



Threshold quantities and Lyapunov functions for ordinary differential equations epidemic models with mass action and standard incidence functions

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ABSTRACT

This paper presents a novel algebraic method for the construction of Lyapunov functions to study global stability of the disease-free equilibrium points of deterministic epidemic ordinary differential equation models with mass action and standard incidence functions. The method is named as **Jacobian-Determinant method**. In our method, a direct algebraic procedure that also relies only on determinant of the Jacobian matrix of the infected subsystem is developed to determine a threshold quantity, \mathcal{R}'_0 akin to the basic reproduction number, \mathcal{R}_0 of such class of models. The developed technique is applied on a wide variety of models to construct Lyapunov functions to study the global stability of the infection-free critical points. Further, implementation of our method reveals that the threshold quantity is the same as (or the square) of the basic reproduction numbers as obtained using the next-generation matrix method. It is further observed that even for models that do not use the standard or mass action incidence, the threshold quantity is still related to the basic reproduction numbers as obtained with the next-generation matrix method.

1. Introduction

Mathematical models have been very helpful in enhancing our understanding of the dynamics of infectious diseases. The volume of literature on mathematical models following the advent of the COVID-19 pandemic further illustrates this assertion [1–4]. As more information about diseases is discovered, the complexity of the models that seek to describe these diseases increases. The increase in complexity and application of mathematical models often necessitates the application of mathematical concepts that hitherto were not used in the field of model.

Despite the tremendous increase in the application of mathematics to understand natural phenomena, the application of differential equations continue to gain attention since the theory of differential equations is quite advanced and the models developed continue to show increased potency in describing the phenomena being studied. Since the eradication or persistence of infectious diseases depends largely on the basic reproduction number, there is hardly any study employing mathematical ordinary differential equation model (ODE) modeling that does not seek to determine the threshold quantity for the disease.

Several techniques have been developed to calculate the basic reproduction number, \mathcal{R}_0 . These methods include the use of the survival

function, the eigenvalues technique, the condition for existence of the endemic equilibrium, the constant term of the characteristic polynomial technique, and the next-generation technique. The eigenvalues technique uses the Routh–Hurwitz criterion to establish conditions under which the characteristic polynomial of the Jacobian matrix of the infected sub-system will be stable and links same to the basic reproduction number [5]. For most ordinary differential equation epidemic models, the conditions under which the endemic equilibrium fails to exist can often be used to determine the basic reproduction number. The techniques that have gained most use in literature are the next generation matrix method [6,7]. These techniques have been largely used because of their mathematical tractability. The basic reproduction numbers obtained using the various method sometimes are not unique even though they all are threshold quantities. These threshold quantities play a major role in the local and often global stability of the equilibrium points of the models. An interesting discussion on global stability for models with a wide variety of incidence functions can be seen in [8].

As noted in [9], the threshold quantities (often called the basic reproduction numbers) obtained using the above mentioned techniques

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may often be different even for the same method depending on the choice of what constitutes transition from one infectious state to another. We note however that despite this obvious difference and the fact that the threshold quantities may not actually represent average number of infections that result from a single infected individual throughout their period of infectiousness, the quantities are often called the basic reproduction number and also play the major role of determining the stability of the infection-free critical points just like \mathcal{R}_0 . Also, it is worth noting that the methods discussed in [5–7] all involve finding spectral radii of next-generation matrices or solving characteristic polynomial equations. These formalism may lend themselves to mathematical intractability, especially for large models. Therefore, the need to develop simpler techniques to obtain threshold quantities for stability of critical points of ODE models cannot be overemphasized. In epidemiological modeling, when the infection-free critical point is globally(asymptotically) stable, then it may be possible to construct a Lyapunov function \mathcal{L} such that whenever a threshold quantity $\mathcal{R}'_0 \leq 1$, then $\frac{d\mathcal{L}}{dt} \leq 0$. There are few straightforward techniques for constructing Lyapunov functions. The Matrix-theoretic and Graph-theoretic methods were proposed to help in the construction of Lyapunov functions for general epidemic models [10]. Even though the matrix-theoretic technique of [10] provides an algebraic routine for constructing Lyapunov functions and seems straightforward, its reliance on the eigenvector of the next-generation matrix $\mathcal{V}^{-1}\mathcal{F}$ may make its application challenging especially for large systems. In this paper, this idea (relationship between $\mathcal{R}'_0 \leq 1$ when $\frac{d\mathcal{L}}{dt} \leq 0$ and Global Asymptotic Stability (GAS) of the infection-free equilibrium point) is explored to develop a routine for constructing Lyapunov functions for a class of epidemic ODE models that involve the mass action and standard incidence functions. The technique also presents a routine for calculating the threshold quantity \mathcal{R}'_0 for such class of epidemic models. The technique developed here is very simple and cheap to use as it relies only on the determinant of the Jacobian matrix of the infected sub-system of the models.

The rest of the paper is organized as follows: In Section 2, the method of interest is developed. Several illustrative examples are presented in Section 3 to demonstrate how the developed method can be used to calculate the threshold quantity of some selected ODE models. The method is further demonstrated in Section 4 to construct Lyapunov functions of some selected models in literature. The method is finally employed in Section 5 to determine the threshold quantities for some models that do not follow the standard/mass action incidence functions; showing the extended applicability of the technique in determining the basic reproduction numbers of epidemic models.

2. Development of the method

The general ODE epidemic models of interest here are of the form

$$\begin{aligned} \frac{dX}{dt} &= f(X, Y), \\ \frac{dY}{dt} &= g(X, Y), \end{aligned} \tag{1}$$

where $X = (X_1, X_2, \dots, X_{m_1})$ and $Y = (Y_1, Y_2, \dots, Y_{m_2})$ represent non-infected and infected compartment populations respectively.

For these type of models, it is often possible to construct a Lyapunov function to determine the global stability of the disease-free equilibrium point \mathcal{E}_0 using

$$\mathcal{L} = \sum_{i=1}^{m_2} K_i Y_i, \quad K_i \geq 0. \tag{2}$$

This is the most often used Lyapunov function candidate and is similar to the one argued for and used in [11].

The time-derivative of the Lyapunov function candidate is then given by

$$\frac{d\mathcal{L}}{dt} = \sum_{i=1}^{m_2} K_i \frac{dY_i}{dt} = \sum_{i=1}^{m_2} K_i g_i(X, Y). \tag{3}$$

Generally, the infected compartments in epidemic ODE models have the form

$$\frac{dY}{dt} = \mathcal{G}_n(X, Y) + \mathcal{G}_l(Y),$$

where $\mathcal{G}_n(X, Y)$ is a nonlinear form that captures the transmission terms involving the movement of uninfected individuals into the infected compartments following effective contact with the infectious individuals. The part $\mathcal{G}_l(Y)$ is a linear form that captures the transition among infected compartments including the movement from one compartment to another due to change in state of infectiousness, and also movement out of compartments due to removal through events like recovery and death. We shall present our technique for the mass action incidence case first and then make a note later for the case of standard incidence. For epidemic ODE models that use mass action, the equations for infected compartments are generally of the form

$$\frac{dY_i}{dt} = \sum_{j=1}^{m_2} \sum_{k=1}^{m_1} \beta_{ij} \eta_{ij} \zeta_{ik} Y_j X_k + \sum_{j=1}^{m_2} \kappa_{ij} Y_j, \tag{4}$$

where $\beta_{ij} \eta_{ij} \zeta_{ik} Y_j X_k$ describe the transmission terms and $\kappa_{ij} Y_j$ describe the transition terms, where

$$\beta_{ij} \geq 0, \eta_{ij} \geq 0, \zeta_{ik} \geq 0 \text{ and } \kappa_{ij} = \begin{cases} \geq 0 & \text{if } i \neq j, \\ < 0 & \text{if } i = j. \end{cases}$$

Substituting Eq. (4) into Eq. (3) gives

$$\frac{d\mathcal{L}}{dt} = \sum_{i=1}^{m_2} K_i \left[\sum_{j=1}^{m_2} \sum_{k=1}^{m_1} \beta_{ij} \eta_{ij} \zeta_{ik} Y_j X_k + \sum_{j=1}^{m_2} \kappa_{ij} Y_j \right],$$

which can be written as

$$\frac{d\mathcal{L}}{dt} = \sum_{j=1}^{m_2} \left[\sum_{i=1}^{m_2} K_i \left(\sum_{k=1}^{m_1} \beta_{ij} \eta_{ij} \zeta_{ik} X_k + \kappa_{ij} \right) \right] Y_j. \tag{5}$$

