



Global Stability of an Epidemic Model with two Infected Stages and Mass-Action Incidence

Mamadou Lamine Diouf^{1,2}, Abderrahman Iggidr¹, Mamadou Sy²

¹ Inria, Université de Lorraine, CNRS.

Institut Elie Cartan de Lorraine, UMR 7502.

ISGMP Bat. A, Ile du Saulcy, 57045 Metz Cedex 01, France.

² UMI-IRD-209 UMMISCO, and LANI

Université Gaston Berger, Saint-Louis, Sénégal.

e-mail: dioufabu@yahoo.fr, Abderrahman.Iggidr@inria.fr, mamadou.sy@ugb.edu.sn

Received: 30 October 2013, accepted: 21 July 2014, published: 31 July 2014

Abstract—The goal of this paper is the establishment of the global asymptotic stability of the model SI with two classes of infected stages and with varying total population size. The incidence used is the mass-action incidence given by

$$(\beta_1 I_1 + \beta_2 I_2) \frac{S}{N}.$$

Existence and uniqueness of the endemic equilibrium is established when the basic reproduction number is greater than one. A Lyapunov function is used to prove the stability of the disease free equilibrium, and the Poincaré-Bendixson theorem allows to prove the stability of the endemic equilibrium when it exists.

Keywords—Epidemic model, Global stability, Mass-action incidence

I. INTRODUCTION

Mathematical analysis became a major tool in the study of the evolution of epidemics. Indeed, more and more models were developed for the

study of some epidemics. In order to model an epidemic disease, the population is divided into various classes. In some cases the population is divided into two senior classes: the class of the susceptible individuals, denoted by S , and the class of the infected individuals, denoted by I . Sometimes, the class of the infected can be split into several classes which allow to highlight the state of the disease. In our case, the infected are divided into two categories, denoted I_1 and I_2 , with I_1 the first stage of the disease and I_2 the worsened case.

If β_1 and β_2 are the per capita transmission rate of the infection in respectively the compartments I_1 and I_2 , there are $\beta_1 I_1 + \beta_2 I_2$ infective contacts. If any contact with a susceptible gives a new infected, then there is $(\beta_1 I_1 + \beta_2 I_2)P(S)$ new infected, where $P(S)$ is the probability for an infected to meet a susceptible. The quantity $(\beta_1 I_1 + \beta_2 I_2)P(S)$ is known in the literature as

the mass action incidence rate. One can notice that most of the classical models of disease use a bilinear mass action incidence $(\beta_1 I_1 + \beta_2 I_2)S$. For example, some of the most famous: the models of Kermack-Mckendrick (1927) and that of Lotka-Volterra (1926).

The goal of our study is to analyze the global stability of the SI_1I_2 model. The system considered can represent, for instance, the modeling of the HIV. For this model we suppose that an infected can have $\frac{S}{N}$ contact of susceptible, then $P(S)$ is given by $\frac{S}{N}$. Also the incidence is given

by $(\beta_1 I_1 + \beta_2 I_2)\frac{S}{N}$, where N represents the total population size: $N = S + I_1 + I_2$. The stability study of systems using this form of incidence is a very interesting subject to which some authors have already devoted some works. The work of C. Simon and J. Jacquez in [18] can be cited. Indeed, these authors addressed the problem for n classes of infected, using some elegant geometrical arguments, but they use a constant recruitment and also they suppose that transition rate from a class of infected to the next class and the rate of disease-induced death are equal. However, in our study, the recruitment is variable and the transition rate (denoted γ) from the first stage of infection I_1 to the second stage I_2 is different from the rate of disease-induced death (denoted d). This makes that for our system the explicit determination of the endemic equilibrium is very difficult if not impossible. So, the stability around possible endemic equilibrium is also more difficult to check than in the case of a constant recruitment. We can also cite more recent works. Particularly, the work of Melese and Gumel in [17], where for the proof of the endemic equilibrium stability, authors make a very strong assumption, which is very difficult to verify. We cite also and specially the work of M. Li, J. Graef, L. Wang and J. Karsai in [15], which deals with a similar system, but the authors used one contact rate. In the works made by C. C. McCluskey (2003) [16] and J. M. Hyman and J. Li (2005) [8], similar models have been considered, but the authors of [8] did not address the question of the global stability of the endemic equilibrium while in [16] the global stability of the endemic equilibrium was proved under the assumption that $\gamma = d$ (i.e., the transition rate from I_1 I_2 is equal to the rate of disease-induced death) and $\beta_1 = \beta_2$. Besides, we mention the work of H. Guo and M. Y. Li (2006), where authors

established the stability of the disease free equilibrium, but for the endemic equilibrium, they used bilinear incidence. We finish by mentioning the paper [10], where the authors considered similar systems but they used bilinear incidence.

