

A Mathematical Model for Predicting Transmission of Dengue Fever

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Abstract:- One of the means for predicting Dengue Fever transmission usually includes, conducting a surveillance of the causal vector in a demarcated area, noting the level of infestation of the vector in the area and computing the House Index (HI), Container Index (CI) and Breteau Index (BI), which are interpreted for possible transmission of the dengue or otherwise. We therefore theorise this physical process and phenomena with a mathematical model in this paper, for predicting the occurrence of dengue fever without going to the field. The main objective of the model is to be able to estimate the time period by which the population of the vector will grow and travel/cover a given area, infest a number of houses and hence translate into a possible transmission of dengue, using the HI specifically. The model we provided is a composite of four key sub-models. The first part of the model represents the phenomenon of the population dynamics of the *Aedes* mosquito which is the vector for dengue transmission; the second part provides the mechanism for predicting the area the mosquitoes will infest over time; the third part estimates the number of houses that may be infested in the area, and the last part computes the HI. In essence, if we introduce one infected female *Aedes* mosquito into a community (a given area) as our initial population, we should be able to estimate by which time the computed HI will translate into the transmission of dengue fever in that community, holding several mathematical assumptions true for our model.

Keywords:- *Mathematical Models; Dengue Fever Transmission; Prediction Models; Epidemiological Models for Dengue Transmission; Process Automation;*

I. INTRODUCTION

Dengue Fever is a global Public Health concern which is viral-transmitted, primarily by the female *Aedes* mosquitoes; principally by the *aegypti* and secondarily by the *albopictus* species. Humans are infected with dengue virus through mosquito bites which may result in subclinical or severe illness, and even death of the infected person [1].

Places with high population of the *Aedes* mosquito are therefore prone to recording an outbreak of the disease; the main spread of the disease occurs when an adult female *Aedes* mosquito bites a human who has the dengue virus, it picks the virus and then transmits it to an uninfected person; there are other minor means of transmission of dengue, such as, from

mother to child through pregnancy and through breastfeeding, and in very rare cases through organ transplant and blood transfusion. [2].

Several countries have had different levels of outbreaks of dengue; even though the disease was only present in a few countries in the 70s, over hundred countries now have many of their citizens infected with the disease, making them endemic areas [1]. The global prevalence of dengue is increasing with a high rate over the years, with about 70% of the disease burden in Asia [3]–[5]. This has raised a lot of international concerns and at the same time triggered both global and localised strategies to stop dengue outbreaks from burdening our world further. Some effective measures include strategies to control the vector, while other efforts are invested in producing effective vaccines for the disease. Since it is only in recent times effective vaccines (especially for children) for dengue are being produced and approved for use [6], much of the efforts skew towards vector control measures, which is mainly to reduce vector densities, to curtail the spread of dengue.

The population of *Aedes* mosquitoes in a given area or a community, directly translates into the possibility of occurrence of dengue in that community [7]. There are consequently, several prediction mechanisms that rely on the population and ecological characteristics of *Aedes* to establish the possibility of outbreaks or otherwise, in an area. The main scheme used for prediction is the computation of different entomological indices which are varied with different focuses on different life stages of the mosquito, thus, the pupae, the larvae and the adult, depending on the objective of an entomological or epidemiological study [8]. The common vector indices used include the Breteau Index (BI), Container Index (CI) and House Index (HI); these indices are computed to monitor vector densities in areas, in order to inform control actions. These indices have been standardised differently with different thresholds for different places [9]. This has resulted in many critiques of the indices as an effective predictive mechanism for dengue. Notwithstanding the critiques, the World Health Organisation (WHO) outlines and encourages entomological surveillances for establishing these indices as an effective means of monitoring outbreaks [10].

The processes that lead to the computation of the indices for determining the transmission of dengue include, employing acceptable and standard means of collecting the *Aedes* mosquito (different life stages of the vector considered

are study-specific) to establish the population and distribution of the vector in a given area under inspection. Basically, the presence of the vector is sought for in houses, where water holding containers are searched, including other means for larvae and pupae. Adult mosquitoes may also be collected through the use of traps, resting collection, human landing techniques etc. There are also other clinical assessment that are usually conducted to confirm the species of the vector; the collected figures of the needed species are then used to compute the HI, BI, or CI, to establish the level of infestation in the area inspected [10].

