

Modeling the Dynamics of Vector-Host Interactions in Avian Communities for Eastern Equine Encephalitis Virus



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Introduction

Eastern Equine Encephalitis (EEE)

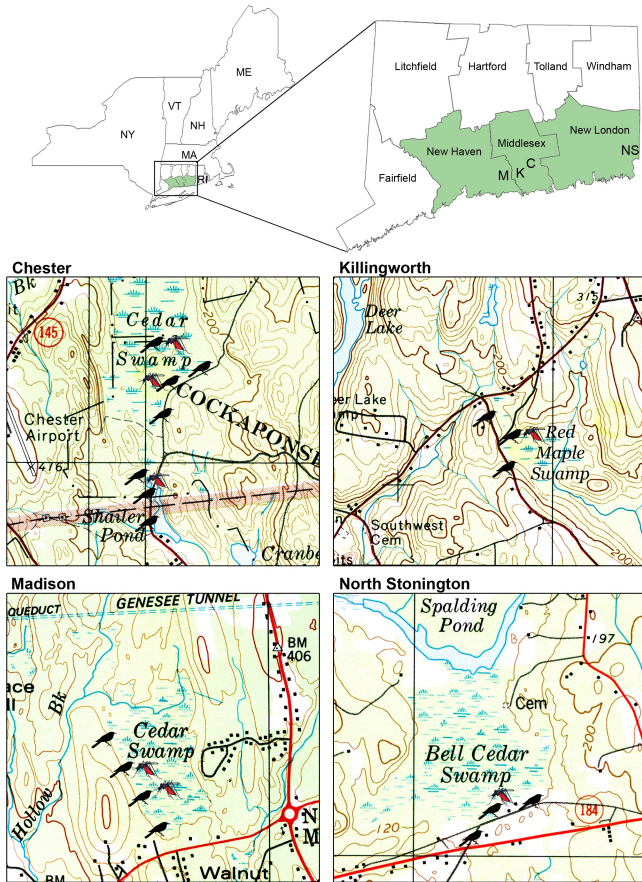
- EEE virus (Togaviridae, Alphavirus) is a highly pathogenic mosquito-borne zoonosis that is responsible for outbreaks of severe disease in humans and equines, resulting in high mortality or severe neurological impairment in most survivors.
- In the past, outbreaks occurred intermittently with no apparent pattern; however, during the last decade we have witnessed annual reoccurrence of virus activity with human and equine cases

Vectors and Hosts

- In the northeastern United States, EEE is maintained in an enzootic cycle involving the ornithophilic mosquito, *Culiseta melanura* and a variety of passerine birds in freshwater swamp habitats.
- It is believed that the various passerine bird hosts allows the disease to overwinter and survive despite a relative lack of mosquito presence

Data Collection

- Over a period of several months, the Connecticut Agricultural Experiment Station (CAES) both collected samples of *Culiseta melanura* and tracked the appearance of various bird species in set locations



- 1127 blood meals were successfully collected and identified to species level
- Greater than 99 percent were from 65 avian hosts in 27 families and 11 orders
- Examination of the blood meals leads us to emphasize our analysis on 8 bird species

Parameters and Assumptions

Feeding Index α

The feeding index α_i assesses the proportion of blood meals from a particular host species i in relation to the proportional abundance of that species in the host community. Hence a feeding index of 1 indicates opportunistic feeding habits, while a feeding index greater than 1 indicates preferential feeding.

$$f_i = \frac{\alpha_i N_i}{\sum_{j=1}^n \alpha_j N_j}$$

Where f_i is the probability that a blood meal was obtained from a specific bird

Fixed Parameters

Due to limited experimental data on the subject, the following were assumed to be fixed for the purposes of the model:

- Bird recruitment rate, b and bird death rate d
- Recovery rate γ is assumed to be constant amongst all bird species
- Mosquito death rate d_v and vector biting rate v

Furthermore studies suggest that infection of a susceptible vector is guaranteed if they feed from of a viremic host, and thus the host-vector transmission rate β_2 is also fixed

Transmission Rates β_i

- Studies suggest that vector-to-host transmission is guaranteed when an infectious vector feeds from a host, and thus the vector-to-host transmission rate was set to 1.
- Limited data exists regarding the value of the host-to-vector transmission rate among the various host species. In order to focus the analysis on the effect of variable biting rates on the model's output, the host-to-vector transmission rate is assumed to be constant across all of the host species
- The all-species host-to-vector transmission rate was determined by fitting the model proportion of birds that became infected over the model period to the observed proportion of seropositives amongst the various bird species from a previous study.