The paper is organized as follows. In Section II, we give the differential system governing the time evolution of the number of individuals in different classes is given, we derive the system governing the dynamics of the proportions and we compute the basic reproduction number \mathcal{R}_0 . In Section III, we prove the existence and uniqueness of the endemic equilibrium when \mathcal{R}_0 is greater than one. The global asymptotic stability of the disease free equilibrium is studied in Section IV by using two Lyapunov functions. The local stability of the disease free equilibrium is given in Section V. We prove in Section VI that the system governing the proportions has no periodic orbit and that the endemic equilibrium is globally asymptotically stable. For the stability of the endemic equilibrium, the Poincaré-Bendixson theory is used.

II. THE MODEL

The SI models are well known in the dynamic of population. In this section, we present the SI model used in this paper. The population of size N is divided into subclasses of individuals who are susceptible, infected into the first stage of the disease and infected into the second stage, with sizes denoted by S , I_1 and I_2 .

The model we consider is given by the system

$$\begin{cases} \dot{S} = bN - (\beta_1 I_1 + \beta_2 I_2)\frac{S}{N} - \mu S, \\ \dot{I}_1 = (\beta_1 I_1 + \beta_2 I_2)\frac{S}{N} - (\mu + \gamma)I_1, \\ \dot{I}_2 = \gamma I_1 - (\mu + d)I_2. \end{cases} \quad (1)$$

Where $N = S + I_1 + I_2$ is the total population size; b and μ represent the per capita birth rate and the per capita natural death rate of the population, respectively. β_1 and β_2 are respectively the per capita transmission rate of the compartments I_1 and I_2 . γ denotes the per capita rate of transfer of infected individuals from the infected stage 1 to stage 2, and d is the disease induced death rate.

The total population size N satisfies the equation:

$$\dot{N} = (b - \mu)N - dI_2.$$

The proportions $s = \frac{S}{N}$, $i_1 = \frac{I_1}{N}$ and $i_2 = \frac{I_2}{N}$ satisfy the following differential system:

$$\begin{cases} \dot{s} = b - bs - (\beta_1 i_1 + \beta_2 i_2)s + dsi_2, \\ \dot{i}_1 = (\beta_1 i_1 + \beta_2 i_2)s - (b + \gamma)i_1 + di_1 i_2, \\ \dot{i}_2 = \gamma i_1 - (b + d)i_2 + di_2^2. \end{cases} \quad (2)$$

We determine the basic reproduction number, which represents the number of secondary cases produced by one infective host in an entirely susceptible population.

We denote by $\mathcal{F}_j(s, i_1, i_2)$ the rate of appearance of new infections in compartment j , and by $\mathcal{V}_j(s, i_1, i_2)$ the rate of transfer of individuals in and out the compartment j by all other means. The matrices \mathcal{F} and \mathcal{V} are given by:

$$\mathcal{F} = \begin{bmatrix} 0 \\ (\beta_1 i_1 + \beta_2 i_2)s \\ 0 \end{bmatrix}$$

and

$$\mathcal{V} = \begin{bmatrix} b - bs - (\beta_1 i_1 + \beta_2 i_2)s + dsi_2 \\ -(b + \gamma)i_1 + di_1 i_2 \\ \gamma i_1 - (b + d)i_2 + di_2^2 \end{bmatrix}.$$

The Jacobian matrices at the disease free equilibrium $(1, 0, 0)$ are:

$$D\mathcal{F} = \begin{pmatrix} 0 & 0 & 0 \\ 0 & \beta_1 & \beta_2 \\ 0 & 0 & 0 \end{pmatrix}$$

and

$$D\mathcal{V} = \begin{pmatrix} -b & -\beta_1 & -\beta_2 + d \\ 0 & -(b + \gamma) & 0 \\ 0 & \gamma & -(b + d) \end{pmatrix}.$$

Let:

$$F = \begin{pmatrix} \beta_1 & \beta_2 \\ 0 & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} -(b + \gamma) & 0 \\ \gamma & -(b + d) \end{pmatrix}.$$

It is well known [3] that the basic reproduction number is the spectral radius of the next generation matrix for the model, namely $-FV^{-1}$. The basic reproduction number of system (2) is then

$$\mathcal{R}_0 = \frac{\beta_1}{b + \gamma} + \frac{\beta_2 \gamma}{(b + \gamma)(b + d)}.$$

III. THE EQUILIBRIUM POINTS

The disease free equilibrium is given by DFE=(1,0,0). In the following, we show the existence and uniqueness of the endemic equilibrium for the system (2) assuming that $b \geq d$. Recall that b and d represent the birth and the disease induced rate, respectively.

