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Analysis of Sub-Models for the Basic Transmission Dynamics of Zika Virus Infection

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ABSTRACT

In this paper, an age-structured model for the transmission dynamics of Zika virus infection that included the effects of vertical transmission in Aedes vectors, and sexual transmission in humans was formulated and analysed. The model was shown to have a unique, positive and bounded solution in a certain uniformly bounded invariant set. The model was validated using the 2016 outbreak data for Colombia using stratified proportionate random sampling to distribute infections according to the age classification in the model. Due to the complex nature of the model, three independent sub-models were extracted and studied individually. In each case, we computed the disease-free equilibrium (DFE) and the basic reproduction number of the sub-models. The reproduction numbers were found to exist if a certain threshold value R_a^0 which corresponds to the vertical reproduction number in the Aedes vectors progeny is less than one. The DFEs of the sub-models were shown to be globally asymptotically stable if their associated reproduction number is less than one. Global sensitivity analysis using PRCC method revealed that vector biting and mortality rates, vector-human ratio parameter and sexual transmission rates are the most sensitive parameters that should be targeted for comprehensive intervention and disease management.

1. Introduction

Zika virus (ZIKV) infection is an emerging arbovirus of the *Flavivirus* family transmitted to humans through the bites of day-time active mosquitoes particularly *Aedes Aegypti* (Lanko *et al*, 2016; CDC, 2019; Shere *et al*, 2021; Rezapour *et al*, 2020). The disease has been proved to be sexually transmitted in humans (CDC, 2019) throughout an extensive period even when the blood sample of the infectious sexually active human is tested negative (Maxian *et al*, 2017). Experimental studies support the claim that, ZIKV can be transmitted vertically in the Aedes vectors progeny, which may provide a means for the arbovirus to persist during adverse climatic conditions due to the resilience of the *Aedes* mosquito's eggs to withstand harsh climate changes (CDC, 2019), or in the absence of susceptible vertebrate host (Saravanan *et al*, 2016). The clinical symptoms of ZIKV includes; fever, myalgia, arthralgia, edema of extremities, maculopapular rash, retro-orbital pain, conjunctivitis, and lymphadenopathies (Rahman *et al* 2019). Previously, Zika virus was of little public health relevance. But since 2007, it has emerged explosively causing series of epidemics in Micronesia, South Pacific and the Americas (Scott *et al*, 2016). The disease captured worldwide attention following the onset of a massive outbreak in Brazil in May 2015, in which by the year 2016, the world health Organization declared ZIKV infection a Public Health Emergency of International Concern (PHEIC) (Saravanan *et al*, 2016). due to its connection with neurological disorders such as Guillain-Barre Syndrome and microcephaly.

Deterministic and mechanistic mathematical modelling technique provides a means for studying dynamics of infectious diseases via compartmental modelling approach. An example of such models can be found in Usman *et al*, (2017), Yuan *et al*, (2021), Al-Maqrashi *et al*, (2022), Sow *et al*, (2022), Wang *et al*, (2024). Therefore, in this paper,

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we will use the deterministic modelling technique to develop a model that incorporates vectorial, vertical and sexual transmission to study the basic transmission dynamics of the ZIKV infection in a completely susceptible hosts namely; the human, adult and aquatic vector hosts. Thus, the developed model will be studied extensively.

2. Model Formulation and Validation

2.1 Formulation of the model

The model in this paper; called the basic transmission dynamics model (BDTM) for the ZIKV infection is an age-structured model with vital dynamics formulated via the Susceptible, Exposed, Infectious, Removed (SEIR) compartmental approach. We categorized the human population $N_H(t)$ at time t into three disjoint age groups namely; pre-sexually active, sexually active and post-sexually active designated by the variables $N_{H1}(t)$, $N_{H2}(t)$ and $N_{H3}(t)$ respectively. Since ZIKV can be transmitted vertically in the *Aedes* vectors progeny, the model further divided the *Aedes* vectors population into adults $N_V(t)$ and aquatic $N_A(t)$ at time t. We also divided the infectious human compartment into symptomatic (reported) and asymptomatic to account for the contribution of unreported ZIKV cases on the dynamics. Two additional compartments i.e., $J_{H.S2}(t)$ and $J_{H.A2}(t)$ are added in the sexually active human population to account for the extended infectiousness period (about 30 days) of the symptomatic and asymptomatic infectious individuals to humans through effective sexual contact. Variables with subscripts H_i for $i=1,2,3$ belongs to the three age-classes defined in this section and that, variables with subscript V and A belongs to the mature and aquatic vector populations respectively. Asymptomatic and symptomatic humans are assumed equally infectious and that, all model parameters are strictly nonnegative. This information is represented by the schematic diagram in Figure (1).

Thus, let

$$s_{h1}=\frac{S_{H1}}{N_H}, e_{h1}=\frac{E_{H1}}{N_H}, i_{h,a1}=\frac{I_{H,A1}}{N_H}, i_{h,s1}=\frac{I_{H,S1}}{N_H}, r_{h1}=\frac{R_{H1}}{N_H}, s_{h2}=\frac{S_{H2}}{N_H}, e_{h2}=\frac{E_{H2}}{N_H}, i_{h,a2}=\frac{I_{H,a2}}{N_H},$$

$$j_{h,a2}=\frac{J_{H,a2}}{N_H}, i_{h,s2}=\frac{I_{H,S2}}{N_H}, j_{h,s2}=\frac{J_{H,S2}}{N_H}, r_{h2}=\frac{R_{H2}}{N_H}, s_{h3}=\frac{S_{H3}}{N_H}, e_{h3}=\frac{E_{H3}}{N_H}, i_{h,a3}=\frac{I_{H,A3}}{N_H}, i_{h,s3}=$$

$$\frac{I_{H,S3}}{N_H}, r_{h3}=\frac{R_{H3}}{N_H}, s_V=\frac{S_V}{N_H}, e_V=\frac{E_V}{N_H}, i_V=\frac{I_V}{N_H}, s_a=\frac{S_A}{N_H}, i_a=\frac{I_A}{N_H}.$$

Suppose a constant parameter m satisfies the relation $m=\frac{N_V}{N_H}$, where m is the vectors-to-human ratio such that, N_V and N_H are the adult vectors and the human populations respectively. Therefore, the description of the model and the schematic diagram in Figure (1) satisfies the following standardized model equations:

$$
\begin{aligned}
\frac{ds_{h1}}{dt} &= \Lambda - \left(\lambda_{h1} + \rho_1 + \mu_H\right) s_{h1}(t), \\
\frac{de_{h1}}{dt} &= \lambda_{h1} s_{h1}(t) - \left(\varepsilon + \rho_1 + \mu_H\right) e_{h1}(t), \\
\frac{di_{h,a1}}{dt} &= (1-q)\varepsilon e_{h1}(t) - \left(\gamma + \rho_1 + \mu_H\right) i_{h,a1}(t), \\
\frac{di_{h,s1}}{dt} &= q\varepsilon e_{h1}(t) - \left(\delta + \rho_1 + \mu_H\right) i_{h,s1}(t), \\
\frac{dr_{h1}}{dt} &= \gamma i_{h,a1}(t) + \delta i_{h,s1}(t) - \left(\rho_1 + \mu_H\right) r_{h1}(t), \\
\frac{ds_{h2}}{dt} &= \rho_1 s_{h1}(t) - \left(\lambda_{h2} + \rho_2 + \mu_H\right) s_{h2}(t), \\
\frac{de_{h2}}{dt} &= \rho_1 e_{h1}(t) + \lambda_{h2} s_{h2}(t) - \left(\varepsilon + \rho_2 + \mu_H\right) e_{h2}(t), \\
\frac{di_{h,a2}}{dt} &= \rho_1 i_{h,a1}(t) + (1-q)\varepsilon e_{h2}(t) - \left(\gamma + \rho_2 + \mu_H\right) i_{h,a2}(t), \\
\frac{dj_{h,a2}}{dt} &= \gamma i_{h,a2}(t) - \left(r + \rho_2 + \mu_H\right) j_{h,a2}(t), \\
\frac{di_{h,s2}}{dt} &= \rho_1 i_{h,s1}(t) + q\varepsilon e_{h2}(t) - \left(\delta + \rho_2 + \mu_H\right) i_{h,s2}(t), \\
\frac{dj_{h,s2}}{dt} &= \delta i_{h,s2}(t) - \left(r + \rho_2 + \mu_H\right) j_{h,s2}(t), \\
\frac{dr_{h2}}{dt} &= \rho_1 r_{h1}(t) + r\left(j_{h,a2}(t) + j_{h,s2}(t)\right) - \left(\rho_2 + \mu_H\right) r_{h2}(t), \\
\frac{ds_{h3}}{dt} &= \rho_2 s_{h2}(t) - \left(\lambda_{h3} + \mu_H\right) s_{h3}(t), \\
\frac{de_{h3}}{dt} &= \rho_2 e_{h2}(t) + \lambda_{h3} s_{h3}(t) - \left(\varepsilon + \mu_H\right) e_{h3}(t), \\
\frac{di_{h,a3}}{dt} &= \rho_2 i_{h,a2}(t) + (1-q)\varepsilon e_{h3}(t) - \left(\gamma + \mu_H\right) i_{h,a3}(t), \\
\frac{di_{h,s3}}{dt} &= \rho_2 i_{h,s2}(t) + q\varepsilon e_{h3}(t) - \left(\delta + \mu_H\right) i_{h,s3}(t), \\
\frac{dr_{h3}}{dt} &= \rho_2\left(r_{h2}(t) + j_{h,a2}(t) + j_{h,s2}(t)\right) + \gamma i_{h,a3}(t) + \delta i_{h,s3}(t) - \mu_H r_{h3}(t), \\
\frac{ds_V}{dt} &= \phi s_a(t) - \left(\lambda_v + \mu_V\right) s_V(t), \\
\frac{de_V}{dt} &= \lambda_v s_V(t) - \left(\kappa + \mu_V\right) e_V(t), \\
\frac{di_V}{dt} &= \kappa e_V(t) + \phi i_a(t) - \mu_V i_V(t), \\
\frac{ds_a}{dt} &= m\theta - \pi\theta i_a(t) - \left(\phi + \xi\right) s_a(t), \\
\frac{di_a}{dt} &= \pi\theta i_a(t) - \left(\phi + \xi\right) i_a(t),
\end{aligned}
\tag{2.1}
$$

subject to the following initial conditions:

$$s_{hi}(0)>0, e_{hi}(0)\geq 0, i_{h,ai}(0)\geq 0,\ j_{h,a2}(0)\geq 0, i_{h,si}(0)\geq 0,\ j_{h,s2}(0)\geq 0, r_{hi}(0)\geq 0,$$
$$s_V(0)>0, e_V(0)\geq 0, i_V(0)\geq 0, s_a(0)>0, i_a(0)\geq 0,$$
$$s_{hi}+e_{hi}+i_{h,ai}+j_{h,a2}+i_{h,si}+j_{h,s2}+r_{hi}\leq 1, s_V+e_V+i_V\leq 1, s_a+i_a\leq 1, \qquad (2.2)$$

with

$$\lambda_{h1}=\lambda_{h3}=\beta_{HV}i_V(t),\ \lambda_{h2}=\beta_{HV}i_V(t)+\beta_{HH}\left(\sigma_{HH}i_{h,a2}(t)+i_{h,s2}(t)+\Phi\left(\sigma_{HH}j_{h,a2}(t)+j_{h,s2}(t)\right)\right),$$
$$\lambda_v=\beta_{VH}\sum_{i=1}^{3}\left(\sigma_{VH}i_{h,ai}(t)+i_{h,si}(t)\right):\ \beta_{HV}=\frac{m\rho_{HV}\sigma_H\sigma_V}{m\sigma_V+\sigma_H},\ \beta_{VH}=\frac{\rho_{VH}\sigma_H\sigma_V}{m\sigma_V+\sigma_H},\ \beta_{HH}=s\rho_{HH};\ i=1,2,3.$$

