# Exploring Vector-Borne Disease through SIR Model:
# Dengue Fever in Singapore

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## Abstract

In this paper, we will be using an SIR model to study the Dengue epidemic in Singapore in 2014. Dengue is one of the most prevalent vector-borne disease in Southeast Asia, and one of the most powerful models to describe the various trends in such diseases is the SIR model, where **S** stands for the susceptible population, **I** the infected population, and **R** the recovered population. While Dengue was more of an endemic in Singapore, as Dengue cases occur every year and at a rather stable number, it behaved like an epidemic in 2014 where there was an unprecedentedly significant surge in the cases from around the 20th week. Our primary goal is to discover the relative magnitude, of the parameters so that the number of infected people produced by our model will be matching the numbers in real life.

## Introduction

### Dengue Fever

Dengue Fever is "transmitted to humans by the bite of an infected" female mosquito from either the Aeges aegypti or the Ae. albopictus family (Ministry of Health, Dengue in Singapore). A female mosquito becomes infected with the Dengue virus, when it sucks the blood of a human that has been infected by Dengue Fever. Dengue Fever can can only be transmitted by mosquitoes, as research has shown that "Dengue fever is not contagious and does not spread directly from person to person." (Ministry of Health, Dengue in Singapore)



Figure 1: Transmitted by the bite of an infected female Aeges aegypti mosquito

For this paper, we will be focusing on the factors that affect the spread of Dengue fever in Singapore. We hope to explain by the end of the paper which factors have been the main factors that contribute to this spread and how the Singaporean Government can do an even better job of preventing the spread of Dengue Fever. To answer our questions, we will be using an SIR model to look at how Dengue Fever has spread in Singapore - the concept of this model will be explained in further detail in the next section. By investigating data from 2014 and employing the five equations, the full SIR for human population (with a focus on the infected population) and SI for mosquitoes populations, we will model the progression of the disease from a typical outbreak to a short-term phaseout in a relatively limited timespan and geographical area (defined below), and examine the relationships between the population of infected humans, infected mosquitoes, and susceptible mosquitoes. In doing this, we mainly hope to have an in-depth understanding of the properties of the Dengue virus on a relatively microscopic level in terms of timespan and area.

### SIR Model

To answer our research question, we will model the spread of Dengue fever in Singapore via an SIR model. An SIR model, according to Wolfram Mathworld, "is an epidemiological model that computes the theoretical number of people infected with a contagious illness in a closed population over time." We will be adapting the general SIR model to better study the epidemic. Instead of three equations in the traditional model (each measuring the rate of change in **S**, **I** and **R** populations), we have five equations that will account for not only the SIR populations of human but also the **SI** populations of mosquitoes (there is no recovered population for mosquitoes).

| | |
|---|---|
| a1 | Likelihood of exposure a susceptible person could have to an infected mosquito |
| a2 | Likelihood of exposure a susceptible mosquito could have to an infected human |
| c1 | Likelihood that a person who is exposed to an infected mosquito actually gets infected |
| c2 | Likelihood that a mosquito who is exposed to an infected human actually gets infected |
| b | Likelihood that person who is infected by Dengue fever recovers in a week |
| r | Weekly number of mosquitoes "recruited" to carry the disease. In other words, number of fully grown mosquitoes who are able to feed off infected human |
| e | Weekly death rate of mosquitos each week (natural death rate and deaths caused by human) |

