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Comment on "Mathematical Modeling towards the Dynamical Interaction of Leptospirosis"

Abid Ali Lashari[*]

Department of Mathematics, Stockholm University, Stockholm, 10691, Sweden.

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Abstract: The aim of this note is to clearly expose the erroneous results concerning the backward bifurcation and stability in the recent literature of mathematical biology. Correct value of the basic reproduction number in [2] is also provided.

Keywords: Jacobian matrix, eigenvalues, stability

1 Introduction

Stability analysis of a mathematical model describing the dynamics of a problem in biology requires a knowledge of the eigenvalues of the Jacobian matrix associated with the matrix [1]. The Routh-Hurwitz criteria give necessary and sufficient conditions for the eigenvalues to lie in the left half of the complex plane. However recent literature in mathematical biology contains instances of authors establishing stability of the Jacobian matrix by using erroneous results concerning eigenvalues of a matrix. Moreover, consequences of erroneously proving backward bifurcation and the global asymptotic stability are also highlighted. Some of the results are stated below.

1. *Eigenvalues of a matrix are invariant under elementary row [or column] operations.* See, for example, Altaf et al. [2].
2. *Moreover, the value of the basic reproduction number R_0 in [2] is not correct and the main theorems presented in Section 4 of [2] are also incorrectly proved.*

The purpose of the present note is to caution against such pitfalls into which an unwary researcher unintentional may fall. We will point out technical problems in [2] and correct some of them. Moreover, we provide the true value of the basic reproduction number as well as the corrected coefficients of the quadratic equation (9) in [2].

2 Falseness of the above statements

The example occurs in the proof of the following theorems of Altaf et al. [2]. The Theorem states:

1. *The DFE about E_1 of the system (1) for $R_0 \leq 1$, stable locally asymptotically , if $\delta_0 > \frac{\mu_0+\alpha_1}{\mu_0 T_4 T_5}$ and $(\mu_0+\alpha_1) > \frac{\delta_h \alpha_h \alpha_1 \lambda_h}{T_1 T_2 T_3}$, otherwise unstable.*
2. *For $R_0 > 1$, the EEE around E_2 of the system (1) is locally asymptotically stable if the following inequalities are satisfied. $\mu_0 > \frac{\beta_1 a_2}{T_3 T_4 T_5}$ and $a_2\delta_0 > \frac{\delta_v \beta_2 \alpha_h \mu_0}{T_1 T_2 T_3(\mu_0+\alpha_1)}$, otherwise unstable.*

In order to prove these results they performed elementary row operation for the Jacobian matrix J_0 (10) (by elementary row operation for the Jacobian matrix J_* (11)). Then, they analyse the eigenvalues of the matrix obtained after elementary row transformation from (10) and (11) to show that all its eigenvalues are negative from which they conclude the above assertions of their theorems. This reasoning would have been valid if elementary row transformation preserved eigenvalues, which however, it does not as the following example shows.

$$A = \begin{pmatrix} 1 & -1 \\ -1 & 2 \end{pmatrix}, \qquad B = \begin{pmatrix} 1 & -1 \\ 0 & 1 \end{pmatrix}.$$

Matrix B has been obtained from A by adding the first row to the second. This is elementary row transformation.

[*] Corresponding author e-mail: abidlshr@yahoo.com

Now eigenvalues of A are $\lambda_1 = \frac{1}{2}(3+\sqrt{5})$ and $\lambda_2 = \frac{1}{2}(3-\sqrt{5})$ whereas B has a repeated eigenvalue $\lambda_{1,2} = 1$. This example shows that the eigenvalues may change after an elementary row transformation. But the determinant remains invariant. Here the determinant of each of A and B is unity.

The eigenvalues for the matrix (10) and of the matrix obtained after elementary row transformation (similarly of matrix (11) and of the matrix obtained after elementary row transformation in [2] are not the same as they violate the well known criteria of the eigenvalues, that the sum of the eigenvalues is equal to the trace of the matrix. Clearly the eigenvalues may change after an elementary row transformation. The above statement may hold in special cases but are false in general [5].

