Modeling the Impact of Host Density on Tick-Borne Lyme Disease Risk

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I aim to answer the following research question: "How does white-footed mouse (*Peromyscus leucopus*) density influence the recruitment and infection dynamics of the Eastern Black-legged tick (*Ixodes scapularis*) from larvae through adults, and how can model-derived infected tick densities be used to predict Lyme disease transmission rates in Montgomery County, Maryland?" To address this, I developed a stage-structured tick model that tracks uninfected and infected ticks through larval, nymphal, and adult life stages, coupled with a simple SIS-like infection process for the white-footed mouse population (divided into susceptible and infected compartments). I also include a compartment for cumulative human Lyme disease infections based on exposure to infected ticks. To enhance the biological realism of the model, realistic temperature data from Montgomery County averaged from 2020 to 2024 is incorporated. This temperature data is used to drive temperature-dependent parameters such as tick mortality and molting rates, ensuring that the seasonal dynamics in the model closely reflect local environmental conditions. Below is an overview of the model's structure, using the exact variable names and parameter definitions from the implementation.

Mouse Model

The Mouse model will be split into two equations that model both susceptible and infected mice. We denote the densities of susceptible and infected mice by S(t) and I(t), respectively, with total mouse density [M0 = S(t) + I(t)]. The mouse dynamics are given by:

$$\frac{dS}{dt} = \mu \mathrm{M}_0 - \beta_{\mathrm{H}}(\mathrm{N_I} + A_{\mathrm{I}})S - \mu S;$$

$$\frac{dI}{dt} = \beta_{\mathrm{H}}(\mathrm{N_I} + A_{\mathrm{I}})S - \mu \mathrm{I}$$

Definitions:

μ : per capita birth/death rate of mice

M_0: constant total mouse density

β_{H}: effective rate at which infected ticks infect mice

$\mathrm{N_I}$ and $\mathrm{A_I}$: densities of infected nymphs and infected adults

In this system, new susceptible mice enter at a rate $\mu \mathrm{M}_0$, susceptible mice become infected upon contact with infected ticks at rate $\beta_{\mathrm{H}}(\mathrm{N_I} + \mathrm{A_I})S$, and both compartments experience losses due to mortality at rate μ .

Tick Model

Ticks progress through three life stages, larvae, nymphs, and adults with each stage subdivided into uninfected and infected compartments. Using the following notations:

Larvae: $L_U(t)$ **(**uninfected) and $L_{\mathrm{I}}(t)$ (infected)

Nymphs: $\mathrm{N}_U(t)$ (uninfected) and $\mathrm{N}_{\mathrm{I}}(t)$ (infected)

Adults: $\mathrm{A}_U(t)$ (uninfected) and $\mathrm{A}_{\mathrm{I}}(t)$ (infected)

Larval Stage -

The dynamics of the larval stages are described by:

$$\frac{dL_U}{dt} = \gamma - \alpha\beta\left(\frac{I}{\mathrm{M}_0}\right)L_U - \mu_L L_U;$$

$$\frac{dL_{\mathrm{I}}}{dt} = \alpha\beta\left(\frac{I}{\mathrm{M}_0}\right)L_U - \mu_L L_{\mathrm{I}}$$

Definitions:

γ : larval production rate

α effective attachment rate (temperature dependent)

β : probability that a larva becomes infected upon feeding on an infected mouse

$\frac{\mathrm{I}}{\mathrm{M}_0}$: fraction of mice that are infected

μ_L: larval mortality rate (temperature dependent)

Nymphal Stage -

Nymphal dynamics are given by:

$$\frac{d\mathrm{N}_U}{dt} = \sigma_L L_U - (\mu_{\mathrm{N}} + \sigma_{\mathrm{N}})\mathrm{N}_U;$$

$$\frac{d\mathrm{N}_{\mathrm{I}}}{dt} = \sigma_L L_{\mathrm{I}} - (\mu_{\mathrm{N}} + \sigma_{\mathrm{N}})\mathrm{N}_{\mathrm{I}}$$

Definitions:

σ_L: molting rate from larvae to nymphs (temperature dependent)

μ_{N}: nymph mortality rate

σ_{N}: The overall exit rate from the nymph stages, including both natural mortality and the initiation of the molting process.

