Modelling the dynamics of direct and pathogens-induced dysentery diarrhoea epidemic with controls

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ABSTRACT
In this paper, the dysentery dynamics model with controls is theoretically investigated using the stability theory of differential equations. The system is considered as SIRSB deterministic compartmental model with treatment and sanitation. A threshold number $R_0$ is obtained such that $R_0 \leq 1$ indicates the possibility of dysentery eradication in the community while $R_0 > 1$ represents uniform persistence of the disease. The Lyapunov–LaSalle method is used to prove the global stability of the disease-free equilibrium. Moreover, the geometric approach method is used to obtain the sufficient condition for the global stability of the unique endemic equilibrium for $R_0 > 1$. Numerical simulation is performed to justify the analytical results. Graphical results are presented and discussed quantitatively. It is found out that the aggravation of the disease can be decreased by using the constant controls treatment and sanitation.

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1. Introduction
Diar rhoea disease is a global problem especially in countries with weak health system and lack of human and financial capacities. Diarrhoea in its various forms is usually one of the five major causes of death in rural areas of Africa. An average of 9 million children, most of them under 5 years, die each year as a result of this disease [29]. Of which cholera and dysentery contribute most of the cases. Epidemics of cholera and dysentery resulted in war and the collapse of the economy of many nations [7]. Dysentery is diarrhoea with visible blood in stools. In most cases it is acute. Shigella (S.flexneri and S.dysenteriae) and amoebiasis are the causative agents of dysentery. Dysentery diarrhoea is the most dangerous and a possible cause of mortality associated with diarrhoea compared to the other types of diarrhoea [45]. Huge scale outbreaks of dysentery are specific risk to general well-being. The death rate could be as high as 15% and can cause an economic crisis during the epidemic.

Dysentery is transmitted through direct human to human interaction and environment to human interaction. According to [32], lack of safe water and poor sanitation are the most important risk factors for increased burden of bacillary dysentery. Population movement
and overcrowding facilitates the disease transmission. As a result, this disease frequently occurs in refuge campus. The elderly, the debilitated and the undernourished of all ages are particularly susceptible to severe disease and death.

In the last two decades, an outstanding achievements have been made in controlling and preventing this disease. World Health organization has introduced preventive methods strategies like the promotion of exclusive breastfeeding, improved complementary feeding practices, Rotavirus immunization, cholera and measles immunization [22]. Antimicrobial, which is the primary treatment for shigellosis, has been given to patients who develop dysentery diarrhoea. Nalidixic acid was also being used as treatment mechanism when epidemic dysentery appeared in Africa and Asia in 1980s and 1990s [35]. Hand washing and safe water have been motivated for years. It is possible to decrease diarrhoea by 40% using hand washing with soap [44].

Mathematical models have been used extensively to help improve our understanding of the dynamics of infectious diseases [27,30,38]. Some of these have considered the interaction between humans [12,26,34]. Others studies focus on the disease dynamics considering multiple transmission pathways [17,25,43]. Environment to host disease transmission is becoming more evident in addition to host to host transmission. Contaminated food, water, soil, and areas can transmit disease to humans. For instance, in [3] the authors considered how the effect of the environment is interpreted in transition and transmission of secondary infectious hosts and free living pathogen. In [31] the authors proposed a coinfection model for listeriosis and anthrax diseases considering the transmissions in both animal and human populations. More recently, [1] studied the effect of animal grazing on the chagas disease levels of the human population by considering two environments (domestic and wild) with the aim to achieve the effect of domestic animal grazing on both the basic reproductive number and the disease levels in the human population. The authors in [24] investigated the biologically likely means for the increase in monthly haemorrhagic fever with renal syndrome by assuming periodic transmission rates and rodent periodic birth rate with vaccination as a control.

Quite recently, several publications have appeared documenting on epidemiological modelling of diarrhoea transmission dynamics with much focus on cholera [6,17,42,48]. Previous researches on cholera models basically differ on how the host to host force of infection and on how the environmental vibrio concentration is formulated. In [15] the authors proposed a cholera dynamics assuming environment to host transmission only, and in [20] the work of [15] is extended to include hyperinfectious vibrios. In both cases, the model is based on logistic response curve in the number of vibros. [28] proposed a new model which includes human to human transmission to the model of [15] to estimate the reproduction number for cholera outbreak in Zimbabwe in the year 2008–2009. The incidence in their model is logistic response curve in the number of vibros and linear in the number of infectious humans. There are also studies on the dynamics of diarrhoeal diseases with controls [4,21]. Most studies have tended to focus on permanent recovery, which is not consistent with the real situation. In order to overcome this limitation, the authors in [5] proposed an SIRSB model with temporary immune periods, which can reveal common diarrhoea propagation. Their study focuses on optimal control and cost-effectiveness analysis of dysentery epidemic model. However, there is still a need to investigate the long-term dynamics of the system.
Therefore, this paper aims to propose a deterministic system for dysentery diarrhoea disease by incorporating constant control measures (treatment for the infected humans and sanitation for the environment), disease-induced death rate and temporary recovery immunity. And investigate the global stability of the disease-free equilibrium using Lyapunov function and LaSalle’s Invariance Principle and the endemic equilibrium using geometric approach. One of this paper’s motivation is to examine the impact of treatment and sanitation on the long-term dynamics of the disease. Our outcomes demonstrate that treatment and sanitation may result in the extinction and persistence of the disease depending on the assumed parameters. The other one is to investigate the effect of the transmission constants and efficacy of the controls on the control of the disease. Furthermore, numeral simulation of the system with and without controls is compared to observe the long-term dynamics of the disease.

The remaining part of this paper is organized as follows: Section 2 presents the system framework. In Section 3 we study the basic reproduction number and existence of equilibria. In Section 4, the stability of equilibria is investigated. In Section 5, numerical analysis and simulation of the system with given parameter values is performed. Brief summary and discussions are shown in the last section.

2. The basic system and its analysis

The total human population size is subdivided into three classes: The class of individuals who are healthy but can contract the disease are called susceptible ($S$). Infected individuals who can transmit the disease are called infectious ($I$). And the number of individuals who have recovered or removed is denoted by $R$. The pathogen population (or concentration of shigella in the environment) is represented by $B$.

Susceptible humans increase at a constant rate of $\Lambda$. It is assumed that incidence between human to human interaction is mass action and environment to human is logistic. $K$ is the pathogen population that yields 25–50% chance of catching dysentery diarrhoea [11]. $\beta_1$ and $\beta_2$ represent rates of ingesting shigella from a contaminated environment and through human to human interaction, respectively. The natural death rate of all human classes is $\mu$. Infected humans contribute to the concentration of shigella at a rate of $\epsilon$. The pathogen population is growing at a rate of $\sigma_1 > 0$ and its natural death rate is $\sigma_2$. It is assumed that $\sigma_2 - \sigma_1 = \sigma > 0$. Recovered individuals lose immunity and return to the susceptible class at a rate of $\alpha$. Infectious ones are assumed to recover at a rate of $\gamma + \epsilon_1 u_1$, where $\gamma$ is the rate of natural recovery, $u_1$ is the rate of treatment. $\rho_1$ proportion of the naturally recovered ones go to the recovered class and the remaining $1 - \rho_1$ proportion instantly become susceptible to reinfection. In addition to this, among the recovered due to treatment, $\rho_2$ portion of them move to a temporary immune state and the remaining immediately become susceptible to reinfection. The disease-induced death rate is $d$. $\epsilon_2 u_2$ is the rate of sanitation.

The two population SIRSB system is described by the following systems of differential equations.

$$\frac{dS}{dt} = \Lambda + \gamma (1 - \rho_1) I + \epsilon_1 u_1 (1 - \rho_2) I + \alpha R - \left( \frac{\beta_1 B}{K + B} + \beta_2 I + \mu \right) S,$$
\[
\frac{dI}{dt} = \left( \frac{\beta_1 B}{K + B} + \beta_2 I \right) S - (\mu + d + \gamma + e_1 u_1) I,
\]
\[
\frac{dR}{dt} = (\gamma \rho_1 + e_1 u_1 \rho_2) I - (\mu + \alpha) R,
\]
\[
\frac{dB}{dt} = \varepsilon I - (\sigma + e_2 u_2) B.
\]

System Equation (1) is studied under the following initial condition
\[
(S(0), I(0), R(0), B(0)) \in R^4_+
\]
where \( R^4_+ \) denotes the nonnegative cone and its lower dimensional faces.

The SIRSB system diagram based on the above assumption is given below (Figure 1).

