Milestone Report: Persistence and transmission dynamics of emerging tick-borne pathogens:

Extending a 2-pathogen, 1-host, 1-vector SIR metapopulation model

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1. Abstract

Novel extensions to a published SIR compartment model describing the dynamics of vector-borne disease in a 2-pathogen/1-vector/1-host system are proposed. The goals of these model extensions are to analyze the resulting changes to the transmission dynamics of two established pathogens induced by the introduction of novel diversity in the form of either a newly emerged (i.e., competing) pathogen or the expansion of the pathogens' ecological niche to new vectors and new hosts. While our proposed model extensions are theoretical by design, we aim to derive plausible initial values gleaned from real-world case studies of applicable vector-borne model systems to demonstrate realistic parameter ranges that may underly similar biological systems as they occur in nature. Extended epidemic models such as those included in this proposal have potential to become valuable tools in the public health science toolbox by helping scientists and decision-makers evaluate threats posed by -for example- the emergence of new vector-borne pathogens or by the expansion of the host or geographic range of established pathogens due to climate change.

KEYWORDS

SIR models, transmission dynamics, vector-borne diseases, metapopulation models

ACM Reference format:

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1 Introduction

The diversity and zoonotic potential of tickborne diseases has been reported with increasing frequency over the past decade, increasing the threat to human and veterinary health (Rondino et al. 2020). Ticks belong to the arachnid order and are classified into two broad types: hard-bodied ticks (family Ixodidae) and soft-bodied ticks (family Argasidae) (Durden and Beati 2013). The ixodid ticks are the most common ectoparasites of humans and mammals in the United States with an average of approximately 50,000 cases of tickborne diseases reported each year, estimated to be 77-95% of the reported cases of vector-borne disease (Rondino et al. 2020; cdc.gov/ticks/data-summary, accessed 2022-10-04). The tick life cycle includes three obligate parasitic stages: larva, nymph, and adult. Each stage is characterized by the need for a blood meal from a suitable host, during which the feeding tick attaches to the host, consumes a meal, and then detaches to molt to the next stage (Figure 1, below).

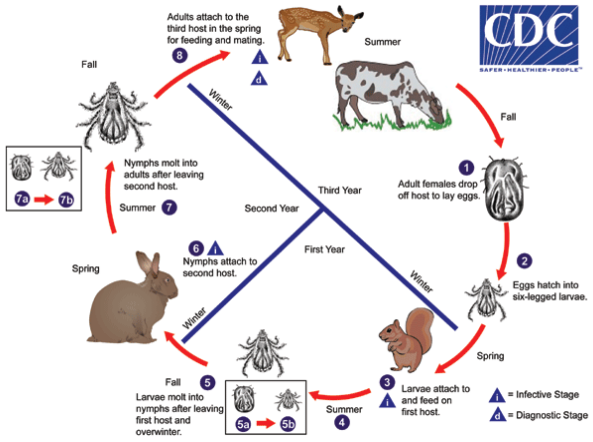

Figure 1: Typical life cycle of tick vectors. Reproduced from URL: https://www.cdc.gov/ticks/tickbornediseases/

During this feeding process, some infectious agents, such as *Rickettsia spp.* (spotted fevers), *Borrelia burgdorferi* (Lyme disease), and *Ehrlichia chaffeensis* (heartwater), which are occasionally present in the host, can be transmitted to the feeding tick via the consumed blood meal (Madison-Antenucci et al. 2020). Following host-to-tick transmission, the newly-acquired pathogen(s) colonize the mid- or hindgut of the tick and can be further transmitted by the tick vector to new hosts on which the infected tick feeds (cdc.gov/ticks/life_cycle_and_hosts, accessed 2022-10-04). Once colonized (="infected"), molting larvae or nymphal ticks retain the commensal pathogen as they advance to their next life stage (known as trans-stadial transmission). Similarly, adult female ticks can vertically transmit infection to her offspring when eggs are laid (called trans-ovarial

transmission), thus the newly hatched larvae are infectious prior to consuming any blood meal and capable of tick-to-host transmission when they attach to their first host (Rondino et al. 2020).

Modelling vector-borne disease with compartment models such as SIR represents a powerful way to examine population dynamics of tick vectors and the zoonotic pathogens they transmit. The standard SIR model can be extended to capture unique dynamics of vector-borne pathogen transmission, including published models which reflect the multiple modes of transmission and additional states/compartments required to accurately describe a biological system that includes the vector(s), host(s), and the infectious agent(s) at play (White et al. 2019). Further extensions to these existing compartment models can better portray the populations dynamics and expected pathogen persistence, defined as the pathogen's ability to survive environmental disturbances, as they occur in nature by attempting to capture additional parameters of natural systems and using fewer simplifying assumptions. In this proposal, we will analyze a published 2-pathogen/1-vector/1-host compartment model (hereafter referred to as the "2-1-1" model) which models the dynamics of two species of rickettsial pathogen, the ixodid tick vector *Amblyomma*, and a white-tailed deer host population. We aim to extend the deterministic differential equations (ODEs) underlying this model to include additional pathogens, vectors, and hosts with an eye towards better understanding the epidemic potential, transmission dynamics, and persistence of the competing pathogen species as additional diversity is introduced into the model. While theoretical, our proposed extensions to the 2-1-1 model may be useful to examine potential scenarios of public health concern such as emerging zoonoses as "old" pathogens expand their ecological niche by gaining new vectors or host species, or in which they may be outcompeted by the introduction of new pathogens.

