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

Feeding Index α

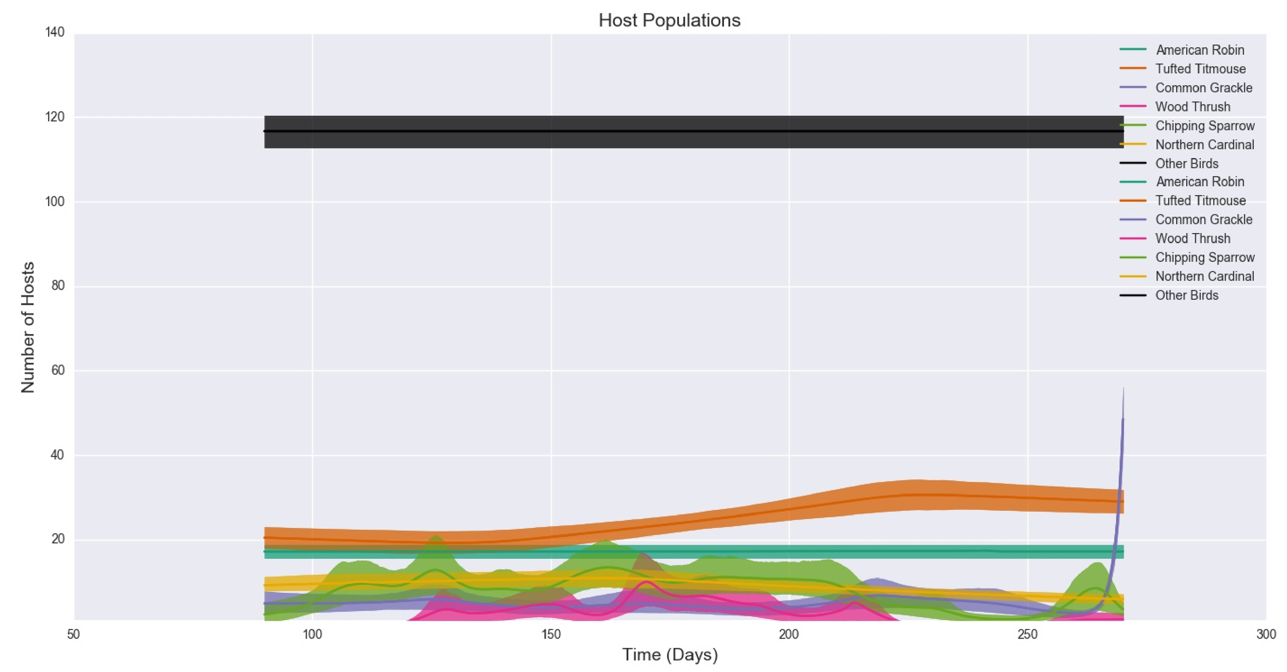
The feeding index α_i assesses the proportion of blood meals from a particular host species i in relation to the proportional abundance of that species in the host community. Hence a feeding index of 1 indicates opportunistic feeding habits, while a feeding index greater than 1 indicates preferential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

$$\alpha_i = \frac{\dfrac{f_i}{\sum\limits_{j=1}^{n} f_j}}{\dfrac{N_i}{\sum\limits_{j=1}^{n} N_j}}$$

Where f_i is the number of blood meals obtained from a specific bird

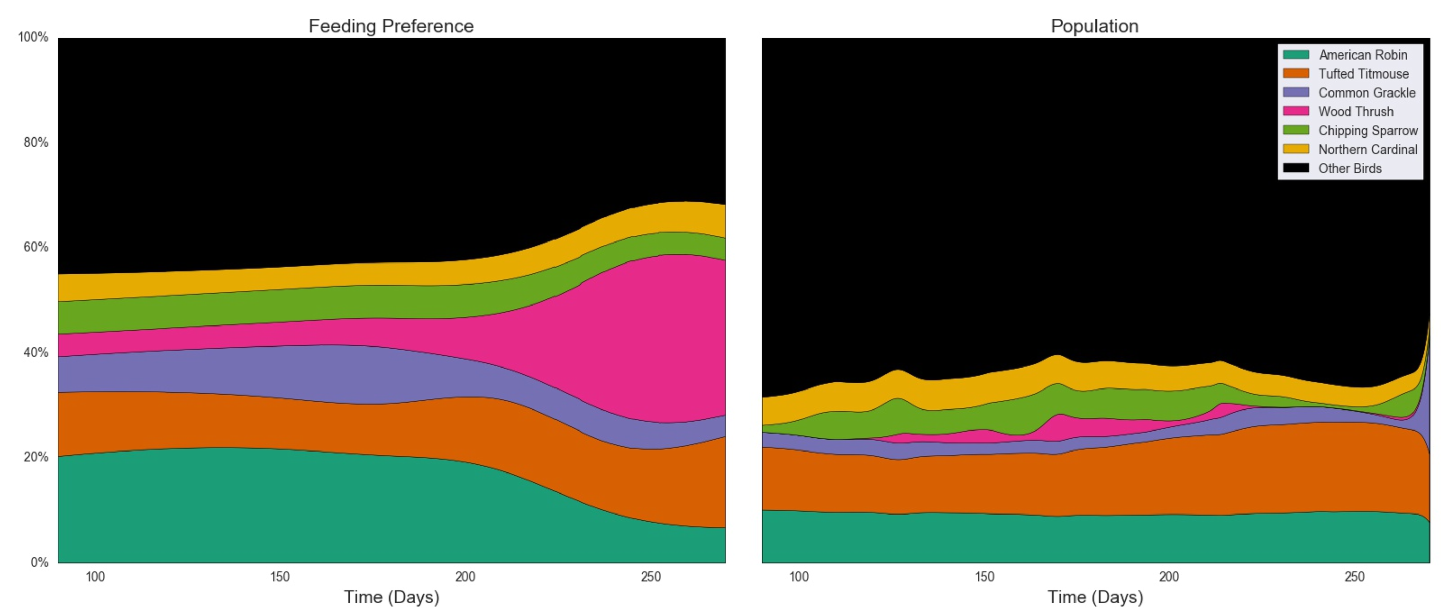
Population Splines

Interpolating Splines were used to create smooth curves of the sampled host populations



Observed Feeding Preference

Utilizing the population splines and calculated feeding indicies, we are able to see the observed feeding preference of the vector.



