

A computational investigation on how visitation affects the reproduction number in a dengue fever model

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ABSTRACT. Dengue fever is transmitted by day-biting mosquitoes in tropical climates and is a major public threat for many countries. Ordinary differential equation models can be used to describe how infectious diseases move throughout populations, and predictions from these models may help in the development of effective treatment strategies. In order to investigate the spread of dengue fever in neighboring communities, a previously developed SIR/SI model of dengue transmission in neighboring communities in Sri Lanka was used to generate the basic reproduction number, R_0 . Parameters for time spent in neighboring communities were varied in order to investigate how time spent in communities of different sizes affects the reproduction number. Results suggest that movement of individuals among communities increases the reproduction number, especially if people are traveling to a population of greater size.

1. Introduction

Dengue fever is a disease spread by mosquitoes in tropical areas and is a major public health threat with more than 2.5 billion people at risk for acquiring the virus (Ranjit and Kissoon, 2011; Sirisena and Noordeen, 2014). *Aedes aegypti* and *Aedes albopictus* mosquitoes are the primary carriers of the dengue virus, laying their eggs closely around homes in tropical areas. Urbanization trends have increased mosquito populations and the prevalence of the disease (Gubler and Clark, 1995; Gubler et al., 2014). Treatments to control the disease have not yet been fully developed; therefore prevention is currently the most effective method to slow the spread of the disease (Laughlin et al., 2012; Sirisena and Noordeen, 2014).

Aedes mosquitoes, more specifically *Ae. aegypti* mosquitoes, are typically the primary carriers of the dengue virus. *Ae. aegypti* spend a majority of their lifetime around the houses where they grow and develop, meaning the people (rather than the mosquitoes themselves) are likely more responsible for transmitting the virus between various communities (World Health Organization, 2009). When the infected mosquito bites a human, the virus binds to white blood cells and reproduces inside the cells. Symptoms expressed of dengue fever include high fever, flu-like symptoms, severe headache, severe eye pain behind the eyes, muscle and/or bone pain, rash, mild bleeding manifestation, and/or low white cell count (CDC, 2012). Fluids from the bloodstream leak into body cavities, resulting in less blood circulating in blood vessels which can eventually result in a loss of blood pressure and a failure of delivery of blood to vital organs (Martina et al., 2009).

Dengue fever and dengue hemorrhagic fever belong to a group of four viruses referred to as serotypes of the disease (DEN-1, DEN-2, DEN-3, and DEN-4). If left untreated, infection can

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lead to serious forms of the disease known as dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS). Infection from one serotype does not result in immunity from the other strains, and contraction of a second serotype leads to an increased risk of developing DHF/DSS (Gubler and Clark, 1995; Gubler et al., 2014). Dengue fever is also a major concern in tropical countries because of increases in reported cases of DHF (Gubler, 1998; Monath, 1994).

The mosquitoes responsible for spreading the virus are primarily active during the daytime. The infection can be contracted through a single bite, humans being the primary host of the virus. Vaccines for dengue fever are not yet well established, but one vaccine has been administered in a few countries (Maron, 2015). Currently, the most effective way to manage the spread of the virus is through preventative measures (World Health Organization, 2009). Mathematical models are used to predict the path of infection transmission and have been used to investigate how measures such as the use of repellents (Dorsett et al., 2016) and genetic interventions (Okamoto et al., 2013; Robert et al., 2013) affect the transmission of vector-borne diseases. Simulating the spread of the disease helps researchers achieve a better understanding of intervention techniques.

Disease transmission within populations is often described using ordinary differential equation (ODE) models. Vector-borne diseases were first described using ODE models by Ross and Macdonald (Macdonald, 1957), and many later models use a similar framework based on susceptible (S) and infected (I) populations (Aneke, 2002; Rodríguez and Torres-Sorando, 2001; Torres-Sorando and Rodríguez, 1997). Additional categories, including individuals removed from the other populations or exposed but not able to infect others, are sometimes also incorporated (Aron and May, 1982; Esteva and Vargas, 1998; Pinho et al., 2010). Disease transmission models may also include movement of individuals to different areas (Auger et al., 2008; Rodríguez and Torres-Sorando, 2001; Torres-Sorando and Rodríguez, 1997) or incorporate discrete modeling structures (Lloyd et al., 2007; MacDonald et al., 1968; Yokley et al., 2014).

