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CONSTRUCTION OF STOCHASTIC MODEL FOR TIME TO DENGUE VIRUS TRANSMISSION WITH THREE PARAMETERS EXPONENTIAL DISTRIBUTION

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ABSTRACT

In this paper deals with the study of a stochastic model for predicting the time to Dengue virus transmission. As the immune capacities of an individual differ and also have its personal resistance, the antigenic diversity threshold is dissimilar for different person. We construct a stochastic model to study the damage process acting on the immune system that is non-linear. The mean of time to Dengue virus transmission and its variance are derived with numerical example.

Keywords: Antigenic diversity threshold, Poisson process, Mittag-Laffler distribution, Dengue virus transmission.

1. Introduction

Dengue Fever (DF) and Dengue Hemorrhagic Fever (DHF), collectively known as “dengue," are mosquito-borne, potentially mortal, flu-like viral diseases that affect humans worldwide. Transmitted to humans by the bite of an infected mosquito Aedesaegypti, dengue is caused by any one of four serotypes are termed as DENV-1, DENV-2, DENV-3, and DENV-4, or antigen-specific viruses; dengue virus is part of the Flaviviridae family. Dengue is one of the most rapidly spreading mosquito-borne viral diseases in the world and inflicts significant health, economic and social burdens on populations. A severe dengue fever can cause increased morbidity and lead into a mortality of 1-10% of its cases, depending on the medical preparedness for early diagnosis and treatment. The severe form of dengue is mediated by an increase in capillary permeability that can cause severe bleeding (e.g. Gastrointestinal bleeding) and plasma leakage resulting in ascites and pleural effusions. Dengue disease is a mosquito-borne condition that has become a major public health concern. Dengue severity can be classified into mild Dengue fever (DF) and severe Dengue or

Dengue hemorrhagic fever (DHF). There is no specific treatment for dengue, and a vaccine is not yet available. Temperature, rainfall and humidity interfere in all stages of vector development from the emergence and viability of eggs, to the size and longevity of adult mosquitoes, as well as their dispersal in the environment. So far, prevention of exposure and vector control remains the only alternatives to prevent dengue transmission.

Mathematical and statistical models describing the transmission of dengue viruses appeared in the study of observations related to pathogenesis of dengue hemorrhagic fever (Fischer, 1970) and providing a better understanding of the nature and dynamics of the transmission of dengue infection, as well as predict outbreaks and simulate the impact of control strategies in disease transmission (Rico-Hesse**,** 2010). The time to Dengue virus transmission by biting mosquito alone is the only mode of Dengue transmission. The bites of mosquitoes are assumed between a seropositive person who is labeled as index case and seropositive state takes place over an incubation period due to the contraction of Dengue to the partner from the index case by the bites of mosquitoes. In this research paper constructing a stochastic model to learn the damage process performing on the immune system that is non-linear and also mean and variance of time to Dengue virus transmission are derived with numerical example.

2. Concepts and terminologies

a. Immune system: A body has its defence efficacy against all infections. It is a complex network of organs, cells and proteins that defend the body against the invasion of foreign disease-bearing organisms such as Dengue.

b. Infection rate: It is the number of new Dengue infections per unit time at calendar time. Because of the varied nature of the mode of infection and also the fact that the time of Dengue transmission is unobservable due to the very wide variations in human immune system.

c. Incidence number :It is the number of Dengue cases diagnosed by calendar year. The number depends on the infection rate and the incubation distribution. It is an indicator, to some extent, of the severity with which the Dengue epidemic is spreading through human population.

d. Dengue incidence: It is the number of new cases that develop in a population per unit time causally per year.

e. Dengue incidence rate: The Dengue infection and incidence are two related concepts. The incidence rate is the ratio of the infective at calendar time to the numbers of infected individuals in the population at the time period.

f. Prevalence rate: It is the number of people infected with Dengue but alive at a calendar time. The prevalence rate is the ratio of the prevalence in the total number of population at the calendar time.

g. Susceptibility :Susceptible individuals are referred to as the non-infected individuals still at risk.