1.1 Feedback Response

We thank the reviewer(s) for providing helpful comments that helped us improve this research further. The reviewers raised interesting points for consideration related to comparisons of our results to similar competing pathogen models and additional potential mathematical analysis of our model, plus a few comments that we felt were minor overall. Based on this feedback, we have revised our research objectives and addressed all comments regarding formatting in this project milestone. Please see the rebuttal below for detailed responses to specific reviewer comments. Our progress to date is further elaborated in the remaining sections to follow.

Comments from reviewer(s):

well written! i agree, your extensions can be interesting to study emerging diseases scenarios
Thank you for the encouragement.

fix the font size issues. seems to be different fonts/sizes in different part of the report. please number the sections as well.

We regret that formatting was a minor detractor from our previous submission. This has been addressed in the project milestone report included in this submission.

your comparison of ABMs vs ODE based models was unclear. is the idea that you want to show a correspondence, or do you want to implement a ABM and calibrate an ODE over its output? and this analysis aim is not given in the goals section.

The initial intent for the inclusion of the agent-based model component was to directly compare the outputs of the deterministic ODE model extensions, which make some simplifying assumptions such as homogenous mixing and do not take the spatial dimension into consideration, with the output of a non-deterministic ABM calibrated with the same parameters as the ODE model. By doing this comparison, we aimed to highlight the important differences between these two types of model for a complex system like our proposed extensions. A detailed explanation of changes made to the research based on this feedback are included in the Activities to Date section.

are there are any interesting phase transitions?

In our view, the most biologically interesting phase transition is perhaps the transovarial dynamic, which allows for pathogen transmission within the vector population between adult females to her offspring (ie. A tick vector can be born in an already infected state). This is a relatively unique feature of tick biology that introduces interesting (albeit admittedly difficult to model) complexity into the typical vector-born pathogen model.

also can any of your hypotheses be answered using any analysis?

Our planned method of answering our stated hypotheses was to compute the extended model curves plus the associated reproductive number values and do simple comparisons (and plausible explanations) to the original values. The comment is intriguing because indeed, it may be possible to infer additional (alternative?) lines of evidence either in support or contradicting our stated hypothesis using some analysis such as the presence of stable equilibria, which could be included in the final report or presentation if suitable time allows to further exploration.

any connections with your new model and the competing virus models we have done in class? might be worth discussing in your reports.

Yes, there are likely to be similarities or overlaps in terms of "competition" between pathogens, in which one (or two in our case) may indeed go extinct over the course of the model time steps. Our hypotheses regarding the invasion reproductive number can be considered a proxy estimation of whether or not competing contagions are expected to persist in the host population over time, with invasion reproductive numbers >= 1.0 considered as likely evidence of persistence (=survival). While

we have not discussed invasion reproductive number in class, we will strive to highlight this in our final report and presentation.

2 Activities to Date

We have made some modifications to the original research plan based on reviewer feedback received at the proposal stage, namely regarding the inclusion of an agent-based model using the same extended SIR model. In light of this feedback and in addition, time constraints and the complexity of the model extensions under study, the proposed use of agent-based modeling as a means to highlight model assumptions did not add sufficient value to the research in our view, and thus will not be pursued further. The remaining research objectives outlined in the initial proposal have not changed.

In brief, our activities to date have primarily focused on the 3-1-1 extension as a proof-of-concept for the extended ODE model. We have identified several additional model assumptions that should be taken under consideration with respect to the biology and natural history of the tick vectors in our models. Namely, we had initially included model states for the transstadial and transovarial pathogen transmission, which have been simplified in our extended ODEs since these introduce substantial complexity into the ODE model that ultimately encapsulate minor differences in resulting transmission patterns.

Additional activities recently undertaken include further exploration of data streams which may provide methods to further estimate or refine initial values for the ODE model parameters, such as case counts of tickborne illness (cdc.gov/ticks/data-summary, accessed 2022-10-24) and estimated animal host population sizes obtained from state Department of Natural Resource surveys (see Relevant Websites section for additional details and URLs). An initial Python-based prototype implementation of the 3-1-1 model is under development and hosted on Github (https://github.com/hseabolt/vectorborne_SIR).

