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Stability analysis and Bifurcation for an Bacterial Meningitis Spreading with Stage Structure: Mathematical Modeling

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Abstract

We introduce a model to describe the evolution of bacterial meningitis epidemics in a non-constant population. We derive the value of the basic reproduction number of our model. We analyze the local and global stability of the disease-free and endemic equilibria. We confirm the results by a numerical analysis of the model.

Keywords: Compartmental models, Epidemics, Bacterial meningitis, Lyapunov functions.

AMS Subject Classification: (2020) 92D30, 34D20, 34D23.

تحليل الاستقرار والتفرعات لانتشار التهاب السحايا الجرثومي مع الفئات العمرية: نمذجة رياضية

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الخلاصة

نقدم إنموذجًا لوصف تطور أوبئة التهاب السحايا الجرثومي في مجموعة سكانية غير ثابتة. نشق قيمة رقم الاستساح الأساسي لنموذجنا. نقوم بتحليل الاستقرار المحلي والكلّي لنقاط التوازن الخالية من المرض والمتوطن. نختتم بالتحليل العددي للنموذج لتأكيد النتائج التي توصلنا إليها.

1. Introduction

A firm grasp of the mechanisms of disease spread is fundamental to understanding, managing and preventing epidemics. Mathematical modeling of infectious diseases, over the last century, has tackled this topic with various approaches and assumptions. Among other models, epidemics have been modelled via a system of ordinary differential equations (ODEs) [1,2,3,4,5,6,7], partial differential equations (PDEs) [8,9,10,11], delay differential equations (DDEs) [12,13,14], stochastic differential equations (SDEs) [15,16,17,18] and networks [19, 20, 21, 22,23].

Each disease depends on its specific characteristics such as the existence of asymptomatic spreaders, the availability of a vaccine, etc., which requires specific modelling assumptions. Modellers set the level of precision in the description of all the nuances with a trade-off between detail and analytical tractability. In particular, in the last year, ever-growing attention has been devoted to the ongoing COVID-19 pandemic [24,25,26,27]. Many researchers tried to explain the fast diffusion of this virus and to predict how different containment techniques may obstruct it [28,29,30].

In this paper, we focus on another specific disease, namely bacterial meningitis, via a system of ODEs which is presented in Section 2. The three most common bacterial agents of this disease are *Streptococcus pneumoniae* (pneumococcus), *Neisseria meningitidis* (meningococcus), and *Haemophilus influenzae* (Hib) [31,32]. In the past, the lethality of meningitis exceeded 50% and even with more modern therapies, it still ranges between 5% and 15% [33,32]. Even when non-lethal, meningitis can have serious health complications, such as memory problems, hearing loss, brain damage and paralysis [34,35]. A vaccine has been available and routinely distributed since the 1980s.

Similar to COVID-19 the diffusion of the disease may happen when an infected individual sneezes or coughs. However, meningitis can be contracted also by eating food contaminated with *Listeria monocytogenes* [36,37]. An interesting characteristic of meningitis, which we decided to include in our model, is the division of the susceptible population into individuals most exposed to the disease (under 20 years old) and less exposed [38].

The organization of this paper is as follows. The model is introduced in Section 2. The boundedness of solutions, the equilibria points and the basic reproduction number are given in Section 3. Sections 4 and 5 are devoted to the necessary conditions to understand the dynamic behavior of the model. The criteria for local and global stability of the nonnegative equilibria are also presented for the proposed model. Section 6 is devoted to numerical simulations. Finally, Section 7 is dedicated to our conclusions and results.

2. Model formulation

In this section, we first construct a biological model which comprises five equations every one of these equations represents part of the population. All individuals in the first equation represent the susceptible class but under 20 years old and they are most exposed to disease and denoted by (S_n). The individuals less vulnerable to disease (20 years old and older) are represented by the second equation and denoted by (S_a). The vaccinated individuals are represented by the third equation and denoted by (V). The fourth equation represents the infected individuals and is denoted by (I). The last equation denoted by (R) represents the recovered individuals. From the above assumptions, the biological model of Bacterial Meningitis can be described by the following system of nonlinear ODEs:

$$\left\{ \begin{array}{l} \frac{dS_n}{dt} = (1 - \omega)\pi + (1 - \rho)\gamma R - (\lambda_1 + \mu)S_n - \beta_1 S_n I, \\ \frac{dS_a}{dt} = \omega\pi + \rho\gamma R - (\lambda_2 + \mu)S_a - \beta_2 S_a I, \\ \frac{dV}{dt} = \lambda_1 S_n + \lambda_2 S_a - \mu V - \sigma\beta_3 V I, \\ \frac{dI}{dt} = (\beta_1 S_n + \beta_2 S_a + \sigma\beta_3 V)I - (\mu + \varepsilon + \alpha)I, \\ \frac{dR}{dt} = \alpha I - (\mu + \gamma)R. \end{array} \right. \quad (1)$$

With initial conditions $S_n(0) > 0, S_a(0) > 0, V(0) \geq 0, I(0) \geq 0, R(0) \geq 0$.

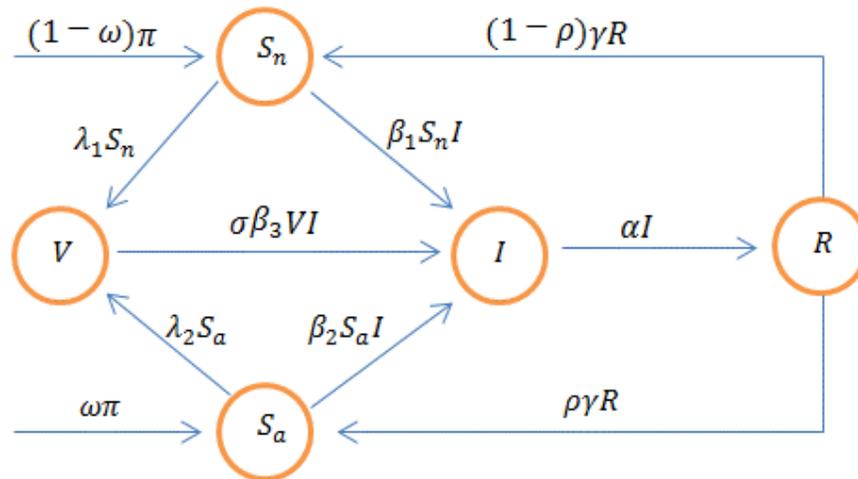


Figure 1: Flow diagram for system (1).

For clarity, we omit the arrows that represent the death in each compartment. We recall that the death rate is μ for all compartments except I , it increases to $\mu + \varepsilon$ due to the non-negligible mortality of the disease. The parameters in the model (1) are as follows: π is the recruitment rate with fraction $\omega \in [0, 1]$ which divides the susceptible individuals entering the population into more and less exposed, μ is the natural death rate, $\lambda_i, i = 1, 2$, are the vaccination rates of the two classes of susceptible individuals, $\beta_i, i = 1, 2, 3$, are the infection rates, α is the recovery rate from the disease, ε is the increase in the death rate

due to disease, σ is the failure in vaccination $\sigma \in [0, 1]$, and γ is the loss in immunity rate. The flow between the various compartments of the system (1) is depicted in Figure 1.