h. Seronegative: The time interval between the points of infection to the time at which the antibodies specific to Dengue are detected is called seronegative.

i. Seropositive: The onset of the production of antibodies in the patient is called seropositive.

j. Time to Dengue virus transmission: The process of change over from seronegative to seropositive is called the time to Dengue virus transmission. In other words, the infected individual remains strong until he develops detectable Dengue antibodies. The event of development of Dengue antibodies after infection is known as time to Dengue virus transmission.

k. Incubation period :The time duration between infections to develop of Dengue is called the incubation period. In another way, the time duration between time to Dengue virus transmission and Dengue when the time of infection is not known.

l. Viral load: The ability to measure the amount of virus in the blood is one of the most exciting advances in the study of Dengue infection.

m. Antigenic diversity threshold: If more and more Dengue is being transmitted by bites of mosquito from the infected person to the uninfected person, the antigenic diversity crosses a particular level that is known as the antigenic diversity threshold. Then there is a collapse of the immune system and hence time to Dengue virus transmission immediately takes place.

3. Nature of the study

The World Health Organization (WHO) ranks dengue among the most important infectious diseases with major impact on international public health (2002). The geographical distribution is expanding and the transmission rates are increasing (2007). Recent estimates indicate that approximately 3.5 billion people, ~55% of the world's population live in countries at risk for locally acquired dengue virus (DENV) infection (2007). DENV transmission and disease are determined by a complicated combination of factors involving the (i) virus, (ii) mosquito vector, (iii) human host and (iv) environment. Many interrelated factors such as biological and demographic issues influence dengue epidemiology and transmission. However, act in isolation and non-climatic variables, including population growth, human movement and environmental changes may have had far more to do with the global resurgence in dengue witnessed over recent decades than any direct effects of climate. The influences of climatic and non-climatic determinants of current and future dengue transmission are difficult to disentangle. The challenge in refining models of dengue transmission to maximize their utility in predicting the location, magnitude and timing of future dengue epidemics or emotional peaks in endemic cycles is to use data at appropriate spatial scales so that relevant ecological, social and demographic variables that operate on a local or regional scale can be incorporated into the model.

4. Need for the study

Dengue remains an enormous public health threat globally and in India, which will remain a major public health issue for the coming decades. The disease burden poses major pressure on health care services and has social and economic implications. Development of mathematical and statistical tools is needed and may require community participation for containment of dengue transmission. Knowledge of the virulence of the virus, including sequential infection, host factors, host immune response in dengue pathogenesis may promote treatment and intervention strategies.

5. Scope of the study

In spite of control measures, dengue has become a major public-health problem in India. Epidemics of increasing magnitude regularly occur against a background of an established endemic situation. Concomitantly, the number of severe dengue cases has risen over time. In India, the number of deaths will occur when the patients with suspected dengue infection tend to seek medical help at a relatively late stage after fever onset. An early diagnosis and proper treatment of dengue cases can reduce the risk of development of severe disease.

6. Importance of the study

The importance of understanding dengue incidence temporally and spatially is its utility in understanding the pathogenesis of dengue illness and disease severity. Important questions generated from this information are the role of herd immunity from the previous year's dengue transmission in modifying dengue disease in the subsequent year and how serotype-specific DENV transmission and infection rates are affected. In order to better understand the importance of individual-level risk factors for dengue, especially how individuals' knowledge may contribute to vector abundance and consequently dengue transmission. Dengue incidence and its temporal and spatial diversity in a population are important in designing dengue vaccine efficacy studies and estimating the population and geographic location required to assess statistical efficacy.

7. Objectives

Because of hardy associated with bites of mosquitoes, this work concentrates primarily on estimating the dynamics of the Dengue transmission by the bites of mosquitoes, as more than 95% of Dengue transmission accounts for bites of mosquitoes.

