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STABILITY ANALYSIS OF SEXUAL AND SYMPTOMATIC VECTOR-BORNE ZIKA VIRUS TRANSMISSION USING GRAPH THEORY

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ABSTRACT:
Zika virus (ZIKV) is primarily transmitted through infected Aedes mosquitoes, while sexual transmission provides an additional pathway for disease spread. In this study, a deterministic ZIKV transmission model is formulated using a weighted directed graph to incorporate both vector-borne and sexual transmission pathways, with particular consideration of symptomatic and asymptomatic human infections. The human and mosquito epidemiological compartments are represented as vertices, while transmission, progression, recovery, and removal processes are assigned as biologically meaningful edge weights. The resulting graph structure provides a systematic representation of the interactions among the different epidemiological states. The disease-free equilibrium E_0 is identified by setting all exposed and infected compartments to zero. To investigate its local stability, the infected subsystem is linearised at E_0 and represented through the Jacobian decomposition $J = F - V$, where F describes the appearance of new infections and V represents transitions and removal processes. The characteristic equation of the Jacobian is derived, and the Routh–Hurwitz criterion is applied to establish the stability conditions. In particular, $\mathcal{R}_0 < 1$ provides the threshold for local asymptotic stability of the disease-free equilibrium, whereas $\mathcal{R}_0 > 1$ indicates the potential for disease invasion. The proposed framework links the graph-based representation of ZIKV transmission with equilibrium stability analysis

KEYWORDS AND PHRASES: zika virus, basic reproduction number, asymptomatic, sexual transmission, graph theory, disease-free equilibrium, stability analysis
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1. INTRODUCTION

Zika virus (ZIKV) is a mosquito-borne flavivirus transmitted primarily by infected Aedes mosquitoes and is associated with neurological complications and congenital abnormalities [1,9]. Sexual transmission also contributes to ZIKV spread, particularly through asymptomatic infections [2], and several mathematical models have incorporated symptomatic and asymptomatic infected individuals alongside sexual transmission [3]. In earlier work, we developed a graph-theoretic model of ZIKV transmission in which the human and mosquito epidemiological compartments were represented as vertices of a weighted directed graph, with transmission and transition processes represented by weighted edges [4]. A graph-based reproduction number R_N was introduced using the graph energy and IOTA energy of the resulting adjacency matrix and was validated using real-world ZIKV incidence data [7].

In this study, we develop a deterministic Zika virus transmission model using a directed weighted graph framework. The proposed digraph represents the epidemiologically relevant transmission pathways and transitions among susceptible, exposed, symptomatic, asymptomatic, and recovered human compartments, together with susceptible, exposed, and infectious mosquito compartments. The edge weights are assigned according to the corresponding biological processes, thereby providing a structured representation of both sexual and vector-borne transmission [8]. Based on this graph representation, the Jacobian matrix at the disease-free equilibrium (DFE) is formulated to derive the basic reproduction number $\mathcal{R}_0$ and investigate the local dynamics and stability of the disease-free state [6]. This formulation provides a systematic framework for relating the transmission structure of the digraph to the epidemiological threshold of the model.

The disease-free equilibrium E_0 is first identified, and the infected subsystem is linearised about this equilibrium to obtain the Jacobian matrix. The characteristic equation is then analysed using the Routh–

Hurwitz criterion to establish conditions under which all eigenvalues have negative real parts and hence E_0 is locally asymptotically stable. In particular, the resulting threshold $\mathcal{R}_0$ distinguishes the conditions for disease elimination from those permitting disease invasion [5]. The analysis further examines the roles of sexual transmission, symptomatic and asymptomatic infections, mosquito biting, transmission, recovery, and mosquito mortality parameters in determining the stability threshold. Thus, the present study complements our earlier graph-based reproduction number R_N by providing a stability-based epidemiological analysis of the proposed ZIKV transmission structure.

2. Construction of the Digraph

The transmission dynamics are represented by a directed weighted graph $D = (V, E)$ with eight epidemiological compartments as vertices: susceptible (S_H), exposed (E_H), symptomatic infectious (I_{HS}), asymptomatic infectious (I_{HA}), and recovered (R_H) humans, and susceptible (S_V), exposed (E_V), and infectious (I_V) mosquitoes. The directed edges, weighted by the parameters in Table 1, represent human progression from susceptible to exposed to symptomatic/asymptomatic infectious states, recovery of infectious individuals, human-to-mosquito and mosquito-to-human transmission, and mosquito progression from susceptible to exposed to infectious states [8].

