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Deterministic and Stochastic Nonlinear Schistosomiasis Model with Delay and Vaccination

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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Abstract

A worldwide approach is needed to combat schistosomiasis, one that addresses the disease's mollusc problem, treats parasitised individuals, and enhances hygienic circumstances by getting rid of human waste. This paper presents a deterministic SIR delayed epidemiological model with vaccination that accounts for the dynamics of parasites in both molluscs and humans. Then, we will alter some of the coefficients to create a new stochastic SIR model that includes vaccination and delay, so expanding the range of possible control tactics. Using the Lyapunov function, we may analyse the above model to determine the necessary and sufficient conditions for the regularity, existence, and uniqueness of a global solution.

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Furthermore, we examine the stochastic asymptotic stability of both the endemic and disease-free equilibrium points in this model. Finally, we present applications that highlight our overall findings.

Keywords: Schistosomiasis control strategy; basic reproduction number; local stability; global stability; epidemic model; lyapunov function; ito's formula.

1 Introduction

Mathematical modeling of infectious diseases has evolved since the 18th century, starting with (Bernoulli, 1760) where Bernoulli used probability to demonstrate the benefits of smallpox inoculation. In (Ross, 1902), R. Ross formalized malaria transmission using mathematical models based on the life cycles of mosquitoes and human infection, establishing the groundwork for epidemic modeling. In (Kermack & McKendrick, 1927), Kermack and McKendrick introduced the SIR model (Susceptible-Infected-Recovered), which uses ordinary differential equations to divide the population into compartments, and remains a cornerstone in epidemic modeling. This model was later expanded to include variations like SEIR (adding an Exposed compartment) (Lotka, 1910) and SIS (for diseases without permanent immunity). In the 1970s, the development of stochastic models in (Kermack & McKendrick, 1932) allowed the incorporation of random effects into the spread of diseases, particularly in small populations. These models have greatly influenced the study of infectious diseases and control strategies over time.

Neglected tropical diseases (NTDs) represent a significant public health challenge, often overlooked in universal healthcare coverage. Among these, schistosomiasis stands out for its severe impact on affected communities, especially in Africa, where up to 90% of cases occur. Schistosomiasis is caused by Schistosoma parasites found in contaminated freshwater, leading to chronic pain, liver damage, and intestinal or urinary complications (OMS, 2019). Each year, an estimated 800,000 people die from this disease, which is spread through both human and mollusc hosts. The parasitic life cycle involves eggs entering freshwater via human excreta, where larvae infect molluscs before eventually reaching human hosts (Professeur Aubri & Docteur Gauzère, 2021). These infections are expanding with the development of irrigation systems, further complicating control efforts (The Merck Version Manual for Healthcare Professionals). Given these severe effects, integrating NTDs into healthcare initiatives is crucial for improving life quality in vulnerable populations.

See the schistosoma life cycle (source: Center for Disease Control and Prevention).

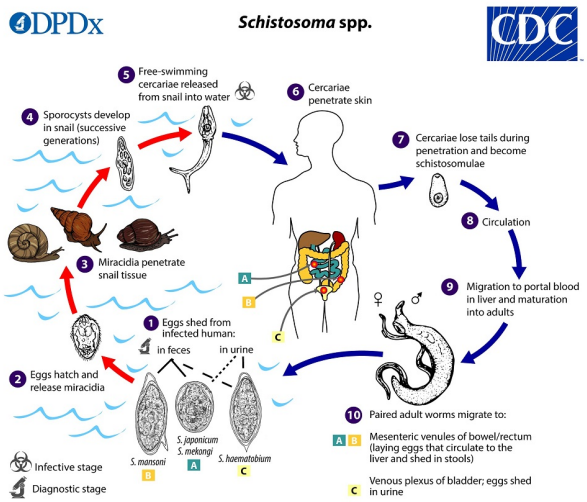

Fig. 1. Schistosoma life cycle

P. A. Cissé evaluates multiple mathematical models in his thesis (Cissé, 2015) in order to maintain the model of Gao et al. (Gao, Liu, Luo, & Xie, 2011). Gao et al. demonstrated in their article that artificial control strategies based on mathematical models would be more successful in controlling the disease if they focused on preventing the disease from spreading from humans to snails rather than blocking it from happening that way. Nevertheless, research has not been done on the impact of a delay in parasite transmission in either the intermediate or final host.

