

# An Early-Season Model of West Nile Virus in Birds of Rutherford County, TN

## Abstract

We adapt a West Nile Virus (WNV) epidemic model that demonstrates the interaction between avian hosts and mosquito vectors into a more comprehensive, early-season model by adding intrinsic growth and death rates of hosts, as well as horizontal transmission. We then parameterize this model based on bird demographics in Rutherford County, TN and investigate the effect of our modifications on the basic reproduction number,  $R_0$ . The behavior of a single-host model and a multi-compartment model which categorize the bird groups by WNV mortality rates are compared. It is seen that an epidemic will occur followed by stabilization of host populations dependent on host susceptibility to the virus.

## Model Diagram

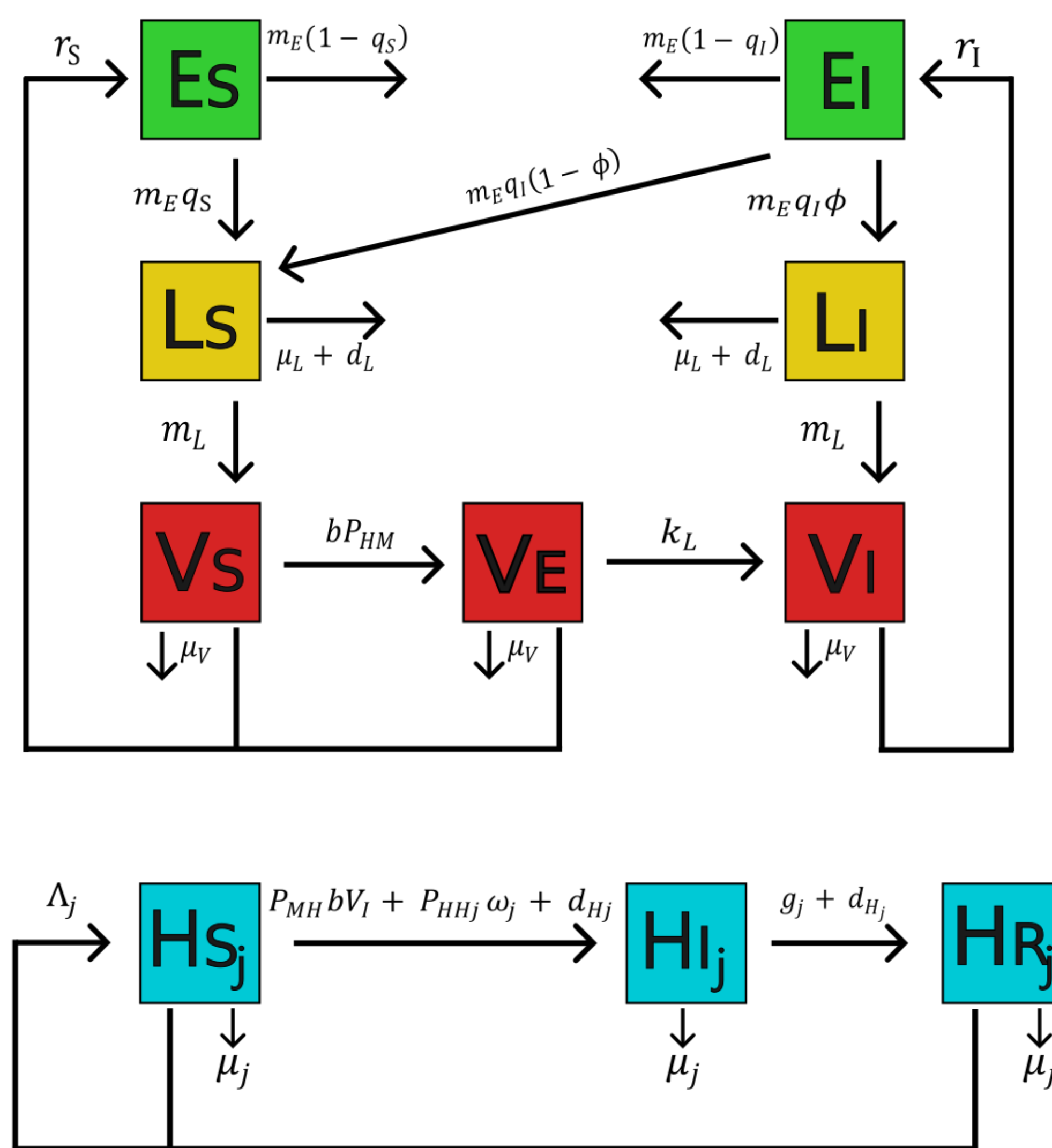


Figure 1: Vector classes include eggs (E), larvae (L), and adult mosquitoes (V). All avian hosts (H) are adults in this model. S, E, I, R, refer to susceptible, exposed, infected, and recovered individuals, respectively.  $j \in \{1, 2, 3\}$  for bird categories with 0%, 1 – 49%, and > 50% WNV mortality.

## Multi-Compartment Model

$$\begin{aligned} \frac{dH_{Sj}}{dt} &= \Lambda_j(H_{Sj} + H_{Rj}) - P_{MH}bV_i \frac{H_{Sj}}{N_{Hj}} - P_{HHj}\omega_j \frac{H_{Sj}}{N_{Hj}} \\ &\quad - \frac{d_{Hj}}{C_{Hj}} N_{Hj} H_{Sj} - \mu_{Hj} H_{Sj} \\ \frac{dH_{Ij}}{dt} &= P_{MH}bV_i \frac{H_{Sj}}{N_{Hj}} + P_{HHj}\omega_j \frac{H_{Sj}}{N_{Hj}} - \gamma_{Hj} H_{Ij} - g_{Ij} H_{Ij} \\ &\quad - \frac{d_{Hj}}{C_{Hj}} N_{Hj} H_{Ij} - \mu_{Hj} H_{Ij} \\ \frac{dH_{Rj}}{dt} &= g_{Ij} H_{Ij} - \frac{d_{Hj}}{C_{Hj}} N_{Hj} H_{Rj} - \mu_{Hj} H_{Rj} \\ \frac{dE_S}{dt} &= r_s(V_S + V_E) - m_E E_S \\ \frac{dE_I}{dt} &= r_i V_I - m_E E_I \\ \frac{dL_S}{dt} &= m_E q_s E_S + m_E q_i(1-\phi) E_I - \mu_L L_S - m_L L_S \\ &\quad - \frac{d_L}{C_L} (L_S + L_I) L_S \\ \frac{dL_I}{dt} &= m_E q_i \phi E_I - \mu_L L_I - m_L L_I - \frac{d_L}{C_L} (L_S + L_I) L_I \\ \frac{dV_S}{dt} &= m_L L_S - \sum_j \frac{bP_{HjM} V_S H_{Ij}}{N_{Hj}} - \mu_V V_S \\ \frac{dV_E}{dt} &= \sum_j \frac{bP_{HjM} V_S H_{Ij}}{N_{Hj}} - k_L V_E - \mu_V V_E \\ \frac{dV_I}{dt} &= m_L L_I + k_L V_E - \mu_V V_I \end{aligned}$$

where  $d_L = \frac{m_L r_s q_s}{\mu_V} - \mu_L - m_L$  and  $d_{Hj} = \Lambda_j - \mu_{Hj}$

## Parameterization

Using eBird observation data, we find the 25 most prevalent bird species in Rutherford County, TN. Parameters are determined through a literature search. For bird species with insufficient data, we extrapolate from the closest relative or use the average value of known species.

Parameter	Variable
$\Lambda_j$	Birth Rate
$\mu_j$	Death Rate
$g_j$	Recovery Rate
$\gamma_{Hj}$	WNV-Induced Death Rate
$P_{HjM}$	Host-to-Vector Transmission Host Group $j$
$P_{HHj}$	Horizontal Transmission

## Basic Reproduction Number

The basic reproduction number,  $R_0$ , represents the mean number of secondary infections produced by one infectious individual in a homogeneous susceptible population. Here we calculate  $R_0$  via the next-generation matrix method:

$$FV^{-1} = \begin{bmatrix} \frac{\omega_j P_{HHj}}{s_j} & \frac{b m_L P_{MH} \phi q_i}{\mu_V t} & \frac{b m_L P_{MH}}{\mu_V t} & \frac{b k_L P_{MH}}{\mu_V (k_L + \mu_V)} & \frac{b P_{MH}}{\mu_V} \\ 0 & \frac{m_L \phi q_i r_i}{\mu_V t} & \frac{m_L r_i}{\mu_V t} & \frac{k_L r_i}{\mu_V (k_L + \mu_V)} & \frac{r_i}{\mu_V} \\ 0 & 0 & 0 & 0 & 0 \\ \frac{b C_L m_L P_{HjM}}{C_{Hj} \mu_V s_j} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

where  $s_j = g_j + \gamma_j + \mu_j + C_{Hj} d_{Hj}$  and  $t = m_L + \mu_L + C_L d_L$