3. Basic properties and existence equilibria points

In this section, we discuss the boundedness and the existence of equilibrium points and the definition of the basic reproduction number for system (1). Clearly, by adding all the equations of the model (1), we obtain the equation governing the total population $N(t)$. This equation can be bounded from above by

$$\frac{dN}{dt} \leq \pi - \mu N,$$

Where $(t) = S_n + S_a + V + I + R$. In particular, we remark that the total population is not constant, contrary to what is assumed in most compartmental models. By solving the last linear differential equation, we get that the total population is asymptotically bounded by the constant:

$$\lim_{t \rightarrow +\infty} N(t) \leq \frac{\pi}{\mu}.$$

Hence, the biologically feasible is a closed set.

$$\Omega = \left\{ (S_n, S_a, V, I, R) \in \mathbb{R}_+^5, S_n + S_a + V + I + R \leq \frac{\pi}{\mu} \right\},$$

which is a positively invariant for system (1), for initial conditions starting in Ω . Now, we discuss the existing conditions of all equilibrium points of the system (1). System(1) has up to two equilibrium points that depend on the values of its parameters. The disease-free equilibrium point denoted by e_0 which is given by $e_0 = (S_{n0}, S_{a0}, V_0, 0, 0)$, where

$$\begin{cases} S_{n0} = \frac{(1-\omega)\pi}{\lambda_1 + \mu}, \\ S_{a0} = \frac{\omega\pi}{\lambda_2 + \mu}, \\ V_0 = \frac{\lambda_1 S_{n0} + \lambda_2 S_{a0}}{\mu}. \end{cases} \quad (2)$$

The basic reproduction number of system (1) by using the results are firstly introduced in [39], then they are generalized in [40, 41]. We refer in particular to [42, Prop. 1] for a detailed application of this method. Thus, the basic reproduction number can be written by

$$\mathcal{R}_0 = \frac{\pi[(1-\omega)(\lambda_2 + \mu)(\mu\beta_1 + \sigma\beta_3\lambda_1) + \omega(\lambda_1 + \mu)(\mu\beta_2 + \sigma\beta_3\lambda_2)]}{\mu(\lambda_1 + \mu)(\lambda_2 + \mu)(\mu + \varepsilon + \alpha)} \quad (3)(3)$$

The other equilibrium point of system(1), which exists in the biologically relevant region if $\mathcal{R}_0 > 1$ is the endemic equilibrium point, and is denoted by e_1 . The point e_1 satisfies the following system

$$\begin{cases} (1 - \omega)\pi + (1 - \rho)\gamma R - (\lambda_1 + \mu)S_n - \beta_1 S_n I = 0, \\ \omega\pi + \rho\gamma R - (\lambda_2 + \mu)S_a - \beta_2 S_a I = 0, \\ \lambda_1 S_n + \lambda_2 S_a - \mu V - \sigma\beta_3 V I = 0, \\ (\beta_1 S_n + \beta_2 S_a + \sigma\beta_3 V)I - (\mu + \varepsilon + \alpha)I = 0, \\ \alpha I - (\mu + \gamma)R = 0, \\ I \neq 0. \end{cases} \quad (4) \quad (4)$$

From the first, the second and the fifth equations of system(4), we obtain

$$\left\{ \begin{array}{l} S_{n1} = \frac{(1-\omega)\pi(\mu+\gamma)+\alpha\gamma(1-\rho)I_1}{(\mu+\gamma)(\lambda_1+\mu+\beta_1I_1)}, \\ S_{a1} = \frac{\omega\pi(\mu+\gamma)+\alpha\gamma\rho I_1}{(\mu+\gamma)(\lambda_2+\mu+\beta_2I_1)}, \\ R_1 = \frac{\alpha I_1}{\mu+\gamma}. \end{array} \right. \tag{5}$$

Therefore, by substituting the values of system(5) in the remaining equations of system(4), we obtain

$$f(V, I) = r_1I^2 + r_2I + r_3VI^3 + r_4VI^2 + r_5VI + r_6V + r_7 = 0, \tag{6}$$

$$g(V, I) = n_1I^2 + n_2I + n_3VI^2 + n_4VI + n_5V + n_6 = 0. \tag{7}$$

Here

$$\begin{aligned} r_1 &= \alpha\gamma(\lambda_1\beta_2(1 - \rho) + \rho\lambda_2\beta_1), \\ r_2 &= \pi(\mu + \gamma)((1 - w)\lambda_1\beta_2 + w\lambda_2\beta_1) + \alpha\gamma(\lambda_1(1 - \rho)(\lambda_2 + \mu) + \rho\lambda_2(\lambda_1 + \mu)), \\ r_3 &= -\sigma\beta_1\beta_2\beta_3(\gamma + \mu), \\ r_4 &= -(\gamma + \mu)(\mu\beta_1\beta_2 + \sigma\beta_2\beta_3(\lambda_1 + \mu) + \sigma\beta_1\beta_3(\lambda_2 + \mu)), \\ r_5 &= -(\gamma + \mu)(\mu\beta_2(\lambda_1 + \mu) + \mu\beta_1(\lambda_2 + \mu) + \sigma\beta_3(\lambda_1 + \mu)(\lambda_2 + \mu)), \\ r_6 &= -\mu(\gamma + \mu)(\lambda_1 + \mu)(\lambda_2 + \mu), \\ r_7 &= \pi(\gamma + \mu)(\lambda_1(1 - w)(\lambda_2 + \mu) + \lambda_1w(\lambda_1 + \mu)), \\ n_1 &= \beta_1\beta_2(\alpha\gamma - (\gamma + \mu)(\mu + \epsilon + \alpha)), \\ n_2 &= \pi\beta_1\beta_2(\gamma + \mu) + \alpha\gamma(\beta_1(1 - \rho)(\lambda_2 + \mu) + \rho\beta_2(\lambda_1 + \mu) \\ &\quad - (\gamma + \mu)(\mu + \epsilon + \alpha)(\beta_1(\lambda_2 + \mu) + \beta_2(\lambda_1 + \mu))), \\ n_3 &= \sigma\beta_1\beta_2\beta_3(\gamma + \mu) \\ n_4 &= \sigma\beta_3(\gamma + \mu)(\beta_2(\lambda_1 + \mu) + \beta_1(\lambda_2 + \mu)), \\ n_5 &= \sigma\beta_3(\gamma + \mu)(\lambda_1 + \mu)(\lambda_2 + \mu), \\ n_6 &= -(\gamma + \mu)(\mu + \epsilon + \alpha)(\lambda_1 + \mu)(\lambda_2 + \mu)(R_0 - 1). \end{aligned}$$

Clearly, as $I \rightarrow 0$, the two isoclines reduce to

$$f(V) = r_6V + r_7 = 0 \tag{8}$$

$$g(V) = n_5V + n_6 = 0. \tag{9}$$

Equations (8) and (9) have a unique positive intersection point with V -axis, which is given by

$$\bar{V} = -\frac{r_7}{r_6},$$

$$\hat{V} = -\frac{n_6}{n_5}.$$

Then, straightforward computations show that the isoclines (6) and (7) have a unique intersection positive point (V_1, I_1) when $\bar{V} < \hat{V}$, provided that

$$\frac{dI}{dV} = -\frac{\partial f/\partial V}{\partial f/\partial I} > 0, \tag{10}$$

$$\frac{dI}{dV} = -\frac{\partial g/\partial V}{\partial g/\partial I} < 0. \tag{11}$$

Now, in addition to (10)-(11), the condition $R_0 > 1$ guarantees the existence of e_1 .

4. Local Stability analysis

In this Section, we discuss the local stability of the two equilibria points that are described in Section 3.

