Comparing the effects of host species richness on different metrics of disease

Michael H. Cortez*
Department of Biological Science
Florida State University
Tallahassee, FL 32306
(850) 645-8692
mcortez@fsu.edu

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*Corresponding author
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ABSTRACT: Changes in host species richness can increase or decrease the risk of infection and levels of disease in communities. In this study, I review theoretical predictions for direct and environmental transmission pathogens about how host additions and removals affect three commonly used metrics of disease: the pathogen community reproduction number ($\mathcal{R}_0$), focal host infection prevalence (the proportion of infected individuals), and focal host infected density. I extend this body of theory by applying sensitivity analysis to a multihost mathematical model and exploring how variation in non-focal host competence (i.e., the ability to transmit a pathogen), non-focal host density, and the pathogen transmission mechanism affect each disease metric. My results yield insight about which biological mechanisms cause host additions and removals to increase or decrease each disease metric, and they identify when and why metrics respond differently (e.g., responses in focal host infection prevalence and infected density can differ when there are large changes in focal host density). My results explain and unify theoretical prior predictions about host species richness-disease relationships. I discuss areas of future research where advances in theory could help explain empirical relationships between host biodiversity and disease.

1 Introduction

Biodiversity in communities is changing rapidly due to anthropogenic effects and species invasions (Cardinale et al., 2012; Dirzo et al., 2014; Dornelas et al., 2014; Doherty et al., 2016). For host-pathogen systems, gains and losses of host species can alter levels of disease and disease risk. Indeed, reviews and meta-analyses have argued and found that increased host species richness can increase or decrease disease (Keesing et al., 2010; Randolph and Dobson, 2012; Salkeld et al., 2013; Wood et al., 2014; Civitello et al., 2015; Ostfeld and Keesing, 2017; Rohr et al., 2019). Understanding the drivers of host species richness-disease relationships is important for predicting changes in disease in focal hosts, assessing whether changes in disease levels in one population increase or decrease the risk of infection and spillover in other populations, and population management, e.g., wildlife managers can use culling and removal of host species to control levels of disease (Laurenson et al., 2004; Donnelly et al., 2006).

Despite the observed variation in how disease levels respond to changes in host species richness, we have a limited understanding of the mechanisms causing that variation and their context-dependent effects. This has led to calls for theory on host richness-disease relationships and, more generally, host biodiversity-disease relationships (Buhnerkempe et al., 2015; Johnson et al., 2015; Halsey, 2019; Rohr et al., 2019). Current theory predicts that responses to host additions and removals are affected by host competence (the ability to transmit the pathogen to susceptible individuals), interspecific host competition, and the pathogen transmission mechanism (Dobson, 2004; Rudolf and Antonovics, 2005; Joseph et al., 2013; Mihaljevic et al., 2014; O'Regan et al., 2015; Strauss et al., 2015; Faust et al., 2017; Cortez and Duffy, 2020; Cortez, 2021); specific predictions are discussed in the next section. While this body of work provides insight into how host species richness can affect levels of disease, general predictions are unclear because studies make different assumptions about the characteristics of the host and pathogen species.

Another limitation is that current theory is unclear about how the metric of disease

influences predictions. Three metrics of disease commonly used in empirical and theoretical studies are: (i) the pathogen's community reproduction number ($\mathcal{R}_0^C$), which is the average number of new infections produced by a single infected individual in an otherwise susceptible community; (ii) focal host infection prevalence, that is, the proportion of infected individuals in a focal population (I/N); and (iii) focal host infected density (I). Increases and decreases in the second metric in response to host species additions are often called amplification and dilution, respectively (Keesing et al., 2006; Rohr et al., 2019). The choice of metric is important because theoretical studies predict that changes in host species richness can have effects of different signs on the three metrics (Roche et al., 2012; Roberts and Heesterbeek, 2018). As an empirical example, fungal infection prevalence in *Daphnia dentifera* increases but infected density decreases when *D. lumholtzi* is added present (Searle et al., 2016). In contrast, both infection prevalence and infected density in *D. lumholtzi* increase when *D. dentifera* is present. Current theory is limited in its ability to explain these patterns, but understanding them is important because the metrics provide different information about disease dynamics and disease risk. Specifically, $\mathcal{R}_0^C$ provides a measure of the risk of an outbreak and how fast an outbreak will grow. In comparison, infection prevalence and infected density provide measures of disease burden for a focal population and, depending on interspecific host contact rates, the potential for a pathogen to spread or spillover into another population or species. In total, in order to understand how host species richness affects disease dynamics and disease risk, additional theory is needed to explain why similar versus different responses are observed for the same metric and between metrics of disease.

In this study, I review the theoretical predictions about the relationships between host species richness and the three metrics of disease, focusing on pathogens with direct transmission (transmission via host-host contact) and environmental transmission (transmission via infectious propagules that are shed into an environment). I then use a multihost mathematical model to explore the factors influencing the relationships between each metric of disease and host species richness. Building on prior work (Roberts and Heesterbeek, 2018; Cortez

and Duffy, 2021; Cortez, 2021), I do this by using sensitivity analysis to calculate how each metric responds to variation in host competence, host density, and the pathogen transmission mode. My results explain and extend prior predictions about host species richness-disease relationships.

2 Current theory on how host species richness affects disease and its limitations

Many studies have reviewed and debated the empirical evidence for positive and negative effects of host species richness on levels of disease (Keesing et al., 2010; Randolph and Dobson, 2012; Salkeld et al., 2013; Wood et al., 2014; Civitello et al., 2015; Ostfeld and Keesing, 2017; Rohr et al., 2019). Here, I review current theory for directly and environmentally transmitted pathogens.

The foundational work in Keesing et al. (2006) predicts that disease risk in a focal host increases when host additions or removals increase host encounter rates (α), increase transmission rates (Δ), increase susceptible host densities (S), decrease mortality rates of infected individuals (μ), and decrease host recovery rates (ν). These predictions are derived from an equation describing changes in infected host density,

$$\frac{dI}{dt} = \overbrace{\alpha \Delta S I}^{\text{infection}} - \overbrace{(\mu + m)}^{\text{mortality}} + \overbrace{\nu}^{\text{recovery}} \tag{1}$$

where S and I are susceptible and infected host densities, respectively, and m is the non-disease mortality rate. The predicted responses are based on the idea that increases and decreases in the growth rate of infected individuals (dI/dt) increase and decrease disease risk, respectively. While the five mechanisms are defined for direct transmission pathogens (i.e., transmission via host-host contact), analogues exist for environmental transmission pathogens (i.e., transmission via infectious propagules shed into the environment; Johnson

and Thieltges 2010) and vector-borne pathogens (Ostfeld and Keesing, 2000; Keesing et al., 2006). A key limitation of these predictions is that they focus on changes in the growth rate of infected individuals and do not directly address other quantities measured in populations (e.g., infection prevalence and infected density).

Other theoretical studies have explored how the presence and absence of host species affect the pathogen's community reproduction number ($\mathcal{R}_0^C$) and infection prevalence (I^*/N^*, where N^* is total host density) and infected density (I^*) of a focal host at equilibrium. For density-dependent direct transmission (DDDT) models (host-host contact rates are proportional to the density of infected individuals), host additions often increase $\mathcal{R}_0^C$ and focal host infection prevalence (Dobson, 2004; Rudolf and Antonovics, 2005; Faust et al., 2017), but both metrics can decrease if there is strong interspecific competition (Joseph et al., 2013; Mihaljevic et al., 2014; O'Regan et al., 2015; Cortez, 2021). For frequency-dependent direct transmission (FDDT) models (host-host contact rates are proportional to the frequency of infected individuals), host additions often decrease $\mathcal{R}_0^C$ and focal host infection prevalence (Dobson, 2004; Rudolf and Antonovics, 2005; Joseph et al., 2013; Mihaljevic et al., 2014), but both metrics can increase if added host species have sufficiently high intraspecific and interspecific transmission rates (O'Regan et al., 2015; Faust et al., 2017). Combined, this suggests that host additions increase $\mathcal{R}_0^C$ and focal host infection prevalence more often under DDDT than FDDT (Dobson, 2004; Rudolf and Antonovics, 2005; Mihaljevic et al., 2014; Faust et al., 2017).

For environmental transmission (ET) models (transmission via infectious propagules shed into the environment), responses in $\mathcal{R}_0^C$ and focal host infection prevalence depend on interspecific host competition and whether host species are net producers (sources) or net removers (sinks) of infectious propagules (Cáceres et al., 2014; Cortez and Duffy, 2021; Cortez, 2021; Espira et al., 2022). In particular, added host species are more likely to increase $\mathcal{R}_0^C$ and focal host infection prevalence if they are sources (Cortez, 2021; Espira et al., 2022). Added host species are also more likely to increase focal host infection prevalence

if they have stronger competitive effects on sink hosts than on source hosts (Cortez, 2021).