For ODE models, the total population is often bounded above by some constant (that is $N(t) \leq \mathcal{N}$ and consequently $X_k \leq \mathcal{N}$) and when mass action and standard incidence functions are used, the inequality $N(t) \leq \mathcal{N}$ can often be used to reduce Eq. (5) into an inequality of the form

$$\frac{d\mathcal{L}}{dt} \leq \sum_{j=1}^{m_2} \left[\sum_{i=1}^{m_2} K_i \left(\sum_{k=1}^{m_1} \beta_{ij} \eta_{ij} \zeta_{ik} \mathcal{N} + \kappa_{ij} \right) \right] Y_j. \tag{6}$$

Now, if the infection-free equilibrium point is globally asymptotically stable when $\mathcal{R}'_0 \leq 1$ and \mathcal{L} is a Lyapunov function, then the right-hand-side of Eq. (6) can be written in the following form

$$\begin{aligned} &\sum_{j=1}^{m_2} \left[\sum_{i=1}^{m_2} K_i \left(\sum_{k=1}^{m_1} \beta_{ij} \eta_{ij} \zeta_{ik} \mathcal{N} + \kappa_{ij} \right) \right] Y_j \\ &= \xi (\mathcal{R}'_0 - 1) \sum_{j=1}^{m_2} \mathcal{T}_j Y_j, \quad \mathcal{T}_j \geq 0, \xi > 0. \end{aligned} \tag{7}$$

By comparing coefficients of Y_j in Eq. (7), the following system of linear equations is established.

$$\sum_{i=1}^{m_2} K_i \left(\sum_{k=1}^{m_1} \beta_{ij} \eta_{ij} \zeta_{ik} \mathcal{N} + \kappa_{ij} \right) = \xi (\mathcal{R}'_0 - 1) \mathcal{T}_j, \quad \forall j = 1, 2, \dots, m_2. \tag{8}$$

Let $M_{ij} = \sum_{k=1}^{m_1} \beta_{ij} \eta_{ij} \zeta_{ik} \mathcal{N} + \kappa_{ij}$, then the above equations can be written as

$$\sum_{i=1}^{m_2} K_i M_{ij} = \xi (\mathcal{R}'_0 - 1) \mathcal{T}_j, \quad j = 1, 2, \dots, m_2. \tag{9}$$

In the case of standard incidence functions, it can be shown that $M_{ij} = \sum_{k=1}^{m_1} \beta_{ij} \eta_{ij} \zeta_{ik} + \kappa_{ij}$.

The solution of the system of equations in Eq. (9) is given by

$$K_i = \frac{\xi (\mathcal{R}'_0 - 1) |M^i|}{|M|}, \quad i = 1, 2, \dots, m_2, \tag{10}$$

where, $|M|$ is the determinant of M and $|M^i|$ is the determinant of M^i which is obtained by replacing the i th column of M with the vector $\mathcal{T} = [\mathcal{T}_{j,1}] = \mathcal{T}_j, j = 1, 2, \dots, m_2$.

The natural question that arises now is, how the \mathcal{T}_j s should be chosen. Here, we define \mathcal{T}_j as the infectivity factor of the j th infected compartment. For mass action and standard incidence functions, these coefficients are often of the form $\beta_{ij}\eta_{ij}$, where β_{ij} and η_{ij} are associated with infectivity of the infected compartments. The infectivity factors are often the constant coefficients of the infected states in the force of infection. We note here that, if Y_j does not contribute to infection (as in the case of non-infectious exposed persons), then $\beta_{ij}\eta_{ij} = 0$.

Now, since $\frac{\xi(\mathcal{R}'_0-1)}{|M|}$ is a common factor then following normalized versions of the solutions in (10) will also do for Lyapunov coefficients.

$$K_i = |M^i|, \quad i = 1, 2, \dots, m_2, \tag{11}$$

Therefore, \mathcal{R}_0 is not needed in our method to defined the Lyapunov coefficients. Our method only requires the Jacobian of the infected sub-system and the infectivity vector \mathcal{T} , which is derived from the force of infection function to determine the Lyapunov coefficients. The following result is thus in order.

Lemma 2.1. *A simpler choice of the Lyapunov coefficients is $K_i = ||M^i||$, that is, the absolute values of the determinant of M^i .*

Also, since $\frac{\xi(\mathcal{R}'_0-1)}{|M|}$ is a common factor in the Lyapunov coefficients (See Eq. (10)), then we can normalize the Lyapunov coefficients by setting the common factor to a constant (that is $\frac{\xi(\mathcal{R}'_0-1)}{|M|} = \xi_1$). The following result is thus established.

Lemma 2.2. *The threshold quantity of the epidemic model (1) can be determined by M as follows*

$$\mathcal{R}'_0 = \frac{\xi_1}{\xi} |M| + 1.$$

The factor $\xi_2 = \xi/\xi_1$ can be chosen such that $|M| = \xi_2 \left(\frac{B}{D} - 1\right)$, in that case, $\mathcal{R}'_0 = \frac{B}{D}$, where B is the part that contains the transmission factors such as probability of infection, contact rate or infectivity/susceptibility factors, and D is the part containing only transmission and other non-transmission terms.

Since the determinant of the Jacobian matrix of the infected sub-system vanishes when threshold quantity is unity (ie $\mathcal{R}'_0 = 1$), we name \mathcal{R}'_0 as the vanishing-determinant ratio of the given model.

From Eq. (9), the following result is obtained.

Lemma 2.3. *The matrix, M is characterized as follows:*

- (i) *The quantities, M_{ij} are the (j, i) th components of the Jacobian of the infected subsystem.*
- (ii) *The matrix M is therefore, the transpose of the Jacobian of the infected subsystem evaluated at \mathcal{E}_0 .*
- (iii) *Since $|M| = |M^T|$, then \mathcal{R}'_0 can be obtained from the Jacobian of the infected subsystem evaluated at \mathcal{E}_0 .*

Conjecture 2.1. *If $|M| = B - D$, then $|M^i| \geq 0$ and if $|M| = D - B$, then $|M^i| \leq 0$, so that K_i is always nonnegative.*

Since M is the transpose of the Jacobian of the infected subsystem and M^i is obtained by replacing the i th column of M with \mathcal{T} , then the following result is established.

Lemma 2.4. *Let \mathcal{J} be the Jacobian of the infected subsystem of the epidemic model (1) evaluated at the infection-free equilibrium and let \mathcal{T} be as defined above. Then the Lyapunov coefficients are given by $K_i = ||\mathcal{J}^i||$, where \mathcal{J}^i is obtained by replacing the i th column of \mathcal{J} with \mathcal{T} .*

In Section 3, we present some motivating examples to illustrate how the developed algorithm can be used to determine the threshold quantity of some models in literature. Also, in Section 4, we also illustrate by way of example how the technique can be used to construct Lyapunov functions for some models in literature.

3. Illustrative examples on determining \mathcal{R}'_0

In this section, we present a number of examples from literature to illustrate the applicability of our proposed method in determining the threshold quantity of some models in literature.

3.1. Example 1: An SEI model with two latent states

This example is the taken from the motivating examples of [7] and is given by

$$\left. \begin{aligned} \frac{dS}{dt} &= \mu N - \frac{\beta SI}{N} - \mu S, \\ \frac{dE_1}{dt} &= \frac{p\beta SI}{N} - (v_1 + \mu) E_1, \\ \frac{dE_2}{dt} &= \frac{(1-p)\beta SI}{N} - (v_2 + \mu) E_2, \\ \frac{dI}{dt} &= v_1 E_1 + v_2 E_2 - (\gamma + \mu) I, \\ \frac{dR}{dt} &= \gamma I - \mu, R. \end{aligned} \right\} \tag{12}$$

The Jacobian of the infected subsystem evaluated at the disease-free equilibrium $\mathcal{E}_0 = (1, 0, 0, 0, 0)$ is given by

$$\mathcal{J}(\mathcal{E}_0) = \begin{bmatrix} -(v_1 + \mu) & 0 & v_1 \\ 0 & -(v_2 + \mu) & v_2 \\ p\beta & (1-p)\beta & -(\gamma + \mu) \end{bmatrix},$$

whose determinant is given by

$$|\mathcal{J}(\mathcal{E}_0)| = \beta [v_1 (v_2 + \mu) p + v_2 (1-p) (v_1 + \mu)] - (v_2 + \mu) (v_1 + \mu) (\gamma + \mu),$$

which can be written as

$$|\mathcal{J}(\mathcal{E}_0)| = (v_2 + \mu) (v_1 + \mu) (\gamma + \mu) \times \left[\frac{\beta (v_1 (v_2 + \mu) p + v_2 (1-p) (v_1 + \mu))}{(v_2 + \mu) (v_1 + \mu) (\gamma + \mu)} - 1 \right].$$

Here we have $\xi = (v_2 + \mu) (v_1 + \mu) (\gamma + \mu)$ and the threshold quantity is obtained as

$$\mathcal{R}'_0 = \frac{\beta (v_1 (v_2 + \mu) p + v_2 (1-p) (v_1 + \mu))}{(v_2 + \mu) (v_1 + \mu) (\gamma + \mu)},$$

which is the same as the basic reproduction number obtained in [7].