The development of prevention and intervention methods for combating the spread of mosquito-borne diseases should consider how mobile populations affect disease spread (Osorio et al., 2004). The previous study in Reagan et al. (2019) developed an SIR/SI model of dengue fever transmission using the visitation model of malaria presented in Torres-Sorando and Rodríguez (1997) with the existing model of dengue fever in Esteva and Vargas (1998). The current study extends the investigation from Reagan et al. (2019) to consider how visiting different communities affects the basic reproduction number.

The basic reproduction number represents the expected number of new infections that arise from a single infected subject in a population where all subjects are susceptible to acquiring the disease (Chowell et al., 2007). This study will investigate how the amount of time spent in a neighboring community affects the reproduction number produced from the already developed model in Reagan et al. (2019). By adjusting the fraction of time an individual spends in each patch, we can observe the trends and changes in reproduction number, and determine which visitation patterns have the largest impact on the variation in reproduction number. This information will improve the understanding of the outbreak patterns in these communities and could lead to more effective intervention strategies.

2. Model Background

A previous study developed a model for the transmission of dengue fever between interacting neighboring communities (Reagan et al., 2019). This model combined the SIR model for dengue

fever in Esteva and Vargas (1998) with the visitation model for malaria transmission in Torres-Sorando and Rodriguez (1997). The study in Reagan et al. (2019) focused on simulating dengue transmission among three communities in Sri Lanka: the city of Colombo with a population of about 648,000 (worldatlas.com, 2015a), the smaller city Sri Jayawardenapura Kotte with a population of about 115,000 (worldatlas.com, 2015b), and the town of Peliyagoda with a population of about 31,000 (Time.is, 2016). Humans are at risk for being bitten at home and while they are away, therefore being at risk for acquiring or spreading the virus in a community other than their own.

The SIR/SI model of dengue transmission among three neighboring communities is based on the assumption that the human population would remain constant, and infection with only a single serotype was represented (Reagan et al., 2019). The system of differential equations from Reagan et al. (2019) is presented below.

$$\begin{aligned} \frac{dS_{h1}(t)}{dt} = & \mu_h N_{h1} - \frac{\beta_h b}{N_{h1}^* + m} (T_{11} S_{h1}(t) I_{v1}(t)) - \frac{\beta_h b}{N_{h2}^* + m} (T_{12} S_{h1}(t) I_{v2}(t)) \dots \quad (2.1) \\ & - \frac{\beta_h b}{N_{h3}^* + m} (T_{13} S_{h1}(t) I_{v3}(t)) - \mu_h S_{h1}(t) \end{aligned}$$

$$\begin{aligned} \frac{dS_{h2}(t)}{dt} = & \mu_h N_{h2} - \frac{\beta_h b}{N_{h2}^* + m} (T_{22} S_{h2}(t) I_{v2}(t)) - \frac{\beta_h b}{N_{h1}^* + m} (T_{21} S_{h2}(t) I_{v1}(t)) \dots \quad (2.2) \\ & - \frac{\beta_h b}{N_{h3}^* + m} (T_{23} S_{h2}(t) I_{v3}(t)) - \mu_h S_{h2}(t) \end{aligned}$$

$$\begin{aligned} \frac{dS_{h3}(t)}{dt} = & \mu_h N_{h3} - \frac{\beta_h b}{N_{h3}^* + m} (T_{33} S_{h3}(t) I_{v3}(t)) - \frac{\beta_h b}{N_{h1}^* + m} (T_{31} S_{h3}(t) I_{v1}(t)) \dots \quad (2.3) \\ & - \frac{\beta_h b}{N_{h2}^* + m} (T_{32} S_{h3}(t) I_{v2}(t)) - \mu_h S_{h3}(t) \end{aligned}$$

$$\begin{aligned} \frac{dI_{h1}(t)}{dt} = & \frac{\beta_h b}{N_{h1}^* + m} (T_{11} S_{h1}(t) I_{v1}(t)) + \frac{\beta_h b}{N_{h2}^* + m} (T_{12} S_{h1}(t) I_{v2}(t)) \dots \quad (2.4) \\ & + \frac{\beta_h b}{N_{h3}^* + m} (T_{13} S_{h1}(t) I_{v3}(t)) - (\mu_h + \gamma_h) I_{h1}(t) \end{aligned}$$

