STOCASTIC ANALYSIS TO CONTROL DENGUE

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Abstract

This article investigates a dengue transmission model incorporating control techniques, utilizing the Homotopy Perturbation Method (HPM) for both analytical and numerical solutions. The study evaluates the stability theory and the basic reproduction number to understand disease dynamics. Graphical representations generated with MATLAB software indicate that dengue infection can be reduced to a manageable level through the applied control strategies.

Keywords: Mathematical model, Stability theory, basic reproduction number, Fuzzy control system, Simulation result

Introduction

Dengue remains one of the most prevalent and dangerous mosquito-borne diseases globally, with an estimated 390 million new infections annually, 96 million of which are symptomatic. The majority of these cases occur in Asia, with Africa, the Americas, and Oceania experiencing lower infection rates. Dengue is transmitted primarily by Aedes aegypti and Aedes albopictus mosquitoes and is caused by four closely related serotypes of the dengue virus (DENV-1 through DENV-4). While recovery from one serotype provides lifelong immunity against that specific strain, cross-immunity to other serotypes is partial and temporary, increasing the risk of severe dengue upon subsequent infections. Symptoms include high fever, severe headache, muscle and joint pain, and rash. Currently, there is no specific treatment for dengue, and the effectiveness of vaccines varies based on prior immunity and serotype.

Vector control remains the primary strategy for managing dengue transmission. This approach can be chemical, environmental, or biological. Chemical methods involve insecticides and larvicides, while environmental methods focus on reducing mosquito breeding sites. Biological control includes the use of natural predators or genetically modified mosquitoes, with Wolbachia-based methods showing promise due to their self-sustaining nature. Mechanical control through mass trapping has also shown effectiveness but is less commonly modeled.

This article reviews the use of mathematical models to understand and control dengue transmission. It highlights recent developments in modeling vector control methods, particularly those incorporating Wolbachia and other biological controls. The review spans literature from the past decade, focusing on gaps and advancements in vector control strategies and their integration into dengue transmission models. The findings aim to inform future research and improve the effectiveness of dengue control interventions.

Literature review

A substantial proportion of the global dengue burden is reported by the WHO African Region, which accounted for 95% of all dengue cases and 96% of dengue-related deaths in 2020 [1]. Segun I. Oke et al. [2] utilized an iterative forward-backward Runge-Kutta fourth-order scheme to assess the impact of various control strategies—such as bed nets, treatment, and insecticides—on malaria transmission and the infected population. Pardi Affandi [4] focused on South Kalimantan, developing a modified dengue distribution model and applying optimal control to the SIR model of malaria spread in the region.

Fekadu Tadege Kobe et al. [3] extended the basic SIR epidemic model by incorporating protection and treatment compartments, demonstrating that dengue transmission can be effectively managed with proper intervention strategies. Jacob C. Koella [5] highlighted that malaria endemicity could be better controlled using imagicides compared to parricides, and variations in transmission parameters significantly influence control outcomes. Marlies Craig et al. [6] proposed a straightforward computational approach to model malaria transmission, considering the biological constraints of climate on parasite and vector growth, and validated their model with recent field data.

This work [6] aimed to explore the impact of uncertain parameters on malaria models, building on the foundational SIR model developed by Kermack and McKendrick [7]. The study incorporated fuzzy set theory to address uncertainties in biological models, as initially discussed by Zadeh [6]. Many models in this domain have addressed the uncertainties inherent in fuzzy models and parameter spaces [7]. While fuzzy epidemic models have often focused on infectious diseases [8], dynamic systems with fuzzy transmission rates have been explored [11]. These models account for unknown recovery and transmission rates, and fuzzy sets are used to represent uncertain variables [12].

Preliminaries

Definition 1:

Let X is a non-empty crisp set. A fuzzy subset S of X is denoted by $\widetilde{S}$ and is defined as $\widetilde{S} = \{(x, \mu_{S(x)}) : x \epsilon X\}$ Where μ_S : X→ [0,1] is a membership function associated with a fuzzy set $\widetilde{S}$ which describes the degree of belongingness of x with X. Here we use the membership function μ(x) to indicate the fuzzy subsets $\tilde{S}$. Also, μ(x) is called fuzzy number if X is the set of real numbers.