4.1 Disease free equilibrium point

To analyze the local stability of the disease-free equilibrium point that is given in (2), we look at the eigenvalues of the Jacobian evaluated in that point. The Jacobian of the system (1) is

$$J(e^*) = \begin{bmatrix} -(\lambda_1 + \mu + \beta_1 I) & 0 & 0 & -\beta_1 S_n & (1 - \rho)\gamma \\ 0 & -(\lambda_2 + \mu + \beta_2 I) & 0 & -\beta_2 S_a & \rho\gamma \\ \lambda_1 & \lambda_2 & -(\mu + \sigma\beta_3 I) & -\sigma\beta_3 V & 0 \\ \beta_1 I & \beta_2 I & \sigma\beta_3 I & M(S_n, S_a, V) & 0 \\ 0 & 0 & 0 & \alpha & -(\mu + \gamma) \end{bmatrix}, \quad (12)$$

where

$$M(S_n, S_a, V) = (\beta_1 S_n + \beta_2 S_a + \sigma\beta_3 V) - (\mu + \varepsilon + \alpha).$$

In particular, evaluating (12) in (2), we obtain

$$J(e_0) = \begin{bmatrix} -(\lambda_1 + \mu) & 0 & 0 & -\beta_1 S_{n0} & (1 - \rho)\gamma \\ 0 & -(\lambda_2 + \mu) & 0 & -\beta_2 S_{a0} & \rho\gamma \\ \lambda_1 & \lambda_2 & -\mu & -\sigma\beta_3 V_0 & 0 \\ 0 & 0 & 0 & M(S_{n0}, S_{a0}, V_0) & 0 \\ 0 & 0 & 0 & \alpha & -(\mu + \gamma) \end{bmatrix}. \quad (13)$$

Four of the eigenvalues of (13) are clearly $-(\lambda_1 + \mu) < 0$, $-(\lambda_2 + \mu) < 0$, $-\mu < 0$ and $-(\mu + \gamma) < 0$. The remaining eigenvalue $M(S_{n0}, S_{a0}, V_0)$ can be checked to be ≥ 0 if and only if the basic reproduction number \mathcal{R}_0 that is given by (3), is ≥ 1 . Hence, if $\mathcal{R}_0 < 1$, the disease-free equilibrium point that is given in (2) is locally stable, whereas if $\mathcal{R}_0 > 1$ the disease-free equilibrium point that is given in (2) is locally unstable.

4.2 Endemic equilibrium point

To analyze the local stability of the endemic equilibrium point that is given in (5), we use a similar strategy to the one that is used in [27, Sec. 4]. The Jacobian of the system (1) is given in (12). If we evaluate it at the endemic equilibrium point, we obtain

$$J(e_1) = \begin{bmatrix} -(\lambda_1 + \mu + \beta_1 I_1) & 0 & 0 & -\beta_1 S_{n1} & (1 - \rho)\gamma \\ 0 & -(\lambda_2 + \mu + \beta_2 I_1) & 0 & -\beta_2 S_{a1} & \rho\gamma \\ \lambda_1 & \lambda_2 & -(\mu + \sigma\beta_3 I_1) & -\sigma\beta_3 V_1 & 0 \\ \beta_1 I_1 & \beta_2 I_1 & \sigma\beta_3 I_1 & 0 & 0 \\ 0 & 0 & 0 & \alpha & -(\mu + \gamma) \end{bmatrix} \quad (14)$$

since from the fourth equation of (4) we obtain $M(S_{n1}, S_{a1}, V_1) = 0$. Applying Gershgorin's first theorem, we obtain that the eigenvalues of (14) lie in the union of the following circles in the complex plane:

- center in $-(\lambda_1 + \mu) - \beta_1 I_1 + 0_i$, radius $R_1 = \min\{\lambda_1 + \beta_1 I_1, \beta_1 S_{n1} + (1 - \rho)\gamma\}$;
- center in $-(\lambda_2 + \mu) - \beta_2 I_1 + 0_i$, radius $R_2 = \min\{\lambda_2 + \beta_2 I_1, \beta_2 S_{a1} + \rho\gamma\}$;
- center in $-\mu - \sigma\beta_3 I_1 + 0_i$, radius $R_3 = \min\{\lambda_1 + \lambda_2 + \sigma\beta_3 V_1, \sigma\beta_3 I_1\}$;
- center in $0 + 0_i$, radius $R_4 = \min\{(\beta_1 + \beta_2 + \sigma\beta_3)I_1, \beta_1 S_{n1} + \beta_2 S_{a1} + \sigma\beta_3 V_1 + \alpha\}$;
- center in $-(\mu + \gamma) + 0_i$, radius $R_5 = \min\{\gamma, \alpha\}$.

The only circle which does not provide an eigenvalue with a negative real part is the fourth, hence, (14) has four eigenvalues with a negative real part and a fifth to be determined.

However, to the best of our efforts, we are not able to analytically prove the local stability of the endemic equilibrium point for values of $\mathcal{R}_0 > 1$. We conjecture that this is true. Our numerical exploration of the model seems to confirm this result, but due to the high dimension of the system, and the non-trivial Jacobian matrix, an analytical proof seems to be hardly achievable.

5.Global Stability analysis

In this section, we verify the conditions that guarantee global stability analysis of the two equilibria that are found in Section 3 of the system (1). We prove that exploiting LaSalle’s method [43] through the definition of specific Lyapunov functions.

5.1 Disease-free equilibrium point

We introduce the following restrictions on the variable space:

$$\begin{aligned} \left[1 - \frac{S_n}{S_{n0}} + \frac{S_n V}{S_{n0} V_0} \left(1 - \frac{S_{n0}}{S_n}\right)\right] &\leq 0, \\ \left[1 - \frac{S_a}{S_{a0}} + \frac{S_a V}{S_{a0} V_0} \left(1 - \frac{S_{a0}}{S_a}\right)\right] &\leq 0 \\ \alpha I - (\mu + \gamma)R &\leq 0. \end{aligned} \tag{15}$$

If the initial conditions of the system lie in the set that is described by (15), we are able to prove the following:

Theorem 1. For orbits evolving in the set described by (15), if $\mathcal{R}_0 \leq 1$, then the disease-free equilibrium point e_0 of the system(1) is asymptotically stable.

Proof. We introduce the following Lyapunov function:

$$L_1 = \int_{S_{n0}}^{S_n} \left(1 - \frac{S_{n0}}{x}\right) dx + \int_{S_{a0}}^{S_a} \left(1 - \frac{S_{a0}}{x}\right) dx + \int_{V_0}^V \left(1 - \frac{V_0}{x}\right) dx + I + R.$$

The derivative of $L_1(t)$ with respect to the time variable t is

$$\frac{dL_1}{dt} = \left(1 - \frac{S_{n0}}{S_n}\right) \frac{dS_n}{dt} + \left(1 - \frac{S_{a0}}{S_a}\right) \frac{dS_a}{dt} + \left(1 - \frac{V_0}{V}\right) \frac{dV}{dt} + \frac{dI}{dt} + \frac{dR}{dt}. \tag{16}$$