In this article, we separate the host snails (uninfected, infected, and resistant), cercariae, and miracidia, as well as the human population (uninfected and unexposed, uninfected and exposed, and infected humans). The structure of this document is as follows. The deterministic model is formulated in the following section. In Section 3, the stochastic model will be introduced, its fundamental breeding number will be ascertained, and adequate criteria for the overall stability of the disease-free equilibrium will be established. To demonstrate the findings, several numerical simulations will be shown in Section 4.

2 Formulation and Analysis of the Deterministic Model

2.1 Gao et al. model (2011)

The initial model we propose is based on the research conducted by Gao et al. (Gao et al., 2011), which uses an Ordinary Differential Equation to represent the dynamics of schistosomiasis transmission. In this model, both the host and snail populations are divided into two groups: susceptible individuals (S_1 and S_2) and infected individuals (I_1 and I_2). Additionally, M and P represent the cercariae and miracidia populations, respectively. The incidence rate, which is the rate of new infections, is a crucial factor in modeling communicable diseases as it influences the qualitative behavior of the models and their ability to accurately depict disease dynamics. In this case, the incidence rate is saturated and nonlinear, expressed as $\frac{\beta SI}{1+aS}$, $\frac{\beta SI}{1+bS^2}$ and $\frac{\beta SI}{1+aS+bS^2}$.

Refer to the transmission diagram for schistosomiasis.

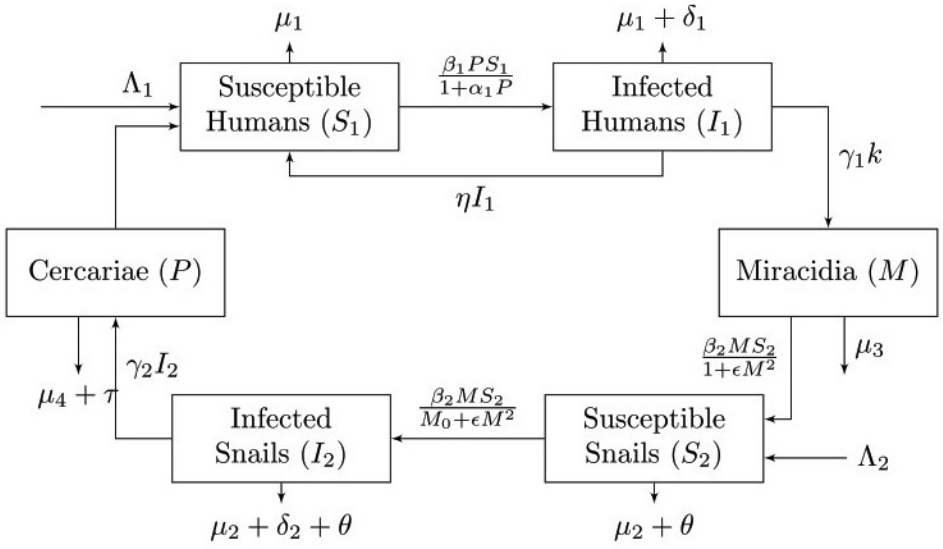

Fig. 2. Schistosomiasis transmission diagram

Gao & al. have developed the following model:

$$\begin{cases} \dfrac{dS_1}{dt} = \Lambda_1 - \dfrac{\beta_1 P S_1}{1+\alpha_1 P} - \mu_1 S_1 + \eta I_1 \\ \dfrac{dI_1}{dt} = \dfrac{\beta_1 P S_1}{1+\alpha_1 P} - (\mu_1 + \delta_1 + \eta) I_1 \\ \dfrac{dM}{dt} = k\gamma_1 I_1 - \mu_3 M \\ \dfrac{dS_2}{dt} = \Lambda_2 - \dfrac{\beta_2 M S_2}{M_0 + \varepsilon M^2} - (\mu_2 + \theta) S_2 \\ \dfrac{dI_2}{dt} = \dfrac{\beta_2 M S_2}{M_0 + \varepsilon M^2} - (\mu_2 + \delta_2 + \theta) I_2 \\ \dfrac{dP}{dt} = \gamma_2 I_2 - (\mu_4 + \tau) P \end{cases} \tag{2.1}$$

