Electronic Supplementary Material for The Tortoise or the Hare? Impacts of Within-Host Dynamics on Transmission Success of Arthropod-Borne Viruses

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Model description

Our model extends the model presented in Althouse et al. (2012) [1]. Briefly, vectores and hosts are born susceptible to arbovirus infection, and are infected at a rate proportional to the number of bites given or received per day and the probability of infection. These transmission probabilities vary seasonally to represent the fluctuation in per bite transmission probability due to seasonally varying processes. After infection, vertebrate hosts recover at a fixed rate and vectors are infected for the remainder of their life. We assume no disease induced mortality.

We explore differences in duration of infectiousness in the vertebrate host using the method of stages [] to expand the infected compartment into multiple infectious compartments. In a standard SIR model, the infectious period is exponentially distributed with mean equal to the mean duration of infectiousness $(1/\gamma)$. In essence, the method of stages sums n independent exponentially distributed waiting times (time spent in each infectious class), resulting in a gamma distributed duration of infectiousness with mean equal to the mean duration of infectiousness $(1/\gamma)$ and variance $1/n\gamma^2$. We explore four cases, chosen arbitrarily, but inspired by actual patterns in arbovirus replication kinetics: mean duration 4 days with variance either 4 days (dark solid curve) or 1.6 days (dark dashed curve) (similar to dengue virus in nonhuman hosts []), and mean duration 25 days with variance either 25 days (light solid curve) or 12.5 days (light dashed curve) (similar to bluetounge virus in cattle []). We account for correlation between duration of infectiousness and viral titer by allowing each of the n infectious compartments to contribute independently to transmission. If all compartments contribute equally, there is no correlation, if only the first or final few compartments contribute, there is correlation. This approximates the relation between magnitude of viremia and transmissibility (*i.e.*, tortoise versus hare strategies). Again, due to the generality of the model, these distributions were chosen to illustrate the effects of correlated titers on transmission.

In this paper, we focus briefly on the one-vector ($j = 1$), one-vertebrate host case ($i = 1$). All parameters are given in Table 1

Model equations

We extend the stochastic version of the arbovirus transmission model presented in [1], which uses a Gillespie stochastic simulation algorithm [2] with the Binomial Tau leap approximation (BTL) [3]. BTL was chosen here for efficiency, computational speed and to avoid negative population sizes [3, 4].

The transition rates for our stochastic model are below:

$$
\begin{aligned}
S_{v_j} \to S_{v_j} + 1 &= \mu_{v_j}(S_{v_j}(t) && (1)\\
S_{v_j} \to S_{v_j} - 1 &= \nu_{v_j} S_{v_j} && (2)\\
\left.\begin{array}{r} S_{v_j} \to S_{v_j} - 1 \\ I_{v_j} \to I_{v_j} + 1 \end{array}\right\} &= \sum_i r_{v_j h_i} \beta_{h_i v_j}(t) \left(\sum_n I_{n,h_i} \right) S_{v_j}/N_j && (3)\\
I_{v_j} \to I_{v_j} + 1 &= \rho I_{v_j} && (4)\\
I_{v_j} \to I_{v_j} - 1 &= \nu_{v_j} I_{v_j} && (5)\\
S_{h_i} \to S_{h_i} + 1 &= \mu_{h_i} N_{h_i} && (6)\\
S_{h_i} \to S_{h_i} - 1 &= \nu_{h_i} S_{h_i} && (7)\\
\left.\begin{array}{r} S_{h_i} \to S_{h_i} - 1 \\ I_{1,h_i} \to I_{1,h_i} + 1 \end{array}\right\} &= \sum_j r_{v_j h_i} \beta_{v_j h_i}(t) I_{v_j} S_{h_i}/N_j && (8)\\
\left.\begin{array}{r} I_{1,h_i} \to I_{1,h_i} - 1 \\ I_{2,h_i} \to I_{2,h_i} + 1 \end{array}\right\} &= \mathbf{B} n \gamma I_{1,h_i} && (9)\\
\cdots & && (10)\\
\left.\begin{array}{r} I_{n-1,h_i} \to I_{n-1,h_i} - 1 \\ I_{n,h_i} \to I_{n,h_i} + 1 \end{array}\right\} &= \mathbf{B} n \gamma I_{n-1,h_i} && (11)\\
I_{\cdot,h_i} \to I_{\cdot,h_i} - 1 &= \nu_{h_i} I_{\cdot,h_i} && (12)\\
\left.\begin{array}{r} R_{h_i} \to R_{h_i} + 1 \\ I_{h_i} \to I_{h_i} - 1 \end{array}\right\} &= \gamma_{h_i} I_{h_i} && (13)\\
R_{h_i} \to R_{h_i} - 1 &= \nu_{h_i} R_{h_i} && (14)\\
& && (15)
\end{aligned}
$$

