-3}	[24]
α_{pa}	The effect on first-year perennials by annuals	6.8×10^{-4}	[24]
α_{pP}	The effect on first-year perennials by adult perennials	0.7	[24]
α_{aa}	Competition between annuals	1.1×10^{-3}	[24]
α_{ap}	Effect on annuals of first-year perennials	3.4×10^{-7}	[24]
α_{aP}	Effect on annuals of adult perennials	0.7	[24]

TABLE 5.1: Description of model parameters and values used for initial model analysis and simulation. Values were estimated from empirical work in California grasslands. Discrete and continuous units are year⁻¹ (except ϵ and λ which are unitless), and competition parameters are individual⁻¹.

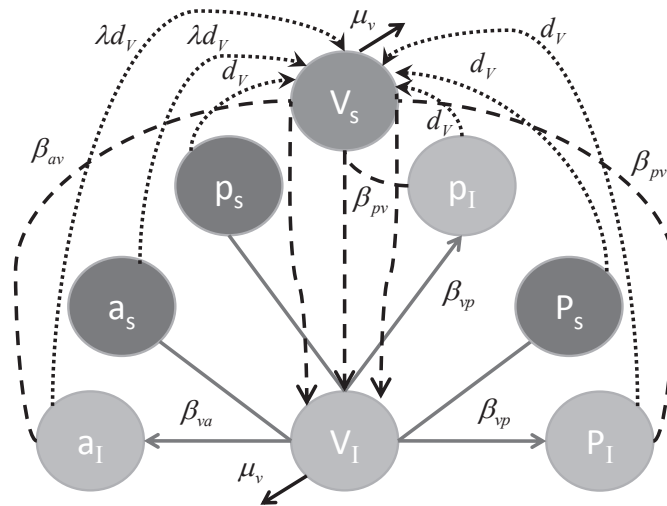


FIGURE 5.2: Transfer diagram for the growing season depicting the population dynamics of vectors and the disease transmission between hosts and vectors.

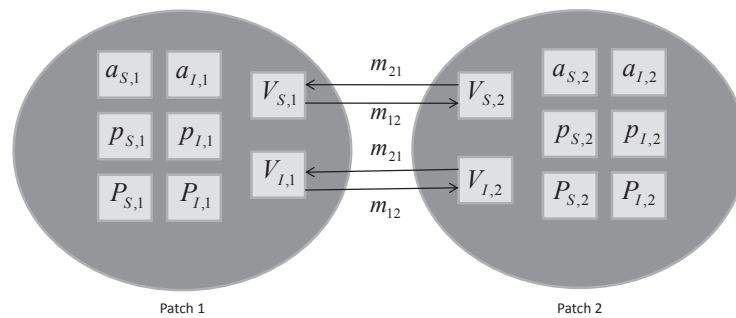


FIGURE 5.3: Patch diagram for two patches, depicting the different compartments in each patch, and the movement of vectors between patches.

species for which we have many experimental and observational estimates represent some of the most important native and invasive grasses in the system. In addition, species we have examined span the range of characteristics from extremely widespread to extremely restricted West Coast ranges as well as locally abundant and always rare within communities. Although B/CYDV infection has been documented in at least 33 native and 80 exotic grasses in California [92], we focus on two common grasses, *Elymus glaucus*, a native perennial, and *Bromus hordeaceus*, an exotic annual, because these species have among the broadest ranges of West Coast grassland species. They have been the focus of our own multiyear B/CYDV monitoring and, among the native perennials, the best-quality published prevalence data are available for *E. glaucus* [94]. Although we parameterize the model for these two species for our numerical simulations (see parameter values in Table 1), we also conduct sensitivity analyses by varying the different epidemiological parameters within the range exhibited by other grass species in field and laboratory studies. This allows us to examine how B/CYDV may control competitive outcomes depending on the composition of the host community.

For the estimation of the dispersal coefficient we note that movement involves leaving, moving between, and arriving in patches and is notoriously complicated to estimate on very small animals, such as aphids. Therefore we use simulations to examine the effect of different aphid migration rates on B/CYDV transmission in a patch framework.

5.5 Analysis of a Two Patch Model

In order to better understand the dynamics of the full model that includes spatial heterogeneity, seasonality, competition, and disease dynamics, we consider the growing season dynamics in one and two patches. In particular, we find the basic reproduction number for the growing season dynamics in an isolated population and in two patches under an additional assumption about adult perennial death rates. Since the dry season

dynamics decrease the number of infected organisms through the death of all infected annuals and infected aphids and the reduced survival of infected perennials, the basic reproduction number for the growing season will give us a good approximation of the initial spread of the virus.

5.5.1 Computation of the Basic Reproduction Number, R_0

In order for the basic reproduction number to be defined, we assume that there is a small death rate for perennial adults, d_P , during the growing season. Omitting a growing season death rate for adult perennials was a simplifying assumption of the non-spatial model in [24]. Based on numerical sensitivity analysis we choose appropriate values of d_P that do not significantly change the outcome of the model (see Figure 4). This assumption changes only equations (5.3.1c) and (5.3.1d) to the following:

$$\frac{dP_{S,j}}{dt} = -\beta_{vp}V_{I,j}P_{S,j} - d_PP_{S,j}, \quad (5.5.1)$$

$$\frac{dP_{I,j}}{dt} = \beta_{vp}V_{I,j}P_{S,j} - d_PP_{I,j}. \quad (5.5.2)$$

We chose $d_P = 0.1$ so that, neglecting the dry season, the average lifespan of a perennial is 10 years.

With this additional assumption, we will use the next generation matrix method [144] to determine the basic reproduction number for the one-patch case, or an isolated population. Let $X = (p_S, P_S, a_S, V_S, p_I, P_I, a_I, V_I)^T$. Then we can rewrite system (5.3.1a)-(5.3.1h) in the form

$$\frac{dX}{dt} = \mathcal{F}(X) - \mathcal{V}(X), \quad (5.5.3)$$

where $\mathcal{F}(X)$ represents a vector function for the new infectious cases and $\mathcal{V}(X)$ contains all other dynamics. We compute the Jacobian of $\mathcal{F}$ and $\mathcal{V}$ and evaluate these at the disease free equilibrium (DFE), $E^* = (p_S^*, P_S^*, a_S^*, V_S^*, 0, 0, 0, 0)$. Let F and V be the matrices defined by

$$F = \left[\frac{\partial \mathcal{F}_i}{\partial x_j}(E^*) \right]; \quad V = \left[\frac{\partial \mathcal{V}_i}{\partial x_j}(E^*) \right], \quad (5.5.4)$$

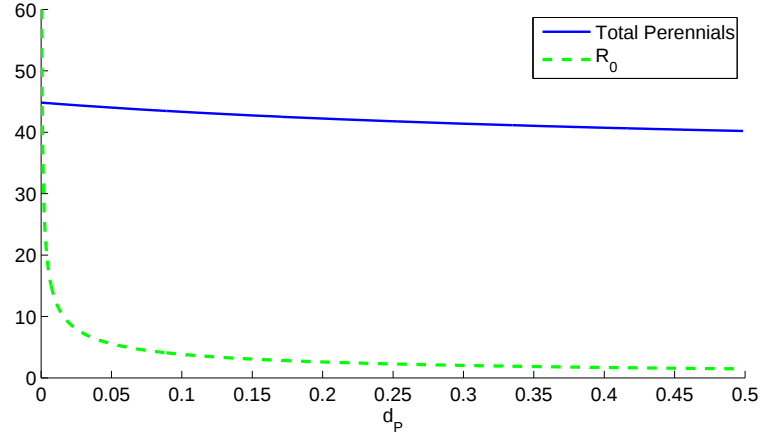


FIGURE 5.4: We plot d_P versus $\mathcal{R}_0$ (dotted line) and d_P versus total adult perennial equilibrium values (solid line) in the disease-free scenario for one patch. In this case, regardless of d_P , the disease-free equilibrium value for annuals is 0.

where $5 \leq i, j \leq 8$ and x_j is the j th component of the vector X defined in (5.5.3).

Computing these matrices we have

$$F = \begin{bmatrix} 0 & 0 & 0 & \beta_{vp}P_S^* \\ 0 & 0 & 0 & \beta_{vp}P_S^* \\ 0 & 0 & 0 & \beta_{va}a_S^* \\ \beta_{pv}V_S^* & \beta_{pv}V_S^* & \beta_{av}V_S^* & 0 \end{bmatrix}, \quad (5.5.5)$$

and

$$V = \begin{bmatrix} \epsilon_p \mu_p \eta_p(E^*) & 0 & 0 & 0 \\ 0 & d_P & 0 & 0 \\ 0 & 0 & \epsilon_a \mu_a \eta_a(E^*) & 0 \\ 0 & 0 & 0 & \mu_V \end{bmatrix}. \quad (5.5.6)$$

The basic reproduction number, $R_{0,1}$, is given as

$$R_{0,1} = \rho(FV^{-1}), \quad (5.5.7)$$

where $\rho(A)$ is the spectral radius of the matrix A . The spectral radius of the matrix FV^{-1}

is given by the formula

$$R_{0,1} = \sqrt{R^{V_p}(R^p + R^P) + R^{V_a}R^a}, \quad (5.5.8)$$

where

$$R^p = \frac{\beta_{vp}P_S^*}{\epsilon_p\mu_p\eta_p(E^*)}, \quad (5.5.9a)$$

$$R^P = \frac{\beta_{vp}P_S^*}{d_P}, \quad (5.5.9b)$$

$$R^a = \frac{\beta_{va}a_S^*}{\epsilon_a\mu_a\eta_a(E^*)}, \quad (5.5.9c)$$

$$R^{V_p} = \frac{\beta_{pv}V_S^*}{\mu_V}, \quad (5.5.9d)$$

$$R^{V_a} = \frac{\beta_{av}V_S^*}{\mu_V}. \quad (5.5.9e)$$

For the baseline parameter values chosen, simulations indicate that in the disease free scenario perennials and annuals do not coexist. When the disease free patch is perennial-only $R^a = 0$ and when the patch is annual-only then $R^p = R^P = 0$. The parameter $R_{0,1}$ is proportional in both cases to the transmission terms and the equilibrium populations of both vector and plants while varying inversely with vector and plant death rates. For seedling perennials and annuals, these death rates depend in part upon the reduction of biomass due to infection.

Next we compute the basic reproduction number for the growing season in two patches. Let $E_1^* = (p_{S,1}^*, P_{S,1}^*, a_{S,1}^*, V_{S,1}^*, 0, 0, 0, 0)$, $E_2^* = (p_{S,2}^*, P_{S,2}^*, a_{S,2}^*, V_{S,2}^*, 0, 0, 0, 0)$ be the disease-free equilibrium for patch 1 and patch 2 respectively. Then, using the next generation method [11, 10],

$$F = \begin{bmatrix} F_1 & \mathbf{0} \\ \mathbf{0} & F_2 \end{bmatrix}, \quad (5.5.10)$$

where, $\mathbf{0}$ denotes a 4×4 matrix of all zeros, and for $i = 1, 2$, the 4×4 matrices, F_1, F_2

are defined as

$$F_i = \begin{bmatrix} 0 & 0 & 0 & \beta_{vp}P_{S,i}^* \\ 0 & 0 & 0 & \beta_{vp}P_{S,i}^* \\ 0 & 0 & 0 & \beta_{va}a_{S,i}^* \\ \beta_{pv}V_{S,i}^* & \beta_{pv}V_{S,i}^* & \beta_{av}V_{S,i}^* & 0 \end{bmatrix}. \quad (5.5.11)$$

We also define the matrix

$$V = \begin{bmatrix} V_1 & M_{12} \\ M_{21} & V_2 \end{bmatrix}, \quad (5.5.12)$$

where for $i, j = 1, 2, i \neq j$,

$$V_i = \begin{bmatrix} \epsilon_p \mu_p \eta_p(E_i^*) & 0 & 0 & 0 \\ 0 & d_P & 0 & 0 \\ 0 & 0 & \epsilon_a \mu_a \eta_a(E_i^*) & 0 \\ 0 & 0 & 0 & \mu_V + m_{ji} \end{bmatrix}, \quad (5.5.13)$$

and

$$M_{ij} = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -m_{ij} \end{bmatrix}. \quad (5.5.14)$$

The basic reproduction number for the whole system, R_0^C , where $R_{0,i}$ is the basic reproduction number for patch i alone and assuming that migration is symmetric so that $m_{12} = m_{21} = m$, is

$$R_0^C = \frac{1}{\sqrt{2}} \sqrt{R^* + (R_{0,1}^2 + R_{0,2}^2)(R_{\mu_V} + R_m)}, \quad (5.5.15)$$

where

$$R_{\mu_V} = \frac{\mu_V}{2m + \mu_V}, \quad (5.5.16)$$

$$R_m = \frac{m}{2m + \mu_V}, \quad (5.5.17)$$

and where

$$R^* = \sqrt{R_{\mu_V}(R_{0,1}^2 - R_{0,2}^2)^2 + R_m^2(R_{0,1}^2 + R_{0,2}^2)^2}. \quad (5.5.18)$$

We remark that if both patches are identical and inhabited by the same single species, then $R_{0,2} = R_{0,1}$. In addition if migration of vectors between patches is very small so R_m is negligible and R_{μ_V} is close to one, then $R_0^C \approx R_{0,1}$. Thus, the basic reproduction number for the system simply becomes the basic reproduction number for the individual identical patches.