The objectives are:

- To realize the dynamics of Dengue in an infected individual so that control measures can be adopted in order to slow down the severity of the disease
- To learn the transmission dynamics of Dengue infection in a susceptible person so that the efficient strategies for controlling the spread of the epidemic can be implemented
- To categorize the statistical pattern of recognition of the time to Dengue virus transmission
- To derive the distribution of the time to Dengue virus transmission
- To grant the nature and extent of uncertainty in time to Dengue virus transmission with respect to the viral load, bite rate and antigenic diversity threshold

8. Assumptions and Notations

- Bites of mosquito are the only source of Dengue transmission.
- Damages to individuals are caused by transmission of Dengue at each bite and the inter arrival time between the bites are independent, identically distributed random variables.
- The damage process acting on the immune system of an infected individual is non-linear and cumulative.
- The total damage caused exceeds a threshold level, which itself is a random variable, the Dengue virus transmission occurs and the person is recognized as infected.
- The process that generates the bites, the sequence of damages and threshold are mutually independent.

and the model parameters are:

- Bites rate of the infected person (a)
- Intensity of the Dengue of the infected person (β)
- Antigenic diversity threshold (λ)

9. Stochastic model for time to Dengue virus transmission with three parameters Exponential distribution

9.1 Distribution of time to Dengue virus transmission

Let us consider a susceptible population whose major mode of transmission is through bites of mosquitoes. Assume that at time t=0, a new member tested Dengue negative enters the population and makes bites of mosquito with members of the susceptible population.

Let the bites of mosquito occur at random time points which is assumed to follow the Poisson distribution with parameter 'a' which is given as

$$p(t) = \frac{(at)^k \ e^{-at}}{k!}, \quad a > 0, \ t > 0 \ and \quad \text{k=1,2,3,.....}$$

Let G(t) be the distribution function of the inter arrival between the bites which follows Mittag-Leffler distribution. The distribution function of Mittag-Leffler distribution (Pillai, 1990) is given by

$$G_{a,\beta}(t) = \sum_{k=1}^{\infty} \frac{(-1)^{(k-1)}}{\Gamma(\beta k+1)} (at)^{\beta k}, \ t \geq 0, a > 0 \, and \, 0 < \beta \leq 1$$

Let the time to Dengue virus transmission of the individual be represented by the random variable T. We obtain the distribution of time to Dengue virus transmission by a stochastic model based on the

above assumptions with linear damage process acting on the immune system, we have the following theorem.

If the number of bites is an Alpha-Poisson process with parameters 'a' and 'β' and inter bite time is a Mittag-Leffler distribution while the threshold level is an exponential distribution $f(x) = \beta\lambda(1 - e^{-\lambda\,(x-\theta)})^{\beta-1} e^{-\lambda\,(x-\theta)}$ with parameter 'λ', 'β' and 'θ' then the probability density function of time to Dengue virus transmission is a three parameters Weibull distribution.

The density function of the distribution of time to Dengue virus transmission given as

$$f(t) = \begin{cases} \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1)C_i \; a \left[\frac{\left[(1+i)\lambda\right]^{\beta}}{a^{\beta} + \left[(1+i)\lambda\right]^{\beta}} \right] e^{-(at)\left[\frac{\left[(1+i)\lambda\right]^{\beta}}{a^{\beta} + \left[(1+i)\lambda\right]^{\beta}}\right]}, & t > 0, \lambda \; and \; \beta > 0 \\ 0 & , otherwise \end{cases}$$

Consider S(t) = P{no infection in (0,t)}

= P{T > t}

= $\sum_{K=1}^{\infty} P$ {Number of time to Dengue virus transmission before t given exactly k contact in (0,t) with intensity β }× P {exactly k contacts in (0,t) with intensity α }

$$= \left\{ \sum_{K=1}^{\infty} V_k(t) \right\} X \left\{ \sum_{K=1}^{\infty} X_i < Y \right\}$$