Taken together, current theory points to possible general rules about how host competence, host competition, and the pathogen transmission mechanism affect host species richness-disease relationships. In addition, current theory suggests responses in $\mathcal{R}_0^C$ and infection prevalence are similar. This is useful to modelers because $\mathcal{R}_0^C$ is typically easier to compute than infection prevalence. However, current theory is limited in two key ways. First, studies make different assumptions about the number of host species, the strength of interspecific host interactions, and the rates and mechanisms of disease transmission. For example, some FDDT studies (Dobson, 2004; Joseph et al., 2013; Mihaljevic et al., 2014) assume interspecific competition is absent and interspecific transmission rates are lower than intraspecific transmission rates whereas other studies (O'Regan et al., 2015; Faust et al., 2017) assume interspecific competition is present and intraspecific and interspecific transmission rates are comparable. This makes it difficult to identify which assumptions are responsible for differences in model behavior. Second, prior studies have shown that the three metrics can respond differently to host additions and removal (Keesing et al., 2006; Roche et al., 2012; Roberts and Heesterbeek, 2018). Indeed, Keesing et al. (2006) noted that variation in transmission rates (via α or Δ) could result in infection prevalence and infected density changing in different directions under some conditions (page 488). Differences in the choice of metric between studies makes it difficult to compare predictions and determine if specific mechanisms have similar or different effects on each metric.

These limitations point to a need for theory that can extend and unify the results for each particular metric as well as explain why predictions differ between metrics. The following presents the model and approach I use as a step toward addressing this need.

3 Models and Methods

3.1 Single-habitat n-host environmental transmission model

I focus on the model in Cortez (2021) of n competing host species and a shared environmentally transmitted pathogen. Throughout, host 1 is the focal host and the others are non-focal hosts. Infection occurs when susceptible individuals encounter infectious propagules (e.g., spores) in the environment that were shed by infected individuals. All host species shed infectious propagules into a shared habitat and are equally exposed to the infectious propagules. Examples of environmentally transmitted pathogens include the human pathogens *Vibrio cholera* and *Giardia lamblia* (Kaper et al., 1995; Wolfe, 1992), the fungal pathogen *Metschnikowia bicuspidata* of *Daphnia* species (Strauss et al., 2015; Searle et al., 2016), the chytrid fungus *Batrachochytrium dendrobatidis* of amphibians (Daszak et al., 2003; Skerratt et al., 2007), whirling disease in fish (Hedrick et al., 1998; Bartholomew and Reno, 2002), and trematode parasites of snails (Johnson et al., 2012).

Each host species is divided into subpopulations of susceptible (S_i), infected (I_i), and recovered (R_i) individuals, where the total density for host i is $N_i = S_i + I_i + R_i$. The model describes the changes in each host class and infectious propagule density (P),

$$\frac{dS_i}{dt} = \underbrace{F_i(\cdot)}_{\text{reproduction}} - \underbrace{\beta_i S_i P}_{\text{infection}} - \underbrace{m_i S_i}_{\text{mortality}} + \underbrace{\gamma_i R_i}_{\text{loss of immunity}} \tag{2a}$$

$$\frac{dI_i}{dt} = \underbrace{\beta_i S_i P}_{\text{infection}} - \underbrace{(\mu_i + m_i) I_i}_{\text{mortality}} - \underbrace{\nu_i I_i}_{\text{recovery}} \tag{2b}$$

$$\frac{dR_i}{dt} = \underbrace{\nu_i I_i}_{\text{recovery}} - \underbrace{(\xi_i + m_i) R_i}_{\text{mortality}} - \underbrace{\gamma_i R_i}_{\text{loss of immunity}} \tag{2c}$$

$$\frac{dP}{dt} = \underbrace{\sum_{j=1}^{n} \chi_j I_j}_{\text{shedding}} - \underbrace{\sum_{j=1}^{n} (u_{S_j} S_j + u_{I_j} I_j + u_{R_j} R_j) P}_{\text{uptake}} - \underbrace{\delta P}_{\text{degradation}} \tag{2d}$$

The parameter values are summarized in Table 1 and additional details are provided in Appendix S1. In equation (2a), host i susceptible density increases due to reproduction (F_i), decreases due to non-disease mortality ($m_i S_i$), and increases due to waning immunity ($\gamma_i R_i$). In equation (2b), host i infected density increases due to new infections ($\beta_i S_i P$) and decreases due to mortality ($\mu_i I_i + m_i I_i$) and recovery ($\nu_i Y_i$). Because infection occurs when infectious propagules are taken up by susceptible individuals, the transmission parameter is the product of the uptake rate of susceptible individuals and the per infectious propagule probability of infection ($\beta_i = p_i u_{S_i}$). In equation (2c), host i recovered density increases due to recovery ($\nu_i I_i$) and decreases due to mortality ($m_i R_i + \xi_i R_i$) and waning immunity ($\gamma_i R_i$). I assume susceptible individuals and recovered individuals are identical except that recovered individuals may experience increased mortality due to prior exposure to the pathogen ($\xi_i \geq 0$). In equation (2d), infectious propagule density increases due to shedding by infected individuals (first sum) and decreases due to uptake of infectious propagules by all individuals of all host species (second sum) and degradation (δP).

The reproduction rates, F_i, account for intraspecific and interspecific host competition. For the numerical simulations presented in figures, I use the Lokta-Volterra competition functions,

$$F_i(\cdot) = r_i(S_i + b_i I_i + R_i)\left[1 - \sum_j \alpha_{ij}(S_i + e_{ij} I_j + R_j)\right] \tag{3}$$

where for host i, r_i is the maximum exponential growth rate, b_i is the reduction in growth rate for infected individuals, α_{ij} is the per capita competitive effect of host j, and e_{ij} determines if infected individuals of host j are weaker ($e_{ij} < 1$), equal ($e_{ij} = 1$), or stronger ($e_{ij} > 1$) competitors than susceptible individuals. The latter accounts for the possibility that infected individuals may be stronger competitors when infection causes increased appetite or resource acquisition rates (Ponton et al., 2011; Shikano and Cory, 2016; Bernardo and Singer, 2017).

I assume the n host species stably coexist in the presence and absence of the pathogen, respectively, at a disease-free equilibrium ($p^{\ddagger}$ with densities $S_i^{\ddagger}$) and an endemic equilibrium

(p^* with densities S_i^*, I_i^* and R_i^*). Without this assumption, my equilibrium-based analyses are biologically uninformative.

3.2 Model Generality

The predictions for the environmental transmission (ET) model (2) apply to direct transmission models (Cortez, 2021). This is because the ET model (2) can reduce to a model with density-dependent direct transmission (DDDT), frequency-dependent direct transmission (FDDT), or direct transmission that is intermediate to DDDT and FDDT; see Box 1. Thus, analyzing model (2) provides a way to extend and unify prior results for ET, DDDT, and FDDT.

In Appendix S2, I extend my results to an n-habitat version of the model which allows for partially overlapping habitats. This is needed to fully explain all of the results from prior DDDT and FDDT studies; see Appendix S2.2 for details. Because a full analysis of the n-habitat model is not tractable, Appendix S2 primarily focuses on systems where (i) interspecific host competition is absent and (ii) each host species has low shedding and uptake rates in the habitats of other host species (which results in interspecific transmission being lower than intraspecific transmission). These assumptions align with those of prior studies on DDDT and FDDT models (Dobson, 2004; Joseph et al., 2013; Mihaljevic et al., 2014). The main text focuses on the simpler 1-habitat model because the results from the 1-habitat and n-habitat models are qualitatively similar.

3.3 Defining host competence, source, and sink

My mathematical analysis identifies two quantities that characterize how well the host species transmit the pathogen. Host competence is the ability of an infected individual to transmit the pathogen to susceptible conspecifics. I define host competence as

$$\mathcal{R}_{0,i}(\infty) = \frac{\chi_i}{m_i + \mu_i + \nu_i} \cdot \frac{\beta_i}{u_{S_i}} \tag{4}$$

which is the average number of new infected conspecifics produced by a single infected individual of host i in an arbitrarily large population; see Appendix S1.4 for additional details. Higher competence hosts have larger values of $\mathcal{R}_{0,i}(\infty)$.

The second characteristic is the host's per capita net production rate of infectious propagules at equilibrium,

$$\begin{aligned}\varphi_i &= \frac{1}{I_i^*}\left(\overbrace{\chi_i I_i^*}^{\text{shedding}} - \overbrace{[u_{S_i}S_i^* + u_{I_i}I_i^* + u_{R_i}R_i^*]P^*}^{\text{uptake}}\right) \\ &= \overbrace{\chi_i}^{\text{shedding}} - \overbrace{\frac{(\mu_i + m_i + \nu_i)}{\beta_i}u_{S_i} - u_{I_i}P^* - \frac{\nu_i}{\xi_i + m_i + \gamma_i}u_{R_i}P^*}^{\text{uptake}}.\end{aligned} \tag{5}$$

(The second line follows from solving the equilibrium conditions $dI_i/dt = 0$ and $dR_i/dt = 0$ for S_i^* and R_i^*.) Source hosts are net producers of infectious propagules, meaning the host's per capita shedding rate is larger than its per capita uptake rate ($\varphi_i > 0$). Sink hosts are net removers of infectious propagules, meaning the host's per capita shedding rate is smaller than its per capita uptake rate ($\varphi_i < 0$). Sink and source also apply to hosts of direct transmission pathogens because of the connection between direct and environmental transmission models (Box 1). For DDDT, all hosts are sources ($\varphi_i > 0$) because DDDT corresponds to no uptake in the ET model (2). For FDDT, hosts are sources ($\varphi_i > 0$) when their interspecific transmission rates are sufficiently large and sinks ($\varphi_i < 0$) otherwise; see Appendix S1.4 for details.

Competence and sink/source are related, but distinct. Source and sink describe the net instantaneous rate of production of infectious propagules whereas competence accounts for the lifetime production of infectious propagules and host infection rates. Consequently, high and low competence often means source and sink, respectively, but not always. In particular, high competence hosts are sinks or small sources when they have low mortality and recovery rates (μ_i and ν_i, making $\mathcal{R}_{0,i}(\infty)$ large) and small shedding rates (χ_i, making

φ_i negative or small and positive). Low competence hosts are large sources when they have high mortality and recovery rates ($\mu_i + \nu_i$, making $\mathcal{R}_{0,i}(\infty)$ small) and large shedding rates (χ_i, making φ_i large and positive).