5.5.2 Sensitivity Analysis

Here we include background for the sensitivity analysis performed in the next section. Sensitivity analysis, here in the context of deterministic differential equations, quantifies the dependence of the output of a model on the input of a model. When parameters or initial conditions vary, so does the model output. There are many ways to approach sensitivity analysis, but the method used in this chapter is forward sensitivity analysis. We follow the approach of [74] in the rest of this section. For an initial value problem

$$u' = f(u, t; p), \quad u(0) = u_0,$$

forward sensitivity analysis estimates how the solution u or some function of the solution $J(u)$ changes with perturbations of a parameter p . Essentially, forward sensitivity analysis aims to compute the partial derivatives $\partial u / \partial p$ or $\partial J(u) / \partial p$. One common way to compare sensitivity to various parameters is to compute a normalized sensitivity index.

Definition 5.5.2.1 (Definition 1.4.1 [74]) *Let $J(u)$ be a function which depends on the forward solution u which depends on parameter p . Let δp be a perturbation to the parameter p and let δJ denote the resulting perturbation in $J(u)$. The normalized sensitivity index is defined as*

$$S_p = \left(\frac{\delta J}{J} \right) / \left(\frac{\delta p}{p} \right) \quad (5.5.19)$$

where $J, p \neq 0$. When the function is differentiable, the sensitivity index can be re-written as

$$S_p = \frac{p}{J} \frac{dJ}{dp}. \quad (5.5.20)$$

Notice that often the chain rule is need to compute S_p in the definition (5.5.20).

Forward sensitivity analysis is local, depending on the particular solution of the system at fixed parameter values. In other words, it computes sensitivity to a parameter perturbed around a particular value, in our case around the parameters estimated by the data or around the expected value of a parameter based on the literature. In this chapter we will use forward sensitivity analysis to help determine the most important parameters to the success of invasion by a pathogen ($\mathcal{R}_0$) and to the cumulative number of infected organisms. This can give important insight into possible control methods for a pathogen as well as general qualitative information about the behavior of the system.

5.5.3 Sensitivity Analysis of R_0 to Parameters

In order to better understand why the native perennials are susceptible to invasion by non-native annuals in the presence of disease, we found the relative importance of all parameters to the initial spread of B/CYDV using R_0 for one and two patches. The initial successful spread of B/CYDV depends on R_0 for the growing season, while the endemic coexistence equilibrium values indicate long term persistence of the virus and thus long term coexistence of annuals and perennials. We therefore computed the sensitivity indices of R_0 to the parameters of the model in order to understand what factors are most important in disease prevalence and exotic invasion.

The sensitivity index $\frac{dR_0}{d\xi}$ is a linear estimate of the number of unit change in R_0 as a result of a unit change in the parameter ξ . Such sensitivity indices depend on the physical units of state variables and parameters, and hence we cannot compare different sensitivity indices. To make comparison feasible, and make the sensitivity analysis independent of the units of the model, we use normalized sensitivity indices as defined below.

Definition 5.5.3.1 *A normalized sensitivity index for the state variable R_0 , with respect to the parameter ξ , denoted as $\psi_{R_0}^\xi$, is the ratio of relative change in R_0 , to the relative*

change in the parameter ξ , and is defined as [128, 36]:

$$\psi_{R_0}^\xi = \frac{\partial R_0}{\partial \xi} \cdot \frac{\xi}{R_0}. \quad (5.5.21)$$

The coefficient $\psi_{R_0}^\xi$, represents a linear estimate of the percentage change in the state variable R_0 caused by a one percent change in the parameter ξ .

Since we have an analytic expression for R_0 for one and two patches we can explicitly compute the sensitivity indices for R_0 with respect to all the parameters in our model. We evaluate the sensitivity indices at the baseline parameters (see Table 1) for our two patch model. Many of the sensitivity indices depend on the disease-free equilibrium population sizes of perennials and annuals (see appendix for an example), so changing demographic parameters will affect the indices.

The results of this sensitivity analysis are tabulated in Table 2. Based on these results we make the following observations. The sensitivity indices for two perennial (or annual) patches (not shown in Table 2) with very small migration rates are essentially the same as those for one perennial (or annual) patch (see Table 2). For the annual-only patches, $R_0 = R_{0,1}$ is most sensitive to ϵ_a , the fractional reduction in fecundity of infected annuals. If ϵ_a is increased by 10% then R_0 is decreased by 45.46%. If the transmission rates between aphids and annuals, β_{av} or β_{va} , increase or decrease by 10% then R_0 increases or decreases by 5%. The sensitivity indices with respect to μ_V and μ_a , the death rate of aphids and annuals, are constant at -0.5 so that if μ_V or μ_a are increased by 10% then R_0 decreases by 5%. R_0 is just slightly less sensitive to α_{aa} , the competition coefficient between annuals, than it is to μ_V and μ_a . For this case, the sensitivity indices for α_{pa} and α_{Pa} are always zero since $p_S^* = P_S^* = 0$. In summary, the initial spread of B/CYDV in annual-only patches is most sensitive to the fractional reduction in fecundity of infected annuals, the disease transmission rates between aphids and annuals, the death rates of aphids and annuals, and the competitive effect of annuals on each other, in the given order of importance.

In perennial-only patches, R_0 increases by 5% when either β_{pv} or β_{vp} increase by 10%. R_0 decreases by 5% when μ_V increases by 10%. R_0 also decreases by 4.98% when d_P , the growing season death rate of adult perennials, increases by 10%. Neither ϵ_p , μ_p , α_{pP} , nor α_{pp} have much effect on the value of R_0 (see Table 2). For this case, the sensitivity index for α_{ap} is always zero since $a_S^* = 0$. So, the initial spread of B/CYDV in perennials is most sensitive to the adult perennial death rate, disease transmission rates, and aphid death rate for perennial-only patches.

Next we consider two patches that are not identical. When one patch is annual and one is perennial, the annual patch dynamics dominate the initial spread of the virus. R_0^C is most sensitive to ϵ_a as with the annual-only patches. In fact, if ϵ_a is increased by 1%, R_0^C decreases by 4.5%. The rest of the parameters related to annual plants are relatively less important (see Table 2) while the parameters related to perennials have little effect on the value of R_0^C . In Table 2 the migration rate used is rather high. When the migration rate is lower, the perennials are even less significant to the initial spread of disease in the two patch system. The dominant role of annuals in initial spread of B/CYDV is due to their higher density, higher transmission rates, and aphid preference for and increased fecundity on the annual species we are considering. Ultimate persistence of the virus, however, depends almost entirely on the perennials since disease is not maintained in annuals during the dry season and there is no vertical transmission.

5.5.4 Numerical Simulations for the Two Patch Model

For our baseline values, if disease is present, the exotic and native species will be able to coexist, in part due to a basic reproduction number for perennial-only patches greater than one. It may be important for conservation and restoration design to consider the case when a patch of perennials would not support the virus alone but faces invasion by an exotic and competent reservoir for B/CYDV.

We performed numerical simulations for two patches, one perennial only, and one

annual only patch. Perennial disease transmission rates are kept small enough so that a perennial-only patch will have a basic reproduction number less than one ($R_{0,1} < 1$) when there is no migration of vectors between patches. The nearby annual-only patch has baseline annual-aphid transmission rates resulting in a high basic reproduction number, $R_{0,2}$, for that patch. Since we are concerned primarily with the presence of disease in the perennial patch, we consider the sensitivity of $R_{0,1}$ to aphid migration rates. However, equation (5.5.15) indicates that the basic reproduction number for the whole system is proportional to $R_{0,1}$ and $R_{0,2}$ so when $R_{0,1}$ increases, R_0^C increases as well. When migration of vectors is symmetric between the perennial patch and the annual patch, the perennial patch basic reproduction number, $R_{0,1}$ increases with the increase of migration and quickly moves above one. When vectors migrate only from the annual to the perennial patch, $R_{0,1}$ for the perennial patch increases even more quickly and is slightly more sensitive to the migration rates. For both of these cases, $R_{0,1}$ increases as the migration rates of the vectors increase. Thus, movement of vectors between the annual and perennial patches results in persistence of the pathogen in perennials that would not otherwise occur. When vectors migrate only from perennial to annual patch, however, the perennial patch basic reproduction number $R_{0,1}$ decreases slightly as migration increases while the basic reproduction number for the annual patch remains virtually unchanged. These results confirm that the disease dynamics of the annual patches dominate the initial spread and success of the virus and migration behavior of vectors can in fact change the disease dynamics of a perennial-only patch.

5.6 Large Scale Numerical Simulations

For our larger scale numerical simulations we examined the full spatial model with 20 patches arranged linearly, as shown in Figure 5.5. Initial simulations with this model were conducted using within-patch transmission rates high enough for annual grasses to increase in abundance in infected mixed-host patches (see Table 1 for initial parameter

Table 2

Parameter	Annual-only Patch	Perennial-only Patch	One of Each
R_0	343.09	4.8131	310.5801
Sensitivity Indices	$R_{0,1}$	$R_{0,2}$	R_0^C
ϵ_a	-4.5455	0	-4.4961
β_{av}	0.5	0	0.4946
β_{va}	0.5	0	0.4946
μ_V	-0.5	-0.5	-0.4696
μ_a	-0.5	0	-0.4946
α_{aa}	-0.3346	0	-0.3308
β_{pv}	0	0.5	1.2457×10^{-5}
β_{vp}	0	0.5	1.2457×10^{-5}
d_P	0	-0.4986	-1.2423×10^{-5}
ϵ_p	0	-0.0014	-3.4077×10^{-8}
μ_p	0	-0.0014	-3.4077×10^{-8}
α_{pP}	0	-0.0013	-3.2787×10^{-8}
α_{pp}	0	-4.4660×10^{-7}	-1.1127×10^{-11}
m_{12}, m_{21}	0	0	-.0250

TABLE 5.2: Normalized sensitivity indices for R_0 . Note that these rates are in 1/year units. The other parameters used are total time = 100, $\tau = 40/100$, $b_A = 200$, $b_P = 45$, $\mu_V = 10$, $\mu_a = 1$, $\mu_p = 0.5$, $d_V = 13.2$, $d_P = 0.1$, $\alpha_{aa} = 1.1 \times 10^{-3}$, $\alpha_{ap} = 3.4 \times 10^{-7}$, $\alpha_{aP} = 0.7$, $\alpha_{pp} = 1.3 \times 10^{-3}$, $\alpha_{pa} = 6.8 \times 10^{-4}$, $\alpha_{pP} = 0.7$, $\lambda = 1.5$, $\epsilon_a = 0.11$, $\epsilon_p = 0.5$, $\beta_{av} = 0.04$, $\beta_{pv} = 0.02$, $\beta_{vp} = 0.2$, $\beta_{va} = 0.4$, $\sigma_{PS} = 0.88$, $\sigma_{PI} = 0.77$, $m_{12} = m_{21} = .6$, 10 initial annuals for the annual-only, and 4 seedling perennials and 10 adult perennials for the perennial-only patch.

values). Under a global connectivity scenario (identical aphid migration rates between each patch) every patch becomes infected with B/CYDV, even when aphid migration rates are very low ($\leq 10^{-12}\text{yr}^{-1}$). Under this scenario B/CYDV prevalence is so high in annual-only, perennial-only, and mixed-host patches (even when migration rates are very low) that increasing the migration rate does not have a large effect on prevalence. In addition, varying the proportion of patches occupied by perennial grasses does not significantly affect B/CYDV persistence or prevalence; prevalence in each perennial patch remains constant and prevalence in annual patches is 100% by the end of each growing season.

When aphid migration is not global, increasing patch connectivity leads to an increase in the number of infected patches when the simulations are allowed to run to long-term equilibrium (Figure 5.6). Patch connectivity is determined by the number of neighboring patches an aphid can reach when it emigrates from a patch (Figure 5.5). Connectivity is unlikely to be global because aphid dispersal between patches is limited by distance and landscape heterogeneity. An increase in patch connectivity could be the result of either a decrease in the distance between patches or an increase in the distance that individual aphids can travel. As the number of infected patches increases, B/CYDV prevalence at the regional level increases. However, patch-level prevalence depends only on the distance of the patch from the initial source of infection and not the regional-level prevalence.

When each patch is connected with only one or two neighboring patches (in a linear chain), increasing the proportion of perennial-only patches leads to a linear increase in the proportion of infected patches (assuming that all perennial patches are initially infected). However, if we start with B/CYDV in a single source patch, the relationship between the proportion of perennial-occupied patches and B/CYDV prevalence is nonlinear over intermediate timeframes (Figure 5.7). Initial increases in the proportion of perennial patches increase global B/CYDV prevalence by increasing the number of infected patches; but, above a threshold, increasing the number of perennial patches leads to a decline in

the number of infected patches over the first 50 years of the simulation. Although when the simulation is allowed to run to equilibrium, all perennial patches eventually become infected, it can take 50+ years for B/CYDV to reach the furthest patches from the initial source of infection. This occurs because in mixed host patches further away from the initial source of infection the perennial grasses outcompete annual grasses before B/CYDV can arrive in the patch. In this case, increasing the proportion of perennial grasses leads to a decline in the regional level presence of annual grasses (Figure 5.8). The lower transmission rates to and from perennial grasses reduces the number of patches to which B/CYDV can travel within the growing season.

