A Dynamical System Model of Dengue Transmission for Rio de Janeiro, Brazil

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A Dynamical System Model of Dengue Transmission for Rio de Janeiro, Brazil

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Abstract
The dengue virus is a serious concern in many parts of the world, including Brazil. As data indicates, a prominent vector for dengue is the mosquito \textit{Aedes aegypti}. By using the dengue incidence records from the Brazilian SINAN database, we estimate the population of \textit{A. aegypti} within the city of Rio de Janeiro. Using historical climate data for Rio de Janeiro and the computed population estimates, we extend an existing model for the population dynamics of mosquitoes to incorporate precipitation in aquatic stages of development for \textit{A. aegypti}.

Keywords: Dengue Transmission, \textit{Aedes aegypti}, Rio de Janeiro, Sensitivity Analysis, Vertical Transmission

1 Introduction

Dengue virus is of increasing concern globally. The dengue virus is transmitted through infected mosquitoes—primarily of the species \textit{Aedes aegypti}. Global warming has been increasing the habitable regions for \textit{A. aegypti}, thereby increasing the global areas at risk of dengue outbreaks [4, 23].

Although most dengue cases are sub-clinical, severe dengue cases can often result in significant health complications or death. Vaccination against the dengue virus offers only partial protection. For example, there are four dengue serotypes, and vaccination against any single serotype has led to increased risk of mortality in the case of infection by another serotype. As a result, effective options for vaccination against the dengue virus have only recently been developed [7, 23].

The main vector of dengue is the \textit{Aedes} family of mosquito, and \textit{A. aegypti} specifically. Dengue transmission occurs through the female mosquito population. An infected female mosquito that bites an uninfected human may infect that human. Furthermore, an infected human that has been bitten by an uninfected female mosquito may infect the biting mosquito [4, 7, 23].

The main vector of dengue is the \textit{Aedes} family of mosquito, and \textit{A. aegypti} specifically. Dengue transmission occurs through the female mosquito population. An infected female mosquito that bites an uninfected human may infect that human. Furthermore, an infected human that has been bitten by an uninfected female mosquito may infect the biting mosquito [4, 7, 23].

Given the key role played by \textit{A. aegypti} in spreading dengue, refinements to \textit{A. aegypti} population models improve our ability to predict and to prepare for dengue outbreaks. As to be expected, there is a history of dynamic system models for mosquito populations, especially in connection to dengue transmission and how these models have evolved over time [11, 22].

We have restricted our approach to describing two specific efforts to create dynamical system models of mosquito populations. One study outlined a general mosquito population lifecycle for the \textit{Anopholes} mosquitoes in southern France in the presence and absence of certain control strategies [3]. A different study utilized a simplified model for the \textit{A. aegypti} lifecycle to compare dengue transmission between dengue population models that involve infection with Wolbachia, and those that do not [14]. The model that we have developed was motivated by both of these approaches.

The main study that influenced the development of our model incorporated a relatively general model of the mosquito lifecycle into their two-state model of mosquito populations [3]. Their model involves three aquatic stages: egg, larva, pupa, and four adult stages of the mosquito: emerging adult, host-seeking, gravid (the egg developmental stage), and ovipositing (the stage where a mosquito moves between different oviposition sites to lay eggs). Their model is stated to require some adaptation for other mosquito genuses, because their subject mosquito genus, \textit{Anopholes}, has certain features that may not be present in other mosquitoes. Most importantly, the \textit{Anopholes} mosquito enters diapause, while \textit{A. aegypti} does not [3]. As a result of this difference, we do not need to use a two-state model to study the effects of diapause on the mosquito population; we only need to consider one state for our dynamical system.

The other study that influenced our model's development involved a two-stage mosquito lifecycle model for \textit{A. aegypti} that distinguishes between only the aquatic
and adult stage of life \[14\]. This study approximated the impact of seasonally varying environmental factors, such as temperature by using a periodic mortality function in the adult population dynamics. It is important to note that because this model does not explicitly consider the impact of temperature or precipitation on population dynamics, it is less informative in regards to how changes in environmental variables impact population dynamics and thereby dengue incidence.