**Theorem 2.1:** The solutions of Equation (1) with positive initial data remain positive for all \( t > 0 \). Furthermore,
\[
\limsup_{t \to \infty} N(t) \leq \frac{\Lambda}{\mu} \quad \text{and} \quad \limsup_{t \to \infty} B \leq \frac{\varepsilon \Lambda}{\mu (\sigma + e_2 u_2)}.
\]

**Proof:** To show the positivity of the solutions, let \( T = \sup \{ t > 0 : S > 0, I > 0, R > 0, B > 0 \} \in [0, t] \). Thus, \( T > 0 \). The first equation of Equation (1) can be written as
\[
\frac{dS}{dt} = \Lambda + \gamma (1 - \rho_1) I + e_1 u_1 (1 - \rho_2) I + \alpha R - (\lambda + \mu) S \geq \Lambda - (\lambda + \mu) S,
\]
where \( \lambda = \frac{\beta_1 B}{K + B} + \beta_2 I \). We thus have
\[
\frac{d}{dt} \left[ S(t) \exp \left\{ \int_0^t \lambda(u) \, du + \mu t \right\} \right] \geq \Lambda \exp \left\{ \int_0^t \lambda(u) \, du + \mu t \right\}.
\]

**Figure 1.** Schematic diagram for the flow of dysentery diarrhoea transmission.
Hence
\[ S(T) \exp \left\{ \int_0^T \lambda(u) \, du + \mu T \right\} - S(0) \geq \int_0^T \Lambda \exp \left\{ \int_0^T \lambda(v) \, dv + \mu T \right\} \, dT. \]

So that
\[ S(T) \geq S(0) \exp \left\{ - \left( \int_0^T \lambda(u) \, du + \mu T \right) \right\} + \exp \left\{ - \left( \int_0^T \lambda(u) \, du + \mu T \right) \right\} \times \left\{ \int_0^T \Lambda \exp \left\{ \int_0^T \lambda(v) \, dv + \mu T \right\} \, dT \right\} > 0. \]

Using similar approach, it could be shown that all other state variables of the model remain positive for all time \( t > 0 \). \[ \square \]

Furthermore, adding the first 3 equations of system Equation (1) gives that
\[
\frac{dN}{dt} = \Lambda - \mu N - dI \leq \Lambda - \mu N,
\]
and from the last equation of system (1) we get
\[
\frac{dB(t)}{dt} = \varepsilon I - (\sigma + e_2 u_2)B \leq \varepsilon N - (\sigma + e_2 u_2)B.
\]

Thus,
\[
\Lambda - (\mu + d)N \leq \frac{dN(t)}{dt} \leq \Lambda - \mu N(t),
\]
which follows that,
\[
\frac{\Lambda}{\mu + d} \leq \liminf_{t \to \infty} N(t) \leq \limsup_{t \to \infty} N(t) \leq \frac{\Lambda}{\mu}.
\]

Similarly,
\[
-(\sigma + e_2 u_2)B(t) \leq \frac{dB(t)}{dt} \leq \varepsilon N - (\sigma + e_2 u_2)B(t) \leq \varepsilon \frac{\Lambda}{\mu} - (\sigma + e_2 u_2)B(t).
\]

It follows that,
\[
0 \leq \liminf_{t \to \infty} B(t) \leq \limsup_{t \to \infty} B(t) \leq \frac{\varepsilon \Lambda}{\mu (\sigma + e_2 u_2)}.
\]

Hence,
\[
\limsup_{t \to \infty} N(t) \leq \frac{\Lambda}{\mu} \quad \text{and} \quad \limsup_{t \to \infty} B(t) \leq \frac{\varepsilon \Lambda}{\mu (\sigma + e_2 u_2)}.
\]

Henceforth, system Equation (1) is studied in the following feasible region
\[
\Lambda = \left\{ (S, I, R, B) \mid 0 \leq S, I, R, N \leq \frac{\Lambda}{\mu}, 0 \leq B \leq \frac{\varepsilon \Lambda}{\mu (\sigma + e_2 u_2)} \right\}. \tag{3}
\]

and we denote the interior of \( \Lambda \) by \( D \) and its boundary by \( \partial \Lambda \). It is easy to show that the closed set \( \Lambda \) is positively invariant and attracting with respect to system Equation (1).
3. Reproduction number and equilibria

3.1. Reproduction number

Using the next generation approach of [16]; it is possible to calculate the basic reproduction number, $R_0$. The basic reproduction number, $R_0$, is the average number of secondary infectious individuals caused by an average primary infectious individual in its entire period in a completely susceptible population. It is the threshold parameter.

Based on the assumption of [3], the pathogen population cannot maintain itself through growth in the environment. Thus, the environment is considered as an extended state of host infectiousness, where the pathogen shedding into and growth within the environment are considered as transitions within the initial infectious state of the host population. Therefore, the shedding and growth rate of the pathogen are placed in the $V$ matrix rather than the $F$ matrix.

**Proposition 3.1:** The basic reproduction number $R_0$ in the absence of controls is given by

$$R_0 = \rho(FV^{-1}) = \frac{\Lambda \beta_2}{\mu(\mu + d + \gamma)} + \frac{\Lambda \beta_1 \epsilon}{\mu(\mu + d + \gamma)K\sigma}. \quad (4)$$

To use the approach in [16] we write the right hand side of System (1) as $F - V$, where

$$F = \begin{pmatrix} \frac{\beta_1 BS}{K + B} + \beta_2 IS \\ 0 \end{pmatrix}, \quad V = \begin{pmatrix} (\mu + d + \gamma)I \\ -\epsilon I + \sigma B \end{pmatrix}.$$  

System (1) has one disease-free equilibrium $E_0 = (\Lambda/\mu, 0, 0, 0) \in \partial \Delta$. Then the Jacobian matrices of $F$ and $V$ evaluated at the disease-free equilibrium are

$$F = \begin{pmatrix} \frac{\beta_2 \Lambda}{\mu} \\ 0 \end{pmatrix}, \quad V = \begin{pmatrix} \mu + d + \gamma \\ -\epsilon \sigma \end{pmatrix}. \quad (5)$$

The nonnegative matrix, $FV^{-1}$, is the next generation matrix of System (1).

$$FV^{-1} = \begin{pmatrix} \frac{\Lambda \beta_2}{\mu(\mu + d + \gamma)} + \frac{\Lambda \beta_1 \epsilon}{\mu(\mu + d + \gamma)K\sigma} \\ 0 \end{pmatrix}.$$  

The basic reproduction number Equation (4) is the spectral radius $\rho(FV^{-1})$ of the matrix $FV^{-1}$ which is:

$$R_0 = \rho(FV^{-1}) = \frac{\Lambda \beta_2}{\mu(\mu + d + \gamma)} + \frac{\Lambda \beta_1 \epsilon}{\mu(\mu + d + \gamma)K\sigma}.$$  

To see that the controls can be used to reduce $R_0$, one just needs to follow the same procedure used to obtain (4). The basic reproduction number in case the controls $u_1$ and $u_2$ are present is given by

$$R_0(u_1, u_2) = \rho(FV^{-1}) = \frac{\Lambda \beta_2}{\mu(\mu + d + \gamma + e_1 u_1)} + \frac{\Lambda \beta_1 \epsilon}{\mu(\mu + d + \gamma + e_1 u_1)K(\sigma + e_2 u_2)}.$$  

It can be easily shown that the reproduction number $R_0$ decreases with implementing the controls $u_1$ and $u_2$. 
According to [8], the contribution of each transmission pathway in a disease outbreak is separable. Hence, the control efforts can be focused on infectious humans or the contaminated environment depending on the amount of effort required to reduce $R_0(u_1,u_2)$ to less than one. As a result, it is possible to write $R_0(u_1,u_2)$ as

$$R_0(u_1,u_2) = \frac{\Lambda \beta_2}{\mu(\mu + d + \gamma + e_1 u_1)} + \frac{\Lambda \beta_1 \epsilon}{\mu(\mu + d + \gamma + e_1 u_1) K(\sigma_2 + e_2 u_2)(1 - \frac{\sigma_1}{\sigma_2 + e_2 u_2})}.$$  

Using Taylor’s series expansion, we have,

$$\left(1 - \frac{\sigma_1}{\sigma_2 + e_2 u_2}\right)^{-1} = \left(1 + \frac{\sigma_1}{\sigma_2 + e_2 u_2} + \left(\frac{\sigma_1}{\sigma_2 + e_2 u_2}\right)^2 + \text{higher order terms}\right).$$

Thus,

$$R_0(u_1,u_2) = \frac{\Lambda \beta_2}{\mu(\mu + d + \gamma + e_1 u_1)} + \frac{\Lambda \beta_1 \epsilon}{\mu(\mu + d + \gamma + e_1 u_1) K(\sigma_2 + e_2 u_2)}$$

$$+ \frac{\Lambda \beta_1 \epsilon}{\mu(\mu + d + \gamma + e_1 u_1) K(\sigma_2 + e_2 u_2) \sigma_2 + e_2 u_2} + \text{higher order terms}.$$  