Figure 5.8 also shows that the ability of annuals to coexist with perennials depends on the distance of the patch from initial source of infection as well as the proportion of perennials in the patch system. Only patches within 3 jumps of the initial source of infection receive infected aphid immigrants early enough in the growing season for annuals to overcome their competitive inferiority in the absence of the pathogen. However, simulations of the invasion by annuals in perennial only patches reveal that annuals can invade perennial patches once B/CYDV has become established in the patch. Thus only perennial patches that remain disease-free because they are not connected to any other patches via migration, or are only distantly connected to other perennially infected patches, will remain resistant to invasion from annual grasses.

B/CYDV prevalence at the patch and regional levels is higher when there are mixed patches containing both host species rather than patches containing either all annual or all perennial grasses. The higher transmission rates associated with annual grasses lead to higher prevalence levels in juvenile perennial grasses in mixed patches compared to perennial-only patches (85% versus 60% at equilibrium). In addition, the average abundances of both annual grasses and perennial grasses are reduced in mixed patches. Perennial biomass is reduced by 4.5% and 20.5% in adults and juveniles respectively, and annual biomass can be reduced by up to 30% depending on prevalence.

Thus we can conclude from our numerical simulations that if invasion by annuals

grasses occurs in a patch system where B/CYDV has already established in perennial grasses then annuals will be able to invade all infected patches. However if the introduction of B/CYDV and annual grasses occurs simultaneously, then the success of the annuals will depend on where within the patch system they invade relative to the introduction of B/CYDV. While annuals will be able to invade patches close to the initial site of infection, they will fail to invade patches further from the infection source because they will be outcompeted by perennials before B/CYDV becomes prevalent enough in the patch to counter their competitive inferiority. However, these perennial patches will become susceptible to annual invasion over time as they reach an equilibrium-level of B/CYDV prevalence.

On the west coast of the US, fragmented grassland habitat is arranged along both a north-south and an elevational gradient. Although grasslands in California are dominated by invasive annuals, grasslands in Oregon and at higher elevations tend to remain perennial-dominated. Our sensitivity analysis showed that R_0 is more sensitive to aphid migration rates when transmission rates are lower than predicted for California grasslands. This suggests that a combination of lower B/CYDV transmission rates in perennial-dominated populations and a shorter growing season could prevent annuals from establishing in these populations at a higher latitude or elevation. The simulation results also show that if B/CYDV were initially introduced into a population in Southern California, annuals would be outcompeted at the northern end of the range before the virus became prevalent enough in those populations. The results of the sensitivity analysis suggest that these northern perennial populations could then remain resistant to invasion by annuals if transmission rates were low enough to prevent annual reintroduction.

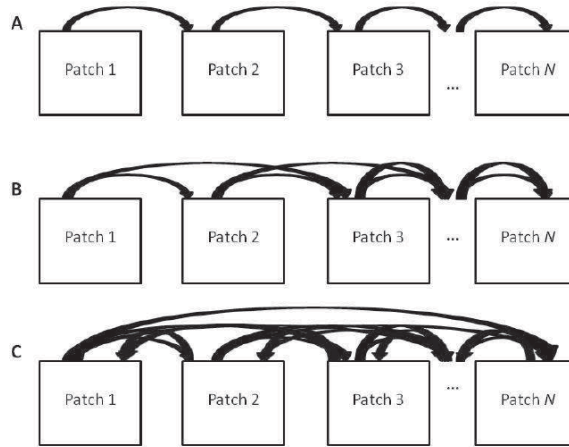


FIGURE 5.5: Linear arrangement of 20 patches used in numerical simulations. Three scenarios included are: (a) aphid migration is unidirectional and to the next patch only, (b) aphid migration is unidirectional and to the two nearest patches, and (c) aphids migration occurs between every patch at the same rate (global connectivity scenario).

5.7 Discussion and Conclusions

The landscape-scale composition and configuration of host communities, along with vector movement patterns among patches, are essential determinants of pathogen spread and prevalence in fragmented landscapes [111, 113]. Pathogen spread depends on host composition (e.g. presence of reservoirs, probability of transmission) and vector density and dispersal, all of which can vary among patches in a complex landscape. Management can increase connectivity, elevating transmission of multi-host pathogens, as is the case with fire suppression increasing connectivity among hosts susceptible to sudden oak death (*Phytophthora ramorum*; see [104]). Landscape-scale host composition also influences the dynamics of many multi-host pathogens, including spread of sudden oak death in California oaks [40], Lyme disease prevalence [29, 4, 28], West Nile virus dynamics [3], hantavirus prevalence in rodents [87], and the spread of foot and mouth disease [80]. Here we have shown that the spatial configuration of the patch system, host composition within patches,

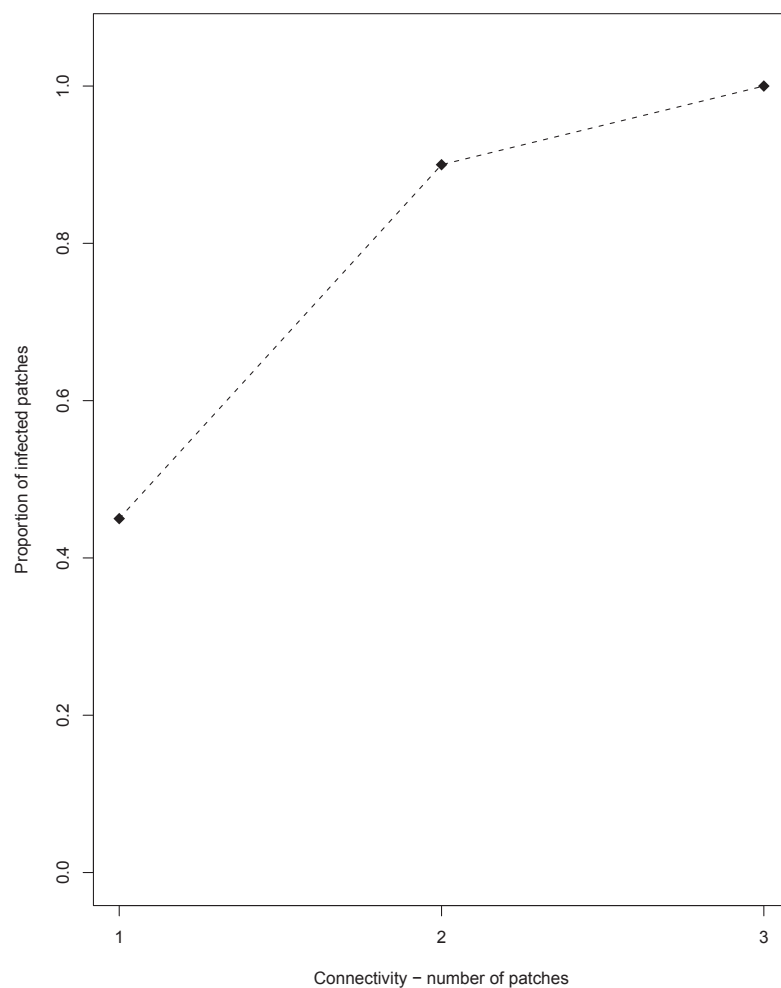


FIGURE 5.6: Proportion of 20 patches that are infected with B/CYDV as a function of the number of neighboring patches that are connected via aphid migration (1, 2, or 3). Figure shows simulation results for scenario where patches contain either all perennial or all annual patches. Points represent the mean proportion of patches infected when the percentage of patches contains perennial grasses is varied from 5% to 100%.

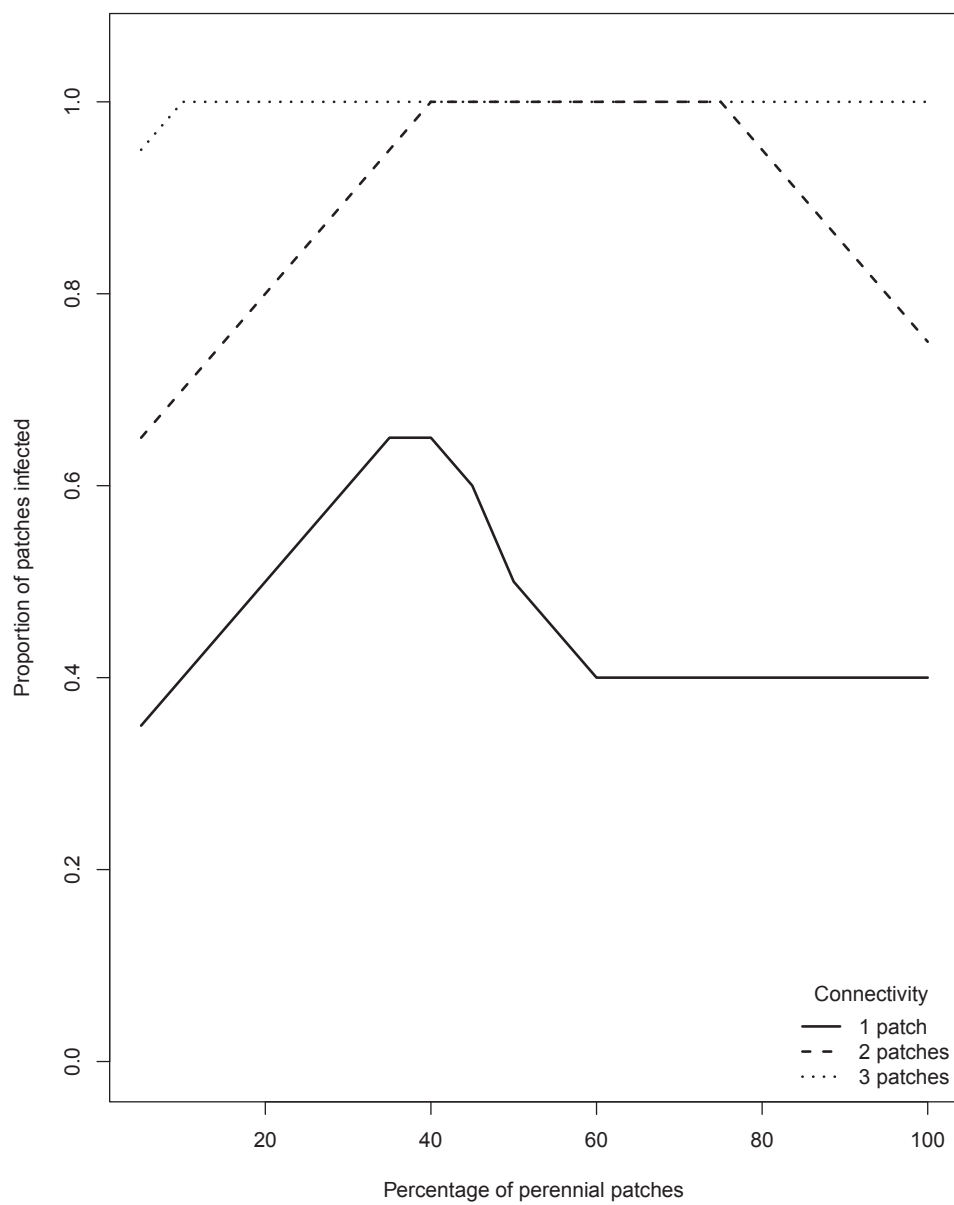


FIGURE 5.7: The proportion of infected patches as a function of the percentage of patches containing perennial grasses when aphids can migrate to the nearest 1, 2, or 3 patches.

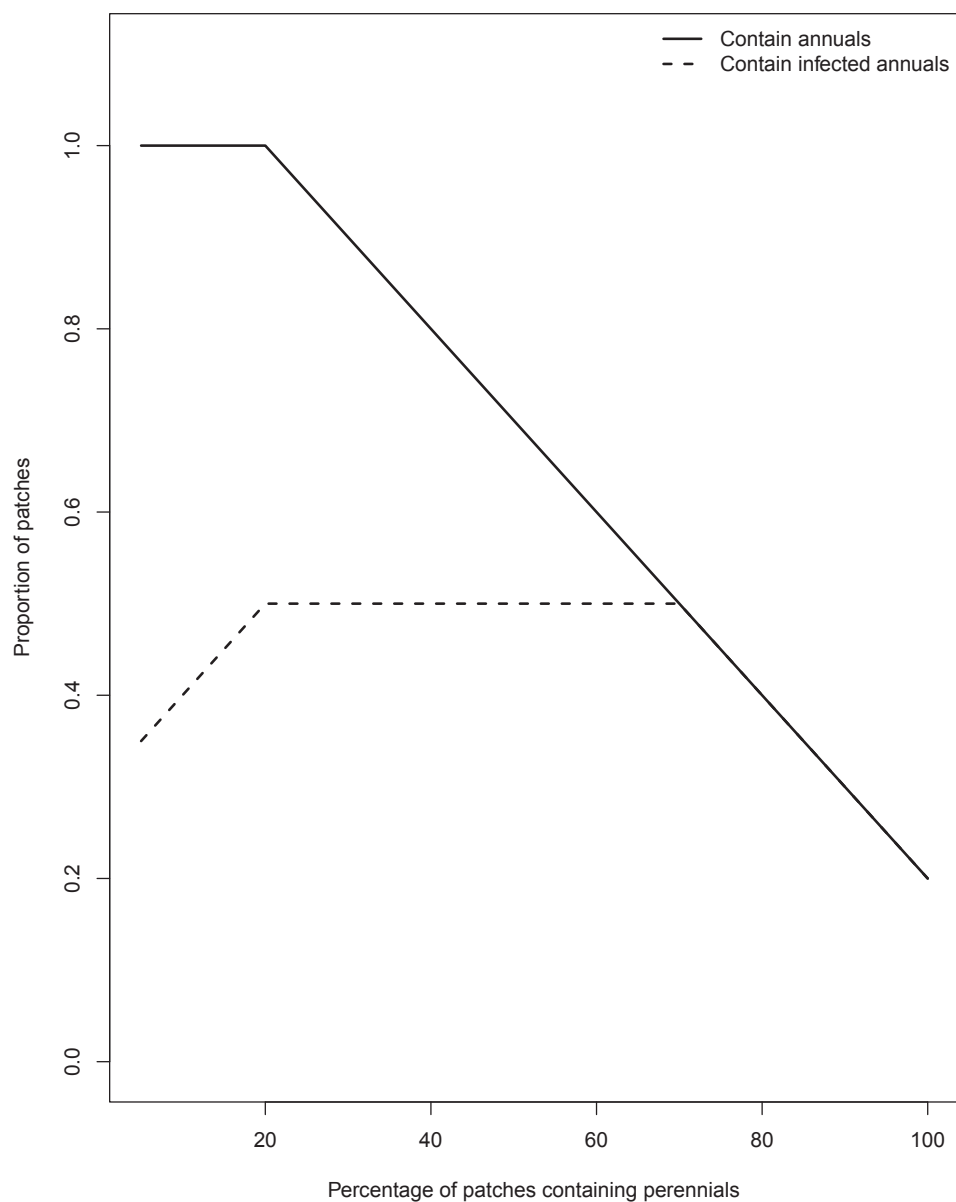


FIGURE 5.8: Proportion of 20 initial patches that contain annual grasses at equilibrium as a function of the number of patches containing perennial grasses in the presence of B/CYDV. Each patch initially contains either annual grasses only, or a mixture of annuals and perennials. B/CYDV is initially present in a single mixed host patch and subsequently spreads via aphid migration.