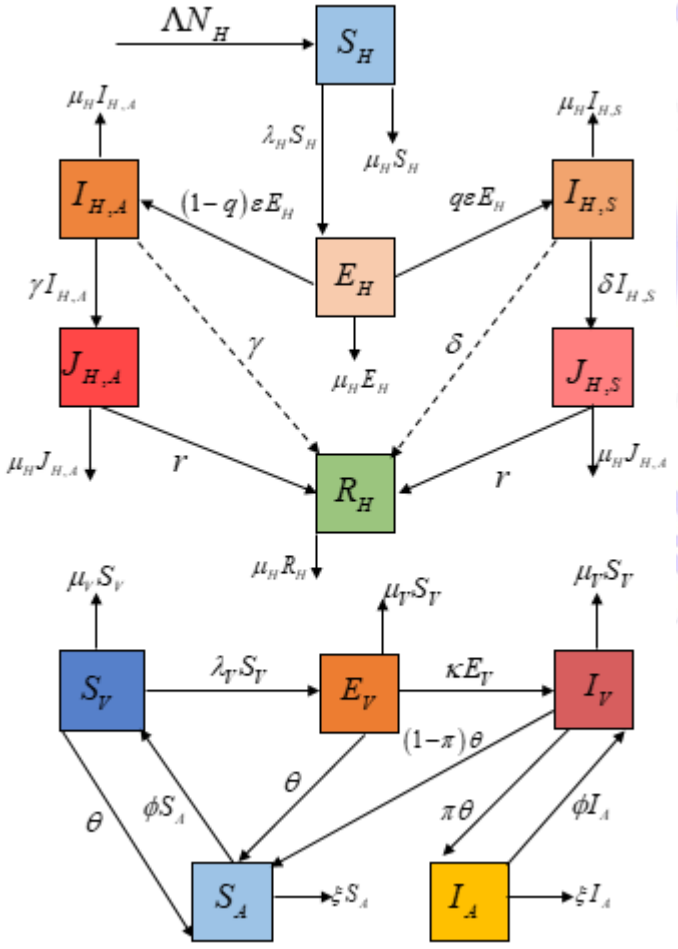

Figure 1: Schematic Diagram of the Basic Dynamics Model

2.2 Existence, uniqueness, positivity and boundedness of solution

Theorem 2.1.: *(Existence, uniqueness and positivity). Let the model in* (2.1) *together with the initial condition in* (2.2) *be represented by the system*

$$\frac{dx}{dt} = f(t,x), \quad x(0) = x_0; \quad x \in \mathbb{R}_+^{22}. \tag{2.3}$$

Suppose $J = [0,a]$ *and* $Z = \overline{B(x_0,b)}$, *where* $f : J \times Z \to \mathbb{R}_+^{22}$ *is Lipschitz with Lipschitz constant* L *and* $|f(x)| \le M$ *for all* $x \in Z$, *then, the model has a unique solution* $x \in C^0(J,Z)$ *as long as the time-interval is chosen with* a *satisfying* $0 < a < \min\left(\frac{1}{L}, \frac{b}{M}\right); Lb < 1$. *Moreover, the solution* $x(t)$ *of the model with nonnegative initial conditions remain positive for all* $t > 0$.

Proof:

To begin the proof, we start by showing f is Lipschitz. Thus, we can write the model system in the form

$$f(y) = Ax + \mathbf{g}(x) + \mathbf{h}$$

where A, $\mathbf{g}$ and $\mathbf{h}$ are matrices of orders (22×22), (22×1) and (22×1) respectively, representing the linear, nonlinear and the constant terms in the standardized model. By the definition of the Lipschitz operator L in the work of Coddington & Levinson (1955), we have;

$$\begin{aligned}
\left\| f(x(t)) - f(x^*(t)) \right\| &= \left\| Ax(t) - Ax^*(t) + \mathbf{g}(x(t)) - \mathbf{g}(x^*(t)) + \mathbf{h}(x) - \mathbf{h}(x^*) \right\|, \\
&= \left\| Ax(t) - Ax^*(t) + \mathbf{g}(x(t)) - \mathbf{g}(x^*(t)) \right\|, \\
&\le \left\| A(x(t) - x^*(t)) + \mathbf{g}(x(t)) - \mathbf{g}(x^*(t)) \right\|, \\
&\le \|A\| \|x - x^*\| + \left\| \mathbf{g}(x) - \mathbf{g}(x^*) \right\|, \\
&\le (\|A\| + \Psi) \|x - x^*\|, \\
&\le L \|x - x^*\|, \qquad L = \|A\| + \Psi < \infty.
\end{aligned}$$

Integrating (2.3) from 0 to t (w.r.t), and applying the initial condition, we obtain

$$x(t) = x_0 + \int_0^t f(x(s))ds \tag{2.4}$$

.

Therefore, $x(t)$ in (2.4) is a solution of model (2.3) if and only if it is a solution of (2.4). From (2.4),

define a new operator Γ on a bounded function $Z = \overline{B(x_0, b)}$ from a closed interval $[0, a]$ to $\mathbb{R}^{22}$ such that

$$\Gamma(z(t)) = x_0 + \int_0^t f(z(d))ds, \tag{2.5}$$

satisfying $\Gamma(0) = x_0$. Now, we need to show that, the operator Γ is a contraction mapping [15].

Consequently, we need to show that, the operator Γ maps a complete metric space $C^0(J, Z)$ to itself. To do that, we will impose a condition on a that strictly guarantees $\Gamma(z(t)) \in Z$ for all time $t \in J$, given any $z(t) \in Z$ by

$$\begin{aligned} |\Gamma(z(t)) - x_0| &= Sup_{t\in J}\left|\int_0^t f(z(s))ds\right|, \\ &\leq \int_0^a |f(z(s))|ds, \\ &\leq Ma, \quad but \;\; a < \min\left(\frac{1}{L}, \frac{b}{M}\right), \\ &\leq b. \end{aligned} \tag{2.6}$$

Therefore, this imposed strict restriction ensures that, $\Gamma(z(t)) \in Z$ for all time $t \in J$. Finally, we show that the operator Γ is a contraction mapping on $C^0(J, Z)$. Thus, given any two functions $z_1, z_2 \in C^0(J, Z)$, by the definition of Γ in (2.4), we have

$$\begin{aligned} |\Gamma(z_1(t)) - \Gamma(z_2(t))| &= Sup_{t\in J}\left|\int_0^t [f(z_1(s)) - f(z_2(s))]ds\right|, \\ &\leq Sup_{t\in J}\left(\int_0^t |f(z_1(s)) - f(z_2(s))|ds\right), \\ &\leq \int_0^t |f(z_1(s)) - f(z_2(s))|ds, \\ &\leq L\int_0^t |z_1(s) - z_2(s)|ds, \\ &\leq Lb|z_1(s) - z_2(s)|. \end{aligned} \tag{2.7}$$

since $Lb < 1$, then, the mapping Γ is a contraction on $C^0(J, Z)$. Thus using Contraction Mapping Theorem

(Robert & Klaus, 2009), we conclude that, there exist a unique fixed point $z \in C^0(J, Z)$ for the standardized model.

To prove positivity of the model solution, we used the first equation in (2.1) for the pre-sexually active susceptible humans as reference. Therefore, let

$$t_* = \sup\{s_{hi}(0) > 0, e_{hi}(0) \geq 0, i_{h,ai}(0) \geq 0, j_{h,a2}(0) \geq 0, i_{h,si}(0) \geq 0, j_{h,s2}(0) \geq 0, r_{hi}(0) \geq 0, s_V(0) > 0, e_V(0) \geq 0, i_V(0) \geq 0, s_a(0) > 0, i_a(0) \geq\}.$$

By appropriate technique, using the first equation in the system (2.1), we can see that

$$s_{h1}(t) = s_{h1}(0) \times \exp\left(-\int_0^{t_*} \lambda_{h1}(u)\,du - \rho_1 t - \mu_H t\right) + \exp\left(-\int_0^{t_*} \lambda_{h1}(u)\,du - \rho_1 t - \mu_H t\right) \times \int_0^{t_*} \Lambda \exp\left(\int_0^{z} \lambda_{h1}(u)\,du - \rho_1 z - \mu_H z\right) dz > 0. \quad (2.9)$$

Meanwhile, in the same, it can be shown that

$$s_{h2}(t) > 0, s_{h3}(t) > 0, e_{hi}(t) > 0, i_{h,ai}(t) > 0, j_{h,a2}(t) > 0, i_{hsi}(t) > 0, j_{h,s2}(t) > 0, r_{hi}(t) > 0,$$
$$s_V(t) > 0, e_V(t) > 0, i_V(t) > 0, s_a(t) > 0, i_a(t) > 0,$$

for all $t > 0;\quad (i = 1, 2, 3)$. Hence, all the solution of the basic dynamics model in proportions with nonnegative initial conditions are positive for all $t > 0$.

Lemma 2.1. *(Boundedness of solution and invariant region): The closed set*

$$D = \{D_h \cup D_V \cup D_a \subset \mathbb{R}_+^{17} \times \mathbb{R}_+^3 \times \mathbb{R}_+^2 \subseteq \mathbb{R}_+^{22} : D_h = (s_{hi}, e_{hi}, i_{h,ai}, j_{h,a2}, i_{h,si}, j_{h,s2}, r_{hi}) \in \mathbb{R}_+^{17},$$
$$D_V = (s_V, e_V, i_V) \in \mathbb{R}_+^3, D_a = (s_a, i_a) \in \mathbb{R}_+^2;\ s_{h1} \leq \frac{\Lambda}{\rho_1 + \mu_H},\ s_{h2} \leq \frac{\rho_1}{\rho_2 + \mu_H} \times \frac{\Lambda}{\rho_1 + \mu_H},$$
$$s_{h3} \leq \frac{\rho_1 \rho_2}{\mu_H(\rho_2 + \mu_H)} \times \frac{\Lambda}{\rho_1 + \mu_H}, s_V \leq \frac{m\theta\phi}{\mu_V(\phi + \xi)}, s_a \leq \frac{m\theta}{\phi + \xi}, e_{hi} \geq 0, i_{h,ai} \geq 0, j_{h,a2} \geq 0,$$
$$i_{h,si} \geq 0, j_{h,s2} \geq 0, r_{hi} \geq 0, e_V \geq 0, i_V \geq 0, i_a \geq 0, \quad \forall\ i = 1, 2, 3,$$

is positively invariant and attracting set for the solutions of the standardized model in proportions.

Proof:

By the Comparison Theorem and the use of appropriate calculus techniques on the system (2.1), we can see that;

$$0 \le \liminf_{t\to\infty} s_{h1}(t) \le \limsup_{t\to\infty} s_{h1}(t) \le \frac{\Lambda}{\rho_1+\mu_H},$$

$$0 \le \liminf_{t\to\infty} s_{h2}(t) \le \limsup_{t\to\infty} s_{h2}(t) \le \frac{\Lambda}{\rho_1+\mu_H}\times\frac{\rho_1}{\rho_2+\mu_H},$$

$$0 \le \liminf_{t\to\infty} s_{h3}(t) \le \limsup_{t\to\infty} s_{h3}(t) \le \frac{\Lambda}{\rho_1+\mu_H}\times\frac{\rho_1}{\rho_2+\mu_H}\times\frac{\rho_2}{\mu_H}. \qquad (2.10)$$

Therefore, in the absence of the disease, in the humans, i.e. when $e_{hi} = i_{h,ai} = j_{h,a2} = i_{h,si} = j_{h,s2} = r_{hi} = 0\ (\forall i = 1,2,3);$ the human population is represented by the value $s_{h1} + s_{h2} + s_{h3} \le N_h \le \frac{\Lambda}{\mu_H}$. Obviously, $0 \le \liminf_{t\to\infty} N_h(t) \le \limsup_{t\to\infty} N_h(t) \le \frac{\Lambda}{\mu_H}$ which implies $N_h(t) > 0$. Hence, the feasible solution $\left(s_{hi}(t), e_{hi}(t), i_{h,ai}(t), j_{h,a2}(t), i_{h,si}(t), j_{h,s2}(t), r_{hi}(t)\right);\ (i = 1,2,3)$ of the human population in the standardized basic transmission dynamics model system enters the positively invariant region $D_h \subseteq \mathbb{R}_+^{17}$.