$$\begin{aligned} \frac{dI_{h2}(t)}{dt} = & \frac{\beta_h b}{N_{h2}^* + m} (T_{22} S_{h2}(t) I_{v2}(t)) + \frac{\beta_h b}{N_{h1}^* + m} (T_{21} S_{h2}(t) I_{v1}(t)) \dots \quad (2.5) \\ & + \frac{\beta_h b}{N_{h3}^* + m} (T_{23} S_{h2}(t) I_{v3}(t)) - (\mu_h + \gamma_h) I_{h2}(t) \end{aligned}$$

$$\begin{aligned} \frac{dI_{h3}(t)}{dt} = & \frac{\beta_h b}{N_{h3}^* + m} (T_{33} S_{h3}(t) I_{v3}(t)) + \frac{\beta_h b}{N_{h1}^* + m} (T_{31} S_{h3}(t) I_{v1}(t)) \dots \quad (2.6) \\ & + \frac{\beta_h b}{N_{h2}^* + m} (T_{32} S_{h3}(t) I_{v2}(t)) - (\mu_h + \gamma_h) I_{h3}(t) \end{aligned}$$

$$\frac{dR_{h1}(t)}{dt} = \gamma_h I_{h1}(t) - \mu_h R_{h1}(t) \quad (2.7)$$

$$\frac{dR_{h2}(t)}{dt} = \gamma_h I_{h2}(t) - \mu_h R_{h2}(t) \quad (2.8)$$

$$\frac{dR_{h3}(t)}{dt} = \gamma_h I_{h3}(t) - \mu_h R_{h3}(t) \quad (2.9)$$

$$\frac{dS_{v1}(t)}{dt} = A_1 - \frac{\beta_v b}{N_{h1}^* + m} (T_{11}S_{v1}(t)I_{h1}(t) + T_{21}S_{v1}(t)I_{h2}(t) + T_{31}S_{v1}(t)I_{h3}(t)) - \mu_v S_{v1}(t) \quad (2.10)$$

$$\frac{dS_{v2}(t)}{dt} = A_2 - \frac{\beta_v b}{N_{h2}^* + m} (T_{22}S_{v2}(t)I_{h2}(t) + T_{12}S_{v2}(t)I_{h1}(t) + T_{32}S_{v2}(t)I_{h3}(t)) - \mu_v S_{v2}(t) \quad (2.11)$$

$$\frac{dS_{v3}(t)}{dt} = A_3 - \frac{\beta_v b}{N_{h3}^* + m} (T_{33}S_{v3}(t)I_{h3}(t) + T_{13}S_{v3}(t)I_{h1}(t) + T_{23}S_{v3}(t)I_{h2}(t)) - \mu_v S_{v3}(t) \quad (2.12)$$

$$\frac{dI_{v1}(t)}{dt} = \frac{\beta_v b}{N_{h1}^* + m} (T_{11}S_{v1}(t)I_{h1}(t) + T_{21}S_{v1}(t)I_{h2}(t) + T_{31}S_{v1}(t)I_{h3}(t)) - \mu_v I_{v1}(t) \quad (2.13)$$

$$\frac{dI_{v2}(t)}{dt} = \frac{\beta_v b}{N_{h2}^* + m} (T_{22}S_{v2}(t)I_{h2}(t) + T_{12}S_{v2}(t)I_{h1}(t) + T_{32}S_{v2}(t)I_{h3}(t)) - \mu_v I_{v2}(t) \quad (2.14)$$

$$\frac{dI_{v3}(t)}{dt} = \frac{\beta_v b}{N_{h3}^* + m} (T_{33}S_{v3}(t)I_{h3}(t) + T_{13}S_{v3}(t)I_{h1}(t) + T_{23}S_{v3}(t)I_{h2}(t)) - \mu_v I_{v3}(t) \quad (2.15)$$

