ARTICLE

Dengue incidence in Baguio City: An application of a compartmental model to Baguio City data for years 2011 to 2022

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ABSTRACT

Baguio City's dengue incidence data for years 2011 to 2022 exhibit three-year cycles of increasing amplitudes. However, current epidemiological models do not capture this behavior. This study modifies the dengue disease model presented in the paper by de los Reyes and Escaner (2018), introducing two key modifications: (1) incorporating logistic growth in the human population and (2) including seasonality in mosquito population growth. With the observed multi-year cycles for disease progression in the city, the model is calibrated to Baguio data to estimate epidemiologically important parameters such as transition rate from susceptible to hospitalized humans, vector biting rate, transmission probability from human to vector and vector to human. A constrained-ODE optimization routine is used to determine model parameter values that produce model curves capturing the dynamics of dengue incidence in Baguio. Using these estimated parameters, simulations are presented with variations observed over cycles each spanning 3 years. Reproduction numbers are calculated, with values ranging from 1.39 (2011–2013) to 1.67 (2014–2016). Sensitivity analysis and parameter bootstrapping are also performed to determine confidence intervals. Results of the study yield city-specific parameter estimates which can guide policy makers in forecasting, in evaluating the impact of interventions, as well as in making decisions towards optimizing the timing and intensity of vector-control measures.

INTRODUCTION

Dengue is a human viral infection primarily transmitted to humans by the bite of female mosquitoes in the *Aedes* genus, mainly by *Aedes aegypti* and in some cases, by *Aedes albopictus* (Bhatt et al. 2013). Symptoms, which usually manifest 4 – 10 days after infection, include high fever, vomiting, and rashes, while a majority of cases are asymptomatic. Secondary infections have a greater risk of severe dengue and may lead to death (World Health Organization 2024).

Dengue incidence has surged significantly in recent decades, with reported cases rising from 500 thousand in 2000 (World Health Organization 2023) to more than 14 million in 2024 (European Centre for Disease Prevention and Control 2024). However, the reported cases substantially undertestimate the true scale of the dengue epidemic, as many countries lack robust detection and reporting mechanisms. One study suggests that approximately 390 million people are infected each year, with the majority of cases occurring in the Asia-Pacific region (Bhatt et al. 2013). In the Philippines, the Department of Health reported 43,732 dengue cases from January to February, 2025, which is 56% higher than the cases recorded for the same period in 2024 (Department of Health 2025). The City Health Services Office of Baguio City, Philippines reported 260 dengue cases

KEYWORDS

Epidemiology; Dengue model; seasonal vector population; reproduction numbers; sensitivity analysis; parameter estimation; bootstrapping

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from January to April, 2025, with 93 admitted to the hospital (Refuerzo 2024b).

The Communicable Disease Control Service of the Department of Health in the Philippines (DOH), formulated the National Dengue Prevention and Control Programme, initially piloted in Region 7 and the National Capital Region (NCR) of the Philippines (Dominguez 1997). The program aims to reduce dengue morbidity and mortality rates by integrated vector control, effective case diagnosis and management, fever surveillance, epidemic contingency planning and research. The DOH also encouraged the community to apply the enhanced 4S strategy as well as implementation of other program policies and guidelines (see Department of Health n.d.). In Baguio City, the city government implemented Ordinance No. 66 series of 2016 called the "Anti-Dengue Ordinance of the City of Baguio" (Refuerzo 2024a). The ordinance aims to enhance case surveillance, public awareness campaign and clean-up drives throughout the city. The city also conducts '"Denguerra'' (War against Dengue) program', a clean-up drive by barangay officials, police officers, and residents to search for and destroy mosquito breeding sites every Thursday. To intensify case surveillance, an online system for citizen self-reporting was also launched (Refuerzo 2024b).

Mathematical models study the spread of communicable diseases to gain insights for control strategies (Brauer 2017). In the Philippines, these mathematical models incorporating dengue incidence are mostly composed of statistical and compartmental models. Statistical models use correlation and time-series analysis to understand climatic and environmental factors that affect dengue-related mortality and forecast epidemics (Acosta and Nacion 2024; Seposo et al. 2024; Marigmen and Addawe 2022b; Marigmen and Addawe 2022a). Deterministic models use compartments whose interactions are described using differential equations to capture the evolution of infections and describe the parameters that greatly affect the dynamics (Cawiding et al. 2025; de los Reyes and Escaner IV 2018; Libatique et al. 2017). The study of de los Reyes and Escaner IV (2018), in particular, modified a susceptible-infected-removed (SIR) vector-host transmission model by incorporating a compartment for individuals who seek healthcare at the onset of the disease. Using the reported Philippine dengue incidence data obtained from years 2014 to 2015, they were able to fit their model and estimate parameter values. Their findings indicate that very few dengue-infected individuals seek treatment.

Southeast Asian countries, where dengue virus is endemic, observe a surge of dengue cases during specific months of the year. This includes many parts of Indonesia (Fauzi et al. 2022; Dhewantara et al. 2019), Thailand (Phanitchat et al. 2019), Singapore (Rajarethinam et al. 2018), Vietnam (Col´on-Gonz´alez et al. 2021) and Philippines (Seposo et al. 2024). For instance in Baguio City, Philippines, dengue cases are observed to increase from June to July and decrease from August to December (Marigmen 2024). Interestingly, data on dengue incidence in Baguio City from 2011 to 2024 call attention to apparent cyclic behavior over three-year periods, see Figure 3. This observed seasonality of dengue cases is often attributed to climatic factors like precipitation and temperature, population density, and human mobility (Cawiding et al. 2025; Marigmen and Addawe 2022a; Zhu et al. 2019; Costa et al. 2022).

Several models have been introduced in the literature to capture the seasonality of dengue epidemics. For instance, Aguiar, Ballesteros, and Stollenwerk (2011) added a seasonal forcing (using a cosine function) into a two-strain host-host dengue model and showed good comparison to seasonal empirical dengue data. Lourenco and Reccker (2013) observed multi-annual dengue epidemic outbreaks in their proposed spatially explicit, multi-strain agent-based model. Rashkov and Kooi (2021) used cosine waves to describe seasonally changing mosquito populations in a two-strain host-vector model. The bifurcation analysis of their model asserts the importance of incorporating seasonal mosquito population dynamics in studying yearly spikes of dengue incidences. They remarked that annual periodic dengue epidemics are due to the periodicity of mosquito populations.

Focusing only on mosquito population dynamics, Mancuso and collaborators (2023) used a non-autonomous logistic model of mosquito population with periodic net growth rate and carrying capacity. The resulting parameters accurately capture the inter-annual and intraseasonal variability of mosquito populations within a single geographic region. A variancebased sensitivity analysis highlights the influence each parameter has on the peak magnitude and timing of the mosquito season.

In this study, we include the seasonal pattern of mosquito population growth observed by Lourenco (2013) and Mancuso (2023) and their respective collaborators, and modify the compartmental model introduced by de los Reyes and Escaner IV (2018). This is not only to fit the yearly dengue incidence rate in Baguio City but also to capture the 3-year cycle of increasing amplitudes of dengue infection in the city. Sensitive parameters of the model are determined using partial rank correlation coefficient (PRCC). Unknown parameter values are estimated by fitting the model to the data from the Baguio City Health Services Office (HSO). Confidence intervals of the estimated parameters are also obtained through bootstrapping. This model, as well as the parameter values, can be used to forecast dengue infections in the city and can serve as guide for policy-making.

