Modeling Importation of Vector Based Infectious Disease in SIR Models

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Abstract

This research paper is an attempt at modeling the risk of vector borne infectious disease importation to a previously disease free country by means of travel. Two population models are considered, the disease free country with human population and the vector population within the disease free country. In the model, travelers from an outside country infected with a disease travel to a disease free country with a known vector population capable of carrying that infectious disease. The spread of infection is then estimated using human-vector interaction rate and probability of infection with each interaction. The models are continuous, stochastic models. These models are then applied to simulate the potential risk of spread of chikungunya fever on Saint Martin Island.

Introduction

Throughout our lives, no matter where we live we are likely to hear of the next new pandemic. In recent years, these have included infectious diseases such as the Zika virus, Ebola, SARS, H1N1, and the West Nile virus. According to LaDeau et al., emerging infectious diseases are on the rise around the world with the increased globalization of travel and trade, human population growth, and climate change (1444). Infectious diseases can be spread through various means, such as animal to human, human to human, or from food or water to humans. Infectious disease modeling can be used to assist in predicting and controlling the spread of these infectious diseases. For research purposes, we focused on chikungunya fever that is modeled using a zoonotic system where the pathogens originate from contact with an infected aedes aegypti mosquito and infected humans are not infectious to other humans but are infectious to mosquitoes (LaDeau et al. 1444). The zoonotic system of infection and factors such as infected individuals traveling to uninfected areas combine to model a widespread infectious disease pandemic.

Model Development

Dynamic compartmental models, which are used in epidemiology, use differential equations to represent susceptible (S), exposed (E), infected (I), and recovered (R) states, or SEIR, to model transmission of the disease within the population. Susceptible are the members of the population who have yet to come into contact with an

infected individual or animal. Exposed are those that have come into contact with an infected individual or animal but have yet to show signs of infection and may or may not be infected. Infected are those that have been infected and are not yet recovered. Recovered are those members of the population that have recovered from being infected either through surviving the infectious disease and gaining immunity or have succumbed to the disease and died. For this research, we evaluated the population using only a SIR model, meaning the exposed are accounted for in the susceptible portion of the population. The model also includes two parameters to model rate of change from susceptible to infected and from infected to recovered. This model assumes that once an individual of the population has recovered, they are no longer susceptible to the infectious disease, mosquitoes do not recover, and accounts for births and deaths, assuming a constant population size.

Globalization is then taken into account for our overall model. People from infected subpopulations are likely to travel to uninfected subpopulations and start the spread of the disease in these areas. Uninfected individuals may travel to infected areas and bring the disease back to their areas with them. This required finding a model to represent movement to and from these locations by populations of infected and uninfected individuals, thereby increasing the number of infected and susceptible in the areas being traveled to and decreasing the number of infected and susceptible in the area traveled from. Smith et al. discusses the distribution of different types of infectious diseases currently around the globe (1908) and Lopez et al. uses several models to show importation and deportation rates of infection using SIR modeling.

Subpopulations will have different rates of infection and recovery. This is accounted for in our model, using varying linear combinations for parameters of rates of infection and recovery for each subpopulation. Weiss and Anthony discuss the increased chances of infection and exposure due to increased human-animal interaction in globalization as well as increased infection rates due to poor medical care or poverty potentially weakening the immune systems of the populations (574).

The model is based on the zoonotic system of infection. The model accounts for rates of infection for individuals being exposed to infected mosquitoes. This was included in our parameter for rate of change from susceptible to infected. This means an increased rate of infection due to animals not being considered in our population of our model, but being considered a factor in increased susceptibility of our human populations.

The final model includes the SIR models of the country's human population as well as the mosquito population, importation rate of infection from travelers, rate of change parameters for susceptible to infected and infected to recovered that account for bite exposure, human exposure, and becoming immune following recovery, and the includes death and births of both populations, assuming a constant population. This model was used to simulate a widespread infectious disease pandemics caused by zoonotic systems of infection given subpopulation parameter rates of infection, population size, travel information, initial start values for number of infected, and area of emergence, specifically the spread of chikungunya fever throughout Saint Martin Island.

Fig. 1 Vector and Human Population Equations

Human Population

$$\frac{dS_H}{dt} = \gamma_H N - \frac{rT_{HM} I_M S_H}{N} - \mu_H S_H$$

$$\frac{dI_H}{dt} = rT_{HM} I_M S_H - \mu_H I_H - \nu I_H - \mu_D I_H + \delta$$

$$\frac{dR_H}{dt} = \nu I_H - \mu_H R_H$$

Vector Population

$$\frac{dS_M}{dt} = \gamma_M N2 - \frac{rT_{HM} I_H S_M}{N2} - \mu_M S_M$$

$$\frac{dI_M}{dt} = rT_{HM} I_H S_M - \mu_M I_M$$

Note: $N=S_H+I_H+R_H$ and $N2=S_M+I_M$, this allows for population to remain constant and never reach zero