After some algebraic simplification, we can rewrite it as follows:

$$\begin{aligned} \left(1 - \frac{S_{n0}}{S_n}\right) \frac{dS_n}{dt} &= \left(1 - \frac{S_{n0}}{S_n}\right) [(1 - \rho)\gamma R - (\lambda_1 + \mu)S_n - \beta_1 S_n I + (\lambda_1 + \mu)S_{n0}] \\ &= (\lambda_1 + \mu)S_{n0} \left[2 - \frac{S_n}{S_{n0}} - \frac{S_{n0}}{S_n}\right] + (1 - \rho)\gamma R \left[1 - \frac{S_{n0}}{S_n}\right] + \beta_1 S_{n0} I \left[1 - \frac{S_n}{S_{n0}}\right] \end{aligned} \tag{17}$$

$$\begin{aligned} \left(1 - \frac{S_{a0}}{S_a}\right) \frac{dS_a}{dt} &= \left(1 - \frac{S_{a0}}{S_a}\right) [\rho\gamma R - (\lambda_2 + \mu)S_a - \beta_2 S_a I + (\lambda_2 + \mu)S_{a0}] \\ &= (\lambda_2 + \mu)S_{a0} \left[2 - \frac{S_a}{S_{a0}} - \frac{S_{a0}}{S_a}\right] + \rho\gamma R \left[1 - \frac{S_{a0}}{S_a}\right] + \beta_2 S_{a0} I \left[1 - \frac{S_a}{S_{a0}}\right] \end{aligned} \tag{18}$$

$$\begin{aligned} \left(1 - \frac{V_0}{V}\right) \frac{dV}{dt} &= \left(1 - \frac{V_0}{V}\right) [\lambda_1 S_n + \lambda_2 S_a - \mu V - \sigma\beta_3 V I - \lambda_1 S_{n0} - \lambda_2 S_{a0} + \mu V_0] \\ &= \frac{\lambda_1 S_{n0} V_0}{V} \left[1 - \frac{S_n}{S_{n0}} - \frac{V}{V_0} + \frac{S_n V}{S_{n0} V_0}\right] + \sigma\beta_3 V_0 I \left[1 - \frac{V}{V_0}\right] \\ &\quad + \frac{\lambda_2 S_{a0} V_0}{V} \left[1 - \frac{S_a}{S_{a0}} - \frac{V}{V_0} + \frac{S_a V}{S_{a0} V_0}\right] + \mu V_0 \left[2 - \frac{V_0}{V} - \frac{V}{V_0}\right] \end{aligned} \tag{19}$$

$$\frac{dI}{dt} = (\beta_1 S_n + \beta_2 S_a + \sigma\beta_3 V)I - (\mu + \varepsilon + \alpha)I. \tag{20}$$

$$\frac{dR}{dt} = \alpha I - (\mu + \gamma)R. \tag{21}$$

Now by substituting equations (17)-(21) in equation (16), we obtain

$$\begin{aligned} \frac{dL_1}{dt} = & (\lambda_1 + \mu)S_{n0} \left[2 - \frac{S_n}{S_{n0}} - \frac{S_{n0}}{S_n} \right] + (1 - \rho)\gamma R \left[1 - \frac{S_{n0}}{S_n} \right] + \beta_1 S_{n0} I \left[1 - \frac{S_n}{S_{n0}} \right] \\ & + (\lambda_{21} + \mu)S_{a0} \left[2 - \frac{S_a}{S_{a0}} - \frac{S_{a0}}{S_a} \right] + \rho\gamma R \left[1 - \frac{S_{a0}}{S_a} \right] + \beta_2 S_{a0} I \left(1 - \frac{S_a}{S_{a0}} \right) \\ & + \frac{\lambda_1 S_{n0} V_0}{V} \left[1 - \frac{S_n}{S_{n0}} - \frac{V}{V_0} + \frac{S_n V}{S_{n0} V_0} \right] + \sigma\beta_3 V_0 I \left[1 - \frac{V}{V_0} \right] \\ & + \frac{\lambda_2 S_{a0} V_0}{V} \left[1 - \frac{S_a}{S_{a0}} - \frac{V}{V_0} + \frac{S_a V}{S_{a0} V_0} \right] + \mu V_0 \left[2 - \frac{V_0}{V} - \frac{V}{V_0} \right] \\ & + (\beta_1 S_n + \beta_2 S_a + \sigma\beta_3 V)I - (\mu + \varepsilon + \alpha)I + \alpha I - (\mu + \gamma)R. \end{aligned}$$

If conditions (15) are satisfied, the largest invariant subset $\frac{dL_1}{dt} \leq 0$, is e_0 . Then as a consequence of LaSalle’s theorem, the disease free equilibrium of system (1) is globally asymptotically stable.

5.2 Endemic equilibrium point

We introduce the following restrictions on the variable space:

$$\begin{aligned} \left[1 - \frac{S_{n1}}{S_n} + \frac{I}{I_1} \left(1 - \frac{S_n}{S_{n1}} \right) \right] & \leq 0, \\ \left[1 - \frac{S_{a1}}{S_a} + \frac{I}{I_1} \left(1 - \frac{S_a}{S_{a1}} \right) \right] & \leq 0, \\ \left[1 - \frac{R}{R_1} + \frac{RS_a}{R_1 S_{a1}} \left(1 - \frac{R_1}{R} \right) \right] & \leq 0, \\ \left[1 - \frac{V_1}{V} + \frac{I}{I_1} \left(1 - \frac{V}{V_1} \right) \right] & \leq 0, \\ \left[1 - \frac{I}{I_1} + \frac{IR}{I_1 R_1} \left(1 - \frac{I_1}{I} \right) \right] & \leq 0. \end{aligned} \tag{22}$$

If the initial conditions of the system lie in the set described by (22), we are able to prove the following:

Theorem 2. For orbits evolving in the set described by (22), if $\mathcal{R}_0 > 1$, the endemic equilibrium point e_1 of (1) is asymptotically stable.

Proof. We introduce the following Lyapunov function:

$$L_2 = \int_{S_{n1}}^{S_n} \left(1 - \frac{S_{n1}}{x} \right) dx + \int_{S_{a1}}^{S_a} \left(1 - \frac{S_{a1}}{x} \right) dx + \int_{V_1}^V \left(1 - \frac{V_1}{x} \right) dx + \int_{I_1}^I \left(1 - \frac{I_1}{x} \right) dx + \int_{R_1}^R \left(1 - \frac{R_1}{x} \right) dx.$$

The derivative of $L_2(t)$ with respect to the time variable t is

$$\frac{dL_2}{dt} = \left(1 - \frac{S_{n1}}{S_n} \right) \frac{dS_n}{dt} + \left(1 - \frac{S_{a1}}{S_a} \right) \frac{dS_a}{dt} + \left(1 - \frac{V_1}{V} \right) \frac{dV}{dt} + \left(1 - \frac{I_1}{I} \right) \frac{dI}{dt} + \left(1 - \frac{R_1}{R} \right) \frac{dR}{dt} \tag{23}$$

After some algebraic simplification we can rewrite it as follows

$$\begin{aligned} \left(1 - \frac{S_{n1}}{S_n} \right) \frac{dS_n}{dt} = & (\lambda_1 + \mu)S_{n1} \left[2 - \frac{S_n}{S_{n1}} - \frac{S_{n1}}{S_n} \right] + \beta_1 S_{n1} I_1 \left[1 - \frac{S_{n1}}{S_n} + \frac{I}{I_1} \left(1 - \frac{S_n}{S_{n1}} \right) \right] \\ & + \frac{(1-\rho)\gamma S_{n1} R_1}{S_n} \left[1 - \frac{R}{R_1} + \frac{RS_n}{R_1 S_{n1}} \left(1 - \frac{R_1}{R} \right) \right]. \end{aligned} \tag{24}$$

$$\begin{aligned} \left(1 - \frac{S_{a1}}{S_a} \right) \frac{dS_a}{dt} = & (\lambda_2 + \mu)S_{a1} \left[2 - \frac{S_a}{S_{a1}} - \frac{S_{a1}}{S_a} \right] + \beta_2 S_{a1} I_1 \left[1 - \frac{S_{a1}}{S_a} + \frac{I}{I_1} \left(1 - \frac{S_a}{S_{a1}} \right) \right] \\ & + \frac{\rho\gamma S_{a1} R_1}{S_a} \left[1 - \frac{R}{R_1} + \frac{RS_a}{R_1 S_{a1}} \left(1 - \frac{R_1}{R} \right) \right]. \end{aligned} \tag{25}$$