The paper is organized as follows. The construction and analysis of the model is discussed in Section 2. The computation of the reproduction number as well as the sensitivity analysis of parameters are also included in this section. We then provide parameter estimation, bootstrapping and simulations in Section 3. Finally, discussions and recommendations are summarized in the last section.

A MODEL OF DENGUE TRANSMISSION

Model construction

We consider the single-strain host-vector compartments introduced by de los Reyes and Escaner IV (2018). The susceptible (S_h), the unhospitalized or unmonitored infectious (I_h), the healthcare-seeking infected (J_h), and the removed or recovered (R_h) individuals constitute the human population. The sum of these populations is denoted by $N_h(t)$. Similarly, the susceptible (S_v), and the infectious (I_v) vectors constitute the vector population. The sum of these two classes is the total vector population, denoted by $N_v(t)$. We include in our model a carrying capacity K_h for humans and K_v for vectors.

Table 1: Model Compartments considered in this study

Compartment	Description
S_h	Susceptible humans
I_h	Unmonitored infectious humans
J_h	Healthcare-seeking infected humans
R_h	Recovered humans
S_v	Susceptible mosquito vectors
I_v	Infectious mosquito vectors

In the proposed model illustrated in Figure 1, the susceptible human population $S_h(t)$ increases as the total population $N_h(t)$ grows logistically at a rate of b_h, with growth constrained by a carrying capacity K_h. Susceptible individuals are infected when an infected female mosquito bites them; here the mosquito population has a biting rate of B per week, with a transmission probability of C_{vh}. Because some individuals seek healthcare at the onset of symptoms, a fraction, α, of the infected population is added in $J_h(t)$ while the non-healthcare seeking infected individuals stay in the $I_h(t)$ compartment. The recovery rate of non-healthcare-seeking individuals and the healthcare-seeking individuals are denoted by γ and θ, respectively, and the recovered individuals from $I_h(t)$ and $J_h(t)$ move into the $R_h(t)$ compartment. Finally, each class of the human population, $S_h(t)$, $I_h(t)$, $J_h(t)$, and $R_h(t)$ has a mortality rate of μ_h.

The susceptible vector population goes through a seasonal increase (over the year) at the rate of $b_v(t)$, constrained by a carrying capacity K_v. The $b_v(t)$ value takes note of the baseline (mean) value of the vectors' oviposition b_{vm}, the magnitude of its oscillation b_{vs}, and its peaks b_{vp}. Mosquitoes then get infected at a rate of C_{hv} by those individuals who have not received healthcare treatment (I_h). Each class of the vector population has a seasonal yearly mortality rate of $\mu_v(t)$, whereby this incorporates the baseline (mean) values of the vectors' mortality μ_{vm}, the magnitude of oscillation μ_{vs}, and its peaks μ_{vp}.

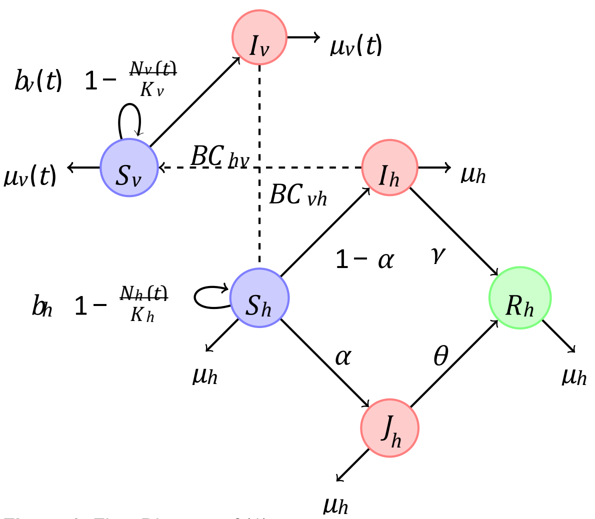


Figure 1: Flow Diagram of (1)

The model is described by the following system of ordinary differential equations (ODEs) where the time variable t is measured in weeks:

$$
\begin{aligned}
\frac{dS_h(t)}{dt} &= b_h N_h(t)\left(1-\frac{N_h(t)}{K_h}\right) - BC_{vh}\frac{I_v(t)S_h(t)}{N_h(t)} - \mu_h S_h(t),\\
\frac{dI_h(t)}{dt} &= (1-\alpha)BC_{vh}\frac{S_h(t)I_v(t)}{N_h(t)} - \gamma I_h(t) - \mu_h I_h(t),\\
\frac{dJ_h(t)}{dt} &= \alpha BC_{vh}S_h(t)\frac{I_v(t)}{N_h(t)} - \theta J_h(t) - \mu_h I_h(t),\\
\frac{dR_h(t)}{dt} &= \gamma I_h(t) + \theta J_h(t) - \mu_h R_h(t),\\
\frac{dS_v(t)}{dt} &= b_v(t)N_v(t)\left(1-\frac{N_v(t)}{K_v}\right) - \left(BC_{hv}\frac{I_h(t)}{N_h(t)} + \mu_v(t)\right)S_v(t),\\
\frac{dI_v(t)}{dt} &= BC_{hv}S_v\frac{I_h(t)}{N_h(t)} - \mu_v(t)I_v(t),
\end{aligned} \tag{1}
$$

where

$$b_v(t) = b_{vm}\left(1 - b_{vs}cos\left(\frac{2\pi(t-b_{vp})}{52}\right)\right) \tag{2}$$

$$\mu_v(t) = \mu_{vm}\left(1 - \mu_{vs}cos\left(\frac{2\pi(t-\mu_{vp})}{52}\right)\right) \tag{3}$$

with nonnegative initial conditions $S_h(0)$, $I_h(0)$, $R_h(0)$, $S_v(0)$, and $I_v(0)$.

In comparison to the model of de los Reyes and Escaner IV 2018, we introduce the carrying capacity for the human population as well as the periodic behavior of the vector population growth. The model parameters are summarized in the following table.

Table 2: Parameters used in the dengue transmission model.

Parameter	Description	Units	Range
b_h	Birth rate of humans	human births per 10,000 population per week	[0,1]
μ_h	Mortality rate of humans	human deaths per 10,000 population per week	[0,1]
B	Vector biting rate	number of bites per mosquito per week	[0,4]
C_{hv}	Transmission probability from human to vector	dimensionless	[0,1]
C_{vh}	Transmission probability from vector to human	dimensionless	[0,1]
γ	Non-seeking healthcare recovery rate	proportions per week	[0,1]
θ	Healthcare-seeking recovery rate	proportions per week	[0,1]
b_{vm}	Mean per capita oviposition rate	proportions per week	[0,1]
μ_{vm}	Mean mortality rate of vectors	proportions per week	[0,1]
b_{vs}	Magnitude of oscillation of the oviposition rate	dimensionless	[0,1]
μ_{vs}	Magnitude of oscillation of vector mortality rate	dimensionless	[0,1]
b_{vp}	Determines the peaks the oviposition rate	week	[0,52]
μ_{vp}	Determines the peaks of vector mortality rate	week	[0,52]
K_h	Human carrying capacity	humans	$[0,3\times10^6]$
K_v	Vector carrying capacity	mosquitoes	$[0,10^7]$
α	Transition rate from susceptible to healthcare-seeking infected	dimensionless	[0,1]

Existence

The expressions for ODEs in equation (1) are composed of linear terms, rational terms, and time-dependent oscillatory functions. The linear terms in (1) as well as the trigonometric functions are Lipschitz continuous since they have bounded derivatives. The rational terms are also Lipschitz continuous as long as $N_h(t)$, K_h, $K_v \geq 0$. Given $N_h(0)$, K_h, $K_v > 0$, the Picard-Lindel¨of theorem guarantees that there exists a unique continuous solution to (1) for some interval $[0,T]$ for $T > 0$. If these values remain positive (which is shown in the next subsection), the Picard-Lindelöf theorem can be used to establish existence and uniqueness of solutions for the interval $[0,+\infty)$.