N_{hi} and N_{vi} represent the human and vector population sizes in patch i . N_h is the total human population size, with N_{hi} representing the fixed (home) population of each patch i . T_{ij} is the fraction of the day that humans living in patch i spend visiting a different patch, j , during the day while interacting with mosquitoes in patch j . T_{ij} values are fractions of the day and the model is based on average populations based on these fractions. Humans are assumed to be in only one patch at a time,

$$T_{ii} = \left(1 - \sum_j T_{ij} \right), \quad (2.16)$$

and the number of humans in a particular patch was calculated using

$$N_{hj}^* = \sum_i T_{ij} N_{hi} \quad (2.17)$$

μ_h represents the per capita human birth and death rate assuming a constant population, and μ_v is a per capita mortality rate of the mosquitoes. γ_h is a constant recovery rate for the humans, b is the average number of bites per mosquito per day, β_h is the probability that the disease is transmitted from vector to human, β_v is the transmission probability from human to mosquito, and m is the number of alternative hosts available for mosquitoes to bite per patch (Esteva and Vargas, 1998). A_i represents the constant recruitment rate for mosquitoes in patch i .

Fixed parameter values used in equations (2.1)-(2.17) are presented in Table 2.1. As previously mentioned, the number of humans in each patch, N_{hi} , were based on communities in Sri Lanka. Patch 1 will represent Colombo ($N_{h1} = 325000$), Patch 2 will represent Sri Jayawardenepura Kotte ($N_{h2} = 110000$), and Patch 3 will represent Peliyagoda ($N_{h3} = 32000$). T_{ij} were based on generalized amounts of time spent working (Reagan et al., 2019).

TABLE 2.1. Parameter values used in equations (2.1)-(2.17).

Parameter	Symbol	Value	Source
Per capita human birth and death rate	μ_h	0.0000457	(Esteva and Vargas, 1998)
Per capita mortality rate in mosquitoes	μ_v	0.25	(Esteva and Vargas, 1998)
Average number of bites per mosquito per day	b	0.5	(Esteva and Vargas, 1998)
Transmission probability from vector to human	β_h	0.75	(Esteva and Vargas, 1998)
Transmission probability from human to vector	β_v	1	(Esteva and Vargas, 1998)
Number of alternative hosts available per patch	m	0	(Esteva and Vargas, 1998)
Human recovery rate	γ_h	0.1428	(Esteva and Vargas, 1998)
Recruitment rate for patch i	A_i	$\frac{1}{3}N_{vi}$	(Soewono and Supriatna, 2001)

TABLE 2.2. Visitation parameter values, T_{ij} , from Reagan et al. (2019).

		j TO		
		Colombo (Patch 1)	Sri Jayawardenepura Kotte (Patch 2)	Peliyagoda (Patch 3)
i FROM	Colombo (Patch 1)	1	0	0
	Sri Jayawardenepura Kotte (Patch 2)	0.05	0.95	0
	Peliyagoda (Patch 3)	0.08	0.04	0.88

The mosquito (or vector) population, N_{vi} , was assumed to be two times the human population within each patch, i.e., $2N_{hi} = N_{vi}$. This assumption was based on previously used ratios (around 4 to 1 (Hughes and Britton, 2013) and 2 to 1 (Kuniyoshi and dos Santos, 2017)).

The investigation in Reagan et al. (2019) set values for T_{ij} based on work expectations and using a 24-hour day. The assumptions for the visitation times are as follows:

- 12% of the time of the population of Peliyagoda is assumed to be spent in Colombo (8%) and in Sri Jayawardenepura Kotte (4%).
- 5% of the time of the population of Sri Jayawardenepura Kotte is spent in Colombo, and the population of Sri Jayawardenepura Kotte. is assumed to spend a negligible percentage of time in Peliyagoda.
- People in Colombo are assumed to stay in Colombo.

The resulting values for the various T_{ij} are presented in Table 2.2. The parameter values in Table 2.2 were considered baseline values for the current study.

3. Simulation Methods

The basic reproduction number, R_0 , was calculated using the model from Reagan et al. (2019) with various values of T_{ij} . R_0 was calculated using the method from Van den Driessche and

Watmough (2002) and described in Browne et al. (2014). Specific parameter values were used in generating R_0 , including population numbers for the particular communities being modeled. Additionally, parameter values presented in Section 2 were used to calculate R_0 .

A systematic investigation was performed, which generated R_0 under different visitation conditions. Values used for T_{ij} to generate R_0 are presented in tables with resulting R_0 values in Section 4. All simulations were run in Mathematica[®], Version 12.0. Values for T_{ij} in all simulations satisfied Equation (2.16), although some sets of visitation times may not be realistic in terms of time physically spent in multiple locations (considering the ability to move among the three areas, time for sleep, etc.) A wide-ranging set of semi-realistic values of T_{ij} were identified and used to generate R_0 . Based on the results using these visitation times, more focused investigations were performed. The investigation was based on the assumption that most individuals whose home was in Colombo would stay completely or primarily in Colombo (Patch 1). Hence, the more focused investigations considered changes in visitation for individuals in Sri Jayawardenepura Kotte (Patch 2) and Peliyagoda (Patch 3).