These processes even though are effective, they are quite involving and strenuous. Some surveillances may take months or even years; on the score of this background and constraints, we explored the possibility of a mechanism (mathematical scheme) that can provide some insight of how the transmission of dengue may occur overtime, with some initial estimated population of *Aedes* mosquito in a given area. It is important to note that, our theoretical effort for automating the process is not intended to replace the physical surveillance efforts, but rather, to offer a computational mechanism that allows us to predict some possible outcome of transmission before even going to the field. This therefore should be considered more as analogous and complementary than a replacement.

II. OTHER RELATED WORKS

Mathematical models have become very imperative for solving real world situations, especially for the fact that our world is fast advancing with increasing complex problems that cannot be solved by common sense and rational reasoning. Different forms of models have often been used to underline the logical frameworks for automation in different works of life, even in fields with non-structured or non-formalised systems such as Natural Language Processing [11]–[13], and some Social Science concepts [14].

Mathematical models have been used heavily in epidemiological studies, where a lot of efforts have been made by several researchers to model different concepts of dengue fever as well as its vector for different research objectives.

While some researchers have provided models based on the population dynamics of the host and vector of dengue, for instance: Esteva and Vargas [15], [16] proposed models for the transmission of dengue for two different population sizes in two different research works; one with constant human population and variable vector population, and the other with variable human population size. In the former, they established an epidemic equilibrium for dengue via an analysis based on the results of theory of competitive systems and stability of orbits, where the vector population is asymptotically constant. In the later, they used the theory of competitive systems, centre manifold theorem and matrices to determine a global asymptotic stability of the equilibrium points. Other researchers [17] have also drawn their modelling efforts for dengue infections based on the features of antibody dependent enhancement within the host which is then related to transmission by the vector, using partial differential equations and numerical methods. Whiles others have also modelled as

well as analysed other models targeting dengue vaccines in relation to the dynamics of the spread of the disease [18].

There have been extensive and comprehensive systematic reviews of mathematical [19], [20] and statistical [21] models of dengue and its dynamics, spanning up to 10 years or more of research work, mostly from scientific papers, espousing elaborate and diversified efforts researchers have contributed in very phenomenal ways to the understanding of the epidemiology of the dengue disease. We cannot over emphasise the rewards of these research works. We have however found a lean gap in these researches, which is not a technical weakness *per se*, but a shift of attention away from providing a model that can project a time period dengue transmission may occur if an infected vector is introduced into a host population given the dynamics of vector population growth in a community. This is the crux of our model where we underpin the novelty of our research in providing a mathematical framework that underscores events that lead to dengue transmission and at the same time predicting the time a transmission may occur.

III. METHODOLOGY

This research is conducted based on abstract mathematical modelling principles [22], mainly for presenting the physical process and epidemiological phenomena for predicting dengue fever in a given area. We employed dynamic modelling techniques, since our model is principally transient, and depends on changes of events and processes over time. We also chose an analytical approach instead of numerical, for building our mathematical theories, mainly because our main focus is to provide a generic mathematical system that is able to give insight to the population dynamics of *Aedes* mosquitoes, as well as present the events of infestation of houses in a given area by the mosquitoes and consequently predict the transmission of dengue over a period of time.

We considered the WHO guidelines for determining the infestation levels of *Aedes*. Three main indices are usually considered in the prediction of dengue transmission, and are computed as follows [10];

$$\text{Breteau Index (BI)} = \frac{\text{Number of positive containers}}{\text{houses infested}} \times 100$$

$$\text{Container Index (CI)} = \frac{\text{Number of positive containers}}{\text{Containers inspected}} \times 100$$

$$\text{House Index (HI)} = \frac{\text{Infested houses}}{\text{Houses inspected}} \times 100$$

We however, used only the HI in our mathematical system because; on one hand, we find it sufficient for our prediction goal, and on the other hand, we find it challenging to use the BI and CI in our system; this is because, we find it not feasible to model a process to predict the number of infested containers in houses, since there is no way of telling how many containers a house can have, and since BI and CI are computed using the number of infested containers, they are seemingly not plausible for our system.