with

$$
\begin{aligned}
\beta_{h_i v_j}(t) &= b_{h_i v_j}[1 + c_j \cdot \cos(t * 2\pi/365)] && (16)\\
\beta_{v_j h_i}(t) &= b_{v_j h_i}[1 + c_j \cdot \cos(t * 2\pi/365)] && (17)\\
N_{v_j} &= S_{v_j} + I_{v_j} && (18)\\
N_{h_i} &= S_{h_i} + I_{h_i} + R_{h_i} && (19)\\
N_j &= \sum_i \left(\frac{r_{v_j h_i}}{\sum_i r_{v_j h_i}} \right) N_{h_i}. && (20)
\end{aligned}
$$

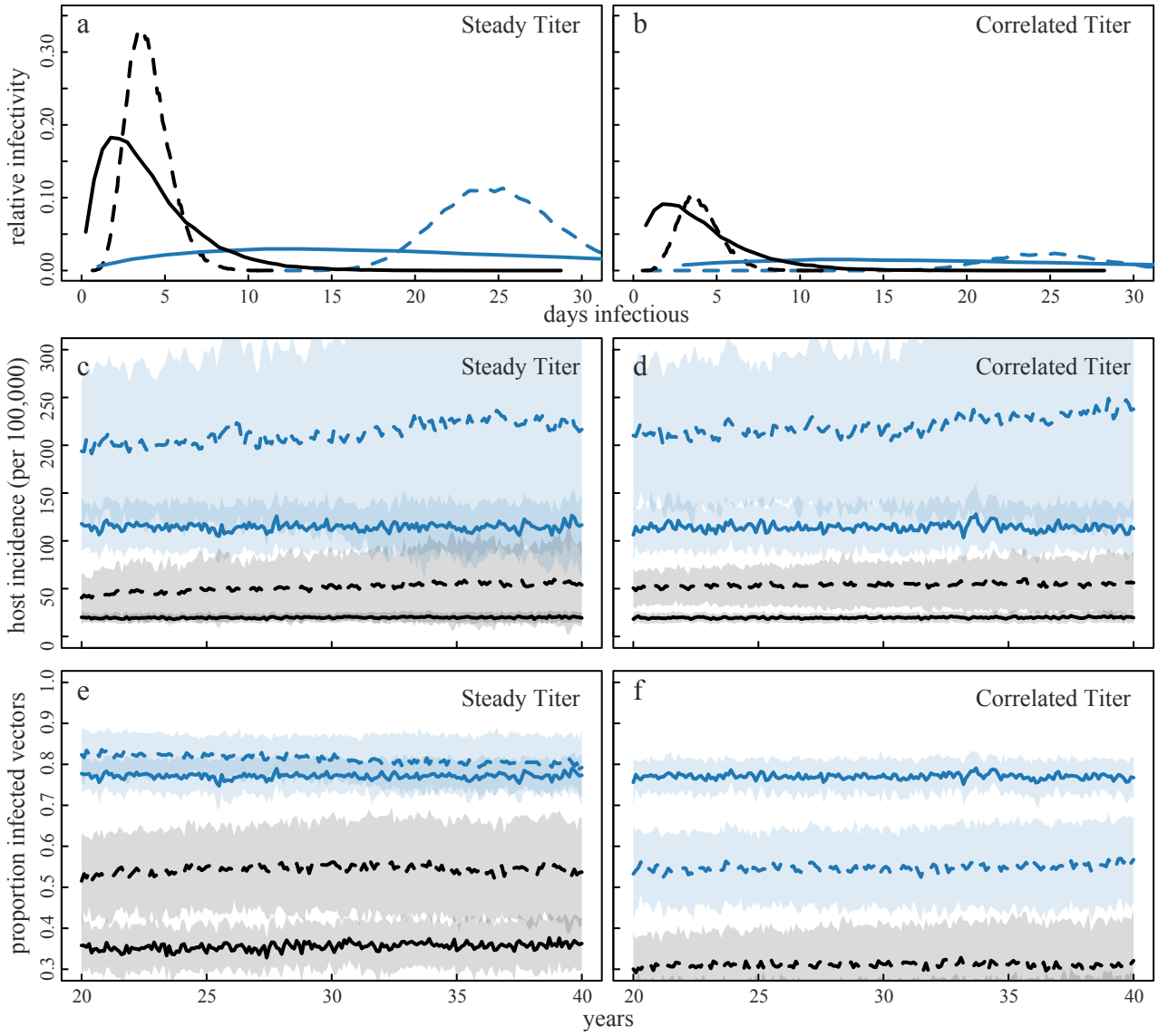
As the number of infectious stages, n, increases, the variance decreases and we see a more peaked distribution. Here, **B**is a vector multiplying the infectious compartments to simulate the effects of viremia magnitude on transmission. In the steady titer case, **B**is the n length identity vector. In the correlated titer case, for $n = 2$, $\mathbf{B} = (1, 1/300)$, for $n = 10$, $\mathbf{B} = (1/300, 1/300, 1/300, 1, 1, 1, 1, 1, 1, 1)$, and for $n = 50$, **B**is $1/300$ for the first 40 entries and 1 for the last 10.