In addition to arising naturally in the calculations, these definitions provide a density-independent ranking of the host species from highest to lowest competence and from largest source to largest sink. This avoids complications that arise when densities shift as host species are added or removed from a community. However, the rankings can differ across environments because both definitions depend on the non-disease mortality rates, m_i.

3.4 Computing the sensitivities of disease metrics

I use model (2) to predict how additions and removals of non-focal hosts affect three disease metrics: (i) the parasite's basic reproduction number for the community ($\mathcal{R}_0^C$), (ii) focal host infection prevalence at equilibrium (I_1^*/N_1^*), and (iii) focal host infected density at equilibrium (I_1^*). Because explicit formulas do not exist for the metrics except in special cases, I cannot directly compute how additions and removals of non-focal hosts affect each metric. However, it is possible to compute explicit formulas for the slopes of the relationships between each metric of disease and non-focal host competence ($\mathcal{R}_{0,n}(\infty)$), non-focal host equilibrium density (N_n^*), and the pathogen transmission mode. The signs of the slopes yield insight into the effects of additions/removals on each metric of disease. As in prior studies (Roberts and Heesterbeek, 2018; Cortez and Duffy, 2021; Cortez, 2021), I compute the slopes using local sensitivities (i.e., derivatives). Here, I describe the idea behind the approach. Box 2 and Appendix S2.5 explain how the $\mathcal{R}_0^C$ sensitivities are computed using the theory for stage-structured models. Appendix S1.6 explains how the sensitivities of the other two metrics are computed using the Jacobian-based approach in Cortez and Duffy (2021) and Cortez (2021).

The slopes of the relationships between each metric of disease and non-focal host competence are computed using derivatives with respect to non-focal host's transmission (β_n), mortality

(μ_n), recovery (ν_n), shedding (χ_n), and uptake ($u_{S_i}, u_{I_i}, u_{R_i}$) rates. For example, the sensitivities for the non-focal host's shedding rate are computing using the derivatives,

$$\frac{\partial \mathcal{R}_0^C}{\partial \chi_n}, \quad \frac{\partial}{\partial \chi_n} \frac{I_1^*}{N_1^*}, \quad \frac{\partial I_1^*}{\partial \chi_n}. \tag{6}$$

Positive and negative values imply that each metric increases and decreases, respectively, as the non-focal host's shedding rate increases. This yields insight about the effects of host additions because positive (negative) values suggest that additions of non-focal hosts with higher shedding rates are more likely to increase (decrease) each metric.

Similarly, the slopes of the relationships between each metric of disease and non-focal host density are computed using the derivatives

$$\frac{d\mathcal{R}_0^C}{dN_n^\ddagger}, \quad \frac{d}{dN_n^*} \frac{I_1^*}{N_1^*}, \quad \frac{dI_1^*}{dN_n^*} \tag{7}$$

where $N_n^\ddagger$ and N_n^* are the densities of host n at the disease-free and endemic equilibria, respectively. Positive and negative values imply that each metric increases and decreases, respectively, as non-focal host's density increases. This yields insight about the effects of host additions because the effect of adding a non-focal host to the community is predicted by the slope of the response as non-focal host density is increased from zero to its equilibrium value. In particular, positive and negative values suggest that the addition of the non-focal host will increase and decrease, respectively, each metric of disease.

In total, the sensitivity formulas identify the specific conditions under which each metric has positive versus negative relationships with non-focal host competence, non-focal host density, and the pathogen transmission mechanism. Comparing those conditions yields insight into when the three metrics will have similar or different responses to host additions and removals.

4 Results

I first present the general mechanisms causing the sensitivities for the three metrics to differ in sign. I then compare how the metrics respond to changes in non-focal host competence, non-focal host density, and the pathogen transmission mode.

4.1 General mechanisms for why sensitivities can have different signs

The three general mechanisms explaining why the sensitivities for the metrics can differ in sign are (1) differences in the definitions of competence and source/sink, (2) density-mediated feedbacks driven by disease-induced mortality, and (3) large changes in focal host density.

For mechanism 1, differences in the definitions of competence and source/sink can cause the sensitivities of $\mathcal{R}_0^C$ to differ in sign from the sensitivities of focal host infection prevalence and infected density. Specifically, the sensitivity formulas for $\mathcal{R}_0^C$ depend on host competence ($\mathcal{R}_{0,i}(\infty)$) whereas the sensitivity formulas for focal host infection prevalence and infected density depend on whether hosts are sources or sinks (φ_i). Consequently, predictions for $\mathcal{R}_0^C$ can disagree with predictions for the other two metrics when high competence hosts are sinks or small sources or when low competence hosts are large sources.

For mechanism 2, density-mediated feedbacks driven by disease-induced mortality can cause the sensitivities of $\mathcal{R}_0^C$ to differ in sign from the sensitivities of the other two metrics. In particular, $\mathcal{R}_0^C$ depends on the disease-free equilibrium densities ($N_i^{\ddagger}$), which are only affected by density-mediated feedbacks due to competition. In contrast, focal host infection prevalence and infected density are affected by density-mediated feedbacks due to both competition and disease-induced mortality. If total disease-induced mortality rates for the focal host ($\mu_1 I_1$) greatly increase or decrease, then the feedbacks due to disease-induced mortality will be strong and the sensitivity of $\mathcal{R}_0^C$ can differ from the sensitivities of the

other two metrics.

For mechanism 3, large changes in focal host density can cause the sensitivities of focal host infection prevalence and focal host infected density to differ in sign. The mathematical reason is the quotient rule from calculus implies that the sensitivities to non-focal host density (equation (7)) are related by

$$\overbrace{\frac{dI_1^*}{dN_n^*}}^{\substack{\text{Change in}\\ \text{infected density}}} = N_1^* \overbrace{\frac{d}{dN_n^*}\frac{I_1^*}{N_1^*}}^{\substack{\text{Change in}\\ \text{infection prevalence}}} + \frac{I_1^*}{N_1^*} \overbrace{\frac{dN_1^*}{dN_n^*}}^{\substack{\text{Change in}\\ \text{total density}}}. \tag{8}$$

The same relationship applies to the sensitivities to parameter values (equation (6)). The sensitivities of infected density (left side of equation) and infection prevalence (first term on the right side of the equation) can only differ in sign if the changes in total focal host density (second term on the right side of the equation) are large and in the opposite direction as the changes in infection prevalence. For example, increased density of host n could increase focal infection prevalence ($[d/dN_n^*][I_1^*/N_n^*] > 0$) but also decrease focal host infected density ($dI_1^*/dN_n^* < 0$) because of large decreases in focal host density ($dN_1^*/dN_n^* < 0$). My calculations show that the sensitivities of focal host infection prevalence and infected density have opposite signs only if (i) the focal host is a sink or small source and a subset of the non-focal hosts are large sources or (ii) the focal host is more strongly regulated by interspecific competition and disease than by intraspecific competition; see Remark S1.6 of Appendix S1.2.5 and Appendix S1.6 for mathematical details.

4.2 Sensitivities of metrics to non-focal host competence

Intuition suggests that higher competence in the non-focal host (larger $\mathcal{R}_{0,n}(\infty)$) will lead to increases in all metrics of disease. For $\mathcal{R}_0^C$, this intuition is always correct; see Appendix S1.5 for mathematical details. For example, increased transmission rates (β_i; Figure 1A) and decreased mortality rates (μ_i; Figure 1D) of a non-focal host always increase $\mathcal{R}_0^C$.

These predictions explain why $\mathcal{R}_0^C$ always increased with increased host competence in prior studies of direct (Dobson, 2004; Joseph et al., 2013; O'Regan et al., 2015; Huang et al., 2019) and environmental (Feng et al., 2009; Espira et al., 2022) transmission pathogens; see Appendix S3.

In contrast, increased competence of a non-focal host often increases focal host infection prevalence, but not always. Specifically, increases in the non-focal host's shedding rate (χ_n) or decreases in its uptake rates ($u_{S_n}, u_{I_n}, u_{R_n}$) always increase focal host infection prevalence. Increases in the non-focal host's transmission parameter (β_n) and decreases in its mortality and recovery rates (μ_n, ν_n) often increase focal host infection prevalence (black circles and red triangles in Figure 1BE). However, decreased focal host infection prevalence is also possible; here, I focus on the two most biologically likely scenarios and refer the reader to Cortez (2021) and Appendix S1.6.3 for additional details. First, increases in the non-focal host's transmission parameter (β_n) can decrease focal host infection prevalence when the non-focal host is a large source ($\varphi_n > 0$) and interspecific competition is sufficiently strong (blue squares in Figure 1B). Second, decreases in the non-focal host's mortality and recovery rates (μ_n, ν_n) can decrease focal host infection prevalence when the non-focal host is a large sink ($\varphi_n < 0$; blue squares in Figure 1E). For both scenarios, increased competence of host n causes shifts in its densities that reduces the production of infectious propagules, which causes decreases in focal host infection prevalence.