Mathematical Model

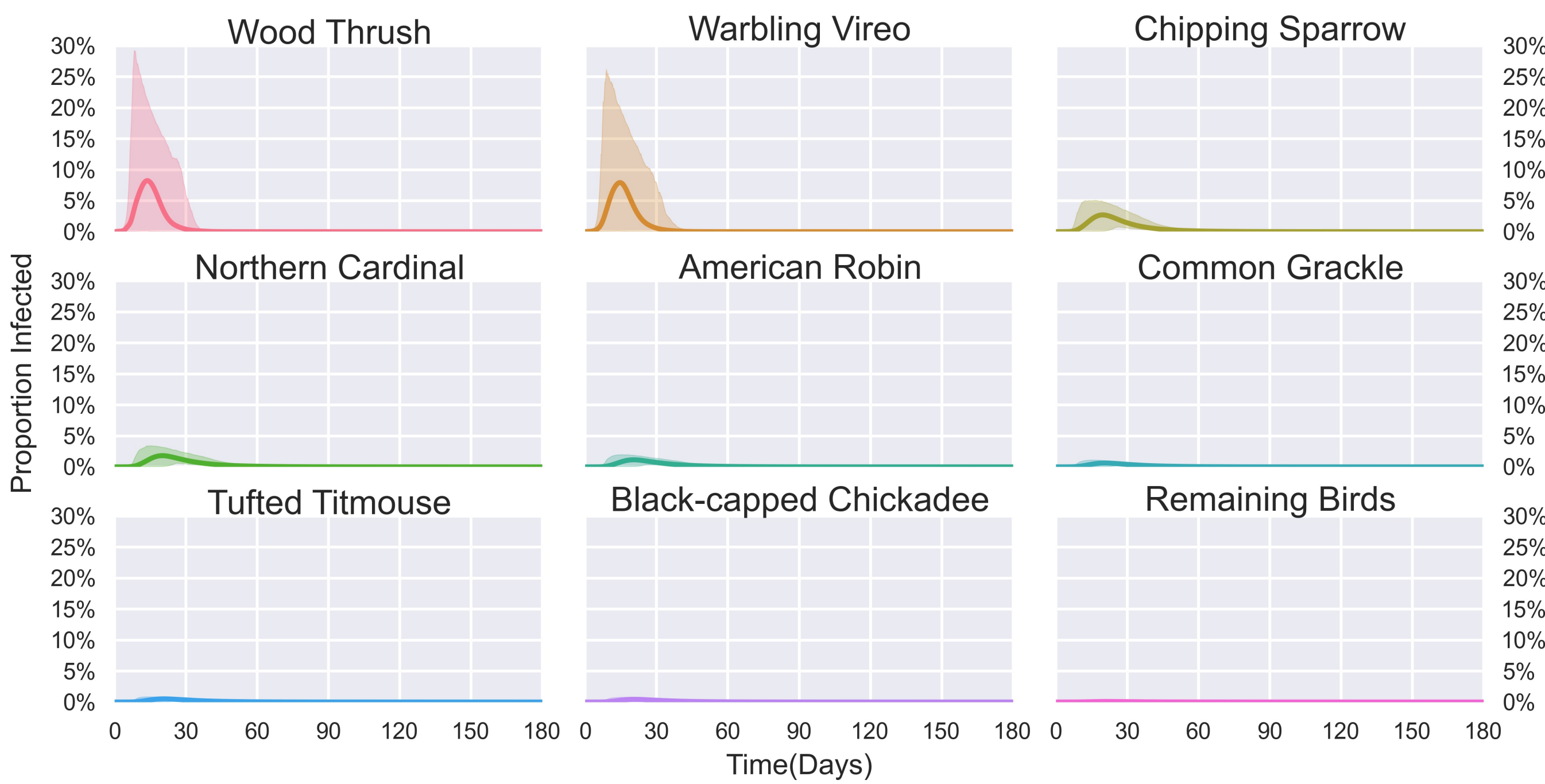
We choose to focus on 8 preferential host species, and a ninth consisting of all other birds. This leaves us with a system of 29 differential equations (with $i=1,2,...,9$).

$$\begin{aligned} \frac{dS_i}{dt} &= bN_i - \lambda_b S_i - dS_i & \lambda_b &= \frac{\beta_1 v I_v \sum \alpha_i}{\sum \alpha_i N_i} \\ \frac{dI_i}{dt} &= \lambda_b S_i - \gamma_b I_i - d_{EEE} I_i - dI_i \\ \frac{dR_i}{dt} &= \gamma_b I_i - dR_i & \lambda_v &= \frac{\beta_2 v \sum \alpha_I I_i}{\sum \alpha_i N_i} \\ \frac{dI_v}{dt} &= \lambda_v S_v - d_v I_v \\ \frac{dS_v}{dt} &= r(t)N_v - d_v I_v \end{aligned}$$

Markov Chain Monte Carlo

- Utilizing Markov chain Monte Carlo methods, 1000 samples were selected for both the counts and blood meals.
- From each of these samples, the feeding indices for each of the selected bird species were calculated
- We have reported the median and 95% confidences intervals for the calculated proportion infected for each host species.

Results



Conclusions and Future Work

Conclusions

Due to their low overall populations and high feeding index, the wood thrush and warbling vireo quickly have populations become highly infectious, which is then followed by a decline as there remain few susceptible birds of these species to infect. As a result of this, however, the number of infectious mosquito's rises drastically, and thus the infection rates of the remaining bird species slowly increases.

Future Questions

- For the purposes of this model bird populations were assumed to be constant over the course of the infection, data exists suggesting that at least certain bird species in the area shift over the course of the summer, which we are currently in the process of implementing.
- The Wood Thrush had a relatively small population appear at each location, but in three locations it had a disproportionately high blood meal count, leading to an extremely high feeding index.

Funding

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