It has the following biological meaning:

$$R_2(u_1,u_2) = \frac{\Lambda \beta_1 \epsilon}{\mu(\mu + d + \gamma + e_1 u_1)},$$

a primary case in the human population makes an infectious contact with humans at a rate of $\beta_2 \Lambda/\mu$ over the mean infectious period of $1/(\mu + d + \gamma + e_1 u_1)$.

$$R_{11}(u_1,u_2) = \frac{\Lambda \beta_1 \epsilon}{\mu(\mu + d + \gamma + e_1 u_1) K(\sigma_2 + e_2 u_2)},$$

a primary case in the human population makes an infectious contact with the environment at a rate of $\epsilon \Lambda/\mu K$ over the mean infectious period of $1/(\mu + d + \gamma + e_1 u_1)$ and a primary case in the environment makes an infectious contact with humans at a rate of $\beta_1$ over the mean infectious period of $1/(\sigma_2 + e_2 u_2)$.

$$R_{12}(u_1,u_2) = \frac{\Lambda \beta_1 \epsilon}{\mu(\mu + d + \gamma + e_1 u_1) K(\sigma_2 + e_2 u_2) \sigma_2 + e_2 u_2},$$

a primary case in the human population makes an infectious contact with the environment at a rate of $\epsilon \Lambda/\mu K$ over the mean infectious period of $1/(\mu + d + \gamma + e_1 u_1)$ and a primary case in the environment makes an infectious contact with humans at a rate of $\beta_1$ over the mean infectious period of $1/(\sigma_2 + e_2 u_2)$, a fraction $\sigma_1/(\sigma_2 + e_2 u_2)$ of which survive and become infectious.

Hence, $R_0(u_1,u_2) = R_2(u_1,u_2) + R_{11}(u_1,u_2) + R_{12}(u_1,u_2)$ represents the total contribution to the infected population and the pathogen population made by the hosts and pathogens of original case. The higher order terms represent the contribution in the higher generation.
3.2. Sensitivity of the basic reproduction number

The system robustness to parameter values is measured by the sensitivity of the reproduction number to these parameters. Hence, studying its sensitivity is important in system dynamics.

**Proposition 3.2:** ([37, Proposition 3.1.]) The inequality $R_0(u_1, u_2) \leq R_0$ is satisfied for any value of the system parameters.

Thus, the basic reproduction number decreases with $u_1$ and $u_2$.

**Proposition 3.3:** The basic reproduction number increases with $\beta_2$, $\beta_1$, $\varepsilon$, $\Lambda$.

**Proof:** This follows from the fact that

$$\frac{\partial R_0(u_1, u_2)}{\partial \beta_1} > 0, \quad \frac{\partial R_0(u_1, u_2)}{\partial \varepsilon} > 0, \quad \frac{\partial R_0(u_1, u_2)}{\partial \Lambda} > 0, \quad \frac{\partial R_0(u_1, u_2)}{\partial \varepsilon} > 0$$

for any parameter values.

The sensitivity of a variable with respect to system parameters is usually measured by sensitivity index.

**Definition 3.4:** ([37, Definition 3.1.] and [14]) The normalized forward sensitivity index of a variable $\Pi$ that depends differentiably on a parameter $\theta$ is defined by

$$\gamma_\Pi^\theta = \frac{\partial \Pi}{\partial \theta} \frac{\theta}{|\Pi|}.$$

Notice that $\gamma_\Pi^\theta$ has a maximum value of magnitude 1. $\gamma_\Pi^\theta = 1$ implies an increase (decrease) of $\theta$ by $y\%$ increases (decreases) $\Pi$ by $y\%$. On the other hand, $\gamma_\Pi^\theta = -1$ indicates an increase (decrease) of $\theta$ by $y\%$ decreases (increases) $\Pi$ by $y\%$.

**Proposition 3.5:** The normalized forward sensitivity index of $R_0$ with respect to $u_1$, $u_2$, $\beta_2$, $\beta_1$ is given by

$$\gamma_{u_1}^{R_0(u_1, u_2)} = -\frac{bu_1}{\mu + d + \gamma + e_1 u_1}, \quad \gamma_{u_2}^{R_0(u_1, u_2)} = -\frac{e_2 u_2}{\sigma + e_2 u_2} \left( \frac{R_1(u_1, u_2)}{R_1(u_1, u_2) + R_2(u_1, u_2)} \right),$$

$$\gamma_{\beta_2}^{R_0(u_1, u_2)} = \frac{R_2(u_1, u_2)}{R_1(u_1, u_2) + R_2(u_1, u_2)}, \quad \gamma_{\beta_1}^{R_0(u_1, u_2)} = \frac{R_1(u_1, u_2)}{R_1(u_1, u_2) + R_2(u_1, u_2)}.$$

**Proof:** This follows immediately from Definition 3.4.

3.3. Existence of endemic equilibrium

System Equation (1) has a unique positive equilibrium $E^* = (S^*, I^*, R^*, B^*) \in D$ given as

$$B^* = \frac{\varepsilon I^*}{\sigma + e_2 u_2}, \quad R^* = \frac{(\gamma (\rho_1 + e_1 u_1 \rho_2)) I^*}{\alpha + \mu},$$
\[ S^* = \frac{\Lambda + (\gamma (1 - \rho_1) + e_1 u_1 (1 - \rho_2) + \alpha \left( \frac{\gamma (\rho_1 + e_1 u_1 \rho_2)}{\alpha + \mu} \right) - (\mu + d + \gamma + e_1 u_1) I^*}{\mu}, \]

and \( I^* \) is the positive solution of the quadratic equation

\[ AI^{*2} + BI^* + C = 0, \quad (5) \]

where

\[ A = \frac{\beta_2 \varepsilon}{\alpha + \mu} ((\alpha + \mu)(\mu + d) + \mu(\gamma \rho_1 + e_1 u_1 \rho_2)), \]

\[ B = \varepsilon (\mu(\mu + d + \gamma + e_1 u_1) - \beta_2 \Lambda) \]

\[ + (\beta_1 \varepsilon + \beta_2 K(\sigma + e_2 u_2)) \left( \frac{1}{\mu + \alpha} ((\alpha + \mu)(\mu + d) + \mu(\gamma \rho_1 + e_1 u_1 \rho_2)) \right), \]

\[ C = \mu K(\sigma + e_2 u_2)(\mu + d + \gamma + e_1 u_1)(1 - R_0). \]

\( A \) is positive and the solutions of Equation (5) depend on the signs of \( B \) and \( C \). It follows that:

**Theorem 3.6:** System Equation (1)

(i) Always has the disease-free equilibrium.

(ii) If \( R_0 > 1 \), it has a unique endemic equilibrium, \( E^* \).

(iii) If \( 0 \leq R_0 \leq 1 \), there is no endemic equilibrium.

4. **Stability of equilibria**

This section is devoted to analytic conditions for the stability of the disease-free and endemic equilibria.

4.1. **Local stability of the disease-free equilibrium**

**Theorem 4.1:** The disease-free equilibrium, \( E_0 \), of system Equation (1) is locally asymptotically stable if \( R_0 \leq 1 \) and is unstable if \( R_0 > 1 \).

**Proof:** Local stability is analysed by the Jacobian matrix of system Equation (1) at \( E_0 \). That is:

\[ J(E_0) = \begin{pmatrix}
-\mu & -\beta_2 \frac{\Lambda}{\mu} + \gamma (1 - \rho_1) + e_1 u_1 (1 - \rho_2) & \alpha & -\frac{\beta_1 \Lambda}{K \mu} \\
0 & \beta_2 \frac{\Lambda}{\mu} - (\mu + d + \gamma e_1 u_1) & 0 & \frac{\beta_1 \Lambda}{K \mu} \\
0 & \gamma \rho_1 + e_1 u_1 \rho_2 & -(\alpha + \mu) & 0 \\
0 & \varepsilon & 0 & -(\sigma + e_2 u_2)
\end{pmatrix} \]

The characteristic polynomial of the Jacobian matrix at \( E_0 \) is:

\[ (\lambda + \mu)(\lambda + \alpha + \mu)(\lambda^2 + a_1 \lambda + a_2) = 0, \]

where

\[ a_1 = (\mu + d + \gamma + e_1 u_1 + \sigma + e_2 u_2) - \frac{\beta_2 \Lambda}{\mu}, \]
\[ a_2 = (\mu + d + \gamma + e_1 u_1)\sigma + e_2 u_2)(1 - R_0). \]

If \( R_0 < 1, a_1 < 0 \) and \( a_1 a_2 > 0 \). Thus, according to the Routh Hurwitz criterion, the quadratic equation, \( \lambda^2 + a_1 \lambda + a_2 = 0 \), has negative real roots only. Consequently, the disease-free equilibrium, \( E_0 \) is locally asymptotically stable. By existence of equilibria Theorem 3.6 above, \( E_0 \) is the only equilibrium at \( R_0 = 1 \) which shows that \( E_0 \) is locally asymptotically stable when \( R_0 \leq 1 \). If \( R_0 > 1 \), then \( a_2 < 0 \) and the quadratic equation has one positive root. Hence, \( E_0 \) is unstable with the dimension of the stable manifold, \( \dim W^s(E_0) = 3 \) and unstable manifold, \( \dim W^u(E_0) = 1 \) [12, Theorem 3.1].