In the equation (2.1), I_1 means the population of infected humans, S_1 the population of susceptible humans , I_2 the population of infected mollusks, S_2 the population of susceptible mollusks, M the population of miracidium and P the population of cercariae.
The settings

- Λ_1 and Λ_2 respectively represent the average number of births per unit time of humans and mollusks
- θ represents the rate of elimination of mollusks
- τ represents the rate of elimination of cercariae
- η represents the treatment rate of infected humans I_1
- k represents the quantity of eggs accompanying the faeces of an infected human in I_1
- γ_1 is the rate of miracidium released by a hatched egg
- γ_2 is the rate of cercariae released by infected mollusc in I_2
- μ_1, μ_2, μ_3 and μ_4 represent the natural death rates of humans, mollusks, miracidia and cercariae, respectively.
- δ_1 and δ_2 respectively the death rates due to infection of individuals and mollusks
- β_1 and β_2 represent respectively the probability of transmission by contact between $S_1 - P$ and between $S_2 - M$

Control policy settings

- θ control focused on the elimination of mollusks
- τ control focused on the elimination of cercariae
- η control focused on the treatment of infected humans

This model, although interesting, does not take into account:

- nor delays in infections of molluscs and humans;
- nor the geographical positions of some molluscs which are not exposed to miracidium infection;
- nor the geographical position of some humans who are in risk-free areas;
- nor chemoprophylaxis.

2.2 SIR delay model taking into account the dynamics of cercariae and miracidia

Considering the aforementioned observations, we suggest a vaccine delay model that accounts for all preventive and control measures: Humans are either immunised against the parasite or unable to come into contact with it because of their location or proximity to a risk area; molluscs are either incompatible with the parasite or unable to come into contact with it because the area is either infected with cercariae or all of the infected humans use latrines. Humans and mollusc populations will be split into susceptible S_i, infected I_i, and recovered R_i $(i \in \{1;2\})$ under these circumstances. The percentage of the vaccinated population that is incompatible or lives in a low-risk location is denoted by λ_i. Index 1 pertains to the human population, while Index 2 deals with the mollusc population. Since there currently appears to be a resistance phenomenon or at least less sensitivity of schistosome to praziquantel in specific endemic places and in people swiftly reinfesting themselves, any sick person who is still in touch with infected water will be regarded unhealed. (Klotz, 2003) A patient with an infection must discharge eggs for at least $h_0 > 0$. A miracidium developed from an egg has a lifespan of $h_1 > 0$. In a mollusc, the time it takes for a miracidium to change into cercariae is $h_2 > 0$. A cercaria's period of infectivity is $h_3 > 0$. With $i \in \{0;1;2;3\}$, let $H_i = \sum_{j=0}^{i} h_j$, and $H_4 = h_0 + \sum_{j=0}^{3} h_j$. With an incidence rate of the kind $\beta_1 S_1(t) \int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)} \varphi_3(u)du$, the susceptible class S_1 is where new sick individuals are recruited into the human population, where the contact rate is β_1 with a force of φ_1 and within a maximum delay. Similarly, in molluscs, the incidence rate takes the form $\beta_2 S_2(t) \int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)} \varphi_1(u)du$. Furthermore, the number of miracidia and cercariae is determined by a function φ_{i+1}. The function φ_{i+1} is a Lebesgue integrable function reflecting the infectiousness of the parasite (Anderson & May, 1991), such that $\int_{H_i}^{H_{i+1}} \varphi_{i+1}(u)du = 1$. and $\int_{H_i}^{H_{i+1}} u\varphi_{i+1}(u)du < +\infty$. We can take $\varphi_{i+1}(u) = \frac{e^{\frac{H_{i+1}-u}{H_{i+1}-H_i}}}{(H_{i+1}-H_i)(e-1)}$

(Refer to the transmission diagram for schistosomiasis).