Parameter	Description	Baseline Value
t	Time in days	
$r_{v_j h_i}$	Biting rate per day to hosts by vector j [5, 6]	0.5 days^{-1}
$b_{h_i v_j}$	Baseline transmission probability, from host i to vector j	0.3
$b_{v_j h_i}$	Baseline transmission probability, vector j to host i [5, 7, 8]	0.3
c_j	Percent of the magnitude of seasonal variation	0.1, 0
μ_{h_i}	Host birth rate (= 1/lifespan)	$1/(60 * 365)$ days^{-1}
ν_{h_i}	Host death rate, set equal to birth rate	
γ_{h_i}	Host recovery rate [9, 10, 11]	1/4 days^{-1}, 1/25 days^{-1},
μ_{v_j}	Vector j birth rate	1/7 days^{-1}
ν_{v_j}	Vector death rate, set equal to birth rate	
N_{v_j}	Initial vector population	10,000
N_{p+i}	Initial host population	15,000

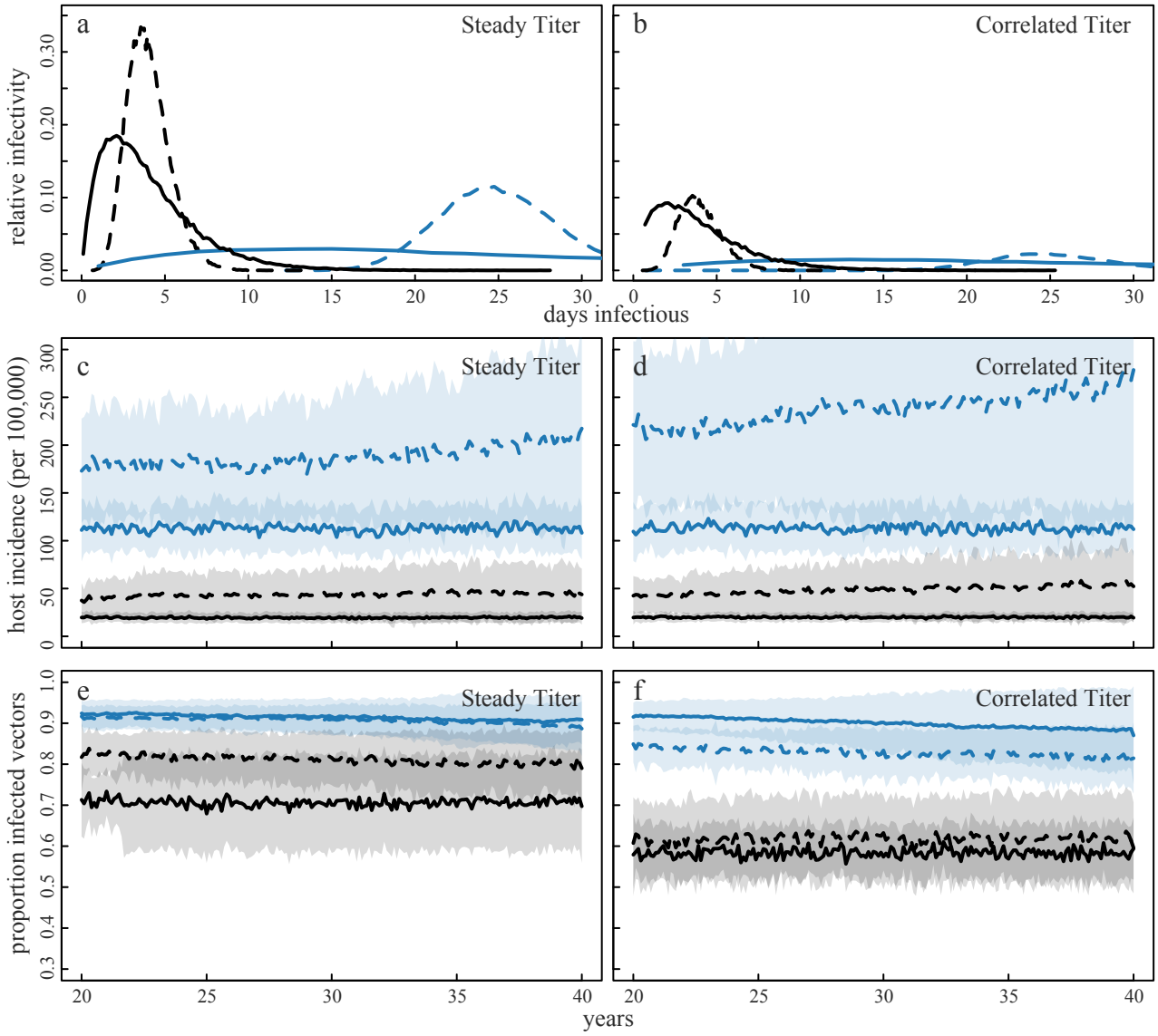
Table 1: **Model Parameters** Justifications for baseline values not given above are given in subsequent sections.