When comparing the metrics, non-focal host competence often has effects of the same sign on all metrics (black circles in Figure 1). However, the non-focal host can have effects of different sign on $\mathcal{R}_0^C$ versus the other two metrics when the non-focal host is a large source or sink (blue squares in 1). This is due to density-mediated feedbacks (mechanism 2) where changes in non-focal host competence alter infectious propagule densities, which affects disease-induced mortality in the focal host. In addition, non-focal host competence can have effects of opposite sign on focal host infection prevalence and infected density due to large changes in focal host density (mechanism 3) when (i) the focal host is more

strongly regulated by the disease or interspecific competition than intraspecific competition (red triangles in Figure 1A-C) or (ii) the focal host is a sink or small source and other hosts are large sources (red triangles in Figure 1D-F).

4.3 Sensitivities of metrics to non-focal host density

Here, I compare how non-focal host density affects each disease metric, which yields insight into how host species additions and removals affect each metric. The response of each metric depends on how the densities of all host species shift as the density of the non-focal host increases. In the following formulas, $\alpha_{in}^{total\ddagger}$ and α_{in}^{total*} denote the total competitive effects (i.e., direct + indirect effect) of host n on host i at the disease-free and endemic equilibria (see Appendix S1.2.5 for details). The total competitive effects can be positive or negative depending on the strength and asymmetry of interspecific host competition across the community.

The sensitivity of $\mathcal{R}_0^C$ to non-focal host density is

$$\frac{d\mathcal{R}_0^C}{dN_n^\ddagger} = C_n^\ddagger \overbrace{\left(\mathcal{R}_{0,n}(\infty) - \mathcal{R}_0^C\right)}^{\text{relative competence of host } n} + \sum_{i<n} C_i^\ddagger \overbrace{\left(\mathcal{R}_{0,i}(\infty) - \mathcal{R}_0^C\right)}^{\text{relative competence of host } i} \overbrace{\alpha_{in}^{total\ddagger}}^{\text{total competitive effect on host } i} \tag{9}$$

where the $C_i^\ddagger$ are positive constants; see Appendix S1.5.1. Equation (9) shows that the change in $\mathcal{R}_0^C$ depends on whether the competence of each host species relative to $\mathcal{R}_0^C$ is high ($\mathcal{R}_{0,i}(\infty) - \mathcal{R}_0^C > 0$) or low ($\mathcal{R}_{0,i}(\infty) - \mathcal{R}_0^C < 0$) and whether the non-focal host has a positive ($\alpha_{in}^{total\ddagger} > 0$) or negative ($\alpha_{in}^{total\ddagger} < 0$) total competitive effect on each species. When interspecific competition is absent ($\alpha_{in}^{total} = 0$), the non-focal host increases $\mathcal{R}_0^C$ when its competence is sufficiently high ($\mathcal{R}_{0,i}(\infty) - \mathcal{R}_0^C > 0$; black circles in Figure 2A) and decreases $\mathcal{R}_0^C$ otherwise ($\mathcal{R}_{0,i}(\infty) - \mathcal{R}_0^C < 0$; black circles in Figure 2D). However, when interspecific competition is present, the non-focal host can decrease $\mathcal{R}_0^C$ when the non-focal host has more negative or less positive total competitive effects on source hosts

(blue squares in Figure 2A) and increase $\mathcal{R}_0^C$ when the non-focal host has more negative or less positive total competitive effects on sink hosts (blue squares in Figure 2D).

The effect of increased non-focal host density on focal host infection prevalence has a similar form,

$$\frac{d}{dN_n^*}\frac{I_1^*}{N_1^*} = \overbrace{C_n^*\varphi_n}^{\text{host } n \text{ is sink/source}} + \sum_i C_i^* \overbrace{\varphi_i}^{\text{host } i \text{ is sink/source}} \overbrace{\alpha_{in}^{total*}}^{\text{total competitive effect on host } i} \tag{10}$$

where the C_i^* are positive constants; see Appendix S1.6.2. The interpretation of equation (10) is the same except that high and low competence are replaced with source and sink, respectively. In particular, when interspecific competition is absent ($\alpha_{in}^{total*} = 0$), focal host infection prevalence increases when the non-focal host is a source ($\varphi_n > 0$; black circles in Figure 2BC) and decreases when the non-focal host is a sink ($\varphi_n < 0$; black circles in Figure 2EF). However, those patterns can be reversed if the non-focal host has more negative (or less positive) total competitive effects on source hosts (blue squares in Figure 2BC) or sink hosts (blue squares in Figure 2EF).

When comparing the metrics, increased non-focal host density often has effects of the same sign on all metrics (black circles in Figure 3). However, responses in $\mathcal{R}_0^C$ can differ in sign from the other two metrics due to differences in the definitions of competence and source/sink (mechanism 1), i.e., when the non-focal host is a high competence sink or a low competence source (blue squares in Figure 3). In addition, responses in focal host infection prevalence and infected density can differ in sign due to large changes in focal host density (mechanism 3) when (i) the focal host is more strongly regulated by disease or interspecific competition than intraspecific competition (red triangles in Figure 3BCEF) or (ii) the focal host is a sink or small source and other hosts are large sources.

These predictions explain prior results for environmental transmission models (Table 2); see Appendix S3.2 for mathematical details. First, in prior studies (Rudge et al., 2013; Fenton et al., 2015; Espira et al., 2022) added high competence sources increased $\mathcal{R}_0^C$ and focal host infection whereas added low competence sinks decreased both metrics because

those studies assumed no interspecific competition ($\alpha_{in}^{total} = 0$). Second, other studies of two-host models (Cáceres et al., 2014; Searle et al., 2016) assumed the focal host was a source ($\varphi_1 > 0$) and there was strong interspecific competition ($\alpha_{1n}^{total} < 0$ where $n = 2$). Consequently, a low competence non-focal sink host will necessarily decrease $\mathcal{R}_0^C$ and focal host infection prevalence (Cáceres et al., 2014), but an added non-focal source host can increase focal host infection prevalence (Searle et al., 2016). Third, the added non-focal source host in Searle et al. (2016) increased focal host infection prevalence, but decreased focal host infected density. This difference is due to large changes in focal host density (mechanism 3) caused by the focal host being a small source and the non-focal host being a very large source.

Translating the predictions to direct transmission models explains prior results for density-dependent (DDDT) and frequency-dependent (FDDT) direct transmission models (Table 2); mathematical details are provided in Appendix S3.1. Under DDDT, all hosts have high competence ($\mathcal{R}_{0,i}(\infty) - \mathcal{R}_0^C > 0$) and are sources ($\varphi_i > 0$). Thus, equations (9) and (10) are positive in the absence of interspecific competition ($\alpha_{in}^{total} = 0$) and negative only if interspecific competition is sufficiently strong ($\alpha_{in}^{total} < 0$). This explains why host additions always increased $\mathcal{R}_0^C$ and focal host infection prevalence in the absence of interspecific competition (Begon et al., 1992; Dobson, 2004; Rudolf and Antonovics, 2005; McCormack and Allen, 2007; Faust et al., 2017; Huang et al., 2019), but host additions decreased those metrics when interspecific competition was sufficiently strong (Bowers and Turner, 1997; Peixoto and Abramson, 2006; Joseph et al., 2013; Mihaljevic et al., 2014; O'Regan et al., 2015).

Under FDDT, a non-focal host is a source if has sufficiently high interspecific transmission rates and a sink otherwise (mathematical details given in Special Cases B and C of Appendix S2.4.2 and Special Case 2 of Appendix S2.5.2). Prior studies of FDDT models assume interspecific transmission rates are fractions of intraspecific transmission rates (i.e, $\hat{\beta}_{ij} = c_j\hat{\beta}_{jj}$ where $c_j < 1$), which means a non-focal host is source only if it has sufficiently high

competence. As a result, additions of lower competence non-focal hosts decreased $\mathcal{R}_0^C$ and focal host infection prevalence (Dobson, 2004; Rudolf and Antonovics, 2005; Faust et al., 2017; Mihaljevic et al., 2014), but additions of sufficiently high competence non-focal hosts increased both metrics (Joseph et al., 2013; O'Regan et al., 2015).

4.4 Sensitivities of metrics to pathogen transmission mechanism

Prior studies (e.g., Dobson 2004; Rudolf and Antonovics 2005; Mihaljevic et al. 2014; Faust et al. 2017) suggest that host additions decrease all three disease metrics more often under frequency-dependent direct transmission (FDDT) than density-dependent direct transmission (DDDT), but not always for focal host infection prevalence (Cortez and Duffy, 2021; Cortez, 2021). I explore this further by comparing how the response of each disease metric to host additions depends on the pathogen transmission mechanism.

To explain the approach, I use $\mathcal{R}_0^C$ as a concrete example (see Appendices S1.5.3 and S2.4.5 for mathematical details). The goal is to determine if larger increases or larger decreases in $\mathcal{R}_0^C$ occur under FDDT or DDDT when a subcommunity of m resident species ($m < n$) has species $m+1, ..., n$ added to it. To do this, I use a new parameter, q, that converts model (2) from a FDDT form ($\delta = 0$) to a DDDT form ($u_{S_i} = u_{I_i} = u_{R_i} = 0$). To allow for a fair comparison between the FDDT and DDDT forms of the model, the change of parameters varies the host uptake and degradation rates while holding constant the value of $\mathcal{R}_0^C$ for the m-species subcommunity. I then compute how $\mathcal{R}_0^C$ for the full n-species community changes using the sensitivity $\partial\mathcal{R}_0^C/\partial q$. Positive values mean host additions cause larger decreases (or smaller increases) in $\mathcal{R}_0^C$ under FDDT than DDDT. Negative values mean that host additions cause larger increases (or smaller decreases) in $\mathcal{R}_0^C$ under FDDT than DDDT. The same approach is used for focal host infection prevalence and infected density, with the only difference being that the change of parameters holds constant the host and propagule densities at the endemic equilibrium for the m-species subcommunity; this allows for a fair comparison with those two metrics (see Appendices S1.6.4 and S2.5.4

for details).