Nonnegativity of Solutions

The model describes human and mosquito population growth. For this to be biologically meaningful, the solutions $S_h(t)$, $I_h(t)$, $J_h(t)$, $R_h(t)$, $S_v(t)$ and $I_v(t)$ for each of the state variables, assuming non-negative initial data, should remain non-negative for all time *t*. That is, suppose

$$
\begin{aligned}
&S_h(0)\geq 0,\quad I_h(0)\geq 0,\quad J_h(0)\geq 0,\quad R_h(0)\geq 0,\quad K_h>N_h(0)>0,\\
&S_v(0)\geq 0,\quad I_v(0)\geq 0,\quad K_v>N_v(0)>0.
\end{aligned} \tag{4}
$$

The total human and vector populations are

$$N_h(t)=S_h(t)+I_h(t)+J_h(t)+R_h(t)$$

and

$$N_v(t)=S_v(t)+I_v(t),$$

respectively. From the model equations,

$$
\begin{aligned}
\frac{dN_h(t)}{dt}&=b_hN_h(t)\left(1-\frac{N_h(t)}{K_h}\right)-\mu_hS_h(t),\\
\frac{dN_v(t)}{dt}&=b_v(t)N_v(t)\left(1-\frac{N_v(t)}{K_v}\right)-\mu_h(t)N_v(t),
\end{aligned}
$$

which are logistic equations with carrying capacity $K_h>0$ and $K_v>0$, respectively. Since the total human and vector populations have positive initial conditions less than the carrying capacity and assuming that the birth rates are larger than the death rates of each population, respectively, then we are assured that $0<N_h(t)<K_h$ and $0<N_v(t)<K_v$ for all $t\geq 0$.

Now, starting with nonnegative initial population values for the compartments, due to the continuity of the expressions for the derivatives in the model, there exists

$$t^*=\sup\{t>0:\ S_h(t)\geq 0, I_h(t)\geq 0, J_h(t)\geq 0, R_h(t)\geq 0, S_v(t)\geq 0, I_v(t)\geq 0\},$$

such that $t^*>0$. We have at t^*,

$$
\begin{aligned}
\frac{dS_h(t)}{dt}+\left(BC_{vh}\frac{I_v(t)}{N_h(t)}+\mu_h\right)S_h(t)&\geq 0,\\
\frac{dJ_h(t)}{dt}+(\theta+\mu_h)J_h(t)&\geq 0,\\
\frac{dI_h(t)}{dt}+(\gamma+\mu_h)I_h(t)&\geq 0,\\
\frac{dR_h(t)}{dt}+\mu_hR_h(t)&\geq 0.
\end{aligned}
$$

This results in

$$
\begin{aligned}
S_h(t^*)&\geq S_h(0)e^{-\int_0^{t^*}\left(BC_{vh}\frac{I_v(t)}{N_h(t)}+\mu_h\right)^{dt}}\geq 0,\\
J_h(t^*)&\geq J_h(0)e^{-(\theta+\mu_h)^{t^*}}\geq 0,\\
I_h(t^*)&\geq I_h(0)e^{-(\gamma+\mu_h)^{t^*}}\geq 0,\\
R_h(t^*)&\geq R_h(0)e^{-\mu_h{}^{t^*}}\geq 0.
\end{aligned}
$$

The same expressions for $S_v(t^*)$ and $I_v(t^*)$ given nonnegative values for both quantities. Hence all compartments have nonnegative population values.

Boundedness

For the model to be epidemiologically significant, all solutions must be bounded. Because each of the compartment contents for the human population are nonnegative values, we have, from the equation $\frac{dN_h(t)}{dt}=b_hN_h(t)\left(1-\frac{N_h(t)}{K_h}\right)-\mu_hN_h(t)$ that $\frac{dN_h(t)}{dt}\leq b_hN_h(t)\left(1-\frac{N_h(t)}{K_h}\right)$. This implies that $\limsup_{t\to\infty}N_h(t)\leq K_h$. So each of S_h, I_h, J_h, R_h are also bounded by K_h in $[0,+\infty)$. Hence each vector compartment population is also bounded by K_v in $[0,+\infty)$. Therefore, the dengue transmission model described in (1) is well-posed, that is, the model solution exists, is unique given initial conditions, with nonnegative and bounded values for each population within the feasible region.

Disease-free Periodic State

The disease-free state occurs when the infected compartments I_h, J_h, I_v and recovered compartment R_h have zero elements. This implies $S_h=N_h$ and $S_v=N_v$. Our model (1) then reduces to

$$\frac{dS_h(t)}{dt}=\left[b_h\left(1-\frac{S_h(t)}{K_h}\right)-\mu_h\right]S_h(t) \tag{5}$$

$$\frac{dS_v(t)}{dt}=\left[b_v(t)\left(1-\frac{S_v(t)}{K_v}\right)-\mu_v(t)\right]S_v(t) \tag{6}$$

Denote by $E^*=(S_h^*,I_h^*,J_h^*,R_h^*,S_v^*,I_v^*)$ the steady state of our model. It is clear from the above equations that the trivial point $E^0=(0,0,0,0,0,0)$ and $E^1=(K_h(1-\mu_h/b_h),0,0,0,0,0)$ are equilibrium points of (1). System (1) also has a periodic steady-state

$$E^2(t)=(K_h(1-\mu_h/b_h),0,0,0,S_{v0}(t),0) \tag{7}$$

where $S_{v0}(t)=K_v\left(1-\frac{\mu_v(t)}{b_v(t)}\right)$. Note that $E^2(t)$ becomes an equilibrium point only when $b_{vs}=\mu_{vs}$ and $b_{vp}=\mu_{vp}$. The state $(0,0,0,0,S_{v0}(t),0)$, though technically also a disease-free steady state, is not considered since we are interested in the epidemiological effect of dengue disease on human populations.

Reproduction Number

The basic reproduction number R_0 describes the number of new infections caused by an infected individual in a disease-free susceptible population (Heesterbeek 2002). We consider using a time-averaged approach to calculate the basic reproduction number (Ma and Ma 2006; Wesley and Allen 2009). In this method, we replace any time-varying parameter with their longtime averages, reducing the system into an autonomous system. Note that we have two timedependent parameters, namely, $b_v(t)$ and $\mu_v(t)$. Since these parameters are periodic functions, the long time averages can be computed as

$$\langle b_v\rangle=\frac{1}{\omega_1}\int_0^{\omega_1}b_v(t)\,dt \text{ and } \langle\mu_v\rangle=\frac{1}{\omega_2}\int_0^{\omega_2}\mu_v(t)\,dt$$

where ω_1 and ω_2 are the periods of $b_v(t)$ and $\mu_v(t)$, respectively. It is clear from (2) and (3) that the period is $\omega_1=\omega_2=52$ and that

$$\langle b_v\rangle=b_{vm} \text{ and } \langle\mu_v\rangle=\mu_{vm}. \tag{8}$$

Using such values instead of the time-dependent parameters is equivalent to finding the value of R_0 when the periodic disease-free steady-state $E^2(t)$ of (1) is an equilibrium point.