2.1 Data Collection Process

Data collection has consisted of going through relevant papers and government data sets to get rough numbers around pathogen transmission statistics, tick populations, disease prevalence in various mammalian hosts, mammalian host populations, and proportion of host populations likely to be exposed to ticks. To do this we have been looking at various government websites specifically those concerning National Parks, Disease Reporting, and Wild Life Management. Most of the data seen so far have been rough estimates of mammalian populations in different locales with yearly resolution. We have not seen any time-series data related to tick nor pathogen populations so far.

3 Results To Date

We do not have initial results (e.g. basic reproductive numbers or invasion reproductive numbers) available at this time while we complete the derivation of the proposed ODE extensions and implement/test code. For brevity in this report, we have provided the 3-1-1 model's extended ODE equations and detailed explanation of their terms in Appendix A at the end of this document. Appendix B contains additional tables describing the states of our compartment model and where applicable, estimated initial values for all three of the proposed model extensions.

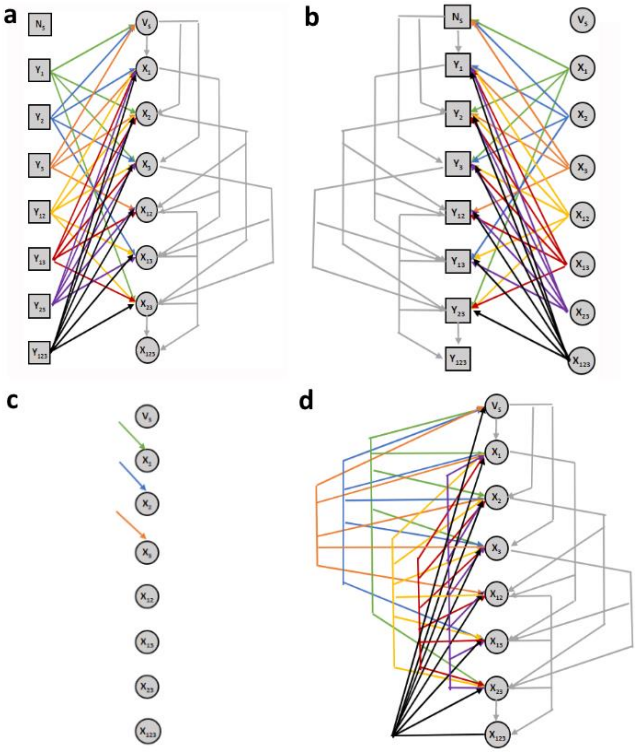

Figure S1: Extended compartment model diagram showing transitions as potential routes of transmission. The colored and black lines represent the transmission of a pathogen from one organism to another. The grey lines represent the transition of an organism from one epidemiological compartment to the next. We assume that in all cases a coinfected tick will only transmit one of its pathogens at a time. Sub-figure a) Outlines Host to Tick transmission flow, b) Outlines Tick to Host transmission flow, c) Outlines Transovarial and Transstadial transmission within the model, d) Outlines how transmission can occur via tick cofeeding

3 Future Activities

Planned future activities include completion of the additional two ODE model extensions, implementations of all three model extensions in Python, and lastly the associated comparison of results towards our initial stated hypotheses. The reviewer queries regarding phase transitions and comparison with the previously

studied competing virus model will be more thoroughly explored in the comparative analysis activities

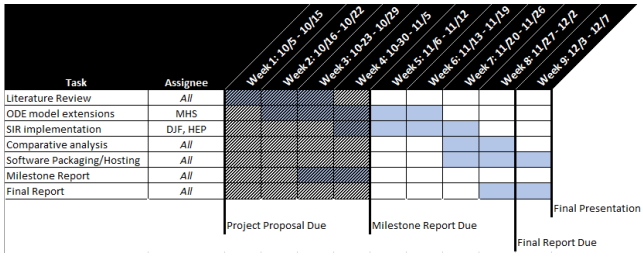

Figure 3: Revised Gantt chart describing activities to date, remaining estimated project timeline, and tentative assignment of tasks to specific team members.