3.2. Example 2: A treatment model of TB

This example is also taken from [6] and is given by

$$\left. \begin{aligned} \frac{dS}{dt} &= b - \frac{\beta_1 SI}{N} - dS, \\ \frac{dE}{dt} &= \frac{\beta_1 SI}{N} + \frac{\beta_2 Tj}{N} + pr_2 I - (d + v + r_1) E, \\ \frac{dI}{dt} &= vE - (d + r_2) I, \\ \frac{dT}{dt} &= qr_2 I + r_1 E - \frac{\beta_2 TI}{N} - dT, \end{aligned} \right\} \tag{13}$$

with the infection-free critical point given by $\mathcal{E}_0 = (1, 0, 0, 0)$.

The infected sub-system is given by

$$\begin{aligned} \frac{dE}{dt} &= \frac{\beta_1 SI}{N} + \frac{\beta_2 Tj}{N} + pr_2 I - (d + v + r_1) E \\ \frac{dI}{dt} &= vE - (d + r_2) I. \end{aligned}$$

The Jacobian of the infected subsystem evaluated at the infection-free critical point is given by

$$J(\mathcal{E}_0) = \begin{bmatrix} -(d + v + r_1) & pr_2 + \beta_1 \\ v & -(d + r_2) \end{bmatrix},$$

so that

$$J(\mathcal{E}_0) = (d + v + r_1)(d + r_2) - vpr_2 - \beta_1 v,$$

and the threshold quantity is obtained as

$$\mathcal{R}'_0 = \frac{\beta_1 v}{(d + v + r_1)(d + r_2) - vpr_2},$$

which is the same as the basic reproduction number found in [6].

3.3. Example 3: An SEI model with two host categories

The SEI model of [7] is considered here. The infected subsystem presented is given by

$$\left. \begin{aligned} \frac{dE_1}{dt} &= \frac{\beta_1 S_1 I_2}{N_2} - (v_1 + \mu) E_1, \\ \frac{dE_2}{dt} &= \frac{\beta_2 S_2 I_1}{N_1} - (v_2 + \mu) E_2, \\ \frac{dI_1}{dt} &= v_1 E_1 - (\gamma_1 + \mu) I_1, \\ \frac{dI_2}{dt} &= v_2 E_2 - (\gamma_2 + \mu) I_2. \end{aligned} \right\} \quad (14)$$

The Jacobian of the subsystem evaluated at the DFE is given by

$$J(\mathcal{E}_0) = \begin{bmatrix} -(v_1 + \mu) & 0 & 0 & \beta_1 \\ 0 & -(v_2 + \mu) & \beta_2 & 0 \\ v_1 & 0 & -(\gamma_1 + \mu) & 0 \\ 0 & v_2 & 0 & -(\gamma_2 + \mu) \end{bmatrix},$$

whose determinant is given by

$$|J(\mathcal{E}_0)| = (\gamma_2 + \mu)(\gamma_1 + \mu)(v_2 + \mu)(v_1 + \mu) - v_1 v_2 \beta_1 \beta_2,$$

so that we have

$$|J(\mathcal{E}_0)| = -(\gamma_2 + \mu)(\gamma_1 + \mu)(v_2 + \mu) \times (v_1 + \mu) \left(\frac{v_1 v_2 \beta_1 \beta_2}{(\gamma_2 + \mu)(\gamma_1 + \mu)(v_2 + \mu)(v_1 + \mu)} - 1 \right).$$

Therefore, the threshold quantity is given by

$$\mathcal{R}'_0 = \frac{v_1 v_2 \beta_1 \beta_2}{(\gamma_2 + \mu)(\gamma_1 + \mu)(v_2 + \mu)(v_1 + \mu)}.$$

We note that, the threshold quantity obtained here is the square of the basic reproduction number of the model obtained using the next-generation matrix method.

3.4. Example 4: A Malaria model with chemo-therapy

The model of Makinde and Okusun [12] is given by

$$\left. \begin{aligned} \frac{dS_h}{dt} &= (1 - (p_1 + p_2)u_1) \mu_h N_h \\ &\quad + (1 - \rho)(\tau u_2 + r) I_h - \frac{\beta_1 \epsilon I_v S_h}{N_h} - \mu_h S_h + \kappa R_h, \\ \frac{dE_h}{dt} &= p_1 u_1 \mu_h N_h + \frac{\beta_1 \epsilon I_v S_h}{N_h} - (\mu_h + \alpha_1) E_h, \\ \frac{dI_h}{dt} &= p_2 u_1 \mu_h N_h + \alpha_1 E_h - (\tau u_2 + \psi + r + \mu_h) I_h, \\ \frac{dR_h}{dt} &= \rho(\tau u_2 + r) I_h - (\kappa + \mu_h) R_h, \\ \frac{dS_v}{dt} &= \mu_v N_v - \frac{\beta_2 \phi \epsilon I_h S_v}{N_h} - (v u_3 + \mu_v) S_v, \\ \frac{dE_v}{dt} &= \frac{\beta_2 \phi \epsilon I_h S_v}{N_h} - (v u_3 + \alpha_2 + \mu_v) E_v, \\ \frac{dI_v}{dt} &= \alpha_2 E_v - (v u_3 + \mu_v) I_v. \end{aligned} \right\} \quad (15)$$

The infected compartments are E_h, I_h, E_v and I_v and hence the Jacobian of the infected subsystem evaluated at the disease-free equilibrium point is given by

$$J(\mathcal{E}_0) = \begin{bmatrix} -(\mu_h + \alpha_1) & 0 & 0 & \frac{\beta_1 \epsilon \phi S_h^0}{N_h^0} \\ \alpha_1 & -(\tau u_2 + \psi + r + \mu_h) & 0 & 0 \\ 0 & \frac{\beta_2 \phi \epsilon S_v^0}{N_h^0} & -(v u_3 + \alpha_2 + \mu_v) & 0 \\ 0 & 0 & \alpha_2 & -(v u_3 + \mu_v) \end{bmatrix},$$

whose determinant is given by

$$|J(\mathcal{E}_0)| = (\mu_h + \alpha_1)(\tau u_2 + \psi + r + \mu_h)(v u_3 + \alpha_2 + \mu_v)(v u_3 + \mu_v) - \frac{\alpha_1 \beta_2 \phi^2 \epsilon^2 S_v^0 \beta_1 S_h^0 \alpha_2}{(N_h^0)^2}.$$

The threshold quantity is therefore given by

$$\mathcal{R}'_0 = \frac{\alpha_1 \beta_2 \phi^2 \epsilon^2 \beta_1 \alpha_2}{(\mu_h + \alpha_1)(\tau u_2 + \psi + r + \mu_h)(v u_3 + \alpha_2 + \mu_v)(v u_3 + \mu_v)} \frac{S_h^0 S_v^0}{(N_h^0)^2}.$$

In [12], the basic reproduction number was obtained for the uncontrolled ($u_1 = u_2 = u_3 = 0$) normalized ($S_h = N_h, S_v/N_h = m$) problem. If we use those simplifications, we obtain

$$\mathcal{R}'_0 = \frac{\beta_1 \beta_2 \epsilon^2 \phi^2 \alpha_1 \alpha_2 m}{(\mu_h + \alpha_1)(\psi + r + \mu_h)(\alpha_2 + \mu_v) \mu_v}.$$

We note again that, the threshold quantity obtained here is the square of the basic reproduction number was obtained in [12].

We make the following conjecture.