Adult Stage -

Adult dynamics are given by:

$$\frac{d\mathrm{A}_U}{dt} = \sigma_{\mathrm{N},a} N_U - \rho_{\mathrm{A}} \left(\frac{\mathrm{I}}{\mathrm{M}_0}\right) \mathrm{A}_U - \mu_{\mathrm{A}} \mathrm{A}_U;$$

$$\frac{d\mathrm{A}_{\mathrm{I}}}{dt} = \sigma_{\mathrm{N},a} N_{\mathrm{I}} - \rho_{\mathrm{A}} \left(\frac{\mathrm{I}}{\mathrm{M}_0}\right) \mathrm{A}_U - \mu_{\mathrm{A}} \mathrm{A}_{\mathrm{I}}$$

Definitions:

$\sigma_{\mathrm{N},a}$: recruitment rate from nymphs to adults

ρ_{A}: probability that an uninfected adult becomes infected

μ_{A}: adult mortality rate

Tick to Human Transmission -

The model accounts for the cumulative number of human infections, $\mathrm{H}_i(t)$, given by:

$$\frac{d\mathrm{H}_i}{dt} = \lambda\psi(\mathrm{N}_{\mathrm{I}} + \mathrm{A}_{\mathrm{I}});$$

Definitions:

λ : rate of human-tick contact

ψ : probability of Lyme disease transmission per tick bite.

$\mathrm{N}_{\mathrm{I}} + \mathrm{A}_{\mathrm{I}}$: total density of infected ticks

Temperature and Density Dependence -

Several of my parameters are functions of temperature. These parameters are modified by a Gaussian function of the form:

$$\mathrm{X}(\mathrm{T}) = \mathrm{X}_0 \exp\left[-\frac{(\mathrm{T}-\mathrm{T}_{opt,\mathrm{X}})2}{2\sigma_{\mathrm{X}}^2}\right];$$

Where:

X_0: baseline value for the parameter

$\mathrm{T}_{opt,\mathrm{X}}$: is the optimal temperature for that process

σ_X: describes the sensitivity to that temperature

T : current temperature

Methods -

The model is implemented in R using the deSolve package for numerical integration of the ordinary differential equations.

Parameterization:

Realistic parameter values are assigned based on literature and local data. Temperature data from Montgomery County (2020–2024) drives the temperature-dependent parameters via the Gaussian modifier.

Simulation:

The system of ODEs is solved over weekly time steps for multiple years. Parameter sweeps (varying M_0) are performed to assess the impact of host density.

Analysis:

Time series plots of $S(t)$, $I(t)$, $L_U(t)$, $L_I(t)$, $N_I(t)$, $A_I(t)$ and $H_i(t)$ are generated. Graphs relating host density (M_0) to key outputs (peak N_I and cumulative H_i) are produced.

Inference:

Sensitivity analyses determine how seasonal temperature variations and changes in M_0 affect tick infection dynamics and human risk. Thresholds for host density that significantly alter Lyme disease risk are identified.