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APPENDIX A: ODE DERIVATIONS FOR EXTENDED 3-1-1 SIR MODEL

Tick-to-host vector-borne transmission of single pathogen:

$$\frac{dY_i}{dt} = \left[A_i\left(\frac{N - Y_i - Y_j - Y_k - Y_{ij} - Y_{ik} - Y_{jk} - Y_{ijk}}{N}\right)\left(X_i + X_{ij} + X_{ik} + X_{ijk}\right)\right] + \left[r_{ij}Y_{ij} + r_{ik}Y_{ik}\right] - \left[A_{ij}\left(\frac{Y_i}{N}\right)\left(X_j + X_{ij} + X_{jk} + X_{ijk}\right) + A_{ik}\left(\frac{Y_i}{N}\right)\left(X_k + X_{ik} + X_{jk} + X_{ijk}\right)\right] - \left[\beta\left(\frac{NY_i}{K}\right) + (b + r_i)Y_i\right]$$

- **First bracket:** Host-to-tick transmission rate for a single pathogen multiplied by the proportion of susceptible hosts multiplied by the summation of ticks infected with pathogen *i, j, k*, = 1, 2, or 3
- **Second bracket:** summation of recovery rate of hosts coinfected by pathogen (1,2) or (1,3)
- **Third bracket:** Host-to-tick transmission rate for coinfection multiplied by proportion of hosts infected with pathogen i, multiplied by the summation of ticks infected with pathogen i, summed for each possible coinfection (Aij + Aik)
- **Last bracket:** growth rate multiplied by proportion of hosts infected with pathogen i over the carrying capacity; death rate and recovery rate multiplied by host infected with pathogen i

Tick-to-host vector-borne transmission of Coinfection for two pathogens:

$$\frac{dY_{ij}}{dt} = \left[A_{ij}\left(\frac{Y_i}{N}\right)\left(X_j + X_{ij} + X_{jk} + X_{ijk}\right) + A_{ji}\left(\frac{Y_j}{N}\right)\left(X_i + X_{ij} + X_{ik} + X_{ijk}\right)\right] + \left[r_{ij,k}Y_{ijk}\right] - \left[A_{ij,k}\left(\frac{Y_{ij}}{N}\right)\left(X_k + X_{ik} + X_{jk} + X_{ijk}\right)\right] - \left[\beta\frac{NY_{ij}}{K} + \left(b + r_{ij} + r_{ji}\right)Y_{ij}\right]$$

- **First bracket:** coinfection transmission rate for i→ij multiplied by proportion of hosts infected with pathogen i multiplied by summation of ticks with pathogen j. add together the reverse situation (coinfection transmission rate for j→ij multiplied by proportion of hosts infected with pathogen j multiplied by summation of ticks with pathogen i)
- **Second bracket:** recovery rate of hosts infected with pathogens i,j,k but lose k multiplied by the number of hosts infected with pathogens i,j,k
- **Third bracket:** coinfection transmission rate of ij→ijk multiplied by the proportion of host infected with pathogens ij multiplied by the summation of ticks with pathogen k
- **Forth bracket:** growth rate multiplied total population (N) and hosts coinfected with pathogens ij over the carrying capacity; death rate plus recovery rates of losing pathogen i or j multiplied by the hosts infected with both pathogens ij

Tick-to-host vector-borne transmission of Coinfection for three pathogens:

$$\frac{dY_{ijk}}{dt} = \left[A_{ij,k}\left(\frac{Y_{ij}}{N}\right)\left(X_k + X_{ik} + X_{jk} + X_{ijk}\right) + A_{ik,j}\left(\frac{Y_{ik}}{N}\right)\left(X_j + X_{ij} + X_{jk} + X_{ijk}\right) + A_{jk,i}\left(\frac{Y_{jk}}{N}\right)\left(X_i + X_{ij} + X_{ik} + X_{ijk}\right)\right] - \left[\beta\frac{NY_{ijk}}{K} + \left(b + r_{ij,k} + r_{ik,j} + r_{jk,i}\right)Y_{123}\right]$$

- First bracket: coinfection transmission rate for ij→ijk multiplied by proportion of hosts infected with pathogen ij multiplied by summation of ticks with pathogen k. add together the reverse situations (ik→ijk + jk→ijk)
- Second: bracket: growth rate time total population (N) and host with pathogens i,j,k over the carrying capacity; death rate plus recovery rate of losing a single pathogen (ijk→ij or ijk→ik or ijk→jk) multiplied by hosts infected with pathogens i,j,k

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NOTE from paper: *Transovarial contransmission is not included in the model; and observed $\gamma 12 + \gamma 21 \leq 1$ to avoid double transmission by coinfected ticks.*

Host-to-tick vector-borne transmission for one pathogen:

$$\frac{dX_i}{dt} = \left[\widehat{A}_i\left(\frac{Y_i + Y_{ij} + Y_{ik} + Y_{ijk}}{N}\right)\left(V - X_i - X_{ij} - X_{ik} - X_{ijk}\right)\right] + \left[\widehat{\beta}\left(\gamma_i X_i + \gamma_{ij} X_{ij} + \gamma_{ik} X_{ik} + \gamma_{ijk} X_{ijk}\right)\right] + \left[\mu_1\frac{\left(V - X_i - X_j - X_k - X_{ij} - X_{ik} - X_{jk} - X_{ijk}\right)\left(X_i + X_{ij} + X_{ik} + X_{ijk}\right)}{V}\right] - \left[\widehat{A}_{ij}\left(\frac{Y_j + Y_{ij} + Y_{jk} + Y_{ijk}}{N}\right)X_i + \widehat{A}_{ik}\left(\frac{Y_k + Y_{ik} + Y_{jk} + Y_{ijk}}{N}\right)X_i\right] - \left[\mu_{ij}\frac{\left(X_j + X_{ij} + X_{jk} + X_{ijk}\right)X_i}{V} + \mu_{ik}\frac{\left(X_k + X_{ik} + X_{jk} + X_{ijk}\right)X_i}{V}\right] - \left[\widehat{\beta}\frac{VX_i}{MN} + \hat{b}X_i\right]$$