In modelling the transmission of dengue, \[14\] used an SEI model within the adult stage of mosquitoes, and an SEIR model in the human population. They constrain themselves to modelling only a single serotype of dengue, and do not consider the contribution of vertical transmission of dengue, when an infected mosquito passes dengue to the next generation. These are common choices in dengue transmission models.

Although it is not common in models of \(A.\ aegypti\) to incorporate precipitation, some research identifies it as an important determinant of carrying capacity for the larval stage within urban/suburban environments \[12\]. The key study found that rainfall in poor suburban environments was shown to be effective at generating more oviposition sites for \(A.\ aegypti\) and led to greater productivity of existing oviposition sites \[12\]. We interpret these results to mean that in a large urban/suburban environment, rainfall increases the environmental carrying capacity of the aquatic stages of \(A.\ aegypti\).

Another largely ignored feature of dengue transmission is vertical transmission. A meta analysis of global research regarding vertical transmission of dengue was conducted and found significant evidence that vertical transmission of dengue occurs in \(A.\ aegypti\) \[9\]. A specific study regarding vertical transmission of dengue in \(A.\ aegypti\) in South and Central America had been conducted and found that the vertical transmission rate of \(A.\ aegypti\) is about 8 percent \[6\].

We develop a dynamical system model of dengue transmission which is motivated by the models in \[3\] and \[14\]. Our system of dengue transmission consists of a seven-stage mosquito lifecycle model, paired with an SEIR human model. Our approach aims to more precisely model the different stages of life of the mosquito than in \[14\]. This improves the validity of our model by allowing it to account for a broad range of sources of variation, such as the impact of precipitation on carrying capacity. Compared to the model presented by \[3\], our model incorporates the presence of dengue and is adapted to the \(A.\ aegypti\) species rather than the genus \textit{Anopholes}. Additionally, our model incorporates vertical transmission of dengue within \(A.\ aegypti\).

\[\frac{dE_{i}}{dt} = \beta (A_{o,s} + A_{o,e} + (1 - \rho)A_{o,i}) - (\mu_{E} + f_{E})E_{s}\]

\[\frac{dL_{i}}{dt} = f_{E}E_{s} - \left( m_{L}(1 + (L_{s} + L_{i})/\kappa_{L}) + f_{L} \right) L_{s}\]

\[\frac{dP_{s}}{dt} = f_{L}L_{s} - (m_{P} + f_{P})P_{s}\]

\[\frac{dP_{i}}{dt} = \beta P_{a,i} - (\mu_{E} + f_{E})E_{i}\]

\[\frac{dL_{i}}{dt} = f_{E}E_{i} - \left( m_{L}(1 + (L_{s} + L_{i})/\kappa_{L}) + f_{L} \right) L_{i}\]

\[\frac{dP_{i}}{dt} = f_{L}L_{i} - (m_{P} + f_{P})P_{i}\]

\[\frac{dA_{m,s}}{dt} = f_{P}P_{s}\sigma \exp\left(-\mu_{em}(1 + (P_{s} + P_{i})/\kappa_{P})\right) - (m_{A} + \gamma_{Aem})A_{m,s}\]

\[\frac{dA_{o,s}}{dt} = \gamma_{Aem}A_{m,s} + \gamma_{Ao}A_{o,s} - (m_{A} + b)A_{h,s}\]

\[\frac{dA_{o,e}}{dt} = b(I_{p}(1 - d_{tp}) + (1 - I_{p}))A_{h,s} - (m_{A} + f_{Ag})A_{g,s}\]

\[\frac{dA_{m,e}}{dt} = f_{Ag}A_{g,s} - (m_{A} + \gamma_{Ag})A_{m,e}\]

\[\frac{dA_{h,e}}{dt} = \gamma_{Ag}(1 - d_{m,i})A_{o,e} - (m_{A} + b)A_{h,e}\]

\[\frac{dA_{h,i}}{dt} = bA_{h,e}(1 - d_{m,i}) + bd_{tp}A_{h,i} - (m_{A} + f_{Ag})A_{g,e}\]