Where $V_k(t)$ = Probability of k contacts in (0,t) with intensity β (i.e., the Poisson distribution with parameter 'a')

$$V_k(t) = \frac{(at)^k \; e^{-at}}{k!}, \quad a > 0, \; t > 0 \qquad k = 1,2,3,\ldots$$

$$f(x) = \beta \;\; \lambda \;\; (1 - e^{-\lambda\,(x-\theta)})^{\beta-1} \; e^{-\lambda\,(x-\theta)}$$

$$P(X < Y) \quad = \int_{\theta}^{\infty} G(x) \beta \;\; \lambda \;\; (1 - e^{-\lambda\,(x-\theta)})^{\beta-1} \; e^{-\lambda\,(x-\theta)} dx$$

$$\text{where } G^*(\lambda) = \int_{\theta}^{\infty} G(x) \, \beta \;\; \lambda \;\; (1 - e^{-\lambda\,(x-\theta)})^{\beta-1} \; e^{-\lambda\,(x-\theta)} dx$$

$$\lim it \begin{matrix} x = \theta \; , \; z = 0 \\ x = \infty \; , \; z = \infty \end{matrix}$$

Let u = x- θ, x = u + θ, dx = du

$$P(X < Y) = \beta\lambda \int_{\theta}^{\infty} G(u+\theta) \, (1 - e^{-\lambda u})^{\beta-1} e^{-\lambda u} du \begin{cases} (a+b)^n = \sum_{i=0}^{n} nC_i \; a^{n-i} b^i \\ and \\ (a-b)^n = \sum_{i=0}^{n} (-1)^i nC_i \; a^{n-i} b^i \end{cases}$$

$$P(X < Y) \quad = \beta\lambda \int_{\theta}^{\infty} G(u+\theta) \left[\sum_{i=0}^{\beta-1} (-1)^i (\beta-1)C_i \, (1)^{\beta-1-i} \left[e^{-\lambda u}\right]^i \right] e^{-\lambda u} du$$

$$= \beta\lambda \left[\sum_{i=0}^{\beta-1} (-1)^i (\beta-1) C_i \; g^* \left[\frac{(1+i)\lambda}{(1+i)\lambda} \right] \right]$$

$$P(X < Y) = \beta \left[\sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i \, g^*[(1+i)\lambda] \right]$$

$$p(\sum_{i=1}^{k} X < Y) = \beta \left[\sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i \left(g^*[(1+i)\lambda] \right)^k \right]$$

where $g^*(\lambda)$ is the Laplace Transform of g(x) and $g_x(x)$ = p.d.f of $\sum_{K=0}^{\infty} X_i$

$$S(t) = \left\{ \sum_{K=0}^{\infty} V_k(t) \right\} \left[\beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i \left(g^*[(1+i)\lambda] \right)^k \right]$$

$$= \sum_{K=0}^{\infty} \frac{(at)^{\beta k} \, e^{-(at)^\beta}}{k!} \left[\beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i \left(g^*[(1+i)\lambda] \right)^k \right]$$

$$= e^{-(at)^\beta} \sum_{k=0}^{\infty} \frac{(at)^{\beta k}}{k!} \beta \left[\sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i \left(g^*[(1+i)\lambda] \right)^k \right]$$

$$= \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) \, C_i \; e^{-(at)\left[1 - g^*[(1+i)\lambda]\right]}$$

Since the probability density function of X follows Mittag – Leffler then

$$g^*(u) = \frac{a^\beta}{a^\beta + u^\beta}$$

$$g^*(1+i)\lambda = \frac{a^\beta}{a^\beta + [(1+i)\lambda]^\beta}$$

$$1 - g^*(1+i)\lambda = \frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta}$$

L(t) = 1- S(t) is called Prevalence function

$$= 1 - \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) \, C_i \; e^{-(at)\left[1 - g^*[(1+i)\lambda]\right]}$$

$$L(t) = 1 - \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) \, C_i \; e^{-(at)\left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta}\right]}$$

The probability density function of time t of Dengue virus transmission is given by

$$f(t) = \frac{d}{dt} L(t)$$

$$= \frac{d}{dt} \left\{ 1 - \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i \; e^{-(at)\left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta}\right]} \right\}$$

$$f(t) = \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i \; a \left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta} \right] e^{-(at)\left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta}\right]}$$

The above function is in the form of three parameters Weibull distribution. Subsequently, we show how the distribution of time to Dengue virus transmission can be generated from the

stochastic model derived from the Dengue transmission. The distribution of time to Dengue virus transmission depends on the stochastic variations in the viral intensity, bite rate and antigenic diversity threshold.