and patch connectivity affect not only the ability of B/CYDV to invade a fragmented system, but also determine whether the pathogen facilitates the invasion of a non-native host species. Below we discuss these three factors in the context of the analysis conducted for our focal B/CYDV system, and we make broad observations and conclusions that could apply to other similar systems.

The spatial structure of host populations can influence the spread of infectious disease, as well as the spatial pattern of disease prevalence. Here we have shown that the spatial configuration of the host community can interact with the timing of pathogen and invasive host arrival to determine the ability of the pathogen to invade local populations and influence competition between annual and perennial grass species. In our numerical simulations, long term pathogen persistence and prevalence depended on the abundance of perennial grasses in a patch system, with increasing perennial patch occupancy generally leading to an increase in B/CYDV prevalence at the regional level because perennial patches serve as a long-term pathogen reservoirs, whereas annual-only patches do not maintain the pathogen between growing seasons. However, high proportions of perennial patches can slow the spread of B/CYDV during the growing season because both aphid fecundity and transmission rates are lower for perennial grasses than annuals. Thus, mixed species patches or mixtures of patches with differing host composition tend to have the highest prevalence rates because of the balance among pathogen residence time, pathogen transmission probability, and vector fecundity.

The viral-induced reduction in annual host fecundity was the most important factor controlling the successful initial spread of B/CYDV in mixed populations of annuals and perennials and in perennial-only populations that were connected to annual populations via aphid dispersal. Because annual hosts are superior to perennials for vector fecundity in this system, the suppressive effect of infection on annuals and the amplification via vector density interact to control the rate of pathogen spatial spread. The baseline value for B/CYDV's effect on annual fecundity was based on observations of the exotic annual *Bromus hordeaceus* in California grasslands. However, the impact of the virus on host

fecundity will vary by host species and also be mediated by environmental conditions [134]. Therefore, in our focal system, B/CYDV prevalence levels in perennial populations will depend on both the identity of nearby annual grasses as well as the environmental conditions experienced by the annuals. If the reduction in annual fecundity is higher than we estimated, annual grasses may not be able to invade perennial populations. More generally, host composition can feed back to control pathogen spread rates in a patchy system.

Spatial connectivity can control both dispersal rates and local species densities. In animal communities, both hosts and vectors can move among patches; however, in our focal community, among-patch host movement is negligible, whereas vector dispersal is key. Landscape-scale host composition can interact with vector dispersal to control disease spread and epidemics, as in our case study. Similarly, bean dwarf mosaic virus, a whitefly-transmitted virus that infects both soybeans and common bean plants causes severe disease in the latter. In Argentina, increased soybean acreage shifted the landscape-scale host composition, leading to the emergence of bean dwarf mosaic virus and threatening local common bean production [45]. In multi-host communities where hosts also move among patches, this will add further complexity that warrants future exploration. In mixed-host communities, hosts vary in infection tolerance and probability of transmission; our results suggest that this variation can interact with patch connectivity to affect pathogen persistence and prevalence. This has important implications for both conservation and understanding species invasions. For example, increased patch connectivity, a common management scheme for endangered species, can lead to increased pathogen transmission and prevalence [65, 64]. Our results suggest that this is especially true for mixed-host communities. If hosts differ strongly in their pathogen tolerance, a less tolerant species of concern could be driven to extinction in a highly connected landscape [72], particularly by a vector-transmitted disease [44].

Species invasions can shape the composition of communities, species coexistence, and biodiversity in fragmented patch systems, and pathogens have been implicated in species

invasions in the B/CYDV system and others. For example, in the United Kingdom the invasive grey squirrel and an introduced parapox virus are causing declines in the native red squirrel population through resource competition and pathogen-mediated apparent competition [125, 143]. In the B/CYDV system coexistence of annual and perennial grasses requires B/CYDV to reduce the competitive advantage of perennial grasses [24]. Our current results modify this non-spatial understanding. In the context of a fragmented patch system, the ability of annuals to invade depends on the timing of invasion with respect to the introduction of disease, the spatial locations where these invasions happen, and the composition and configuration of the patch system. Thus, our current results suggest that connectivity can interact with arrival time and host infection tolerance to determine the success or failure of an invasion.

5.8 Normalized Sensitivity Indices

Following are the normalized sensitivity indices for the annual-only patch:

$$\psi_{R_{0,1}}^{\mu_V} = \frac{\mu_V}{R_{0,1}} \frac{1}{2R_{0,1}} \left(\frac{-\beta_{av}V_S^*}{\mu_V^2} \frac{\beta_{va}a_S^*}{\epsilon_a\mu_a(1 + \alpha_{aa}a_S^*)} \right) \quad (5.8.1)$$

$$\psi_{R_{0,1}}^{\beta_{av}} = \frac{\beta_{av}}{R_{0,1}} \frac{1}{2R_{0,1}} \left(\frac{V_S^*}{\mu_V} \frac{\beta_{va}a_S^*}{\epsilon_a\mu_a(1 + \alpha_{aa}a_S^*)} \right) \quad (5.8.2)$$

$$\psi_{R_{0,1}}^{\beta_{va}} = \frac{\beta_{va}}{R_{0,1}} \frac{1}{2R_{0,1}} \left(\frac{\beta_{av}V_S^*}{\mu_V} \frac{a_S^*}{\epsilon_a\mu_a(1 + \alpha_{aa}a_S^*)} \right) \quad (5.8.3)$$

$$\psi_{R_{0,1}}^{\epsilon_a} = \frac{\epsilon_a}{R_{0,1}} \left(\frac{1}{2R_{0,1}} \frac{\beta_{av}V_S^*}{\mu_V} \frac{-\beta_{va}a_S^*}{\epsilon_a^2\mu_a(1 + \alpha_{aa}a_S^*)} \right) \quad (5.8.4)$$

$$\psi_{R_{0,1}}^{\mu_a} = \frac{\mu_a}{R_{0,1}} \left(\frac{1}{2R_{0,1}} \frac{\beta_{av}V_S^*}{\mu_V} \frac{-\beta_{va}a_S^*}{\epsilon_a\mu_a^2(1 + \alpha_{aa}a_S^*)} \right) \quad (5.8.5)$$

$$\psi_{R_{0,1}}^{\alpha_{aa}} = \frac{\alpha_{aa}}{R_{0,1}} \left(\frac{1}{2R_{0,1}} \frac{\beta_{av}V_S^*}{\mu_V} \frac{-\beta_{va}(a_S^*)^2}{\epsilon_a\mu_a^2(1 + \alpha_{aa}a_S^*)^2} \right) \quad (5.8.6)$$

Normalized sensitivity indices for the perennial-only patch:

$$\psi_{R_{0,1}}^{\beta_{pv}} = \frac{\beta_{pv}}{R_{0,1}} \frac{1}{2R_{0,1}} \frac{V_S^*}{\mu_V} \left(\frac{\beta_{vp} p_S^*}{\epsilon_p \mu_p (1 + \alpha_{pp} p_S^* + \alpha_{Pp} P_S^*)} + \frac{\beta_{vp} P_S^*}{d_P} \right) \quad (5.8.7)$$

$$\psi_{R_{0,1}}^{\mu_V} = \frac{\mu_V}{R_{0,1}} \left(\frac{1}{2R_{0,1}} \left(\frac{-\beta_{pv} V_S^*}{\mu_V^2} \left(\frac{\beta_{vp} p_S^*}{\epsilon_p \mu_p (1 + \alpha_{pp} p_S^* + \alpha_{Pp} P_S^*)} + \frac{\beta_{vp} P_S^*}{d_P} \right) \right) \right) \quad (5.8.8)$$

$$\psi_{R_{0,1}}^{\beta_{vp}} = \frac{\beta_{vp}}{R_{0,1}} \frac{1}{2R_{0,1}} \frac{\beta_{pv} V_S^*}{\mu_V} \left(\frac{p_S^*}{\epsilon_p \mu_p (1 + \alpha_{pp} p_S^* + \alpha_{Pp} P_S^*)} + \frac{P_S^*}{d_P} \right) \quad (5.8.9)$$

$$\psi_{R_{0,1}}^{\mu_p} = \frac{\mu_p}{R_{0,1}} \left(\frac{1}{2R_{0,1}} \frac{-\beta_{pv} V_S^*}{\mu_V} \frac{\beta_{vp} p_S^*}{\epsilon_p \mu_p^2 (1 + \alpha_{pp} p_S^* + \alpha_{Pp} P_S^*)} \right) \quad (5.8.10)$$

$$\psi_{R_{0,1}}^{\alpha_{pp}} = \frac{\alpha_{pp}}{R_{0,1}} \left(\frac{1}{2R_{0,1}} \frac{\beta_{pv} V_S^*}{\mu_V} \frac{-\beta_{vp} (p_S^*)^2}{\epsilon_p \mu_p (1 + \alpha_{pp} p_S^* + \alpha_{Pp} P_S^*)^2} \right) \quad (5.8.11)$$

$$\psi_{R_{0,1}}^{\alpha_{pP}} = \frac{\alpha_{pP}}{R_{0,1}} \left(\frac{1}{2R_{0,1}} \frac{\beta_{pv} V_S^*}{\mu_V} \frac{-\beta_{vp} P_S^* p_S^*}{\epsilon_p \mu_p (1 + \alpha_{pp} p_S^* + \alpha_{pP} P_S^*)^2} \right) \quad (5.8.12)$$

$$\psi_{R_{0,1}}^{d_P} = \frac{d_P}{R_{0,1}} \frac{1}{2R_{0,1}} \left(\frac{\beta_{pv} V_S^*}{\mu_V} \frac{-\beta_{vp} P_S^*}{d_P^2} \right) \quad (5.8.13)$$

$$\psi_{R_{0,1}}^{\epsilon_p} = \frac{\epsilon_p}{R_{0,1}} \frac{1}{2R_{0,1}} \frac{\beta_{pv} V_S^*}{\mu_V} \frac{-\beta_{vp} p_S^*}{\epsilon_p^2 \mu_p^2 (1 + \alpha_{pp} p_S^* + \alpha_{pP} P_S^*)} \quad (5.8.14)$$

For the normalized sensitivity indices computed above, $p_S^*, P_S^*, a_s^*, V_S^*$ are the equilibrium values of susceptible seedling perennials, adult perennials, annuals, and vectors for the growing season dynamics. These equilibrium values are computed numerically by running the numerical simulation for 100 years and using the values for each group at the end of the growing season.