4. Results

Resulting values of R_0 are presented in Table 4.1–Table 4.7. Each table lists the values of T_{ij} used to generate R_0 . Table 4.1 presents the beginning overall simulations. Tables 4.2–4.4 present results when the visitation times were held as in Reagan et al. (2019) except in Patch 2. In Table 4.3, results are presented for simulations where T_{21} values were increased, representing an increase in visitation time from individuals in Patch 2 traveling to Patch 1. As T_{21} values increase, R_0 values increase. However, Table 4.4, which includes simulation results for individuals from Patch 2 spending higher visitation time in Patch 3, does not show a similar R_0 trend.

Tables 4.5–4.7 present results for when the visitation times remained as used in Reagan et al. (2019) for Patch 1 and Patch 2 but were changed for Patch 3. In all three tables, R_0 increases as visitation time outside Patch 3 increases. Both Colombo (Patch 1) and Sri Jayawardenepura Kotte (Patch 2) have significantly higher populations than Peliyagoda (Patch 3), and the trend of increasing R_0 with increasing visitation time in one patch is consistent with the results for Patch 2 if the patch being visited has a higher population.

A trend of increasing R_0 can be seen in Tables 4.3, 4.6, and 4.7, which all show results from simulations where visitation times are increasing in a patch that has a higher population than the one of the individual’s origin. A similar trend is not seen for Table 4.4, which shows simulation results for individuals in Patch 2 spending time in a patch of smaller population (Patch 3). Note that some values are unreasonable (95% of the time, individuals from Patch 2 will not be in Patch 1, for example) but are used to investigate general trends. The simulated R_0 results versus the visitation time in single patch of increased visitation are plotted in Figures 4.1(a)–4.2(b).

The calculated reproduction number, R_0 in Reagan et al. (2019) was 3.29. Using visitation times that reflect no visitation (i.e., $T_{ij} = 1$ when $i = j$ and $T_{ij} = 0$ when $i \neq j$), R_0 was calculated to be 3.241. All other resulting R_0 values as a part of this investigation were greater than 3.241.

5. Discussion and Conclusions

A previous study developed a model of dengue fever transmission incorporating human mobility among three communities in Sri Lanka (Reagan et al., 2019). The current study ran multiple simulations to generate the basic reproduction number, R_0 , using the model from Reagan et al. (2019)

TABLE 4.1. Wide-range investigation using semi-realistic values of T_{ij} to generate R_0 . All of the time values have been rounded to three decimal places except for those denoted with an asterisk (*). The first line is from the original simulation in Reagan et al. (2019), which is presented for reference.

T_{11}	T_{12}	T_{13}	T_{21}	T_{22}	T_{23}	T_{31}	T_{32}	T_{33}	R_0
1	0	0	0.05	0.95	0	0.08	0.04	0.88	3.290
1	0	0	0.375	0.675	0	0.25	0.125	0.625	3.469
1	0	0	0.375	0.675	0	0.08	0.04	0.88	3.412
1	0	0	0.05	0.95	0	0.25	0.125	0.625	3.375
1	0	0	0.37495*	0.62495*	0.0001*	0.375	0.625	0	3.463
0.958	0.042	0	0.05	0.95	0	0.08	0.04	0.88	3.283
0.917	0.083	0	0.05	0.95	0	0.08	0.04	0.88	3.293
0.958	0	0.042	0.05	0.95	0	0.08	0.04	0.88	3.253
0.917	0	0.083	0.05	0.95	0	0.08	0.04	0.88	3.265
1	0	0	0.042	0.958	0	0.08	0.04	0.88	3.288
1	0	0	0.083	0.917	0	0.08	0.04	0.88	3.298
1	0	0	0	0.958	0.042	0.08	0.04	0.88	3.290
1	0	0	0	0.917	0.083	0.08	0.04	0.88	3.284
1	0	0	0.05	0.95	0	0.042	0	0.958	3.268
1	0	0	0.05	0.95	0	0.083	0	0.917	3.275
1	0	0	0.05	0.95	0	0	0.042	0.958	3.271
1	0	0	0.05	0.95	0	0	0.083	0.958	3.292

TABLE 4.2. In-depth investigation on visitation from individuals in Sri Jayawardenepura Kotte (Patch 2). Between each case, the time that people from Patch 2 remained in Patch 2 was decreased by 0.1, and this difference was split and added between Patch 1 and 3. The first line is from the original simulation in Reagan et al. (2019), which is presented for reference.