### 4.2. Global stability of the disease-free equilibrium

**Theorem 4.2:** The disease-free equilibrium, \( E_0 \), of system Equation (1) is globally asymptotically stable in \( \Lambda \) if \( R_0 \leq 1 \).

**Proof:** We set the Lyapunov function

\[ L = \varepsilon I + (\mu + d + \gamma + u_1)B. \]

Differentiating \( L \) in the solutions of system Equation (1) we get

\[
L' = \varepsilon I' + (\mu + d + \gamma + e_1 u_1)B',
= \varepsilon \left( \frac{\beta_1 B S}{K + B} + \beta_2 I S - (\mu + d + \gamma + e_1 u_1) \right)
+ (\mu + d + \gamma + e_1 u_1) (\varepsilon I - (\sigma + e_2 u_2)B)
\leq \varepsilon \beta_2 \left( \frac{\Lambda}{\mu} \right)^2 + \varepsilon^2 \left( \frac{\Lambda}{\mu} \right)^2 \left( \frac{\beta_1}{K + e_2 u_2} - (\mu + d + \gamma + e_1 u_1) \right)
= \frac{\varepsilon \Lambda}{\mu (\mu + d + \gamma + e_1 u_1)} \left( \frac{\Lambda \beta_2}{\mu (\mu + d + \gamma + e_1 u_1)} + \frac{\Lambda \beta_1 \varepsilon}{\mu (\mu + d + \gamma + e_1 u_1) K (\sigma + e_2 u_2)} - 1 \right)
= \frac{\varepsilon \Lambda}{\mu (\mu + d + \gamma + e_1 u_1)} (R_0 - 1).
\]

\( L' < 1 \) when \( R_0 < 1 \). Furthermore, \( L' = 0 \) if and only if \( R_0 = 1 \). Therefore, the largest compact invariant set in \( \{(S, I, R, B) \mid L'(I, B) = 0\} \) is the singleton, \( E_0 = (\Lambda/\mu, 0, 0, 0) \). By LaSalle’s Invariance Principle the disease-free equilibrium is globally asymptotically stable in \( \Lambda \). ■

### 4.3. Global stability of the endemic equilibrium

we employ the geometric approach developed by [23] to analyse the global stability of this model. The mathematical framework is summarized below.
Suppose that $D \subset \mathbb{R}^n$ be a bounded open set and the map $x \mapsto f(x)$ defined by $f : D \mapsto \mathbb{R}^n$ be a $C^1$ function. Let each solution $x(t)$ of the following the differential equation

$$\frac{dx}{dt} = f(x) \tag{6}$$

be uniquely determined by its initial value $x(0, x_0) = x_0$, and denote this solution by $x(t, x_0)$. A subset $K$ is said to be absorbing in $D$ if $x(t, K) \subset K$ for any compact subset $K_1 \subset D$ and sufficiently large $t$. An open set $D \subset \mathbb{R}^n$ is simply connected if each closed curve in $D$ can be continuously deformed to a point within $D$.

**The global stability problem.** Suppose the following assumptions are true for system Equation (6):

(H1) $D$ is simply connected;
(H2) There exists a compact absorbing set $K \subset D$;
(H3) The system Equation (6) has a unique equilibrium point $\bar{x}$ in $D$.

Find conditions under which the local stability of $\bar{x}$ in $D$ implies it is global stable.

Suppose $\| \cdot \|$ denotes a vector norm on $\mathbb{R}^n$ and the operator norm which it induces for linear mappings from $\mathbb{R}^n$ to $\mathbb{R}^n$. For $n \geq 2$, a Bendixson criterion is a condition satisfied by $f$ which precludes the existence of nonconstant periodic solutions of Equation (6). It is said to be robust under $C^1$ local perturbation of $f$ at $x_0 \in D$ if, for each sufficiently small $\epsilon > 0$ and neighbourhood $U$ of $x_0$, it is also satisfied by $g \in C^1(D \mapsto \mathbb{R}^n)$ such that the support supp$(f - g) \subset U$ and $|f - g|_{C^1} < \epsilon$, where the distance between the two functions is

$$|f - g|_{C^1} = \sup \left\{ |f(x) - g(x)| + \left| \frac{\partial f}{\partial x}(x) - \frac{\partial g}{\partial x}(x) \right| : x \in D \right\}.$$ 

A function $g \in C^1(D \mapsto \mathbb{R}^n)$ is called a $C^1$ local $\epsilon$-perturbation of $f$ at $x_0 \in D$ if there exists an open neighbourhood $U$ of $x_0$ in $D$ such that the support supp$(f - g) \subset U$ and $|f - g|_{C^1} < \epsilon$. A point $x_0 \in D$ is wandering for Equation (6) if there exists a neighbourhood $U$ of $x_0$ and $T > 0$ such that $U \cap x(t, U)$ is empty for all $t > T$. Thus, all equilibria and omega and alpha limit points are nonwandering.

Let $\| \cdot \|$ represents a vector norm in $\mathbb{R}^n$ and the norm of $n \times n$ matrices it induces. The Lozinskiǐ measure $\mu_1(A)$ of $n \times n$ of matrix $A$ with respect to the induced matrix norm $\| \cdot \|$ in $\mathbb{R}^n$ is defined as

$$\mu_1(A) = \lim_{h \to 0^+} \frac{|I + hA| - 1}{h}.$$ 

**Lemma 4.3:** The Lozinskiǐ measure of a real $n \times n$ matrix $A$ with respect to the matrix norm induced by the $l_1$ vector norm, is given by

$$\mu_1(A) = \max_j \left( A_{jj} + \sum_{i \neq j} |A_{ij}| \right).$$

Let the map $P : D \mapsto R_{\mathbb{C}}^{(2)}\times(\overline{2})$ be a $C^1$ and nonsingular matrix valued function for all $x \in D$, and let $\mu_1$ be the Lozinskiǐ measure on $R_{\mathbb{C}}^{(2)}\times(\overline{2})$. Suppose that system Equation (6)
has a compact absorbing set $K$. Define the quantity $q$ as

$$q = \limsup_{t \to \infty} \sup_{x_0 \in K} \frac{1}{t} \int_0^t \mu_1(A(x(s,x_0))) \, ds,$$

where $A(x) = P_f(x)P^{-1}(x) + P_j(x)J^{[2]}(x)P^{-1}(x)$. The matrix $P_f$ is obtained by replacing each entry $P_{ij}$ of $P$ by its derivative in the direction of $f$ with

$$P_f(x) := \frac{dP(x(t,x_0))}{dt}, \quad J(x) := \frac{\partial f}{\partial x}(x).$$

Under the assumptions of $(H_1)$ and $(H_2)$, it is proved in [23, Theorem 4.4] that if

$$\mu_1\left(P_f(x)P^{-1}(x) + P_j(x)J^{[2]}(x)P^{-1}(x)\right) \leq -g < 0 \quad \text{on } K, \quad (7)$$

then no simple closed rectifiable curve in $D$ can be invariant with respect to system Equation (6). $J^{[2]}(x) = (\partial f^{[2]}/\partial x)(x)$ is the second additive compound matrix of $\partial f/\partial x)(x)$. Criterion Equation (7) allows a choice of $R^{(n)} \times (\mathbb{Q})$ different matrix functions and arbitrary vector norms $|\cdot|$ in deriving sufficient conditions for global stability. It is pointed out in [23] that condition Equation (7) is equivalent to assuming $V(x,y) = |A(x)y|$ as a Lyapunov function whose derivative with respect to $n + (\mathbb{Q})$ dimensional system

$$\frac{dx}{dt} = \frac{\partial f}{\partial x}(x), \quad \frac{dy}{dt} = \frac{\partial f^{[2]}}{\partial x}(x(t,x_0))y$$

is negative definite. This rules out any simple closed rectifiable curve which is invariant in $D$.

The existence of a compact absorbing set in $D$ is equivalent to proving the uniform persistent of system Equation (1) [18, Theorem 4.2]; that is, there exists $\eta > 0$ such that each solution $(S(t),I(t),R(t),B(t))$ of Equation (1) with initial value $(S(0),I(0),R(0),B(0)) \in D$ satisfies

$$\min \left\{ \liminf_{t \to \infty} S(t), \liminf_{t \to \infty} I(t), \liminf_{t \to \infty} R(t), \liminf_{t \to \infty} B(t) \right\} \geq \eta.$$

**Theorem 4.4:** System Equation (1) is uniformly persistent in $D$ if and only if $R_0 > 1$.

**Proof:** We are using the combination of the methods given in [10], [12, Theorem 3.4], and [34, Lemma 3.4]. To do that, let the semi-flow of system Equation (1) is denoted by $\phi, X = \Lambda, X_1 = D$, and $X_2 = \partial \Lambda$.