For the normalized sensitivity indices of R_0^C , we note that for parameter ξ

$$\frac{\partial R_0^C}{\partial \xi} = \frac{\partial R_0^C}{\partial R_{0,1}} \frac{\partial R_{0,1}}{\partial \xi} + \frac{\partial R_0^C}{\partial R_{0,2}} \frac{\partial R_{0,2}}{\partial \xi} + \frac{\partial R_0^C}{\partial R_{\mu_V}} \frac{\partial R_{\mu_V}}{\partial \xi} + \frac{\partial R_0^C}{\partial R_m} \frac{\partial R_m}{\partial \xi}. \quad (5.8.15)$$

Then we can use the sensitivity indices given before for $R_{0,1}$ and the following to compute

the sensitivity indices of R_0^C :

$$\begin{aligned} \frac{\partial R_0^C}{\partial R_{0,1}} &= \frac{1}{4R_0^C} \left(\frac{1}{2R^*} [2R_{\mu_V}(R_{0,1}^2 - R_{0,2}^2)2R_{0,1} + 2R_m^2(R_{0,1}^2 + R_{0,2}^2)2R_{0,1}] \right. \\ &\quad \left. + 2(R_{\mu_V} + R_m)R_{0,1} \right) \end{aligned} \quad (5.8.16)$$

$$\begin{aligned} \frac{\partial R_0^C}{\partial R_{0,2}} &= \frac{1}{4R_0^C} \left(\frac{1}{2R^*} [-2R_{\mu_V}(R_{0,1}^2 - R_{0,2}^2)2R_{0,2} + 2R_m^2(R_{0,1}^2 + R_{0,2}^2)2R_{0,2}] \right. \\ &\quad \left. + 2(R_{\mu_V} + R_m)R_{0,2} \right) \end{aligned} \quad (5.8.17)$$

$$\frac{\partial R_0^C}{\partial R_{\mu_V}} = \frac{1}{4R_0^C} \left(\frac{1}{2R^*} (R_{0,1}^2 - R_{0,2}^2)^2 + (R_{0,1}^2 + R_{0,2}^2) \right) \quad (5.8.18)$$

$$\frac{\partial R_0^C}{\partial R_m} = \frac{1}{4R_0^C} \left(\frac{1}{2R^*} 2R_m(R_{0,1}^2 - R_{0,2}^2)^2 + (R_{0,1}^2 + R_{0,2}^2) \right) \quad (5.8.19)$$

6 NETWORK MODEL FOR THE SPREAD OF RINDERPEST

6.1 Introduction

This chapter is the interdisciplinary chapter resulting from an internship at Los Alamos National Laboratory. It represents work with a team from multiple disciplines and institutions. We use mathematical methods to model and analyze the introduction and spread of rinderpest in livestock in the United States. This model is a multi-patch, multi-host disease model similar to those discussed in Chapters 2-4 but on a larger scale, applied to five hosts and approximately 3,000 patches. Since the model is for livestock, competition between species is not included. We see here, as in Chapter 5, that adding spatial heterogeneity to a multi-host disease model can change the outcome of and give additional insight into the non-spatial model.

Animal diseases, such as foot-and-mouth disease and avian influenza, are increasingly important in world economics, national security, and biodiversity. Introduction of an exotic livestock disease to the United States (US) either by natural or anthropogenic means could have serious economic and public health consequences. Direct costs due to recent outbreaks of mad cow disease and foot-and-mouth disease in the United Kingdom cost billions of dollars in death of animals, culling, and vaccination. Although direct costs can be enormous, indirect costs such as loss in livestock exports are often much greater. In addition to economic loss, animal diseases are often a human public health threat. Many animal diseases (e.g., avian flu, tularemia, monkeypox) are zoonotic and can be spread from animals to humans.

To help prepare for the possibility of a serious animal disease epidemic, we created a spatially explicit stochastic model for multi-host animal diseases to better understand their spread in the US. The model uses county-level data and between-state animal transportation rates to capture both the intra-county and inter-county behavior of an epidemic.

The model is flexible and can be used to simulate many types of animal diseases among various animal groups (poultry, cattle, pigs, etc.) while incorporating surveillance and response strategies.

Rinderpest is a virus closely related to human measles and canine distemper that affects cloven-hoofed animals such as cows, pigs, sheep, and wild or domestic buffalo [141, 96]. This virus can cause high morbidity and mortality in naive populations, is highly transmissible and has a long history of devastating livestock herds and wildlife in Europe, Asia, and Africa [96, 77]. During World War II, vaccinations for rinderpest were developed and produced in response to a possible threat of rinderpest introduced to the US [147].

Rinderpest has a fairly short incubation period of 4 to 5 days followed by 1 to 2 weeks of clinical signs, including fever, loss of appetite, lesions, diarrhea, dehydration, and death. Clinical signs can continue for many weeks as animals recovering from the acute phase suffer debility, secondary infection e.g. skin disease, eye pathology and other manifestations. In its most virulent form and with a high density population of naive animals, rinderpest is a fast-moving disease that requires a large number of susceptible animals to persist [119, 123]. There are avirulent strains of rinderpest that have occurred in many different situations, but we will focus on virulent and/or rapidly spreading strains. Mariner et al. [96] estimated the reproductive number of the more virulent lineage of rinderpest to be 4.4 and the 1.2 for the less virulent lineage.

A relatively mild form of rinderpest endemic to cattle can have devastating effects on wildlife populations and vice versa. Domestic cattle and wild or domestic buffalo have the highest death rates due to rinderpest but it also affects sheep, goats, pigs, and many wildlife species [20]. Additionally, wildlife populations may be an important source of re-infection of rinderpest [85]. European bison and deer were susceptible to rinderpest with high mortality rates. White-tailed deer have also been infected experimentally, so it is likely they and other wildlife species could be a factor in the spread of rinderpest in the United States. For the past decade, the Food and Agriculture Organization of the United

Nations has been working on eradicating the disease through vaccination and intense surveillance and was officially considered eradicated in October, 2010 [51]. Rinderpest virus was last confirmed in wild buffalo in Kenya in 2001-2 and there is no confirmed case or serological evidence of circulation of virus amongst wildlife since then. Equivocal serology from cattle due to rinderpest has not been confirmed in any location or livestock population within the declared infection zone of the Somali ecosystem of East Africa since that period and all vaccination has ceased since 2003 [51, 53].

However, due to severity of rinderpest epidemics-and like smallpox- it will remain a disease to research if it were to infect animal populations outside the laboratory. If rinderpest were to emerge in the US, the loss in livestock would likely be devastating. Rinderpest has never been detected in North America so there is no immunity to the disease among our livestock or wildlife. Historically, introduction into nine herds causes high death rates [90]. In the 1890s, the effects on cattle herds in eastern Africa and large portions of sheep, goat, and ungulate wildlife populations were severe, changing the distribution of animals in many regions of Africa. Consequences of this epidemic for people living in the area included famine for some pastoral groups in sub-Saharan Africa, including the Maasai. It was also a catalyst for the re-emergence of human diseases such as sleeping sickness, which were temporarily absent due to the loss of tsetse fly hosts in regions of Africa caused by rinderpest mortality [90, 99, 123]. If rinderpest entered the US, it could be devastating to animal agriculture, wildlife, and the economy. To investigate effective responses to an introduction of rinderpest to the US, we have adapted our spatial epidemiology model specifically to the behavior of primary hosts of rinderpest.

James and Rossiter [123], Lefevre et al. [141], and Mariner et al. [96] have previously developed mathematical models for the spread of rinderpest in Africa. All three incorporate different vaccination programs and stochasticity to explore the spread of rinderpest in cattle herds within parts of Africa where the disease is either endemic or has been present in the past. Their models do not include multiple hosts or spatial heterogeneity, both of which are important to the spread of rinderpest. The models were used for previously

exposed or vaccinated herds and some of the parameter values would not be accurate for an epidemic in the US, since rinderpest is an exotic disease for the US and all animals would be immunologically naive. Our model extends and expands the ideas in these models to include multiple mitigation strategies, spatial spread among counties on a network, multiple host categories, and the effects of rinderpest on naive herds. Our objective was to model a rinderpest outbreak in the US to determine agricultural and veterinary practices that minimize the risk of catastrophic damage from this exotic disease. Using an epidemiological model, we explore the effectiveness of various mitigation strategies such as surveillance, quarantine, vaccination, movement control, and culling, which are incorporated in the model. We determine the sensitivity of the model to these strategies and compare results for different responses in order to minimize risk and damage. For rinderpest, the relevant groups of livestock are sheep, hogs and pigs, dairy cows, cattle on feed, and beef cattle. The mathematical model was used to estimate the extent of spread in, and the relevance of, each of these groups. Because there are no data for rinderpest in the US, our model is useful for creating a plan of action should an outbreak occur.

6.2 Methods

Here we present a two-stage hybrid model of the spread of a multi-host infectious disease among agricultural animals in the US using rinderpest as a case study. The model incorporates large-scale interactions between US counties and the small-scale dynamics of disease spread within a county. The large-scale interactions and spread of disease between counties is stochastic. To model within county dynamics, we analyze a distribution of solutions to deterministic equations (see Section 6.3) with parameters sampled from the ranges in Table 6.1. The model is designed to be as general as possible so that it can be adapted to varying parameter values and situations.

TABLE 6.1

Par	Description	Baseline	Range	Ref.
ι_i^I	infectivity of species i in stage I	0.00000023	N/A	[99]
ι_i^L	infectivity of species i in stage L (subclinical)	0.000000115	N/A	[85]
ι_i^C	infectivity of species i in stage C (carrier)	0.000000115	N/A	[99]
s_4^s	susceptibility of susceptible stage feedlot cattle	5.0	N/A	[107, 109, 115]
s_i^s	susceptibility of animals besides feedlot in stage S	22.5	N/A	[109]
$r(X)$	1/measure of density of animals in county x		N/A	[108, 141]
a	constant of proportion for contact rate	5	N/A	N/A
β_{ij}^{mn}	transmission rate from type j in stage n to type i in stage m		N/A	[37, 77, 109, 120]
r_{V_s}	reduced susceptibility of vacci- nated susceptible animals	0.5	N/A	[13, 14, 15]
r_{V_e}	reduced infectivity of vaccinated quiescent infected animals	0.5	N/A	[15, 132]
Continued on next page				

TABLE 6.1 – continued

Par	Description	Baseline	Range	Ref.
λ_L	rate of progression from latent to infectious stage (1/ residency time in stage)	1/4.5 days	1/ 3-6	[116, 114]
λ_C	rate of progression from carrier to recovered	1/ 698.75 days	1/120-1277.5	[55]
λ_I	rate of progression from infectious to recovered	1/ 6 day	1/ 4-8 days	[55, 85]
λ_{V_s}	rate of progression from vaccinated susceptible to recovered	1/ 10.5 days	1/ 7-14	[55]
λ_{V_e}	rate of progression from vaccinated quiescent infected to recovered	1/698.75 days	1/ 120-1277.5	[85]
λ_R	rate of progression from recovered to susceptible	0	0	N/A
θ_L	ratio of infected progress to clinical symptoms	0.975	0.95-1	[85]
θ_D	ratio of infectious that die	0.9	0.8-1.0	[116]
ϵ_q	efficacy of quarantine (ratio of susceptible successfully quarantined)	0.5	0.1-0.9	[13]
ϵ_{v_s}	efficacy of vaccine for susceptibles (will move into immune)	0.775	0.6-0.95	[77]
ϵ_{v_e}	efficacy of vaccine for exposed (latent only)	0.775	0.6-0.95	[119, 77]
ϵ_c	efficacy of culling	0.5	N/A	[53, 121]
ϵ_s	efficacy of short-range movement control	0.5	0.1-0.9	N/A
Continued on next page				

TABLE 6.1 – concluded

Par	Description	Baseline	Range	Ref.
ϵ_l	efficacy of long-range movement control	0.5	0.1-0.9	N/A
T_l	time after detection until inter-state movement restricted	6.5 days	1-14 days	N/A
T_{v1}	time after first detection in U.S. until vaccine widely available	33.5 days	7-60 days	N/A
T_{v2}	time after further detection locally until vaccine available	17 days	N/A	N/A
T_q	time after detection until quarantine implemented	2 days	1-3 days	N/A
T_c	time after detection until culling implemented	2 days	1-3 days	N/A
η	number of infected animals needed to trigger official detection	50	N/A	N/A
k	constant of proportionality for long-range movement kernel	0.001	N/A	N/A

TABLE 6.1: Model parameter description and disease input ranges used with supportive references.

6.3 Intra-County Model

We begin with the micro-scale intra-county model in which deterministic equations modeling disease spread within a county are solved for parameters sampled randomly from across their ranges. First, we assumed that there is no natural death of hosts, so that animals in the model die due to infection or culling. For this case study, the “types”

of animals are beef cattle, dairy cattle, cattle on feed, sheep and goats, and pigs. We will refer to each of the susceptible, infectious, recovered, dead, vaccinated, quarantined, etc compartments as a disease stage. Within each county there is no heterogeneity for livestock distributions in respect to the number of farms accounting for the number of animals. Each susceptible host of type i in county x , denoted S_i^x , has a certain probability, namely μ_{ij}^{mn} , of becoming infected with the pathogen due to contact with another infected animal of type j . This probability is based on the susceptibility to disease of animal type i in stage m , denoted s_i^m , the infectivity of animal type j in stage n , denoted ι_j^n , and a scaled contact rate based on the density of farm animals in the county, denoted $e^{-r(x)/a}$ where $r(x) = 1/\sqrt{N/A}$. Here, N is the total number of all types of animals in the county, A is the area of the county, and a is a constant of proportionality referred to as the characteristic length of local spread. The transmission rate, or probability of infection, is

$$\mu_{ij}^{mn} = (\text{infectivity})(\text{susceptibility})(\text{contact rate})(\text{fraction infected})$$

where *fraction infected* = $\frac{n_j}{N}$ for n_j the number of animals in (infected) stage n of type j and represents the probability that a contact is with an infected individual. For our case, we then rewrite the transmission probability as

$$\mu_{ij}^{mn} = (\text{infectivity})(\text{susceptibility}) \frac{(\text{contact rate})}{(\text{total population})} (\text{number infected})$$

So, the probability of species i in stage m becoming infected by species j in stage n is $\mu_{ij}^{mn} = \iota_j^n s_i^m e^{-r(x)/a} n_j = \beta_{ij}^{mn} n_j$ where $e^{-r(x)/a}$ is the true contact rate scaled by the total number of animals, N . Also note that for very low densities, $e^{-r(x)/a}$ behaves linearly, and as density increases, $e^{-r(x)/a}$ approaches 1 as its slope approaches zero. We use a transmission function that moves between a linear dependence at low animal density and saturates at high animal density.