Proposition III.1. *If $\mathcal{R}_0 > 1$, the endemic equilibrium exists and is unique.*

Proof: At the equilibrium, the third equation of (2) gives:

$$i_1^* = \frac{b + d}{\gamma} i_2^* - \frac{d}{\gamma} i_2^{*2}. \quad (3)$$

Replacing i_1^* by its expression in the second equation of (2), we have after simplification by γi_2^* :

$$\begin{aligned} \beta_1(b + d) - \beta_1 di_2^* + \beta_2 \gamma s^* - (b + \gamma)(b + d) \\ + d(b + d)i_2^* + d(b + d)i_2^{*2} - d^2 i_2^{*2} = 0. \end{aligned} \quad (4)$$

Also, in (4) we replace s^* by its expression given by: $s^* = 1 - i_1^* - i_2^* = 1 - \frac{b + d}{\gamma} i_2^* - \frac{d}{\gamma} i_2^{*2} - i_2^*$, then i_2^* is solution of the polynomial:

$$P(i_2^*) = a_3(i_2^*)^3 + a_2 i_2^{*2} + a_1 i_2^* + a_0 = 0,$$

where

$$\begin{aligned} a_3 &= -\beta_1 \frac{d^2}{\gamma}, \\ a_2 &= 2\beta_1 d \frac{b + d}{\gamma} + \beta_1 d + \beta_2 d - d^2, \\ a_1 &= -\beta_1 \frac{(b + d)^2}{\gamma} - \beta_1(b + d) - \beta_1 d - \beta_2(b + d) \\ &\quad - \beta_2 \gamma + d(b + \gamma) + d(b + d), \text{ and} \\ &= -\mathcal{R}_0(b + d)(b + \gamma) \left(1 + \frac{b + d}{\gamma}\right) \\ &\quad 4 - \beta_1 d + d(2b + d + \gamma) \\ a_0 &= \beta_1(b + d) + \beta_2 \gamma - (b + d)(b + \gamma) \\ &= (b + d)(b + \gamma)(\mathcal{R}_0 - 1). \end{aligned}$$

Using the fact that $\mathcal{R}_0 > 1$, it is easy to show that: $a_3 < 0$, $a_2 > 0$, $a_1 < 0$, and $a_0 > 0$.

We have $P(i_2^*) = 0 \Leftrightarrow Q(i_2^*) = \mathcal{R}_0$, where Q is the polynomial given by

$$\begin{aligned} Q(i_2^*) &= -\frac{a_3}{k} (i_2^*)^3 - \frac{a_2}{k} i_2^{*2} - \frac{a_1}{k} i_2^* + 1, \text{ and} \\ k &= (b + d)(b + \gamma). \end{aligned}$$

We have:

$$Q(0) = 1$$

$$Q(1) = \frac{\beta_1(b^2 + b\gamma + d\gamma) + \gamma(b(b - d + \gamma) + \beta_2(b + \gamma))}{k}.$$

Also

$$Q(1) - \mathcal{R}_0 = b \frac{\beta_1 b + \beta_2 \gamma + b\gamma + \gamma^2 - d\gamma}{k\gamma},$$

which is positive if and only if

$$\beta_1 b + \beta_2 \gamma + b\gamma + \gamma^2 > d\gamma. \tag{5}$$

The relation (5) is satisfied thanks to the assumption $b \geq d$. Thus, $1 = Q(0) < \mathcal{R}_0 < Q(1)$.

Let us localize exactly the domain of i_2^* . We have

$$i_1^* + i_2^* < 1, \tag{6}$$

and since, by relation (3), $i_1^* = \frac{b+d}{\gamma}i_2^* - \frac{d}{\gamma}i_2^{*2}$, we deduce that i_2^* must verify the following inequality:

$$R(i_2^*) = -d i_2^{*2} + (b + d + \gamma)i_2^* - \gamma < 0.$$

The discriminant of the polynomial R is $\Delta_R = (b + d + \gamma)^2 - 4d\gamma = b^2 + 2b(d + \gamma) + (d - \gamma)^2 > 0$. The roots of R are $r_1 = (b + d + \gamma - \sqrt{\Delta_R})/2d$ and $r_2 = (b + d + \gamma + \sqrt{\Delta_R})/2d$. We have: $r_1 < \gamma/2d < r_2$, and with the assumption $b \geq d$ we have $r_2 > 1$. i_2^* must satisfy $0 < i_2^* < \min\{r_1, 1\} \leq \min\{\gamma/2d, 1\}$, that is i_2^* must belong to the interval $I = (0, \min\{r_1, 1\}) \subset (0, \min\{\gamma/2d, 1\})$. On the other hand, we have

$$Q(r_1) - \mathcal{R}_0 = (1/(2k))[b(b + d + \gamma + \sqrt{\Delta_R})] > 0.$$

Since $Q(0) = 1 < \mathcal{R}_0$, $Q(r_1) > \mathcal{R}_0$, and $Q(1) > \mathcal{R}_0$, the graph of Q intersects the horizontal line $y = \mathcal{R}_0$ at least one time in I .

Now let us show that there is exactly one intersection in I .

The derivative of Q is:

$$Q'(i_2^*) = -(1/k)(3a_3 i_2^{*2} + 2a_2 i_2^* + a_1).$$

Note that by Descartes rules of signs there is no negative root. On the other hand, the discriminant of Q' is $\Delta = a_2^2 - 3a_3 a_1$, we then have two cases:

- If $\Delta \leq 0$, Q' is positive on \mathbb{R} .