$$\begin{aligned} \left(1 - \frac{V_1}{V} \right) \frac{dV}{dt} = & \frac{\lambda_1 S_{n1} V_1}{V} \left[1 - \frac{S_n}{S_{n1}} + \frac{S_n V}{S_{n1} V_1} \left(1 - \frac{S_{n1}}{S_n} \right) \right] + \frac{\lambda_2 S_{a1} V_1}{V} \left[1 - \frac{S_a}{S_{a1}} + \frac{S_a V}{S_{a1} V_1} \left(1 - \frac{S_{a1}}{S_a} \right) \right] \\ & + \mu V_1 \left[2 - \frac{V}{V_1} - \frac{V_1}{V} \right] + \sigma\beta_3 V_1 I_1 \left[1 - \frac{V_1}{V} + \frac{I}{I_1} \left(1 - \frac{V}{V_1} \right) \right] \end{aligned} \tag{26}$$

$$\begin{aligned} \left(1 - \frac{I_1}{I}\right) \frac{dI}{dt} &= \frac{\beta_1 S_{n1} I_1^2}{I} \left[1 - \frac{I}{I_1} + \frac{S_n I^2}{S_{n1} I_1^2} \left(1 - \frac{I_1}{I}\right)\right] + \frac{\beta_2 S_{a1} I_1^2}{I} \left[1 - \frac{I}{I_1} + \frac{S_a I^2}{S_{a1} I_1^2} \left(1 - \frac{I_1}{I}\right)\right] \\ &+ \frac{\sigma \beta_3 V_1 I_1^2}{I} \left[1 - \frac{I}{I_1} + \frac{V I^2}{V_1 I_1^2} \left(1 - \frac{I_1}{I}\right)\right] + (\mu + \varepsilon + \alpha) I_1 \left[2 - \frac{I_1}{I} - \frac{I}{I_1}\right] \end{aligned} \tag{27}$$

$$\left(1 - \frac{R_1}{R}\right) \frac{dR}{dt} = \frac{\alpha I_1 R_1}{R} \left[1 - \frac{I}{I_1} + \frac{I R}{I_1 R_1} \left(1 - \frac{I_1}{I}\right)\right] + (\mu + \gamma) R_1 \left[2 - \frac{R}{R_1} - \frac{R_1}{R}\right]. \tag{28}$$

Now by substituting equations (24)-(28) in equation (23), we obtain

$$\begin{aligned} \frac{dL_2}{dt} &= (\lambda_1 + \mu) S_{n1} \left[2 - \frac{S_n}{S_{n1}} - \frac{S_{n1}}{S_n}\right] + \beta_1 S_{n1} I_1 \left[1 - \frac{S_{n1}}{S_n} + \frac{I}{I_1} \left(1 - \frac{S_n}{S_{n1}}\right)\right] \\ &+ \frac{(1-\rho)\gamma S_{n1} R_1}{S_n} \left[1 - \frac{R}{R_1} + \frac{R S_n}{R_1 S_{n1}} \left(1 - \frac{R_1}{R}\right)\right] + (\lambda_2 + \mu) S_{a1} \left[2 - \frac{S_a}{S_{a1}} - \frac{S_{a1}}{S_a}\right] \\ &+ \beta_2 S_{a1} I_1 \left[1 - \frac{S_{a1}}{S_a} + \frac{I}{I_1} \left(1 - \frac{S_a}{S_{a1}}\right)\right] + \frac{\rho \gamma S_{a1} R_1}{S_a} \left[1 - \frac{R}{R_1} + \frac{R S_a}{R_1 S_{a1}} \left(1 - \frac{R_1}{R}\right)\right] \\ &+ \frac{\lambda_1 S_{n1} V_1}{V} \left[1 - \frac{S_n}{S_{n1}} + \frac{S_n V}{S_{n1} V_1} \left(1 - \frac{S_{n1}}{S_n}\right)\right] + \frac{\lambda_2 S_{a1} V_1}{V} \left[1 - \frac{S_a}{S_{a1}} + \frac{S_a V}{S_{a1} V_1} \left(1 - \frac{S_{a1}}{S_a}\right)\right] \\ &+ \mu V_1 \left[2 - \frac{V}{V_1} - \frac{V_1}{V}\right] + \sigma \beta_3 V_1 I_1 \left[1 - \frac{V_1}{V} + \frac{I}{I_1} \left(1 - \frac{V}{V_1}\right)\right] \\ &+ \frac{\beta_1 S_{n1} I_1^2}{I} \left[1 - \frac{I}{I_1} + \frac{S_n I^2}{S_{n1} I_1^2} \left(1 - \frac{I_1}{I}\right)\right] + \frac{\beta_2 S_{a1} I_1^2}{I} \left[1 - \frac{I}{I_1} + \frac{S_a I^2}{S_{a1} I_1^2} \left(1 - \frac{I_1}{I}\right)\right] \\ &+ \frac{\sigma \beta_3 V_1 I_1^2}{I} \left[1 - \frac{I}{I_1} + \frac{V I^2}{V_1 I_1^2} \left(1 - \frac{I_1}{I}\right)\right] + (\mu + \varepsilon + \alpha) I_1 \left[2 - \frac{I_1}{I} - \frac{I}{I_1}\right] \\ &+ \frac{\alpha I_1 R_1}{R} \left[1 - \frac{I}{I_1} + \frac{I R}{I_1 R_1} \left(1 - \frac{I_1}{I}\right)\right] + (\mu + \gamma) R_1 \left[2 - \frac{R}{R_1} - \frac{R_1}{R}\right]. \end{aligned}$$

If the conditions (22) are satisfied, the largest invariant subset $\frac{dL_2}{dt} \leq 0$, is e_1 . Then as a consequence of LaSalle’s theorem, the endemic equilibrium point of system (1) is globally asymptotically stable.

6. Numerical simulation

The interaction between the various compartments of the system (1) exhibits convergence towards either the disease-free equilibrium e_0 , in the case $\mathcal{R}_0 < 1$, or the endemic equilibrium e_1 , in the case $\mathcal{R}_0 > 1$. In this section, we provide numerous numerical simulations of our model to confirm the theoretical discussions that are established in the previous sections. All the simulations of system (1) are executed using the Matlab and MatCont programs. To examine the stability of the equilibria points as a result of variations of the parameters, we have used the following values as initial conditions for the population $(S_n(0), S_a(0), V(0), I(0), R(0))$.

$$\begin{aligned} &(150, 750, 25, 10, 150) ; (500, 1500, 100, 4000, 50); \\ &(300, 1000, 200, 200, 300) ; (1000, 50, 1000, 1000, 750). \end{aligned} \tag{29}$$

We refer to Figures 2 and 3 for plots of solutions to system (1). The values of the parameters that are used in Figure 2 are:

$$\begin{aligned} &\omega = 0.3; \pi = 500; \rho = 0.1; \gamma = 0.3; \lambda_1 = 0.01; \beta_1 = 0.0002; \mu = 0.1; \\ &\lambda_2 = 0.01; \beta_2 = 0.0001; \sigma = 0.001; \beta_3 = 0.00001; \varepsilon = 0.001; \alpha = 0.2. \end{aligned} \tag{30}$$

For the values (30) and in accordance with Theorem 2, Figure 2 shows the convergence towards the endemic point e_1 . In such a setting, meningitis remains endemic.