We thought through the several natural and controlled conditions that influence the population, spatial and ecological dynamics of the *Aedes* mosquitos as well as other plausible characteristics for the transmission of dengue in a community. We have however limited our model to positive and negative growth factors, as well as a carrying capacity mechanisms as our control measures to keep our model simple.

IV. PROPOSED MODEL AND SOLUTIONS

A. Model 1: Population Dynamics of Aedes Mosquitoes

We denote *A* for *Aedes* mosquitoes, such that, *dA* is the population change in *A* as a function of change in time *dt*. We also denote δ as the rate of positive change in *A*, and *m* as the rate of declined change in *A*, while *k* is the carrying capacity or limiting factor of exponential growth of the population of *A*.

$$\frac{dA}{dt} = \delta A \left(1 - \frac{A}{k}\right) - mA$$

Solution of the Model

$$dA = \left(\delta A \left(1 - \frac{A}{k}\right) - mA\right) dt$$

$$kdA = (-\delta A^2 + k\delta A - kmA)dt$$

$$\frac{dt}{k} = -\frac{dA}{\delta A^2 + (km - k\delta)A}$$

Separable Equation;

$$M(A)d(A) = N(t)dt$$

We integrate both sides, thus;

$$\int \frac{1}{k} dt = \int -\frac{1}{\delta A^2 + (km - k\delta)A} dA$$

Left Integral (Li)

$$\int \frac{1}{k} dt = \frac{t}{k} + C$$

Right Integral (Ri)

$$\int -\frac{1}{\delta A^2 + (km - k\delta)A} dA - \int \frac{1}{A(\delta A - k\delta + km)} dA$$

For;

$$x = \frac{A}{\delta A - k\delta + km}$$

$$A = (\delta A - k\delta + km)x$$

$$A = \frac{k\delta - km}{\delta} - \frac{km - k\delta}{\delta(\delta x - 1)}$$

$$dA = \frac{km - k\delta}{(\delta x - 1)^2} dx$$

$$\begin{aligned} &= - \int -\frac{1}{(k\delta - km)x} dx \\ &= \frac{1}{k\delta - km} \ln(|x|) = \frac{\ln(|x|)}{k\delta - km} \\ &= \frac{\ln(|A|)}{k\delta - km} - \frac{\ln(|\delta A - k\delta + km|)}{k\delta - km} \\ &\quad \frac{\ln\left(\frac{A}{\delta A - k\delta + km}\right)}{k\delta - km} \end{aligned}$$

therefore; Li = Ri

$$\frac{t}{k} + C = \frac{\ln\left(\frac{A}{\delta A - k\delta + km}\right)}{k\delta - km}$$

$$e^{\frac{t}{k} + C} = e^{\frac{\ln\left(\frac{A}{\delta A - k\delta + km}\right)}{k\delta - km}}$$

$$A = \frac{kme^{mt}}{C\delta e^{\delta t} - \delta e^{mt}} + \frac{ke^{mt}}{C\delta e^{\delta t} - e^{mt}} - \frac{km}{\delta} + k$$

where *C* is constant and *a* = *a*(*t*).

The rate of change δ of *A* is the growth factor which is as a result of change in the production of eggs *db* that mature into mosquitoes, which are then introduced into the population over time. We therefore define δ as;

$$\delta = \frac{db}{dt}$$

However, since one female *Aedes* mosquito is considered to lay a particular number of eggs within its lifespan, we can consider an average constant of eggs from one female mosquito affecting the overall population of mosquitoes over time. We denote that average constant as μ .