T_{11}	T_{12}	T_{13}	T_{21}	T_{22}	T_{23}	T_{31}	T_{32}	T_{33}	R_0
1	0	0	0.05	0.95	0	0.08	0.04	0.88	3.290
1	0	0	0.1	0.85	0.05	0.08	0.04	0.88	3.310
1	0	0	0.15	0.75	0.1	0.08	0.04	0.88	3.357
1	0	0	0.2	0.65	0.15	0.08	0.04	0.88	3.399
1	0	0	0.25	0.55	0.2	0.08	0.04	0.88	3.438
1	0	0	0.3	0.45	0.25	0.08	0.04	0.88	3.472
1	0	0	0.35	0.35	0.3	0.08	0.04	0.88	3.499
1	0	0	0.4	0.25	0.35	0.08	0.04	0.88	3.518
1	0	0	0.45	0.15	0.4	0.08	0.04	0.88	3.516
1	0	0	0.5	0.05	0.45	0.08	0.04	0.88	3.465

TABLE 4.3. In-depth investigation on visitation from individuals in Sri Jayawardenepura Kotte (Patch 2). Between each case, the time that people from Patch 2 remained in Patch 2 was decreased by 0.1, and this difference was added to Patch 1. The first line is from the original simulation in Reagan et al. (2019), which is presented for reference.

T_{11}	T_{12}	T_{13}	T_{21}	T_{22}	T_{23}	T_{31}	T_{32}	T_{33}	R_0
1	0	0	0.05	0.95	0	0.08	0.04	0.88	3.290
1	0	0	0.15	0.85	0	0.08	0.04	0.88	3.320
1	0	0	0.25	0.75	0	0.08	0.04	0.88	3.359
1	0	0	0.35	0.65	0	0.08	0.04	0.88	3.401
1	0	0	0.45	0.55	0	0.08	0.04	0.88	3.443
1	0	0	0.55	0.45	0	0.08	0.04	0.88	3.484
1	0	0	0.65	0.35	0	0.08	0.04	0.88	3.523
1	0	0	0.75	0.25	0	0.08	0.04	0.88	3.559
1	0	0	0.85	0.15	0	0.08	0.04	0.88	3.597
1	0	0	0.95	0.05	0	0.08	0.04	0.88	3.763

TABLE 4.4. In-depth investigation on visitation from individuals in Sri Jayawardenepura Kotte (Patch 2). Between each case, the time that people from Patch 2 remained in Patch 2 was decreased by 0.1, and this difference was added to Patch 3. The first line is from the original simulation in Reagan et al. (2019), which is presented for reference.

T_{11}	T_{12}	T_{13}	T_{21}	T_{22}	T_{23}	T_{31}	T_{32}	T_{33}	R_0
1	0	0	0.05	0.95	0	0.08	0.04	0.88	3.290
1	0	0	0.05	0.85	0.1	0.08	0.04	0.88	3.311
1	0	0	0.05	0.75	0.2	0.08	0.04	0.88	3.352
1	0	0	0.05	0.65	0.3	0.08	0.04	0.88	3.383
1	0	0	0.05	0.55	0.4	0.08	0.04	0.88	3.405
1	0	0	0.05	0.45	0.5	0.08	0.04	0.88	3.418
1	0	0	0.05	0.35	0.6	0.08	0.04	0.88	3.422
1	0	0	0.05	0.25	0.7	0.08	0.04	0.88	3.414
1	0	0	0.05	0.15	0.8	0.08	0.04	0.88	3.378
1	0	0	0.05	0.05	0.9	0.08	0.04	0.88	3.278

with various visitation times. The reproduction numbers from this analysis were between 3.253 and 3.763. The smallest generated R_0 resulted from individuals staying in their home communities, or patches, which supports the idea that population movement increases rates of infection.