\[\frac{dA_{m,i}}{dt} = f_{Ag}(1 - d_{m,i})A_{g,e} - (m_{A} + \gamma_{Ae})A_{m,i}\]

\[\frac{dA_{o,i}}{dt} = f_{P}P_{\sigma}\exp\left(-\mu_{em}(1 + (P_{s} + P_{i})/\kappa_{P})\right) - (m_{A} + \gamma_{Aem})A_{m,i}\]

\[\frac{dA_{m,i}}{dt} = \gamma_{Aem}A_{m,i} + \gamma_{Ao}(A_{o,i} + A_{o,e}) + bd_{m,i}A_{h,e} - (m_{A} + b)A_{h,i}\]

\[\frac{dA_{h,i}}{dt} = b(A_{h,i} + d_{m,i}A_{h,e}) - (m_{A} + f_{Ag})A_{g,i}\]

\[\frac{dA_{o,i}}{dt} = f_{Ag}(A_{g,i} + d_{m,i}A_{g,e}) - (m_{A} + \gamma_{Ag})A_{m,i}\]

\[\frac{dH_{e}}{dt} = bd_{tp}A_{h,i}H_{e} - \gamma_{H}H_{e}\]

\[\frac{dH_{i}}{dt} = \gamma_{H}H_{e} - rH_{i}\]

\[\frac{dH_{i}}{dt} = rH_{i}\]

Our mosquito lifecycle model generally follows that developed in \[3\]. For example, we consider 3 aquatic stages:
We use \[ f \] in [3], which we describe later at the end of this section. We represent the various stages of susceptible, exposed, and infected mosquitoes by additional subscripts \( s, e, \) and \( i \), respectively. It is worth noticing that while the entire lifecycle of the mosquito is present in the susceptible and infected stages, exposed mosquitoes only exist in the host seeking, gravid, and ovipositing adult stage. This is because we do not model exposure to dengue as being vertically transmittable, and exposure can only occur through blood feeding which occurs in the host-seeking stage. Because we include vertical transmission of dengue in our model, we must consider the aquatic stage for infected mosquitoes. To our knowledge, this is not common in models of dengue transmission.

It should also be noted that the differential equations that represent the human population are computed as a percentage of the total human population. Meanwhile, the differential equations for the mosquito equations represent the population levels.

Table 1 presents all of the relevant parameters to our model. It should be noted that a significant number of parameters are derived from parameters for the \textit{Anopholes} genus of mosquito, and therefore are likely accurate only within magnitude to the actual parameters for \textit{A. aegypti}.

The only parameter that specifically warrants explanation is \( TDD_E \). The value of 42 is computed from the assumption that a typical daily temperature in a tropical climate is 21°C and the finding of [21] that \textit{A. aegypti} eggs generally develop in 2 days in a tropical climate. This estimate is therefore fairly coarse.

There are four forms of temperature- or precipitation-dependent functions within the system of equations. The \( f_E, f_{A_s}, m_L, \) and \( m_P \) terms are taken from [3], and represent temperature-dependent transition and mortal-

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \kappa_L )</td>
<td>Precipitation-dependent carrying capacity for the larva and pupa</td>
<td>( 2000148 )</td>
</tr>
<tr>
<td>( \kappa_P )</td>
<td>Precipitation-dependent carrying capacity for the adult mosquitoes</td>
<td>( 6 \times 10^{-4} )</td>
</tr>
<tr>
<td>( f_L(T) )</td>
<td>Biting rate function</td>
<td>( \frac{f_P(T)}{4} )</td>
</tr>
<tr>
<td>( m_L(T) )</td>
<td>Egg laying rate</td>
<td>( e^{-T/2} + \mu_L )</td>
</tr>
<tr>
<td>( m_P(T) )</td>
<td>Pupae hatching rate</td>
<td>( e^{-T/2} + \mu_P )</td>
</tr>
</tbody>
</table>
| \( m_A(T) \) | Adult biting rate | \( \begin{cases} 
0.1 - 0.00667T & \text{if } m_A(T) \geq \mu_A \\
0.000148T^2 & \text{if } m_A(T) < \mu_A 
\end{cases} \) |