9.2 Probability of time to Dengue virus transmission

The probability of time to Dengue virus transmission is calculated for various intervals by defining

$$p_i = \int_{t_i}^{t_{i+1}} f(t)\, dt \qquad for\ i = 1, 2, 3.....$$

$$where\ f(t) = \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i\, a \left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta} \right] e^{-(at)\left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta} \right]}, t > 0, \lambda > 0$$

$$p_i = \int_{t_i}^{t_{i+1}} \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i\, a \left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta} \right] e^{-(at)\left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta} \right]} dt$$

$$Let\ \ M_i = a \left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta} \right]$$

$$p_i = \int_{t_i}^{t_{i+1}} \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i\, M_i\, e^{-M_i t} dt$$

$$p_i = \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i \left[e^{-a\left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta} \right] t_i} - e^{-a\left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta} \right] t_{i+1}} \right]$$

where$t_i$and t_{i+1} has one width of class interval width

9.3 Performance of measures to time to Dengue virus transmission

The expected time to Dengue virus transmission and its variance are obtained below:

The expected time to Dengue virus transmission and its variance are obtained below:

$$E[T] = \int_0^\infty t\ f(t)\, dt$$

$$E[T] = \int_0^\infty t\ \ \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i\, a \left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta} \right] e^{-(at)\left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta} \right]} dt$$

$$Let = \mathrm{M_i} = a \left[\frac{[(1+i)\lambda]^\beta}{a^\beta + [(1+i)\lambda]^\beta} \right] \qquad and\ \ y = t\ M_i \qquad \frac{dy}{M_i} = dt$$

$$E[T] = \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i\, M_i \int_0^\infty \frac{y}{M_i} e^{-y}\, \frac{dy}{M_i}$$

$$E[T] = \frac{\beta}{a} \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} \left[\frac{a^\beta + [(1+i)\lambda]^\beta}{[(1+i)\lambda]^\beta} \right] (\beta-1) C_i$$

$$E[T^2] = \int_0^\infty t^2\ f(t)\, dt$$

$$E[T^2]=\int_0^{\infty} t^2 \quad \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i \; a\left[\frac{[(1+i)\lambda]^{\beta}}{a^{\beta}+[(1+i)\lambda]^{\beta}}\right] e^{-(at)\left[\frac{[(1+i)\lambda]^{\beta}}{a^{\beta}+[(1+i)\lambda]^{\beta}}\right]} \; dt$$

Let $M_i = a\left[\frac{[(1+i)\lambda]^{\beta}}{a^{\beta}+[(1+i)\lambda]^{\beta}}\right]$ and $y = t\, M_i$ $\frac{dy}{M_i} = dt$

$$E[T^2]= \beta \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} (\beta-1) C_i \; M_i \int_0^{\infty} \left(\frac{y}{M_i}\right)^2 e^{-y} \; \frac{dy}{M_i}$$

$$E[T^2] = \frac{2\beta}{a^2} \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} \left[\frac{a^{\beta}+[(1+i)\lambda]^{\beta}}{[(1+i)\lambda]^{\beta}}\right]^2 (\beta-1) C_i$$

$V[T] = E[T^2] - E[T]$

$$= \left\{\frac{2\beta}{a^2} \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} \left[\frac{a^{\beta}+[(1+i)\lambda]^{\beta}}{[(1+i)\lambda]^{\beta}}\right]^2 (\beta-1) C_i\right\} - \left[\frac{\beta}{a} \sum_{i=0}^{\beta-1} \frac{(-1)^i}{(1+i)} \left[\frac{a^{\beta}+[(1+i)\lambda]^{\beta}}{[(1+i)\lambda]^{\beta}}\right] (\beta-1) C_i\right]^2$$

This is the mean and variance of time to Dengue virus transmission when the bite rate is Poisson process and the antigenic diversity threshold is generalized exponential distribution with three parameters.