Conjecture 3.1. *The threshold quantity \mathcal{R}'_0 presented in this paper is the basic reproduction number as determined using the next-generation method.*

From the last two examples in Sections 3.3 and 3.4, we note that the threshold quantities obtained with our novel method here are not exactly as those in the cited literature. In fact the values obtained here are the squares of those obtained in the cited literature. It is however easy to observe that the threshold quantities of the examples in Sections 3.3 and 3.4 have a special character different from those of the other models; the existence of product of transmission probabilities or powers of contact rates. The following remark is thus in order.

Remark 3.1. Whenever \mathcal{R}'_0 contains a product of transmission probabilities or powers of contact rates, then $\mathcal{R}_0 = \sqrt{\mathcal{R}'_0}$.

4. Illustrative examples on constructing Lyapunov function candidates

In this section, the developed technique is used to construct some Lyapunov functions of some selected models. These examples are specifically chosen in order to compare the result of the developed technique and the Lyapunov functions that had been constructed in the literature.

4.1. An SEIR model with lapse

This model is the SEIR model with relapse taken from [13] by [10] and is given by

$$\left. \begin{aligned} \frac{dS}{dt} &= \Lambda - \beta SI - dS, \\ \frac{dE}{dt} &= \beta SI - (d + \epsilon) E, \\ \frac{dI}{dt} &= \epsilon E + \eta R - (d + \gamma + \alpha) I, \\ \frac{dR}{dt} &= \gamma I - (d + \eta) R. \end{aligned} \right\} \quad (16)$$

The infected subsystem include E , I and R and hence the jacobian of the infected subsystem evaluated at the disease-free equilibrium $(\frac{\Lambda}{d}, 0, 0, 0)$ is given by

$$J = \begin{bmatrix} -(d + \epsilon) & \frac{\beta\Lambda}{d} & 0 \\ \epsilon & -(d + \gamma + \alpha) & \eta \\ 0 & \beta & 0 \end{bmatrix},$$

and the infectivity vector is given by $\mathcal{T} = (0, \beta, 0)$.

The Lyapunov coefficients are thus given by

$$\begin{aligned} K_1 = |J^1| &= \begin{vmatrix} 0 & \beta & 0 \\ \epsilon & -d - \gamma - \alpha & \eta \\ 0 & \gamma & -d - \eta \end{vmatrix} = \epsilon\beta(d + \eta), \\ K_2 = |J^2| &= \begin{vmatrix} -d - \epsilon & \frac{\beta\Lambda}{d} & 0 \\ 0 & \beta & 0 \\ 0 & \gamma & -d - \eta \end{vmatrix} = (d + \epsilon)\beta(d + \eta), \\ K_3 = |J^3| &= \begin{vmatrix} -d - \epsilon & \frac{\beta\Lambda}{d} & 0 \\ \epsilon & -d - \gamma - \alpha & \eta \\ 0 & \beta & 0 \end{vmatrix} = (d + \epsilon)\eta\beta. \end{aligned}$$

After scaling the coefficients, we get

$$K_1 = 1, K_2 = \frac{d + \epsilon}{\epsilon}, K_3 = \frac{(d + \epsilon)\eta}{\epsilon(d + \eta)},$$

which are the same as found in [10].

4.2. The smoking model of [14]

The model is given by

$$\left. \begin{aligned} \frac{dP}{dt} &= \mu N - \frac{\beta PS}{N} - \mu P, \\ \frac{dS}{dt} &= \frac{\beta PS}{N} + \alpha Q_t - (\mu + \gamma) S, \\ \frac{dQ_t}{dt} &= \gamma(1 - \sigma) S - (\alpha + \mu) Q_t, \\ \frac{dQ_p}{dt} &= \gamma\sigma S - \mu Q_p. \end{aligned} \right\} \quad (17)$$

The infected subsystem is given by

$$\left. \begin{aligned} \frac{dS}{dt} &= \frac{\beta PS}{N} + \alpha Q_t - (\mu + \gamma) S, \\ \frac{dQ_t}{dt} &= \gamma(1 - \sigma) S - (\alpha + \mu) Q_t, \end{aligned} \right\}$$

so that the Jacobian evaluated at $\mathcal{E}_0 = (1, 0, 0, 0)$ is given by

$$J = \begin{bmatrix} \beta - (\gamma + \mu) & \alpha \\ \gamma(1 - \sigma) & -(\alpha + \mu) \end{bmatrix}, \text{ and } \mathcal{T} = (\beta, 0)^T.$$

Therefore

$$\begin{aligned} K_1 = |J^1| &= \begin{vmatrix} \beta & 0 \\ \gamma(1 - \sigma) & -(\alpha + \mu) \end{vmatrix} = \beta(\alpha + \mu), \\ K_2 = |J^2| &= \begin{vmatrix} \beta - (\gamma + \mu) & \alpha \\ \beta & 0 \end{vmatrix} = \beta\alpha, \end{aligned}$$

which can be scaled to $K_1 = \alpha + \mu$, $K_2 = \alpha$ which are the same as found in [14].

4.3. Application of technique to models with backward bifurcation

4.3.1. A TB model with exogenous re-infection [15]

$$\left. \begin{aligned} \frac{dS}{dt} &= \Pi - \frac{\beta(W_T \eta_T + T)S}{N} - \mu S, \\ \frac{dL}{dt} &= \frac{f\beta(\eta_T W_T + T)S}{N} + \rho W_T - \frac{\eta_R \beta(\eta_T W_T + T)L}{N} - (\alpha + \mu)L, \\ \frac{dT}{dt} &= \frac{(1-f)\beta(\eta_T W_T + T)S}{N} + \frac{\eta_R \beta(\eta_T W_T + T)L}{N} + \alpha L - (\tau + \mu + \delta)T, \\ \frac{dW_T}{dt} &= \tau T - (\rho + \mu)W_T. \end{aligned} \right\}$$

The infected subsystem include $\frac{dL}{dt}$, $\frac{dT}{dt}$, and $\frac{dW_T}{dt}$ and its Jacobian evaluated at the disease-free equilibrium of the model is given by

$$J = \begin{bmatrix} -(\alpha + \mu) & f\beta & f\beta\eta_T + \rho \\ \alpha & (1-f)\beta - (\tau + \mu + \delta) & (1-f)\beta\eta_T \\ 0 & \tau & -(\rho + \mu) \end{bmatrix}.$$

The determinant of J is then obtained as

$$|M| = |J(\mathcal{E}_0)| = \beta((1-f)\mu + \alpha)(\tau\eta_T + \mu + \rho) - [\mu(\tau + \mu + \delta)(\mu + \rho + \alpha) + \alpha\rho(\delta + \mu)]$$

so that the threshold quantity is given by $\mathcal{R}'_0 = \frac{\beta((1-f)\mu + \alpha)(\tau\eta_T + \mu + \rho)}{\mu(\tau + \mu + \delta)(\mu + \rho + \alpha) + \alpha\rho(\delta + \mu)}$ which is the same as the basic reproduction number of the model.

Now, for this model the interactivity vector \mathcal{T} is given by $\mathcal{T} = (0, \beta, \beta\eta_T)$, so that the Lyapunov coefficients are obtained as follows:

$$\begin{aligned} K_1 = |M^1| &= \begin{vmatrix} 0 & \beta & \beta\eta_T \\ \alpha & (1-f)\beta - \tau - \mu - \delta & (1-f)\beta\eta_T \\ 0 & \tau & -\rho - \mu \end{vmatrix} \\ &= \alpha\beta(\tau\eta_T + \mu + \rho), \end{aligned}$$

$$K_2 = |M^2| = \begin{vmatrix} -\alpha - \mu & f\beta & f\beta\eta_T + \rho \\ 0 & \beta & \beta\eta_T \\ 0 & \tau & -\rho - \mu \end{vmatrix} = (\alpha + \mu)\beta(\tau\eta_T + \mu + \rho),$$

$$\begin{aligned} K_3 = |M^3| &= \begin{vmatrix} -\alpha - \mu & f\beta & f\beta\eta_T + \rho \\ \alpha & (1-f)\beta - \tau - \mu - \delta & (1-f)\beta\eta_T \\ 0 & \beta & \beta\eta_T \end{vmatrix} \\ &= ((\alpha + \mu)(\tau + \mu + \delta)\eta_T + \rho\alpha)\beta. \end{aligned}$$

Now, the time derivative of the Lyapunov function candidate $\mathcal{L} = K_1 L + K_2 T + K_3 W_T$ is simplified to obtain

$$\begin{aligned} \frac{d\mathcal{L}}{dt} &= \left(\frac{((\mu(1-f) + \alpha)S + \eta_R \mu L)}{N} \times \frac{\mathcal{R}'_0}{((1-f)\mu + \alpha)} - 1 \right) \beta(W_T \eta_T + T), \end{aligned}$$

so that $\mathcal{R}'_0 < 1$ is not sufficient for GAS which suggests the presence of backward bifurcation as shown in [16]. Now, if $\eta_R = 0$ then the time-derivative of the Lyapunov function becomes $\frac{d\mathcal{L}}{dt} = \left(\frac{S\mathcal{R}'_0}{N} - 1\right) \beta (W_T \eta_T + T)$, which is negative whenever $\mathcal{R}'_0 < 1$ indicating GAS of the disease-free equilibrium in the absence of exogenous re-infection.