The third form of climate-dependent function is found in the models \( \kappa_L \) and \( \kappa_P \). These models represent the variation of the carrying capacity for the larva and pupa aquatic stages based upon precipitation. We assume a simple linear model for each case.

\[
\kappa_L(R) = \alpha_{L,0} + \alpha_{L,1}R \\
\kappa_P(R) = \alpha_{P,0} + \alpha_{P,1}R
\]

The fourth temperature-dependent function present is the biting rate function \( b(T) \). Previous studies such as [21] have identified that biting frequency increases with temperature. The simplest model for such a phenomena is a simple linear model for each case.

\[
b(T) = b_0 + b_1T
\]

The \( \alpha_{X,0}, \alpha_{X,1}, b_0, \) and \( b_1 \) parameter values are not known, so we consider our model with a range of parameter values. The ranges we consider for these parameters are given in Table 2. Table 2 also depicts the results of a global sensitivity analysis across many other uncertain or unknown parameters.

2.1 Initial Conditions and Simulations

The model was simulated by implementing a numerical method in python. The numerical method that was chosen was Euler’s Method with a step size of one-tenth. We started the simulation with 500,000 susceptible host-seeking adult mosquitoes, 1000 infected host-seeking

![Figure 1: Human-mosquito model flow chart.](image-url)
Dynamical System Model of Dengue Transmission
Schmidt, Whipple, Chellamuthu, Xie

(a) Daily average temperature. (b) Mean interpolated daily precipitation.

Figure 2: Climate data used in model.

Table 1: Parameter values used for the human-mosquito model and simulation.

<table>
<thead>
<tr>
<th>Constant</th>
<th>Description</th>
<th>Value</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\beta$</td>
<td>Number of eggs laid by ovipositing females (per females)</td>
<td>about 200</td>
<td>[17]</td>
</tr>
<tr>
<td>$\rho$</td>
<td>Probability of vertical transmission</td>
<td>0.078</td>
<td>[6]</td>
</tr>
<tr>
<td>$\sigma$</td>
<td>Sex-ratio at the emergence</td>
<td>0.5</td>
<td>[5]</td>
</tr>
<tr>
<td>$d_{tp}$</td>
<td>Dengue transmission probability per bite</td>
<td>0.216</td>
<td>[14]</td>
</tr>
<tr>
<td>$d_{m,i}$</td>
<td>Dengue incubation rate in mosquitoes (day$^{-1}$)</td>
<td>0.1</td>
<td>[14]</td>
</tr>
<tr>
<td>$r$</td>
<td>Recovery rate from dengue, Humans</td>
<td>1/5</td>
<td>[14]</td>
</tr>
<tr>
<td>$\mu_E$</td>
<td>Egg mortality rate (day$^{-1}$)</td>
<td>0.1</td>
<td>[11] &amp; educated guess</td>
</tr>
<tr>
<td>$\mu_L$</td>
<td>Minimum larva mortality rate (day$^{-1}$)</td>
<td>0.08</td>
<td>[11] &amp; educated guess</td>
</tr>
<tr>
<td>$\mu_P$</td>
<td>Minimum pupa mortality rate (day$^{-1}$)</td>
<td>0.1</td>
<td>[11] &amp; educated guess</td>
</tr>
<tr>
<td>$\mu_{em}$</td>
<td>Mortality rate during adult emergence (day$^{-1}$)</td>
<td>0.17</td>
<td>[16]</td>
</tr>
<tr>
<td>$\mu_A$</td>
<td>Minimum adult mortality rate (day$^{-1}$)</td>
<td>1/30</td>
<td>[11] &amp; educated guess</td>
</tr>
<tr>
<td>$T_E$</td>
<td>Minimal temperature needed for egg development ($^\circ$C)</td>
<td>16</td>
<td>[18]</td>
</tr>
<tr>
<td>$TDD_E$</td>
<td>Total number of degree-days necessary for egg development ($^\circ$C)</td>
<td>about 42</td>
<td>[24]</td>
</tr>
<tr>
<td>$\gamma_{Aem}$</td>
<td>Development rate of emerging adults (day$^{-1}$)</td>
<td>0.25</td>
<td>[11]</td>
</tr>
<tr>
<td>$\gamma_{Ao}$</td>
<td>Transition rate from oviposition site-seeking to host-seeking adults (day$^{-1}$)</td>
<td>2</td>
<td>[11] &amp; educated guess</td>
</tr>
<tr>
<td>$\gamma_H$</td>
<td>Progression rate from exposed to infectious human</td>
<td>1/5.5</td>
<td>[14]</td>
</tr>
<tr>
<td>$T_{Ag}$</td>
<td>Minimal temperature needed for egg maturation ($^\circ$C)</td>
<td>9.9</td>
<td>[11]</td>
</tr>
<tr>
<td>$TDD_{Ag}$</td>
<td>Total number of degree-days necessary for egg maturation ($^\circ$C)</td>
<td>36</td>
<td>[11]</td>
</tr>
</tbody>
</table>
Figure 3: Susceptible mosquitoes.