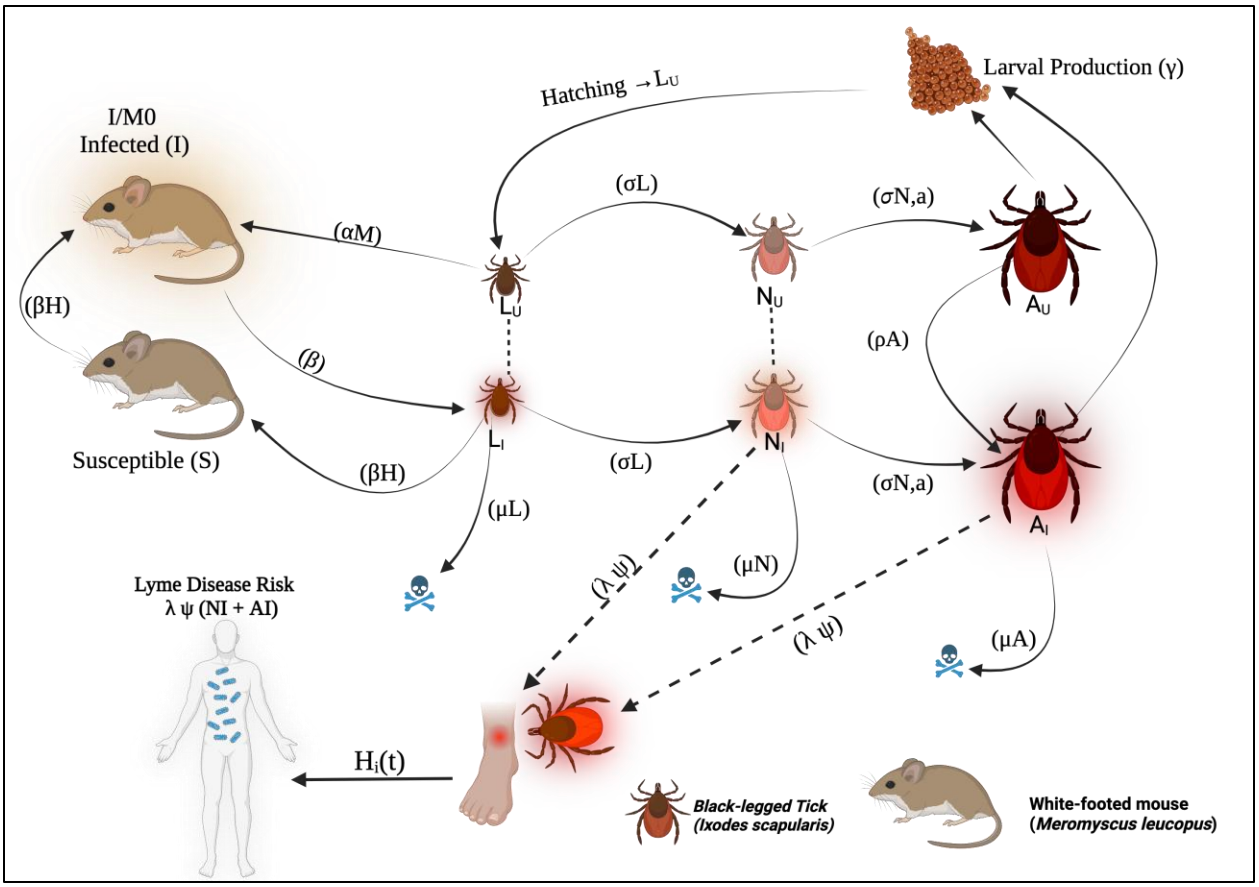

Figure 1. SIS mouse model and stage-structured tick model for Lyme disease transmission. Mice are split into susceptible (S) and infected (I), with total density M0.Ticks progress from larvae to nymphs to adults, each stage subdivided into uninfected or infected compartments. Infection occurs when ticks feed on infected mice (I/M0). Humans acquire Lyme disease from infected nymphs and adults. Arrows represent transitions, feeding, and infection events; parameter labels refer to the main text.

Anticipated Results -

Time-Series Dynamics of Ticks

I plan to generate a plot of tick densities (uninfected and infected larvae, nymphs, and adults) over a one-year cycle (on the x-axis), revealing seasonal fluctuations driven by temperature-dependent parameters. I anticipate that larval densities will peak during specific times of the year, likely in spring or early summer followed by nymph and adult peaks as molting progresses. Infected compartments should generally lag behind their uninfected counterparts, reflecting the time required for ticks to acquire infection from infected mice. This seasonal pattern will illustrate how temperature (through mortality and molting rates) and host density (through feeding rates) jointly shape tick infection dynamics.

Relationship Between Host Density and Infection Outcomes

I also intend to run parameter sweeps in which I vary the total mouse density M_0. For each value of M_0, I will record both the peak infected nymph density (the maximum value of $N_I$during the

simulation) and the cumulative human infections (H_i) after a defined period (one year). Plotting these outcomes against M_0 (on the x-axis) should clarify whether there is a threshold beyond which further increases in host density yield diminishing returns in infection or an increasing trend where higher mouse densities steadily lead to greater tick infection prevalence and Lyme disease risk. If host density is high enough, I expect that abundant infected hosts could drive up tick infection rates and, as a result increase the cumulative human infections.

By comparing the predicted patterns of seasonal peaks in each tick stage and the relationship between M_0 and infected tick prevalence/human risk I can determine whether and how host density serves as a critical driver of Lyme disease dynamics under realistic temperature conditions for Montgomery County, Maryland.