4.3.2. The risk-structured model of [15]

This model was used in [15] to illustrate that, stratification of the Susceptible class may cause backward bifurcation. The model is given by

$$\left. \begin{aligned} \frac{dS_l}{dt} &= (1-f)\pi + \psi_h S_h - \frac{\beta I S_l}{N} - \psi_l S_l - \mu S_l, \\ \frac{dS_h}{dt} &= f\pi + \psi_l S_l - \frac{\theta_h \beta I S_h}{N} - \psi_h S_h - \mu S_h, \\ \frac{dE}{dt} &= \frac{\beta (S_h \theta_h + S_l) I}{N} - (\sigma + \mu) E, \\ \frac{dI}{dt} &= \sigma E - (\gamma + \mu + \delta) I, \end{aligned} \right\}$$

where S_l and S_h are low-risk and high-risk Susceptibles respectively with different levels of Susceptibilities. The Jacobian of the infected subsystem at the disease-free equilibrium point is given by

$$J = \begin{bmatrix} -(\sigma + \mu) & \frac{\beta(S_h^* \theta_h + S_l^*)}{N^*} \\ \sigma & -(\gamma + \mu + \delta) \end{bmatrix}$$

whose determinant is given by $-\frac{\sigma(S_h \theta_h + S_l) \beta}{N} + (\sigma + \mu)(\gamma + \mu + \delta)$ so that the threshold quantity can be given by

$$\mathcal{R}'_0 = \frac{\beta \sigma (\theta_h S_h^* + S_l^*)}{N^* (\sigma + \mu) (\gamma + \mu + \delta)}.$$

Now, the vector \mathcal{T} for this model is given by $\mathcal{T} = (0, 1)$ so that the Lyapunov coefficients are obtained as follows:

$$K_1 = |M^1| = \left\| \begin{matrix} 0 & 1 \\ \sigma & -(\gamma + \mu + \delta) \end{matrix} \right\| = \sigma,$$

$$K_2 = |M^2| = \left\| \begin{matrix} -(\sigma + \mu) & \frac{\beta(S_h \theta_h + S_l)}{N} \\ 0 & 1 \end{matrix} \right\| = \sigma + \mu.$$

The time derivative of the Lyapunov function candidate $\mathcal{L} = K_1 E + K_2 I$ can be simplified into

$$\frac{d\mathcal{L}}{dt} = \left(\frac{(S_h \theta_h + S_l) N^*}{(S_h^* \theta_h + S_l^*) N} \mathcal{R}'_0 - 1 \right) I.$$

We observe that $\mathcal{R}'_0 < 1$ does not guarantee GAS of the disease-free equilibrium, suggesting the presence of backward bifurcation. We also observe that if there is no risk difference among Susceptibles (ie. $\theta_h = 1$) then the time-derivative of the Lyapunov function reduces to $\frac{d\mathcal{L}}{dt} \leq (\mathcal{R}'_0 - 1) I$.

5. Application of the developed technique on other model types

In this section, the developed technique is applied to other models that do not use the standard and mass action incidence functions in order to check the generalizability of the technique to such type of models.

5.1. Example 5: A model of Cholera model [17]

This model is chosen because it applies the saturated incidence function which is of a different form from the standard/mass action incidence.

The Cholera model [17] is given by

$$\left. \begin{aligned} \frac{dS}{dt} &= (1-\rho)A - \frac{\beta SB}{K+B} + \theta V - (\phi + \mu_1)S, \\ \frac{dV}{dt} &= \rho A + \phi S - \frac{\sigma \beta VB}{K+B} - (\theta + \mu_1)V, \\ \frac{dI}{dt} &= \frac{\beta SB}{K+B} + \frac{\sigma \beta VB}{K+B} - (d + \alpha + \mu_1)I, \\ \frac{dB}{dt} &= \eta I - \mu_2 B. \end{aligned} \right\} \tag{18}$$

The infected subsystem is given by

$$\left. \begin{aligned} \frac{dI}{dt} &= \frac{\beta SB}{K+B} + \frac{\sigma \beta VB}{K+B} - (d + \alpha + \mu_1)I, \\ \frac{dB}{dt} &= \eta I - \mu_2 B, \end{aligned} \right\}$$

with the Jacobian given by

$$J(\mathcal{E}_0) = \begin{bmatrix} -(d + \alpha + \mu_1) & \frac{\beta S}{K} + \frac{\beta \sigma V}{K} \\ \eta & -\mu_2 \end{bmatrix}.$$

Now,

$$|J(\mathcal{E}_0)| = \mu_2 (d + \alpha + \mu_1) - \frac{\beta \eta (S^0 + \sigma V^0)}{K},$$

so that the threshold quantity is given by

$$\mathcal{R}'_0 = \frac{\beta \eta (S^0 + \sigma V^0)}{K \mu_2 (d + \alpha + \mu_1)},$$

which is the same as the basic reproduction number found in [17], using the next-generation matrix technique of [6].

5.2. Example 6: A Maize Streak Virus Disease model [18]

This example is the Maize Streak Virus Disease model of [18] given by

$$\left. \begin{aligned} \frac{dS_m}{dt} &= r S_m \left(1 - \frac{N_m}{K}\right) + (1-\epsilon) \rho E_m - \frac{\beta_{hm} S_m I_h}{N_h} - \frac{a S_m N_h}{1 + A S_m}, \\ \frac{dE_m}{dt} &= \frac{\beta_{hm} S_m I_h}{N_h} - \frac{a E_m N_h}{1 + A E_m} - (\rho + \mu_m) E_m, \\ \frac{dI_m}{dt} &= \epsilon \rho E_m - \frac{a I_m N_h}{1 + A I_m} - (\alpha + \mu_m) I_m, \\ \frac{dS_h}{dt} &= b - \frac{\beta_{mh} S_h (E_m + I_m)}{N_m} - \mu_h S_h, \\ \frac{dI_h}{dt} &= \frac{\beta_{mh} S_h (E_m + I_m)}{N_m} - \mu_h I_h, \end{aligned} \right\} \tag{19}$$

The infected subsystem is given by

$$\left. \begin{aligned} \frac{dE_m}{dt} &= \frac{\beta_{hm} S_m I_h}{N_h} - \frac{a E_m N_h}{1 + A E_m} - (\rho + \mu_m) E_m, \\ \frac{dI_m}{dt} &= \epsilon \rho E_m - \frac{a I_m N_h}{1 + A I_m} - (\alpha + \mu_m) I_m, \\ \frac{dI_h}{dt} &= \frac{\beta_{mh} S_h (E_m + I_m)}{N_m} - \mu_h I_h, \end{aligned} \right\}$$

whose Jacobian matrix evaluated at the DFE $\mathcal{E}_0 = (S_m^0, 0, 0, S_h^0, 0)$ is given by

$$J(\mathcal{E}_0) = \begin{bmatrix} -(aS_h^0 + \rho + \mu_m) & 0 & \frac{\beta_{hm} S_m^0}{S_h^0} \\ \epsilon \rho & -(aS_h^0 + \alpha + \mu_m) & 0 \\ \frac{\beta_{mh} S_h^0}{S_m^0} & \frac{\beta_{mh} S_h^0}{S_m^0} & -\mu_h \end{bmatrix}.$$

The determinant of $\mathcal{J}(\mathcal{E}_0)$ is given by

$$\begin{aligned} |\mathcal{J}(\mathcal{E}_0)| &= (aS_h + \varepsilon\rho + \alpha + \mu_m) \beta_{mh} \beta_{hm} \\ &\quad - \mu_h (aS_h + \alpha + \mu_m) (aS_h + \rho + \mu_m) \\ &= \mu_h (aS_h^0 + \alpha + \mu_m) (aS_h^0 + \rho + \mu_m) \\ &\quad \times \left[\frac{(aS_h^0 + \varepsilon\rho + \alpha + \mu_m) \beta_{mh} \beta_{hm}}{\mu_h (aS_h^0 + \alpha + \mu_m) (aS_h^0 + \rho + \mu_m)} - 1 \right]. \end{aligned}$$

Therefore, the basic reproduction number is given by (using

Remark 3.1) $\mathcal{R}'_0 = \sqrt{\frac{(aS_h^0 + \varepsilon\rho + \alpha + \mu_m) \beta_{mh} \beta_{hm}}{\mu_h (aS_h^0 + \alpha + \mu_m) (aS_h^0 + \rho + \mu_m)}}$, which is the same as obtained in [18].