The possible progressions through the disease states of our model, which begin in the susceptible state, S , and progress to either recovered, R , or dead, D , are diagrammed in Figure 6.1. After becoming infected, a susceptible host can move into either a subclinical “latent” state or a subclinical “carrier” non-progressing state with probability θ_L or $1 - \theta_L$

respectively. The host in the subclinical latent (incubation) stage, L_i^x , with infectivity ι_i^L remains for a residence time of $1/\lambda_L$ upon which the host transitions into a symptomatic infectious stage, I_i^x . The hosts in the carrier stage, C_i^x , have an infectivity of ι_i^C but never exhibit clinical signs and after a residency time of $1/\lambda_C$ move into a recovered, immune stage, R_i^x . We will refer to L_i^x and C_i^x as the quiescent infected group. Meanwhile, hosts in the infectious stage will have infectivity ι_i^I and remain infectious with time of $1/\lambda^I$ after which they will either die or recover with probability θ_D and $1 - \theta_D$ respectively. The recovered class remains immune for life.

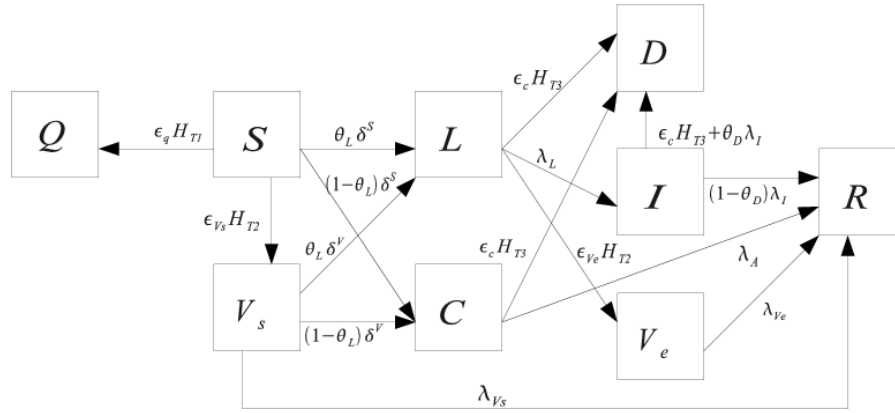


FIGURE 6.1: Description of the intra-county disease progression model. See Table 6.1 for specific symbol descriptions used in the model.

The intra-county portion of the model also includes mitigation processes such as vaccination, quarantine, and culling, as well as the response time and efficacy of each of these control measures. After 50 hosts are infected in a county, the disease is officially detected with a corresponding time of detection, τ_d , and control measures are implemented with an appropriate time lag. The first response to detection is quarantine. At the time of quarantine, t_1 , uninfected hosts are isolated and thus removed from the susceptible compartment. Here, ϵ_q is the efficacy of the quarantine, so that the total number of animals of type i successfully quarantined are $\epsilon_q S_i^x$. The quarantine has a time lag, T_q , of 1-2 days. We used a wide range for between 7 and 60 days when vaccines become

widely available after the first time disease is detected in the US and we used an average of 33.5 days to become available locally after subsequent detection of disease in a county. We wanted to test for the impacts of having vaccines ready versus a longer time period for vaccine development. For ϵ_{v_s} and ϵ_{v_e} the efficacy of vaccination on susceptible and quiescent infected animals respectively, the total number of successfully vaccinated animals of type i at the time of vaccination, t_2 , is $\epsilon_{v_s}S_i^x + \epsilon_{v_e}(L_i^x + C_i^x)$. There is a lag between time of vaccination and immunity so vaccinated susceptibles are moved into a temporary stage V_s with residency time $1/\lambda_{V_s}$ and susceptibility to disease reduced by a factor of r_{V_s} so that $\beta_{ij}^{V_s M} = r_{V_s}\beta_{ij}^{SM}$ where M is one of the infectious states. Similarly, vaccinated latent animals (in L_i^x) are moved into stage V_e with residency time $1/\lambda_{V_e}$ with infectivity reduced by a factor of r_{V_e} so that $\beta_{ij}^{MV_e} = r_{V_e}\beta_{ij}^{ML}$. It is assumed that vaccinated carriers exhibit no different behavior than un-vaccinated carriers so that carriers that are vaccinated simply remain in the C_i^x , or carrier, stage.

Lastly, we consider culling, which has a lag time of 1-2 days after detection and an efficacy of ϵ_c . Culling can occur in two instances: if a county is under surveillance for the disease, then both infectious and quiescent infected groups are culled at time t_3^* , whereas if a county is not under official surveillance, then only clinical infectious animals are culled at time t_3 . Notice that this implies the ideal situation where no susceptible or recovered animals are culled. A county will be put under surveillance if it is within 20 miles of another known infected county that is under quarantine (this happens if the number of clinical infectious animals in the county is greater than $\nu = 50$ and enough time, T_q , has elapsed for a quarantine to be put into place) or if the county itself is under quarantine. This surveillance zone estimate is a conservative estimate based on the average surveillance zone size of 30 km for foot and mouth epidemics in Europe. Since accurate pen-side tests for rinderpest are available, good surveillance and methodical separation of infected animals is possible.

The equations for the intra-county model are then

$$\frac{dS_i^x}{dt} = -\delta_i^s(x)S_i^x - \epsilon_q S_i^x \mathcal{H}_{t_1} - \epsilon_{v_s} S_i^x \mathcal{H}_{t_2} \quad (6.3.1)$$

$$\frac{dV_{s_i}^x}{dt} = -\delta_i^v(x)V_{s_i}^x - \lambda_{V_s} V_{s_i}^x + \epsilon_{v_s} S_i^x \mathcal{H}_{t_2} \quad (6.3.2)$$

$$\frac{dL_i^x}{dt} = \theta_L(\delta_i^s(x)S_i^x + \delta_i^v(x)V_{s_i}^x) - \lambda_L L_i^x - \epsilon_{v_e} L_i^x \mathcal{H}_{t_2} - \epsilon_c L_i^x \mathcal{H}_{t_3^*} \quad (6.3.3)$$

$$\frac{dC_i^x}{dt} = (1 - \theta_L)(\delta_i^s(x)S_i^x + \delta_i^v(x)V_{s_i}^x) - \lambda_C C_i^x - \epsilon_c C_i^x \mathcal{H}_{t_3^*} \quad (6.3.4)$$

$$\frac{dI_i^x}{dt} = \lambda_L L_i^x - \lambda_I I_i^x - \epsilon_c I_i^x \mathcal{H}_{t_3^*} \quad (6.3.5)$$

$$\frac{dV_{e_i}^x}{dt} = -\lambda_{v_e} V_{e_i}^x + \epsilon_{v_e} L_i^x \mathcal{H}_{t_2} \quad (6.3.6)$$

$$\frac{dR_i^x}{dt} = \lambda_{v_s} V_{s_i}^x + \lambda_C C_i^x + (1 - \theta_D)\lambda_I I_i^x + \lambda_{v_e} V_{e_i}^x \quad (6.3.7)$$

$$\frac{dD}{dt} = \theta_D \lambda_I I_i^x + \epsilon_c (L_i^x + C_i^x) \mathcal{H}_{t_3^*} + \epsilon_c I_i^x \mathcal{H}_{t_3^* \cup t_3} \quad (6.3.8)$$

where

$$\delta_i^s(y) = \sum_j (\beta_{ij}^{SL} L_j^y + \beta_{ij}^{SC} C_j^y + \beta_{ij}^{SI} I_j^y + r_{V_e} \beta_{ij}^{SL} V_{e_j}^y) \quad (6.3.9)$$

$$\delta_i^v(y) = \sum_j (r_{V_s} (\beta_{ij}^{SL} L_j^y + \beta_{ij}^{SC} C_j^y + \beta_{ij}^{SI} I_j^y) + r_{V_s} r_{V_e} \beta_{ij}^{SL} V_{e_j}^y) \quad (6.3.10)$$

and

$$\mathcal{H}_A = \mathcal{H}_A(t) = \begin{cases} 0 & t \notin A \\ 1 & t \in A \end{cases}$$

Finally, t_1^x is the set of all times when a quarantine occurs in county x , t_2^x the set of all times when vaccination occurs in county x , t_3^x when culling occurs in a county x not under surveillance, and $t_{3^*}^x$ the set of all times when culling occurs in a county x under surveillance. For this model, mitigation is conducted on the day scale so that the SIR-type model is run for a full day in a county and at the end of that day mitigation strategies are implemented and numbers of animals in each stage are updated accordingly before running the SIR-type model for the next day.

6.4 Inter-County Model

Next, we discuss the macro-scale inter-county and inter-state model. Figure 6.2 shows the density of cattle in the US with county-level resolution. This and similar data for the other animal classifications are available from the 2007 agricultural census and the cattle are split into beef cattle, dairy cattle, cattle on feed as used in the model [108]. Each susceptible county, x , has a probability of becoming infected of $p_x(t) = 1 - e^{-\Gamma_x(t)}$ where $e^{-\Gamma_x(t)}$ is the probability of *not* becoming infected and

$$\Gamma_x(t) = \sum_i \sum_y [\delta_i^s(y, t) S_i^x + \delta_i^v(y, t) V_{si}^x] [\chi_s(t) \kappa_s(x, y) + \chi_l \kappa_l(x, y)] \quad (6.4.1)$$

for i the number of species and y the number of counties. We use χ to indicate reduced long or short range movement due to movement control measures put into place after detection of a disease and use κ as a long or short range movement kernel. For this model

$$\chi_s = \begin{cases} 1 & t < \tau_d \\ \epsilon_s & t \geq \tau_d \end{cases} \quad (6.4.2)$$

$$\chi_l = \begin{cases} 1 & t < \tau_d + T_l \\ \epsilon_l & t \geq \tau_d + T_l \end{cases} \quad (6.4.3)$$

$\kappa_s(x, y) = e^{-\frac{\|r_x - r_y\|}{a}}$ and $\kappa_l(x, y) = 1 - e^{-k \sum_i g_i(x, y) \Delta t}$. Here, a is a constant of proportionality for short-range movement seen as the length scale of transmission resulting from animal-to-animal contact and fomites, $\|r_x - r_y\|$ is the distance between counties x and y (on a sphere), k is a constant of proportionality for long-range movement, and Δt is the time step being used. For our simulations, $\Delta t = 0.125$ (approximately 1/8 day). Also, $g_i(x, y)$ is the frequency of inter-state movement from state y into state x based on data from the US Department of Agriculture [135].

We chose 16 starting locations for the epidemic as case studies for our model. To determine starting locations, we picked two counties from the top ten counties for number of each of the groups of animals we considered (dairy cattle, feedlot cattle, beef cattle,

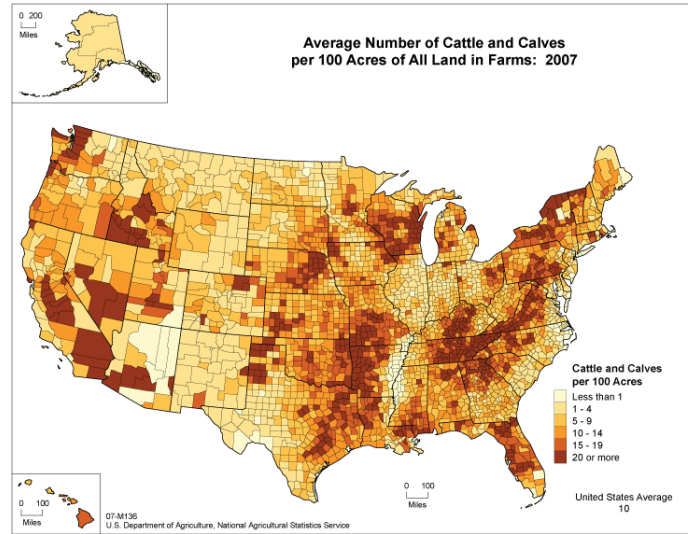


FIGURE 6.2: Density of cattle and calves in the US by county.

sheep, and pigs). In addition, we started the epidemics in each of the different animal groups to add variation and less predictability to the scenarios. There were several counties with high populations for multiple groups so we minimized duplication by choosing from among the top ten. We also chose several counties (in Florida, Arizona, California, and Wyoming) that have much livestock but are geographically separated from other counties with significant livestock density or numbers. These isolated counties were chosen in order to see the comparative effects of short and long distance movement and movement control for various regions in the United States.

6.5 Results

We ran our model 400 times for each of 16 starting locations throughout the US, exploring different combinations of the various disease properties and mitigation param-

ters, as well as simple stochastic variation. The majority of simulation runs each produce more than a ten-fold increase in the number of cases in a few days after the start of the epidemic. A few days later, and at much lower levels, the recovered and dead populations rise, reflecting the high mortality rate of rinderpest in cattle. Shortly after the sharp rise of symptomatic animals, a massive quarantine program appears, and culling of symptomatic animals. The next two months of the epidemic reflect a steady spread of disease to new counties and the subsequent application of quarantine and culling to contain the spread in each new region. Within the model, the duration of quarantine is indefinite, although in reality, the quarantine could be lifted once an effective vaccination program occurs.