Figure 4: Infected mosquitoes.
adult mosquitoes and 16 million susceptible humans. The number of initial host seeking mosquitoes was chosen to be large enough to let the simulation stabilize itself after one year. Meanwhile the initial amount of susceptible humans was based off of population data of the state of Rio de Janeiro, Brazil. Six years were simulated under these initial conditions. It is noted that decreasing the step size did not yield significant differences in the results, thus in order to cut down on computing power, a step size of one-tenth felt sufficient for our purposes.

We used climate data depicted in Figure 2 for the simulations. The temperature data depicted in Figure 2 was assembled from [19]. The precipitation data depicted in Figure 2 was sourced from [19]. We note that we could not find daily precipitation data for Rio de Janeiro. We resorted to interpolating daily precipitation data as the monthly average precipitation computed from monthly climate data (from SINAN disease reporting system), generates predictions shown in Figure 3. We focus our fitted model around the outbreak years 2015 and 2016 for computational feasibility. We provide a brief warmup and cooldown period in order to allow the population model to stabilize, and to prevent the model from only fitting the outbreaks.

We notice that our model partially captures the outbreak phenomena. However, the peaks and troughs are not entirely represented. It is likely that our model does not fully capture these phenomena possibly because it fails to account for the effect of population density in the transmission of dengue. It has been noted that highly populated and poor urban regions accelerate the spread of dengue [12]. Our model does not account for this concentration effects.

Figure 9 compares the predictive performance of our model using precipitation varying carrying capacity with a constant carrying capacity model. The fixed carrying capacity model is obtained by setting $\alpha_{E,1} = 0$ and $\alpha_{P,1} = 0$. We notice that the variable carrying capacity term better captures the outbreak dynamics in the observed data.

3 Results

3.1 Mosquitoes

From our simulation, we can see that the mosquito population follows an annual cycle for population highs and lows. From Figure 3, we observe for each yearly maximum that there are approximately $9 \times 10^{11}$ susceptible host-seeking mosquitoes. Meanwhile the average low is $2 \times 10^{11}$ susceptible host-seeking mosquitoes. This conforms with our knowledge that there are mosquitoes year-round in Rio de Janeiro, Brazil.

The susceptible aquatic mosquitoes population follows a nearly identical sinusoidal pattern. We can observe that at any given peak there are approximately 300–400 times more susceptible eggs than there are susceptible ovipositing mosquitoes. All of this can be further observed in Figure 5.

The infected mosquitoes population also follows a yearly cycle. There is an approximate average of 4000 infected host-seeking mosquitoes for each peak. Similarly, there is an average of only 1500 infected host-seeking mosquitoes for each yearly base. This can be observed in Figure 4. This number of infected host-seeking mosquitoes could be a reasonable estimation because our data suggests that the amount of infected humans at any given time is around the same magnitude. Figure 4 showcases the inclusion of vertical transmission in our model.

Figures 5 and 6 roughly depict the impact of 10 and 50 percent uncertainty in the egg mortality parameter $\mu_E$ on population of susceptible eggs and host seeking susceptible mosquitoes. We notice that the resulting change in the number of host-seeking susceptible mosquitoes is dramatic. The peak population of host seeking susceptible mosquitoes is roughly doubled by a decrease in $\mu_E$ by 50 percent. These plots suggest that the parameter $\mu_E$—which is not well established in the literature—should be precisely measured in order to better model the population dynamics of A. aegypti.