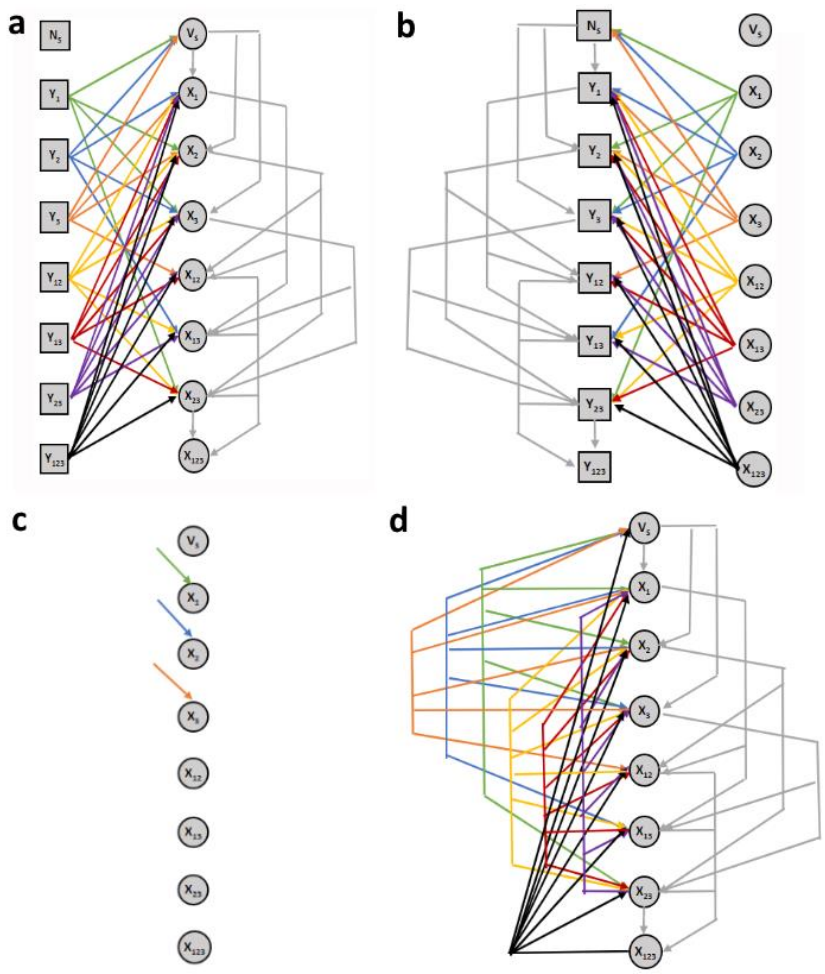
- First bracket: transmission rate of pathogen i multiplied by proportion of hosts with pathogen i multiplied by the number of susceptible vectors in the population
- Second bracket: growth rate multiplied by transovarial and transstadial transmission rate (i.e. proportion of infected females' (X_i or X_{ij}) offspring with transovarial transmission is γ_i (γ_{ij} for coinfected females) and is regarded the same as ticks maintaining the pathogen between life stages)
- Third bracket: cofeeding transmission rate multiplied by proportion of susceptible tick population multiplied by the proportion of ticks infected with pathogen i
- Forth bracket: summation of host-to-tick transmission rate (i→ij or i→ik infection) multiplied by proportion of host with pathogen j/k multiplied by ticks infected with pathogen i.
- Fifth bracket: summation of cofeeding transmission (i→ij or i→ik) multiplied by the proportion of ticket with pathogen j/k multiplied by number of ticks with pathogen i.
- Sixth bracket: growth rate multiplied by vector population time ticks with pathogen i over maximum number of ticks per host (M) times host population size; death rate times number of ticks with pathogen i.