Similarly, in the same manner, we can see that;

$0 \le \liminf_{t\to\infty} s_V(t) \le \limsup_{t\to\infty} s_V(t) \le \frac{m\theta\phi}{\mu_V(\phi+\xi)}$ and $0 \le \liminf_{t\to\infty} s_a(t) \le \limsup_{t\to\infty} s_a(t) \le \frac{m\theta}{\phi+\xi}$.

Therefore, in the absence of the ZIKV infection in the adult *Aedes* vectors and vertical transmission in the aquatic *Aedes* vectors populations, the adult and aquatic *Aedes* vectors populations are represented by $s_V(t) \le N_v(t) \le \frac{m\theta\phi}{\mu_V(\phi+\xi)}$ and $s_a(t) \le N_a(t) \le \frac{m\theta}{\phi+\xi}$ respectively. Thus, obviously, $0 \le \liminf_{t\to\infty} N_v(t) \le \limsup_{t\to\infty} N_v(t) \le \frac{m\theta\phi}{\mu_V(\phi+\xi)}$ and $0 \le \liminf_{t\to\infty} N_a(t) \le \limsup_{t\to\infty} N_a(t) \le \frac{m\theta}{\phi+\xi}$, which implies $N_v(t) > 0$ and $N_a(t) > 0$. Hence, the feasible solutions $\left(s_V(t), e_V(t), i_V(t)\right)$ of the adult *Aedes* vectors and $\left(s_a(t), i_a(t)\right)$ of the aquatic *Aedes* vectors in the standardized model system enters the positively invariant sets $D_V \subseteq \mathbb{R}_+^3$ and $D_a \subseteq \mathbb{R}_+^2$ respectively.

Thus, $D = \left(D_h \cup D_V \cup D_a\right) \subseteq \mathbb{R}_+^{22}$ is a positively invariant set being the union of finite invariant sets. Clearly, under dynamics described by the standardized basic dynamics model (2.1), the closed set $D = \left\{D_h \cup D_V \cup D_a \subset \mathbb{R}_+^{17} \times \mathbb{R}_+^3 \times \mathbb{R}_+^2\right\}$ is hence positively invariant and attracting set, and all the model solutions are uniformly bounded in the set.

2.3 Model validation and parameter estimation

To validate the model and estimate values for some of the model parameters, we fitted the model with real-time data for the 2016 Zika outbreak in Colombia as used and published in the work of Biswas *et al.* (2020). This data was

initially reported by the Colombian National Institute of Health, SIVIGILA as stated by Aranda *et al.* (2019). All efforts to obtain categorized data that fits the age classification by the model proved difficult. In view of this, we applied proportionate stratified random sampling technique (Muhammad, 2024) implemented on the *R* software package to estimate the distribution of infections in the three age classes of the age-structured model (2.1) by assuming ZIKV infection is uniformly distributed among all individuals. We also assumed that, the demography of all age classes in the model agrees with the age proportions of the population of Colombia in the year 2016 as reported in Wikipedia Demographics of Colombia, and the sexual classification of individuals in the work of Sanchez_Franco & Gonzalez Uribe (2021). This approach, often called age standardization in epidemiology, adjusts demographic differences and provides a baseline infection estimate for each age group. Therefore, using the known demographic distribution of the populations, this allowed us to estimate the age-specific infection counts from the total number of infected individuals in the reported data by ensuring all infected individuals are fully represented in the new data set. This is justified by the work of Chen (2001), that, if rates are unknown or assumed equal across partitions (age groups), distributions in proportion to the total population in each partition (age group) is an accepted demographic adjustment. The adjusted estimations for the infected individuals in the three age groupings are presented in Table (1) and the result of the experiment is presented in Fig. (2). The human and mosquito related parameter values estimated by the model and other baseline parameter values source from existing literature are presented in Table (2) and Table (3).

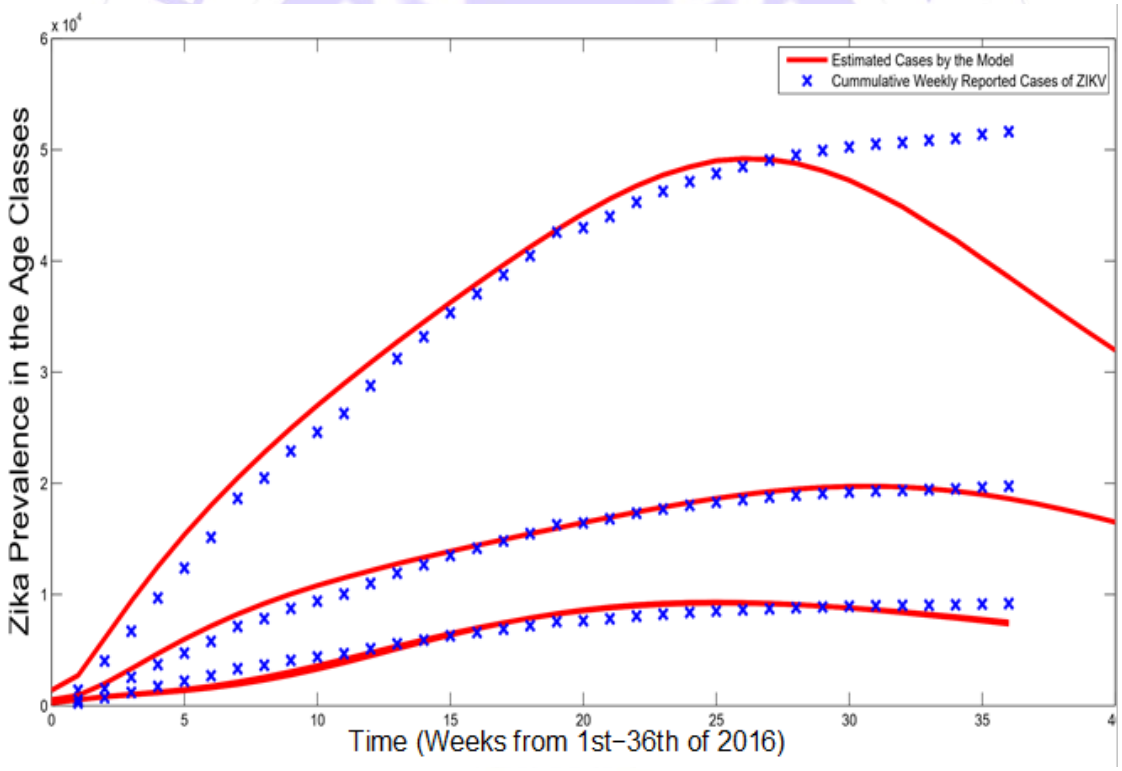

Figure 2: Cumulative ZIKV Prevalence in the Age-Classes

Table 1: Estimated Weekly Cumulative ZIKV Cases

Week	Age-Class-1	Age-Class-2	Age-Class-3	Cumulative
1	532	1393	248	2173
2	1538	4024	716	6278
3	2559	6694	1191	10444
4	3703	9687	1723	15113
5	4731	12378	2202	19311
6	5789	15145	2693	23627
7	7126	18645	3316	29087
8	7828	20481	3643	31952
9	8751	22896	4072	35719
10	9401	24598	4375	38374
11	10048	26289	4676	41013
12	10999	28778	5118	44895
13	11932	31219	5552	48703
14	12682	33179	5901	51762
15	13506	35336	6284	55126
16	14160	37048	6589	57797
17	14813	38756	6893	60462
18	15471	40479	7199	63149
19	16275	42582	7573	66430
20	16432	42990	7646	67068
21	16816	43995	7824	68635
22	17309	45286	8054	70649
23	17686	46273	8229	72188
24	18015	47134	8383	73532
25	18292	47857	8511	74660
26	18535	48492	8624	75651
27	18753	49064	8726	76543

28	18926	49516	8806	77248
29	19085	49931	8880	77896
30	19206	50249	8937	78392
31	19308	50516	8984	78808
32	19361	50654	9008	79023
33	19434	50847	9043	79324
34	19501	51020	9074	79595
35	19640	51384	9139	80163
36	19734	51630	9182	80546

Table 2: Baseline Human Parameter Values

Parameter	Description	Value	Source
Λ	Birth rate	$\frac{3}{200}\times\frac{1}{52}week^{-1}$	(Macrotrends)
μ_H	Human mortality rate	$\frac{1}{200}\times\frac{1}{52}week^{-1}$	(World Bank)
$\frac{1}{\varepsilon}$	Human incubation period	$\frac{10}{7}weeks$	Estimated
$\frac{1}{\delta}$	Symptomatic infectious period	$\frac{4}{7}weeks$	(Kucharski *et al*, 2016)
$\frac{1}{\gamma}$	Symptomatic infectious period	$\frac{5}{7}weeks$	(Kucharski *et al*, 2016)
$\frac{1}{r}$	Sexually active hum. inf. period	$\frac{30}{7}weeks$	(Maxian *et al*, 2017)
ρ_1	Maturity rate from age class 1	$\frac{1}{16}\times\frac{1}{52}week^{-1}$	(Maxian *et al*, 2017)
ρ_2	Maturity rate from age class 2	$\frac{1}{49}\times\frac{1}{52}week^{-1}$	(Maxian *et al*, 2017)
ρ_{HH}	Prob. of trans. through sex. cont.	0.99	Estimated
σ_{HH}	Reduction in sex trans. by asymp. hum.	0.99	Estimated
Φ	Reduction in sex trans. by hum in J class	0.81	Estimated
s	Sexual contact rate	$0.2week^{-1}$	Estimated
q	Proportion of asymptomatic ZIKV inf.	0.4	Estimated

Table 3: Baseline Vector and Human-Vector Interaction Parameter Values

Parameter	Description	Value	Source
μ_V	Vector mortality rate	$\frac{7}{13} week^{-1}$	(Moreno *et al*, 2017)
$\frac{1}{\kappa}$	Vector incubation period	$\frac{10}{7} weeks$	(Maxian *et al*, 2017)
σ_{VH}	Reduction in trans. by aymp. hum.	0.3	Estimated
σ_H	Vector biting rate	$10.64 week^{-1}$	Estimated
σ_V	Vector gonotrophic constant	0.39	Estimated
π	ZIKV vertical trans. rate in vectors	$\frac{1}{290}$	(Saravanan *et al*, 2016)
θ	Egg laying rate	$0.00003 week^{-1}$	Estimated
ϕ	Aquatic maturity rate	$0.0808 week^{-1}$	Estimated
ξ	Aquatic mortality rate	$\frac{399}{10000} week^{-1}$	Estimated
ρ_{HV}	Prob. of trans. from vector to human	0.72	Estimated
ρ_{VH}	Prob. of trans. from human to vector	0.31	Estimated
m	Vector-human ratio	735.40	Estimated

3 Pre-sexually Active Humans Sub-Model

Due to complexity of the standardized ZIKV basic dynamics model, the model analysis may not be straight forward easy. Therefore, in view of this, we will extract and analyse independent sub-model systems from the BTDM. In this section, we extracted a sub-model system from the BTDM comprising of the pre-sexually active humans, adult and aquatic Aedes vectors to form a sub-system.