Figures 7 and 8 roughly depict the impact of 10 and 50 percent uncertainty in the ovipositing transition rate parameter $\gamma_{Ao}$ on the population of susceptible eggs and total host seeking susceptible mosquitoes. We notice that the resulting change in the number of host seeking susceptible mosquitoes is less dramatic than was observed for the case of $\mu_E$. The peak population of host seeking susceptible mosquitoes is increased by about 25 percent as a result of a decrease in $\mu_E$ by 50 percent.

3.2 Humans

Our model, fitted to Rio de Janeiro observed dengue incidence data (from SINAN disease reporting system), generates predictions shown in Figure 3. We focus our fitted model around the outbreak years 2015 and 2016 for computational feasibility. We provide a brief warmup and cooldown period in order to allow the population model to stabilize, and to prevent the model from only fitting the outbreaks.

We notice that our model partially captures the outbreak phenomena. However, the peaks and troughs are not entirely represented. It is likely that our model does not fully capture these phenomena possibly because it fails to account for the effect of population density in the transmission of dengue. It has been noted that highly populated and poor urban regions accelerate the spread of dengue [12]. Our model does not account for this concentration effects.

Sobol global sensitivity analysis identifies which model parameters explain the greatest proportion of variation in model output over a given domain of possible param-
Figure 5: Impact of 10 percent deviation in egg mortality.

Figure 6: Impact of 50 percent deviation in egg mortality.

Figure 7: Impact of 10 percent deviation in ovipositing transition rate.
Figure 8: Impact of 50 percent deviation in ovipositing transition rate.

(a) Susceptible eggs sensitivity.  
(b) Host seeking susceptible mosquitoes.

Figure 9: Impact of 50 percent deviation in ovipositing transition rate.

(a) Fixed carrying capacity.  
(b) Variable carrying capacity.
Table 2: The total sensitivity indices computed by Sobol sensitivity analysis. The range column indicates the range of values over which the global search was conducted. The ** and * next to constant terms indicate parameters deemed very sensitive and somewhat sensitive, respectively.

<table>
<thead>
<tr>
<th>Constant</th>
<th>Description</th>
<th>Total Sensitivity</th>
<th>95 Percent CI (±)</th>
<th>Search Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\alpha_{L,0}$</td>
<td>$\kappa_L$ parameter 1</td>
<td>$1.87 \times 10^{-13}$</td>
<td>$1.35 \times 10^{-4}$</td>
<td>[1e9, 1e15]</td>
</tr>
<tr>
<td>$\alpha_{L,1}$</td>
<td>$\kappa_L$ parameter 2</td>
<td>$9.18 \times 10^{-14}$</td>
<td>$1.92 \times 10^{-6}$</td>
<td>[1e9, 1e15]</td>
</tr>
<tr>
<td>$\alpha_{P,0}$</td>
<td>$\kappa_P$ parameter 1</td>
<td>$9.13 \times 10^{-15}$</td>
<td>$7.2 \times 10^{-7}$</td>
<td>[1e9, 1e15]</td>
</tr>
<tr>
<td>$\alpha_{P,1}$</td>
<td>$\kappa_P$ parameter 2</td>
<td>$1.35 \times 10^{-15}$</td>
<td>$2.74 \times 10^{-7}$</td>
<td>[1e9, 1e15]</td>
</tr>
<tr>
<td>$A_{h,s}$ **</td>
<td>Initial $A_{h,s}$ population</td>
<td>$8.64 \times 10^{-7}$</td>
<td>$17.53$</td>
<td>[1e3, 1e9]</td>
</tr>
<tr>
<td>$b_0$ **</td>
<td>$b$ parameter 1</td>
<td>$1.06 \times 10^{-7}$</td>
<td>$10371.15$</td>
<td>[0.001, 1]</td>
</tr>
<tr>
<td>$b_1$ **</td>
<td>$b$ parameter 2</td>
<td>$1.06 \times 10^{-7}$</td>
<td>$0.859882$</td>
<td>[0.001, 1]</td>
</tr>
<tr>
<td>$\mu_E$ *</td>
<td>Egg mortality rate</td>
<td>$1.39 \times 10^{-10}$</td>
<td>$0.027654$</td>
<td>[0.01, 3]</td>
</tr>
<tr>
<td>$\mu_L$ *</td>
<td>Larva mortality rate</td>
<td>$1.83 \times 10^{-10}$</td>
<td>$0.00757$</td>
<td>[0.01, 3]</td>
</tr>
<tr>
<td>$\mu_P$ *</td>
<td>Pupa mortality rate</td>
<td>$2.42 \times 10^{-10}$</td>
<td>$0.038703$</td>
<td>[0.01, 3]</td>
</tr>
<tr>
<td>$\mu_{EM}$ *</td>
<td>Emerging adult mortality rate</td>
<td>$1.93 \times 10^{-9}$</td>
<td>$0.015903$</td>
<td>[0.01, 3]</td>
</tr>
<tr>
<td>$\gamma_{Aem}$ *</td>
<td>Emerging adult development rate</td>
<td>$2.14 \times 10^{-10}$</td>
<td>$0.003008$</td>
<td>[0.01, 0.4]</td>
</tr>
<tr>
<td>$\gamma_{Ao}$ **</td>
<td>Transition rate from ovipositing to host seeking</td>
<td>$9.75 \times 10^{-4}$</td>
<td>$171354.9$</td>
<td>[0.01, 2]</td>
</tr>
</tbody>
</table>