Simulation results suggest that the reproduction number increases with additional population movement, especially if the movement is from individuals from a smaller population to a larger population. This increase is likely due to susceptible humans coming into contact with a larger population of (potentially) infected individuals. Simulation results for individuals moving from

TABLE 4.5. In-depth investigation on visitation from individuals in Peliyagoda (Patch 3). Between each case, the time that people from Patch 3 remained in Patch 3 was decreased by 0.1, and this difference was split and added between Patch 1 and 2. The first line is from the original simulation in Reagan et al. (2019), which is presented for reference.

T_{11}	T_{12}	T_{13}	T_{21}	T_{22}	T_{23}	T_{31}	T_{32}	T_{33}	R_0
1	0	0	0.05	0.95	0	0.08	0.04	0.88	3.290
1	0	0	0.05	0.95	0	0.13	0.09	0.78	3.325
1	0	0	0.05	0.95	0	0.18	0.14	0.68	3.361
1	0	0	0.05	0.95	0	0.23	0.19	0.58	3.398
1	0	0	0.05	0.95	0	0.28	0.24	0.48	3.434
1	0	0	0.05	0.95	0	0.33	0.29	0.38	3.470
1	0	0	0.05	0.95	0	0.38	0.34	0.28	3.506
1	0	0	0.05	0.95	0	0.43	0.39	0.18	3.542
1	0	0	0.05	0.95	0	0.48	0.44	0.08	3.578

TABLE 4.6. In-depth investigation on visitation from individuals in Peliyagoda (Patch 3). Between each case, the time that people from Patch 3 remained in Patch 3 was decreased by 0.1, and this difference was added to Patch 1. The first line is from the original simulation in Reagan et al. (2019), which is presented for reference.

T_{11}	T_{12}	T_{13}	T_{21}	T_{22}	T_{23}	T_{31}	T_{32}	T_{33}	R_0
1	0	0	0.05	0.95	0	0.08	0.04	0.88	3.290
1	0	0	0.05	0.95	0	0.18	0.04	0.78	3.318
1	0	0	0.05	0.95	0	0.28	0.04	0.68	3.349
1	0	0	0.05	0.95	0	0.38	0.04	0.58	3.381
1	0	0	0.05	0.95	0	0.48	0.04	0.48	3.416
1	0	0	0.05	0.95	0	0.58	0.04	0.38	3.450
1	0	0	0.05	0.95	0	0.68	0.04	0.28	3.486
1	0	0	0.05	0.95	0	0.78	0.04	0.18	3.521
1	0	0	0.05	0.95	0	0.88	0.04	0.08	3.557

their patch of origin to a patch of higher population showed a trend of increasing R_0 with increasing visitation time in the patch with more people. However, values for the visitation time were used for some simulations that would exceed typical movement for employment or day-to-day activities.

Many of the population values are held as constants in the model, such as overall and patch population sizes. More sophisticated structures for modeling the populations in the individuals in each patch could strengthen the predictions. Additionally, no climate considerations are incorporated in the model nor have infections from multiple serotypes. Refinements to the model could help identify how to target intervention methods (regionally) to best combat disease spread. Additionally, different prevention methods may be more effective in urban settings than rural ones (and

TABLE 4.7. In-depth investigation on visitation from individuals in Peliyagoda (Patch 3). Between each case, the time that people from Patch 3 remained in Patch 3 was decreased by 0.1, and this difference was added to Patch 2. The first line is from the original simulation in Reagan et al. (2019), which is presented for reference.

T_{11}	T_{12}	T_{13}	T_{21}	T_{22}	T_{23}	T_{31}	T_{32}	T_{33}	R_0
1	0	0	0.05	0.95	0	0.08	0.04	0.88	3.290
1	0	0	0.05	0.95	0	0.08	0.14	0.78	3.336
1	0	0	0.05	0.95	0	0.08	0.24	0.68	3.385
1	0	0	0.05	0.95	0	0.08	0.34	0.58	3.435
1	0	0	0.05	0.95	0	0.08	0.44	0.48	3.485
1	0	0	0.05	0.95	0	0.08	0.54	0.38	3.534
1	0	0	0.05	0.95	0	0.08	0.64	0.28	3.583
1	0	0	0.05	0.95	0	0.08	0.74	0.18	3.631
1	0	0	0.05	0.95	0	0.08	0.84	0.08	3.678