3.1 Pre-sexually active humans sub-model equations

Thus, the sub-model system

$$\begin{aligned}
\frac{ds_{h1}}{dt} &= \Lambda - \left(\lambda_{h1} + \rho_1 + \mu_H\right) s_{h1}(t), \\
\frac{de_{h1}}{dt} &= \lambda_{h1} s_{h1}(t) - \left(\varepsilon + \rho_1 + \mu_H\right) e_{h1}(t), \\
\frac{di_{h,a1}}{dt} &= (1-q)\varepsilon e_{h1}(t) - \left(\gamma + \rho_1 + \mu_H\right) i_{h,a1}(t), \\
\frac{di_{h,s1}}{dt} &= q\varepsilon e_{h1}(t) - \left(\delta + \rho_1 + \mu_H\right) i_{h,s1}(t), \\
\frac{dr_{h1}}{dt} &= \gamma i_{h,a1}(t) + \delta i_{h,s1}(t) - \left(\rho_1 + \mu_H\right) r_{h1}(t), \\
\frac{ds_V}{dt} &= \phi s_a(t) - \left(\lambda_{v1} + \mu_V\right) s_V(t), \\
\frac{de_V}{dt} &= \lambda_{v1} s_V(t) - \left(\kappa + \mu_V\right) e_V(t), \\
\frac{di_V}{dt} &= \kappa e_V(t) + \phi i_a(t) - \mu_V i_V(t), \\
\frac{ds_a}{dt} &= m\theta - \pi\theta i_a(t) - \left(\phi + \xi\right) s_a(t), \\
\frac{di_a}{dt} &= \pi\theta i_a(t) - \left(\phi + \xi\right) i_a(t),
\end{aligned} \tag{3.1}$$

$$\begin{aligned}
&s_{h1}(0) > 0, e_{h1}(0) \geq 0, i_{h,a1}(0) \geq 0, i_{h,s1}(0) \geq 0, r_{h1}(0) \geq 0, \\
&s_V(0) > 0, e_V(0) \geq 0, i_V(0) \geq 0, s_a(0) > 0, i_a(0) \geq 0, \\
&s_{h1} + e_{h1} + i_{h,a1} + i_{h,s1} + r_{h1} \leq 1, \quad s_V + e_V + i_V \leq 1, \quad s_a + i_a \leq 1
\end{aligned}$$

where;

$$\lambda_{h1} = \beta_{HV} i_V(t), \lambda_{v1} = \beta_{VH}\left(\sigma_{VH} i_{h,a1}(t) + i_{h,s1}(t)\right): \ \beta_{HV} = \frac{m\rho_{HV}\sigma_H\sigma_V}{m\sigma_V + \sigma_H}, \ \beta_{VH} = \frac{\rho_{VH}\sigma_H\sigma_V}{m\sigma_V + \sigma_H}; \ N_v = mN_{h1}.$$

Clearly, if $N_{h1} \leq 1,$ then, $0 \leq \liminf_{t\to\infty} N_v \leq \limsup_{t\to\infty} N_v \leq m.$ Using Theorem (2.1), we can show that, there exist a unique, positive and bounded solution $\left(s_{h1}(t), e_{h1}(t), i_{h,a1}(t), i_{h,s1}(t), r_{h1}(t), s_V(t), e_V(t), i_V(t), s_a(t), i_a(t)\right)$ for all $t > 0$ for the pre-sexually

active humans sub-model in (3.1) on a closed positively invariant set

$$D_1 = \{D_{h1} \cup D_V \cup D_a \subset \mathbb{R}_+^5 \times \mathbb{R}_+^3 \times \mathbb{R}_+^2 \subseteq \mathbb{R}_+^{10} : D_{h1} = (s_{h1}, e_{h1}, i_{h,a1}, i_{h,s1}, r_{h1}) \in \mathbb{R}_+^5; s_{h1} \leq \frac{\Lambda}{\rho_1 + \mu_H},$$

$$e_{h1} \geq 0, i_{h,a1} \geq 0, i_{h,s1} \geq 0, r_{h1} \geq 0, D_V = (s_V, e_V, i_V) \in \mathbb{R}_+^3; s_V \leq \frac{m\theta\phi}{\mu_V(\phi + \xi)}, e_V \geq 0, i_V \geq 0,$$

$$D_a = (s_a, i_a) \in \mathbb{R}_+^2; \quad s_a \leq \frac{m\theta}{\phi + \xi}, e_{hi} \geq 0, i_{h,ai} \geq 0, j_{h,a2} \geq 0, i_a \geq 0,$$

3.2 The DFE and epidemic reproduction number for the pre-sexually active humans sub-model

The disease-free equilibrium (DFE) of the pre-sexually active human sub-model is given as

$$E_0^1 = \left(s_{h1}^0, e_{h1}^0, i_{h,a1}^0, i_{h,s1}^0, r_{h1}^0, s_V^0, e_V^0, i_V^0, s_a^0, i_a^0\right) = \left(\frac{\Lambda}{\rho_1 + \mu_H}, 0, 0, 0, 0, \frac{m\theta\phi}{\mu_V(\phi + \xi)}, 0, 0, \frac{\theta\phi}{\phi + \xi}, 0\right)$$

To compute the basic reproduction number for the sub-model system (3.1) using the next-generation matrix method, we use the definition and notations in the works of Diekman *et al*, (1990) and Van den Drische & James (2002) for the associated matrices F_{h1} and V_{h1} for the new infectious terms and the remaining transition terms evaluated at the DFE, E_0^1 is given as:

$$F_{h1} = \begin{pmatrix} 0 & 0 & 0 & 0 & \frac{\Lambda\rho_{HV}m\sigma_H\sigma_V}{(\rho_1 + \mu_H)(m\sigma_V + \sigma_H)} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{m\theta\phi\rho_{VH}\sigma_H\sigma_V\sigma_{VH}}{\mu_V(\phi + \xi)(m\sigma_V + \sigma_H)} & \frac{m\theta\phi\rho_{VH}\sigma_H\sigma_V}{\mu_V(\phi + \xi)(m\sigma_V + \sigma_H)} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$V_{h1}=\begin{pmatrix} \varepsilon+\rho_1+\mu_H & 0 & 0 & 0 & 0 & 0 \\ -(1-q)\varepsilon & \gamma+\rho_1+\mu_H & 0 & 0 & 0 & 0 \\ -q\varepsilon & 0 & \delta+\rho_1+\mu_H & 0 & 0 & 0 \\ 0 & 0 & 0 & \kappa+\mu_V & 0 & 0 \\ 0 & 0 & 0 & -\kappa & \mu_V & -\phi \\ 0 & 0 & 0 & 0 & -\pi\theta & \phi+\xi \end{pmatrix}$$

Therefore, the basic reproduction number for the pre-sexually active human sub-population via the sub-model is the dominant eigenvalue of $\left(F_{h1}V_{h1}^{-1}\right)$ obtained as:

$$R_{h1}^0=\sqrt{R_{h,a1}^0+R_{h,s1}^0} \qquad (3.2)$$

where;

$$R_{h,a1}^0=\frac{\Lambda\rho_{HV}\rho_{VH}\sigma_{VH}\sigma_H^2\sigma_V^2\kappa m^2\theta\phi(1-q)\varepsilon}{\mu_V^2(\rho_1+\mu_H)(\varepsilon+\rho_1+\mu_H)(\gamma+\rho_1+\mu_H)(m\sigma_V+\sigma_H)^2(\kappa+\mu_V)(\phi+\xi)(1-R_a^0)}$$

$$R_{h,s1}^0=\frac{\Lambda\rho_{HV}\rho_{VH}\sigma_H^2\sigma_V^2\kappa m^2\theta\phi q\varepsilon}{\mu_V^2(\rho_1+\mu_H)(\varepsilon+\rho_1+\mu_H)(\delta+\rho_1+\mu_H)(m\sigma_V+\sigma_H)^2(\kappa+\mu_V)(\phi+\xi)(1-R_a^0)}$$

such that, $R_a^0=\frac{\pi\theta\phi}{\mu_V(\phi+\xi)}$; is the vertical reproductive number of the ZIKV infection in the aquatic vectors population. Clearly, R_{h1}^0 exist (i.e. $R_{h1}^0\geq 0$) if and only if $0\leq R_a^0<1$. The global sensitivity indices of the pre-sexually active humans reproduction number is presented in Figure (3).

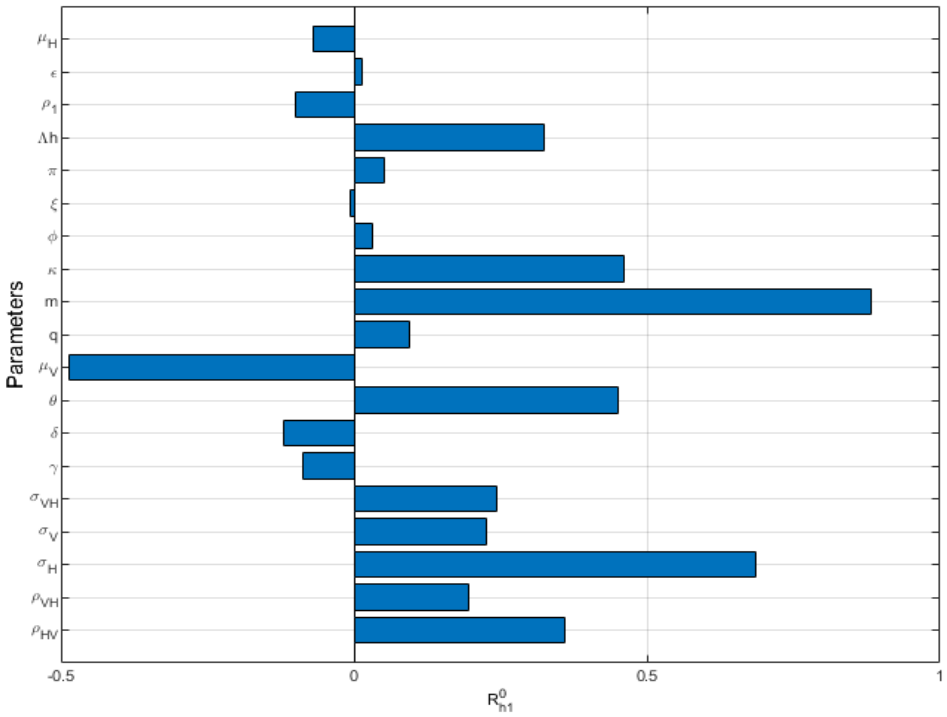

Figure 3: PRCC Results for R^0_{h1}

Remark 3.1. *Let* $R^0_{h1} = \sqrt{R^0_{h,a1} + R^0_{h,s1}}$ *be the epidemic reproduction number of the pre-sexually active humans sub-model. Then, the threshold values* $R^0_{h,a1}$ *and* $R^0_{h,s1}$ *are the individual infectious periods or the number of secondary infections contributed by the asymptomatic pre-sexually active humans and the symptomatic pre-sexually active humans respectively.*

Consequently, using Theorem (2) of Van den Drische and James (2002), we summarize the following result:

Theorem 3.1. *The DFE* E^1_0 *of the pre-sexually active humans' sub-model system in* (3.1) *is locally asymptotically stable (LAS) in* $D_1 \subset D_{h1} \times D_v \times D_a$ *whenever* $R^0_{h1} < 1$ *and unstable if* $R^0_{h1} > 1$..

3.2.1 Global asymptotic stability of the DFE, E^1_0

Theorem 3.2. *The DFE* E^1_0 *of the pre-sexually active humans' sub-model system is globally asymptotically stable (GAS) in* $D_1 \subset D_{h1} \times D_v \times D_a$ *when* $R^0_{h1} < 1$ *and unstable otherwise.*

Proof: Thus, given the DFE

$$E_0^1 = \left(\frac{\Lambda}{\rho_1 + \mu_H}, 0, 0, 0, 0, \frac{m\theta\phi}{\mu_V(\phi+\xi)}, 0, 0, \frac{\theta\phi}{\phi+\xi}, 0 \right),$$

there exist a nonzero matrix J such that, the system comprising of the infectious classes of the pre-sexually active humans sub-model can be written in the form:

$$\frac{d\chi}{dt} = (F_{h1} - V_{h1})\chi - J\chi, \qquad \chi = \left[e_{h1}, i_{h,a1}, i_{h,s1}, e_V, i_V, i_a \right]^T, \tag{3.3}$$

Where F_{h1} and V_{h1} were defined earlier. Thus, solving the right-hand of (3.3) for J using correspondence, we have

$$J = \begin{pmatrix} 0 & 0 & 0 & 0 & \beta_{HV} s_{h1}^0 \left(1 - \frac{s_{h1}}{s_{h1}^0}\right) & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \beta_{VH}\sigma_{VH} s_V^0 \left(1 - \frac{s_V}{s_V^0}\right) & \beta_{VH} s_V^0 \left(1 - \frac{s_V}{s_V^0}\right) & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

with $s_{h1}^0 = \frac{\Lambda}{\rho_1 + \mu_H}$, $s_V^0 = \frac{m\theta\phi}{\mu_V(\phi+\xi)}$, $\beta_{HV} = \frac{m\rho_{HV}\sigma_H\sigma_V}{m\sigma_V + \sigma_H}$ and $\beta_{VH} = \frac{\rho_{VH}\sigma_H\sigma_V}{m\sigma_V + \sigma_H}$. At equilibrium levels; we have $\left(1 - \frac{s_{h1}}{s_{h1}^0}\right) > 0$ and $\left(1 - \frac{s_V}{s_V^0}\right) > 0$. Therefore, obviously, $J \geq 0$ since $s_{h1} \leq s_{h1}^0$ and $s_V \leq s_V^0$ in the invariant set D_1.