Define the continuous semi-flow $\phi : [0, \infty) \times X \mapsto X$ by $\phi(t,x) = x(t)$ and let $x(t,x_0)$ denote the solution of system Equation (1) satisfying $x(0,x_0) = x_0$. Firstly, we show that $\phi$ is dissipative. This is proved by virtue of Theorem 2.1; all solutions of $\phi$ initiated in $X$ ultimately enter a set $K$ and stay therein forever. $K$ is bounded and closed and hence compact. Consequently, $\phi$ is dissipative. Secondly, we need to find an invariant set, $\Omega$ in the boundary of $X$ such that $\phi$ is continuous semi-flow with respect to $\Omega$. To do so, denote the omega limit set of the solution $x(t,x_0)$ of $\phi$ starting in $X$ by $\omega(x_0)$ (which exists by
Theorem 2.1), we need to determine the following set:

\[ \Omega = \bigcup_{y \in Y} \omega(y), \text{ where } Y = \{x_0 \in X_2 | x(t, x_0) \in X_2, \forall t > 0\} . \]

From system Equation (1) it follows that all solutions starting in the boundary of \( X \) leave the boundary except the solutions emanating from \( S \)-axis. Implying that the \( S \)-axis is an invariant set, and hence, \( Y = \{(S, 0, 0, 0)|0 < S \leq \frac{\Delta}{\mu}\} \). Furthermore, it is easy to see that \( \Omega \) is the equal to the set \( \{E_0\} \) as all solutions initiated on the \( S \)-axis converge to \( E_0 \). In fact, \( \phi \) in the set \( Y \) is given by

\[ \frac{dS}{dt} = \Lambda - \mu S. \]

It is proved in theorem 4.2 that \( E_0 \) is globally asymptotically stable for \( R_0 \leq 1 \). Consequently, any solution \((S(t), I(t), R(t), B(t))\) of \( \phi \) initiating from \( Y \) is such that \((S(t), I(t), R(t), B(t)) \rightarrow E_0 \). Consequently, \( E_0 \) is a covering of \( \Omega \). Moreover, \( \Omega \) is isolated since it is the maximal invariant subset of \( E_0 \). Since \( \frac{dS}{dt} = \Lambda - \mu S \) is a linear ordinary differential equation with unique acyclic solution, \( \Omega \) is acyclic.

In what follows we show the weakly persistence of \( \phi \). It is enough to show \( E_0 \) is a weak repeller of \( X_1 \) [34, Lemma 3.4]. By definition, \( E_0 \) is a weak repeller for \( X_1 \) if for every solution, \( x(t, x_0) \), starting in \( x_0 \in X_1 \)

\[ \lim_{t \rightarrow +\infty} \sup d(x(t, x_0), E_0) > 0. \] (8)

Equation (8) is satisfied if the following equation holds [38, Lemma 3.5]

\[ W^s(E_0) \cap X_1 = \emptyset. \] (9)

To show this, suppose that Equation (9) does not hold for some solution \( x(t, x_0) \) starting in \( x_0 \in X_1 \). In view of the fact that the closed positive orthant is positively invariant for \( \phi \), it follows that \( \limsup_{t \rightarrow +\infty} d(x(t, x_0), E_0) = 0 = \liminf_{t \rightarrow +\infty} d(x(t, x_0), E_0) \) and thus \( \lim_{t \rightarrow +\infty} x(t, x_0) = E_0 \), which is clearly impossible if Equation (9) holds.

What remains to be shown is that Equation (9) holds. To that end, recall that the Jacobian matrix of system Equation (1) at \( E_0 \) is unstable if \( R_0 > 1 \). Assume that there exists an omega limit set \((S(t), I(t), R(t), B(t))\) such that \( \lim_{t \rightarrow +\infty} S(t) = \Lambda/\mu \), \( \lim_{t \rightarrow +\infty} I(t) = \lim_{t \rightarrow +\infty} R(t) = \lim_{t \rightarrow +\infty} B(t) = 0 \). It follows for small enough \( \epsilon \) that, \( (\Lambda/\mu) - \epsilon \leq S(t) \leq (\Lambda/\mu) + \epsilon, 0 \leq I(t) \leq \epsilon, 0 \leq R(t) \leq \epsilon, 0 \leq B(t) \leq \epsilon \) for \( t \geq 0 \). Thus, \((S/(K + B)) \geq (((\Lambda/\mu) - \epsilon)/(K + \epsilon)) = (\Lambda/\mu K) - (2\Lambda \epsilon/\mu (K + \epsilon))\).

From the second and the last equations of system Equation (1), we obtain

\[ \frac{dI}{dt} \geq \beta_1 \frac{\Lambda B}{\mu K} - 2 \epsilon \beta_2 I \left( \frac{\Lambda}{\mu} - \epsilon \right) - (\mu + d + \gamma + \epsilon_1) I, \]

\[ \frac{dB}{dt} = \epsilon I - (\sigma + \epsilon_2) B. \] (10)
Consider the matrix \( M_{F-V-\varepsilon} \) defined by

\[
M_{F-V-\varepsilon} = \begin{pmatrix}
\beta_2 \left( \frac{\Lambda}{\mu} - \varepsilon \right) - (\mu + d + \gamma + e_1 u_1) & \frac{\beta_1 S K}{(K+B)^2} - \varepsilon \\
\varepsilon & (\sigma + e_2 u_2)
\end{pmatrix}.
\]

\( M_{F-V-\varepsilon} \) admits a positive off-diagonal element. The Perron-Frobenius property implies that there is a positive eigenvector \( v = (v_1, v_2) \) for the maximum eigenvalue, \( \rho(M_{F-V-\varepsilon}) = R_0(\varepsilon) \), which is positive [30, Definition 2.1]. Let us consider the following system:

\[
\begin{align*}
\frac{dz_1}{dt} &= \left( \beta_2 \left( \frac{\Lambda}{\mu} - \varepsilon \right) - (\mu + d + \gamma + e_1 u_1) \right) z_1 + \left( \frac{\beta_1 S K}{(K+B)^2} - \varepsilon \right) z_2, \\
\frac{dz_2}{dt} &= \varepsilon z_1 - (\sigma + e_2 u_2) z_2.
\end{align*}
\]

Let \( z(t) = (z_1(t), z_2(t)) \) be a solution of Equation (11) through \((I_{v_1}, B_{v_2})\) at \( t = t_0 \), where I and B are positive and satisfy \( I_{v_1} < I(t_0) \) and \( B_{v_2} < B(t_0) \). Since the semi-flow of Equation (11) is monotone and \( M_{F-V-\varepsilon} v > 0 \), it follows that \( \lim_{t \to +\infty} z_i(t) \to +\infty \). Thus, \( z(t) \notin W^s(E_0) \) and \( z(t) \notin X \) contradicting that all solutions emanating from the S-axis converge to \( E_0 \) and the boundedness of the solutions of system Equation (1). This results in \( W^s(E_0) \cap X_1 = \emptyset \). Thus, \( E_0 \) is a weak repeller for \( X_1 \) and \( \phi \) is weakly persistent system. We conclude that \( \phi \) is uniformly persistent.

In what follows, we prove the global stability of the unique endemic equilibrium based on the theory outlined above. To do so let \( x = (S, I, R, B) \) and denote the right hand side of system Equation (1) by \( f(x) \). By the uniform persistence Theorem 4.4, (\( H_2 \)) is satisfied and obviously Equation (1) has unique equilibrium solution \( E^* \in D \) for \( R_0 > 1 \). Consequently, (\( H_1 \)) and (\( H_2 \)) are satisfied.

**Theorem 4.5:** If \( R_0 > 1 \), then the unique endemic equilibrium, \( E^* \), of system Equation (1) is globally asymptotically stable in \( D \) and \( E_0 \) is unstable if

\[
\mu > \max \{ \alpha, d + \gamma (1 - \rho_1) + e_1 u_1 (1 - \rho_2) - \alpha, \varepsilon + \gamma \rho_1 + u_1 \rho_2 - \alpha \}
\]

is satisfied.

**Proof:** By Theorem 4.4, when \( R_0 > 1 \), there is a compact absorbing set \( K \) in \( D \) which is absorbing for system Equation (1).