Host-to-tick vector-borne transmission for two pathogens:

$$\frac{dX_{ij}}{dt} = \left[\widehat{A}_{12}\left(\frac{Y_j + Y_{ij} + Y_{jk} + Y_{ijk}}{N}\right)X_i + \widehat{A}_{ji}\left(\frac{Y_i + Y_{ij} + Y_{ik} + Y_{ijk}}{N}\right)X_j\right] + \left[\mu_{ij}\frac{\left(X_j + X_{ij} + X_{jk} + X_{ijk}\right)X_i}{V} + \mu_{ji}\frac{\left(X_i + X_{ij} + X_{ik} + X_{ijk}\right)X_j}{V}\right] - \left[\widehat{\beta}\frac{VX_{ij}}{MN} + \hat{b}X_{ij}\right]$$

Host-to-tick vector-borne transmission for three pathogens:

$$\frac{dX_{ijk}}{dt} = \left[\widehat{A}_{ij,k}\left(\frac{Y_k + Y_{ik} + Y_{jk} + Y_{ijk}}{N}\right)X_{ij} + \widehat{A}_{ik,j}\left(\frac{Y_j + Y_{ij} + Y_{jk} + Y_{ijk}}{N}\right)X_{ik} + \widehat{A}_{jk,i}\left(\frac{Y_i + Y_{ij} + Y_{ik} + Y_{ijk}}{N}\right)X_{jk}\right] + \left[\mu_{ij,k}\frac{\left(X_k + X_{ik} + X_{jk} + X_{ijk}\right)X_{ij}}{V} + \mu_{ik,j}\frac{\left(X_j + X_{ij} + X_{jk} + X_{ijk}\right)X_{ik}}{V} + \mu_{jk,i}\frac{\left(X_i + X_{ij} + X_{ik} + X_{ijk}\right)X_{jk}}{V}\right] - \left[\widehat{\beta}\frac{VX_{ijk}}{MN} + \hat{b}X_{ijk}\right]$$



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APPENDIX B: SUPPLEMENTARY TABLES

State Variable	Description	Initial Value	Model Extension
N	Total Number of Hosts	20	
N_1	Number of Host Species 1	10	2-1-2
N_2	Number of Host Species 2	10	2-1-2
V	Total Number of Ticks	4000	
V_1	Number of Vector Species 1	3000	2-2-1
V_2	Number of Vector Species 2	1000	2-2-1
Y_1	Number of Hosts Infected with Pathogen 1	1	
X_1	Number of Ticks Infected with Pathogen 1	200	
Y_2	Number of Hosts Infected with Pathogen 2	0	
X_2	Number of Ticks Infected with Pathogen 2	150	
Y_3	Number of Hosts Infected with Pathogen 3	0	3-1-1
X_3	Number of Ticks Infected with Pathogen 3	175	3-1-1
Y_{12}	Number of Coinfected Hosts with Pathogens 1,2	0	
X_{12}	Number of Coinfected Ticks with Pathogens 1,2	10	
Y_{13}	Number of Coinfected Hosts with Pathogens 1,3	0	3-1-1
X_{13}	Number of Coinfected Ticks with Pathogens 1,3	10	3-1-1
Y_{23}	Number of Coinfected Hosts with Pathogens 2,3	0	3-1-1
X_{23}	Number of Coinfected Ticks with Pathogens 2,3	5	3-1-1
Y^*	Number of Coinfected Hosts with Pathogens 1,2,3	0	3-1-1
X^*	Number of Coinfected Ticks with Pathogens 1,2,3	1	3-1-1

Table S1: Description of state variables according to proposed model extensions (partially reproduced from White et al. 2019). Rows using gray highlighting indicate new state variables unique to this study. Text is additionally colored to visually separate states unique to specific model extensions.