By the Comparison Theorem [28], it follows that (3.3) can be written as:

$$\frac{d\chi}{dt} \leq (F_{h1} - V_{h1})\chi - J\chi. \tag{3.4}$$

Using the Comparison Theorem method as applied by Shaban & Mofi (2014) [29], we need to show that, the eigenvalues of the matrix

$$F_{h1}-V_{h1}=\begin{pmatrix} -a & 0 & 0 & 0 & a_{15} & 0 \\ (1-q)\varepsilon & -b & 0 & 0 & 0 & 0 \\ q\varepsilon & 0 & -c & 0 & 0 & 0 \\ 0 & a_{42} & a_{43} & -(\kappa+\mu_V) & 0 & 0 \\ 0 & 0 & 0 & \kappa & -\mu_V & \phi \\ 0 & 0 & 0 & 0 & \pi\theta & -(\phi+\xi) \end{pmatrix} \tag{3.5}$$

have negative real parts if and only if $R_{h1}^0<1$, where

$$a_{15}=\frac{\Lambda\rho_{HV}m\sigma_H\sigma_V}{(\rho_1+\mu_H)(m\sigma_V+\sigma_H)},\ a_{42}=\frac{m\theta\phi\rho_{VH}\sigma_H\sigma_V\sigma_{VH}}{\mu_V(m\sigma_V+\sigma_H)(\phi+\xi)} \text{ and } a_{43}=\frac{m\theta\phi\rho_{VH}\sigma_H\sigma_V}{\mu_V(m\sigma_V+\sigma_H)(\phi+\xi)}.$$

Thus, we row-reduce the matrix in (3.5) to obtain

$$F_{h1}-V_{h1}=\begin{pmatrix} -a & 0 & 0 & 0 & a_{15} & 0 \\ 0 & -ab & 0 & 0 & (1-q)\varepsilon a_{15} & 0 \\ 0 & 0 & -ac & 0 & q\varepsilon a_{15} & 0 \\ 0 & 0 & 0 & -a^2bc(\kappa+\mu_V) & c_{45} & 0 \\ 0 & 0 & 0 & 0 & c_{55} & a^2bc(\kappa+\mu_V)\phi \\ 0 & 0 & 0 & 0 & 0 & c_{66} \end{pmatrix} \tag{3.6}$$

such that, $c_{45}=aba_{42}q\varepsilon a_{15}+aca_{41}(1-q)\varepsilon a_{15},\quad c_{55}=\kappa c_{45}-a^2bc(\kappa+\mu_V)\mu_V$ and $c_{66}=-\pi\theta\phi a^2bc(\kappa+\mu_V)-c_{55}(\phi+\xi)$. Therefore, the characteristic equation of (3.6) after substitutions gives the following eigenvalues:

$$\lambda_1=-(\varepsilon+\rho_1+\mu_H),\quad \lambda_2=-(\varepsilon+\rho_1+\mu_H)(\gamma+\rho_1+\mu_H),\quad \lambda_3=-(\varepsilon+\rho_1+\mu_H)(\delta+\rho_1+\mu_H),$$
$$\lambda_4=-(\varepsilon+\rho_1+\mu_H)^2(\gamma+\rho_1+\mu_H)(\delta+\rho_1+\mu_H)(\kappa+\mu_V),$$
$$\lambda_5=-\mu_V(\varepsilon+\rho_1+\mu_H)^2(\gamma+\rho_1+\mu_H)(\delta+\rho_1+\mu_H)(\kappa+\mu_V)\left[1-\left(R_{h1}^0\right)^2\right],$$
$$\lambda_5=-\mu_V(\varepsilon+\rho_1+\mu_H)^2(\gamma+\rho_1+\mu_H)(\delta+\rho_1+\mu_H)(\kappa+\mu_V)(\phi+\xi)\left(1+R_a^0\right)\left[1-\left(R_{h1}^0\right)^2\right]^2.$$

Obviously, $\lambda_i<0;\ i=1,2,3,4.$ For $\lambda_{5,6}<0,$ we require that $\left(R_{h1}^0\right)^2=\left(R_{h,a1}^0+R_{h,s1}^0\right)<1.$ Therefore, it follows that, the linearized differential inequality system in (3.4) is stable for $\left(R_{h1}^0\right)^2<1.$ Consequently, $(e_{h1},i_{h,a1},i_{h,s1},e_V,i_V,i_a)\to(0,0,0,0,0,0)$ as $t\to\infty$ Thus, substituting $e_{h1}=i_{h,a1}=i_{h,s1}=e_V=i_V=i_a=0$

in (3.4) gives $s_{h1}(t)\to s_{h1}^0$, $s_V(t)\to s_V^0$ and $s_a(t)\to s_a^0$ in D_1 as $t\to\infty$. Therefore, $\left(s_{h1}(t),e_{h1}(t),i_{h,a1}(t),i_{h,s1}(t),r_{h1}(t),s_V(t),e_V(t),i_V(t),s_a(t),i_a(t)\right)\to\left(s_{h1}^0,0,0,0,0,s_V^0,0,0,s_a^0,0\right)$ as $t\to\infty$ for $R_{h1}^0<1$. Thus, the DFE E_0^1 is GAS if $R_{h1}^0<1$..

4 Sexually active humans sub-model

In this section, we will extract a special case, independent sub-model system from the standardized model comprising of the sexually active humans, adult Aedes vectors and the aquatic vectors. Recruitment into the exposed, infectious and removed human sub populations from the age class 1 through maturity/aging-out is considered negligible in the dynamics. Thus, the sub-model and its analysis is presented as follows:

4.1 Sexually active humans sub-model equations

The special case (with constant recruitment) sexually active humans' sub-model equations are given as:

$$\begin{aligned}
\frac{ds_{h2}}{dt}&=\frac{\rho_1\Lambda}{\rho_1+\mu_H}-(\lambda_{h2}+\rho_2+\mu_H)s_{h2}(t),\\
\frac{de_{h2}}{dt}&=\lambda_{h2}s_{h2}(t)-(\varepsilon+\rho_2+\mu_H)e_{h2}(t),\\
\frac{di_{h,a2}}{dt}&=(1-q)\varepsilon e_{h2}(t)-(\gamma+\rho_2+\mu_H)i_{h,a2}(t),\\
\frac{dj_{h,a2}}{dt}&=\gamma i_{h,a2}(t)-(r+\rho_2+\mu_H)j_{h,a2}(t),\\
\frac{di_{h,s2}}{dt}&=q\varepsilon e_{h2}(t)-(\delta+\rho_2+\mu_H)i_{h,s2}(t),\\
\frac{dj_{h,s2}}{dt}&=\delta i_{h,s2}(t)-(r+\rho_2+\mu_H)j_{h,s2}(t),\\
\frac{dr_{h2}}{dt}&=r\left(j_{h,a2}(t)+j_{h,s2}(t)\right)-(\rho_2+\mu_H)r_{h2}(t),\\
\frac{ds_V}{dt}&=\phi s_a(t)-(\lambda_{v2}+\mu_V)s_V(t),\\
\frac{de_V}{dt}&=\lambda_{v2}s_V(t)-(\kappa+\mu_V)e_V(t),\\
\frac{di_V}{dt}&=\kappa e_V(t)+\phi i_a(t)-\mu_V i_V(t),\\
\frac{ds_a}{dt}&=m\theta-\pi\theta i_a(t)-(\phi+\xi)s_a(t),\\
\frac{di_a}{dt}&=\pi\theta i_a(t)-(\phi+\xi)i_a(t),
\end{aligned}\qquad (4.1)$$

$$s_{h2}(0)>0, e_{h2}(0)\geq 0, i_{h,a2}(0)\geq 0,\ j_{h,a2}(0)\geq 0, i_{h,s2}(0)\geq 0,\ j_{h,s2}(0)\geq 0, r_{h2}(0)\geq 0,$$
$$s_V(0)>0, e_V(0)\geq 0, i_V(0)\geq 0, s_a(0)>0, i_a(0)\geq 0,$$
$$s_{h2}+e_{h2}+i_{h,a2}+j_{h,a2}+i_{h,s2}+j_{h,s2}+r_{h2}\leq 1, \quad s_V+e_V+i_V\leq 1, \quad s_a+i_a\leq 1$$

where;

$$\lambda_{h2}=\beta_{HV}i_V(t)+\beta_{HH}\left(\sigma_{HH}i_{h,a2}(t)+i_{h,s2}(t)+\Phi\left(\sigma_{HH}j_{h,a2}(t)+j_{h,s2}(t)\right)\right), \lambda_v=\beta_{VH}\left(\sigma_{VH}i_{h,a1}(t)+i_{h,s1}(t)\right)$$

such that, $\beta_{HV}=\dfrac{m\rho_{HV}\sigma_H\sigma_V}{m\sigma_V+\sigma_H}$, $\beta_{VH}=\dfrac{\rho_{VH}\sigma_H\sigma_V}{m\sigma_V+\sigma_H}$, $\beta_{HH}=s\rho_{HH}$; $N_v=mN_{h1}$. Clearly, if $N_{h1}\leq 1$, then, $0\leq \liminf_{t\to\infty} N_v\leq \limsup_{t\to\infty} N_v\leq m$. Using Theorem (2.1), we can show that, there exist a unique, positive and bounded solution $\left(s_{h2}(t), e_{h2}(t), i_{h,a2}(t), j_{h,a2}(t), i_{h,s2}(t), j_{h,s2}(t), r_{h2}(t), s_V(t), e_V(t), i_V(t), s_a(t), i_a(t)\right)$ for all $t>0$ for the sexually active humans sub-model in (4.1) on a closed positively invariant set

$$D_2=\left\{D_{h2}\cup D_V\cup D_a\subset \mathbb{R}_+^7\times\mathbb{R}_+^3\times\mathbb{R}_+^2\subseteq\mathbb{R}_+^{12}:\ D_{h2}=\left(s_{h2}, e_{h2}, i_{h,a2}, j_{h,a2}, i_{h,s2}, j_{h,s2}, r_{h2}\right)\in\mathbb{R}_+^7;\right.$$
$$s_{h2}\leq\frac{\rho_1\Lambda}{(\rho_1+\mu_H)(\rho_2+\mu_H)},\ e_{h2}\geq 0, i_{h,a2}\geq 0,\ j_{h,a2}\geq 0, i_{h,s2}\geq 0,\ j_{h,s2}\geq 0, r_{h2}\geq 0,\ D_V=\left(s_V, e_V, i_V\right)\in\mathbb{R}_+^3;$$
$$\left.s_V\leq\frac{m\theta\phi}{\mu_V(\phi+\xi)},\ e_V\geq 0, i_V\geq 0,\ D_a=\left(s_a, i_a\right)\in\mathbb{R}_+^2;\ \ s_a\leq\frac{m\theta}{\phi+\xi}, e_{hi}\geq 0, i_{h,ai}\geq 0,\ j_{h,a2}\geq 0, i_a\geq 0,\right.$$

for all $t>0$.