Condition	$R_0$
Late-Season Model	1.23
Single Compartment Model	1.61 (1.57) $\}$
Host Group 1	2.14
Host Group 2	2.90
Host Group 3	3.53 (2.81) $\}$
Multi-Compartment Model	4.87 (4.57) $\}$

$\}$ : calculated without horizontal transmission

## Multi-Compartment Results

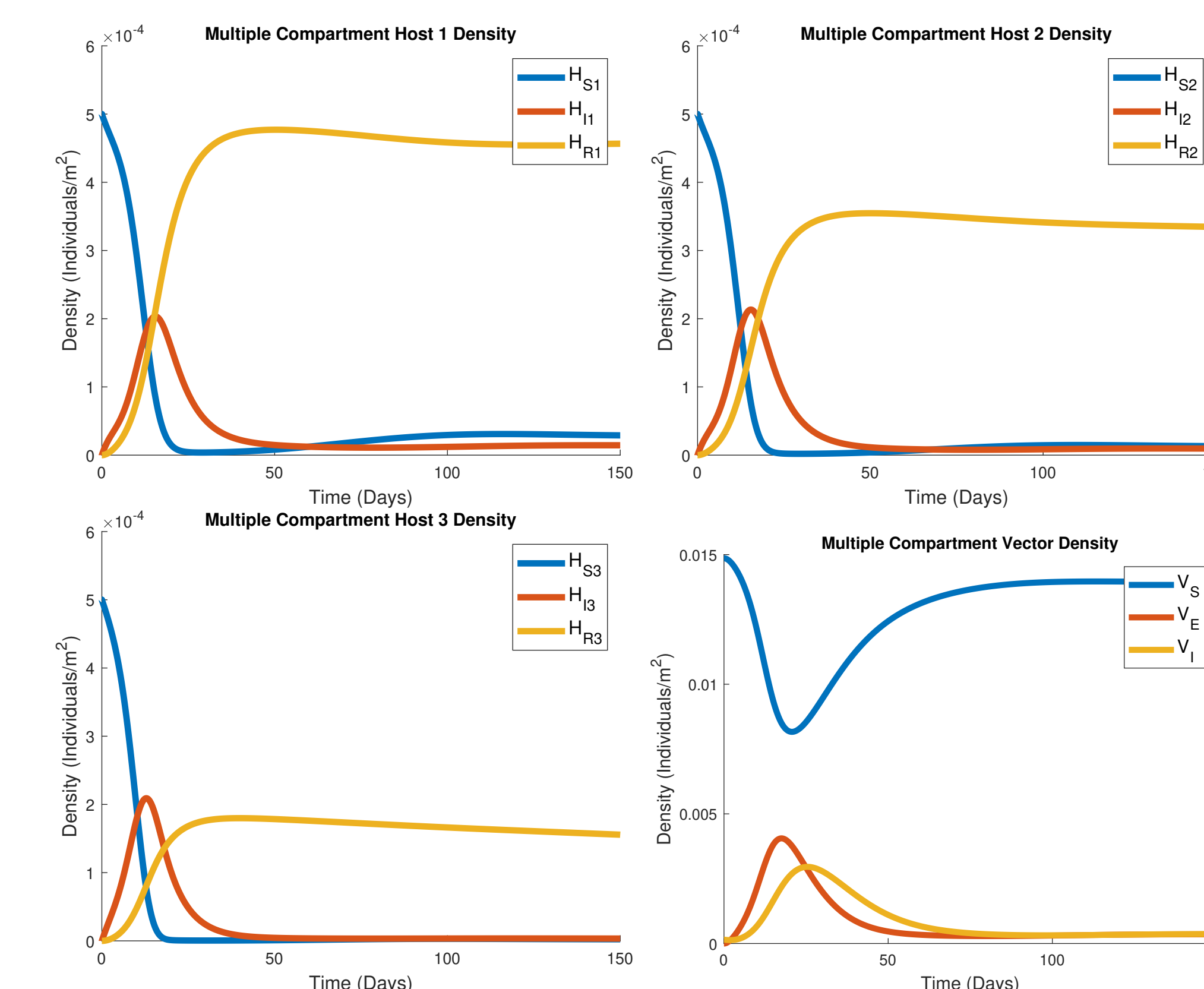


Figure 2: Multi-compartment model running for 150 days starting from the disease-free equilibrium.