For $\mathcal{R}_0^C$, host additions cause larger decreases (or smaller increases) in $\mathcal{R}_0^C$ under FDDT than DDDT if (i) there is no interspecific competition (Figure 4A), (ii) added host species are sufficiently weak intraspecific and interspecific competitors, or (iii) added host species have higher uptake rates than resident host species (black circles and red triangles in Figure 4D). However, additions can cause larger increases (or smaller decreases) in $\mathcal{R}_0^C$ under FDDT than DDDT when added host species are stronger intraspecific and interspecific competitors and have lower uptake rates than resident host species (blue squares in Figure 4D).

Host additions are more likely to cause larger decreases (or smaller increases) in focal host infection prevalence under FDDT than DDDT when the added host species (i) are weak intraspecific and interspecific competitors and (ii) have lower competence than resident host species. For direct transmission models where interspecific transmission rates are fractions of intraspecific transmission rates (i.e, $\hat{\beta}_{ij} = c_j\hat{\beta}_j$ where $c_j < 1$), condition (ii) implies that added host species have relatively lower rates of interspecific transmission (smaller c_j) than resident host species; see Appendix S2.5.4 for details. Host additions are more likely to cause larger increases (or smaller decreases) in focal host infection prevalence under FDDT than DDDT when the opposite conditions hold. Consequently, in the absence of interspecific competition, an added low competence host causes smaller increases in focal host infection prevalence under FDDT than DDDT (black circles and blue squares in Figure 4B), but an added high competence host can cause the opposite (red triangles in Figure 4B). When interspecific competition is present, an added host can cause larger increases in focal host infection prevalence under FDDT than DDDT when it is a strong interspecific competitor or has high competence (blue squares and red triangles in Figure 4E, respectively).

When comparing the metrics, the pathogen transmission mechanism often has effects of the same sign on all metrics (black circles in Figure 4). However, responses in $\mathcal{R}_0^C$ can

differ in sign from the other two metrics when the added host species are large sources (red triangles in Figure 4DEF). This is due to density-mediated feedbacks (mechanism 2) where the added large sources increase infectious propagule density, which increases disease-induced mortality in the focal host. In addition, responses in focal host infection prevalence and infected density can have opposite signs due to changes in focal host density (mechanism 3) when the focal host is more strongly regulated by disease or interspecific competition than intraspecific competition (blue squares and red triangles in Figure 4A-C).

These predictions explain patterns in prior studies comparing DDDT and FDDT models. First, the $\mathcal{R}_0^C$ predictions explain why $\mathcal{R}_0^C$ increased more often under DDDT than FDDT in the absence of interspecific competition (Dobson, 2004; Rudolf and Antonovics, 2005; Joseph et al., 2013; Mihaljevic et al., 2014), but not when interspecific competition was stronger (Joseph et al., 2013; Mihaljevic et al., 2014). Second, Rudolf and Antonovics (2005) and Faust et al. (2017) observed that host additions decreased focal host infection prevalence more often under FDDT than DDDT because those studies assumed low interspecific transmission and no interspecific competition, respectively.

5 Discussion and Future Directions

Altered host species richness can change the risk and levels of disease in empirical communities (LoGiudice et al., 2008; Randolph and Dobson, 2012; Wood et al., 2016; Civitello et al., 2015; Rohr et al., 2019). In this study, I explored how variation in non-focal host competence, non-focal host density, and the pathogen transmission mechanism affects three common disease metrics: the pathogen's community reproduction number ($\mathcal{R}_0^C$) and focal host infection prevalence (I_1^*/N_1^*) and infected density (I_1^*) at equilibrium. My sensitivity-based results identify the factors influencing the slopes of the responses of each disease metric. That yields insight into the conditions under which host additions and removals increase

or decrease each disease metric, and it explains how observed relationships between host species richness and disease in prior theoretical studies were driven by host and pathogen characteristics and the disease metric (Table 2).

The three metrics provide insight about different aspects of disease dynamics and disease risk: $\mathcal{R}_0^C$ is a measure of the risk and speed of an outbreak in a community whereas infection prevalence (I/N) and infected density (I) are measures of disease burden in a population. Agreement across all metrics is an ideal situation for disease management strategies that use culling or host removal (Laurenson et al., 2004; Donnelly et al., 2006) because disease risk and disease burden can be simultaneously minimized by removing or suppressing species in a community. However, cases where the metrics respond differently to altered host species richness are potentially problematic because they imply that reducing disease risk could potentially increase disease burden, and vice versa. For example, removing a high competence, small source host from a community reduces the risk of an outbreak in that community (by lowering $\mathcal{R}_0^C$) but potentially increases disease burden in a focal population if the pathogen becomes established (by increasing I_1^*/N_1^* or I_1^*). Disagreement between infection prevalence and infected density is problematic as well because it means that disease burden can increase in one metric and decrease in another. For example, removal of a large source host may decrease focal host infection prevalence (I_1^*/N_1^*), but also increase infected density (I_1^*), because of large changes in focal host density; this is the scenario observed in Searle et al. (2016). Such scenarios could increase or decrease the risk of spillover into novel host populations depending on whether interspecific contact rates depend on infected host densities or frequencies.

Identifying when metrics agree and disagree also facilitates predictions about the effects of altered host biodiversity. $\mathcal{R}_0^C$ is often much easier to compute than infection prevalences and infected densities. When the responses in $\mathcal{R}_0^C$ and the other two metrics agree, predictions about $\mathcal{R}_0^C$ will yield qualitatively correct predictions about responses in infection prevalences and infected densities. To determine if the metrics agree or not, my results indicate that competence, net production of infectious propagules (sink/source), and levels of interspecific

competition are important quantities to estimate for each host species. These may be difficult to accurately estimate in some systems. However, the sensitivities show how underestimating or overestimating parameters will affect predictions. For example, an underestimated shedding rate will lead to underestimated values of all three metrics in most cases (because all sensitivities are positive), but infected density could be overestimated if the focal host is strongly regulated by interspecific competition or disease (which yields a negative sensitivity for infected density). For systems where accurate estimates are available, my results can help explain observed patterns. For example, for the studies of environmentally transmitted pathogens that used models parameterized to an empirical system (Rudge et al., 2013; Cáceres et al., 2014; Fenton et al., 2015; Searle et al., 2016), my results explain how increases and decreases in each metric are driven by the characteristics of the host and pathogen species; see Appendix S3.2 for details. Thus, in addition to explaining and unifying results from prior theoretical studies, the theory in this study shows promise for explaining some of the variation in responses to altered host species richness observed across empirical systems (Civitello et al., 2015; Halliday and Rohr, 2019).

Looking forward, fully explaining the variation in responses observed across all empirical systems will require advances in theory in four areas. First, additional theory is needed to address other metrics, including peak infection prevalence or infected density (Roche et al., 2012), community prevalence (Suzán et al., 2009; Searle et al., 2011), disease incidence (Haas et al., 2011), infectious propagule density (Roberts and Heesterbeek, 2018; Cortez and Duffy, 2020), and infection intensity (Hechinger and Lafferty, 2005; Becker et al., 2014). Exploring these metrics is important because they can provide different information about disease burden and disease risk. Second, more theory is needed to extend our understanding of multi-host systems where host species have non-competitive interspecific interactions (Rohr et al., 2015), including systems where pathogens obligately switch between host species during their life cycle (Hechinger and Lafferty, 2005; Hopkins et al., 2016). Combined, the first and second areas would help address a current need to understand how the interactions

between parasites, pathogens, and their ecosystems shape disease burden and the risk of disease emergence (Cunningham et al., 2017).

Third, additional theory is needed to explain why increased host species richness often, but not always, decreases disease for vector-borne pathogens in empirical studies (Ezenwa et al., 2006; Keesing et al., 2009; Moore and Borer, 2012; Xavier et al., 2012) and theoretical studies (Saul, 2003; Normal et al., 1999; Ogden and Tsao, 2009; Miller and Huppert, 2013). Because vectors are analogous to infectious propagules, some of the variation may be explained by the net production of infected vectors by each host species (analogous to φ_i). However, this analogy is limited because vectors can have complex dynamics and behavior (e.g., biting preferences), which may influence how host additions affect disease metrics (Miller and Huppert, 2013; Marini et al., 2017).

Fourth, new theory is needed to explain why host species can have temporally varying effects on disease metrics. For example, empirical studies show that an additional host species can have effects of the same sign at all points in time (e.g., always decreasing focal host infection prevalence; Strauss et al. 2015) or effects of varying sign (e.g., transition from decreased to increased focal host infection prevalence; Dallas et al. 2016). My results suggest a possible explanation for the temporally varying effects: a low competence source host could decrease infection prevalence early in time because decreases in $\mathcal{R}_0^C$ imply slower rates of spread, but also increase infection prevalence later in time because it is a net producer of infectious propagules. However, future work is needed to fully explore when and why host species have temporally variable effects on disease dynamics.

While more theory is needed in the four areas listed above, this study and others (Roberts and Heesterbeek, 2018; Cortez, 2021) demonstrate that sensitivity-based approaches can help advance understanding. This study showed that sensitivity analysis can help explain and extend results from prior theoretical studies. That in turn yields insight into the mechanisms influencing the relationships between host species richness and disease in empirical systems.