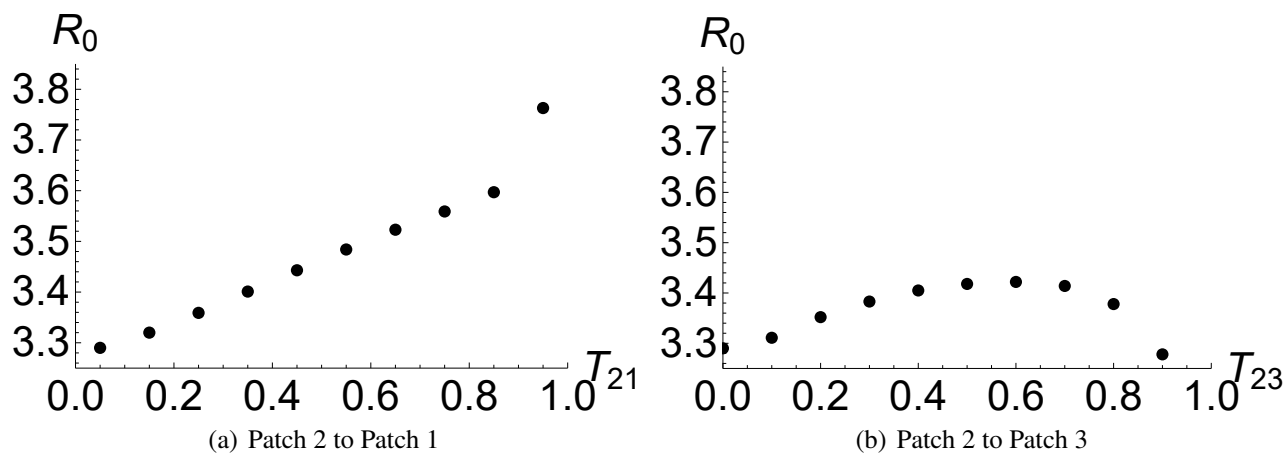


FIGURE 4.1. Predicted changes in R_0 resulting from increased visitation time from individuals in Sri Jayawardenepura Kotte (Patch 2) to another patch.

vice versa), and tailoring community-specific strategies may have a greater impact than a single intervention method.

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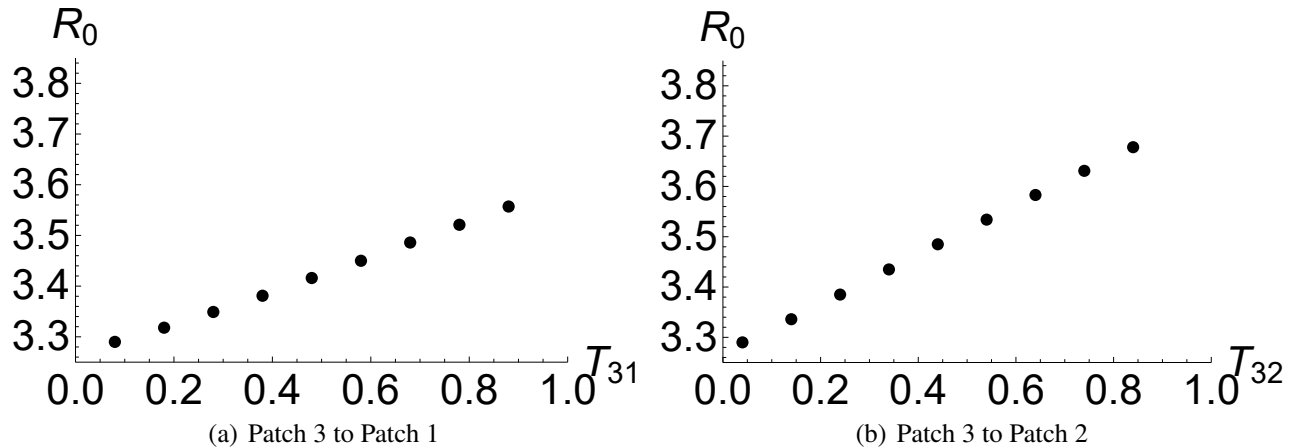


FIGURE 4.2. Predicted changes in R_0 resulting from increased visitation time from individuals in Peliyagoda (Patch 3) to another patch.

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