The spatial-temporal spread of a severe epidemic can be seen in Figure 6.3, showing the map of the US, colored according to the day each county sees its first case of rinderpest. The epidemic was seeded in Weld County, Colorado, on day 0, and spread to California almost immediately (black circles). By day 11, the disease has already spread to over a dozen locations throughout the US, seeding the second explosion of cases, during days 11 to 16. During the longest phase of the epidemic, from week 3 to 9, nearly all of the 70 million beef cattle in the nation are quarantined, with almost one million beef cattle culled. Rinderpest epidemics spread to essentially every area in the country that contains significant populations of beef cattle. As the rate of the growth of new infections levels off, a great deal of effort and activity is being expended during this portion of the epidemic, as the spread is mitigated by a combination of a quarantine (which reduces the effective reproductive number below one) and the rapid identification and culling of newly symptomatic animals that results from imperfections in the quarantine.

6.6 Sensitivity to Model Parameters

The worst-case scenario represents only one of many possible instantiations of a rinderpest epidemic (Figure 6.3). We explored the sensitivity of consequence to variation

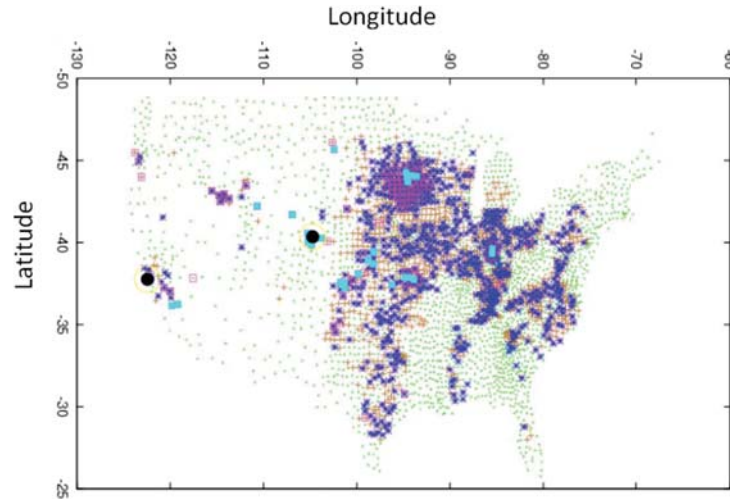


FIGURE 6.3: Geographic progression of one epidemic seeded in Weld County, Colorado. All counties are shown with green crosses and counties impacted by the epidemic by days 2, 11, 21, 51, and 101 are shown with various symbols.

in nearly all model parameters. Figure 6.4 illustrates how the total number of dead beef cattle depends on the starting location of the epidemic, as well as the effectiveness of the quarantine. Epidemics were seeded with 100 infected animals of one type (beef cattle, milk cattle, feedlot cattle, swine, or sheep) in one of 16 counties selected to be illustrative of geographic diversity in the epidemiology. Quarantine efficacy was defined to be the fraction of animals protected from infection by the quarantine and was allowed to vary from 0.1 (only a ten percent reduction in infection) to 0.9, representing a ten-fold decrease in the likelihood of disease spread. This parameter involves all possible modes of spread, including animals moving, spread by wildlife, animals being transported, and disease spread with fomites by humans. Considerations such as asymptomatic spread also appear here. The impact of the time between detection of rinderpest in a county and initiation of culling (varied from 1 to 4 days) was nearly as large as that of quarantine efficacy, but most model parameters had a smaller impact on the overall number of animals infected by the epidemic.

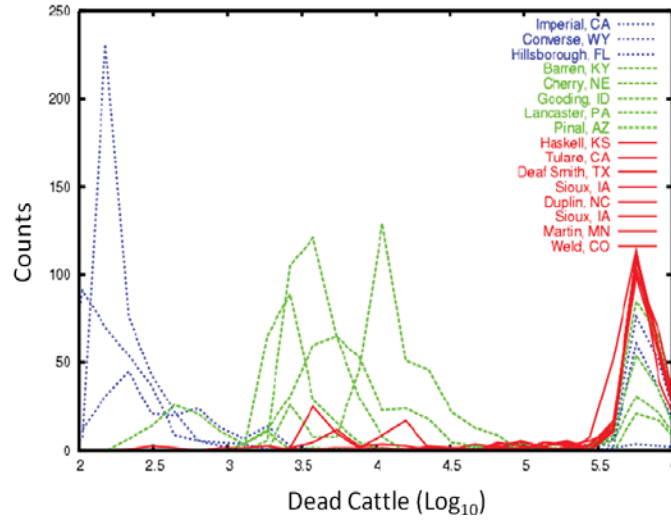


FIGURE 6.4: Consequence realized over 400 runs of varying disease and mitigation parameters for epidemics started at the 16 locations (three groups). Counts are the number of simulation runs with the number of total dead cattle.

The normalized forward sensitivity index of a variable to a parameter is the ratio of the relative change in the variable to the relative change in the parameter. Since all variables depend on many nodes in the network of counties and probability of infection is stochastic, the sensitivity indices were computed numerically based on the mean of approximately 5000 runs starting in 16 different locations. We computed the sensitivity of total number of animals infected to the disease-related parameters. We found that the total number of infected animals increases with the fraction of animals that progress to symptoms, with the fraction of infected animals that die, and with an increase in the incubation period. The number of infected animals is not very sensitive to intrinsic disease parameters over the range they were varied (reflecting plausible values for these parameters). We varied each of these parameters along their range for 16 different starting locations. We then computed the average number of infected animals across the range of each parameter for the 5000 runs. The slope of the best fit line for each parameter versus the average number of infected animals was used to calculate the sensitivity index. See

Parameter	Normalized Forward Sensitivity Index
θ_L^c (ratio infected cows that progress to symptoms)	11.3
θ_L^s (ratio infected sheep that progress to symptoms)	3.4
θ_D (ratio infected that dies)	3.4
θ_L^h (ratio infected hogs that progress to symptoms)	0.5
T_c (time after detection until culling implemented)	0.4
ϵ_s (efficacy short range movement control)	0.3
$1/\lambda_L$ (residency time in latent stage)	0.2
$1/\lambda_{V_s}$ (residency time in vaccinated susceptible)	-0.2
ϵ_l (efficacy long range movement control)	0.2
ϵ_q (efficacy quarantine)	-0.1
$1/\lambda_I$ (residency time in infectious stage)	0.1
$1/\lambda_C$ and $1/\lambda_{V_e}$ (time in carrier stage)	0.1

TABLE 6.2: Sensitivity analysis for significant varied parameter for the simulations.

Table 6.6, of sensitivity indices.

Rinderpest can be controlled with several mitigation strategies. We use sensitivity analysis to quantify the relative impact of various mitigation strategies on the total number of infected cattle. We found that movement control is not very effective in controlling both variables. Culling, on the other hand, is very effective, especially if implemented promptly [140]. Vaccination can be effective for controlling the size of an epidemic, but only if the

vaccine is readily available and stockpiled, which is not currently the case in the US. The last important variable for controlling the epidemic is the time until the epidemic is detected.

6.7 Importance of Geography

The most striking find was dependence of the overall epidemic size on the starting location (Figure 6.4). Overall epidemic size, measured by the number of infected animals for the epidemics started in 16 locations throughout the US, was related to the seed location. Epidemics from the 16 seed locations can be classified according to overall size into small epidemics of 100 to 300 animals (failed epidemics), epidemics infecting 3,000 to 30,000 animals (medium epidemics), and the large epidemics infecting around one million beef cattle. Epidemics infecting 1000 beef cattle or 100,000 beef cattle rarely occur, although several locations readily produce both failed and large epidemics.

6.8 Geographic Flow of Infection

From the simulated data, clustering exists around small and very large epidemics with few cases falling between the two extremes. The conditions under which rinderpest reaches large epidemic levels are related to the origin of the disease and whether or not the disease moves into certain key counties in high-livestock-density areas of the US. We have indicated the starting locations of the failed, medium, and large epidemics with appropriately colored symbols in Figure 6.2 of the density of beef cattle. Further examination of the simulation results indicate that the large epidemics passed through the Midwest at some point early in the epidemic.

The variation in spatial origin and size of observed epidemics suggests further ex-

amination of the dependence of the epidemic size on response time and effectiveness of movement controls. Because the parameter values were sampled from a uniform distribution, it is evident that failed epidemics are significantly more likely to occur in the presence of reduced movement of animals. Equally evident, however, is that movement controls alone are not particularly helpful. Clearly, if movement controls prevent all movement, the epidemic would, by definition, not spread. Our model is merely highlighting that single cases can, quite frequently, get through even stringent movement control schemes.

6.9 Discussion

Determining parameter values for rinderpest is difficult in many cases because there is a paucity of spatial historical data and rinderpest has never been present in the US. We can be relatively confident of disease progression parameters within individual hosts, such as the incubation and infectious periods, as well as death rates experimentally [140, 117], although exploration of ranges for these parameters is clearly prudent.

The epidemiological parameters are somewhat more difficult to quantify. The most reliable indicator is the historical data of the frequency and size of epidemics. In extrapolating the transmission likelihood from historical data, three significant sources of uncertainty must be lumped together. First, are the intrinsic transmissibility of the disease and susceptibility of animals to the virus, which are likely to be higher than past epidemics because of the long-term absence of circulating rinderpest. Second, are the greatly increased size, density, and transport of livestock in the US. Finally, modern agricultural practices are more highly refined than they were when rinderpest last circulated freely, presumably resulting in better control of infectious disease in general. In order to validate the model for transmissibility parameters, we compare qualitative spatial results with what is known from previous outbreaks of rinderpest in nine herds and with well known recent outbreaks of foot-and-mouth disease. It is important to realize that we are

not primarily concerned here with computing the median consequence value for a rinderpest epidemic (that would require quite careful examination of the above three effects). Instead, we aim to explore and quantify the relationship between disease properties, geography, and mitigation strategies to better understand and mitigate the spread of infectious diseases in multi-host populations.

We found that rinderpest spread as expected when started from different geographic locations in the US. For example, in recent foot-and-mouth disease studies it has been shown that number of animals is important in the initial stages of the disease, while density of animals becomes important after the first one to two generations [20, 120]. We would expect then that rinderpest requires a path through densely populated areas and an initially large population of livestock in order to spread widely. This was indeed how the model behaved. For instance, an epidemic started in a county in Idaho caused high death rates in that county but was not able to spread to the rest of the US because Idaho is surrounded by states with very low livestock densities. However, an epidemic started in Iowa spread rapidly throughout the high-density belt from the Midwest through eastern Texas. One difficulty in the modern era is that, even if not surrounded by areas with dense populations of livestock, infected animals may be shipped to areas that are densely populated. We also saw that rinderpest spread quickly, which is to be expected from examining the last continent-wide epidemic in nine herds in Africa in the 1890's. Even though transportation was much slower and less widespread, rinderpest spread from the horn of Africa to the tip of South Africa (about 8000 km) in less than 10 years [90].

Spatial mixing plays an important role in other fast-spreading animal diseases such as foot-and-mouth disease [116], and initial explorations indicate that the same is true for rinderpest. Rinderpest spreads quickly, is highly transmissible, and has a high death rate, so has the potential to burn itself out quickly if enough susceptible animals are not available. Thus, for an initial infection to become an epidemic, rinderpest initially requires a large number of susceptible animals. After the first few generations, high density of hosts is required as with foot-and-mouth disease. So, we assume that rinderpest will

only become a large-scale epidemic if it reaches or begins in the high-number, high-density areas in the Midwest of beef cattle in the US. Because of human mobility we not only have to consider proximity but rate of movement of livestock between areas. For example, although California is geographically distant from other high-density livestock areas in the US, high rates of movement between California and the mid to eastern US result in large epidemics with origins in California. We separated the initial locations into three categories: primarily small epidemics, primarily large epidemics, and bimodal distribution of epidemics. In addition, the importance of wildlife in the propagation of rinderpest should not be understated. Although the data on wildlife required to be incorporated into the model are mostly unavailable, wildlife may be an important part of an epidemic.

In all of the simulations, the overall mortality rate never exceeded a few percent, even though the case fatality rate is nearly unity. This is because we concluded that, even in the worst case, ranchers would be able to control the epidemic by identifying and culling the clearly symptomatic animals. The importance of this mitigative strategy is evident in the dependence of the size of the epidemic on both the efficacy and rapidity of quarantine and the rapidity of culling.

The apparent lack of importance of vaccination evident in the sensitivity analysis does not indicate a lack of importance of a highly efficacious vaccine in controlling rinderpest. It simply reflects our expectation that quarantine and culling of the sporadic outbreaks will be utilized to control the epidemic only until the vaccine can be administered and become effective. Such a dependency would show up strongly in a complete economic consequence analysis, which we have not attempted here.

One important advantage to our epidemiological model is its ability to treat multiple hosts on an equal footing. The hosts can differ in either disease progression properties, such as the greatly decreased disease susceptibility of swine to rinderpest, in comparison to cattle. They can also differ in their epidemiological properties, such as the fact that feedlot cattle do not typically return to mingle with beef cattle once they enter the feed lot. Indeed, the low susceptibility of swine to rinderpest is a significant factor in the

difference from foot-and-mouth epidemic spread across the US. Although our multi-host model treats the different types of livestock appropriately, we only treated wildlife and the spread of disease by humans (through fomites-humans do not contract rinderpest) implicitly, through the imperfection of both long- and short-range movement restrictions. It will be important to return to these questions in future studies.