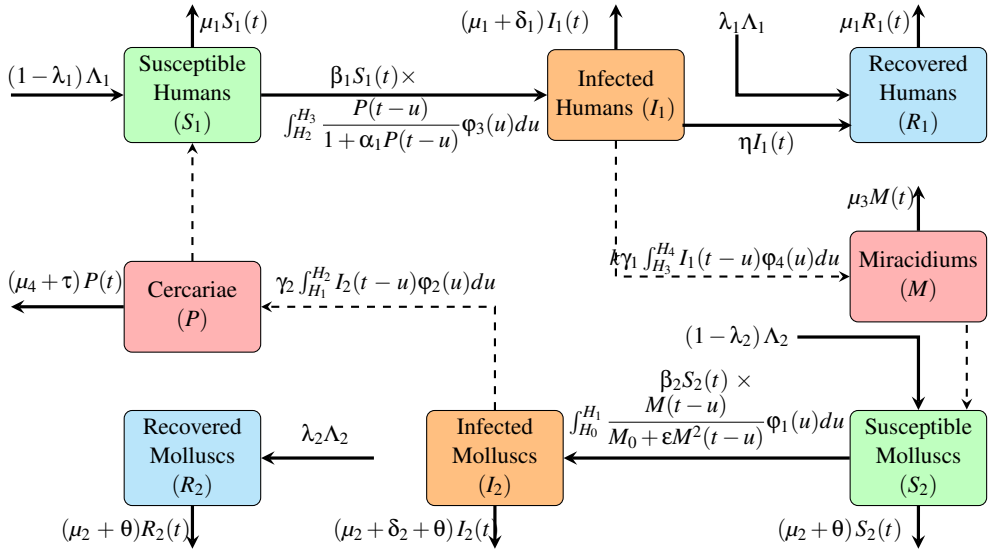

Fig. 3. Detailed Transmission Diagram with Additional Explanations

The equation becomes

$$\begin{cases} \frac{dS_1}{dt}(t) = (1-\lambda_1)\Lambda_1 - \beta_1 S_1(t)\int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du - \mu_1 S_1(t) \\ \frac{dI_1}{dt}(t) = \beta_1 S_1(t)\int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du - (\mu_1+\delta_1+\eta) I_1(t) \\ \frac{dR_1}{dt}(t) = \lambda_1\Lambda_1 + \eta I_1(t) - \mu_1 R_1(t) \\ \frac{dM}{dt}(t) = k\gamma_1\int_{H_3}^{H_4} I_1(t-u)\varphi_4(u)du - \mu_3 M(t) \\ \frac{dS_2}{dt}(t) = (1-\lambda_2)\Lambda_2 - \beta_2 S_2(t)\int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)}\varphi_1(u)du - (\mu_2+\theta) S_2(t) \\ \frac{dI_2}{dt}(t) = \beta_2 S_2(t)\int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)}\varphi_1(u)du - (\mu_2+\delta_2+\theta) I_2(t) \\ \frac{dR_2}{dt}(t) = \lambda_2\Lambda_2 - (\mu_2+\theta) R_2(t) \\ \frac{dP}{dt}(t) = \gamma_2\int_{H_1}^{H_2} I_2(t-u)\varphi_2(u)du - (\mu_4+\tau) P(t) \end{cases} \tag{2.2}$$

Let's pose

$$\phi_3(P(t)) = \int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du; \qquad \phi_1(M(t)) = \int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)}\varphi_1(u)du$$

$$\phi_4(I_1(t)) = \int_{H_3}^{H_4} I_1(t-u)\varphi_4(u)du \qquad \phi_2(I_2(t)) = \int_{H_1}^{H_2} I_2(t-u)\varphi_2(u)du$$