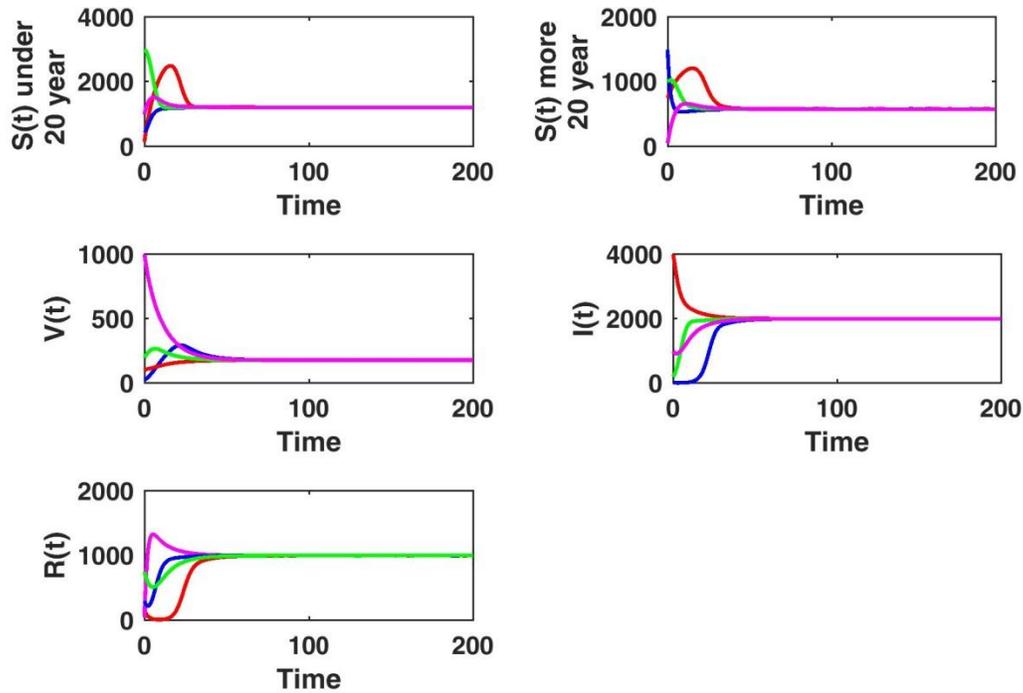


Figure 2: The global asymptotic stability of the endemic equilibrium point e_1 when $\mathcal{R}_0 = 2.567 > 1$. The initial values of each compartment are given in (29), and the parameters in (30).

If we decrease the contact rate between susceptible individuals under 20-year S_n with the infected I to $\beta_1 = 0.00002$, and keep the remaining values listed in equation (30), we bring \mathcal{R}_0 below the threshold value 1. In accordance with Theorem 1, Figure 3 shows the asymptotic stability of the disease-free point e_0 . In such a setting, meningitis becomes extinct, this confirms the intuition that the decrease of the contact rates, even assuming all the other parameters in the model are fixed, allows to control and eradicate the disease.

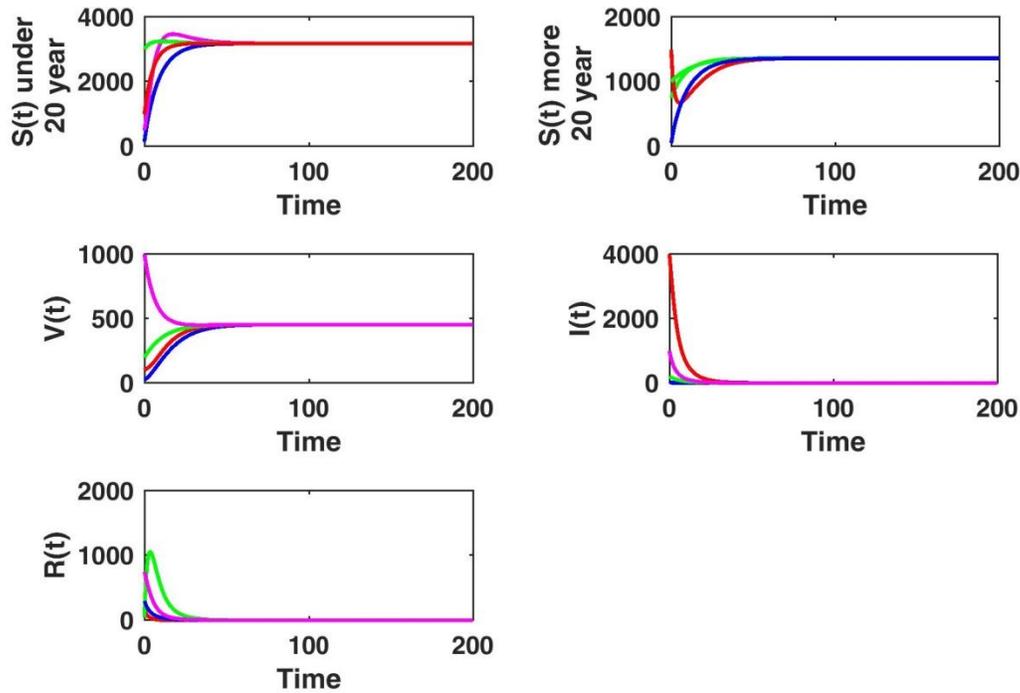


Figure 3: The global asymptotic stability of the disease-free equilibrium point e_0 when $\mathcal{R}_0 = 0.664 < 1$. The initial values of each compartment are given in (29), and the parameters in (30).

In Figure 4, we observe the influence of the parameter λ_1 (vaccination rate of susceptible under 20 years) on the dynamical solution to the model (1). When $\lambda_1 < \lambda_1^* \approx 0.3253$, and keep all the other parameter values constant as in (30), the endemic equilibrium point e_1 is asymptotically stable. However, increasing this value to $\lambda_1 > \lambda_1^* \approx 0.3253$, the disease-free equilibrium point e_0 becomes asymptotically stable. The existence of a bifurcation point between the two chosen values of λ_1 is illustrated in Figures 4a and 4b which is confirmed through the use of the MatCont [44], see Figure 6a. In Figure 5, we show the effect of changing the recovery rate α . Increasing α corresponds to a shortening of the infectious period, i.e. speeding the recovery up. Consider the influence the parameter α has on the basic reproduction number \mathcal{R}_0 . Clearly, if all the other values are fixed, there exists a value $\alpha^* \approx 0.6717$ below which $\mathcal{R}_0 > 1$, and above which $\mathcal{R}_0 < 1$. Using the values (30). if $\alpha < \alpha^*$, the endemic equilibrium e_1 is asymptotically stable.

However, taking $\alpha \geq \alpha^*$, the endemic equilibrium loses its stability, and the trajectory converges towards the disease-free equilibrium e_0 . The existence of a bifurcation point between the two chosen values of α is illustrated in Figures 5a and 5b which is confirmed through the use of the MatCont [44], see Figure 6b. In addition, Figure 7 shows the relationship between \mathcal{R}_0 and several parameters in the model(1).