- If $\Delta > 0$, we have two roots x_1 and x_2 , and $x_1 + x_2 = -(2a_2/3a_3)$. However:

$$\begin{aligned} \frac{-2a_2}{3a_3} &= \frac{4}{3} \frac{b+d}{d} + \frac{2}{3} \left\{ \frac{\gamma}{d} + \frac{\beta_2 \gamma}{\beta_1 d} - \frac{\gamma}{\beta_1} \right\} \\ &= \frac{2}{3} \frac{b+d}{d} + \frac{2}{3} \left\{ \frac{b+d}{d} + \frac{\gamma}{d} + \frac{\beta_2 \gamma}{\beta_1 d} - \frac{\gamma}{\beta_1} \right\} \\ &= \frac{2}{3} \frac{b+d}{d} + \frac{2}{3\beta_1 d} \{ \beta_1(b+d) + \beta_2 \gamma + \beta_1 \gamma - d\gamma \} \\ &= \frac{2}{3} \frac{b+d}{d} + \frac{2}{3\beta_1 d} \{ (b+d)(b+\gamma)\mathcal{R}_0 + \beta_1 \gamma - d\gamma \}. \end{aligned}$$

Thus

$$-2a_2/3a_3 = \frac{2}{3} \frac{b+d}{d} + \frac{2}{3\beta_1 d} \{ b(b+\gamma)\mathcal{R}_0 + bd\mathcal{R}_0 + \beta_1 \gamma + d\gamma(\mathcal{R}_0 - 1) \}.$$

We know that $b(b+\gamma)\mathcal{R}_0 = \beta_1 b + \frac{\beta_2 b \gamma}{b+d}$. Since $b \geq d$, we have $-2a_2/3a_3 > 2$, thus there is at least one root of Q' larger than one.

All these observations show that the graph of Q intersects the line $y = \mathcal{R}_0$ only once. i_1^* is deduced by $i_1^* = \frac{b+d}{\gamma}i_2^* - \frac{d}{\gamma}i_2^{*2}$, and $s^* = 1 - \frac{b+d+\gamma}{\gamma}i_2^* + \frac{d}{\gamma}i_2^{*2}$. Then, the endemic equilibrium exists and is unique. ■

IV. GLOBAL STABILITY OF THE DFE

Theorem IV.1. *If $\mathcal{R}_0 < 1$, the DFE is globally asymptotically stable.*

Proof: To prove Theorem IV.1, we distinguish two cases, the first case corresponds to $\beta_2 \geq d$ and the second is $\beta_2 < d$. In both cases, we use Lyapunov functions.

Case 1: $\beta_2 \geq d$. We consider the following Lyapunov function:

$$V = i_1 + \frac{\beta_2}{b+d} i_2.$$

The derivative of V is:

$$\begin{aligned} \dot{V} &= (\beta_1 i_1 + \beta_2 i_2)s - (b + \gamma)i_1 + d i_1 i_2 \\ &\quad + \frac{\beta_2 \gamma}{b+d} i_1 - \beta_2 i_2 + \beta_2 \frac{d}{b+d} i_2^2. \end{aligned}$$

Since $\beta_1 i_1 s \leq \beta_1 i_1$, we have

$$\begin{aligned} \dot{V} &\leq \beta_1 i_1 + \beta_2 i_2 s - (b + \gamma)i_1 + d i_1 i_2 \\ &\quad + \frac{\beta_2 \gamma}{b+d} i_1 - \beta_2 i_2 + \beta_2 \frac{d}{b+d} i_2^2 \\ &\leq (b + \gamma) \left[\frac{\beta_1}{b + \gamma} + \frac{\beta_2 \gamma}{(b + \gamma)(b + d)} - 1 \right] i_1 \\ &\quad + \beta_2 i_2 (s - 1) + d i_1 i_2 + \beta_2 \frac{d}{b+d} i_2^2, \\ &\leq (b + \gamma)(\mathcal{R}_0 - 1) i_1 + \beta_2 i_2 (s - 1) + d i_1 i_2 \\ &\quad + \beta_2 \frac{d}{b+d} i_2^2. \end{aligned}$$

We know that $\beta_2 i_2 (s - 1) = -\beta_2 i_2 (i_1 + i_2)$, then

$$\begin{aligned} \dot{V} &\leq (b + \gamma)(\mathcal{R}_0 - 1) i_1 + (d - \beta_2) i_1 i_2 \\ &\quad + \left(\frac{d}{b+d} - 1 \right) \beta_2 i_2^2. \end{aligned}$$

Thus

$$\dot{V} \leq (b + \gamma)(\mathcal{R}_0 - 1)i_1 + (d - \beta_2)i_1i_2 - \frac{\beta_2 b}{b + d}\beta_2 i_2^2 \leq 0.$$

It follows that \dot{V} is negative definite when $\mathcal{R}_0 < 1$. When $\mathcal{R}_0 = 1$, the time derivative of V \dot{V} is only nonpositive but in this case LaSalle invariance principle allows to prove the global asymptotic stability of the DFE.