To compute for the reproduction number, we proceed by using the method of the next generation matrix. Let $x=(x_1,x_2,x_3)^\top:=(I_h,J_h,I_v)^\top$, where I_h, J_h, and I_v are the infected states of the system. In order to compute for the value of R_0, it is important to distinguish new infections from all other changes in the population. For $i = 1,2,3$, let $\mathcal{F}_i(x)$ be the input rate of new infections from x_i, $\mathcal{V}_i^+(x)$ be the rate of transfer into x_i by all other means, and $\mathcal{V}_i^-$ be the rate of transfer out of x_i. Set

$$\mathcal{F}(x) = \left(\mathcal{F}_1(x), \mathcal{F}_2(x), \mathcal{F}_3(x)\right)^\top,$$
$$\mathcal{V}^+(x) = \left(\mathcal{V}_1^+(x), \mathcal{V}_2^+(x), \mathcal{V}_3^+(x)\right)^\top,$$
$$\mathcal{V}^-(x) = \left(\mathcal{V}_1^-(x), \mathcal{V}_2^-(x), \mathcal{V}_3^-(x)\right)^\top,$$
$$\mathcal{V}(x) = \mathcal{V}^-(x) - \mathcal{V}^+(x).$$

Recall that the infected compartments have the following dynamics:

$$\frac{dI_h(t)}{dt} = (1-\alpha)BC_{vh}\frac{S_h(t)I_v(t)}{N_h(t)} - \gamma I_h(t) - \mu_h I_h(t),$$
$$\frac{dJ_h(t)}{dt} = \alpha BC_{vh}\frac{S_h(t)I_v(t)}{N_h(t)} - \theta J_h(t) - \mu_h J_h(t),$$
$$\frac{dI_v(t)}{dt} = BC_{hv}\frac{S_v(t)I_h(t)}{N_h(t)} - \mu_h(t)I_v(t).$$

It follows that

$$\mathcal{F}(x)\begin{bmatrix} (1-\alpha)BC_{vh}\frac{S_h(t)x_3}{N_h(t)} \\ \alpha BC_{vh}\frac{S_h(t)x_3}{N_h(t)} \\ BC_{hv}\frac{S_v(t)x_1}{N_h(t)} \end{bmatrix} \text{ and } \mathcal{V}(x)\begin{bmatrix} (\gamma+\mu_h)x_1 \\ (0+\mu_h)x_2 \\ \mu_h(t)x_3 \end{bmatrix}$$

Define F and V as

$$F = \left[\frac{\partial \mathcal{F}}{dx_j}(E^*)\right] \text{ and } V = \left[\frac{\partial \mathcal{V}}{dx_j}(E^*)\right],$$

where $E^*$is some some equilibrium point. We now replace the periodic parameters by (8). Evaluating the matrices at the disease-free equilibrium (7) yields

$$F(E^2) = \begin{bmatrix} 0 & 0 & (1-\alpha)BC_{vh} \\ 0 & 0 & \alpha BC_{vh} \\ BC_{hv}\dfrac{K_v b_h(b_{vm}-\mu_{vm})}{K_h b_{vm}(b_h-\mu_h)} & 0 & 0 \end{bmatrix}$$

and

$$V(E^2) = \begin{bmatrix} \gamma+\mu_h & 0 & 0 \\ 0 & \theta+\mu_h & 0 \\ 0 & 0 & \mu_{vm} \end{bmatrix}.$$

The basic reproduction number is the spectral radius of $F(E^2)V^{-1}(E^2)$, that is, the largest eigenvalue of the obtained next generation matrix. This gives

$$R_0 = \sqrt{\frac{K_v\left(1-\frac{\mu_{vm}}{b_{vm}}\right)}{K_h\left(1-\frac{\mu_h}{b_h}\right)} \cdot \frac{BC_{hv}}{\gamma+\mu_h} \cdot \frac{(1-\alpha)BC_{vh}}{\mu_{vm}}}\,. \tag{9}$$

Let us look at the components of R_0. We see that the first multiplicand under square root, i.e., $K_v\left(1-\frac{\mu_{vm}}{b_{vm}}\right)/K_h\left(1-\frac{\mu_h}{b_h}\right)$, is in fact composed of the steady states of the disease-free dynamics (5)-(6), hence this represents the vector to host ratio. The number of vector infections caused by an infected host is represented by $\frac{BC_{hv}}{\gamma+\mu_h}$ while the number of host infections caused by one infected vector is represented by $\frac{(1-\alpha)BC_{vh}}{\mu_{vm}}$. Taking the geometric mean of the average secondary infections caused by a single host or vector gives the value of R_0.

With the use of time-averaged approach, the basic reproduction number R_0 only captures the onset of the spread of disease in the population. It fails to incorporate the introduced seasonality of vector populations. Thus, we also consider the effective reproduction number $R_e(t)$, which quantifies the progression of the spread of the disease. The effective reproduction number can be computed by following the next generation matrix method without substituting the disease-free equilibrium (Fauzi et al. 2022; S. Zhao et al. 2020). Thus,

$$R_e(t) = \sqrt{\frac{N_v(t)}{N_h(t)} \cdot \frac{S_h(t)}{N_h(t)} \cdot \frac{S_v(t)}{N_v(t)} \cdot \frac{BC_{hv}}{\gamma+\mu_h} \cdot \frac{(1-\alpha)BC_{vh}}{\mu_v(t)}}\,. \tag{10}$$

Sensitivity Analysis

The dynamics of deterministic models are governed by the input parameters which may exhibit uncertainties. Thus, global sensitivity analysis is needed to determine which parameters largely affect the dynamics of the model given perturbations on the parameters (Agusto and Khan 2018; Marino et al. 2008; Wu et al. 2013). The partial rank correlation coefficient (PRCC) measures the sensitivity of an output state variable to parameter values as a linear correlation between the residuals. The PRCC values range between -1 and 1 and positive (negative) values indicate positive (negative) correlation of the model parameters and the state variable. The larger the absolute value of the PRCC, the greater the correlation of the parameter with the output. PRCC is often combined with latin hypercube sampling (LHS) to allow analysis of parameter variations across each uncertainty range (Wu et al. 2013; Agusto and Khan 2018).

The LHS matrices are obtained by assuming that all the model parameters are uniformly distributed and that each parameter is sampled independently. A total of 1000 model simulations are done for each LHS using ±90% of the nominal values in Table 2. A dummy variable is included to show that the sampling method is consistent and robust. The time points used are morbidity weeks 1 to 152. Figure 2 gives the PRCC values of the parameters with respect to the cumulative values of J_h. According to Marino (2008), the PRCC sensitivity analysis method works well for non-linear monotonic relationships.

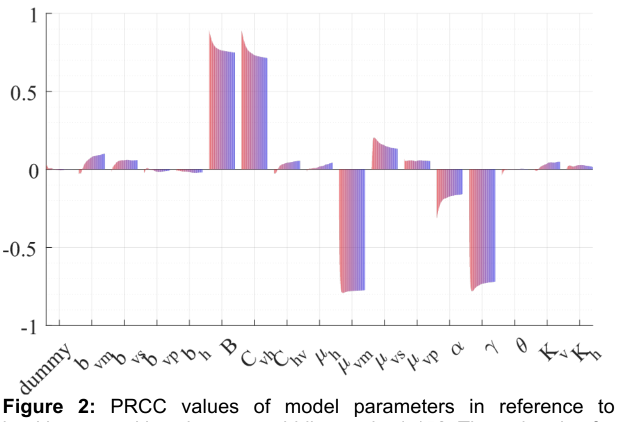


Figure 2: PRCC values of model parameters in reference to healthcare-seeking class at morbidity weeks 1-152. The red region for each parameter represents the PRCC values at earlier weeks (1-76) and the blue region gives PRCC values for weeks (77-152).