5.3. Example 7: An HIV-Malaria co-infection model [19]

A mathematical model proposed to study the dynamics of HIV-Malaria co-infection in a workforce was proposed [19]. The infected subsystem of the model is given by

$$\left. \begin{aligned} \frac{dI_{pa}}{dt} &= r_1 I_{na} + r_3 I_{nd} - (\lambda_m + \delta_1 + \mu) I_{pa}, \\ \frac{dI_{na}}{dt} &= \lambda_a S_h - (\lambda_m + r_1 + \delta_2 + \mu) I_{na}, \\ \frac{dI_{nm}}{dt} &= \lambda_m S_h - (\lambda_a + r_2 + \psi_m + \mu) I_{nm}, \\ \frac{dI_{nd}}{dt} &= \lambda_m (I_{pa} + I_{na}) + \lambda_a I_{nm} - (r_3 + \delta_3 + \psi_m + \mu) I_{nd}, \\ \frac{dA}{dt} &= \delta_1 I_{pa} + \delta_2 I_{na} + \delta_3 I_{nd} - (\psi + \mu) A, \\ \frac{dE_v}{dt} &= \lambda_v S_v - (\delta_m + \nu + \mu_v) E_v, \\ \frac{dI_v}{dt} &= \delta_m E_v - (\nu + \mu_v) I_v. \end{aligned} \right\}$$

The Jacobian of the infected system evaluated at the infection free equilibrium point $\mathcal{E}_0 = (\frac{Q_h}{\mu}, 0, 0, 0, 0, \frac{Q_v}{\nu + \mu_v}, 0, 0)$ of the model is given by

$$\mathcal{J}(\mathcal{E}_0) = \begin{bmatrix} -k_1 & r_1 & 0 & r_3 & 0 & 0 & 0 \\ \beta_a & \beta_a - k_2 & 0 & \beta_a & 0 & 0 & 0 \\ 0 & 0 & -k_3 & 0 & 0 & 0 & \beta_m \varepsilon \phi \\ 0 & 0 & 0 & -k_4 & 0 & 0 & 0 \\ \delta_1 & \delta_2 & 0 & \delta_3 & -k_5 & 0 & 0 \\ 0 & 0 & \frac{\beta_v \varepsilon \phi \mu Q_v}{Q_h(\nu + \mu_v)} & \frac{\beta_v \varepsilon \phi \mu Q_v}{Q_h(\nu + \mu_v)} & 0 & -k_6 & 0 \\ 0 & 0 & 0 & 0 & 0 & \delta_m & -k_7 \end{bmatrix},$$

where

$$\begin{aligned} k_1 &= \delta_1 + \mu, \quad k_2 = r_1 + \delta_2 + \mu, \quad k_3 = r_2 + \psi_m + \mu, \quad k_4 = r_3 + \delta_3 + \psi_m + \mu, \\ k_5 &= \psi + \mu, \quad k_6 = \delta_m + \nu + \mu_v, \quad k_7 = \nu + \mu_v. \end{aligned}$$

The determinant of $\mathcal{J}(\mathcal{E}_0)$ is given by

$$\begin{aligned} |\mathcal{J}(\mathcal{E}_0)| &= \frac{(\psi + \mu)(r_3 + \delta_3 + \psi_m + \mu)}{Q_h(\nu + \mu_v)} [-\beta_a (\mu + \delta_1 + r_1) \\ &\quad + (\mu + \delta_1) (\mu + r_1 + \delta_2)] \times \\ &\quad \left[\frac{\beta_v \varepsilon^2 \phi^2 \mu Q_v \beta_m \delta_m - Q_h (\nu + \mu_v)^2 (\delta_m + \nu + \mu_v) (\mu + r_2 + \psi_m)}{Q_h (\nu + \mu_v)^2 (\delta_m + \nu + \mu_v) (\mu + r_2 + \psi_m)} - 1 \right], \end{aligned}$$

which can be written a

$$\begin{aligned} |\mathcal{J}(\mathcal{E}_0)| &= \Lambda \left(1 - \frac{\beta_a (\mu + \delta_1 + r_1)}{(\mu + \delta_1) (\mu + r_1 + \delta_2)} \right) \\ &\quad \times \left(\frac{\beta_v \varepsilon^2 \phi^2 \mu Q_v \beta_m \delta_m}{Q_h (\nu + \mu_v)^2 (\delta_m + \nu + \mu_v) (\mu + r_2 + \psi_m)} - 1 \right), \end{aligned}$$

where $\Lambda = \frac{(\mu + \delta_1) (\mu + r_1 + \delta_2) (r_3 + \delta_3 + \psi_m + \mu) (\nu + \mu_v)}{(\delta_m + \nu + \mu_v) (\mu + r_2 + \psi_m) (\psi + \mu)}$. We observe that, the quantities

$\frac{\beta_a (\mu + \delta_1 + r_1)}{(\mu + \delta_1) (\mu + r_1 + \delta_2)}$ and $\frac{\beta_v \varepsilon^2 \phi^2 \mu Q_v \beta_m \delta_m}{Q_h (\nu + \mu_v)^2 (\delta_m + \nu + \mu_v) (\mu + r_2 + \psi_m)}$ respectively represent \mathcal{R}_{0H} and \mathcal{R}_{0M}^2 which define the basic reproduction numbers of the HIV and Malaria sub-models in [19].

5.4. Example 8: The HIV-TB co-infection model [16]

The infected subsystem of the model is given by

$$\left. \begin{aligned} \frac{dH_1}{dt} &= \lambda_H S + \lambda_{HT}^1 S + \lambda_M^H S - \lambda_T \psi_1 H_1 \\ &\quad - \lambda_{HT}^2 \psi_1 H_1 - \lambda_M^T \psi_1 H_1 - K_1 H_1, \\ \frac{dH_2}{dt} &= \sigma H_1 + \theta_1 \sigma W_H - \lambda_T \psi_2 H_2 \\ &\quad - \lambda_{HT}^2 \psi_2 H_2 - \lambda_M^T \psi_2 H_2 - K_2 H_2, \\ \frac{dL}{dt} &= l \lambda_T S + l \lambda_{HT}^2 S + l \lambda_M^T S + \rho W_T \\ &\quad - \lambda_H L - \lambda_{HT}^1 L - \lambda_M^H L - \lambda_R L - \lambda_{R1} L - K_3, \\ \frac{dT}{dt} &= (1-l) \lambda_T S + (1-l) \lambda_{HT}^2 S + (1-l) \lambda_M^T S \\ &\quad + \lambda_R L + \alpha L - \lambda_H T + \phi \lambda_{R1} L \\ &\quad - \lambda_M^H T - \lambda_{HT}^1 T - K_4 T, \\ \frac{dI_{HL}^1}{dt} &= \lambda_T \psi_1 H_1 + \lambda_{HT}^2 \psi_1 H_1 + \lambda_M^T \psi_1 H_1 \\ &\quad + \lambda_H L + \lambda_{HT}^1 L + l (\lambda_{HT}^2 W_H + \lambda_T W_H + \lambda_M^T W_H) \\ &\quad + \lambda_M^H L + \lambda_{HT}^1 W_T + \lambda_M^H W_T + \lambda_{R2} I_{HL}^1 - K_5 I_{HL}^1, \\ \frac{dI_{HL}^1}{dt} &= \lambda_H T + \lambda_{HT}^1 T + \lambda_M^H T + (1-l) (\lambda_{HT}^2 W_H \\ &\quad + \lambda_T W_H + \lambda_M^T W_H) + \lambda_{R2} I_{HL}^1 + \theta_1 \alpha I_{HL}^1 \\ &\quad + (1-\phi) \lambda_{R1} L - K_6 I_{HT}^1, \\ \frac{dI_{HL}^2}{dt} &= \lambda_T \psi_2 H_2 + \lambda_{HT}^2 \psi_2 H_2 + \lambda_M^T \psi_2 H_2 \\ &\quad - \lambda_{R2} I_{HL}^2 + (1-\xi) \gamma_{HT} I_{HL}^1 + \theta_1 \sigma W_{HL}^H \\ &\quad + \sigma_{HT} W_{HT}^M + \sigma_T W_{HT}^T - K_7 I_{HL}^2, \\ \frac{dI_{HT}^2}{dt} &= \lambda_{R2} I_{HL}^2 + \theta_2 \alpha I_{HL}^2 + \xi \gamma_{HT} I_{HL}^1 \\ &\quad + \eta_1 \sigma I_{HT}^1 + \sigma_H W_{HT}^H - K_8 I_{HT}^2, \\ \frac{dW_H}{dt} &= \tau_1 H_1 + \tau_2 H_2 - \lambda_{HT}^2 W_H - \lambda_T W_H - \lambda_M^T W_H - K_9 W_H, \\ \frac{dW_T}{dt} &= \tau_3 T - \lambda_{HT}^1 W_T - \lambda_H W_T - \lambda_M^H W_T - K_{10} W_T, \\ \frac{dW_{HL}^H}{dt} &= \tau_1 I_{HL}^1 + \tau_2 I_{HL}^2 - \lambda_{R2} W_{HL} - K_{11} W_{HL}^H, \\ \frac{dW_{HT}^H}{dt} &= \tau_1 I_{HT}^1 + \tau_2 I_{HT}^2 + \theta_1 \alpha W_{HL}^H + \lambda_{R2} W_{HL} - K_{12} W_{HT}^H, \\ \frac{dW_{HT}^T}{dt} &= \tau_3 (I_{HT}^1 + I_{HT}^2) - K_{13} W_{HT}^T, \\ \frac{dW_{HT}^M}{dt} &= \tau_3 W_{HT}^H + \tau_2 W_{HT}^T - K_{14} W_{HT}^M, \end{aligned} \right\} \quad (20)$$

