

Modeling the Dynamics of Lyme Disease in a Tick-Mouse System Subject to Vaccination of Mice Populations

Daniel Carrera-Pineyro¹, Harley Hanes², Adam Litzler³, Andrea

McCormack⁴, Josean Velazquez-Molina⁵, Dr. Christopher Kribs⁶, Dr. Anuj Mubayi⁵, Dr. Karen Rios-Soto⁷

¹*University of the Incarnate Word*

²*Tulane University*

³*The Ohio State University*

⁴*North Center College*

⁵*Arizona State University*

⁶*The University of Texas at Arlington*

⁷*University of Puerto Rico Mayaguez*

`oakman@ilstu.edu`

Lyme disease is one of the most prevalent and the fastest growing vector-borne bacterial illness in the United States, with over 25,000 new confirmed cases and 300,000 associated illnesses every year. The Centers for Disease Control and Prevention estimates that those numbers could be significantly underrepresented. Lyme Disease is caused by the bacteria, *Borrelia burgdorferi*, which humans contract through the bite of *Ixodes scapularis*, commonly known as the deer tick or Eastern blacklegged tick. Ticks receive the pathogen through numerous reservoirs, chiefly the white footed mouse *Peromyscus leucopus*. Our research assesses whether vaccines targeting mice are an effective method to reduce human risk for Lyme Disease. We do this using a system of non-linear difference equations to model transmission dynamics and vector demographics in both tick and mice populations.