We see from Figure 2 that the parameters B, C_{vh}, and μ_{vs} influence cumulative J_h positively while parameters μ_{vm}, α, and γ influence cumulative J_h negatively. It should be noted that the sensitivity of the parameters is different for each morbidity week. There is a high correlation of the said parameters with the cumulative J_h in the first few weeks of morbidity (25-30), then this gradually decreases for the next set of morbidity weeks. But the correlation of parameters μ_{vm} and γ remains high throughout the given morbidity weeks. Control strategies that reduce the value of parameters that positively influence the cumulative J_h or increase the value of the parameters that negatively influence the infected compartments should adequately reduce the spread of dengue infections in the city.

SIMULATIONS, PARAMETER ESTIMATION, AND BOOTSTRAPPING

Epidemiological Data

The daily dengue incidence data from January 2011 to December 2022 acquired from Baguio City Health Service Office is used in this study. These were grouped by morbidity week over three-year periods shown in Figure 3. The graph shows the oscillating behavior in reported dengue cases over each three-year period. There are increasing peaks of dengue cases in morbidity weeks 25-35, 75-95, and 125-145.

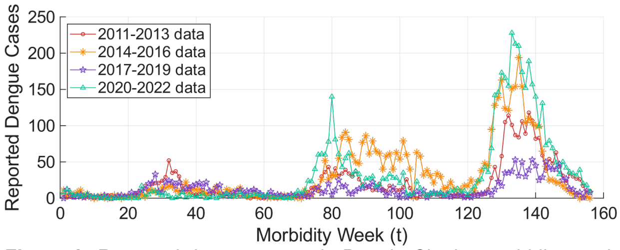


Figure 3: Reported dengue cases in Baguio City by morbidity week over three-year period from 2011-2022.

Parameter Values and initial conditions

The Philippines Statistics Authority (PSA) conducts a population census every 5 years. From their report in 2022 (Philippine Statistics Authority 2022), the total Baguio population for years 2010, 2015 and 2020 are 318676, 345366, and 366358, respectively. The dynamics of the total population N_h are then fitted based on these data to estimate the human birth rate b_h and the mortality rate μ_h listed in Table 2. The best fit model is used to determine the Baguio population at the onset of each three-year cycle, see Table 3.

Since there is no available data for the vector population, conservative estimates are used. Because of intervention measures like destroying mosquito breeding sites in Baguio City, we expect changes in the vector carrying capacity each year, but we set a maximum carrying capacity of the vector population to be 10^7. It is assumed that there are 2000 susceptible vector and 40 infected vector at the start of each three-year cycle. The initial conditions of the other compartments in (1) are listed in Table 4. Here, we assume at the start of each three-year cycle that the number of recovered is half of the human population since we only assume a single strain of dengue virus.

Table 3: Baguio population based on the best fit population model N_h at the onset of each 3-year cycle from 2011 – 2022.

Year	$N_h(0)$
2011–2013	318676
2014-2016	335460
2017-2019	335460
2020-2022	362674

Table 4: Initial conditions of each compartment used in (1).

Parameter	Values
$J_h(0)$	Data from morbidity week 1
$I_h(0)$	$[0.5 \,.\, J_h(0)]$
$R_h(0)$	$[0.5 \,.\, N_h(0)]$
$J_h(0)$	$N_h(0) - I_h(0) - J_h(0) - R_h(0)$
$S_v(0)$	2000
$I_v(0)$	40

A summary of the parameter values used in the model identification are shown in Table 5. Conservative estimates were utilized for parameters with no known values and were subject for further parameter estimation based on data.

Table 5: Parameter values used in the dengue transmission model.

Parameter	Value	References
b_h	0.0078	Data-fitted
μ_h	0.0063	Data-fitted
B	1	(Lizarralde-Bejarano et al. 2017; Twizell et al. 2003)
C_{hv}	0.75	(Lizarralde-Bejarano et al. 2017; Twizell et al. 2003)
C_{vh}	0.375	(Lizarralde-Bejarano et al. 2017; Twizell et al. 2003)
γ	0.5	(Lizarralde-Bejarano et al. 2017)
θ	1	(Lizarralde-Bejarano et al. 2017)
b_{vm}	0.4	Estimated
μ_{vm}	0.8	Estimated
b_{vs}	0.2	Estimated
μ_{vs}	0.2	Estimated
b_{vp}	1	Estimated
μ_{vp}	3	Estimated
K_h	2,215,141	(Baguio City Public Information Office 2022)
K_v	10^6	Estimated
α	0.2	Estimated

Model Identification

We now estimate the parameters in order to fit our model to the reported data. To capture the observed seasonality, the model is fitted for the morbidity weeks over each three-year period. The parameters $\alpha, B, C_{vh}, C_{hv}$ which control the transition of the susceptible human to healthcare-seeking infected compartments as well as $b_{vm}, b_{vs}, b_{vp}, \mu_{vm}, \mu_{vp}$ and K_v which describe the vector population are considered. The model output considered is the healthcare-seeking infected human J_h which is the available epidemiological data. Parameter estimation is employed for each of the parameters by minimizing the sum of least square errors between the model output and reported data for each morbidity week in each three-year period. This is carried out using the `lsqcurvefit` function in MATLAB. The values of the parameter estimates are found in Table 6. The parameter estimates are then used to solve (1) using `ode45` in MATLAB and the resulting dynamics of J_h is compared to the available data, as seen in Figure 4. The evolution of the susceptible and infectious vector population based on the estimated parameters are shown in Figure 5.

It can be deduced from Table 6 that it was during the period of 2014−2016 that the transition rate from susceptible to the infected class seeking healthcare α had the lowest estimated value. In contrast, the value of α is seen to increase in the succeeding years. The vector biting rate B had the largest estimated values while the carrying capacity K_v had the least estimated values for the years 2017−2019. The value of the computed basic reproduction number R_0 is larger on years 2014 − 2016 and 2020 − 2022 as compared to the other years. The effective reproduction number $R_e(t)$ shown in Figure 4, captures the onset of the surge of reported cases in each year.

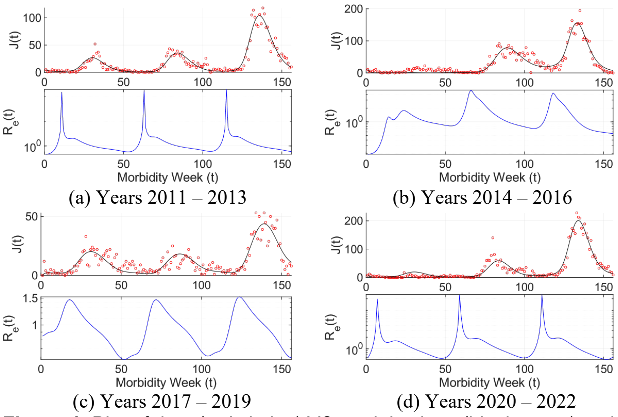


Figure 4: Plot of data (red circles) VS model values (black curve) and the effective reproduction number $R_e(t)$ (blue curve in logarithmic scale) of best fit model.