4.2 The DFE and epidemic reproduction number for the sexually active humans sub-model

Thus, the DFE for the sub-model is:

$$E_0^2=\left(s_{h2}^0, e_{h2}^0, i_{h,a2}^0, j_{h,a2}^0, i_{h,s2}^0, j_{h,s2}^0, r_{h2}^0, s_V^0, e_V^0, i_V^0, s_a^0, i_a^0\right)$$
$$=\left(\frac{\rho_1\Lambda}{(\rho_1+\mu_H)(\rho_2+\mu_H)}, 0,0,0,0,0,0, \frac{m\theta\phi}{\mu_V(\phi+\xi)}, 0, 0, \frac{\theta\phi}{\phi+\xi}, 0\right)$$

Using the next-generation matrix method as defined in the works of Diekman *et al*, (1990) and Van den Drische & James (2002), the basic reproduction number for the sub-model (4.1) was computed by finding the associated matrices F_{h2} and V_{h2} for the new infectious terms and the remaining transition terms, evaluated at the DFE, E_0^2 as follows:

$$F_{h2}=\begin{pmatrix} 0 & \beta_{HH}\sigma_{HH}s_{h2}^{0} & \beta_{HH}\Phi\sigma_{HH}s_{h2}^{0} & \beta_{HH}s_{h2}^{0} & \beta_{HH}\Phi s_{h2}^{0} & 0 & \beta_{HV}s_{h2}^{0} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \beta_{VH}\sigma_{VH}s_{V}^{0} & 0 & \beta_{VH}s_{V}^{0} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix} \tag{4.2}$$

$$V_{h2}=\begin{pmatrix} a & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ -(1-q)\varepsilon & b & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\gamma & c & 0 & 0 & 0 & 0 & 0 \\ -q\varepsilon & 0 & 0 & d & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -\delta & c & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \kappa+\mu_{V} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\kappa & \mu_{V} & -\phi \\ 0 & 0 & 0 & 0 & 0 & 0 & -\pi\theta & \phi+\xi \end{pmatrix} \tag{4.3}$$

where s_{h2}^{0} and s_{V}^{0} are the values of the susceptible sexually active humans and the susceptible mature *Aedes* vectors at the DFE E_{0}^{2} such that, $a=\varepsilon+\rho_{2}+\mu_{H}$, $b=\gamma+\rho_{2}+\mu_{H}$, $c=r+\rho_{2}+\mu_{H}$ and $d=\delta+\rho_{2}+\mu_{H}$. Thus, the epidemic reproduction number for the sexually active human sub-model, i.e. the dominant eigenvalue of $\left(F_{h2}V_{h2}^{-1}\right)$ is simplified and expressed as:

$$R_{h2}^{0}=\frac{\left(R_{h,a2}^{0}+R_{h,s2}^{0}\right)+\sqrt{\left(R_{h,a2}^{0}+R_{h,s2}^{0}\right)^{2}+4\left(R_{V1}^{0}+R_{V2}^{0}\right)}}{2} \tag{4.4}$$

such that;

$$R_{h,a2}^0 = \frac{s\rho_{HH}\sigma_{HH}\left(r+\rho_2+\mu_H+\Phi\gamma\right)\left(1-q\right)\varepsilon\rho_1\Lambda}{\left(\rho_1+\mu_H\right)\left(\rho_2+\mu_H\right)\left(\varepsilon+\rho_2+\mu_H\right)\left(\gamma+\rho_2+\mu_H\right)\left(r+\rho_2+\mu_H\right)},$$

$$R_{h,s2}^0 = \frac{s\rho_{HH}\left(r+\rho_2+\mu_H+\Phi\delta\right)q\varepsilon\rho_1\Lambda}{\left(\rho_1+\mu_H\right)\left(\rho_2+\mu_H\right)\left(\varepsilon+\rho_2+\mu_H\right)\left(\delta+\rho_2+\mu_H\right)\left(r+\rho_2+\mu_H\right)},$$

$$R_{V1}^0 = \frac{\rho_{HV}\rho_{VH}\sigma_H^2\sigma_V^2\sigma_{VH}\kappa m^2\theta\phi\left(1-q\right)\varepsilon\rho_1\Lambda}{\mu_V^2\left(m\sigma_V+\sigma_H\right)^2\left(\rho_1+\mu_H\right)\left(\rho_2+\mu_H\right)\left(\varepsilon+\rho_2+\mu_H\right)\left(\gamma+\rho_2+\mu_H\right)\left(\kappa+\mu_V\right)\left(\phi+\xi\right)\left(1-R_a^0\right)},$$

$$R_{V1}^0 = \frac{\rho_{HV}\rho_{VH}\sigma_H^2\sigma_V^2\kappa m^2\theta\phi q\varepsilon\rho_1\Lambda}{\mu_V^2\left(m\sigma_V+\sigma_H\right)^2\left(\rho_1+\mu_H\right)\left(\rho_2+\mu_H\right)\left(\varepsilon+\rho_2+\mu_H\right)\left(\delta+\rho_2+\mu_H\right)\left(\kappa+\mu_V\right)\left(\phi+\xi\right)\left(1-R_a^0\right)},$$

where $R_a^0 = \dfrac{\pi\theta\phi}{\mu_V\left(\phi+\xi\right)}$. Thus, R_{h2}^0 exist if and only if $0 \le R_a^0 < 1$, i.e., when $\mu_V\left(\phi+\xi\right) > \pi\theta\phi$. Therefore, in the absence of the sexual transmission in the human population, i.e., when $s = \rho_{HH} = 0$, we have;

$$R_{h2}^0 = \sqrt{R_{V1}^0 + R_{V2}^0}$$

which is similar to the basic reproduction number for the pre-sexually active humans sub-model generated via vector-human cross-transmission and the vertical transmission. The global sensitivity indices of the sexually active humans reproduction number is presented in Figure (4).

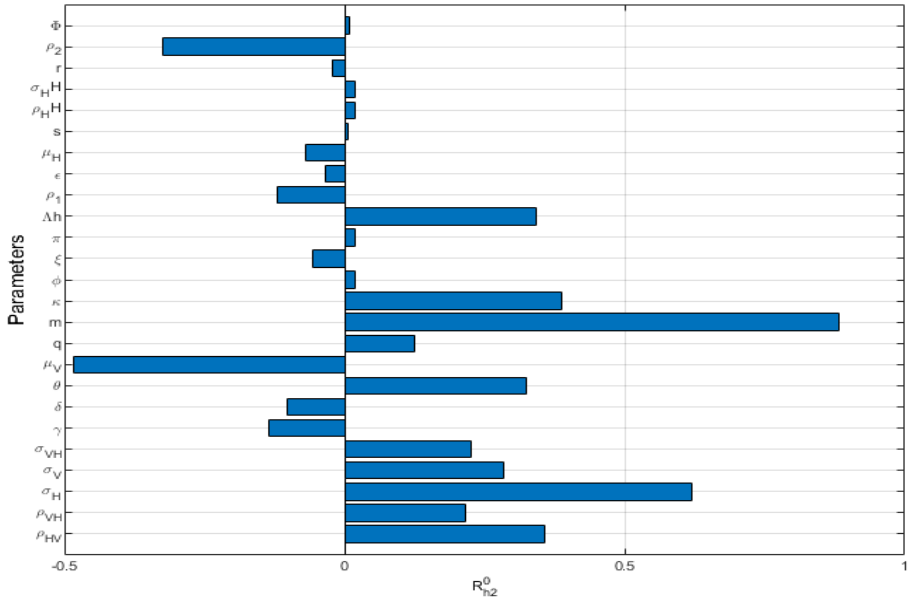

Figure 4: PRCC Results for R^0_{h2}

Remark 4.1. *Given the value of* R^0_{h2} *in* (4.4), *the threshold values* $R^0_{h,a2}$ *and* $R^0_{h,s2}$ *are the individual intrinsic infectious period or the number of secondary infections contributed by the asymptomatic and symptomatic sexually active humans respectively through sexual contacts, while the threshold values* R^0_{V1} *and* R^0_{V2} *are the individual extrinsic infectious period or the number of secondary infections contributed by the asymptomatic and symptomatic sexually active humans respectively through adult Aedes mosquito bites.*

Using Theorem 2 of Van Den Drische and James (2002), the following result is summarized:

Theorem 4.1. *The DFE* E^2_0 *for the sexually active humans sub-model* (4.1) *is locally asymptotically stable (LAS) in* $D_2 \subset D_{h2} \times D_v \times D_a$ *whenever* $R^0_{h2} < 1$ *and unstable if* $R^0_{h2} > 1$.

4.2.1 Global asymptotic stability of the DFE, E^2_0

Theorem 4.2. *The DFE point,* E^2_0 *for the sexually active humans sub-model* (4.1) *is globally asymptotically stable (GAS) in* $D_2 \subset D_{h2} \times D_v \times D_a$ *whenever* $R^0_{h2} < 1$ *and unstable if* $R^0_{h2} > 1$.

Proof:

The proof is based on using the Castillo-Chavez & Song (2004) Theorem. Let the new compartments $X_1(t)$ and $X_2(t)$ describe the uninfected and infected classes of the model system in (4.1) respectively. Thus,

$$X_1(t)=\left[s_{h2}, r_{h2}, s_V, s_a\right]^T, \qquad X_2(t)=\left[e_{h2}, i_{h,a2}, j_{h,a2}, i_{h,s2}, j_{h,s2}, e_V, i_V, i_a\right]^T.$$

Therefore, the system (4.1) can be written as:

$$\frac{dX_1(t)}{dt}=F\left(X_1, X_2\right), \qquad \frac{dX_2(t)}{dt}=G\left(X_1, X_2\right);\ G\left(X_1, \mathbf{0}\right)=\mathbf{0}, \qquad (4.5)$$

where the functions F and G are the corresponding right hand sides of the model system (4.1). By the Castillo-Chavez & Song (2004) Theorem, to guarantee the global asymptotic stability of the DFE, E_0^2, the following conditions (H_1) and (H_2) must be satisfied:

(H_1): $\left(X_1^0, \mathbf{0}\right)=\left[\frac{\rho_1\Lambda}{\left(\rho_1+\mu_H\right)\left(\rho_2+\mu_H\right)}, 0, 0, 0, 0, 0, \frac{m\theta\phi}{\mu_V\left(\phi+\xi\right)}, 0, 0, \frac{m\theta}{\phi+\xi}, 0\right]^T$ is globally asymptotically stable for $\frac{dX_1}{dt}=F\left(X_1, \mathbf{0}\right)=\mathbf{0}$.

(H_2): $\hat{G}\geq 0$ where $\hat{G}\left(X_1, X_2\right)=AX_2-G\left(X_1, X_2\right)$ such that $D_{X_2}G\left(X_1^0, \mathbf{0}\right)$ is an *M*-matrix $\forall\left(X_1, X_2\right)\in D_2$.

To check for the condition (H_1), we have;

$$\frac{dX_1}{dt}=F\left(X_1, \mathbf{0}\right)=\begin{bmatrix}\frac{\rho_1\Lambda}{\rho_1+\mu_H}-\left(\rho_2+\mu_H\right)s_{h2}\\ -\left(\rho_2+\mu_H\right)r_{h2}\\ \phi s_a-\mu_V s_V\\ m\theta-\left(\phi+\xi\right)s_a\end{bmatrix} \qquad (4.6)$$

The behaviour of each of the new compartments in X_1 can be known by solving the system (4.6). Hence, we obtained:

$$\begin{bmatrix} s_{h2} \\ r_{h2} \\ s_V \\ s_a \end{bmatrix} = \begin{bmatrix} \dfrac{\rho_1\Lambda}{(\rho_1+\mu_H)(\rho_2+\mu_H)} + (C_1 + s_{h2}(0))\exp(-(\rho_2+\mu_H)t) \\ r_{h2}(0)\exp(-(\rho_2+\mu_H)t) \\ \dfrac{m\theta\phi}{\mu_V(\phi+\xi)} + (C_2 + s_V(0))\exp(-\mu_V t) \\ \dfrac{m\theta}{\phi+\xi} + (C_3 + s_a(0))\exp(-(\phi+\xi)t) \end{bmatrix} \tag{4.7}$$

where C_1, C_2 and C_3 are arbitrary constants of integration (from 0 to t) with respect to time. Thus, from (4.7), we can clearly see that $\lim_{t\to\infty} X_1(t) = X_1^0$.