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Table 1: Model variables, parameters, and important quantities

Notation	Description
Variables	
S_i	host i susceptible density
I_i	host i infected density
R_i	host i recovered density
$N_i = S_i + I_i + R_i$	host i total density
I_i/N_i	host i infection prevalence (i.e., proportion of infected individuals)
P	infectious propagule density
Parameters	
F_i	reproduction rate
β_i	transmission coefficient
m_i	mortality rate due to non-disease related factors
μ_i	disease-induced mortality rate
ν_i	recovery rate
ξ_i	rate of increased mortality due to prior infection
γ_i	rate of loss of immunity
χ_i	shedding rate of infectious propagules
$u_{S_i}, u_{I_i}, u_{R_i}$	uptake rates of infectious propagules for host classes S_i, I_i, R_i
δ	degradation rate of infectious propagules
Quantities	
$\mathcal{R}_0^C$	pathogen community reproduction number
φ_i	per capita net production of infectious propagules by host i
	defines if host i is a source ($\varphi_i > 0$) or sink ($\varphi_i > 0$)
$\mathcal{R}_{0,i}(\infty) = \beta_i \chi_i / u_{S_i}[m_i + \mu_i + \nu_i]$	competence of host i
α_{in}^{total}	total (direct + indirect) competitive effect of host n on host i
$p^{\ddagger}$	n-species disease-free equilibrium with densities $N_i^{\ddagger}$
p^*	n-species endemic equilibrium with densities N_i^*

Table 2: Predicted effects of the addition of a non-focal host on three metrics of disease

Metric	Transmission Mode†	Interspecific Competition	Predicted response to the addition of a non-focal host	Prior studies‡ explained/generalized
Community reproduction number ($\mathcal{R}_0^C$)	ET	No	Increases if non-focal host has sufficiently high competence or interspecific shedding rates Decreases if non-focal host has sufficiently low competence or interspecific shedding rates	[1]-[3]
		Yes	Increases if hosts with higher competence and interspecific shedding rates increase more or decrease less than hosts with lower competence and interspecific shedding rates Increases if hosts with lower competence and interspecific shedding rates increase more or decrease less than hosts with higher competence and interspecific shedding rates	
	DDDT	No	Always increases	[4]-[6]
		Yes	Increases unless interspecific competition is sufficiently strong	[7]-[10]
	FDDT	No	Increases if non-focal host has sufficiently high competence or interspecific shedding rates Decreases if non-focal host has sufficiently low competence or interspecific shedding rates	[4]
		Yes	Increases if hosts with higher competence and interspecific shedding rates increase more or decrease less than hosts with lower competence and interspecific shedding rates Decreases if hosts with lower competence and interspecific shedding rates increase more or decrease less than hosts with higher competence and interspecific shedding rates	[7]-[10]
Focal host infection prevalence (I_1^*/N_1^*)	ET	No	Increases if non-focal host is a source Decreases if non-focal host is a sink	[11]
		Yes	Increases if source hosts increase more or decrease less than sink hosts Decreases if source hosts decrease more or increase less than sink hosts	[12]-[14]
	DDDT	No	Always increases	[15]-[17]
		Yes	Increases unless interspecific competition is sufficiently strong	[10],[17]-[19]
	FDDT	No	Increases if non-focal host has sufficiently high competence and interspecific transmission rates Decreases if non-focal host has sufficiently low competence and interspecific transmission rates	[16]
		Yes	Increases if hosts with higher competence and interspecific transmission increase more or decrease less than hosts with lower competence and interspecific transmission Decreases if hosts with higher competence and interspecific transmission decrease more or increase less than hosts with lower competence and interspecific transmission	[10],[17]
Focal host infected density (I_1^*)	All		Same as focal host infection prevalence unless (i) Focal host is more strongly regulated by the disease and interspecific competition than by intraspecific competition (ii) Focal host is a sink or small source and some other hosts are large sources	[10],[20]

† ET is environmental transmission; FDDT is frequency-dependent direct transmission; DDDT is density-dependent direct transmission.

‡ Prior studies are [1] Rudge et al. (2013), [2] Fenton et al. (2015), [3] Espira et al. (2022), [4] Dobson (2004), [5] McCormack and Allen (2007), [6]

Huang et al. (2019), [7] O'Regan et al. (2015), [8] Joseph et al. (2013), [9] Mihaljevic et al. (2014), [10] Roberts and Heesterbeek (2018), [11] Rudge et al. (2013), [12] Cáceres et al. (2014), [13] Cortez and Duffy (2021), [14] Cortez (2021), [15] Begon et al. (1992), [16] Faust et al. (2017), [17] Rudolf and Antonovics (2005), [18] Bowers and Turner (1997), [19] Peixoto and Abramson (2006), [20] Searle et al. (2016). Mathematical details are provided in Appendix S3.

7 Figures

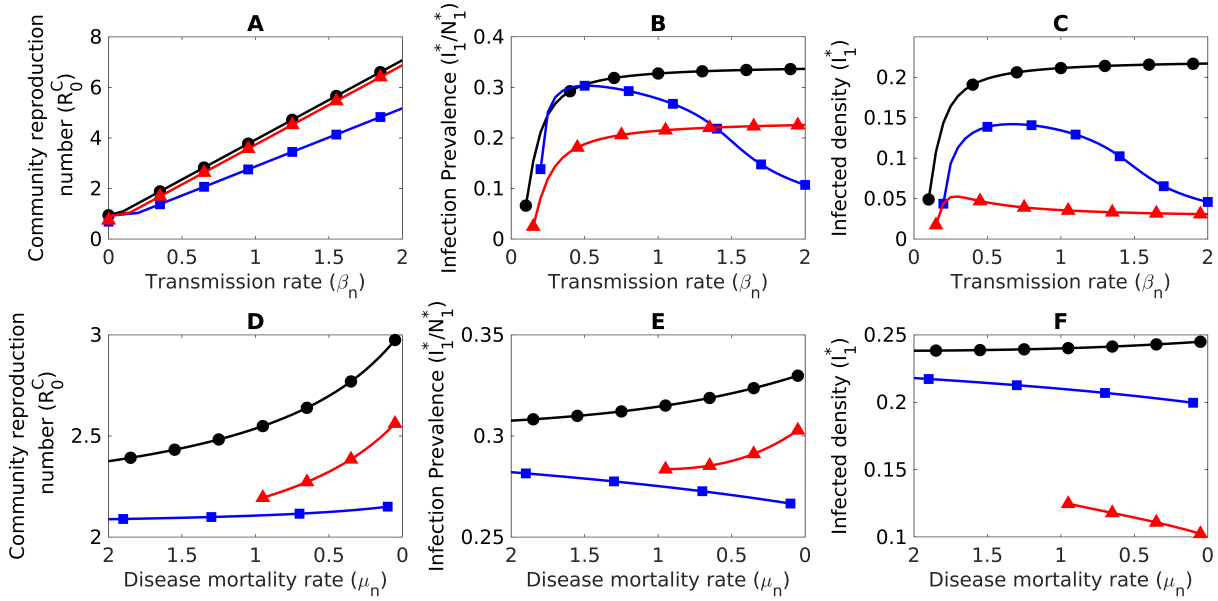

Figure 1: Increased competence of a non-focal host increases all metrics of disease, unless there are strong density-mediated feedbacks due to disease-induced mortality (mechanism 2) or large changes in focal host density (mechanism 3). Note that the x-axes in the bottom row are reversed. (A,D) $\mathcal{R}_0^C$ always increases with increased transmission rates and decreased disease-induced mortality rates of a non-focal host. (B,E) Focal host infection prevalence (I_1^*/N_1^*) increases with increased transmission rates and decreased disease-induced mortality rates of a non-focal host (black circles and red triangles in B,E), unless there are strong density-mediated feedbacks due to disease-induced mortality (mechanism 2), which occurs when interspecific competition is sufficiently large (blue squares in B) or the non-focal host is a large sink (blue squares in E). (C,F) Focal host infected density (I_1^*) responds in the same way as focal host infection prevalence (black circles and blue squares), unless there are large changes in focal host density (mechanism 3), which occurs when the focal host is more strongly regulated by the disease or interspecific competition than intraspecific competition (red triangles in C) or the focal host is a sink and other hosts are large sources (red triangles in F). In each row, curves of the same color are from the same parameterization of a four-host version of model (2); see appendix S4 for parameter values.