where, (see [Box I](#))

$$\begin{aligned} K_1 &= \mu + \sigma + \tau_1, & K_2 &= \mu + \delta_H + \tau_2, & K_3 &= \mu + \alpha, \\ K_4 &= \mu + \delta_T + \tau_3, & K_5 &= \mu + \theta_1 \alpha + \gamma_{HT}, & K_6 &= \mu + \tau_1 + \tau_3 + \eta_1 \sigma, \\ K_7 &= \mu + \theta_2 \alpha + \tau_2 + \delta_{HT}, & K_8 &= \mu + \tau_2 + \tau_3 + \omega \delta_{HT}, & K_9 &= \mu + \theta_1 \sigma, \\ K_{10} &= \mu + \rho, & K_{11} &= \mu + \theta_1 \alpha + \theta_1 \sigma, & K_{12} &= \mu + \sigma_H + \tau_3, \\ K_{13} &= \mu + \sigma_T + \tau_2, & K_{14} &= \mu + \sigma_{HT}. \end{aligned}$$

$$\begin{aligned}
 \lambda_H &= \frac{\beta_H(H_2\eta_2+W_H\eta_H+H_1)}{N}, & \lambda_T &= \frac{\beta_T(W_T\eta_T+T)}{N}, & \lambda_{HT}^1 &= \frac{\beta_H(\eta_D I_{HT}^1+I_{HL1}+c_2\eta_2(\eta_D I_{HT}^2+I_{HL2}))}{N}, \\
 \lambda_{HT}^2 &= \frac{\beta_T(I_{HT}^1+I_{HT}^2)}{N}, & \lambda_M^H &= \frac{\beta_H(W_{HTT}+\eta_H(W_{HLH}+W_{HT}^H+W_{HT}^M))}{N}, & \lambda_M^T &= \frac{\beta_T(W_{HT}^H+\eta_T(W_{HTT}+W_{HT}^M))}{N}, \\
 \lambda_R &= \frac{\beta_T\eta_T T}{N}, & \lambda_R^1 &= \frac{\beta_T\eta_r(I_{HT}^1+I_{HT}^2+W_{HT}^H)}{N}, & \lambda_R^2 &= \frac{\beta_T\eta_r(W_{HT}^H I_{HT}^2+T+I_{HT}^1)}{N}.
 \end{aligned}$$

Box 1.

The Jacobian of the infected subsystem evaluated at the infection-free equilibrium point

$$\begin{aligned}
 \mathcal{E}_0 &= (S = \frac{I}{\mu}, H_1 = 0, H_2 = 0, L = 0, T = 0, \\
 &I_{HL}^1 = 0, I_{HT}^1 = 0, I_{HL}^2 = 0, I_{HT}^2 = 0, W_H = 0, W_T = 0, \\
 &W_{HL}^H = 0, W_{HT}^H = 0, W_{HT}^T = 0, W_{HT}^M = 0),
 \end{aligned}$$

is given by

$$\mathcal{J}(\mathcal{E}_0) = \begin{bmatrix} J_{11} & J_{12} \\ J_{21} & J_{22} \end{bmatrix},$$

where J_{11} , J_{12} , J_{21} and J_{22} are defined in Appendix.

The Determinant of \mathcal{J} is then obtained as

$$\begin{aligned}
 |\mathcal{J}(\mathcal{E}_0)| &= \Gamma [((\sigma\tau_2 + K_2\tau_1)\eta_H + (\tau_1\theta_t + K_9)\sigma\eta_2 \\
 &- \sigma\tau_2\theta_t + K_2K_9)\beta_H + \sigma K_1\tau_2\theta_t - K_1K_2K_9] \times \\
 &[(\eta_T\tau_3 + K_{10})((1-l)K_3 + \alpha l)\beta_T + \alpha\rho\tau_3 - K_3K_4K_{10}],
 \end{aligned}$$

which can be written as

$$\begin{aligned}
 |\mathcal{J}(\mathcal{E}_0)| &= \Gamma\Omega \left[\frac{\beta_H((\sigma\tau_2+K_2\tau_1)\eta_H+(\tau_1\theta_t+K_9)\sigma\eta_2+K_2K_9-\sigma\tau_2\theta_t)}{K_1K_2K_9\sigma K_1\tau_2\theta_t} - 1 \right] \\
 &\times \left[\frac{\beta_T(\eta_T\tau_3+K_{10})((1-l)K_3+\alpha l)}{K_3K_4K_{10}\alpha\rho\tau_3} - 1 \right],
 \end{aligned}$$

where $\Omega = (K_3K_4K_{10}\alpha\rho\tau_3)(K_1K_2K_9\sigma K_1\tau_2\theta_t)$. The quantities $\beta_H \frac{((\sigma\tau_2+K_2\tau_1)\eta_H+(\tau_1\theta_t+K_9)\sigma\eta_2+K_2K_9-\sigma\tau_2\theta_t)}{K_1K_2K_9\sigma K_1\tau_2\theta_t}$ and $\frac{\beta_T(\eta_T\tau_3+K_{10})((1-l)K_3+\alpha l)}{K_3K_4K_{10}\alpha\rho\tau_3}$ are clearly the basic reproduction numbers \mathcal{R}_H and \mathcal{R}_T obtained in [16].

Following the results in the examples and the cited literature in Sections 5.3 and 5.4, the following result is established.

Conjecture 5.1. For epidemic ODE models involving co-infection of n number of diseases, the determinant of the Jacobian of the infected subsystem is of the form

$$|\mathcal{J}(\mathcal{E}_0)| = \Gamma \prod_{k=1}^n \left(\frac{B_k}{D_k} - 1 \right),$$

and the basic reproduction number is given by

$$\mathcal{R}_0 = \max \left\{ \frac{B_k}{D_k}, \forall k = 1, 2, \dots, n \right\}.$$

where $\mathcal{R}_{0k} = \frac{B_k}{D_k}$ is the basic reproduction number of the k th diseases.

Putting all the discussions above together, we summarize algorithm of the developed method in the next section.

6. The algorithms

With all the above, we summarize the algorithms for determination of basic reproduction numbers and Lyapunov functions for epidemic ODE models are as follows:

Algorithm 1: Determination of Lyapunov coefficients:

- Step1** Identify the infected **compartments** of the model.
- Step2** Find the Jacobian \mathcal{J} of the infected subsystem of the model.
- Step3** Evaluate the Jacobian of the infected subsystem at the infection-free critical point, \mathcal{E}_0 (i.e. $M = \mathcal{J}(\mathcal{E}_0)$).