9.3a Mean time to Dengue virus transmission with respect to intensity and bite rate

To find the variation in mean time to Dengue virus transmission, three levels of β=1, 2 and 3 is considered, and the other parameter is kept constant so as to give an antigenic diversity threshold in λ=5. From the Table-1 we observe that the time to Dengue virus transmission happens quickly if the intensity increases in the given antigenic threshold.

Figure-1 shows that the mean time to Dengue virus transmission decreases when the bite rate increases for the given intensity β and antigenic diversity threshold λ. Also, it shows that the mean time to Dengue virus transmission decreases as the intensity increases for the given antigenic diversity threshold and bite rate 'a'.

Table 1: Mean time to Dengue virus transmission when λ=5

a	Mean		
	λ=5		
	β=1	β=2	β=3
1	1.20	1.07	1.02
2	0.70	0.64	0.61
3	0.53	0.52	0.50
4	0.45	0.42	0.39
5	0.40	0.28	0.25
6	0.37	0.15	0.12
7	0.34	0.11	0.10

9.3b Mean time to Dengue virus transmission with respect to antigenic diversity threshold and bite rate

To find the variation in mean time to Dengue virus transmission, three levels of λ =6, 8 and 10 is considered, and the other parameter is kept constant so as to give an intensity in β=1. From the Table-2 we observe that the time to Dengue virus transmission happens slowly if the antigenic diversity threshold increases in the given intensity.

Figure-2 shows that the mean time to Dengue virus transmission decreases when the bite rate increases for the given intensity β and antigenic diversity threshold λ.

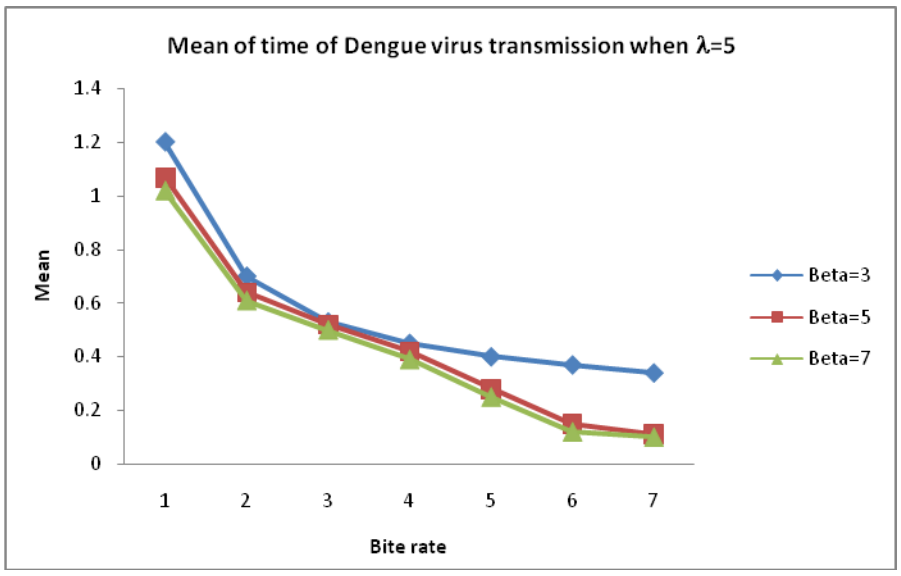

Figure 1: Mean of time to Dengue virus transmission when λ=5

Table-2: Mean of time to Dengue virus transmission when β=1

a	Mean		
	β=1		
	λ=6	λ=8	λ=10
1	1.10	1.13	1.17
2	0.60	0.63	0.67
3	0.43	0.46	0.50
4	0.35	0.35	0.42
5	0.30	0.35	0.37
6	0.27	0.29	0.33
7	0.24	0.27	0.31