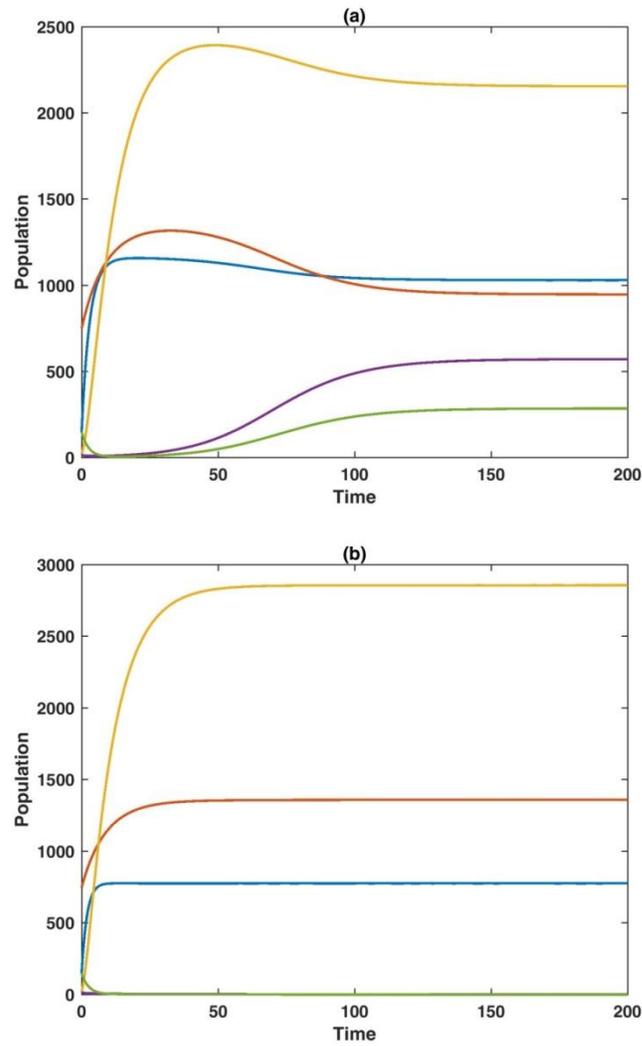


Figure 4: Effect of λ_1 on the dynamics of model (1). (a) For $\lambda_1 = 0.31 < \lambda_1^* \approx 0.3253$ with $\mathcal{R}_0 = 1.034 > 1$. (b) For $\lambda_1 = 0.35 > \lambda_1^* \approx 0.3253$ with $\mathcal{R}_0 = 0.94 < 1$.

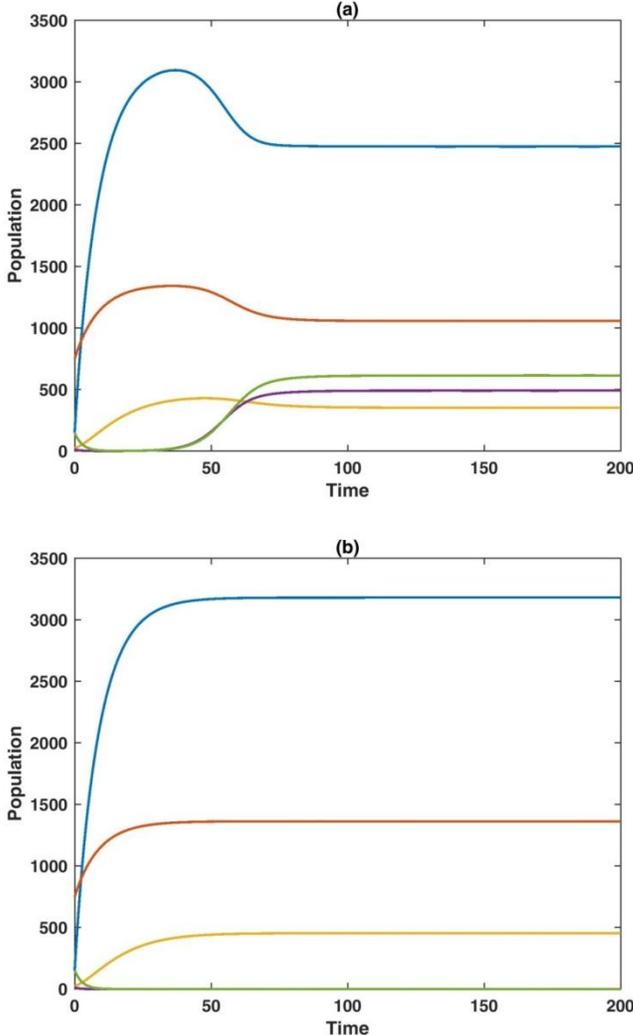


Figure 5: Effect of α on the dynamics of model (1). (a) For $\alpha = 0.6 < \alpha^* \approx 0.6717$ with $\mathcal{R}_0 = 1.31 > 1$. (b) For $\alpha = 0.7 > \alpha^* \approx 0.6717$ with $\mathcal{R}_0 = 0.96 < 1$.