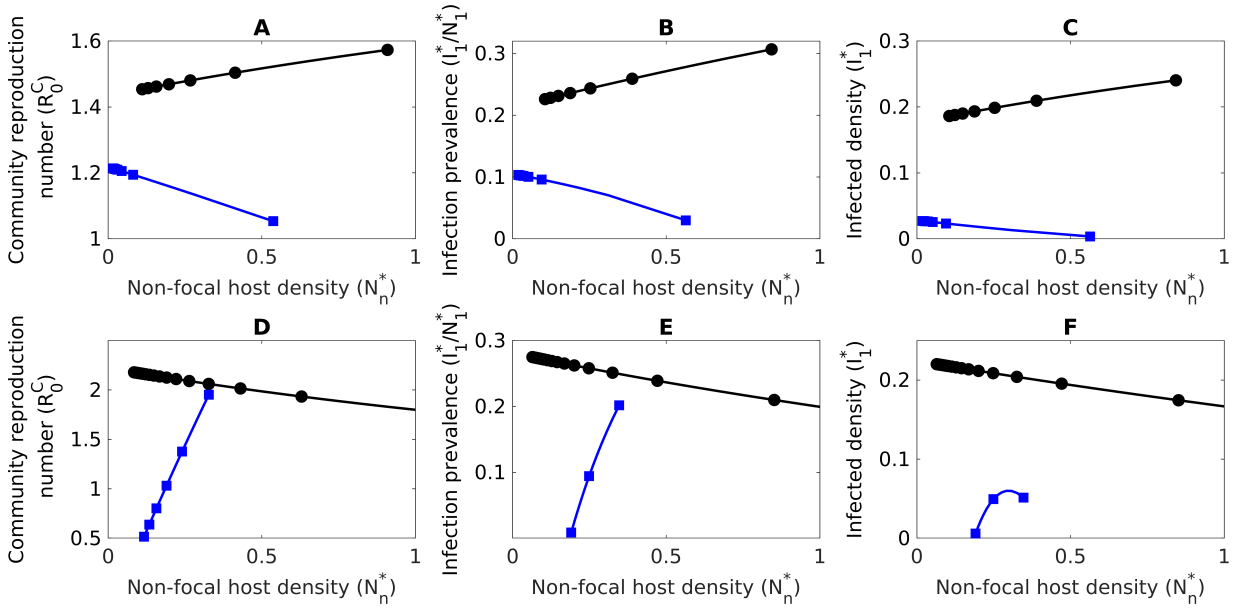

Figure 2: Strong interspecific competition can reverse predictions about the effects of increased non-focal host density on each disease metric. (A-C) Increased density of a high competence non-focal source host increases all disease metrics in the absence of interspecific competition (black circles), but decreases all disease metrics when the non-focal host has more negative (or less positive) total competitive effects on low competence source hosts than high competence sink hosts (blue squares). (D-F) Increased density of a low competence non-focal sink host decreases all disease metrics in the absence of interspecific competition (black circles), but increases all disease metrics when the non-focal host has more negative (or less positive) total competitive effects on low competence sink hosts than high competence source hosts (blue squares). In each row, curves of the same color are from the same parameterization of a four-host version of model (2); see appendix S4 for parameter values.

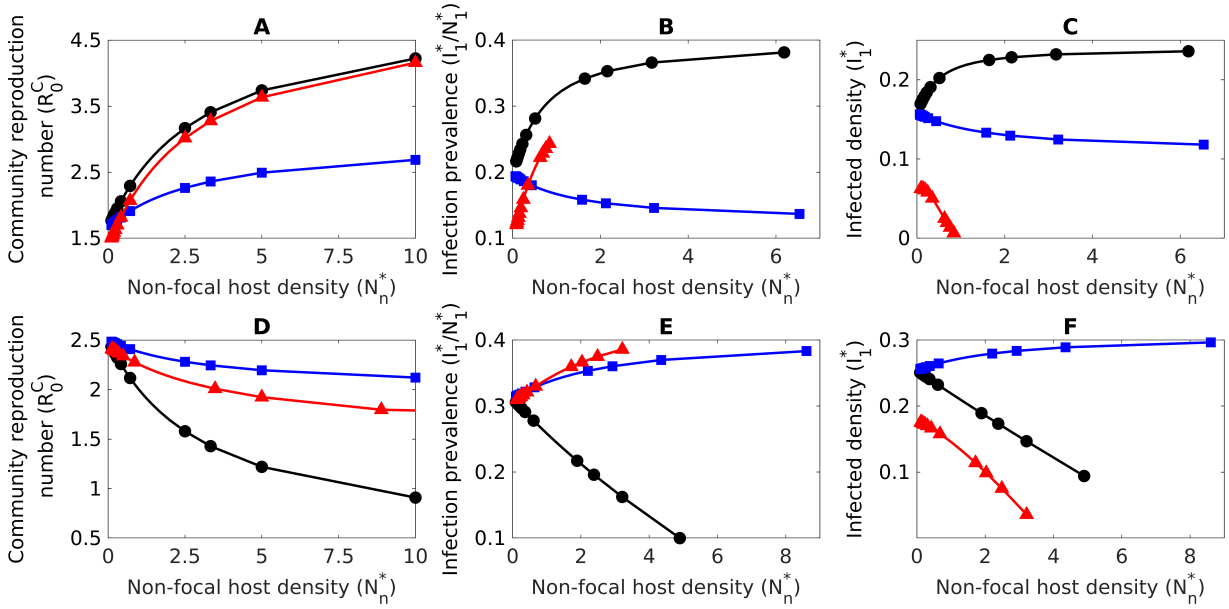

Figure 3: The effects of increased non-focal host density on each of metric of disease depend on whether the non-focal host has high or low competence, the non-focal is a source or sink, and there are large changes in focal host density (mechanism 3). Increased density of the non-focal host (A) always increases $\mathcal{R}_0^C$ when the non-focal host has high competence and (D) always decreases $\mathcal{R}_0^C$ when non-focal host has low competence. (B,C) Increased density of the non-focal host increases focal host infection prevalence (I_1^*/N_1^*) when the non-focal host is a source (black circles and red triangles in B; blue squares and red triangles in E) and decreases focal host infection prevalence when the non-focal host is a sink (blue squares in B; black circles in E). (C,F) Increased density of the non-focal host often increases focal host infected density (I_1^*) when the non-focal host is a source (black circles in C; blue squares in F) and decreases focal host infected density when the non-focal host is a sink (blue squares in C; black circles in F). However, focal host infected density can decrease when the non-focal host is a source if there are large changes in focal host density, which occurs when the focal host is more strongly regulated by disease and interspecific competition than by intraspecific competition (red triangles in CF). In each row, curves of the same color are from the same parameterization of a four-host version of model (2); see appendix S4 for parameter values.

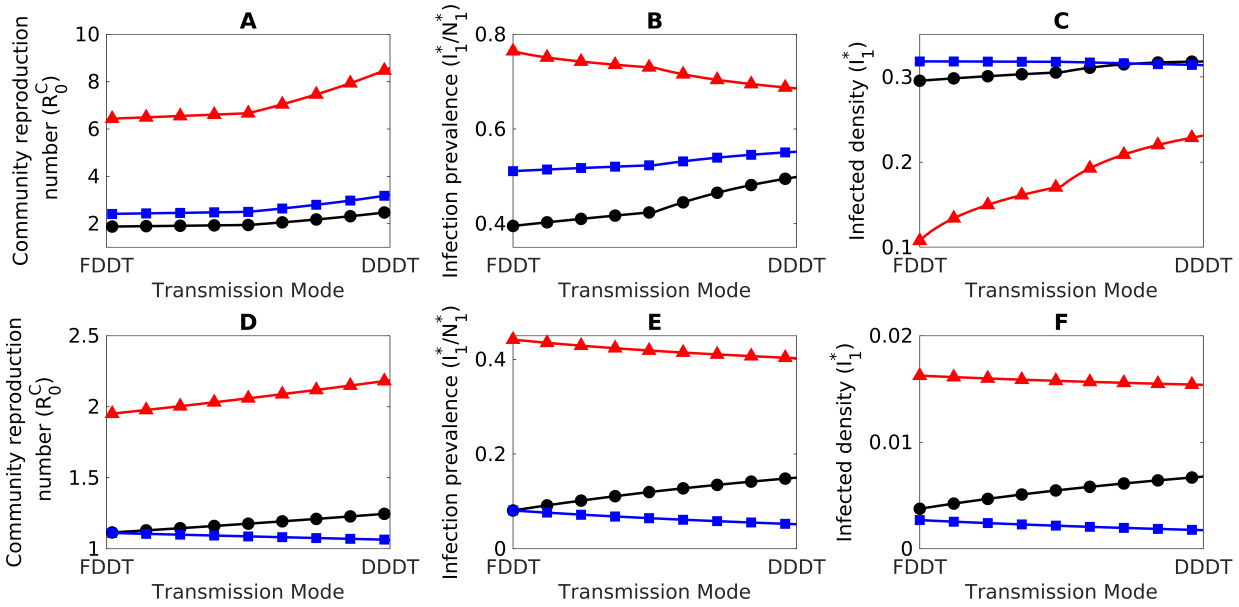

Figure 4: Host additions cause larger decreases or smaller increases in each metric under frequency-dependent direct transmission (FDDT) than density-dependent direct transmission (DDDT), unless the added host species have sufficiently high competence, the added host species are sufficiently strong interspecific competitors, or there are large changes in focal host density. In each panel, a change of parameters is used to convert the environmental transmission model from a FDDT form to a DDDT form; see text for details. Positive slopes mean large decreases or smaller increases in the metric under FDDT than DDDT when a host is added to a community of resident host species; negative slopes mean larger increases or smaller decreases in the metric under FDDT and DDDT. (A,D) Host additions cause smaller increases in $\mathcal{R}_0^C$ under FDDT than DDDT (all curves in A, black circles and red triangles in D), unless interspecific competition is sufficiently strong and the added host has sufficiently smaller uptake rates than resident host species (blue squares in D). (B,E) Host additions cause larger decreases or smaller increases in focal host infection prevalence (I_1^*/N_1^*) under FDDT than DDDT (black circles and blue squares in B, black circles in E), unless the added host has sufficiently high competence or is a strong interspecific competitor (red triangles in B, blue squares and red triangles in E). (C,F) The responses in focal host infected density (I_1^*) are the same as those in focal host infection prevalence (black circles in C, all curves in F), unless there are large changes in focal host density (mechanism 3), which occurs when the focal host is more strongly regulated by disease and interspecific competition than by intraspecific competition (blue squares and red triangles in C). In each row, curves of the same color are from the same parameterization of a four-host version of model (2); see appendix S4 for parameter values.