This implies that;

$$\frac{db}{dt} = \mu A$$

$$db = \mu A dt$$

Separable Equation;

$$M(b) db(A) = N(t) dt$$

$$\int \mu A dt = \int 1 db$$

Left Integral

$$\int \mu A dt = \mu At + C$$

Right Integral

$$\int 1db = b + C$$

Therefore;

$$b = \mu At + C,$$

where C is constant, $t = t(b)$

B. Model 2: Area of Infestation of Mosquitoes Over Time

In this section we provided a mechanism to estimate how the mosquitoes with a changing population from Model 1 move to infest a given area over time, and consequently infest the number of houses in the given area. We consider an average distance r , which a mosquito can move/cover (away from its breeding site). We also compute the average House Density (HD), of a given area for inspection per some unit measure (e.g. m^2/km^2). We modelled the area infested ψ by A as a function of the distance r travelled by the mosquito. We then modeled the change in the distance traveled by A over time t .

Therefore, our model for the area infested by A is;

$$\frac{d\psi(A)}{dr} = \pi r^2$$

Where ψ is the area infested by A , as function of r distance moved. Given that ψ changes at an average rate λ .

$$\frac{dr}{dt} = \lambda$$

$$dr = \lambda dt$$

$$\int dr = \int \lambda dt$$

$$r = \lambda t + C$$

Therefore, solving for the area ψ infested by A ;

$$\frac{d\psi(A)}{dr} = \pi r^2$$

$$d\psi(A) = \pi r^2 dr$$

$$\int d\psi(A) = \int \pi r^2 dr$$

Li

$$\int 1d\psi(A) = \psi(A) + C$$

Ri

following Power Function integral,

$$\int r^n dr = \frac{r^{n+1}}{n+1}, \text{ at } n = 2$$

$$\int \pi r^2 dr = \pi \frac{r^3}{3}$$

$$\int \pi r^2 dr = \frac{\pi r^3}{3} + C$$

Li = Ri

$$\psi(A) = \frac{\pi r^3}{3} + C$$

Solving for $\frac{d}{dr}$

$$\psi(A) = 2\pi r$$

C. Model 3: Number of Houses Infested (H-inf)

Since $\frac{d\psi(A)}{dr}$ is the area Infested by A over distance r , we have to know the number of houses that are in the infested area. First, we estimate the House Density (HD) of the total area under inspection, which is given by;

$HD = \frac{h_n}{\psi_n}$, where h_n is the total number of houses in the area under inspection, and ψ_n is the total area under inspection.

The resultant HD values give us the average number of houses per unit distance. For instance, if the area for inspection is considered in square kilometers, then, the HD value will give us the number of houses per every $1km^2$.

Second, we provide a model to compute the number of Houses Infested (H-inf) using the estimated HD value. This is given as follows;

$$H-inf = HD \times \frac{d\psi(A)}{dr}$$

D. Model 4: House Index Computation and Transmission Prediction

Form Model 3, we can now compute the House Index as follows;

$$HI = \frac{\sum_{x=0}^j H-inf_x}{h_n} \times 100$$

Our h_n is the total number of houses in the demarcated area for inspection, where $n \neq 0$, and $\sum_{x=0}^j H-inf_x$ is the sum total of houses infested with A , as r changes in $\frac{d\psi(A)}{dr}$ over time.

Finally, we consider the time t by which the infestation of A in an area occurs as they travel distance r , will translate into an HI that will be considered as a possible transmission of the disease or otherwise.

The determination or classification of HI into transmission or non-transmission of dengue is done by comparing the HI to a pre-determined or standardised index threshold, which we denote as $t-h$. Therefore, our final classification will be done as follows;

$$\left\{ f(t-h) = \begin{cases} 1, \text{ transmission} & HI \leq t-h \\ 0, \text{ non-transmission} & \text{otherwise} \end{cases} \right| t-h$$

There are many standardised thresholds a researcher can choose to work with, while some are computed for area-specific epidemiological studies, the choice of threshold

however, must be done to strictly conform to the dynamics of the area under study for the prediction (guided by WHO standards).