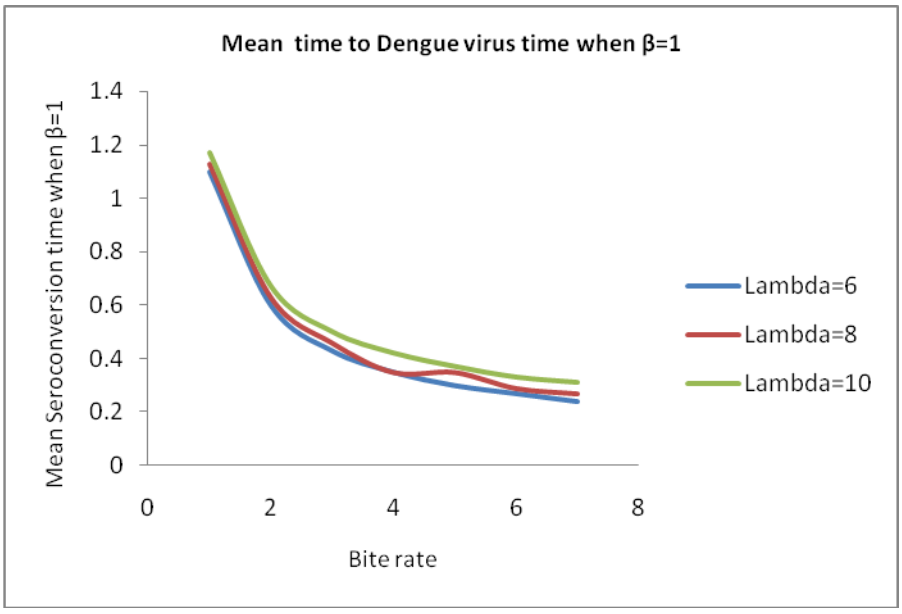

Figure-2: Mean of time to Dengue virus transmission when β=1

9.3c Time variance to Dengue virus transmission with respect to intensity and bite rate

To find the time variance to Dengue virus transmission, three levels of β=1, 2 and 3 is considered, and the other parameter is kept constant so as to give an antigenic diversity threshold in λ=5. From the Table-3 we observe that the Dengue virus transmission happens quickly if the intensity increases in the given antigenic threshold.

Figure-3 shows that the time variance to Dengue virus transmission decreases when the bite rate increases for the given intensity β and antigenic diversity threshold λ. Also, it shows that the time variance to Dengue virus transmission decreases as the intensity increases for the given antigenic diversity threshold and bite rate 'a'. Similarly, when intensity and antigenic diversity threshold increase the Dengue virus transmission happens very quickly.

Table-3: Time variance to Dengue virus transmissionwhen λ=5

a	Variance		
	λ =5		
	β=1	β=2	β=3
1	1.44	1.14	1.04
2	0.49	0.40	0.33
3	0.28	0.26	0.23
4	0.20	0.22	0.21
5	0.16	0.21	0.20
6	0.13	0.21	0.18
7	0.12	0.22	0.13

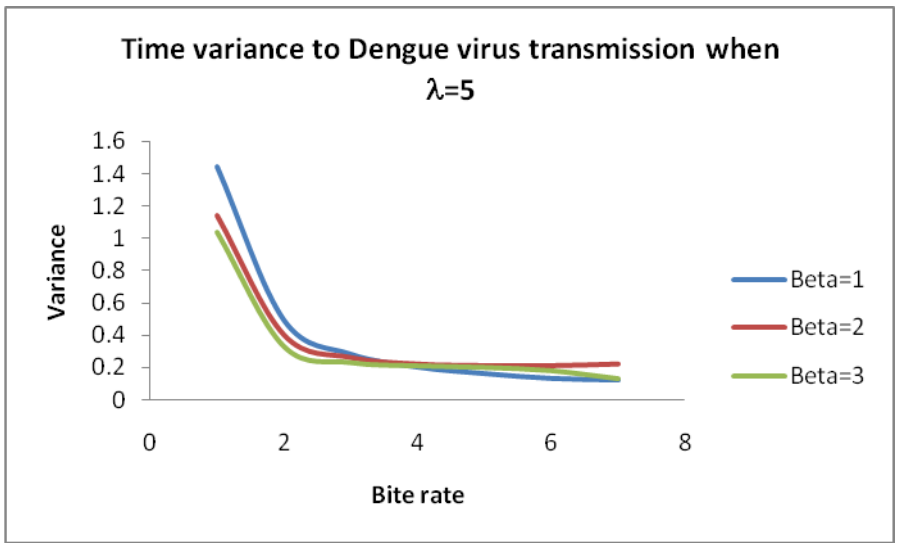

Figure-3: Time variance to Dengue virus transmission when λ=5

9.3d Time variance to Dengue virus transmission with respect to antigenic diversity threshold and bite rate