Figure 2: Model Parameters

## Model Development

We have developed two separate yet interrelated box models, one designed for the human population and another for the mosquito population in Singapore with respect to the Dengue disease.
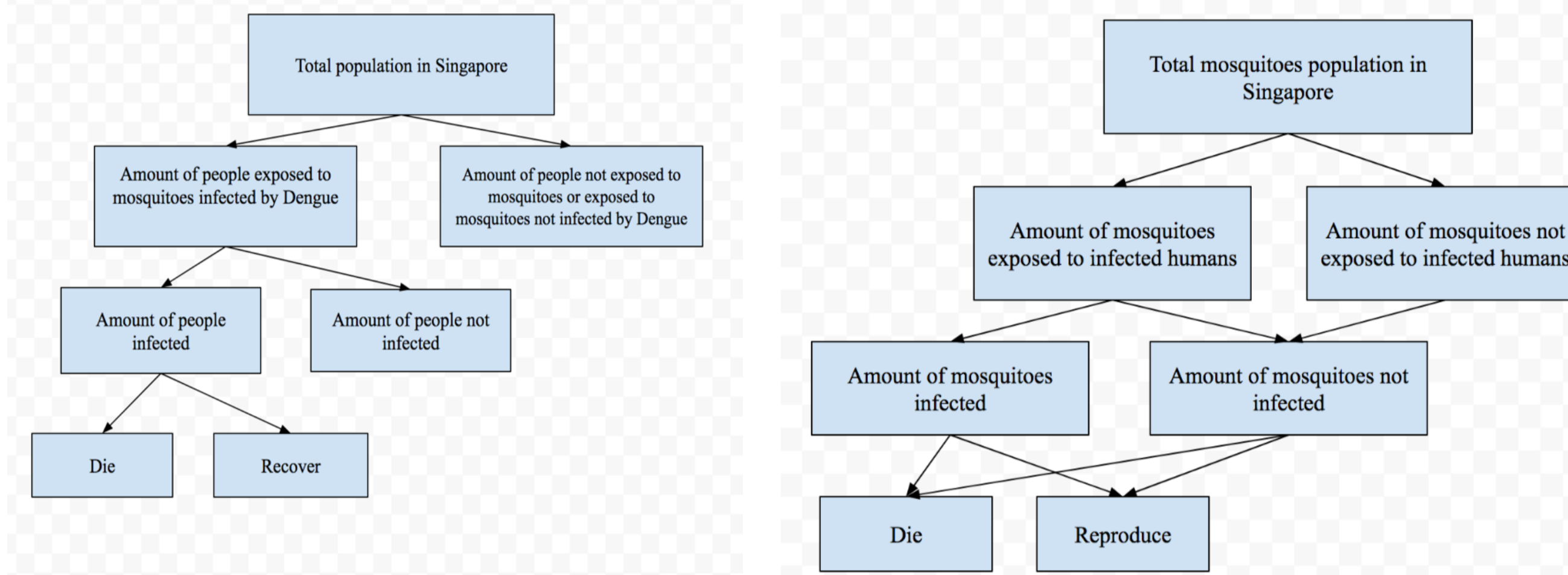


Figure 3: Box Models for Human and Mosquito Populations

## Explaining our Parameters and Initial Values

### Why are c1 and c2 equal?

There are four strains of Dengue virus, and being immune to one does not mean one will never get infected with others. In fact, research has shown that being infected with a different strain of virus could produce more life-threatening effects. Ideally, with only one strain of virus present, humans would most likely have a lower chance of being infected than mosquitoes as humans have much longer lifespans and human cells could learn to become more capable of battling the virus. But with different strains present, humans and mosquitoes are equalized again.

### Why is a1 lower than a2?

We monitored the behaviors of our model and observed that only when parameter a1 is lower than a2, the population of infected human and mosquito follow our predictions: infected human will increase then decrease, so will infected mosquitoes. Humans have greater mobility, and typically office buildings and public transports do not have breeding sites for mosquitoes. However, when a sick person with dengue virus is staying at home, all the mosquitoes in the household are exposed to the virus.

### Why only 55,794 people in Singapore are susceptible?

In order for a person to be susceptible to Dengue fever, they will likely be living in a area that is deemed Aedes positive under the Aedes House Index scale. In a 2014 report, the Singapore Government reported that the overall Aedes House Index (HI) for Singapore was 0.30 percent - this represents the percentage of households that are susceptible to Aedes breeding, which as explained above is what transmits Dengue Fever to people. Since the average household size in Singapore in 2014 was 3.4 people, that means that around 1percent of the Singaporean population (0.30 percent *3.4 people = 1.02 percent of the total population) is susceptible to Dengue Fever. In 2014, the population of Singapore was 5.47 million. 1.02 percent of 5.47 million is 55,794 people which is the number we used as the number of susceptible people in Singapore to Dengue Fever in early 2014.