Step4 Replace the j th row of M with \mathcal{T} to get M^j , $j = 1, 2, \dots, m_2$.

Step5 Find $K_j = ||M^j||$, $j = 1, 2, \dots, m_2$.

Algorithm 2: Determination of \mathcal{R}'_0

- Step1** Identify the infected **compartments** of the model.
- Step2** Find the Jacobian \mathcal{J} of the infected subsystem of the model.
- Step3** Evaluate the Jacobian of the infected subsystem at the infection-free critical point, \mathcal{E}_0 (i.e. $\mathcal{J}(\mathcal{E}_0)$).
- Step4** Find the determinant, $|\mathcal{J}(\mathcal{E}_0)|$.
- Step5** Express the determinant as $|\mathcal{J}(\mathcal{E}_0)| = \xi \left(\frac{B}{D} - 1 \right)$, $\xi \in \mathbb{R}$.
- Step6** Find \mathcal{R}'_0 using $\mathcal{R}'_0 = \frac{B}{D}$.
- Step7** Apply Remark 3.1 and/or Conjecture 5.1 as appropriate.

7. Conclusion

In this paper, a new method which we name the **Jacobian-Determinant method** is presented. The method exploits the use of determinants of Jacobian matrices to find a threshold quantity, \mathcal{R}'_0 akin to (and conjectured to be the same as) the basic reproduction numbers and Lyapunov functions of ODE models with standard/mass action incidence functions. Unlike other techniques which are heuristic or rely on the eigenvectors of next-generation matrices, our method only requires calculation of determinants of the Jacobian matrix of the infected subsystem, making our method very simple to use. Our method is shown to yield the same threshold quantity as the next-generation matrix method of [6]. Since the new method only requires the determinant of the Jacobian of the infected subsystem, it is less computationally expensive and hence cheaper than the next-generation matrix method of [6]. The method also provides a routine for easy construction of Lyapunov functions of the models of interest. The procedure used to develop the technique here considered the global stability of the infection-free equilibrium point. In another study that is being undertaken by the authors, the procedure used here is exploited to see the possibility of constructing Lyapunov functions to study the GAS of endemic equilibria of epidemic ODE models.

CRedit authorship contribution statement

Baba Seidu: Conceptualization, Methodology, Formal analysis, Writing – original draft, Writing – review & editing. **Oluwole D. Makinde:** Methodology, Formal analysis, Writing – original draft, Writing – review & editing. **Joshua Kiddy K. Asamoah:** Conceptualization, Methodology, Formal analysis, Writing – original draft, Writing – review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

No data was used for the research described in the article.

Appendix

$$J_{11} = \begin{bmatrix} \beta_H - K_1 & \beta_H \eta_2 & 0 & 0 & \beta_H & \beta_H \eta_D & \beta_H c_2 \eta_2 \\ \sigma & -K_2 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -K_3 & l\beta_T & 0 & l\beta_T & 0 \\ 0 & 0 & \alpha & (1-l)\beta_T - K_4 & 0 & (1-l)\beta_T & 0 \\ 0 & 0 & 0 & 0 & -K_5 & 0 & 0 \\ 0 & 0 & 0 & 0 & \theta_1 \alpha & -K_6 & 0 \\ 0 & 0 & 0 & 0 & (1-\xi)\gamma_{HT} & 0 & -K_7 \end{bmatrix},$$

$$J_{12} = \begin{bmatrix} \beta_H c_2 \eta_2 \eta_D & \beta_H \eta_H & 0 & \beta_H \eta_H & \beta_H \eta_H & \beta_H & \beta_H \eta_H \\ 0 & \theta_1 \sigma & 0 & 0 & 0 & 0 & 0 \\ l\beta_T & 0 & l\beta_T \eta_T + \rho & 0 & l\beta_T & l\beta_T \eta_T & l\beta_T \eta_T \\ (1-l)\beta_T & 0 & (1-l)\beta_T \eta_T & 0 & (1-l)\beta_T & (1-l)\beta_T \eta_T & (1-l)\beta_T \eta_T \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta_1 \sigma & 0 & \sigma_0 & \sigma_{HT} \end{bmatrix},$$

$$J_{21} = \begin{bmatrix} 0 & 0 & 0 & 0 & \xi\gamma_{HT} & \eta_1 \sigma & \theta_2 \alpha \\ \tau_1 & \tau_2 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \tau_3 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \tau_1 & 0 & \tau_2 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \tau_3 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix},$$

$$J_{22} = \begin{bmatrix} -K_8 & 0 & 0 & 0 & \sigma_H & 0 & 0 \\ 0 & -K_9 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -K_{10} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -K_{11} & 0 & 0 & 0 \\ \tau_2 & 0 & 0 & \theta_1 \alpha & -K_{12} & 0 & 0 \\ \tau_3 & 0 & 0 & 0 & 0 & -K_{13} & 0 \\ 0 & 0 & 0 & 0 & \tau_3 & \tau_2 & -K_{14} \end{bmatrix}.$$

References

- [1] Tuncer N, Timsina A, Nuno M, Chowell G, Martcheva M. Parameter identifiability and optimal control of an SARS-CoV-2 model early in the pandemic. *J Biol Dyn* 2022;16(1):412–38.
- [2] Asamoah JKK, Borna C, Seidu B, Jin Z. Mathematical analysis of the effects of controls on transmission dynamics of SARS-CoV-2. *Alex Eng J* 2020;59(6):5069–78.
- [3] Eikenberry SE, Mancuso M, Iboi E, Phan T, Eikenberry K, Kuang Y, et al. To mask or not to mask: Modeling the potential for face mask use by the general public to curtail the COVID-19 pandemic. *Infect Dis Model* 2020;5:293–308.
- [4] Okuonghae D, Omame A. Analysis of a mathematical model for COVID-19 population dynamics in Lagos, Nigeria. *Chaos Solitons Fractals* 2020;139:110032.
- [5] Yang HM. The basic reproduction number obtained from Jacobian and next generation matrices – A case study of dengue transmission modelling. *Biosystems* 2014;126:52–75.
- [6] Van den Driessche P, Watmough J. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Math Biosci* 2002;180(1–2):29–48.
- [7] Diekmann O, Heesterbeek J, Roberts MG. The construction of next-generation matrices for compartmental epidemic models. *J R Soc Interface* 2010;7(47):873–85.
- [8] Li M-T, Jin Z, Sun G-Q, Zhang J. Modeling direct and indirect disease transmission using multi-group model. *J Math Anal Appl* 2017;446(2):1292–309.
- [9] Li J, Blakeley D, Smith RJ. The failure of R_0 . *Comput Math Methods Med* 2011;2011:1–17.
- [10] Shuai Z, van den Driessche P. Global stability of infectious disease models using Lyapunov functions. *SIAM J Appl Math* 2013;73(4):1513–32.
- [11] Simon CP, Jacquez JA. Reproduction numbers and the stability of equilibria of SI models for heterogeneous populations. *SIAM J Appl Math* 1992;52(2):541–76.
- [12] Makinde OD, Okosun KO. Impact of chemo-therapy on optimal control of malaria disease with infected immigrants. *BioSystems* 2011;104(1):32–41.
- [13] Van Den Driessche P, Wang L, Zou X. Modeling diseases with latency and relapse. *Math Biosci Eng* 2007;4(2):205.
- [14] Sharomi O, Gumel AB. Curtailing smoking dynamics: A mathematical modeling approach. *Appl Math Comput* 2008;195(2):475–99.
- [15] Gumel AB. Causes of backward bifurcations in some epidemiological models. *J Math Anal Appl* 2012;395(1):355–65.
- [16] Sharomi O, Podder CN, Gumel AB, Song B. Mathematical analysis of the transmission dynamics of HIV/TB coinfection in the presence of treatment. *Math Biosci Eng* 2008;5(1):145.
- [17] Zhou X-y, Cui J-a, Zhang Z-h. Global results for a cholera model with imperfect vaccination. *J Franklin Inst B* 2012;349(3):770–91.
- [18] Seidu B, Asamoah JKK, Wiah EN, Ackora-Prah J. A comprehensive cost-effectiveness analysis of control of maize streak virus disease with Holling's Type II predation form and standard incidence. *Results Phys* 2022;40:105862.
- [19] Seidu B, Makinde OD, Seini IY. Mathematical analysis of the effects of HIV-malaria co-infection on workplace productivity. *Acta Biotheor* 2015;63(2):151–82.