Sensitivity analyses

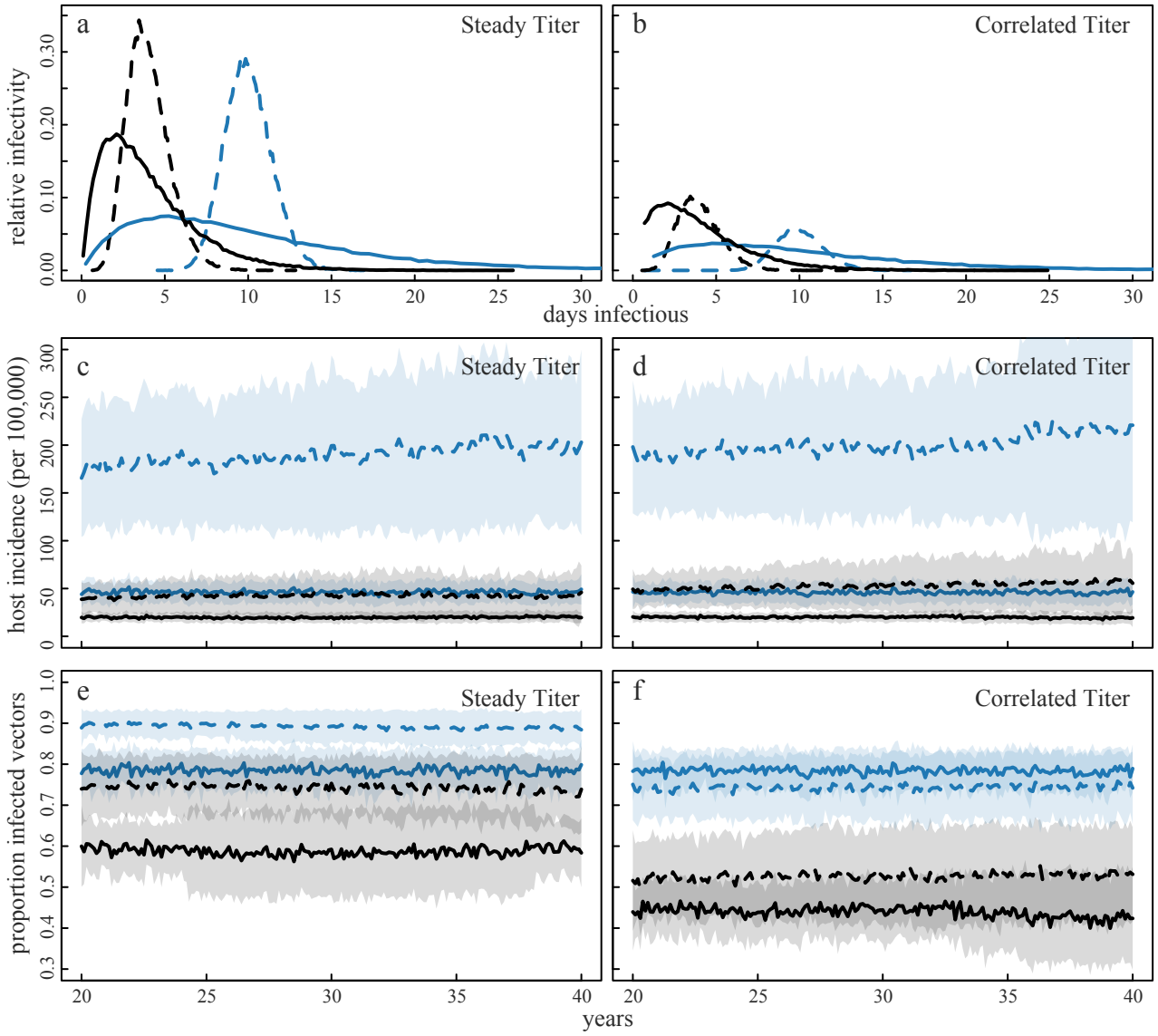
Figures 1 and 2 present model runs with baseline $\beta = 0.1$ and 0.6 respectively; Figure 3 presents model runs with mean infectious durations of 4 days and 10 days; and Figure 4 presents model runs with no seasonality. In all cases, the qualitative results hold.