Over the last decade, a number of authors have studied the phenomenon of backward bifurcation (where the locally-asymptotically stable disease-free equilibrium co-exists with a locally-asymptotically stable endemic equilibrium when $R_0 < 1$) (see e.g. [7] and the references therein). The epidemiological importance of the backward bifurcation phenomenon arising in epidemic modelling is that the classical requirement of $R_0 < 1$ is, although necessary, no longer sufficient for disease elimination. Lashari and Zaman [8] also carried out analysis of the backward bifurcation of their model. In fact, the occurrence of the phenomenon of backward bifurcation in their model discussed in Section 4 is not true because R_0 in [8] is the sum of two positive terms and the fact that $R_0 < 1$ implies both $\frac{\alpha_h\alpha_v b_1 b_2\beta_2\beta_3}{\mu_h\mu_v Q_1 Q_2 Q_3 Q_4}$ and $\frac{\alpha_h b_1\beta_1}{\mu_h Q_1 Q_2}$ are less than unity. From $\frac{\alpha_h b_1\beta_1}{\mu_h Q_1 Q_2} < 1$, it can easily be seen that $b > 0$. Thus, $a > 0$, $b > 0$ and $c > 0$ if $R_0 < 1$. As $b > 0$, when $R_0 < 1$, therefore case (iii) of Theorem 4.1 of [8] does not indicate the possibility of a backward bifurcation.

The phenomenon of backward bifurcation of the model discussed in Section 3.2 may also be not true. In fact, Castillo-Chavez et al. [3] use a comparison theorem to derive sufficient conditions for the global stability asymptotically of the disease free equilibrium of a general disease transmission model when $R_0 < 1$. Clearly, in the case of a backward bifurcation the disease free equilibrium can not be globally asymptotically stabile whenever $R_0 < 1$ [3,4]. In most models, however, one expects a second threshold for global stability [7]. If there are multiple equilibria, then no equilibrium can attract all solutions. (For example, the disease-free equilibrium does not attract the other equilibria.) Thus, no equilibrium is globally asymptotically stable on the full space.

Sometime when there are two equilibria (one disease-free and one endemic) the endemic equilibrium can be shown to be globally asymptotically stable [7]. A more precise statement would be that the endemic equilibrium is globally asymptotically stable amongst solutions for which the disease is present. (This way, the disease-free states are excluded.) Therefore, if the disease free equilibrium is globally asymptotically stable as shown in Section 4 in [2], then the backward bifurcation phenomenon can not occur. Therefore, it is instructive to mention here this incorrect use of mathematics, that could be the result of simple ignorance or unintentional errors, so that in future young researchers should be aware of the harms of these wrong results.

Since, the basic reproduction number, denoted R_0, is the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual [6]. If $R_0 < 1$, then on average an infected individual produces less than one new infected individual over the course of its infectious period, and in this case the disease dies out. If $R_0 > 1$, then each infected individual produces, on average, more than one new infected individual, and hence the disease can invade the population. However, in theorem in Section 4, it is proved that if $R_0 > 1$, (with some other conditions) than the disease free equilibrium is globally asymptotically stable. Unfortunately, that result is against the classical result in mathematical biology that if $R_0 > 1$, then each infected individual produces, on average, more than one new infected individual. In that scenario, the disease free equilibrium can never be globally asymptotically stable. The disease free equilibrium being both locally and globally asymptotically stable (provided there is no scenario of backward bifurcation) when $R_0 \leq 1$, and being unstable when $R_0 > 1$ [4,6].

It is also worthy to point out that the proof of the global stability of the endemic equilibrium is also wrong as well since if $S_v^* = 1$, then $L' = 0$, it is not negative as stated in [2]. Furthermore, the largest compact invariant subset of the set where $L' = 0$, is clearly not the singleton set E_2 (the endemic equilibrium).