The graph $D = (V, E)$ where

$V(D) = \{S_H(= v_1), E_H(= v_2), I_{HS}(= v_3), I_{HA}(= v_4), R_H(= v_5), S_V(= v_6), E_V(= v_7), I_V(= v_8)\}$

$E(D) = \{S_H E_H, E_H I_{HS}, E_H I_{HA}, I_{HS} S_H, I_{HA} S_H, I_{HS} R_H, I_{HA} R_H, I_{HS} S_V, I_{HA} S_V, S_V E_V, E_V I_V, I_V S_H\}$

Figure 1 shows the resulting Zika transmission digraph including both mosquito-borne and sexual transmission pathways, with exposed compartments remaining non-infectious [8].

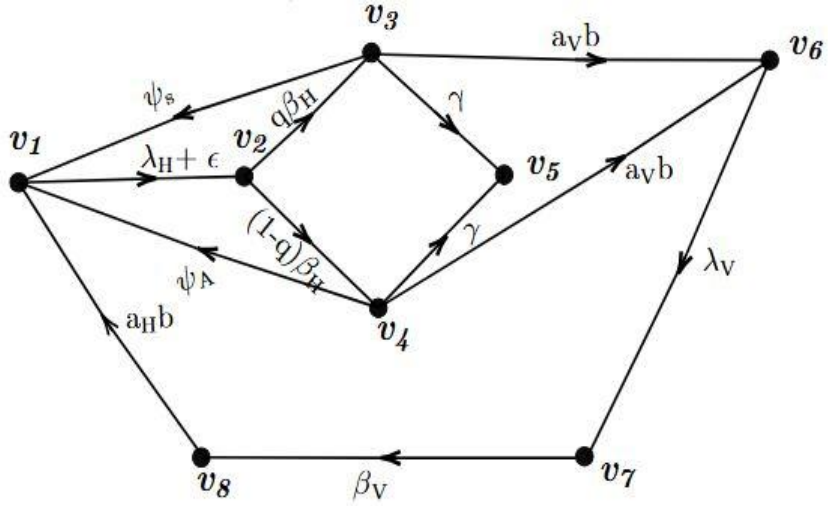


Figure 1: Graphical representation of Zika virus transmission.

Table 1: Descriptions of the parameters used in the model

Parameter	Description
λ_H	Force of infection for human
λ_V	Force of infection for vector
b	Mosquito biting rate
a_H	Transmission probability from an infectious mosquito to a susceptible human per bite
a_V	Transmission probability from an infectious human to a susceptible mosquito per bite
Ψ_S	Rate of sexual transmission (symptomatic)
Ψ_A	Rate of sexual transmission (asymptomatic)
q	Proportion of humans who are symptomatic
β_H	Latency period of Zika in humans
β_V	Latency period of Zika in vectors
γ	Human infectious period
μ_V	Mosquito death rate

3. Disease-Free Equilibrium Point and Basic Reproduction Number

Let * denote the equilibrium value of each compartment. At the disease-free equilibrium (DFE), denoted by E_0, all exposed and infected compartments are absent from both human and mosquito populations. Hence,

$$E_H^* = I_{HS}^* = I_{HA}^* = E_V^* = I_V^* = 0,$$

while the susceptible human and mosquito populations attain their total population sizes,

$$S_H^* = N_H, \qquad S_V^* = N_V.$$

Therefore, the disease-free equilibrium of the proposed eight-compartment model is given by

$$E_0 = (S_H^*, E_H^*, I_{HS}^*, I_{HA}^*, R_H^*, S_V^*, E_V^*, I_V^*) = (N_H, 0,0,0,0, N_V, 0,0). \qquad (1)$$

At this equilibrium, no infectious individuals are present, and consequently both sexual and vector-borne transmission pathways are inactive. The stability of E_0 determines whether a small introduction of Zika virus infection can invade the population or whether the infection will eventually disappear.