Case 2: $\beta_2 < d$: We consider the following Lyapunov function defined on $\{0 < s \leq 1, 0 \leq i_1 \leq 1, 0 \leq i_2 \leq 1\}$:

$$V = s - \ln s + i_1 + \left(\frac{b + \gamma}{\gamma} - \frac{\beta_1}{\gamma}\right)i_2.$$

We obtain

$$\begin{aligned} \dot{V} &= \dot{s}\left(1 - \frac{1}{s}\right) + \dot{i}_1 + \left(\frac{b + \gamma}{\gamma} - \frac{\beta_1}{\gamma}\right)\dot{i}_2 \\ &= (b - bs)\left(1 - \frac{1}{s}\right) - (\beta_1 i_1 + \beta_2 i_2)s + (\beta_1 i_1 + \beta_2 i_2) + ds i_2 - di_2 + (\beta_1 i_1 + \beta_2 i_2)s \\ &\quad - (b + \gamma)i_1 + di_1 i_2 + (b + \gamma)i_1 - \frac{(b + \gamma)(b + d)}{\gamma}i_2 + \frac{d(b + \gamma)}{\gamma}i_2^2 - \beta_1 i_1 \\ &\quad + \beta_1 \frac{b + d}{\gamma}i_2 - \beta_1 \frac{d}{\gamma}i_2^2, \end{aligned}$$

we get :

$$\begin{aligned} \dot{V} &= -\frac{b}{s}(1 - s)^2 + \beta_2 i_2 + di_2(s + i_1 - 1) \\ &\quad - \frac{(b + \gamma)(b + d)}{\gamma}i_2 + \frac{bd}{\gamma}i_2^2 + di_2^2 \\ &\quad + \beta_1 \frac{b + d}{\gamma}i_2 - \beta_1 \frac{d}{\gamma}i_2^2. \end{aligned}$$

We have the followings equalities:

$$\frac{b}{s}(1 - s)^2 = \frac{b}{s}(i_1 + i_2)^2 \text{ and } di_2(s + i_1 - 1) = -di_2^2.$$

Then \dot{V} becomes:

$$\begin{aligned} \dot{V} &= -\frac{b}{s}(i_1 + i_2)^2 + \beta_2 i_2 - \frac{(b + \gamma)(b + d)}{\gamma}i_2 \\ &\quad + \frac{bd}{\gamma}i_2^2 + \beta_1 \frac{b + d}{\gamma}i_2 - \beta_1 \frac{d}{\gamma}i_2^2 \\ &= -\frac{b}{s}(i_1 + i_2)^2 + \frac{(b + \gamma)(b + d)}{\gamma}(\mathcal{R}_0 - 1)i_2 \\ &\quad + \frac{bd}{\gamma}i_2^2 - \beta_1 \frac{d}{\gamma}i_2^2 \\ &= -\frac{b}{s}(i_1 + i_2)^2 - \frac{(b + \gamma)(b + d)}{\gamma}(1 - \mathcal{R}_0)i_2 \\ &\quad - \beta_1 \frac{d}{\gamma}i_2^2 + \frac{bd}{\gamma}i_2^2. \end{aligned}$$

As $1/s \geq 1$ and $i_2 \geq i_2^2$, we have

$$\begin{aligned} \dot{V} &\leq -b(i_1 + i_2)^2 - \frac{(b + \gamma)(b + d)}{\gamma}(1 - \mathcal{R}_0)i_2^2 \\ &\quad - \beta_1 \frac{d}{\gamma}i_2^2 + \frac{bd}{\gamma}i_2^2 \\ &= -bi_1^2 - 2bi_1i_2 - bi_2^2 - \frac{(b + \gamma)(b + d)}{\gamma} \\ &\quad \cdot (1 - \mathcal{R}_0)i_2^2 - \beta_1 \frac{d}{\gamma}i_2^2 + \frac{bd}{\gamma}i_2^2 \\ &= -bi_1^2 - 2bi_1i_2 - \frac{i_2^2}{\gamma}(b\gamma + (b + \gamma)(b + d) \\ &\quad \cdot (1 - \mathcal{R}_0) + \beta_1 d - bd). \end{aligned}$$

Denote by $D = b\gamma + (b + \gamma)(b + d)(1 - \mathcal{R}_0) + \beta_1 d - bd$, then

$$\dot{V} \leq -bi_1^2 - 2bi_1i_2 - D \frac{i_2^2}{\gamma}.$$

Therefore, $\dot{V} \leq 0$ if $D \geq 0$.

If $bd < b\gamma + \beta_1 d$ holds then $D \geq 0$. If not, we rewrite D in the following form:

$$\begin{aligned} D &= b\gamma + (b + \gamma)(b + d) - \beta_1(b + d) - \beta_2\gamma \\ &\quad + \beta_1 d - bd \\ &= b\gamma + b^2 + bd + b\gamma + d\gamma - \beta_1(b + d) \\ &\quad - \beta_2\gamma + \beta_1 d - bd \\ &= b^2 + 2b\gamma + d\gamma - \beta_1 b - \beta_2\gamma \\ &= b(b - \beta_1) + \gamma(2b + d - \beta_2). \end{aligned}$$

The inequality $bd \geq b\gamma + \beta_1 d$ gives $b > \beta_1$, and with the assumption $\beta_2 < d$ we get again $D \geq 0$.