### Why only 200 people are initially infected?

We started with an initial population of 200 people infected due to the data we were given by the Singaporean Government. Their data had around 200 reported cases of Dengue fever in the week before our model begins.

### Why initial number of people recovering is 0?

We decided for the simplicity of our model that the initial number of people that had recovered was 0.

### Why initial number of susceptible mosquitoes is 3200?

Since there is no actual data on the number of mosquitos in Singapore, so we decided to focus on living spaces with mosquitoes instead of the entire island of Singapore (just like how we focused on households when estimating the susceptible population, we are looking at living spaces here). In 2014, an annual average of 0.10 percent of the households in Singapore contained mosquito breeding sites, which comes down to 0.001*5470000/3.4 = 1600 households. If we assume that within each week, there would be two surviving adult Aedes E to carry dengue virus, we can assume that we have 3200 susceptible mosquitoes in the living spaces under inspection.

### Why initial number of infected mosquitoes is 290?

Research on mosquitoes in Singapore by H.L. Lee showed that the "infection rate of the mosquito population is around 10 percent." Thus, since we believe that the 3200 susceptible mosquitoes are 90 percent of the mosquito population, having 290 infected mosquito would represent 10 percent of the total susceptible and infected mosquito population being infected - the total initial susceptible and infected mosquito population is 290+3200=3490, and 10 percent of 3490 is roughly 290.

## Differential Equations and Model Output Graphs

Variables: $h1$ - Susceptible Human Population; $h2$ - Infected Human Population; $h3$ - Recovered Human Population; $m1$ - Susceptible Mosquito Population; $m2$ - Infected Mosquito Population

### 1. Rate of change in the population of susceptible human

$dh1/dt = -a1 * m2 * h1 * c1 + b * h2$

**-a1*m2*h1*c1** measures the change in the number of susceptible people that are exposed to infected mosquitoes. It is a negative rate as we are expecting the number of susceptible people to decrease when more people become infected. Parameter **b** measures the likelihood that person who is infected by Dengue fever recovers in a week. Thus, **b*h2** measures the change in the number of infected people that recover and become susceptible people.

### 2. Rate of change in the population of infected human

$dh2/dt = h1 * a1 * m2 * c1 - b * h2$

The equation for the rate of change in the population of infected human is the flipped version of the equation for the rate of change in the population of susceptible human.

### 3. Rate of change in the population of recovered human

$dh3/dt = b * h2$

As explained above, **b*h2** is related to the rate of recovery, or the proportion of the infected population who are cured of dengue.

### 4. Rate of change in the population of susceptible mosquitoes

$dm1/dt = -a2 * h2 * m1 * c2 + r - e * m1$

**-a2*h2*m1*c2** measures the change in the number of susceptible mosquitoes that are exposed to infected human. It's a negative rate as we are expecting the number of susceptible mosquitoes to decrease when more mosquitoes become infected. There is no recovery for mosquitoes. Parameter **r** measures the number of mosquitoes that are added to the susceptible pool every week. It refers to the weekly number of mosquitoes that are 1) the offspring of both susceptible and infected mosquitoes and 2) survive till adulthood to be able to carry the disease. Parameter **e** measures the weekly death rate of mosquitoes which includes both the natural death rate and deaths caused by human (e.g. regular spray of mosquito repellents in common areas).