The second additive compound matrix \( J^{[2]} \) of the Jacobian matrix \( J \) of the system Equation (1) is:

\[
J^{[2]} = \begin{pmatrix}
M_{11} & 0 & \frac{\beta_1 S K}{(K+B)^2} - \alpha & \frac{\beta_1 S K}{(K+B)^2} - \alpha & 0 \\
M_{21} & M_{22} & 0 & M_{24} & 0 \\
\varepsilon & 0 & M_{33} & 0 & M_{35} \\
0 & M_{42} & 0 & M_{44} & \alpha \\
0 & 0 & \frac{\beta_1 B}{K+B} & 0 & M_{55} \\
0 & 0 & 0 & -\varepsilon & M_{65} \\
0 & 0 & 0 & 0 & M_{66}
\end{pmatrix}
\]
where

\[ M_{11} = -\left( \mu + \frac{\beta_1 B}{K + B} + \beta_2 I + \mu + d + \gamma + e_1 u_1 \right) + \beta_2 S, \]

\[ M_{21} = \gamma \rho_1 + e_1 u_1 \rho_2 = M_{65}, \]

\[ M_{22} = -\left( \mu + \frac{\beta_1 B}{K + B} + \beta_2 I + \mu + \alpha \right), \]

\[ M_{24} = M_{35} = -\beta_2 S + \gamma (1 - \rho_1) + e_1 u_1 (1 - \rho_2), \]

\[ M_{44} = -\left( \mu + \frac{\beta_1 B}{K + B} + \beta_2 I + \mu + \alpha \right), \]

\[ M_{55} = \beta_2 S - (\mu + d + \gamma + e_1 u_1 + \alpha + \mu), \]

\[ M_{66} = -(\alpha + \mu + \sigma + e_2 u_2). \]

Set the matrix-valued function,

\[ P = \begin{pmatrix}
  \frac{a_1}{I} & 0 & 0 & 0 & 0 & 0 \\
  0 & \frac{a_1}{I} & 0 & 0 & 0 & 0 \\
  0 & 0 & \frac{a_1}{I} & 0 & 0 & 0 \\
  0 & 0 & \frac{a_2}{B} & 0 & 0 & 0 \\
  0 & 0 & 0 & \frac{a_2}{B} & 0 & 0 \\
  0 & 0 & 0 & 0 & \frac{a_2}{B} & 0 \\
\end{pmatrix} \]

where \( a_1 \) and \( a_2 \) are arbitrary positive constants. \( P \) is a \( C^1 \) and nonsingular in \( D \). Let the vector field of system Equation (1) is denoted by \( f \). Then

\[ P_f P^{-1} = \text{diag} \left( \frac{-I'}{I}, \frac{-I'}{I}, \frac{-B'}{B}, \frac{-B'}{B}, \frac{-B'}{B} \right), \]

where \( P_f \) is the directional derivative of \( P \) in the direction of \( f \). It follows that

\[ P_f J^{[2]} P^{-1} = \begin{pmatrix}
  M_{11} & \frac{I}{E (1 + K_1 I)} & \frac{I}{E (1 + K_1 I)} & \frac{-\beta S}{\frac{\beta_1 SK}{(K + B)^2} a_1 B} & \frac{-\beta S}{\frac{\beta_1 SK}{(K + B)^2} a_1 B} & \frac{0}{\frac{\beta_1 SK}{(K + B)^2} a_1 B} \\
  0 & M_{22} & 0 & \frac{\beta_1 SK}{(K + B)^2} a_1 B & \frac{\beta_1 SK}{(K + B)^2} a_1 B & \frac{0}{\frac{\beta_1 SK}{(K + B)^2} a_1 B} \\
  0 & 0 & M_{44} & \frac{\beta_1 SK}{(K + B)^2} a_1 B & \frac{\beta_1 SK}{(K + B)^2} a_1 B & \frac{0}{\frac{\beta_1 SK}{(K + B)^2} a_1 B} \\
  0 & 0 & \frac{a_1}{a_2 B} & 0 & 0 & 0 \\
  0 & 0 & 0 & \frac{a_2}{B} & 0 & 0 \\
  0 & 0 & 0 & -\varepsilon & 0 & 0 \\
\end{pmatrix}. \]

The matrix

\[ A = P_f P^{-1} + P_f J^{[2]} \]
can be written in block form

\[
A = \begin{pmatrix}
    A_{11} & A_{12} & A_{13} & A_{14} \\
    A_{21} & A_{22} & A_{23} & A_{24} \\
    A_{31} & A_{32} & A_{33} & A_{34} \\
    A_{41} & A_{42} & A_{43} & A_{44}
\end{pmatrix},
\]

where

\[
A_{11} = M_{11} - \frac{I'}{I}, A_{12} = (0, -\alpha), A_{13} = \left(\frac{\beta_1 SK - a_1 B}{(K + B)^2 a_2 I}, \frac{\beta_1 SK - a_1 B}{(K + B)^2 a_2 I}\right), A_{14} = 0,
\]

\[
A_{21} = (\gamma \rho_1 + e_1 u_1 \rho_2, 0)^T, A_{24} = \left(\frac{\beta_1 SK - a_1 B}{(K + B)^2 a_2 I}, \frac{\beta_1 SK - a_1 B}{(K + B)^2 a_2 I}\right)^T
\]

\[
A_{31} = \left(\frac{\varepsilon}{a_2 B}, 0\right)^T,
\]

\[
A_{34} = (\alpha, 0)^T, A_{41} = 0, A_{42} = (0, -\varepsilon), A_{43} = (0, \gamma \rho_1 + e_1 u_1 \rho_2),
\]

\[
A_{44} = -((\alpha + \mu + \sigma + e_2 u_2) - B'),
\]

\[
A_{23} = \begin{pmatrix} 0 & 0 \\ 0 & 0 \end{pmatrix}, A_{32} = \begin{pmatrix} 0 & 0 \\ 0 & 0 \end{pmatrix}
\]

\[
A_{22} = \begin{pmatrix} M_{22} - \frac{I'}{I} & M_{24} \\ M_{42} & M_{44} - \frac{I'}{I} \end{pmatrix}, A_{33} = \begin{pmatrix} M_{33} - \frac{I'}{I} & M_{24} \\ M_{42} & M_{55} - \frac{B'}{B} \end{pmatrix}
\]

Let \( u = (u_1, u_2, u_3, u_4, u_5, u_6) \) be vectors in \( R^6 \cong R^\langle 6 \rangle \). We select a norm in \( R^6 \) as \( ||(u_1, u_2, u_3, u_4, u_5, u_6)|| = \max\{|u_1|, |u_2| + |u_3|, |u_4| + |u_5|, |u_6|\} \). Using the approach of estimation in [34, Theorem 4.4] and [27, Theorem 2], we have

\[
\mu_1(A) \leq \sup\{g_1, g_2, g_3, g_4\},
\]

where

\[
g_1 = \mu_1(A_{11}) + |A_{12}| + |A_{13}| + |A_{14}|, g_2 = |A_{21}| + \mu_1(A_{22}) + |A_{23}| + |A_{24}|,
\]

\[
g_3 = |A_{31}| + |A_{32}| + \mu_1(A_{33}) + |A_{34}|, g_4 = |A_{41}| + |A_{42}| + |A_{43}| + \mu_1(A_{44}).
\]

\(|A_{ij}|(i \neq j, i, j = 1, 2, 3, 4)\) are matrix norms with respect to the \( l_1 \) vector norm, and \( \mu_1 \) denotes the Lozinski\' measure with respect to the \( l_1 \) norm. It turns out that

\[
\mu_1(A_{11}) = -\left(\mu + \frac{\beta_1 B}{K + B} + \beta_2 I + \mu + d + \gamma + e_1 u_1\right) + \beta_2,
\]

\[
|A_{12}| = \alpha = |A_{34}|, |A_{13}| = \frac{\beta_1 SK - a_1 B}{(K + B)^2 a_2 I} = |A_{24}|, |A_{21}| = \gamma \rho_1 + e_1 u_1 \rho_2 = |A_{43}|,
\]

\[
|A_{14}| = 0 = |A_{32}| = |A_{41}| = |A_{23}|, |A_{31}| = \frac{\varepsilon a_1 I}{a_2 B}, |A_{42}| = \varepsilon, |A_{43}| = \gamma \rho_1 + e_1 u_1 \rho_2.
\]
To calculate $g_1, g_2, g_3, g_4$ we let $a_2 = -a_1$. Then,

$$g_1 = -\left(\mu + \frac{\beta_1 B}{K+B} + \beta_2 I + \mu + d + \gamma + e_1 u_1\right) + \beta_2 S - \frac{I'}{I} + \alpha + \frac{\beta_1 SK}{(K+B)^2} \frac{a_1 B}{a_2 I}.$$ 