N_i is the population's capacity to receive $i (i \in \{1;2\})$
Death rates are assumed to be lower than birth rates in the human population.
Total human population $H = S_1 + I_1 + R_1 \leq N_1$

$$\frac{\Lambda_1}{H} > \mu_1 + \delta_1 \qquad \Lambda_1 > (\mu_1+\delta_1) H \qquad \Lambda_1 - (\mu_1+\delta_1) H > 0 \qquad \frac{dH}{dt} = \Lambda_1 - \mu_1 H - \delta_1 I_1 > 0$$

In snails, the birth rate is assumed to be greater than the sum of death rates and shellfish removal rate. Otherwise the mollusks would disappear with the disease and end of the study. Total snail population $E = S_2 + I_2 + R_2 \leq N_2$

$$\frac{\Lambda_2}{E} > \mu_2 + \delta_2 + \theta \quad \Lambda_2 > (\mu_2+\delta_2+\theta) E \quad \Lambda_2 - (\mu_2+\delta_2+\theta) E > 0 \quad \frac{dE}{dt} = \Lambda_2 - (\mu_2+\theta) E - \delta_2 I_2 > 0$$

The system (2.2) can be rewritten

$$\begin{cases} \dfrac{dS_1}{dt}(t) = (1-\lambda_1)\Lambda_1 - \beta_1 S_1(t)\displaystyle\int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du - \mu_1 S_1(t) \\ \dfrac{dS_2}{dt}(t) = (1-\lambda_2)\Lambda_2 - \beta_2 S_2(t)\displaystyle\int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)}\varphi_1(u)du - (\mu_2+\theta) S_2(t) \\ \dfrac{dI_1}{dt}(t) = \beta_1 S_1(t)\displaystyle\int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du - (\mu_1+\delta_1+\eta) I_1(t) \\ \dfrac{dI_2}{dt}(t) = \beta_2 S_2(t)\displaystyle\int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)}\varphi_1(u)du - (\mu_2+\delta_2+\theta) I_2(t) \\ \dfrac{dR_1}{dt}(t) = \lambda_1\Lambda_1 + \eta I_1(t) - \mu_1 R_1(t) \\ \dfrac{dR_2}{dt}(t) = \lambda_2\Lambda_2 - (\mu_2+\theta) R_2(t) \\ \dfrac{dM}{dt}(t) = k\gamma_1\displaystyle\int_{H_3}^{H_4} I_1(t-u)\varphi_4(u)du - \mu_3 M(t) \\ \dfrac{dP}{dt}(t) = \gamma_2\displaystyle\int_{H_1}^{H_2} I_2(t-u)\varphi_2(u)du - (\mu_4+\tau) P(t) \end{cases} \tag{2.3}$$

The initial conditions of the system (2.3) are:

$$S_1(0)>0 \ , \ S_2(0)>0 \ , \ I_1(0)>0 \ , \ I_2(0)\geq 0 \ , \ R_1(0)>0 \ , \ R_2(0)>0 \ , \ M(0)>0 \ \ et \ \ P(0)\geq 0$$

Let the set $\mathbb{D}$ be where the system is biologically defined.

$$\mathbb{D} = \{X \in \mathbb{R}_+^8 : \forall i \in \{1,2,3,5,6\}\ X_i > 0,\ \forall i \in \{4,7,8\}\ X_i \geq 0,\ \sum_{i=1}^{3} X_{2i-1} < \frac{\Lambda_1}{\mu_1},\ \sum_{i=1}^{3} X_{2i} < \frac{\Lambda_2}{\mu_2+\theta}\}$$