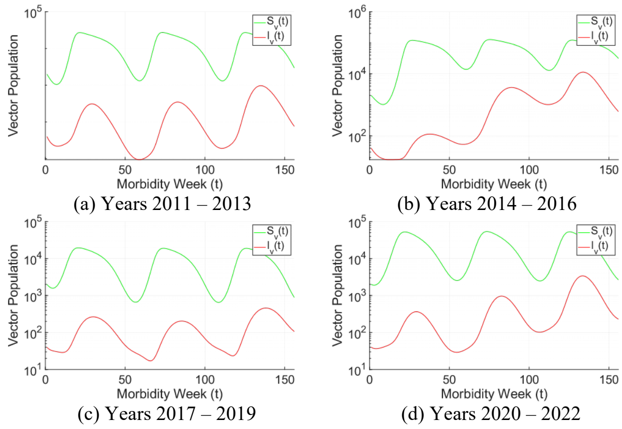


Figure 5: Logarithmic scale plot of susceptible ($\boldsymbol{S_v}$) and infected ($\boldsymbol{I_v}$) vector population of best fit model.

Bootstrapping

We employ parametric bootstrapping in order to quantify parameter uncertainty and construct confidence intervals. This method involves repeatedly sampling multiple observations from the best fit model in order to quantify parameter uncertainty using Poisson distribution, centered on the mean at the time points t (Chowell 2017). As mentioned, we re-estimated parameters for each of the 1,000 simulated synthetic datasets (as shown in Figures 8 and 9 in the appendix). The mean and standard deviation of the datasets are also shown in the appendix. The confidence interval of the re-estimated parameters are shown in Table 7. This shows that the best fit model parameter values (see Table 6) are within ± standard deviations of the mean values of the re-estimated parameters.

The shaded region (in cyan) in the plot for each of the 3-year periods, as seen in Figure 6, indicates the 95% confidence interval. The results provide a good confidence level for the parameter estimates, which implies that the values of the parameters estimated for each 3-year period are reliable.

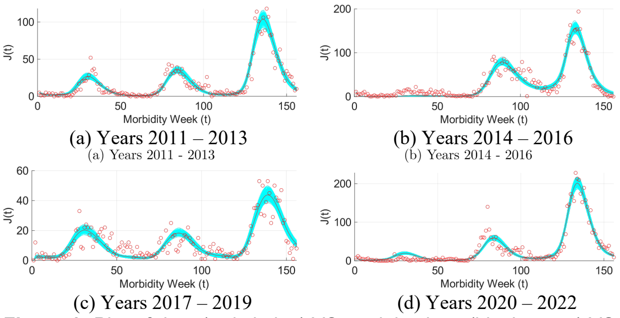
Table 6: Estimated parameters from data through different time periods.

Year	α	B	C_{vh}	C_{hv}	$K_v/10^7$
2011-2013	0.0523	3.2554	0.9052	0.8686	0.0035
2014-2016	0.0198	1.9606	0.9389	0.3472	0.0149
2017-2019	0.0339	4	1	1	0.0036
2020-2022	0.0471	2.6131	0.7657	0.8459	0.0090

Year	b_{vm}	μ_{vm}	b_{vs}	μ_{vs}	b_{vp}	μ_{vp}	R_0
2011-2013	0.7564	0.3558	1.0000	1.0000	4.2367	10.9739	1.3908
2014-2016	0.5498	0.1968	1.0000	0.9757	5.1804	13.6949	1.6747
2017-2019	0.6265	0.4105	1.0000	0.7766	1.0485e-12	4.9139	1.4867
2020-2022	0.4090	0.2559	0.9694	1	1.5585e-05	7.2035	1.6125

Table 7: 95% confidence intervals of parameters from bootstrapping through different time periods.

Parameters	2011-2013	2014-2016	2017-2019	2020-2022
α	[0.0456, 0.0610]	[0.0188, 0.0211]	[0.0305, 0.0427]	[0.0447, 0.0497]
B	[3.0609, 3.6553]	[1.7482, 2.6042]	[3.9167, 4.0501]	[2.4629, 3.2329]
C_{vh}	[0.8652, 0.9635]	[0.8030, 1]	[0.9615, 1]	[0.6992, 0.8723]
C_{hv}	[0.8173, 0.9494]	[0.1877, 0.5665]	[0.9726, 1]	[0.7287, 0.9665]
$K_v/10^7$	[0.0022, 0.0052]	[0.0082, 0.0233]	[0.0030, 0.0043]	[0.0060, 0.0098]
b_{vm}	[0.6658, 0.8413]	[0.4639, 0.7329]	[0.5732, 0.6585]	[0.3578, 0.4970]
μ_{vm}	[0.3100, 0.4249]	[0.1739, 0.2467]	[0.3664, 0.4357]	[0.2216, 0.3109]
b_{vs}	[0.8858, 1]	[0.8907, 1]	[0.9475, 1]	[0.7880, 1]
μ_{vs}	[0.8911, 1]	[0.8711, 1]	[0.7363, 0.8063]	[0.9152, 1]
b_{vp}	[2.5883, 5.6094]	[3.7188, 7.3488]	[0, 0.6543]	[0, 2.2258]
μ_{vp}	[9.0476, 12.5342]	[11.7970, 15.9821]	[4.2584, 6.3356]	[6.5500, 9.1745]
R_0	[1.3282, 1.4278]	[1.5919, 1.6988]	[1.4526, 1.4993]	[1.5188, 1.6300]



(a) Years 2011 – 2013 (b) Years 2014 – 2016

(c) Years 2017 – 2019 (d) Years 2020 – 2022

Figure 6: Plot of data (red circles) VS model values (black curve) VS synthetic models (cyan curve) after parameter estimation.

DISCUSSION

Current knowledge on dengue transmission in Baguio City is obtained from statistical and mathematical modeling studies (Marigmen and Addawe 2022a, 2022b; Marigmen 2024; Libatique et al. 2017). From these studies, seasonal patterns have been observed, and the highest incidence of dengue cases occurs between June and July of each year (Marigmen 2024). In the Philippines, epidemiologically important parameter values related to dengue transmission, like the mosquito biting rate B and transition rate from susceptible to healthcare-seeking infected humans, have also been identified using compartmental models (de los Reyes and Escaner IV 2018). However, specific values for Baguio City have not been identified.

In this study, we consider a well-posed mathematical model that incorporates the dynamics of the mosquito population over a 3-year span. The model parameters are calibrated to dengue incidence data in Baguio City from 2011 to 2022. This modification of earlier models and its fitting to the Baguio dengue incidence data is a significant contribution in the study of dengue transmission in Baguio City. To the best of our knowledge, there are no available studies on mosquito dynamics as this affects dengue transmission in Baguio.

We further incorporate a carrying capacity for the human population and periodic growth of the vector, as a refinement to the model of de los Reyes and Escaner IV (2018). Incorporating human carrying capacity into the model provides realistic dynamics of human population growth in an environment with limited resources. This gives logistic growth rather than exponential growth. Moreover, introducing periodic vector population growth into the model captures seasonal fluctuations in mosquito population due to climatic and environmental factors.

Baguio City has a wet season from May to October and a dry season from November to April. The city is in the highlands and sits on a typhoon belt, hence the unpredictable weather experienced. (Chepenlianskaia and Khan 2023). Taking this into account and the fact that the life cycle of a mosquito is dependent on climate, the model incorporates a time-varying vector population growth rate derived from the study of Mancuso et al. (Chandra and Mukherjee 2022; Mancuso et al. 2023). The time-varying vector population of Mancuso et al. has been used in epidemiological studies such as in studies on the West Nile virus transmission, however, integration of this into dengue transmission has not yet been done. (Mancuso 2023). To our knowledge, there have not been studies in the Philippines that include time-varying vector population growth in the transmission of dengue or any vector-borne disease.

