



May 19th, 9:00 AM - 9:30 AM

## The role of infection on shifts in population cycles in a discrete-time epidemic model

Laura F. Strube

*Virginia Polytechnic Institute and State University, lfstrube@vt.edu*

Ryan H. Hughes

*Virginia Tech, ryanh18@vt.edu*

Lauren M. Childs

*Virginia Polytechnic Institute and State University*

Follow this and additional works at: <https://scholarscompass.vcu.edu/bamm>



Part of the [Life Sciences Commons](#), [Medicine and Health Sciences Commons](#), and the [Physical Sciences and Mathematics Commons](#)

---

<https://scholarscompass.vcu.edu/bamm/2022/thur/23>

This Event is brought to you for free and open access by the Dept. of Mathematics and Applied Mathematics at VCU Scholars Compass. It has been accepted for inclusion in Biology and Medicine Through Mathematics Conference by an authorized administrator of VCU Scholars Compass. For more information, please contact [libcompass@vcu.edu](mailto:libcompass@vcu.edu).

# The Role of Infection on Shifts in Population Cycles in a Discrete-Time Epidemic Model

Strube, Laura F.

Virginia Tech, Department of Mathematics

Hughes, Ryan H.

Virginia Tech, Department of Mathematics

Childs, Lauren M.

Virginia Tech, Department of Mathematics

April 19, 2022

## Abstract

One-dimensional discrete-time population models, such as for logistic or Ricker growth, exhibit periodic and chaotic dynamics. Adding epidemiological interactions into the system increases its dimension and the resulting complexity of its behaviors. Previous work showed that while a discrete SIR model with Ricker growth exhibits qualitatively similar total population dynamics in the presence and absence of disease, a more complicated viral infection (SIV) system does not. Instead, infection in the SIV system shifts the periodic behavior of system in a manner that distinguishes it from the corresponding disease-free system. Here, we examine a SI model with Ricker population growth and show that infection produces a distinctly different bifurcation structure than that of the underlying disease-free system. We use analytic and numerical bifurcation analysis to determine the influence of infection on the bifurcation structure of the system. In addition, we derive the basic reproductive number,  $R_0$ , and determine the influence of population growth and decay parameters on  $R_0$ . Our work shows that even in the SI model, infection dynamics can shift the location of period-doubling bifurcations as well as the onset of chaos.