Mathematical Model

We choose to focus on 6 preferential host species, and a seventh consisting of all other birds. This leaves us with a system of 23 differential equations (with i=1,2,...,9).

$$\frac{dS_i}{dt} = \mathsf{b}N_i - \lambda_b S_i - \mathsf{d}S_i \qquad \lambda_b = \frac{\beta_1 v I_v \sum \alpha_i}{\sum \alpha_i N_i}$$

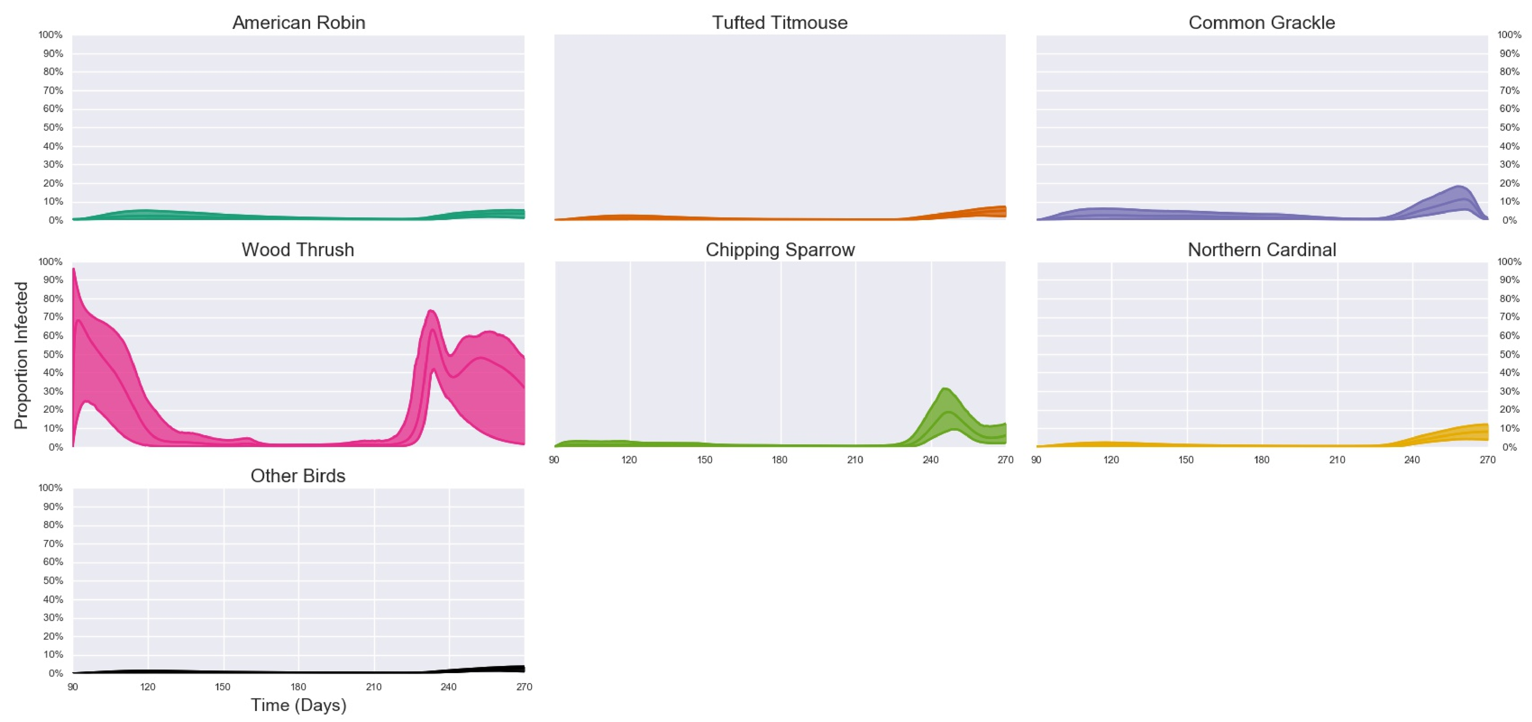
$$\frac{dI_i}{dt} = \lambda_b S_i - \gamma_b I_i - d_{EEE} I_i - \mathsf{d}I_i$$

$$\frac{dR_i}{dt} = \gamma_b I_i - \mathsf{d}R_i \qquad \lambda_v = \frac{\beta_2 v \sum \alpha_I I_i}{\sum \alpha_i N_i}$$

$$\frac{dI_v}{dt} = \lambda_v S_v - d_v I_v$$

$$\frac{dS_v}{dt} = r(t) N_v - d_v I_v$$

Results



Conclusions

Early in the season, the disease persists due to infections from preferntial species such as the Common Grackle and Amerian Robin. Due to a increased feeding preference for Wood Thrush later in the season, in conjucture with the small overall population of Wood Thrush, lead to the population to quickly become infected. This spike in new infections leads to an increase in in infections across all other species.

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