Definition 2:

A Fuzzy set is called Triangular fuzzy number if the membership value can be represented by a Triangular Function. This function by a three parameters F(x: a, b, c) such as:

$$\text{F(x: a,b,c)} = \begin{cases} 0 & x < a \\ \frac{x-a}{b-a}, & a \le x \le b \\ \frac{c-x}{c-b}, & b < x \le c \\ 1 & x > c \end{cases}$$

Definition 3:

Let Ω be a nonempty set and P (Ω) denote the set of all subsets of Ω. Then μ: Ω → [0, 1] is a fuzzy measure [14]. If μ(ϕ) =0 and μ(Ω) =1

for A,BϵP(Ω) ,μ(A)≤ μ(B) if A⊂ B

Let μ: Ω → [0, 1] be an uncertain variable, i.e) μ is a fuzzy subset and μ a fuzzy measure on Ω. Then fuzzy expected value (FEV) of μ is the real number, defined by the sugeno measure.

$$FEV(\mu) = \int \mu d\mu \ = sup\{\min(\alpha, k(\alpha))\}, \quad 0 \le \alpha \le 1$$

Where $k(\alpha) = \mu\{\omega \epsilon \Omega : \mu(\omega) \ge \alpha\}$

Proposed Mathematical model:

In this paper, we propose an SEIR model to analyze the spread of dengue, incorporating uncertain parameters into the framework. This model describes the dynamics between the susceptible, exposed, infected, and recovered individuals within the population. To address dengue transmission, we extend this approach by employing a system of nonlinear ordinary differential equations that accounts for the entire population. The model includes considerations for varying virus loads and their impact on disease transmission.

In this study, we employ the differential equation for $\frac{dS}{dt}$ to model the dynamics of the susceptible population in the context of disease spread. Here, a represents the recruitment

rate, which captures the influx of new individuals into the susceptible group through births or immigration. The term bSI denotes the infection rate, where b is an uncertain parameter reflecting the probability of disease transmission per contact between susceptible S and infected I individuals. Finally, cS accounts for the natural death rate, representing the loss of susceptible individuals due to natural causes. This equation integrates these factors to describe how the number of susceptible individuals changes over time, providing insights into the impact of recruitment, infection, and mortality on disease dynamics.

$$\frac{dS}{dt} = a - b(\vartheta)SI - cS$$

The equation for $\frac{dE}{dt}$ in the proposed model, the dynamics of the exposed population Ein an infectious disease model. Here, bSI represents the rate at which susceptible individuals S become exposed to the disease through contact with infected individuals I, with b being the uncertain transmission rate. The term $-cE$ accounts for the natural death rate of exposed individuals, where ccc is the natural death rate coefficient. Meanwhile, $-dE$ captures the rate at which exposed individuals transition to the infected state, with d representing the uncertain rate of this progression. This equation balances the influx of exposed individuals from new infections against their natural death and progression to the infected stage.

$$\frac{dE}{dt} = b(\vartheta)SI - cE - d(\vartheta)E$$

The equation for $\frac{dI}{dt}$ in the proposed model, the dynamics of the infected population I in an infectious disease framework. The term dE represents the rate at which exposed individuals E develop into the infected state, with d being the uncertain developing rate. The terms $-eI$ and $-gI$ account for the rates of recovery and disease-induced death among infected individuals, where e and g are uncertain recovery and death rates, respectively. Additionally, $-cS$ reflects the impact of the natural death rate c on the susceptible population S, indirectly affecting the infected group. This equation integrates these factors to describe how the infected population evolves over time, balancing new infections against recovery, mortality, and indirect effects from the susceptible population.

$$\frac{dI}{dt} = d(\vartheta)E - eI - gI - cS$$

The equation $\frac{dR}{dt} = eI - d(\vartheta)R$ models the dynamics of the recovered population R in an infectious disease model. It captures the rate at which infected individuals I recover and

transition to the recovered state, with e representing the uncertain recovery rate. The term $-dR$ accounts for the natural death rate of recovered individuals, where d is the natural death rate coefficient. This equation balances the increase in recovered individuals due to recovery eI against the decrease due to natural death dR, thereby describing how the recovered population changes over time.