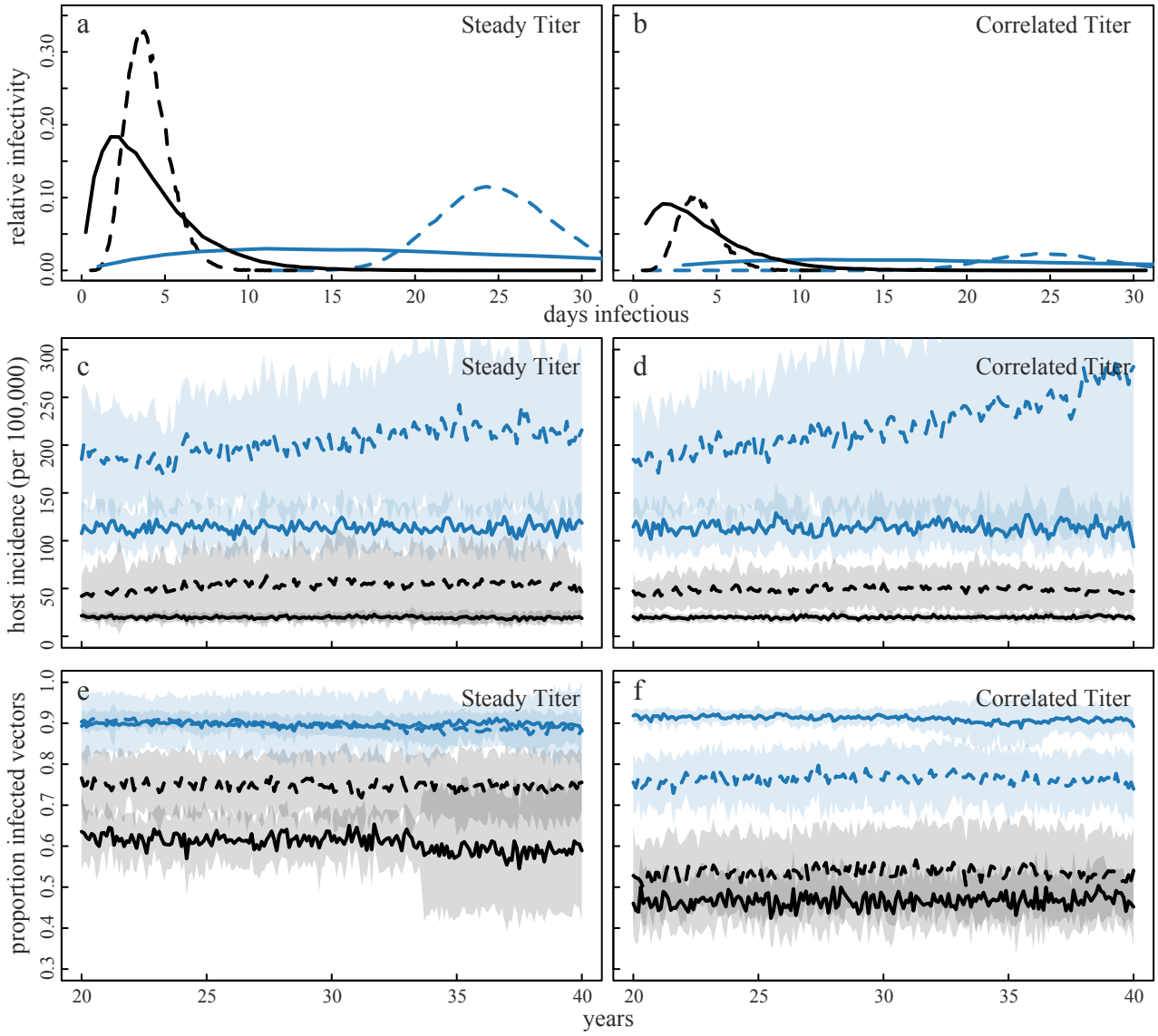
Supplemental Figure 1: **Results of the stochastic arbovirus transmission model with lower transmissibility.** Figure is identical to Figure 3 in the mean text with baseline transmission, β, equal to 0.1.



Supplemental Figure 2: **Results of the stochastic arbovirus transmission model with higher transmissibility.** Figure is identical to Figure 3 in the mean text with baseline transmission, β, equal to 0.6.



Supplemental Figure 3: **Results of the stochastic arbovirus transmission model with shorter durations of infection.** Figure is identical to Figure 3 in the mean text with mean duration of infection equal to 4 days (variance 4 days or 1.6 days) and 10 days (variance of 10 and 2 days).



Supplemental Figure 4: **Results of the stochastic arbovirus transmission model with shorter durations of infection.** Figure is identical to Figure 3 in the mean text with mean duration of infection equal to 4 days (variance 4 days or 1.6 days) and 10 days (variance of 10 and 2 days).

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