Rewriting the second and fourth equations of system Equation (1), we get,

$$\frac{I'}{I} = \frac{\beta_1 BS}{I(K+B)} - \beta_2 S - (\mu + d + \gamma + e_1 u_1),$$

$$\frac{B'}{B} = \frac{\varepsilon I}{B} - (\sigma + e_2 u_2)$$

Substituting $I'/I$ in $g_1$,

$$g_1 = -\left(\mu + \frac{\beta_1 B}{K+B} + \beta_2 S\right) - \frac{\beta_1 BS}{I(K+B)} + \alpha - \frac{\beta_1 SK}{(K+B)^2} \frac{B}{I}$$

$$g_1 \leq -\mu + \alpha.$$

Likewise,

$$\mu_1(A_{44}) = -\left(\alpha + \mu + \sigma + e_2 u_2 + \frac{B'}{B}\right)$$

$$= -\left(\alpha + \mu + \sigma + e_2 u_2 + \frac{\varepsilon I}{B}\right) + \sigma + e_2 u_2$$

and

$$g_4 = -\left(\alpha + \mu + e_2 u_2 + \frac{\varepsilon I}{B}\right) + \varepsilon + \gamma \rho_1 + e_1 u_1 \rho_2$$

$$\leq -\mu + (\varepsilon + \gamma \rho_1 + e_1 u_1 \rho_2 - \alpha).$$

To calculate $\mu_1(A_{22})$ and $\mu_1(A_{33})$, we add the absolute value of the off-diagonal elements to the diagonal ones in each column of $A_{22}$ and $A_{33}$, and then take the maximum of the two sums, i.e.

$$\mu_1(A_{22}) = \max\{-2\mu - \alpha - \frac{I'}{I}, \left(-2\mu - \alpha - \frac{I'}{I}\right) - (\mu + d + \gamma + e_1 u_1)\}$$

$$= -2\mu - \alpha - \frac{I'}{I}.$$

And

$$\mu_1(A_{33}) = \max\{-\mu - (\sigma + e_2 u_2) - \frac{B'}{B}, -\mu - (\sigma + e_2 u_2) - \frac{B'}{B} - (d + \gamma \rho_1 + e_1 u_1 (1 - \rho_2)\}$$

$$= -\mu - (\sigma + e_2 u_2) - \frac{B'}{B}.$$
provided that
\[-\beta_2 S + \gamma (1 - \rho_1) + e_1 u_1 (1 - \rho_2) \geq 0.\]

Thus,
\[
g_2 = \gamma \rho_1 + e_1 u_1 \rho_2 + -2\mu - \alpha - \frac{I'}{I} - \left( \frac{-\beta_1 SK}{(K + B)^2} \right) \frac{B}{I} \leq -\mu + (d + \gamma (1 - \rho_1) + e_1 u_1 (1 - \rho_2) - \alpha). \]

And
\[
g_3 = \varepsilon \frac{a_1}{a_2} \frac{I}{B} - \mu - (\sigma + e_2 u_2) - \frac{B'}{B} + \alpha \leq -\mu + \alpha. \]

The estimate in $\mu_1(A)$ can be written as
\[
\mu_1(A) \leq \sup\{g_1, g_2, g_3, g_4\} = \min\{-g_1, -g_2, -g_3, -g_4\}. \tag{13}\]

Let $g = \min\{\mu - \alpha, \mu - (d + \gamma (1 - \rho_1) + e_1 u_1 (1 - \rho_2) - \alpha), \mu - (\varepsilon + \gamma \rho_1 + e_1 u_1 \rho_2 - \alpha)\}$.

If $\mu > \max\{\mu - \alpha, \mu - (d + \gamma (1 - \rho_1) + e_1 u_1 (1 - \rho_2) - \alpha), \mu - (\varepsilon + \gamma \rho_1 + e_1 u_1 \rho_2 - \alpha)\}$, then $-g < 0$.

Finally,
\[
\mu_1(A) \leq \sup\{g_1, g_2, g_3, g_4\} < -g. \]

This implies that $\mu_1(A(S, I, R, B)) = \mu_1(PfP^{-1} + PfJ^{[2]}P^{-1}) \leq -g < 0$. Along each solution $(S(t), I(t), R(t), B(t))$ of system Equation (1) such that $(S(0), I(0), R(0), B(0)) \in K$ and $t > T$, we have
\[
\frac{1}{t} \int_0^t g_i ds \leq -g < 0, \quad i = 1, 2, 3, 4. \]

Averaging along each solution trajectories as $t \to \infty$ we get
\[
\bar{q} = \limsup_{t \to \infty} \sup_{x_0 \in K} \frac{1}{t} \int_0^t \mu_1(A(x(s, x_0))) \, ds \leq -g < 0. \quad \Box \]

5. Bifurcation analysis and numerical simulations

In this section, we implement the bifurcation analysis and numerical simulations to establish the above theoretical analysis and discuss more dynamical behaviour of system Equation (1). The parameters used for the simulation are given in Table 1.
Table 1. Parameter values.

| Parameters | Meaning | Values | References |
|------------|---------|--------|------------|
| $\Lambda$ | Recruitment rate of susceptible population | Varies | Assumed |
| $\mu$ | Natural death rate of humans | 0.00045662 | [48] |
| $\sigma$ | Net death rate of Shigella pathogen | 0.033333 | Assumed |
| $\gamma$ | Natural recovery rate | 0.0158 | [11] |
| $d$ | Disease-induced death rate | 0.0015 | [48] |
| $K$ | Pathogen population that could cause disease | 200 cells/L | [36] |
| $\alpha$ | Progression rate of recovered | 0.0025 | Assumed |
| $\varepsilon$ | Contribution of each infected person to the concentration of shigella | Varies | Assumed |
| $\rho_1$ | Proportion of individuals naturally recovered | 0.75, 0.5 | Assumed |
| $\rho_2$ | Proportion of individuals recovered by treatment | 0.75, 0.5 | Assumed |
| $e_1$ | Efficacy of treatment | varies | Assumed |
| $e_2$ | Efficacy of sanitation | varies | Assumed |

5.1. Bifurcation analysis

This subsection is devoted to the bifurcation analysis of system Equation (1) on the basis of Section 3. Bifurcation analysis gives an insight of how the equilibrium points depend on $R_0$. In most cases, as $R_0$ crosses 1 to the right, the diseases free equilibrium becomes unstable and there emerges stable endemic equilibrium. $R_0 = 1$ is called a bifurcation point and the graph is bifurcation curve. This qualitative change in behaviour of the system from stable disease-free equilibrium to unstable disease-free equilibrium and stable endemic equilibrium is called forward bifurcation (supercritical bifurcation). In this case, it is assumed that the disease can be eradicated as long as $R_0 < 1$. But in some cases, it is possible that the stable disease free equilibrium can coexist with stable endemic equilibrium as a result the classical approach keeping $R_0 < 1$ does not guarantee disease eradication. This type of bifurcation is called backward bifurcation. In this case, another threshold quantity is needed to eradicate the disease. Further theory and application of bifurcation on epidemic models can found in [2,9].

To investigate the type of bifurcation, consider $R_0 = 1$. Let

$$\beta_1^* := \frac{K(\delta + e_2 u_2)}{\varepsilon \Lambda} - (\mu (\mu + d + \gamma + e_1 u_1) - \beta_2 \Lambda)$$

be the bifurcation parameter. The eigenvalues of the characteristics polynomial at $R_0 = 1$ are $\lambda_1 = -\mu$, $\lambda_2 = -(\alpha + \mu)$, $\lambda_3 = \beta_2 \frac{\Lambda}{\mu} - (\mu + d + \gamma + e_1 u_1 + \sigma + e_2 u_2)$, and $\lambda_4 = 0$. We can observe that the three eigenvalues are real and negative and one is 0 and simple. Based on the bifurcation process of [13], forward bifurcation exists at $R_0 < 1$. Its biological meaning is that as far as $R_0 < 1$ the dysentery diarrhoea epidemic can be eradicated from the population. If parameters change and result in $R_0 > 1$, a small endemic state may occur. The forward bifurcation curve for $R_0$ as a function of $\beta_1$ is given in Figure 2. For $R_0 \leq 1$ the disease-free equilibrium of system Equation (1) is globally stable. Thus, the dysentery epidemic may be eliminated from the population. However, if the reproduction is greater than unity the disease is endemic in the community.

5.2. Numerical analysis and simulation

The theoretical outcome above proves that $R_0$ is a threshold parameter to decide if dysentery diarrhoea persists in the community. In this subsection, we implement
Figure 2. (a) The forward bifurcation curve for $I$ versus $R_0$, when $\Lambda = 0.09$, $\beta_2 = 0.00005$, $e_1 = 1$, $e_2 = 1$, $\alpha = 0.0025$, $u_1 = 0.05$, $u_2 = 0.1$, $\epsilon = 0.20$, $\rho_1 = 0.5$, $\rho_2 = 0$ and other parameters are as in Table 1.

Figure 3. Simulations of system Equation (1) using various initial conditions. In this case, $\Lambda = 0.1$, $\beta_2 = 0.000011$, $\beta_1 = 0.000075$, $e_1 = 1$, $e_2 = 0.1$, $\alpha = 0.0025$, $u_1 = 0.05$, $u_2 = 0.1$, $\epsilon = 0.20$, $\rho_1 = 0.5$, $\rho_2 = 0$ and other parameters are as in Table 1. The corresponding reproduction number is $R_0 = 0.9446$. (a) Infected time series and (b) Pathogen time series.