The intent of this enhancement on previous models is to better capture and visualize the dynamics of dengue-infected mosquitoes in the city. The inclusion of a time-varying vector population in the model adds insight into the observed pattern (from Baguio data for years 2011 to 2022) of disease progression over three-year periods. Study results can be referred to in assessing whether vector management initiatives implemented by the Baguio City Local Government Unit are effective in the prevention of dengue outbreaks. Simulations using the model with parameter values derived from data should be helpful in formulating policy on the management of vector populations.

Figure 3 shows a surge in dengue cases during the period $2014-2016$. This may be due in part to the low value of α, i.e. a large proportion of dengue-infected individuals did not seek hospitalization. This estimated value for α in 2014−2016 is comparable to the estimates of de los Reyes and Escaner (2018) for the years 2014 and 2015, which are low values as well.

Notably, it was in 2016 when City Ordinance No. 66 series of 2016 (called the "Anti-Dengue Ordinance of the City of Baguio") was first implemented (Refuerzo 2024a). This measure may have increased dengue awareness in the community and as a result, substantially increased the proportion of infected individuals seeking healthcare in the succeeding years. Figure 3 shows a significant decrease in dengue infections in the years $2017-2019$.

The reduction in mosquito carrying capacity is notable in $2017-2019$ and is likely attributable to LGU efforts in vector population control. The sustained effort of the city to destroy mosquito breeding sites is apparent in the decrease of K_v from the years $2014-2016$ and $2017-2019$.

The estimated biting rate for all periods is well within the epidemiologically accepted ranges (Lizarralde-Bejarano et al. 2017; Zahid et al. 2023). The changes in the parameter values will have to be further investigated as this may be affected by climatic factors.

The R_0 values 1.67 and 1.61 in the years $2014-2016$ and $2020-2022$, respectively, are larger, compared to that in other years since there is a surge in the number of reported dengue cases during these years. In fact, $R_0 \approx 1.67$ in the years $2014-2016$ is close to the measured $R_0 \approx 1.62$ in 2014 by de los Reyes and Escaner IV (2018).

The estimated seasonal parameter values suggest that there is a year-round abundance of mosquitoes, with strong surges during the rainy season (see Figure 5). This observation is consistent with the findings in (Marigmen and Addawe 2022a), indicating that climatic factors such as increased precipitation led to more favorable breeding sites, consequently raising dengue incidence in the city. Hence, sustained efforts to control and eradicate mosquito breeding grounds should be maintained throughout the year. This suggests that vector-control interventions such as fogging and community-based cleaning efforts are indeed effective measures in mitigating the risk of dengue outbreaks. Further, observations regarding seasonal fluctuations in vector population as well as multi-year cycles of disease incidence would be crucial in formulating strategies for disease control, including the matter of lead times for implementation of mitigation measures. Progression of the (time-dependent) effective reproduction number, see for instance Figure 5, can provide guidance as to timing and intensity of application of mitigation measures. In the future, more advanced interventions, such as the use of Wolbachia-infected mosquitoes (Dorigatti et al. 2018), can also be considered.

The study has had the benefit of access to dengue incidence data covering over 10 years (2011 - 2022). This is significant as study results can then be utilized by local government to make prospective forecasts of disease incidence. The model also allows us to estimate the number of dengue infected individuals who did not seek healthcare, which is not accounted for in the data. Parameter estimates and observations on vector dynamics can be referred to in determining optimal timing, intensity and duration of application of control and mitigation measures, to ensure good outcomes. This can be simulated through our model by adding, for instance, a "harvesting" term in the susceptible vector compartment i.e.,

$$\frac{dS_v(t)}{dt} = b_v(t)N_v(t)\left(1-\frac{N_v(t)}{K_v}\right)-\left(BC_{hv}\frac{I_h(t)}{N_h(t)}+\mu_v(t)\right)S_v(t)-NH_v \quad (11)$$

where

$$H = \begin{cases} c & if\ \tau \le t \le \tau + dH = \\ 0 & otherwise, \end{cases}$$

annually for three years. Here, τ denotes the week when we start reducing vector population, d for the duration in weeks of the process per year, and c for the percentage of removed vector population. In the simulation shown in Figure 7 for the years 2011-2013 where parameters of the best fit model were used, we see the effect of reducing by 0.1 the vector population for a duration of 5 weeks at different starting points. In this scenario, it is best to start reducing the vector population on morbidity week 45 of each year to reduce the number of dengue patients (black line vs red dashed line). We intend to explore optimal cycle and duration in the succeeding studies.

The inclusion of sinusoidal vector birth and death rates in model (1) makes it highly nonlinear. This means that the model is sensitive to initial conditions. Parameter estimates can be made closer to real life scenario by using real data instead of conservative assumptions, e.g. on initial number of susceptible and infected vectors. The sinusoidal vector birth and death rates in the model do not explicitly account for factors affecting these. These rates simply describe the observed seasonality of mosquito population levels. Incorporating factors like environmental conditions, population density, and human mobility, which impact such seasonality could lead to better understanding of the effect of these factors on the spread of dengue disease. One could also modify the model to include multiple strains of dengue. In fact, there are host-host and host-vector multi-strain dengue models in literature that also observed seasonal dengue epidemics (see Aguiar et al. 2011; Lourenço and Recker 2013; Rashkov and Kooi 2021).

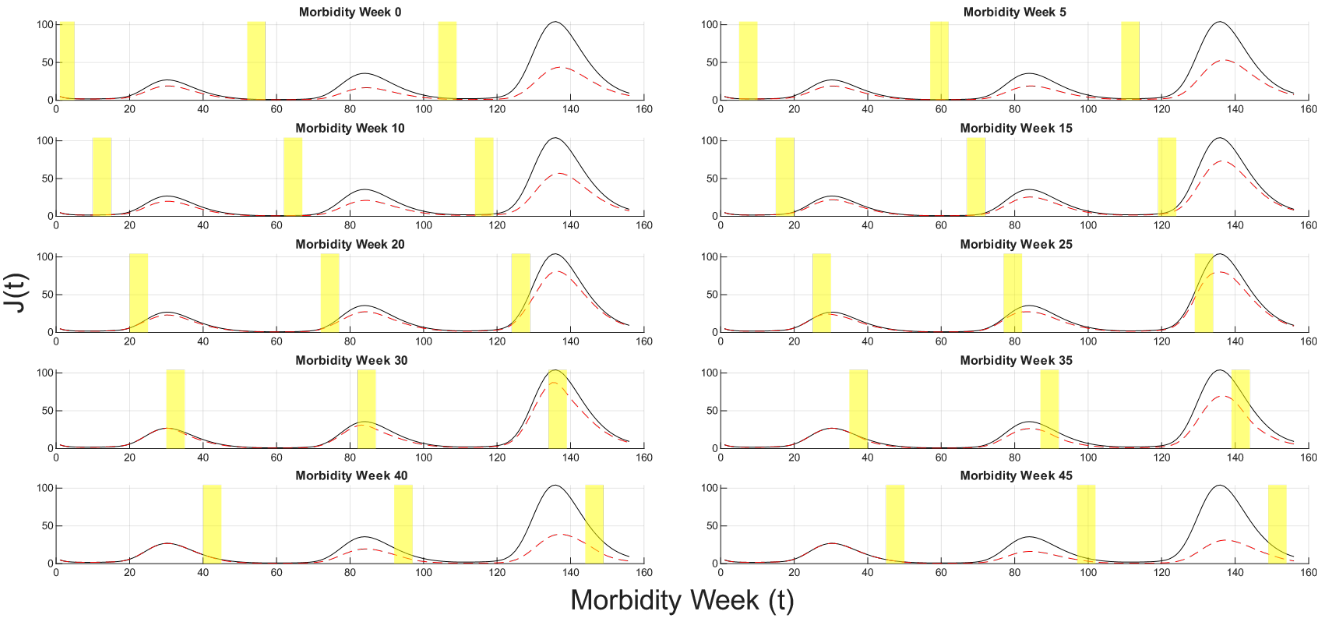
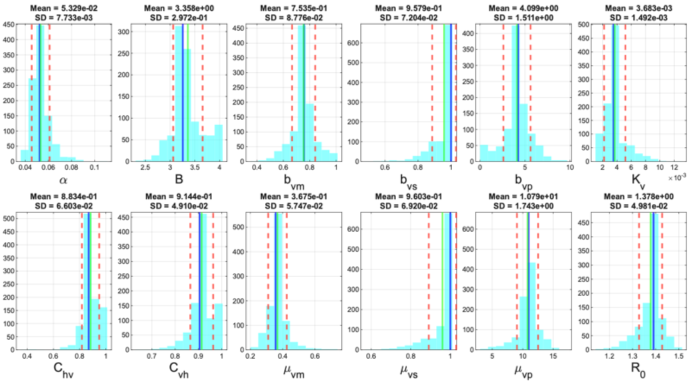