For the local stability analysis, only the exposed and infectious compartments are considered. The infected subsystem is represented as

$$X_I = \{E_H, I_{HS}, I_{HA}, E_V, I_V\},$$

with the infected-state vector

$$x_I = \begin{pmatrix} E_H \\ I_{HS} \\ I_{HA} \\ E_V \\ I_V \end{pmatrix}, \qquad x_I^* = \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}.$$

The local stability of the disease-free equilibrium is determined by analysing the Jacobian matrix evaluated at E_0. The linearized system around the equilibrium is given by

$$\dot{x}_I = J(E_0)x_I,$$

where $J(E_0)$ denotes the Jacobian matrix of the infected subsystem. The equilibrium E_0 is locally asymptotically stable if all eigenvalues λ_i of $J(E_0)$ satisfy

$$\mathrm{Re}(\lambda_i) < 0.$$

This implies that any small perturbation from the disease-free state decreases with time. Conversely, the existence of an eigenvalue with positive real part indicates instability and the possibility of disease invasion.

To obtain the stability conditions, the Jacobian matrix is decomposed into two components representing new infection generation and internal transitions within the infected subsystem. Thus, the linearized system can be written as

$$\dot{x}_I = (F - V)x_I,$$

where F represents the rate of appearance of new infections generated through the transmission pathways of the graph, while V represents the transfer of individuals among exposed and infectious compartments, including progression, recovery, and mortality processes. This decomposition follows the structure of the weighted directed graph, where rows correspond to destination compartments and columns correspond to source compartments.

The elements of the matrices are defined as

$$F_{ij} = \begin{cases} a_{ij}, & \text{if the transition } j \to i \text{ represents a new infection,} \\ 0, & \text{otherwise,} \end{cases}$$

and

$$V_{ij} = \begin{cases} -a_{ji}, & \text{if } j \to i \text{ represents transfer between infected compartments,} \\ \sum_{k \in X_I} a_{ik}, & \text{if } i = j \text{ represents total outflow from compartment } i, \\ 0, & \text{otherwise.} \end{cases}$$

Using the infected subsystem

$$X_I = \{E_H, I_{HS}, I_{HA}, E_V, I_V\},$$

and the parameters defined in Table 1, the Jacobian matrix at the disease-free equilibrium is obtained as

$$J(E_0) = F - V = \begin{pmatrix} 0 & \Psi_S & \Psi_A & 0 & a_H b \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & a_V b & a_V b & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix} - \begin{pmatrix} \beta_H & 0 & 0 & 0 & 0 \\ -q\beta_H & \gamma & 0 & 0 & 0 \\ -(1-q)\beta_H & 0 & \gamma & 0 & 0 \\ 0 & 0 & 0 & \beta_V & 0 \\ 0 & 0 & 0 & -\beta_V & \mu_V \end{pmatrix}.$$

$$\Longrightarrow J(E_0) = \begin{pmatrix} -\beta_H & \Psi_S & \Psi_A & 0 & a_H b \\ q\beta_H & -\gamma & 0 & 0 & 0 \\ (1-q)\beta_H & 0 & -\gamma & 0 & 0 \\ 0 & a_V b & a_V b & -\beta_V & 0 \\ 0 & 0 & 0 & \beta_V & -\mu_V \end{pmatrix}.$$

The characteristic equation of the Jacobian matrix is obtained from

$$\det(J - \lambda I) = 0.$$

Expanding the determinant gives $(-\gamma - \lambda)(\lambda^4 + C_3\lambda^3 + C_2\lambda^2 + C_1\lambda + C_0) = 0$, where

$$\begin{aligned} C_3 &= \mu_V + \beta_H + \beta_V + \gamma, \\ C_2 &= \mu_V\beta_V + \mu_V\beta_H + \mu_V\gamma + \beta_V\beta_H + \beta_V\gamma + \beta_H\gamma - \Psi_S q\beta_H - \Psi_A(1-q)\beta_H, \\ C_1 &= \mu_V\beta_V\beta_H + \mu_V\beta_V\gamma + \beta_V\beta_H\gamma + \mu_V\beta_H\gamma - \mu_V q\beta_H\Psi_S - \beta_V q\beta_H\Psi_S \\ &\quad -\beta_V(1-q)\beta_H\Psi_A - \mu_V(1-q)\beta_H\Psi_A, \\ C_0 &= \mu_V\beta_V\beta_H\gamma - \mu_V q\beta_H\beta_V\Psi_S - \mu_V\beta_V(1-q)\beta_H\Psi_A - q\beta_H\beta_V a_V a_H b^2 \\ &\quad -(1-q)\beta_H\beta_V a_V a_H b^2. \end{aligned} \qquad (2)$$