3 Correction

The coefficients of the equation (9) in [2] are also wrong, the true values of the coefficients A, B, and C are given by

$$\begin{aligned} A &= \lambda_h\delta_h(\alpha_h\alpha_1\beta_2 T_4 T_5 + a_2\alpha_h\alpha_v\beta_1\beta_2) \\ &\quad -T_1T_2T_3\left[T_4T_5(\mu_0+\alpha_1)\beta_2 + a_2\alpha_v\beta_1\beta_2\right], \\ B &= a_1T_3(\alpha_h\alpha_1\beta_2T_4T_5 + a_2\alpha_h\alpha_v\beta_1\beta_2) + \lambda_h\delta_h\alpha_h\alpha_1\delta_0T_4T_5 \\ &\quad -\delta_0(\mu_0+\alpha_1)T_1T_2T_3T_4T_5, \\ C &= a_1\alpha_h\alpha_1\delta_0T_3T_4T_5. \end{aligned} \tag{1}$$

Now, we will find the correct value of the reproduction number R_0. The matrices, F (for the new infection terms) and V (of the transition terms) are given, respectively, by

$$F = \begin{pmatrix} 0 & 0 & 0 & \dfrac{\beta_1 a_1}{\mu_0+\alpha_1} \\ 0 & 0 & 0 & 0 \\ 0 & \dfrac{\beta_2 a_2}{\delta_0} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} T_1 & 0 & 0 & 0 \\ -\alpha_h & T_2 & 0 & 0 \\ 0 & 0 & T_4 & 0 \\ 0 & 0 & -\alpha_v & T_5 \end{pmatrix}.$$

It follows then that the basic reproduction number, denoted by R_0, is given by

$$R_0 = \rho(FV^{-1}) = \sqrt{\frac{a_1 a_2 \alpha_h \alpha_v \beta_1 \beta_2}{\delta_0(\mu_0+\alpha_1)T_1T_2T_4T_5}} \qquad (2)$$

where ρ is the spectral radius (dominant eigenvalue in magnitude) of the next generation matrix FV^{-1} [4,6]. Hence, using Theorem 2 of [6], we have established the following result:

Lemma . The disease free equilibrium, E_1, of the model (1) in [2], is locally asymptotically stable if $R_0 < 1$, and unstable if $R_0 > 1$.

The value of R_0 given by (2) is clearly different from the value of R_0 in [2]. The coefficient C in (1) is independent of R_0. Therefore the discussion in Section 3 of [2] leads to misleading statements. Moreover, the main theorems in Section 4 in [2] are wrongly proved and needs to be revised, since these results based on the erroneously obtained value of the basic reproduction number R_0.

4 Conclusion

This comment has pointed out technical problems in the main results in Ref. [2] and has presented the corrected results. Studies of mathematical models of the spread of Leptospirosis have great impact on health authorities planning and allocation of funds to control the spread of infectious diseases. The effective control decisions of the disease have an important role in the combat of the disease and will be very useful for the public as well as the funding agencies. However such resources are likely to go waste if scientific studies which purport to guide them are based on faulty theoretical basis. The conclusion based on the model propose by Altaf et al. [2] may not be valid and Leptospirosis may still be far from reaching its equilibrium from the community.

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Abid Ali Lashari received the Ph.D degree in Mathematics at School of Natural Sciences (SNS), National University of Sciences and Technology (NUST), H-12 Islamabad, Pakistan. His work is focused on using mathematical approaches to provide some insight into real life phenomena associated with the mathematical modeling of infectious disease. He is mainly working in the field of mathematical modeling of infectious disease such as models of vector borne disease, population dynamics, epidemics dynamics and infectious diseases with optimal control. He has published research papers in international peer reviewed journals of mathematical sciences. Currently, he is employed at Department of Mathematics, Stockholm University, Stockholm, Sweden. He is working with Pieter Trapman on a project entitled ”stochastic models for infectious disease dynamics”.