The explosive spread of rinderpest apparent in Figures 6.3 and 6.4 can be traced to three separate parameters in our model: asymptomatic spread, relatively short incubation times, and a relatively high transmission and susceptibility coefficient. Given the likelihood, even in a naive outbreak, of a percentage of asymptomatic cases and the possibility of an avirulent strain being introduced and spreading widely, with potential subsequent reversion to virulence, asymptomatic animals play an important role in both the long-term outcome of a rinderpest epidemic and in the best surveillance and mitigation strategies. Here, we focus on the virulent strain of rinderpest to simulate a worst-case scenario for impacts. The ultimate ability to control the disease while losing only a few percent of the Nation's livestock can be traced to the clarity of the signs of disease and the existence of an efficacious vaccine, which led to our assumed rapidity and effectiveness of culling and quarantine.

An important outcome of this study is the importance of geography and the density of susceptible hosts to the spread of rinderpest. The relatively small statistical correlation of epidemic size to movement restrictions in comparison to quarantine and culling should not be interpreted to mean that this control measure is of little importance. There are several lessons learned from these simulations for the management of rinderpest or similar disease outbreak in cattle populations in the US. First, it is far cheaper to implement than quarantine or culling, although the economics of the loss of export are considerable. Second, the impact of preventing the spread to the major cattle populations is a thousand-fold decrease in epidemic size and a significant shortening in the duration of quarantine and culling interventions. Third, the actual effectiveness of movement restrictions depends on several key variables, such as the absolute value of the transmissibility of the virus and

the implicit assumptions on the likelihood of spread by fomites or wildlife. Finally, it is impossible to capture the adaptive nature of the mitigative measures in a model such as ours. Our parameter estimates are applied ‘for the long haul’ and may not reflect potential opportunistic mitigation.

These results strongly support the case for complete eradication of rinderpest. The ability to systematically explore the epidemiology of disease will be important when considering the impacts of climate change and emerging disease, and the robustness of modern agricultural practices. It is also important as a stepping stone to controlling zoonotic diseases and understanding the evolutionary pressures of multi-host pathogens in general. The geography and connectedness of populations plays an important role in the outcome of an epidemic. Using this knowledge of animal population density and connectedness can assist in determining critical populations or locations to apply mitigation or control measures for animal movement.

7 CONCLUSION AND FUTURE DIRECTIONS

7.1 Summary of Results

This thesis considered compartmental Susceptible-Infectious-Recovered (SIR) ordinary differential equation models for the spread of a pathogen among competing species. We also modeled spatial heterogeneity using multi-patch models that are graphs (or networks) with systems of differential equations at each vertex. These models can be viewed as either an approximation of spatial diffusion or as a model for patchy environments. For the case of spatio-temporal dynamics of disease spread, a multi-patch model consists of an SIR model on each vertex of a graph or network with movement of species between some or all of the vertices. Methods I used to understand and analyze the models include stability analysis of equilibria, persistence theory and analysis of flow along the boundaries of the system, threshold values for growth and other behaviors, sensitivity analysis, and simulations. In addition, we added stochasticity to a model for spread of disease, sampling across the range of parameters such as susceptibility, infectivity, and efficacy of control strategies.

Understanding the mechanisms that drive coexistence of competing species is an important question in community ecology. The effects of a shared disease on the outcome of competition between two species has been investigated by several authors in the ecological and mathematical ecology communities. Although many papers propose and analyze mathematical models of Lotka-Volterra competition between two species that share a common (generalist) pathogen, some important cases are difficult to analyze. In particular, it has been difficult to find existence and stability conditions of the infected coexistence equilibrium for these models.

Chapters 3 and 4 addressed the effect of interactions between competition and disease dynamics on this endemic coexistence steady state. We considered a competition

model for two species with a generalist pathogen and computed the basic reproduction number, derived analytic forms for equilibria where possible, and performed local and global stability analysis of the equilibria, including the disease-free and infected coexistence equilibria. For models with frequency incidence disease transmission, we prove the existence, uniqueness and global stability of the infected coexistence equilibrium under the assumption that coexistence of the species is feasible using the theory of asymptotically autonomous systems. As is the case for most models with frequency incidence disease transmission, the stability of the coexistence equilibrium depends on the basic reproduction number (BRN) being greater than one. Thus, the frequency incidence disease model exhibits the classic endemic model behavior; the disease dies out below a threshold and approaches an endemic equilibrium above the threshold.

We prove that a conjecture made in [73, 26, 17] about the infected coexistence equilibrium holds for a simplified model. In particular, we show that the conditions under which infected coexistence is stable guarantee that all other equilibria are unstable and vice versa. In addition, we also show that under the simplifying assumptions, the qualitative behavior of the model with mass action disease transmission is identical to the model with frequency incidence disease transmission. This is not true for the full general system with mass action. We hypothesize, then, that for species with very similar intra-specific competition rates and similar (a-virulent) pathogen transmission rates, the choice of incidence functions does not change the conditions under which endemic coexistence is stable, i.e., stability is determined by the basic reproduction number and relative strengths of inter- and intra-specific competition.

In the case of mass action disease transmission we show that, if the death rate due to disease is positive, then disease can reduce the total equilibrium density for each species in isolation. This in turn affects competitive ability indirectly (apparent competition), and is another indication that in the presence of disease, the competitive outcome can change. We hypothesize that one of the driving forces behind the possible switch of competitive outcomes and the difficulty of analysis of the full model is death due to disease. This

force may be magnified by differing rates of transmission between and within species. The results of this research can be found in a technical report [21], and a paper that is in review [22].

In Chapter 4, for cases when stability of the system is difficult to determine, persistence theory was used to show conditions under which species and/or the pathogen persist in the system. Han and Pugliese [61] found conditions for strong uniform persistence of disease and for one or both species for the case of density-dependent birth with competition in the death term. We find that adding competition to the birth term and removing density dependence from death affects the actual equilibrium densities of the computed boundary equilibria but does not qualitatively change the conditions under which the species and/or the disease persist uniformly strongly. This suggests that the particular way in which competition acts on the growth rate of the species does not change the qualitative outcome of our model in the context of strong uniform persistence of both species and the pathogen.

It is also proved using persistence theory that when all other equilibria are unstable, endemic coexistence is strongly uniformly persistent (i.e. there is coexistence of both species and the pathogen). I also present conditions under which each individual species and the disease are strongly uniformly persistent. Although stability of particular interior equilibria and/or limit cycles is not proved, the strong uniform persistence of the system is proved. This is an important result from an ecological perspective, since it guarantees that all variables stay bounded strictly away from zero, thus will not go extinct. In summary, we use persistence theory to complete the analysis of the full model for competition and disease with mass action incidence, showing that persistence of both species and the disease is determined by a few ecologically relevant parameters.

Chapter 5 pursues the question, “Could exotic species alter disease transmission dynamics, which in turn facilitate invasion?” In collaboration with ecologists [106], we considered a model to study the transmission dynamics of Barley Yellow Dwarf Virus (BYDV), an important ecological component of native grasslands in California as well as

patchy meadows in the Cascades. We modeled the spread of the aphid-vectored BYDV on multiple patches for two host grass species, one native and one invasive, including both seasonal and age related dynamics for the grasses. Using simulations, the basic reproduction number, and sensitivity analysis, we have shown that the spatial configuration of the patch system, host composition within patches, and patch connectivity affect not only the ability of BYDV to invade a fragmented system, but also determine whether the pathogen facilitates the invasion of a non-native host species [106].

In animal communities, both hosts and vectors can move among patches; however, in our focal community, among-patch host movement is negligible, whereas vector dispersal is key. Landscape-scale host composition can interact with vector dispersal to control disease spread and epidemics, as in our case study. Similarly, bean dwarf mosaic virus, a whitefly-transmitted virus that infects both soybeans and common bean plants causes severe disease in the latter. In Argentina, increased soybean acreage shifted the landscape-scale host composition, leading to the emergence of bean dwarf mosaic virus and threatening local common bean production. In multi-host communities where hosts also move among patches, this will add further complexity that warrants future exploration.

The landscape-scale composition and configuration of host communities, along with vector movement patterns among patches, are essential determinants of pathogen spread and prevalence in fragmented landscapes [111, 113]. Pathogen spread depends on host composition (e.g. presence of reservoirs, probability of transmission) and vector density and dispersal, all of which can vary among patches in a complex landscape. Management can increase connectivity, elevating transmission of multi-host pathogens, as is the case with fire suppression increasing connectivity among hosts susceptible to sudden oak death (*Phytophthora ramorum*; see [104]). Our results show that for cases such as the BYDV system, mixed species patches or mixtures of patches with differing host composition tend to have the highest prevalence rates because of the balance among pathogen residence time, pathogen transmission probability, and vector fecundity. Further, our results suggest that connectivity can interact with arrival time and host infection tolerance to determine the

success or failure of establishment for newly arriving species.

Chapter 6 (in collaboration with colleagues from various disciplines at Los Alamos National Laboratory) investigates the spread of generalist animal diseases on a large spatial network, using Rinderpest as a case study. We predicted the potential spread of Rinderpest using a two-stage model for the spread of a multi-host infectious disease among agricultural animals in the US, incorporating USDA data for county-level livestock populations and movement. The model includes pigs, sheep, goats, beef cattle, dairy cattle, and cattle on feed as well as mitigation strategies such as quarantine, vaccination, culling, and movement control. I ran simulations of the model for designed scenarios, and performed sensitivity analysis of the parameters. We were not primarily concerned with computing the median consequence value for a rinderpest epidemic (that would require quite careful examination of the above three effects). Instead, we aimed to explore and quantify the relationship between disease properties, geography, and mitigation strategies to better understand and mitigate the spread of infectious diseases in multi-host populations.

We found the size of Rinderpest epidemics were directly related to the origin of the disease and whether or not the disease moved into certain key counties in the high-livestock-density areas of the US, and were sensitive to response time and effectiveness of mitigation strategies [95]. Spatial mixing plays an important role in other fast-spreading animal diseases such as foot-and-mouth disease [116], and initial explorations indicate that the same is true for rinderpest. Rinderpest spreads quickly, is highly transmissible, and has a high death rate, so has the potential to burn itself out quickly if enough susceptible animals are not available. Thus, for an initial infection to become an epidemic, rinderpest initially requires a large number of susceptible animals. After the first few generations, high density of hosts is required as with foot-and-mouth disease. So, we assume that rinderpest will only become a large-scale epidemic if it reaches or begins in the high-number, high-density areas in the Midwest of beef cattle in the US. Because of human mobility we not only have to consider proximity but rate of movement of livestock between areas.

In summary, we find that competition, disease, and space can interact to create complex dynamics. In fact, adding any one of these factors to a model can potentially change the outcome of the model or the conditions under which coexistence of species is possible. It will be important to continue to compare simple models with more complex models in order to understand the situations under which more complexity is necessary to answer the question being asked. As we discovered in Chapters 3 and 4, for some special cases, adding disease dynamics to a model for competing species does not significantly change the conditions for coexistence of the species. However, for other cases, adding disease dynamics can completely switch the competitive outcome, as it does in the case of Barley Yellow Dwarf Virus system. These results help us understand how the forces of infection and competition combine and are implicated in determining community structure in a spatially heterogeneous environment.

Additionally, we find that adding space to a model can give insight into the regional dynamics of a pathogen, especially when there is a fragmented landscape with differing host composition and environmental factors through which the pathogen must spread. As in the case of rinderpest and BYDV, initial location and timing of the pathogen invasion can significantly change the transitory dynamics and/or the final outcome of the system. The ability to systematically explore the epidemiology of disease will be important when considering the impacts of climate change and emerging disease, and the robustness of modern agricultural practices. It is also important as a stepping stone to controlling zoonotic diseases and understanding the evolutionary pressures of multi-host pathogens in general. The geography and connectedness of populations plays an important role in the outcome of an epidemic. Using this knowledge of host population density and connectedness can assist in determining critical populations or locations to apply mitigation or control measures for host or vector movement.

7.2 Future Directions

Relatively little has been done in the way of expanding knowledge of models that combine more complex population dynamics and disease. I plan to continue work on numerical methods specifically for models that include both population dynamics and disease spread. Additionally, it would be interesting to apply persistence theory to a general model for competition between species with disease in only one of the species. This is an important sub-case that has not been well explored in the context of persistence theory.

The BYDV team hopes to compare the results of several different spatially explicit and implicit models for BYDV spread in native grasslands and meadows. It would be interesting to expand this work to other organisms whose competitive outcomes can be changed by the presence of a generalist pathogen. There is much still to be done in the area of spatial models for invasion of both pathogens and exotic species.

The rinderpest model is being adapted to Rift Valley Fever epidemics in East Africa, a mosquito-vector-borne zoonotic disease. In the immediate future, we will further explore and analyze models for mosquito-vector-borne pathogens including analysis of a simpler model for Rift Valley Fever with vertical transmission and a model for Dengue.

The broad impact of this work is a partnership between ecologists, biologists, epidemiologists, and mathematicians to develop significant advances in the theory and application of mathematical models. By applying mathematical models to biological and ecological systems, we increase understanding of disease, pathogen, and population dynamics, contributing significant scientific knowledge to the management and understanding of disease and/or exotic species. Long term, I want to continue to collaborate with interdisciplinary researchers in biological, ecological, and health fields to work on models that will expand knowledge and our problem solving abilities for both environmental and humanitarian issues.

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