We conclude that $\dot{V} \leq 0$ if the assumption $\beta_2 < d$ holds. Once again LaSalle invariance principle allows to conclude. Conclusion: in both cases ($\beta_2 \geq d$ and $\beta_2 < d$), we have proved that the disease free equilibrium is globally asymptotically stable. ■

V. LOCAL STABILITY OF THE ENDEMIC EQUILIBRIUM

With the assumption $b \geq d$ we have the following result:

Theorem V.1. *The endemic equilibrium is asymptotically stable when it exists, i.e., when $\mathcal{R}_0 > 1$.*

Proof: Since $s + i_1 + i_2 = 1$, we can eliminate s in System (2). Therefore, we get the following system:

$$\begin{cases} \dot{i}_1 = (\beta_1 i_1 + \beta_2 i_2)(1 - i_1 - i_2) - (b + \gamma)i_1 + di_1 i_2, \\ \dot{i}_2 = \gamma i_1 - (b + d)i_2 + di_2^2. \end{cases} \tag{7}$$

The Jacobian of system (7) at the endemic equilibrium $(EE = (i_1^*, i_2^*))$ is:

$$J(EE) = \begin{pmatrix} \beta_1 - 2\beta_1 i_1^* - \beta_1 i_2^* - \beta_2 i_2^* - (b + \gamma) + di_2^* & \\ & \gamma \\ \beta_2 - 2\beta_2 i_2^* - \beta_2 i_1^* - \beta_1 i_1^* + di_1^* & \\ & -b - d + 2di_2^* \end{pmatrix}$$

At the endemic equilibrium we have:

$$\beta_1 - 2\beta_1 i_1^* - \beta_1 i_2^* - \beta_2 i_2^* - (b + \gamma) + di_2^* = -\beta_2 i_2^* \frac{1 - i_2^*}{i_1^*} - \beta_1 i_1^*.$$

The determinant of $J(EE)$ is given by:

$$\begin{aligned} \det(J(EE)) &= \beta_2(b + d)i_2^* \frac{1 - i_2^*}{i_1^*} + \beta_1(b + d)i_1^* \\ &\quad - 2\beta_2 d i_2^{*2} \frac{1 - i_2^*}{i_1^*} - 2\beta_1 di_1^* i_2^* \\ &\quad - \beta_2 \gamma + 2\beta_2 \gamma i_2^* + \beta_2 \gamma i_1^* \\ &\quad + \beta_1 \gamma i_1^* - d\gamma i_1^* \\ &= \beta_2(b + d)i_2^* \frac{1 - i_2^*}{i_1^*} + (\beta_1(b + d) \\ &\quad + \beta_2 \gamma) i_1^* + 2\beta_2 i_2^* \left(\gamma - d i_2^* \frac{1 - i_2^*}{i_1^*} \right) \\ &\quad - 2\beta_1 d i_1^* i_2^* - \beta_2 \gamma + \beta_1 \gamma i_1^* \\ &\quad - d\gamma i_1^*. \end{aligned}$$

In the first term of the determinant, we replace $(b + d)i_2^*$ by $\gamma i_1^* + di_2^{*2}$ and we get:

$$\begin{aligned} \det(J(EE)) &= \beta_2 (\gamma i_1^* + di_2^{*2}) \frac{1 - i_2^*}{i_1^*} \\ &\quad + (b + d)(b + \gamma)\mathcal{R}_0 i_1^* \\ &\quad + 2\beta_2 \frac{i_2^*}{i_1^*} (\gamma i_1^* - di_2^* + di_2^{*2}) \\ &\quad - 2\beta_1 di_1^* i_2^* - \beta_2 \gamma + \beta_1 \gamma i_1^* - d\gamma i_1^*. \end{aligned}$$

We replace again $\gamma i_1^* - di_2^* + di_2^{*2}$ by bi_2^* and by developing the first term of the determinant, we get:

$$\begin{aligned} \det(J(EE)) &= \beta_2 \gamma - \beta_2 \gamma i_2^* + \beta_2 d i_2^{*2} \frac{1 - i_2^*}{i_1^*} \\ &\quad + (b + d)(b + \gamma)\mathcal{R}_0 i_1^* + 2\beta_2 b \frac{i_2^{*2}}{i_1^*} \\ &\quad - 2\beta_1 di_1^* i_2^* - \beta_2 \gamma + \beta_1 \gamma i_1^* \\ &\quad - d\gamma i_1^* \\ &= \beta_2 i_2^* \left(-\gamma + di_2^* \frac{1 - i_2^*}{i_1^*} + b \frac{i_2^*}{i_1^*} \right) \\ &\quad + (b + d)(b + \gamma)\mathcal{R}_0 i_1^* + \beta_2 b \frac{i_2^{*2}}{i_1^*} \\ &\quad - 2\beta_1 di_1^* i_2^* + \beta_1 \gamma i_1^* - d\gamma i_1^* \\ &= \beta_2 \frac{i_2^*}{i_1^*} (-\gamma i_1^* + (b + d)i_2^* - d i_2^{*2}) \\ &\quad + (b + d)(b + \gamma)\mathcal{R}_0 i_1^* + \beta_2 b \frac{i_2^{*2}}{i_1^*} \\ &\quad - 2\beta_1 di_1^* i_2^* + \beta_1 \gamma i_1^* - d\gamma i_1^*. \end{aligned}$$