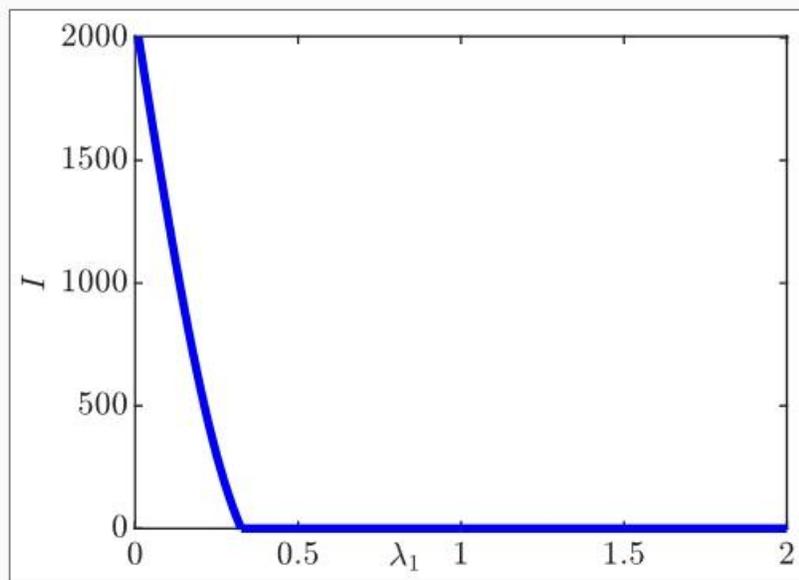
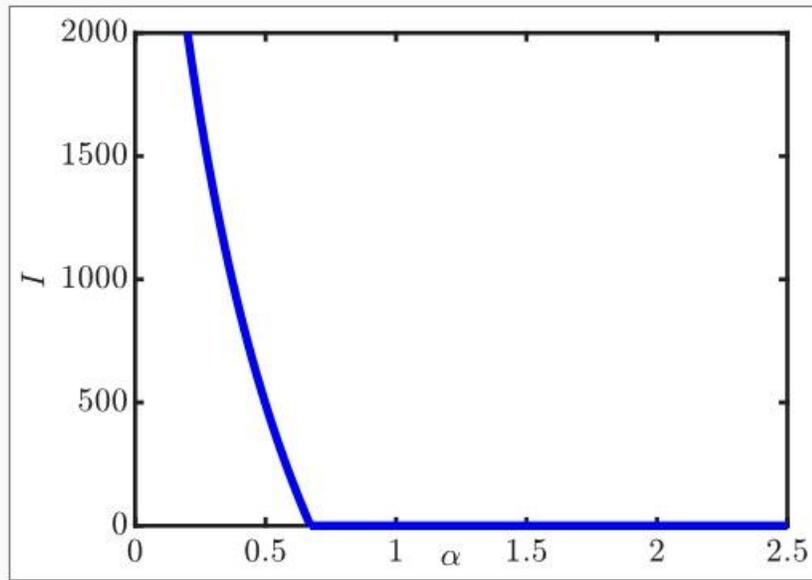
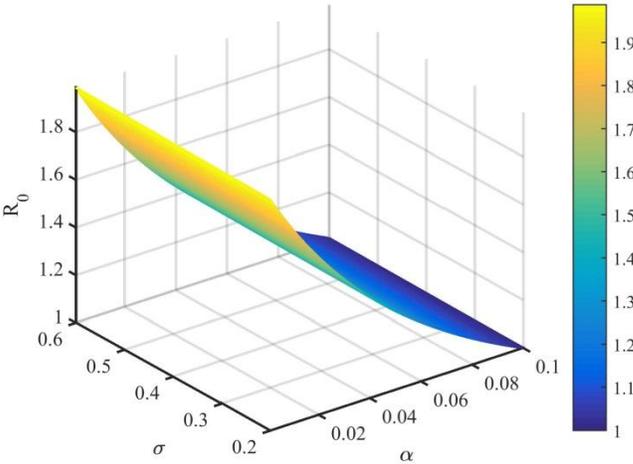
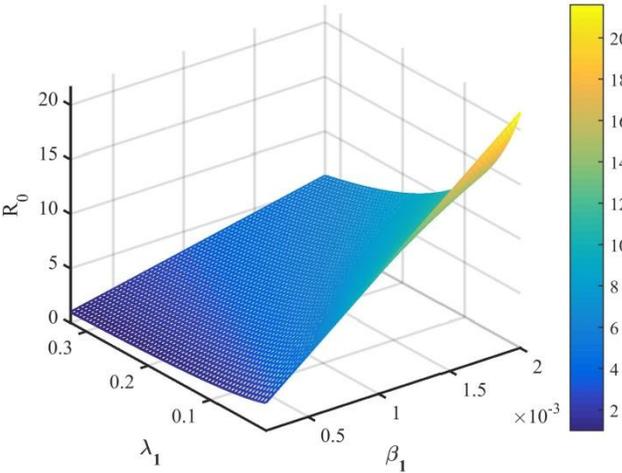
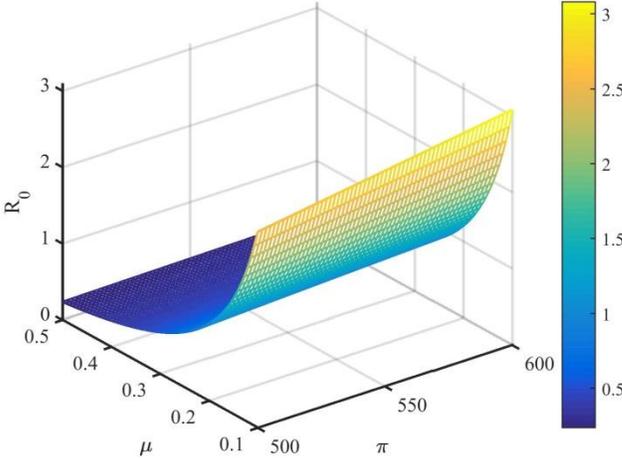


Figure 6: Bifurcation analysis of system (1) for the parameters listed in (30). (a) Bifurcation diagram of the effect of varying λ_1 on the asymptotic values of I . (b) Bifurcation diagram of the effect of varying α on the asymptotic values of I .



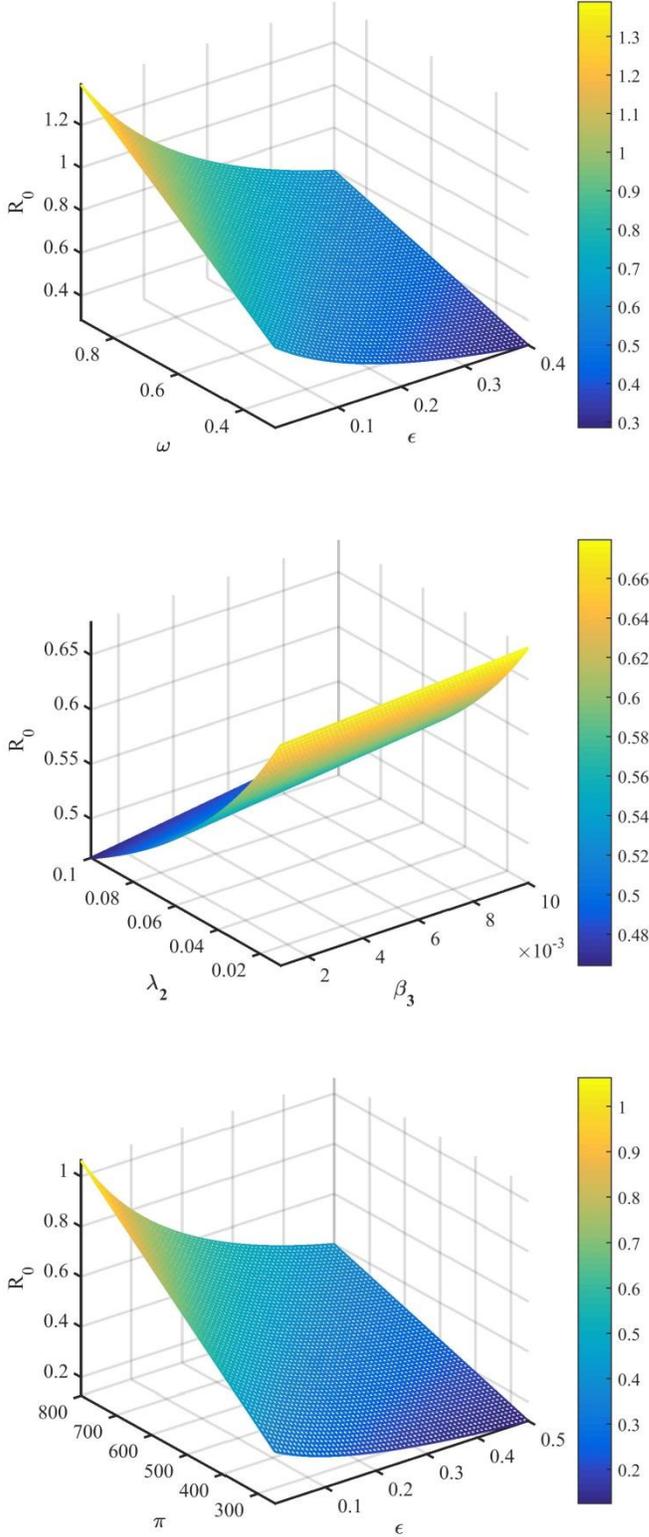


Figure 7: The relationship between \mathcal{R}_0 with some parameters.

7. Conclusions

The behavior of a newly proposed model is analyzed and presented as a nonlinear system of ODE. The model describes the evolution in time of a bacterial meningitis epidemic in a non-constant population. We provided the classic threshold value \mathcal{R}_0 for our model, which proved to be a surprisingly intricate combination of all the parameters in our system. We proved, under some restrictions, that the asymptotic behavior is either convergence towards the disease-free equilibrium point or the endemic equilibrium point. Our numerical analysis confirms the theoretical results regarding the asymptotic behavior of the model. Moreover, our bifurcation analysis provides a glimpse into the possible control measures for such an epidemic. Some of the parameters of the system are embedded in the disease, such as the duration of the immunity window; other parameters such as the contact rates can be reduced through various precautions. Our analysis aims at the qualitative properties of the system, rather than at precise predictions, and we leave the calibration of our model with real-world data as a viable research outlook.

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