Next, we check the second condition in (H_2) by finding the *M*-matrix $A = D_{X_2} G\left(X_1^0, \mathbf{0}\right)$. Thus,

$$A = \begin{Bmatrix} -D_1 & y_1 s_{h2}^0 & y_1\Phi s_{h2}^0 & \beta_{HH} s_{h2}^0 & y_2 s_{h2}^0 & 0 & \beta_{HV} s_{h2}^0 & 0 \\ (1-q)\varepsilon & -D_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & r_1 & -D_3 & 0 & 0 & 0 & 0 & 0 \\ q\varepsilon & 0 & 0 & -D_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & r_1 & -D_3 & 0 & 0 & 0 \\ 0 & \beta_{VH}\sigma_{VH} s_V^0 & 0 & \beta_{VH} s_V^0 & 0 & -D_5 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \kappa & -D_6 & \phi \\ 0 & 0 & 0 & 0 & 0 & 0 & \pi\theta & -D_7 \end{Bmatrix}$$

where $D_1 = \varepsilon + \rho_2 + \mu_H$, $D_2 = \gamma + \rho_2 + \mu_H$, $D_3 = r + \rho_2 + \mu_H$, $D_4 = \delta + \rho_2 + \mu_H$, $D_5 = \kappa + \mu_V$, $D_6 = \mu_V$, $D_7 = \phi + \xi$, $y_1 = \beta_{HH}\sigma_{HH}$ and $y_2 = \beta_{HH}\Phi$. Clearly, A is an *M*-matrix. Therefore,

$$\widehat{G}(X_1, X_2) = D_{X_2} G\left(X_1^0, \mathbf{0}\right) X_2 - G(X_1, X_2) = \begin{bmatrix} \widehat{G}_1 & 0 & 0 & 0 & 0 & \widehat{G}_6 & 0 & 0 \end{bmatrix}^T. \tag{4.8}$$

where $\widehat{G}_1 = \beta_{HH} s_{h2}^0 \left(1 - \dfrac{s_{h2}}{s_{h2}^0}\right)\left(\sigma_{HH}\left(i_{h,a2} + \Phi j_{h,a2}\right) + i_{h,s2} + \Phi j_{h,s2}\right) + \beta_{HV} s_V^0 \left(1 - \dfrac{s_V}{s_V^0}\right) i_V$ and $\widehat{G}_6 = \beta_{HV} s_V^0 \left(1 - \dfrac{s_V}{s_V^0}\right)\left(\sigma_{HV} i_{h,a2} + i_{h,s2}\right)$. If the sexually active human sub-populations are at equilibrium, then $\left(1 - \dfrac{s_{h2}}{s_{h2}^0}\right) > 0$ and $\left(1 - \dfrac{s_V}{s_V^0}\right) > 0$. Obviously, $\widehat{G}(X_1, X_2) \geq 0$ since $s_{h2} \leq s_{h2}^0$ and $s_V \leq s_V^0$ in D_2. Therefore, the condition (H_2) is guaranteed. Thus, by the Castillo-Chavez Theorem (2004) [30], the DFE E_2^0 is globally

asymptotically in D_2 if $R_{h2}^0 < 1$, which conclude the proof.

Remark 4.2. *The biological interpretation of the above result is that, it is possible to eliminate ZIKV infection from the hosts of the sexually active humans sub-model if the disease basic reproduction number, R_{h2}^0, can be brought down to a value less than or equal to one, regardless of initial size of the infectious classes in the sub-model.*

5 Post –sexually active humans sub-model

In this section, we will extract another special case, independent sub-system from the standardized ZIKV basic dynamics model comprising of the post-sexually active humans, adult and aquatic *Aedes* vectors. Thus, the sub-model and its analysis is presented as follows:

5.1 Post –sexually active humans sub-model equations

The special case (with constant recruitment) post sexually active sub-model is given as:

$$\begin{aligned}
\frac{ds_{h3}}{dt} &= \frac{\rho_1\rho_2\Lambda}{(\rho_1+\mu_H)(\rho_2+\mu_H)} - (\lambda_{h3}+\mu_H)s_{h3}(t),\\
\frac{de_{h3}}{dt} &= \lambda_{h3}s_{h3}(t) - (\varepsilon+\mu_H)e_{h3}(t),\\
\frac{di_{h,a3}}{dt} &= (1-q)\varepsilon e_{h3}(t) - (\gamma+\mu_H)i_{h,a3}(t),\\
\frac{di_{h,s3}}{dt} &= q\varepsilon e_{h3}(t) - (\delta+\mu_H)i_{h,s3}(t),\\
\frac{dr_{h3}}{dt} &= \gamma i_{h,a3}(t) + \delta i_{h,s3}(t) - \mu_H r_{h3}(t),\\
\frac{ds_V}{dt} &= \phi s_a(t) - (\lambda_{v3}+\mu_V)s_V(t),\\
\frac{de_V}{dt} &= \lambda_{v3}s_V(t) - (\kappa+\mu_V)e_V(t),\\
\frac{di_V}{dt} &= \kappa e_V(t) + \phi i_a(t) - \mu_V i_V(t),\\
\frac{ds_a}{dt} &= m\theta - \pi\theta i_a(t) - (\phi+\xi)s_a(t),\\
\frac{di_a}{dt} &= \pi\theta i_a(t) - (\phi+\xi)i_a(t),
\end{aligned} \tag{5.1}$$

$$\begin{aligned}
&s_{h3}(0) > 0, e_{h3}(0) \geq 0, i_{h,a3}(0) \geq 0, i_{h,s3}(0) \geq 0, r_{h3}(0) \geq 0,\\
&s_V(0) > 0, e_V(0) \geq 0, i_V(0) \geq 0, s_a(0) > 0, i_a(0) \geq 0,\\
&s_{h3} + e_{h3} + i_{h,a3} + i_{h,s3} + r_{h3} \leq 1, s_V(0) + e_V + i_V \leq 1, s_a + i_a \leq 1,
\end{aligned}$$

with $\lambda_{h3} = \beta_{HV} i_V(t)$ and $\lambda_{V3} = \beta_{VH} \times \left(\sigma_{VH} i_{h,a3}(t) + i_{h,s3}(t)\right)$ such that $\beta_{HV} = \dfrac{\rho_{HV} m \sigma_H \sigma_V}{m\sigma_V + \sigma_H}$, $\beta_{VH} = \dfrac{\rho_{VH} \sigma_H \sigma_V}{m\sigma_V + \sigma_H}$ and $N_v = mN_{h3}$. Note that, if $N_{h3} \le 1$, then, $\lim\limits_{t\to\infty} N_v \le m$.

It follows that, using Theorem (2.1), we can show that, the post-sexually active humans sub-model (5.1) with nonnegative initial conditions, have a unique, positive and bounded solution $\left(s_{h3}(t), e_{h3}(t), i_{h,a3}(t), i_{h,s3}(t), r_{h3}(t), s_V(t), e_V(t), i_V(t), s_a(t), i_a(t)\right)$ in a certain positively invariant set

$D_3 = \left\{ D_{h3} \cup D_v \cup D_a \subset \mathbb{R}_+^5 \times \mathbb{R}_+^3 \times \mathbb{R}_+^2 \subset \mathbb{R}_+^{10} \right.$ with

$D_{h3} = \left(s_{h3}, e_{h3}, i_{h,a3}, i_{h,s3}, r_{h3}\right) \in \mathbb{R}_+^5 : e_{h3} \ge 0, i_{h,a3} \ge 0, i_{h,s3} \ge 0, r_{h3} \ge 0, s_{h3} \le \dfrac{\rho_1 \rho_2 \Lambda}{\mu_H \left(\rho_1 + \mu_H\right)\left(\rho_2 + \mu_H\right)}$;

$N_h > 0$, $D_v = \left(s_V, e_V, i_V\right) \in \mathbb{R}_+^3 : e_V \ge 0, i_V \ge 0, s_V \le \dfrac{m\theta\phi}{\mu_V\left(\phi + \xi\right)}$; $N_v > 0$ and

$\left. D_a = \left(s_a, i_a\right) \in \mathbb{R}_+^2 ; \, i_a \ge 0, s_a \le \dfrac{m\theta}{\phi + \xi} ; N_a > 0 \text{ for all } t > 0 \right\}$.

5.2 The DFE and basic reproduction number for the post-sexually active humans sub-model

The DFE for the post-sexually active humans sub-model is given as:

$$E_0^3 = \left(s_{h3}^0, e_{h3}^0, i_{h,a3}^0, i_{h,s3}^0, r_{h3}^0, s_V^0, e_V^0, i_V^0, s_a^0, i_a^0\right)$$
$$= \left(\frac{\rho_1 \rho_2 \Lambda}{\mu_H \left(\rho_1 + \mu_H\right)\left(\rho_2 + \mu_H\right)}, 0, 0, 0, 0, \frac{m\theta\phi}{\mu_V\left(\phi + \xi\right)}, 0, 0, \frac{m\theta}{\phi + \xi}, 0 \right).$$

The basic reproduction number for the sub-model (5.1) was computed using the next-generation matrix method. Using the definition and notations in Diekman *et al*, (1990) and Van den Drische & James (2002), the associated matrices F_{h3} and V_{h3} for the new infectious terms and the remaining transition terms, evaluated at the DFE E_0^3 are obtained as follows:

$$F_{h3}=\begin{pmatrix} 0 & 0 & 0 & 0 & \dfrac{\Lambda\rho_1\rho_2\rho_{HV}m\sigma_H\sigma_V}{\mu_H\left(\rho_1+\mu_H\right)\left(\rho_2+\mu_H\right)\left(m\sigma_V+\sigma_H\right)} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \dfrac{m\theta\phi\rho_{VH}\sigma_H\sigma_V\sigma_{VH}}{\mu_V\left(m\sigma_V+\sigma_H\right)\left(\phi+\xi\right)} & \dfrac{m\theta\phi\rho_{VH}\sigma_H\sigma_V}{\mu_V\left(m\sigma_V+\sigma_H\right)\left(\phi+\xi\right)} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$V_{h3}=\begin{pmatrix} \varepsilon+\mu_H & 0 & 0 & 0 & 0 & 0 \\ -\left(1-q\right)\varepsilon & \gamma+\mu_H & 0 & 0 & 0 & 0 \\ -q\varepsilon & 0 & \delta+\mu_H & 0 & 0 & 0 \\ 0 & 0 & 0 & \kappa+\mu_V & 0 & 0 \\ 0 & 0 & 0 & -\kappa & \mu_V & -\phi \\ 0 & 0 & 0 & 0 & -\pi\theta & \phi+\xi \end{pmatrix}$$

The basic reproduction number for the post-sexually active human sub-model which is the dominant eigenvalue of the matrix $\left(F_{h3}V_{h3}^{-1}\right)$ is:

$$R_{h3}^0=\sqrt{R_{h,a3}^0+R_{h,s3}^0}$$

such that;

$$R_{h,a3}^0=\frac{\rho_{HV}\rho_{VH}\sigma_H^2\sigma_V^2\sigma_{VH}\kappa m^2\theta\phi\left(1-q\right)\varepsilon\rho_1\rho_2\Lambda}{\mu_H\mu_V^2\left(\rho_1+\mu_H\right)\left(\rho_2+\mu_H\right)\left(\varepsilon+\mu_H\right)\left(\gamma+\mu_H\right)\left(m\sigma_V+\sigma_H\right)^2\left(\kappa+\mu_V\right)\left(\phi+\xi\right)\left(1-R_a^0\right)},$$

$$R_{h,a3}^0=\frac{\rho_{HV}\rho_{VH}\sigma_H^2\sigma_V^2\kappa m^2\theta\phi q\varepsilon\rho_1\rho_2\Lambda}{\mu_H\mu_V^2\left(\rho_1+\mu_H\right)\left(\rho_2+\mu_H\right)\left(\varepsilon+\mu_H\right)\left(\delta+\mu_H\right)\left(m\sigma_V+\sigma_H\right)^2\left(\kappa+\mu_V\right)\left(\phi+\xi\right)\left(1-R_a^0\right)}$$

where, $R_a^0=\dfrac{m\theta\phi}{\mu_V\left(\phi+\xi\right)}$. Thus, R_{h3}^0 exists if and only if, $0\le R_a^0<1$, i.e., when $\mu_V\left(\phi+\xi\right)>\pi\theta\phi$. The global sensitivity indices of the post-sexually active humans reproduction number presented in Figure (5).