## Single-Compartment Results

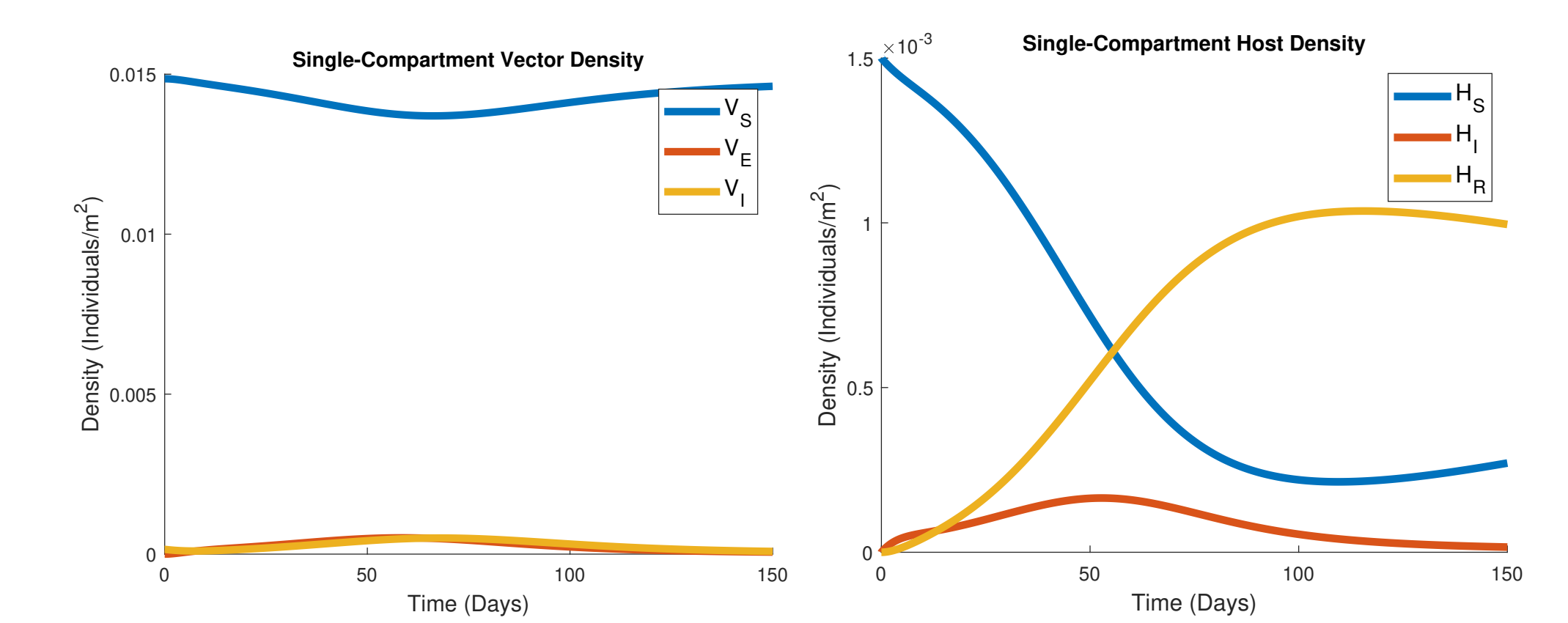


Figure 3: Single-compartment model beginning at the disease-free equilibrium and running for our 150-day season.

## Conclusion

We first expanded upon a previous model of West Nile Virus transmission to incorporate location-specific bird demographics and direct transmission. We then investigated the effects of these new parameters upon the basic reproduction number. Future research will implement optimal control theory to control the vector population, expand the model to include seasonality, and investigate the effects of other environmental parameters on the basic reproduction number.

## Acknowledgements

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## References

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