Parameter	Description	Initial Value	Model Extension
Â1	Host-to-Tick Pathogen 1 Transmission Rate	0.07	
Â2	Host-to-Tick Pathogen 2 Transmission Rate	0.07	
Â3	Host-to-Tick Pathogen 3 Transmission Rate	0.07	3-1-1
Â12	Host-to-Tick Coinfection Transmission Rate Pathogens 1,2	0.035	
Â13	Host-to-Tick Coinfection Transmission Rate Pathogens 1,3	0.035	3-1-1
Â23	Host-to-Tick Coinfection Transmission Rate Pathogens 2,3	0.035	3-1-1
A1	Tick-to-Host Pathogen 1 Transmission Rate	0.02	
A2	Tick-to-Host Pathogen 2 Transmission Rate	0.02	
A3	Tick-to-Host Pathogen 3 Transmission Rate	0.02	3-1-1
A12	Tick-to-Host Coinfection Transmission Rate Pathogens 1,2	0.01	
A13	Tick-to-Host Coinfection Transmission Rate Pathogens 1,3	0.01	3-1-1
A23	Tick-to-Host Coinfection Transmission Rate Pathogens 2,3	0.01	3-1-1
γ1	Tick Transovarial and Transstadial Transmission of Pathogen 1	0.4	
γ2	Tick Transovarial and Transstadial Transmission of Pathogen 2	0.4	
γ3	Tick Transovarial and Transstadial Transmission of Pathogen 3	0.4	3-1-1
γ12	Coinfected Tick Transovarial and Transstadial Transmission (1,2)→1	0.2	
γ21	Coinfected Tick Transovarial and Transstadial Transmission (1,2)→2	0.2	3-1-1
γ13	Coinfected Tick Transovarial and Transstadial Transmission (1,3)→1	0.2	3-1-1
γ31	Coinfected Tick Transovarial and Transstadial Transmission (1,3)→3	0.2	3-1-1
γ23	Coinfected Tick Transovarial and Transstadial Transmission (2,3)→2	0.2	3-1-1
γ32	Coinfected Tick Transovarial and Transstadial Transmission (2,3)→3	0.2	3-1-1
μ1	Tick Cofeeding Transmission Rate of Pathogen 1	0.01	
μ2	Tick Cofeeding Transmission Rate of Pathogen 2	0.01	
μ2	Tick Cofeeding Transmission Rate of Pathogen 3	0.01	3-1-1
μ12	Tick Cofeeding Coinfection Transmission Rate Pathogens 1,2	0.005	
μ13	Tick Cofeeding Coinfection Transmission Rate Pathogens 1,3	0.005	3-1-1
μ23	Tick Cofeeding Coinfection Transmission Rate Pathogens 2,3	0.005	3-1-1
v1	Host Recovery Rate for Pathogen 1	0.166	
v2	Host Recovery Rate for Pathogen 2	0.166	
v3	Host Recovery Rate for Pathogen 3	0.166	3-1-1
v12	Host Recovery Rate of Coinfection Pathogens (1,2)→1	0.166	
v21	Host Recovery Rate of Coinfection Pathogens (1,2)→2	0.166	
v23	Host Recovery Rate of Coinfection Pathogens (2,3)→2	0.166	3-1-1
v32	Host Recovery Rate of Coinfection Pathogens (2,3)→3	0.166	3-1-1
v13	Host Recovery Rate of Coinfection Pathogens (1,3)→1	0.166	3-1-1
v31	Host Recovery Rate of Coinfection Pathogens (1,3)→3	0.166	3-1-1
K	Host Carrying Capacity	20	
M	Maximum Ticks per Host	200	
β	Host Population Growth Rate	0.2	

$\hat{\beta}$	Tick Population Growth Rate	0.75	
b	Host Background Density-Independent Mortality Rate	0	
$\hat{b}$	Tick Background Density-Independent Mortality Rate	0.001	

Table S2: SIR model parameters and initial values for the base 2-1-1 and extended 3-1-1 model (partially reproduced from White et al. 2019). Rows using gray highlighting indicate new state variables unique to this study. Wherever possible, variable symbols follow White et al. (2019).

Parameter	Description	Initial Value	Model Extension
Â11	Host1-to-Tick Pathogen 1 Transmission Rate	0.07	
Â21	Host2-to-Tick Pathogen 1 Transmission Rate	0.07	2-1-2
Â12	Host1-to-Tick Pathogen 2 Transmission Rate	0.07	
Â22	Host2-to-Tick Pathogen 2 Transmission Rate	0.07	2-1-2
Â*1	Host1-to-Tick Coinfection Transmission Rate Pathogens 1,2	0.035	
Â*2	Host2-to-Tick Coinfection Transmission Rate Pathogens 1,2	0.035	2-1-2
A11	Tick-to-Host1 Pathogen 1 Transmission Rate	0.02	
A21	Tick-to-Host2 Pathogen 1 Transmission Rate	0.02	2-1-2
A12	Tick-to-Host1 Pathogen 2 Transmission Rate	0.02	
A22	Tick-to-Host2 Pathogen 2 Transmission Rate	0.02	2-1-2
A*1	Tick-to-Host1 Coinfection Transmission Rate Pathogens 1,2	0.01	
A*2	Tick-to-Host2 Coinfection Transmission Rate Pathogens 1,2	0.01	2-1-2
γ1	Tick Transovarial and Transstadial Transmission of Pathogen 1	0.4	
γ2	Tick Transovarial and Transstadial Transmission of Pathogen 2	0.4	
γ12	Coinfected Tick Transovarial and Transstadial Transmission (1,2)→1	0.2	
μ1	Tick Cofeeding Transmission Rate of Pathogen 1	0.01	
μ2	Tick Cofeeding Transmission Rate of Pathogen 2	0.01	
μ12	Tick Cofeeding Coinfection Transmission Rate Pathogens 1,2	0.005	
v11	Host1 Recovery Rate for Pathogen 1	0.166	
v12	Host1 Recovery Rate for Pathogen 2	0.166	2-1-2
v21	Host2 Recovery Rate for Pathogen 2	0.166	
v22	Host2 Recovery Rate for Pathogen 2	0.166	2-1-2
v11	Host1 Recovery Rate of Coinfection Pathogens (1,2)→1	0.166	
v12	Host1 Recovery Rate of Coinfection Pathogens (1,2)→2	0.166	
v21	Host2 Recovery Rate of Coinfection Pathogens (1,2)→1	0.166	2-1-2
v22	Host2 Recovery Rate of Coinfection Pathogens (1,2)→2	0.166	2-1-2
K1	Host1 Carrying Capacity	20	
K2	Host2 Carrying Capacity	20	2-1-2
M	Maximum Ticks per Host	200	
β1	Host1 Population Growth Rate	0.2	
β2	Host1 Population Growth Rate	0.2	2-1-2
β̂	Tick Population Growth Rate	0.75	
b1	Host1 Background Density-Independent Mortality Rate	0.01	
b2	Host2 Background Density-Independent Mortality Rate	0.01	2-1-2
b̂	Tick Background Density-Independent Mortality Rate	0.001	