Box 1: Relationships between environmental and direct transmission models

Prior studies (Eisenberg et al., 2013; Cortez and Weitz, 2013; Cortez and Duffy, 2021; Cortez, 2021; Espira et al., 2022) have shown that environmental transmission (ET) models can reduce down to models with density-dependent direct transmission (DDDT), frequency-dependent direct transmission (FDDT), or direct transmission that is intermediate to DDDT and FDDT. In general, an environmental transmission model reduces to a direct transmission model when the shedding rates and either the uptake rates or degradation rates are very large. The reason is that very large uptake and degradation rates mean that the infectious propagules only persist in the environment for short periods of time. As a result, a susceptible individual will encounter infectious propagules only if it is in close proximity to an infected individual. Because transmission only occurs when susceptible and infected individuals are in close contact, the environmental transmission pathogen effectively behaves like a direct transmission pathogen.

The 1-habitat ET model (2) reduces down to (i) a DDDT model when uptake is negligible compared to degradation ($U + \delta \approx \delta$), (ii) an FDDT model when degradation is negligible compared to uptake ($\delta \approx 0$) and all uptake rates are equal ($u_{S_i} = u_{I_i} = u_{R_i} = u$), and (iii) a model with transmission intermediate to DDDT and FDDT when uptake and degradation are both non-negligible. Here, I provide a brief mathematical explanation; additional details for the 1-habitat and n-habitat models are provided in Appendices S1.3 and S2.2, respectively. When the shedding rates are large and the uptake or degradation rates are large, the infected density equation in the 1-habitat ET model (2) is approximately described by

$$\frac{dI_i}{dt} = \overbrace{\sum_j \frac{\beta_i \chi_j S_i I_j}{\delta + \sum_k (u_{S_k} S_i + u_{I_k} I_i + u_{R_k} R_i)}}^{\text{infection}} - \overbrace{\mu_i Y_i - m_i Y_i}^{\text{mortality}} - \overbrace{\nu_i Y_i}^{\text{recovery}} . \tag{11}$$

The first term in equation (11) is the sum of the direct transmission rates from each host j to host i; the second and third terms are the mortality rates due to disease and non-disease factors; and the fourth term is the recovery rate. I consider three cases. First, if uptake of infectious propagules is negligible ($\delta + \sum_k u_{S_k} S_i + u_{I_k} I_i + u_{R_k} R_i \approx \delta$), then the transmission rate in equation (11) reduces to $\hat{\beta}_{ij} S_i I_j$ where $\hat{\beta}_{ij} = \beta_i \chi_j / \delta$. This is a DDDT rate because the rate of infection is proportional to the density of infected individuals (I_j). Second, if degradation is negligible ($\delta \approx 0$) and all uptake rates are equal ($u_{S_i} = u_{I_i} = u_{R_i} = u$), then the transmission rate in equation (11) reduces to $\hat{\beta}_{ij} S_i I_j / \sum_k N_k$ where $\hat{\beta}_{ij} = \beta_i \chi_j / u$. This is a FDDT rate because the rate of infection is proportional to the frequency of infected individuals in the community ($I_j / \sum_k N_k$). Third, if uptake and degradation rates are non-negligible, then the direct transmission rate in equation (11) is intermediate to FDDT and DDDT. The rate is more similar to DDDT when degradation is large and uptake small, and the rate is more similar to FDDT under the opposite conditions.

In total, the 1-habitat and n-habitat ET models can be converted from DDDT forms to FDDT forms by varying the magnitudes of the infectious propagule degradation rate and host uptake rates. Consequently, the results for the 1-habitat and n-habitat ET models apply to DDDT and FDDT models, after accounting for the restrictions on the parameter values. This allows one to simultaneously study ET, DDDT, and FDDT pathogens and identify how the transmission mechanism affects model predictions.

Box 2: Connection between $\mathcal{R}_0^C$ and theory for stage-structured models
The pathogen's basic reproduction number, $\mathcal{R}_0^C$, is the average number of new infections produced by a single infected individual in an otherwise susceptible community. The value of $\mathcal{R}_0^C$ determines if a single infected individual will cause an outbreak ($\mathcal{R}_0^C > 1$) or not ($\mathcal{R}_0^C > 1$). Conveniently, $\mathcal{R}_0^C$ for the 1-habitat model (2) has an explicit formula,

$$\mathcal{R}_0^C = \sum_i \frac{\chi_i}{(m_i + \mu_i + \nu_i)} \frac{\beta_i N_i^\ddagger}{U^\ddagger + \delta} \tag{12}$$

where $N_i^\ddagger$ is the density of host i and $U^\ddagger = \sum_j u_{S_j} N_j^\ddagger$ is the total uptake rate of infectious propagules at the disease-free equilibrium; see Appendix S1.5 for mathematical calculations. Each term in the sum defines the average number of new infections a single infected individual of host i will produce in its lifetime. In particular, the first fraction is the shedding rate (χ_j) multiplied by the average duration of infection ($1/[\mu_i+m_i+\gamma_i]$), which equals the average lifetime production of infectious propagules by an infected individual of host i. The second fraction is the infection rate for host i ($\beta_i N_i^\ddagger$) multiplied by the average lifespan of a spore ($1/[U^\ddagger + \delta]$), which equals the average lifetime production of new infected individuals of host i by an infectious propagule. The sensitivities of $\mathcal{R}_0^C$ (e.g., $\partial\mathcal{R}_0^C/\partial\chi_n$ and $d\mathcal{R}_0^C/dN_n^*$) can be computed by differentiating equation (12).

For many models, explicit formulas for $\mathcal{R}_0^C$ cannot be computed. This is true for the n-habitat models analyzed in Appendix S2 and direct transmission models with three or more host species. Consequently, one cannot compute the sensitivities of $\mathcal{R}_0^C$ by differentiating a formula analogous to equation (12). However, the matrix theory developed for discrete-time models of stage-structured populations allows one to derive formulas for the sensitivities of $\mathcal{R}_0^C$, even when an explicit formula for $\mathcal{R}_0^C$ does not exist.

The intuition for the connection between $\mathcal{R}_0^C$ and stage-structured models is that infected individuals of each host species represent different life history "stages" for the pathogen. Matrix models for stage-structured populations describe how each stage contributes to the abundances of all stages in the next time step. Analogously, the Next Generation Matrix (Van den Driessche and Watmough, 2008; Diekmann et al., 2010) describes how the infected class in each host species contributes to infections

in all host species in the next pathogen generation. As a specific example, the Next Generation Matrix for a 3-species version of model (2) is

$$\mathbf{NGM} = \begin{bmatrix} \frac{\chi_1}{\mu_1+m_1+\gamma_1}\frac{\beta_1 N_1^{\ddagger}}{U^{\ddagger}+\delta} & \frac{\chi_2}{\mu_2+m_2+\gamma_2}\frac{\beta_1 N_1^{\ddagger}}{U^{\ddagger}+\delta} & \frac{\chi_3}{\mu_3+m_3+\gamma_3}\frac{\beta_1 N_1^{\ddagger}}{U^{\ddagger}+\delta} \\ \frac{\chi_1}{\mu_1+m_1+\gamma_1}\frac{\beta_2 N_2^{\ddagger}}{U^{\ddagger}+\delta} & \frac{\chi_2}{\mu_2+m_2+\gamma_2}\frac{\beta_2 N_2^{\ddagger}}{U^{\ddagger}+\delta} & \frac{\chi_3}{\mu_3+m_3+\gamma_3}\frac{\beta_2 N_2^{\ddagger}}{U^{\ddagger}+\delta} \\ \frac{\chi_1}{\mu_1+m_1+\gamma_1}\frac{\beta_3 N_3^{\ddagger}}{U^{\ddagger}+\delta} & \frac{\chi_2}{\mu_2+m_2+\gamma_2}\frac{\beta_3 N_3^{\ddagger}}{U^{\ddagger}+\delta} & \frac{\chi_3}{\mu_3+m_3+\gamma_3}\frac{\beta_3 N_3^{\ddagger}}{U^{\ddagger}+\delta} \end{bmatrix}. \quad (13)$$

Entry i, j defines the average number of new infections in host j that a single infected individual of host i will produce in its lifetime. In particular, the first fraction in each entry ($\chi_j/[\mu_j + \nu_j + \gamma_j]$) equals the average lifetime production of infectious propagules by an infected individual of host j. The second fraction in each entry ($\beta_i N_i^{\ddagger}/[U^{\ddagger} + \delta]$) equals the average lifetime production of new infected individuals of host i by an infectious propagule. When the fractions are multiplied, they yield the average lifetime production of new infections in host j by a single infected individual of host i.

For matrix models, the leading eigenvalue of the matrix defines the asymptotic growth rate of the species. Analogously, the leading eigenvalue of the Next Generation Matrix (13) defines the pathogen's reproduction number ($\mathcal{R}_0^C$), which in turn defines the asymptotic growth rate of an outbreak. Importantly, this means that the sensitivity theory for the asymptotic growth rates of stage-structured populations (Caswell, 2019) can be used to compute the sensitivities of $\mathcal{R}_0^C$. I use that theory to compute the sensitivities of $\mathcal{R}_0^C$ for the n-habitat model and direct transmission models with three or more host species, even though explicit formulas for $\mathcal{R}_0^C$ cannot be computed. Mathematical details are given in Appendix S2.4.