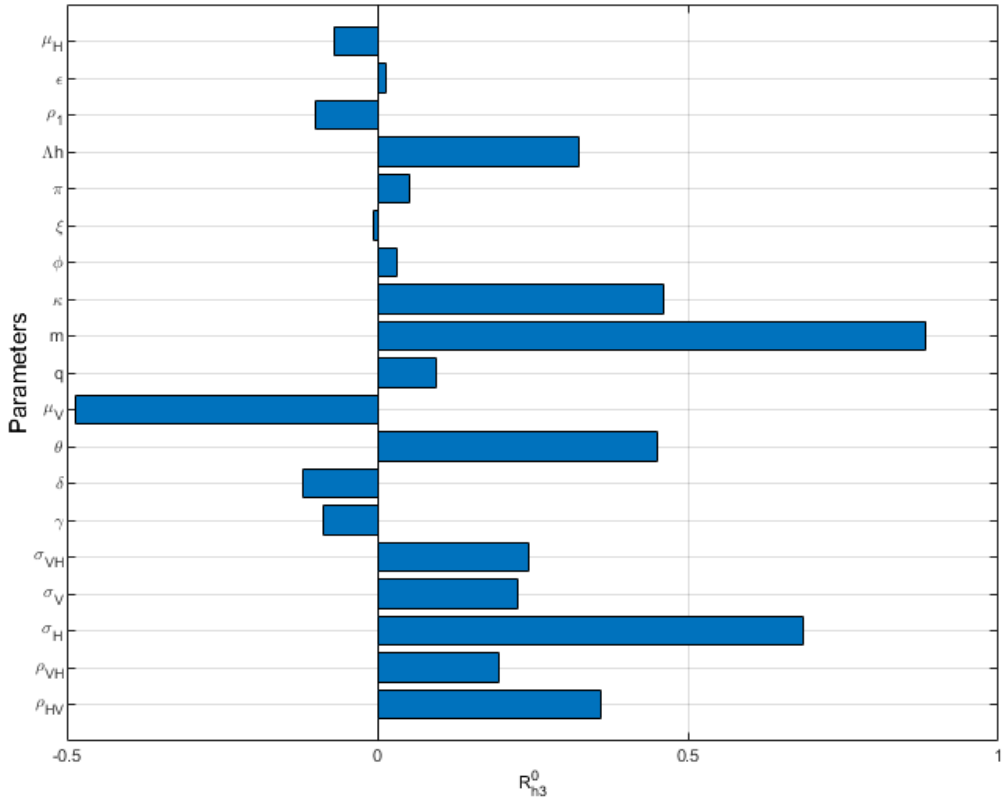

Figure 5: PRCC Results for R^0_{h3}

Remark 5.1. *Given that,* $R^0_{h3} = \sqrt{R^0_{h,a3} + R^0_{h,s3}}$ *, then, the threshold values;* $R^0_{h,a3}$ *and* $R^0_{h,s3}$ *are the individual infectious periods or the number of secondary infections contributed the asymptomatic and the symptomatic post-sexually active humans respectively.*

Therefore, using Theorem 2 of Van Den Driessche & James (2002), the following result is summarized:

Theorem 5.1. *The DFE* E^3_0 *of the post-sexually active humans sub-model system* (5.1) *is locally asymptotically stable (LAS) in* $D_3 \subset D_{h3} \times D_v \times D_a$ *whenever* $R^0_{h3} < 1$ *and unstable if* $R^0_{h3} > 1$.

5.3 Global asymptotic stability analysis of the DFE, E^3_0

Theorem 5.2. *The DFE* E^3_0 *of the post-sexually active humans sub-model system* (5.1) *is globally asymptotically stable (GAS) in* $D_3 \subset D_{h3} \times D_v \times D_a$ *if* $R^0_{h3} < 1$ *and unstable if* $R^0_{h3} > 1$.

Proof. The proof is based on using the Castillo-Chavez & Song (2004) Theorem technique. Let the new

compartments $Y_1(t)$ and $Y_2(t)$ describe the uninfected and infected classes of the model (5.1) respectively. Thus,

$$Y_1(t)=\left[s_{h3}, r_{h3}, s_V, s_a\right]^T \text{ and } Y_2(t)=\left[e_{h3}, i_{h,a3}, i_{h,s3}, e_V, i_V, i_a\right]^T. \qquad (5.3)$$

Therefore, system (5.1) can be written as:

$$\frac{dY_1(t)}{dt}=F(Y_1,Y_2), \quad \frac{dY_2(t)}{dt}=G(Y_1,Y_2); \quad G(Y_1,\mathbf{0})=\mathbf{0}, \qquad (5.4)$$

where the functions F and G are the right-hand sides of the model (5.1). By the Castillo-Chavez & Song (2004) Theorem, to guarantee the global stability of E_0^3, the following conditions (H_1) and (H_2) must be satisfied:

(H_1): $\left(Y_1^0,\mathbf{0}\right)=\left[\frac{\rho_1\rho_2\Lambda}{\mu_H(\rho_1+\mu_H)(\rho_2+\mu_H)}, 0, 0, 0, 0, \frac{m\theta\phi}{\mu_V(\phi+\xi)}, 0, 0, \frac{m\theta}{\phi+\xi}, 0\right]^T$ is globally asymptotically stable for $\frac{dY_1}{dt}=F(Y_1,\mathbf{0})=\mathbf{0}$.

(H_2): $\hat{G}\geq 0$ where $\hat{G}(Y_1,Y_2)=AY_2-G(Y_1,Y_2)$ such that, $A=D_{Y_2}G\left(Y_1^0,\mathbf{0}\right)$ is an *M*-matrix $\forall(Y_1,Y_2)\in D_3$.

To check for the condition (H_1), we have;

$$\frac{dY_1}{dt}=F(Y_1,\mathbf{0})=\begin{bmatrix}\frac{\rho_1\rho_2\Lambda}{(\rho_1+\mu_H)(\rho_2+\mu_H)}-\mu_H s_{h3}\\ -\mu_H r_{h3}\\ \phi s_a-\mu_V s_V\\ m\theta-(\phi+\xi)s_a\end{bmatrix} \qquad (5.5)$$

The behaviour of the new compartments in $Y_1(t)$ can be known by solving the new system obtained in (5.5). Hence,

$$\begin{bmatrix} s_{h3} \\ r_{h3} \\ s_V \\ s_a \end{bmatrix} = \begin{bmatrix} \dfrac{\rho_1\rho_2\Lambda}{\mu_H(\rho_1+\mu_H)(\rho_2+\mu_H)} + \left(C_2 + s_{h3}(0)\right)\exp\left(-\mu_H t\right) \\ r_{h3}(0)\exp\left(-\mu_H t\right) \\ \dfrac{m\theta\phi}{\mu_V(\phi+\xi)} + \left(C_3 + s_V(0)\right)\exp\left(-\mu_V t\right) \\ \dfrac{m\theta}{\phi+\xi} + \left(C_4 + s_a(0)\right)\exp\left(-(\phi+\xi)t\right) \end{bmatrix} \tag{5.6}$$

where C_2, C_3 and C_4 are arbitrary constants of integration from 0 to t with respect to time. Thus, from (5.6), we can clearly see that, $\lim_{t\to\infty} Y_1(t) = Y_1^0$.

Furthermore, we check the second condition (H_2) by finding the *M*-matrix, $A = D_{Y_2} G\left(Y_1^0, \mathbf{0}\right)$ which is a Jacobian matrix of $G(Y_1, Y_2)$ with respect to $\left(e_{h3}, i_{h,a3}, i_{h,s3}, e_V, i_V, i_a\right)$ evaluated at $\left(Y_1^0, \mathbf{0}\right)$. Thus,

$$A = \begin{bmatrix} -(\varepsilon+\mu_H) & 0 & 0 & 0 & \beta_{HV} s_{h3}^0 & 0 \\ (1-q)\varepsilon & -(\gamma+\mu_H) & 0 & 0 & 0 & 0 \\ q\varepsilon & 0 & -(\delta+\mu_H) & 0 & 0 & 0 \\ 0 & \beta_{VH}\sigma_{VH} s_V^0 & \beta_{VH} s_V^0 & -(\kappa+\mu_V) & 0 & 0 \\ 0 & 0 & 0 & \kappa & -\mu_V & \phi \\ 0 & 0 & 0 & 0 & \pi\theta & -(\phi+\xi) \end{bmatrix}$$

Obviously, A is an *M*-matrix. Therefore,

$$\hat{G}(Y_1, Y_2) = D_{Y_2} G\left(Y_1^0, \mathbf{0}\right) Y_2 - G(Y_1, Y_2) = \left[\hat{G}_1, 0, 0, \hat{G}_4, 0, 0\right]^T, \tag{5.7}$$

where $\hat{G}_1 = \beta_{HV} s_{h3}^0 \left(1 - \dfrac{s_{h3}}{s_{h3}^0}\right) i_V$ and $\hat{G}_4 = \beta_{VH} s_V^0 \left(1 - \dfrac{s_V}{s_V^0}\right)\left(\sigma_{VH} i_{h,a3} + i_{h,s3}\right)$. If the post-sexually active humans sub-populations are at equilibrium level, then $1 - \dfrac{s_{h3}}{s_{h3}^0} > 1$ and $1 - \dfrac{s_V}{s_V^0} > 1$ since $s_{h3} \le s_{h3}^0$ and $s_V \le s_V^0$ in D_3. Obviously, $\hat{G}(Y_1, Y_2) \ge 0$, which implies that, the condition (H_2) is guaranteed. Thus, by the Castillo-Chavez Theorem (2004), the DFE, E_0^3 is globally asymptotically stable in D_3 if $R_{h3}^0 < 1$. The proof is complete.

Remark 5.2. *The biological interpretation of the above result is that, the ZIKV infection can b eliminated from the post-sexually active human's sub-model hosts if the threshold quantity* $R_{h3}^0 < 1$ *can be controlled to a numerical value less than unity, regardless of initial size of the infectious classes in the sub-model.*

6 Summary and Conclusion

6.1 Summary

In this paper, a deterministic age-structured model that incorporates vertical transmission in Aedes vectors and sexual transmission in humans into the dynamics of Zika virus infection is formulated. The model is validated using the 2016 ZIKV outbreak data for Colombia where stratified random sampling technique implemented in the *R*-software is used to distribute infections according the age ratio/percentile distribution of the Colombian population as reported by the World Bank in 2016, by ensuring that all infected individuals from the reported data are dully represented in the new estimated data sets. The model is proved to have a unique positive and bounded solution in a certain positively invariant region. Due to the size and nonlinearity of the developed model, we extracted and studied three independent sub-models from the main model namely; pre-sexually active, sexually active and post-sexually active humans sub-models. Each of the sub-model was shown to inherit the basic properties of the main model. We computed the Disease-Free Equilibrium (DFE and the basic reproduction number R0 of each sub-model using the next-generation matrix method. All the three reproduction numbers of the sub-models were found to exist if and only if a unique threshold which represent the vertical reproductive number of the Aedes vectors in the aquatic phase is less than one. Each of the DFEs of the three sub-models was proved to be globally asymptotically stable if the associated R_0 of the sub-model is less than unity. Through global sensitivity analysis using PRCC method, we discovered that, the most sensitive parameters that propagates or minimizes the incidences of the ZIKV infection in the host's populations are the vector biting and mortality rates, vector-human ratio parameter, sexual contact rate and the human recovery rates. Therefore, accordingly, we suggest that, control interventions that minimizes; contacts between mature vectors and humans through the use of bed-nets and residual sprays, direct sexual contacts between humans through the use of condoms (especially during outbreaks) and the use of effective and formal ZIKV treatment can properly and optimally reduce the spread of the disease.

6.2 Conclusion

In this paper, a new mathematical model for the basic transmission dynamics of the Zika virus infection is shown to be well-posed and epidemiologically meaningful through appropriate methods of analysis. The vectorial transmission is observed to be the dominant transmission route from the results of the sensitivity analysis. It is also observed that, sexual transmission route's contribution is significant while the vertical transmission route's contribution in the aquatic vectors is negligible.

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