Table S3: SIR model parameters and initial values for the base 2-1-1 and extended 2-1-2 (2 pathogen, 1 vector, 2 hosts) model, partially reproduced from White et al. 2019. Rows using gray highlighting indicate new state variables unique to this study. Wherever possible, variable symbols follow White et al. (2019).

Parameter	Description	Initial Value	Model Extension
Â11	Host-to-Tick1 Pathogen 1 Transmission Rate	0.07	
Â12	Host-to-Tick1 Pathogen 2 Transmission Rate	0.07	
Â21	Host-to-Tick2 Pathogen 1 Transmission Rate	0.07	2-2-1
Â22	Host-to-Tick2 Pathogen 2 Transmission Rate	0.07	2-2-1
Â*1	Host-to-Tick1 Coinfection Transmission Rate Pathogens 1,2	0.035	
Â*2	Host-to-Tick2 Coinfection Transmission Rate Pathogens 1,2	0.035	2-2-1
A11	Tick1-to-Host Pathogen 1 Transmission Rate	0.02	
A12	Tick1-to-Host Pathogen 2 Transmission Rate	0.02	
A21	Tick2-to-Host Pathogen 1 Transmission Rate	0.02	2-2-1
A22	Tick2-to-Host Pathogen 2 Transmission Rate	0.02	2-2-1
A*1	Tick1-to-Host Coinfection Transmission Rate Pathogens 1,2	0.01	
A*2	Tick2-to-Host Coinfection Transmission Rate Pathogens 1,2	0.01	2-2-1
γ11	Tick1 Transovarial and Transstadial Transmission of Pathogen 1	0.4	
γ12	Tick1 Transovarial and Transstadial Transmission of Pathogen 2	0.4	
γ*1	Coinfected Tick1 Transovarial and Transstadial Transmission (1,2)→1	0.2	
γ21	Tick2 Transovarial and Transstadial Transmission of Pathogen 1	0.6	2-2-1
γ22	Tick2 Transovarial and Transstadial Transmission of Pathogen 2	0.6	2-2-1
γ*2	Coinfected Tick2 Transovarial and Transstadial Transmission (1,2)→1	0.3	2-2-1
µ11	Tick1 Cofeeding Transmission Rate of Pathogen 1	0.01	
µ12	Tick1 Cofeeding Transmission Rate of Pathogen 2	0.01	
µ*1	Tick1 Cofeeding Coinfection Transmission Rate Pathogens 1,2	0.005	
µ21	Tick2 Cofeeding Transmission Rate of Pathogen 1	0.02	2-2-1
µ22	Tick2 Cofeeding Transmission Rate of Pathogen 2	0.02	2-2-1
µ*2	Tick2 Cofeeding Coinfection Transmission Rate Pathogens 1,2	0.1	2-2-1
v1	Host Recovery Rate for Pathogen 1	0.166	
v2	Host Recovery Rate for Pathogen 2	0.166	
v12	Host Recovery Rate of Coinfection Pathogens (1,2)→1	0.166	
v21	Host Recovery Rate of Coinfection Pathogens (1,2)→2	0.166	
K	Host Carrying Capacity	20	
M1	Maximum Ticks1 per Host	150	
M2	Maximum Ticks2 per Host	50	2-2-1
β	Host Population Growth Rate	0.2	
β1	Tick1 Population Growth Rate	0.75	
β2	Tick2 Population Growth Rate	0.75	2-2-1
b	Host Background Density-Independent Mortality Rate	0	
$\hat{b}1$	Tick1 Background Density-Independent Mortality Rate	0.001	
$\hat{b}2$	Tick2 Background Density-Independent Mortality Rate	0.001	2-2-1

Table S4: SIR model parameters and initial values for the base 2-1-1 and extended 2-2-1 (2 vector) model, partially reproduced from White et al. 2019. Rows using gray highlighting indicate new state variables unique to this study. Wherever possible, variable symbols follow White et al. (2019).