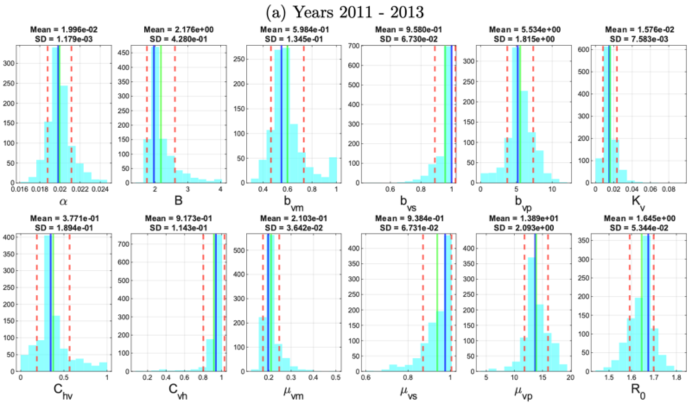
Figure 7: Plot of 2011-2013 best fit model (black line) vs new estimates (red dashed-line) after vector reduction. Yellow bars indicate the duration (5 weeks) of vector reduction (0.1) starting at the given morbidity weeks for each year.

Finally, optimal model parameter values were obtained using numerical methods. Specifically, these values represent local solutions to a given minimization problem and may not necessarily fall within epidemiologically accepted ranges. Moreover, multiple sets of parameter values can produce similar model outputs (Pope et al. 2009). To address this, we used initial parameter values informed by related studies and data from Baguio City and the Philippines. This approach helped ensure that our local solution is reasonably close to the true solution. Additionally, the model was successfully calibrated to dengue incidence data in Baguio City from 2011 to 2022.

Here are the histograms of the parameters from bootstrapping.

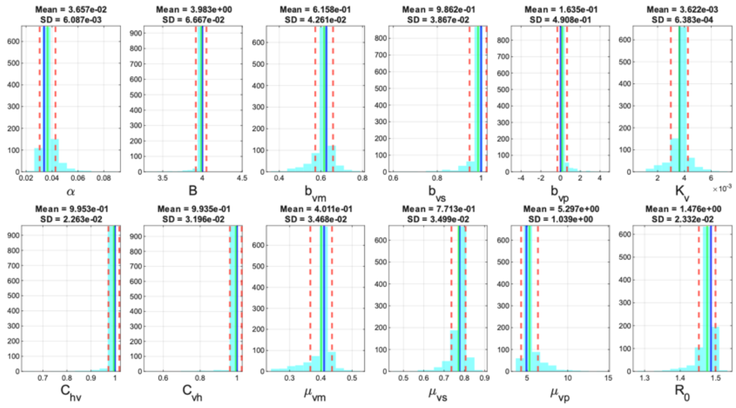


(a) Years 2011 - 2013

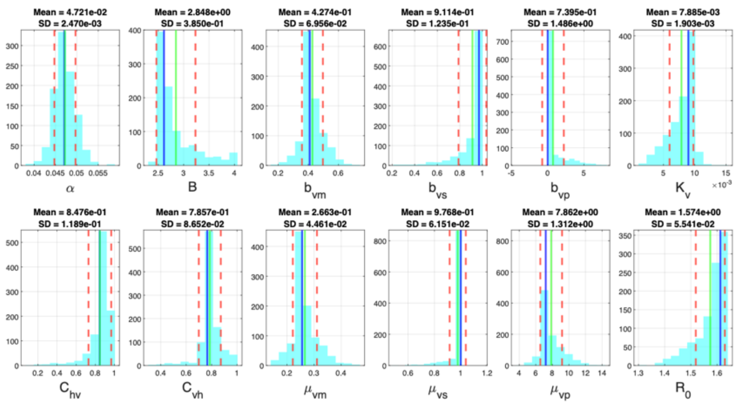


(b) Years 2014 - 2016

Figure 8: Histogram of estimated parameters obtained from bootstrapping. The green line indicates the mean value of the estimated parameters obtained from bootstrapping, and the blue line indicates the estimated parameters obtained from actual data, and the red line represents the lower and upper bounds of the 95% confidence interval.



(a) Years 2017 - 2019



(b) Years 2020 - 2022

Figure 9: Histogram of estimated parameters obtained from bootstrapping. The green line indicates the mean value of the estimated parameters obtained from bootstrapping, and the blue line indicates the estimated parameters obtained from actual data, and the red line represents the lower and upper bounds of the 95% confidence interval.

CONCLUSION

The dengue disease model presented by de los Reyes and Escaner (2018) was modified to analyze dengue incidence in Baguio City from 2011 to 2022, stratified into three-year cycles. The model incorporates periodic growth rates for vectors and carrying capacities for both host and vector populations. The model was proven to be well-posed, and the averaged and effective reproduction numbers were computed. Sensitivity analysis revealed that epidemiologically important parameters such as the transition rate from infected to hospitalized humans, vector biting rate, and bidirectional transmission probabilities, are highly sensitive. Parameter values were determined using a constrained-ODE optimization routine, with confidence intervals obtained via bootstrapping. The estimated parameters accurately capture strong surges in the mosquito population during rainy seasons. Notably, a reduction in mosquito carrying capacity observed from 2017 to 2019 is likely attributable to Local Government Unit (LGU) vector control efforts. These parameter estimates and insights into vector dynamics can serve as a reference for determining the optimal application of control and mitigation measures.

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CONFLICT OF INTEREST

No conflict of interest was reported by the authors.

CONTRIBUTIONS OF INDIVIDUAL AUTHORS

a. Junius Wilhelm G. Bueno conceptualized the model, performed computation work, prepared figures and tables, analyzed parameter estimates, authored and reviewed drafts of the paper, and approved the final draft.
b. Ronmar B. Macarubbo performed computation work, analyzed parameter estimates, authored and reviewed drafts of the paper, and approved the final draft.
c. Mark Ian C. Barreto performed computation work, analyzed parameter estimates, authored and reviewed drafts of the paper, and approved the final draft.
d. Gerald S. Navida performed computation work, analyzed parameter estimates, authored and reviewed drafts of the paper, and approved the final draft.
e. Andrei A. Domogo administered the project, conceptualized the model, analyzed parameter estimates, authored and reviewed drafts of the paper, and approved the final draft.
f. Priscilla S. Macansantos administered the project, conceptualized the model, analyzed parameter estimates, authored and reviewed drafts of the paper, and approved the final draft.

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