Table 1. Parameters and Description

γ_H : human birthrate

r: rate at which humans interact with infection vector (biten by mosquito)

T_{HM}: probability of transmission of infection to human after bite

ϵ : importation via external infection rate

μ_H : natural human death rate

δ : importation via immigration rate (how many immigrants come infected on average)

ν : recovery rate

γ_M : vector birthrate 0.636 per day

μ_M : vector death rate, .12 per day (only female mosquitoes bite)

μ_D : death rate due to the illness

Results

Parameters were optimized in MATLAB using data from Cassadou, et al. The simulation and the data follow the spread of chikungunya fever following the importation to Saint Martin of the disease from October 2013 to December 2013 for a total period of 61 days.

Fig. 2 Initial Results Following Optimization

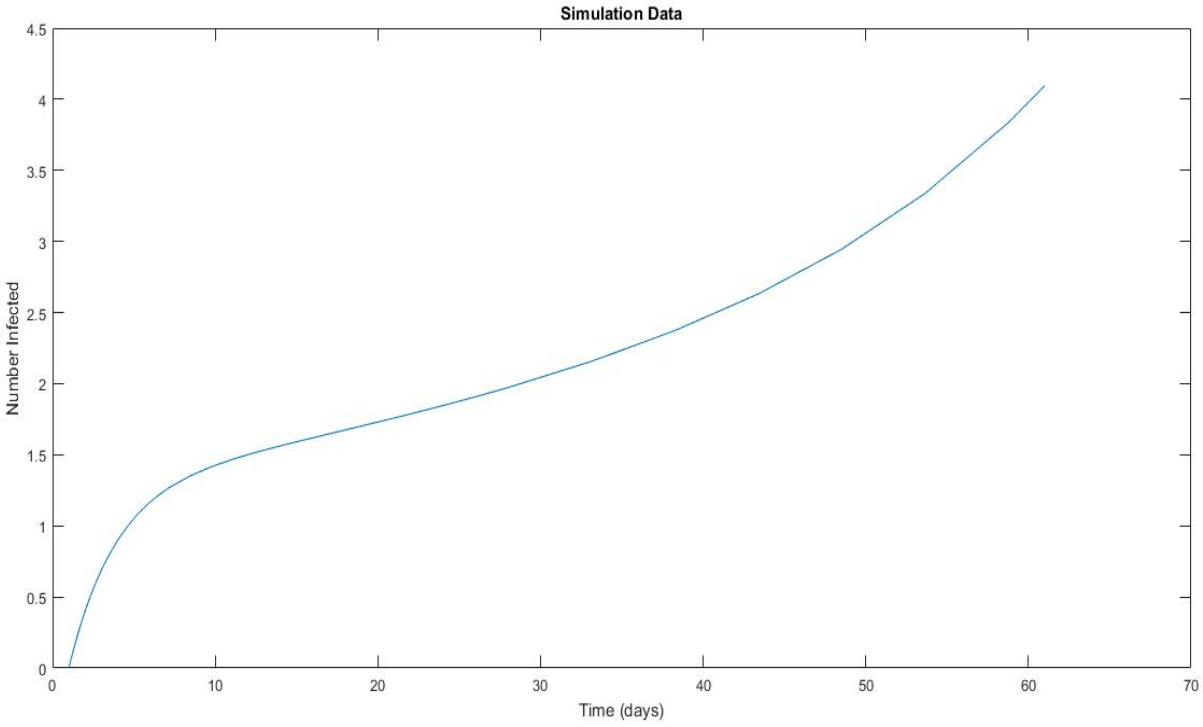


Figure 2 shows the results of this initial simulation. The data was then graphed, seen in Figure 3. Comparison of the two graphs shows that the model is a fairly accurate representation of the spread of chikungunya fever. When attempting to graph any representation of a stochastic model, the results are not usually very accurate due to the randomness seen in the model.