Analysis of fuzzy system:

The imprecise model of dengue infection is created by modifying the SEIR mathematical model. As a result, from disease to disease, the rate of recovery and transmission among individuals varies. The concept of a triangular fuzzy number with a membership function is:

$$\eta(\vartheta) = \begin{cases} 0, & if \quad \vartheta < \bar{\vartheta} - y, \\ \frac{\vartheta - \bar{\vartheta} + y}{y}, & if\ \bar{\vartheta} - y \leq \vartheta \leq \bar{\vartheta}, \\ \frac{-(\vartheta - \bar{\vartheta} - y)}{y}, & if \quad \bar{\vartheta} < \vartheta \leq \bar{\vartheta} + y, \\ 1, & if \quad \vartheta > \bar{\vartheta} + y. \end{cases}$$

Where y is the spread of each of the fuzzy sets assumed by $\vartheta$and $\bar{\vartheta}$is the central value. The linguistic variable's classification is given as weak, medium, and high for the triangular fuzzy number in this imprecise model, expressed by for a fixed $\bar{\vartheta}$. Each description can be thought of as a triangular, fuzzy number. Fig. 2 clearly shows $\eta(\vartheta)$

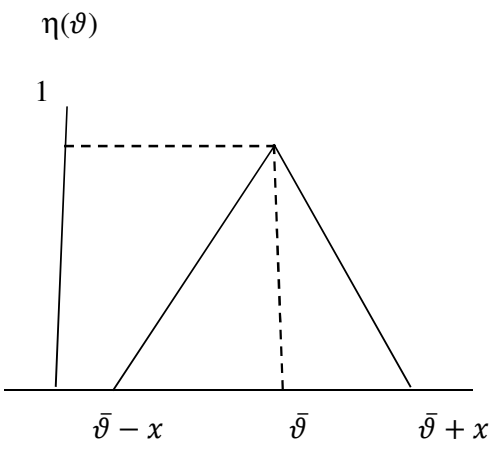


Figure:1 Triangular fuzzy number

According of the population's heterogeneity, we view the transmission rate and recovery rate as being confusing numbers. Assuming that the malaria virus can be transmitted by infected

people, this suggests that those who are susceptible to the disease can also transmit it to others. Let the transmission rate chance be represented. This model treats the transmission rate as a imprecise quantity, and its membership function, which depends on the virus load, is given by:

$$b(\vartheta) = \begin{cases} 0, & if\ \ \vartheta < \vartheta_{min}, \\ \frac{\vartheta - \vartheta_{min}}{\vartheta_M - \vartheta_{min}}, & if\ \ \vartheta_{min} \le \vartheta \le \vartheta_M, \\ 1, & if \vartheta_M \le \vartheta \le \vartheta_{max} \end{cases}$$

A minimum virus load, ϑ_M is an intermediate virus load, and ϑ_{max} is a maximum virus load every individual in a population all are existent. Fig. 3 presents the membership function of transmission rate.

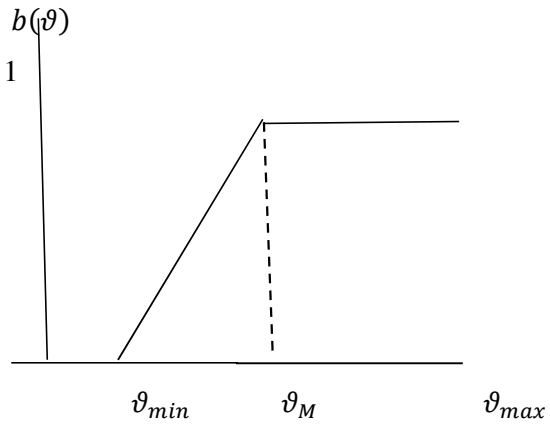


Fig: 3 Membership function of transmission rate

Let $d(\vartheta)$ the virus load dengue the rate of recovery from infectious dengue illnesses. The virus load affects how long it takes to recover from the illness. In this model using the membership function,$d(\vartheta)$ the recovery rate is therefore considered to be a uncertain number: $d(\vartheta) = \frac{(\emptyset_{min}-1)}{\vartheta_{max}}\vartheta + 1$, if $0 < \vartheta < \vartheta_{max}$ Where $0 < \emptyset_{min} < 1$, is the minimal recovery rate for the population of individuals, and where $\vartheta$is the virus load. Fig. 3 demonstrates the recovery rate's membership function.

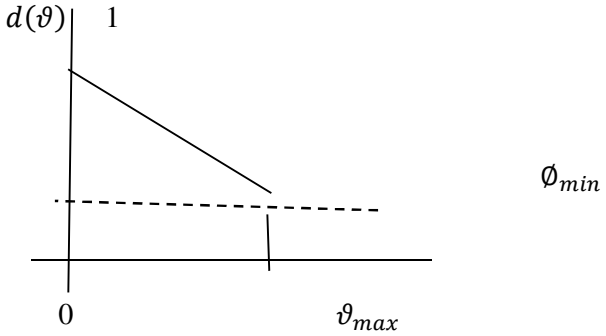


Fig: 3 Membership function of recovery rate

Stability analysis:

Stability analysis of an SEIR dengue model involves examining the equilibrium points where the rates of change of the compartments susceptible (S), exposed (E), infectious (I), and recovered (R) are zero. By constructing and evaluating the Jacobian matrix of the system's differential equations at these equilibrium points, one determines their stability by analyzing the eigenvalues of this matrix. If all eigenvalues have negative real parts, the equilibrium is stable.