### 5. Rate of change in the population of infected mosquitoes

$dm2/dt = a2 * h2 * m1 * c2 - e * m2$

The first part of this equation is similar to a flipped version of the equation for the rate of change in the population of susceptible mosquitoes. We also have **e*m2**, which measures the change in the number of infected mosquitoes that die each week. There is no recovery possibility for mosquitoes, so we don't have to subtract any recovered mosquitoes from the infected mosquitoes population.
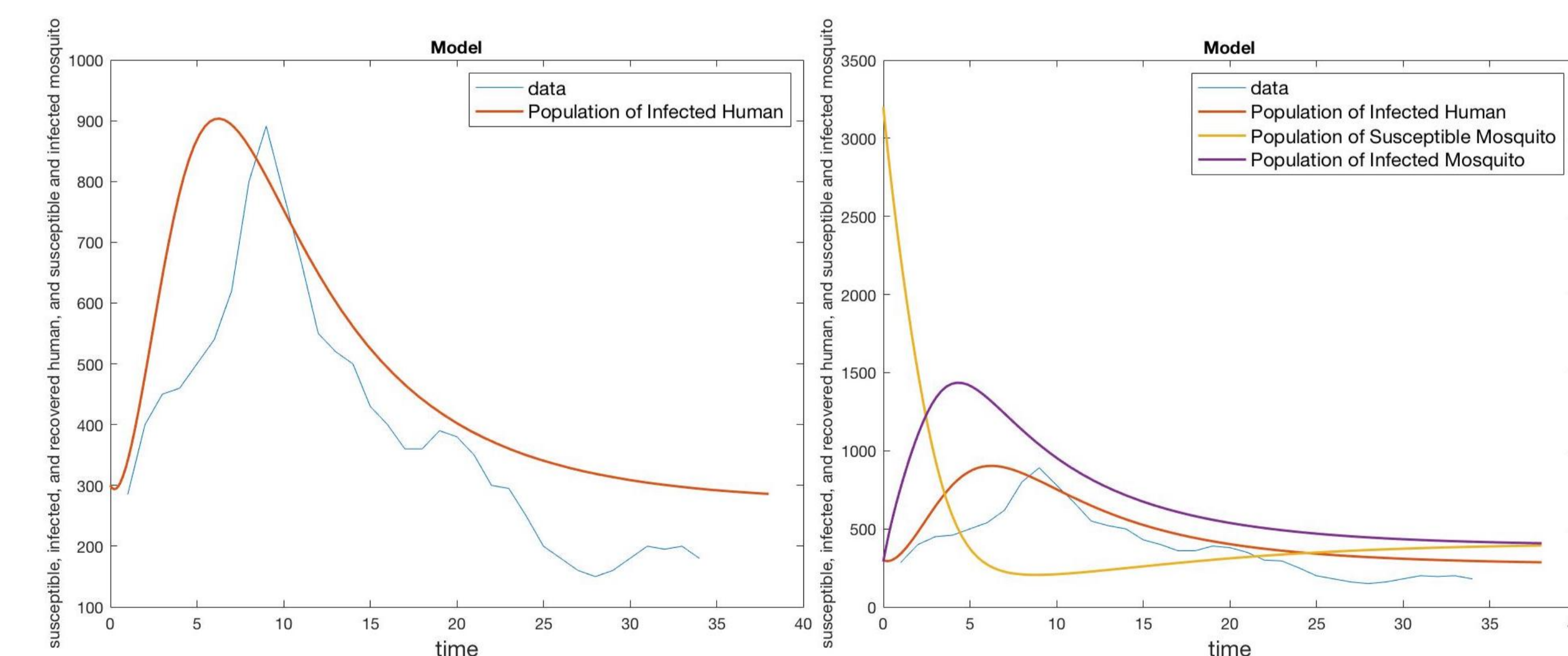


Figure 4: Infected Human Population and Short-Run Full SIR

## Model Discussion

Research has shown that the surge in Dengue cases in 2014 was due to: a) Dengue has 4 strains of virus, being infected with one would still mean that the person is susceptible to the other 3; b) there was a virus mutation from DEN 2 to DEN 1; c) an increased number of households with Aedes Aegypti breeding sites. These conditions primarily correspond to changes in parameters **a1, c1 and r**. To test the validity of our model, we lowered these parameters to simulate what would happen had these changes not occurred. We saw that the number of infected cases decreased significantly from the peak in 2014, which further confirmed the validity of our model.