Thus

$$\begin{aligned} \det(J(EE)) &= b(b + d + \gamma)\mathcal{R}_0 i_1^* + \beta_2 b \frac{i_2^{*2}}{i_1^*} \\ &\quad + d\gamma i_1^* (\mathcal{R}_0 - 1) + \beta_1 i_1^* (\gamma - 2di_2^*). \end{aligned}$$

The determinant is positive because $i_2^* \in (0, \frac{\gamma}{2d})$. Furthermore the trace is negative, because it is given by:

$$\text{tr} J(EE) = -\beta_2 i_2^* \frac{1 - i_2^*}{i_1^*} - \beta_1 i_1^* - b - d + 2di_2^*.$$

Then the endemic equilibrium is asymptotically stable. ■

VI. GLOBAL STABILITY OF THE ENDEMIC EQUILIBRIUM

Since $s + i_1 + i_2 = 1$, we can reduce system (2) to a planar system and hence we can use the Poincaré-Bendixson theorem to investigate the global attraction of the endemic equilibrium when $\mathcal{R}_0 > 1$. To this end, let us consider the following system:

$$\begin{cases} \dot{s} = b(1 - s) - (\beta_1 i_1 + \beta_2(1 - i_1 - s))s + ds(1 - i_1 - s), \\ \dot{i}_1 = (\beta_1 i_1 + \beta_2(1 - i_1 - s))s - (b + \gamma)i_1 + di_1(1 - i_1 - s), \end{cases} \tag{8}$$

defined on the set $\Omega = \{0 \leq s \leq 1, 0 \leq i_1 \leq 1, s + i_1 \leq 1\}$. We establish by the Dulac-Bendixson criterium that there is no periodic orbit for (8).

Theorem VI.1. System (8) has no periodic orbit.

Proof: Consider the function $B(x, y) = \frac{1}{xy}$. We have:

$$B \dot{s}(s, i_1) = \frac{b}{s i_1} - \frac{b}{i_1} - \beta_1 - \frac{\beta_2}{i_1} + \beta_2 + \frac{\beta_2 s}{i_1} + \frac{d}{i_1} - d - \frac{ds}{i_1},$$

thus

$$\frac{\partial}{\partial s} B \dot{s}(s, i_1) = -\frac{b}{s^2 i_1} + \frac{\beta_2}{i_1} - \frac{d}{i_1}.$$

And

$$B \dot{i}_1(s, i_1) = \beta_1 + \frac{\beta_2}{i_1} - \beta_2 - \frac{\beta_2 s}{i_1} - \frac{b + \gamma}{s} + \frac{d}{s} - \frac{d i_1}{s} - d,$$

so

$$\frac{\partial}{\partial i_1} B \dot{i}_1(s, i_1) = -\frac{\beta_2}{i_1^2} + \frac{\beta_2 s}{i_1^2} - \frac{d}{s}.$$

It leads to

$$\begin{aligned} \frac{\partial B \dot{s}(s, i_1)}{\partial s} + \frac{\partial B \dot{i}_1(s, i_1)}{\partial i_1} &= \\ -\frac{b}{s^2 i_1} + \frac{\beta_2}{i_1^2} (s + i_1 - 1) - \frac{d}{i_1} - \frac{d}{s} & \\ \frac{\partial B \dot{s}(s, i_1)}{\partial s} + \frac{\partial B \dot{i}_1(s, i_1)}{\partial i_1} < 0 \quad \forall s, i_1 \in (0, 1]. \end{aligned}$$

By Dulac-Bendixson criterium, we conclude that there is no closed orbit for system (8). ■

Thanks to Theorem VI.1 and the Poincaré-Bendixson theorem we have the following result:

Theorem VI.2. If $\mathcal{R}_0 > 1$ the endemic equilibrium exists and is globally asymptotically stable in $\Omega - \Gamma$, where Γ is the stable manifold of the disease free equilibrium.