Disease free equilibrium point:

The DFE is obtained by equating $\frac{dS}{dt} = 0$, and taking $\mathrm{E} = \mathrm{I} = \mathrm{R} = 0$. We obtained DFE point as $(\frac{a}{c}, 0,0,0)$

Endemic equilibrium point:

The endemic equilibrium points for our proposed is found to be $(\frac{a}{b+I}, \frac{bSI}{c+d}, \frac{dE-cS}{e+g}, \frac{eI}{d})$

Basic reproduction number:

The basic reproduction number is the average number of secondary infections that a single infected person causes over the course of their lifetime R_0 stands for the number. The next generation matrix method [21] is used to determine the system's basic reproduction number, R_0. To determine R_0:

$$R_0 = \frac{b}{d}$$

Fuzzy control system:

In this section, utilizing the imprecise basic reproduction number and the bifurcation parameter α*, we have examined the estimation of the malarial virus under management.

i) The viral load in this instance is low. (i.e) when $\overline{\phi} + x \leq \phi_{min}$ the time. R_f is the imprecise fundamental reproduction number, and it equals zero. It implies that the illness will be wiped out.

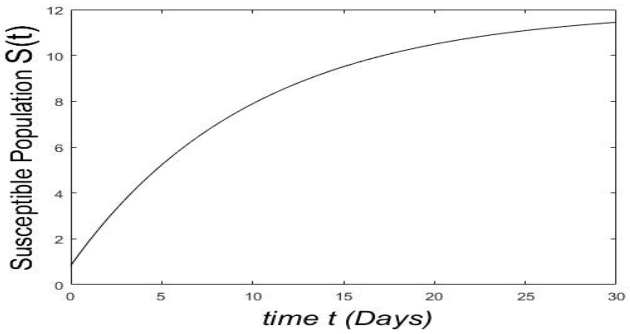
i) The viral load in this instance is Medium. (i.e) when $\overline{\phi} - x \geq \phi_{min}$ and $\overline{\phi} + x \leq \phi_M$ and. There is enough virus load ϕ that R_0 and $R_0(\phi)$ are equal. Additionally, because there is a medium amount of virus present, the average number of secondary cases R_f is higher than the number of secondary cases $R_0(\overline{\phi})$.

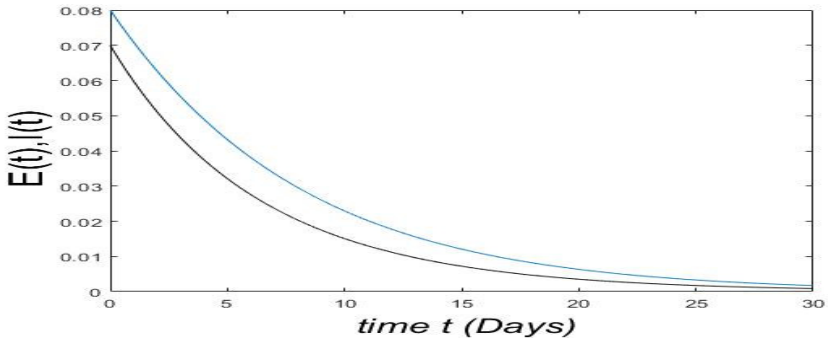
iii) The viral burden in this instance is high. (i.e) when $\bar{\phi} + x \leq \phi_M$ and $\bar{\phi} + x \leq \phi_{max}$ .Specifically, as a result,

$R_f > 1$, the illness will be endemic.

Numerical stimulation by homotopy method:

The dengue cases were analyzed retrospectively from 1998 to 2018, and it is observed that a total of 814,606 cases (incidence rate: 33.46 per million population) reported in India. The inter-annual variability of dengue cases shows that the cases were below 20,000 during 1998 to 2009 periods followed by the year 2010 onwards the cases were rapidly increased and the maximum cases were (188,401 cases) observed during the year 2017.





Conclusion:

The compartmental SEIR epidemic model has been utilized in this paper to examine the population spread. We determined the membership function and derived the imprecise parameters as a function of viral load. The bifurcation and the infection spread model with imprecise parameters were both evaluated by the results, with a focus on the suggested model's study.

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