All sub-models so far are related and interdependent for the complete computation and prediction of the transmission of dengue fever in a community. The model is presented in a very generic form so that it can be useful for different epidemiological estimations, especially when real values are to be given to the model for its output. Since important input and output standard values such as the lifespan, life-cycle, number of eggs, maximum distance travel, survival and death rates as well as indices thresholds of the *Aedes* mosquito can vary dramatically, depending on a number of important factors, our model in its generic form will allow specifying the ideal numeric data at implementation level. The real-life process and phenomena thus, being effectively represented by our composite model, provides the theoretical framework and opportunity for effective automation. The model diagram below makes picturesque the flow, interconnection and function of all subcomponents of the model.

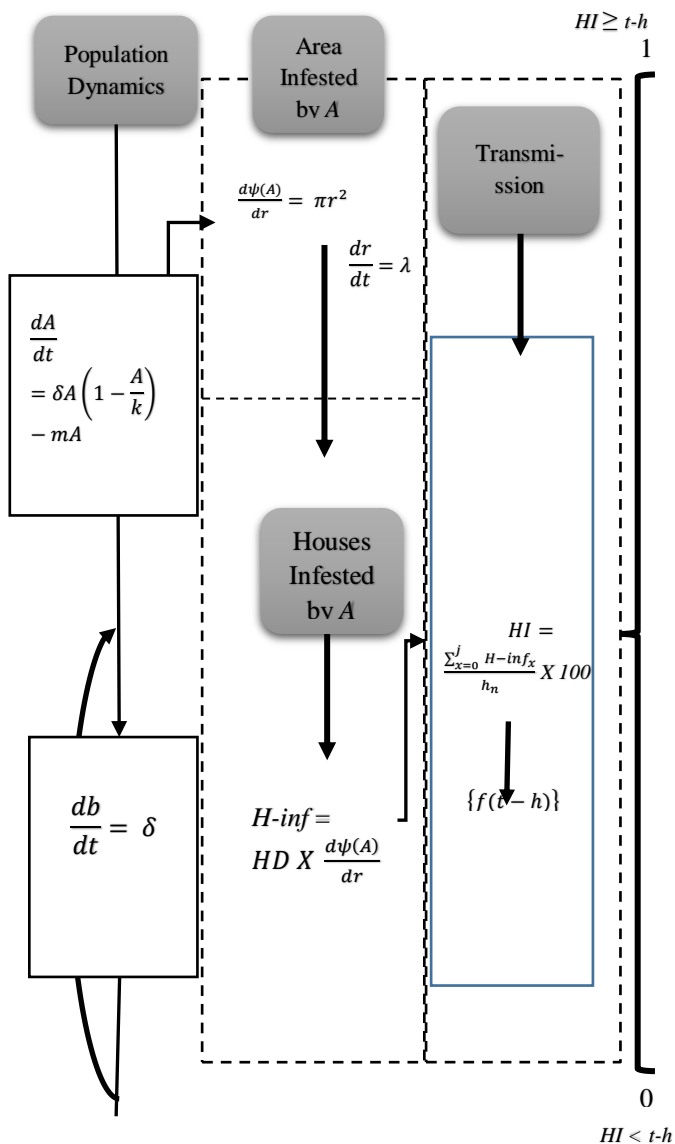


Fig. 1. Composite Model Diagram

V. CONCLUSION

Monitoring the spread of dengue disease can be a very tricky task, since there are several factors that determine the spread of the disease which are not constant over time. It is therefore prudent to have tools that can give us a reasonable picture of how things may seem in the future (on account of the spread of dengue), and when they may be apparent if we assume or estimate an initial population of *Aedes* in a community. This can inform how much time that is available for control actions. We have effectively provided a mathematical model for this purpose, where we modelled the population dynamics of *Aedes* vector, the time it takes for the growing *Aedes* population to infest an area, the number of houses likely to be infested in the area, which consequently allows us to compute the HI for predicting dengue transmission and the time it may occur.

We hope to identify an archetypal case study for our model for future research, so that we can advance our theoretical concepts; we hope to provide an advanced computational tool based on this model that will be tuned to near-precision to augment the control efforts that are already in place for managing the spread of the dengue disease.

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