Fig. 3 Chikungunya Fever on Saint Martin

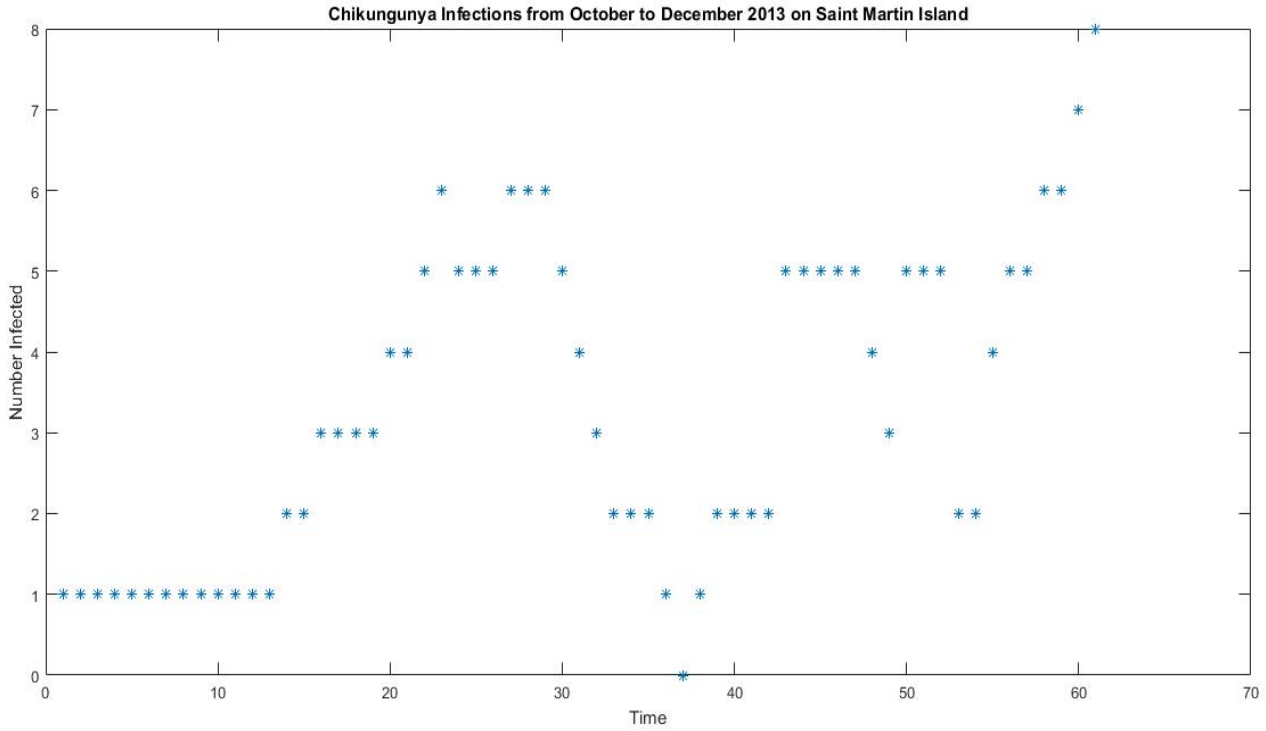
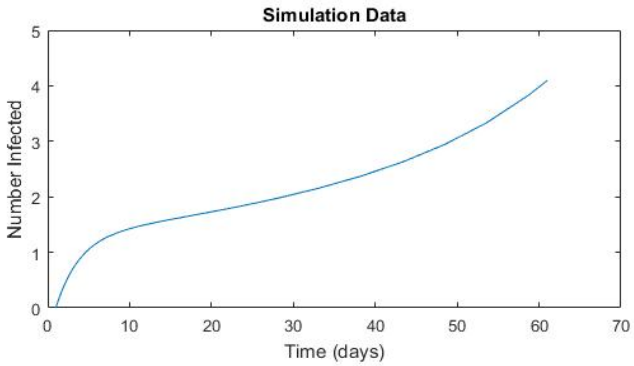
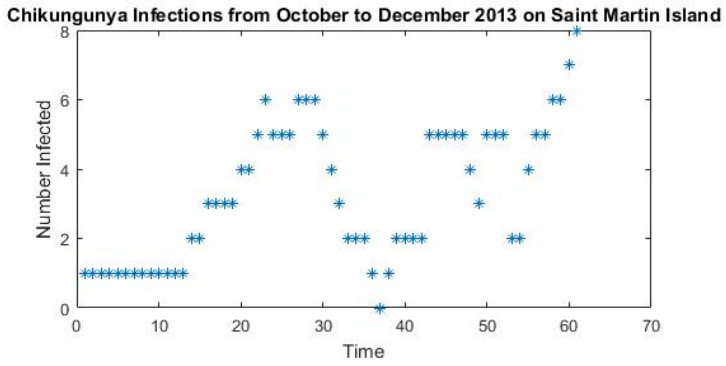


Fig. 4 Side-by-side Comparison of Data versus Simulation





Conclusion

SIR models are important to modeling the spread of infectious diseases. As human populations grow, the risk of infectious disease epidemics grow as well. Being able to accurately model the spread of infectious disease is a pertinent topic of research. Many models used are continuous, deterministic models that do not allow for changes in population and are therefore unable to model comings and goings of modern travelers across the globe. Factoring travelers into our SIR models allows us to more accurately depict the natural movements of the human population and, therefore, more accurately represent the spread of disease. Chikungunya is an emerging infectious disease around the globe, in the same category as dengue fever, malaria, zika, and ebola. It is important to be able to model this disease correctly and efficiently. Future work should be done to garner a better comparison of the model to our data in order to know for certain the accuracy of the model.

References

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