The first factor gives the eigenvalue

$$\lambda = -\gamma < 0,$$

which always satisfies the stability requirement. Therefore, the stability of the disease-free equilibrium depends on the remaining quartic polynomial,

$$\lambda^4 + C_3\lambda^3 + C_2\lambda^2 + C_1\lambda + C_0 = 0.$$

Applying the Routh–Hurwitz criterion to this quartic polynomial provides the conditions required for all eigenvalues to have negative real parts. These conditions lead to the threshold value of the basic reproduction number $\mathcal{R}_0$, which determines whether Zika virus transmission dies out or persists in the population.

Theorem 1 (Local Stability of the Disease-Free Equilibrium). *Let E_0 denote the disease-free equilibrium of the model, and let the characteristic equation of the Jacobian matrix $J = F - V$ evaluated at E_0 be $\lambda^4 + C_3\lambda^3 + C_2\lambda^2 + C_1\lambda + C_0 = 0$, where the coefficients are defined in Eq. (2). Define the basic reproduction number at the disease-free equilibrium,*

$$\mathcal{R}_0 = \sqrt{\frac{\mu_V[q\Psi_S + (1-q)\Psi_A] + a_V a_H b^2}{\mu_V \gamma}}.$$

Then E_0 is locally asymptotically stable if and only if

$$\mathcal{R}_0 < 1, \qquad C_1 > 0, \qquad C_3C_2C_1 > C_1^2 + C_3^2C_0,$$

and E_0 is unstable whenever $\mathcal{R}_0 > 1$.

Proof.

Step 1: Positivity of C_3. Since $\mu_V, \beta_H, \beta_V, \gamma$ are all positive model parameters, $C_3 = \mu_V + \beta_H + \beta_V + \gamma > 0$ (from Eq. (2)) automatically, so this coefficient requires no separate hypothesis.

Step 2: Reduction of C_0 to the threshold parameter. Factor C_0 by collecting the common factor $\beta_H\beta_V$ and using $q + (1-q) = 1$:

$$\begin{aligned} C_0 &= \mu_V\beta_V\beta_H\gamma - \mu_V\beta_H\beta_V[q\Psi_S + (1-q)\Psi_A] - \beta_H\beta_V a_V a_H b^2[q + (1-q)] \\ &= \beta_H\beta_V(\mu_V\gamma - \mu_V[q\Psi_S + (1-q)\Psi_A] - a_V a_H b^2) \\ &= \beta_H\beta_V\mu_V\gamma(1 - (\mathcal{R}_0)^2). \end{aligned}$$

Since $\beta_H, \beta_V, \mu_V, \gamma > 0$, it follows that

$$C_0 > 0 \Leftrightarrow (\mathcal{R}_0)^2 < 1 \Leftrightarrow \mathcal{R}_0 < 1,$$

and conversely $\mathcal{R}_0 > 1$ forces $C_0 < 0$. Since C_0 is the constant term of the quartic factor in the characteristic equation, its sign is determined by $\mathcal{R}_0$. Specifically, $C_0 > 0$ for $\mathcal{R}_0 < 1$, $C_0 = 0$ at $\mathcal{R}_0 = 1$, and $C_0 < 0$ for $\mathcal{R}_0 > 1$. Thus, $\mathcal{R}_0 = 1$ marks the stability threshold, at which C_0 vanishes and $\lambda = 0$ becomes an eigenvalue of the quartic factor.