Numerical simulations to establish the above theoretical analysis and discuss more dynamical behaviour of system (1). Runge-Kutta Fehlberg fourth-fifth order method is used to solve the system of equations in Equation (1) and results are plotted graphically.

5.2.1. Numerical simulation with both controls
Figure 3 shows the global stability of the disease-free equilibrium. Figure 3(a) describes the human size infected with dysentery diarrhoea. It shows that all solution trajectories representing infected humans with dysentery diarrhoea appear to be widespread initially and are monotonically decreasing. Finally, the infected humans drop to zero. The pathogen population is also eliminated from the community when the reproduction number is less than unity (Figure 3(b)).

Figure 4 shows that the disease is endemic in the population. For very small perturbation out of the $S$-axis all solution trajectories converge to the endemic equilibrium except
Figure 4. Simulations of system Equation (1) using various initial conditions. In this case, $\Lambda = 20$, $\beta_2 = 0.000011$, $\beta_1 = 0.000075$, $e_1 = 1$, $e_2 = 1$, $\alpha = 0.0025$, $u_1 = 0.05$, $u_2 = 0.1$, $\varepsilon = 0.20$, $\rho_1 = 0.5$, $\rho_2 = 0$ and other parameters are as in Table 1. The corresponding reproduction number is $R_0 = 25.2917$. Infected humans time series and (b) Pathogen time series.

Figure 5. Variations of the infected humans and pathogen population by varying the intervention efficacy. In this case, the initial values are $(S(0), I(0), R(0), B(0)) = (2000, 10, 10, 10)$, $\Lambda = 2$, $\beta_2 = 0.00011$, $\beta_1 = 0.00075$, $\alpha = 0.0025$, $u_1 = 0.05$, $u_2 = 0.1$, $\varepsilon = 0.20$, $\rho_1 = 0.5$, $\rho_2 = 0$ and other parameters are as in Table 1. (a) Infected humans time series and (b) Pathogen time series.

Those on this axis which stay there forever and converge to $E_0$ along this axis. The convergence of these sufficiently close trajectories to $E_0$ to the endemic equilibrium for any positive initial values shows that the system is uniformly persistent which is compatible with Theorem 4.4. As a consequence, we note from Figure 4(a and b) that for $R_0 > 1$ all solution trajectories starting in the open set $D$ converge to the equilibrium point $\bar{x} \in K$, the compact absorbing set in $D$, for sufficiently large time $t$. The results thus obtained are compatible with Theorem 4.5.

5.2.2. The effect of efficacy of treatment and sanitation

In Figure 5, the variation of infected humans and pathogen population is shown for different values of treatment efficacy $e_1$ and sanitation efficacy $e_2$. It is found that as the intervention efficacy increases, the infected humans and pathogen population decreases. This signifies that by increasing the intervention efficacy, the spread of the infectious disease can be reduced. However, it cannot be significantly controlled.

5.2.3. The effect of the rate of ingesting shigella through human to human interaction

In Figure 6, the variation of infected humans and pathogen population is shown for different values of the transmission rate $\beta_2$. It is found out that as the infection rate $\beta_2$ increases, the infected humans and pathogen population increases. This signifies that the spread of
Fig. 6. Variations of the infected humans and pathogen population by varying the rate of ingesting shigella ($\beta_2$). In this case, the initial values are $(S(0), I(0), R(0), B(0)) = (2000, 10, 10, 10)$, $\Lambda = 2$, $\beta_1 = 0.00075$, $\alpha = 0.0025$, $u_1 = 0.05$, $u_2 = 0.1$, $\varepsilon = 0.20$, $\rho_1 = 0.5$, $\rho_2 = 0$ and other parameters are as in Table 1. (a) Infected humans time series and (b) Pathogen time series.

Fig. 7. Simulations of system Equation (1) with and without controls. In this case, the initial values are $(S(0), I(0), R(0), B(0)) = (1000, 500, 100, 200)$, $\Lambda = 20$, $\beta_2 = 0.000011$, $\beta_1 = 0.000075$, $e_1 = 1$, $e_2 = 1$, $\alpha = 0.0025$, $\varepsilon = 0.20$, $\rho_1 = 0.5$, $\rho_2 = 0$. The reproduction number is $R_0 = 29.9087$ without controls and $R_0 = 7.1108$ with controls. (a) Infected time series and (b) Pathogen time series.

Dysentery diarrhoea disease can be controlled by decreasing the infection rate $\beta_2$. This can be decreased through vaccination of the susceptible population.

5.2.4. Numerical simulation with and without controls

It is pointed out in Section 3 that treatment and sanitation have roles in controlling the disease by reducing the reproduction number. For instance, Figure 7(a and b) describe the humans size infected with dysentery diarrhoea and pathogen population with the intervention of constant treatment and sanitation and without controls respectively. It is apparent from these graphs that it is possible to decrease the infected and pathogen population using controls. In this case $R_0 = R_1 + R_2 = 2.7751 + 27.1336 = 29.9087$ without controls and $R_0 = R_1 + R_2 = 0.5594 + 7.1108 = 7.1108$ with the application of controls.

6. Discussion and conclusions

In this paper, we have proposed a deterministic compartmental dysentery epidemic model with the application of constant controls and analysed the global stability of the system. The environment is assumed a transition. Lyapunov–LaSalle and geometric methods were
used to prove the global stability of the disease-free and endemic equilibrium respectively and obtained new global stability results.

It is established that the basic reproduction number is a sharp threshold parameter and completely determines the global dynamics of the system (Theorem 4.1 and 4.2). It is found out that if $R_0 \leq 1$, the disease dies out. On the other hand, if $R_0 > 1$, the disease is persistent in the community.

Assuming that the environment acts as a transition, transition-reservoir or reservoir of infection, three different $R_0$ expressions are derived [3,8,28][8,26,41,44] considering one of these scenarios and derive $R_0$ can have different structure. Therefore, misinterpreting the role of pathogen growth and shedding may result in overestimating or underestimating the control efforts required in eradicating the infection. Otherwise, the environment becomes a reservoir of the pathogen and targeting the host population will not be sufficient to eradicate the infection.

The dynamics of the dysentery diarrhoea disease can be very complex because of the number of factors involved. In fact, the uniqueness of the EE is highly dependent on the pathogen growth and decay behaviours in the environment. Considering a generalized logistic growth of the pathogen in the environment and limiting the pathogen decay rate to a certain range may result in multiple endemic equilibria leading to rich dynamics of the considered model [33].

This study considers homogeneous mixing population by ignoring the spatial distribution of the population. Many relevant questions can be answered by homogeneous models. However, in other situations heterogeneity is important, i.e., induced by age or spatial structure of the population. Successful infection control can not be achieved by ignoring space (the rate of spatial spread of a pathogen and the influence of density of populations in different classes). For instance, the authors in [39,40] stressed that stationary pattern seen in the spatial distribution of a disease implies a stable state regardless of the initial conditions. Studies on pattern transitions and complexity in spatial epidemics show that a stationary pattern seen in the spatial distribution of a disease implies a stable state regardless of the initial conditions [40,41]. On the other hand, pattern transitions between spatio-temporal can mean an early warning for disease outbreak. They represent either quasi-periodic or oscillatory waves, temporal or spatio-temporal chaos, or even turbulence [19,39]. Human behaviour such as contact precautions and social distancing clearly influence disease prevalence, but disease prevalence can in turn alter human behaviour, forming a coupled, nonlinear system [46,47].

The sufficient condition for the global stability of the endemic equilibrium,

$$\mu > \max \{\alpha, d + \gamma (1 - \rho_1) + e_1 u_1 (1 - \rho_2) - \alpha, \epsilon + \gamma \rho_1 + u_1 \rho_2 - \alpha\},$$

is obtained by choosing matrix-valued function $P(x)$ and estimating the Lozinskiĭ measure for a $6 \times 6$ matrix. This sufficient condition obtained can be improved by choosing different matrix-valued function $P(x)$ and matrix norm. Consequently, the restrictions on the parameters may be weakened and get different sufficient conditions for global stability as far as $R_0 > 1$. Our results agree with the authors in [42] if the parameters $\rho_1$, $\rho_2$, $\alpha$, $d$, $u_1$, $u_2$ are all considered to be zero. The system rules out any complicated behaviour such as limit cycles, homoclinic and heteroclinic orbits (Theorem 4.5). Numerical simulations have found no such behaviour for any parameter values.
It is found out that the implementation of constant controls treatment and sanitation reduce the disease in the community. However, the implementation of constant intervention rates leaves several open questions to social planners which wish to control and/or eradicate the disease in a short period of time. Thus, the implementation of constant and continuous controls is recommended to have a complete picture of the system outcome.

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