It would be strange if this were not the case, as the behavior of *A. aegypti* is known to be important in determining dengue.

### 4 Discussion and Conclusions

In this analysis we have developed a temperature driven multi-compartmental dynamical system model and have applied this model to the region of Rio de Janeiro, Brazil. The main key feature of our model is that it factors in the effect of precipitation on the larva and pupa aquatic stages. Additionally, this model takes into account the effect of vertical transmission between infected mosquitoes and their offspring. Furthermore, this model assumes that half of all mosquitoes that enter adulthood will be female mosquitoes. It is also assumed that there are no infected humans as an initial condition.

We apply our model to the Rio de Janeiro region of Brazil, and find that it fits the observed infected data moderately well. Poor performance in predicting the outbreaks of 2014 and 2015, as well as in modelling the gap between them, might be explained by recognizing the role of the spatial distribution of populations in driving and dampening outbreaks. It is unlikely that our model can be readily adapted to account for such spatial effects.

Additionally, our model is limited by the availability of existing estimates of the *A. aegypti* lifecycle parameters. There is significant uncertainty in all parameter estimates we found. However, variables such as the total degree day requirements—which are integral to many transition functions we used—were not found in our re-
view of the literature. The lack of availability of valid estimates means that models such as ours are of limited precision.

It is worth noting that the dependence on valid parameter estimates is a limitation of most dynamical system models of complex biological phenomena. Such models often involve a large number of parameters which cannot be cheaply measured. In order to determine which parameters should be measured first, we conducted a sensitivity analysis of model parameters by the Sobol method.

The sensitivity analysis we conducted indicates that our model is generally sensitive to $A. aegypti$ lifecycle parameters, and that of those parameters the most sensitive are $\gamma_{Ao}$, $b_0$, $A_{h,s}$, and $b_1$. These parameters describe the transition rate from ovipositing to host seeking, the relation between biting rate and temperature, and the initial mosquito population within the region of interest. In the context of the broadly understood dynamics of dengue, it makes sense that these parameters are highly sensitive as they relate fairly directly to the states and rates at which dengue is transmitted between humans and mosquitoes. We hope that in time basic biological research generates more and better estimates of $A. aegypti$ lifecycle parameters, though we understand the challenges involved in doing so.

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Author Contributions

Benjamin Whipple, Gregory Schmidt, Vinodh Chellamuthu, and Xiaoxia Xie designed the model and analyzed model outputs. Benjamin Whipple and Gregory Schmidt implemented the model using MatLab/Python and did the literature review. Benjamin Whipple conducted the sensitivity analysis.

References