Proof: If $\mathcal{R}_0 > 1$, the Jacobian matrix of system of (8) at the point (1,0) has a negative determinant. Therefore the DFE is unstable, but the eigenvalues of the Jacobian matrix at the DFE are equal to:

$$\begin{aligned} \lambda_{1,2} &= \beta_1 - (b + \gamma) - (b + d) \\ &\pm \sqrt{(\beta_1 - (b + \gamma) - (b + d))^2 - 4(b + \gamma)(b + d)(1 - \mathcal{R}_0)}. \end{aligned}$$

One of the two eigenvalues is negative, which gives that the disease free equilibrium has one dimensional stable manifold Γ . The ω -limit set of the system (8) on $\Omega - \Gamma$

is reduced to the endemic equilibrium point. Because of the local stability of the endemic equilibrium for $\mathcal{R}_0 > 1$, the endemic equilibrium is globally asymptotically stable. ■

VII. CONCLUSION

The model SI is one of the most important epidemiological model. This paper gives a qualitative analysis of the stability of the model with a non-linear incidence. For this incidence, the system is analyzed by considering the differential system satisfied by the proportions, and the theory of Poincaré-Bendixson is used.

It would be interesting to generalize the work to study the system with arbitrary n infected stages. It also would be interesting to find a Lyapunov function for proving the global asymptotic stability of the endemic equilibrium.

REFERENCES

- [1] R. M. Anderson and R. M. May. Infection diseases of Humans. *Oxford University Press*, London 1991.
- [2] L -M. Cai, X. -Z. Li and Ghosh. Global satbility of staged-structured model with a non linear incidence. *Applied Math. Comput.*, 214:73–82, 2009.
- [3] P. van den Driessche and J. Watmough. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Math. Biosci.*, 180:29–48, 2002. [http://dx.doi.org/10.1016/S0025-5564\(02\)00108-6](http://dx.doi.org/10.1016/S0025-5564(02)00108-6)
- [4] H. Guo and M. Y. Li. Global dynamics of a staged progression model for infectious diseases. *Math. Biosci. and eng.*,3(3):513–525, 2006. <http://dx.doi.org/10.3934/mbe.2006.3.513>
- [5] H. W. Hethcote. The Mathematics of infectious diseases. *SIAM*, 42:599–653, 2000.
- [6] H. W. Hethcote and H. R. Thieme. Stability of the endemic equilibrium in epidemic model with subpopulations. *Math. Biosciences*, 75:205–227, 1985. [http://dx.doi.org/10.1016/0025-5564\(85\)90038-0](http://dx.doi.org/10.1016/0025-5564(85)90038-0)
- [7] H. W. Hethcote and J. A. Yorke. Gonorrhoea Transmission Dynamics and control. *Springer Verlag*, 1984.
- [8] J. M. Hyman, J. Li. The reproductive number for an HIV model with differential infectivity and staged progression. *Linear Algebra and its Applications*, 398:101–116, 2005.
- [9] J. M. Hyman, J. Li, E. A. Stanley. The differential infectivity and staged progression models for the transmission of HIV12. *Mathematical Biosciences*, 155(2):77–109,1999.
- [10] A. Iggidr, J. Mbang, G. Sallet, and J.-J. Tewa. Multi-compartment models. *Discrete Contin. Dyn. Syst. Supplements*, suppl. volume(Dynamical Systems and Differential Equations. Proceedings of the 6th AIMS International Conference.):506–519, September 2007.

- [11] A. Korobeinikov. Lyapunov functions and global properties for SEIR and SEIS epidemic models. *Math.Med.Biology*, 21:75-83, 2004.
- [12] A. Korobeinikov and P. K. Maini. Non-linear incidence and stability of infectious disease models. *Math.Med.Biology*, 22:113-128, 2005. <http://dx.doi.org/10.1093/imammb/dqi001>
- [13] J. P. LaSalle. The stability of dynamics systems. *CBMS-NSF Regional Conf. Ser. in Appl.Math. 25, SIAM, Philadelphia*, 1976.
- [14] S. A. Levin. Descartes' Rule of Sign-How hard can it be?
- [15] M. Y. Li, J. R. Graef, L Wang and J Karsai. Global dynamics of a SEIR with varying total population size. *Mathematical biosciences*, 160:191-213, 1999.
- [16] C. C. McCluskey. A model of HIV/AIDS with staged progression and amelioration. *Mathematical Biosciences*, 181:1-16, 2003.
- [17] D. Y. Melesse and A. B. Gumel. Global asymptotic properties of an SEIRS model with multiple infectious stages. *Math. Anal. and Appl.*,366:202-217, 2010. [http://dx.doi.org/10.1016/S0025-5564\(02\)00149-9](http://dx.doi.org/10.1016/S0025-5564(02)00149-9)
- [18] C. P. Simon and J. A. Jacquez. Reproduction Numbers and the stability of equilibria of SI models for heterogeneous population. *SIAM*, 52(2):541-576, April 1992.
- [19] S. M. Moghadas and A. B. Gumel. Global stability of a two stage epidemic model with generalised two stage incidence. *Mathematics and computers and simulation*, 60:107-118, 2002.
- [20] H. R. Thieme. Global stability of the endemic equilibrium in infinite dimension: Lyapunov functions and positive operator. *Journal of differentiel equation*, 250(9):3772-3801, 2011.