Step 3: Routh–Hurwitz array. For the quartic $\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4 = 0$ with $(a_1, a_2, a_3, a_4) = (C_3, C_2, C_1, C_0)$, the Routh array is

$$\begin{array}{lccc} \lambda^4 & 1 & a_2 & a_4 \\ \lambda^3 & a_1 & a_3 & 0 \\ \lambda^2 & b_1 = \dfrac{a_1a_2 - a_3}{a_1} & a_4 & \\ \lambda^1 & c_1 = \dfrac{b_1a_3 - a_1a_4}{b_1} & & \\ \lambda^0 & a_4 & & \end{array}$$

All roots of the characteristic polynomial have strictly negative real part if and only if every entry of the first column is positive: $a_1 > 0$, $b_1 > 0$, $c_1 > 0$, $a_4 > 0$. Since $a_1 = C_3 > 0$ always (Step 1), the conditions $b_1 > 0$ and $c_1 > 0$ reduce, after clearing denominators, to

$$b_1 > 0 \;\Leftrightarrow\; C_3C_2 > C_1, \qquad c_1 > 0 \;\Leftrightarrow\; C_3C_2C_1 > C_1^2 + C_3^2C_0.$$

Step 4: Removing redundant conditions. Suppose $C_1 > 0$, $C_0 > 0$, and $C_3C_2C_1 > C_1^2 + C_3^2C_0$ hold. Dividing the last inequality by $C_1C_3 > 0$ gives

$$C_2 > \frac{C_1}{C_3} + \frac{C_3C_0}{C_1} > 0,$$

so $C_2 > 0$ is implied. Dividing instead by $C_1 > 0$ gives

$$C_3C_2 > C_1 + \frac{C_3^2C_0}{C_1} > C_1,$$

so $C_3C_2 > C_1$ is also implied. Hence the independent hypotheses reduce exactly to

$$C_1 > 0, \qquad C_0 > 0 \text{ (i.e. } \mathcal{R}_0 < 1), \qquad C_3C_2C_1 > C_1^2 + C_3^2C_0,$$

which together are necessary and sufficient for all first-column Routh entries to be positive, and therefore for local asymptotic stability of E_0.

Step 5: Instability. If $\mathcal{R}_0 > 1$, Step 2 gives $C_0 < 0$. Hence, the first-column Routh entry corresponding to the λ^0 row is negative. Therefore, the Routh–Hurwitz criterion is not satisfied, and at least one eigenvalue of J has positive real part. Consequently, E_0 is unstable whenever $\mathcal{R}_0 > 1$. ■

Observation 1. The threshold $\mathcal{R}_0$ combines the sexual-transmission contribution $\mu_V[q\Psi_S + (1-q)\Psi_A]$ and the vector-borne contribution $a_V a_H b^2$. The term $q\Psi_S + (1-q)\Psi_A$ reflects the effect of symptomatic and

asymptomatic infection states on sexual transmission. Hence, both symptomatic status and sexual transmission play important roles in determining whether $\mathcal{R}_0$ exceeds 1.

Observation 2. Since $C_0 = \beta_H \beta_V \mu_V \gamma (1 - (\mathcal{R}_0)^2)$, stability requires the product of mosquito mortality μ_V and human recovery rate γ to outweigh the combined transmission terms. Thus increasing mosquito mortality (vector control) and shortening the human infectious period (faster recovery) act jointly to bring $\mathcal{R}_0$ below 1.

4. CONCLUSION

The graph-theoretic framework combined with the Routh–Hurwitz stability theorem provides a rigorous analytical foundation for understanding Zika virus transmission dynamics. By formulating the Jacobian through the F and V matrices extracted from the directed graph, the local stability of the disease-free equilibrium is determined by the basic reproduction number $\mathcal{R}_0$. The derived conditions confirm that the DFE is locally asymptotically stable when $\mathcal{R}_0 < 1$, whereas $\mathcal{R}_0 > 1$ leads to instability and potential persistence of infection. The analysis further shows that sexual transmission through symptomatic and asymptomatic infectious individuals contributes to the transmission threshold, while mosquito mortality and human recovery rate play important roles in reducing $\mathcal{R}_0$. Thus, strengthening vector control and improving recovery can support disease elimination. Overall, the graph-based approach provides an alternative to conventional ODE-based analysis for examining transmission and stability, while offering useful insights into the combined effects of sexual transmission, symptomatic status, mosquito mortality, and recovery on Zika virus persistence and control.

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