To find the time variance to Dengue virus transmission, three levels of λ =6, 8 and 10 is considered, and the other parameter is kept constant so as to give an intensity in β=5. From the Table-4 we observe that the Dengue virus transmission happens quickly if the antigenic diversity threshold increases in the given intensity.

Figure-4 shows that the time variance to Dengue virus transmission decreases when the bite rate increases for the given intensity β and antigenic diversity threshold λ. Also, it shows that the

time variance to Dengue virus transmission decreases as the antigenic diversity threshold increases for the given intensity and bite rate 'a'. Similarly, when intensity and antigenic diversity threshold increase the Dengue virus transmission happens very quickly.

Table 4: Variance of time to Dengue virus transmissionwhen β=5

a	Variance		
	β=1		
	λ=6	λ=8	λ=10
1	1.36	1.27	1.21
2	0.44	0.39	0.36
3	0.25	0.21	0.19
4	0.17	0.14	0.12
5	0.13	0.11	0.09
6	0.11	0.09	0.07
7	0.10	0.08	0.06

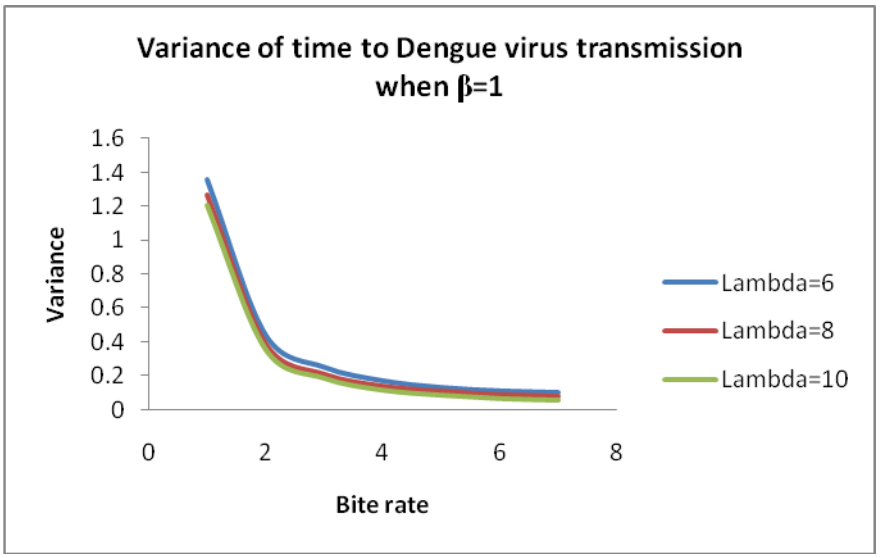

Figure 4: Variance of time to Dengue virus transmissionwhen β=5

From the above Figures 1, 2, 3 and 4 of mean and variance of time to Dengue virus transmission, we observe that the mean time to Dengue virus transmission is less than the variance of time to Dengue virus transmission for the same parametric values. These coincide with the results of Venkatesan and Nanthakumar (2004) that the time distributions of Dengue virus transmission have larger variance than mean.

10. Conclusion

In the study of Dengue epidemic the time to Dengue virus transmission is an inevitable component. Since the bite rate is non observable in most cases one mosquito would expect that the spread of Dengue would have an impact on the human life. In this research article we constructed a stochastic model for the time to Dengue virus transmission and it is noted that mean time to Dengue virus transmission is less than the variance of time to Dengue virus transmission.

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WEBSITES

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