2.3 Existence and uniqueness of solutions

The system (2.3) is described by a system of nonlinear differential equations which can be rewritten in the following matrix form :

$$X'(t) = F(X(t))$$

Where

$$X(t)=\begin{pmatrix} S(t)\\ I(t)\\ R(t)\\ V(t)\end{pmatrix}\quad S(t)=\begin{pmatrix} S_1(t)\\ S_2(t)\end{pmatrix}\quad I(t)=\begin{pmatrix} I_1(t)\\ I_2(t)\end{pmatrix}\quad R(t)=\begin{pmatrix} R_1(t)\\ R_2(t)\end{pmatrix}\quad V(t)=\begin{pmatrix} M(t)\\ P(t)\end{pmatrix}$$

$$F(X)=\begin{pmatrix} F_1(x_1,\ \ldots\ ,x_8)\\ F_2(x_1,\ \ldots\ ,x_8)\\ F_3(x_1,\ \ldots\ ,x_8)\\ F_4(x_1,\ \ldots\ ,x_8)\\ F_5(x_1,\ \ldots\ ,x_8)\\ F_6(x_1,\ \ldots\ ,x_8)\\ F_7(x_1,\ \ldots\ ,x_8)\\ F_8(x_1,\ \ldots\ ,x_8)\end{pmatrix}=\begin{pmatrix} (1-\lambda_1)\Lambda_1-\beta_1x_1\phi_3(x_8)-\mu_1x_1\\ (1-\lambda_2)\Lambda_2-\beta_2x_2\phi_1(x_7)-(\mu_2+\theta)x_2\\ \beta_1x_1\phi_3(x_8)-(\mu_1+\delta_1+\eta)x_3\\ \beta_2x_2\phi_1(x_7)-(\mu_2+\delta_2+\theta)x_4\\ \lambda_1\Lambda_1+\eta x_3-\mu_1x_5\\ \lambda_2\Lambda_2-(\mu_2+\theta)x_{6.}\\ k\gamma_1\phi_4(x_3)-\mu_3x_7\\ \gamma_2\phi_2(x_4)-(\mu_4+\tau)x_8\end{pmatrix}$$

The system (2.3) can be written

$$\begin{cases}\dfrac{dX}{dt}(t)=F(X(t))\\ X_0=g\end{cases}\tag{2.4}$$

Either

$$h=\max_{1\le i\le 4}h_i$$

For $g\in\mathcal{C}([-h,0],\mathbb{R}^8)$, the norm g is defined by

$$\|g\|=\sup_{\theta\in[-h;0]}\|g(\theta)\|$$

Let's note

$$X_0=(S_1(0),S_2(0),I_1(0),I_2(0),R_1(0),R_2(0),M(0),P(0))$$

Theorem 2.1. *For all $X_0\in\overline{\mathbb{D}}$, there is a unique maximal solution of the system (2.3) verifying $X(0)=X_0$*

Proof.

Lemma 2.2. ***Theorem of Existence and Uniqueness (Cauchy-Lipschitz)***

Consider the differential system: $\begin{cases}\dot{x_1}&=&f_1(t,x_1,...,x_n)\\ \dot{x_2}&=&f_2(t,x_1,...,x_n)\\ \vdots&\vdots&\vdots\\ \dot{x_n}&=&f_n(t,x_1,...,x_n)\end{cases}$

where f_i are defined and continuous on a common domain $\Delta\subset\mathbb{R}\times\mathbb{R}^n$ and have partial derivatives with respect to x_i that are continuous on Δ (for $i=1,...,n$) .

Then, given real numbers t_0 and $a_1,a_2,...,a_n$ such that $(t_0,a_1,a_2,...,a_n)$ belongs to Δ, there exists a unique solution $(u_1(t)$, $u_2(t),...,u_n(t))$ defined on a maximal interval I containing t_0 that satisfies the initial conditions $u_1(t_0)=a_1,u_2(t_0)=a_2,...,u_n(t_0)$ $=a_n$.

By applying the previous lemma to F, since F is a function of class $\mathcal{C}^\infty$ on $\mathbb{R}^8$, hence F locally Lipschitzian; We therefore deduce the existence and uniqueness of a maximal solution. □

Positivity of the vector $X(t)$

Theorem 2.3. *$\mathbb{D}$ is invariant with respect to the system (2.3): no trajectory leaves $\mathbb{D}$*

Proof. Let $X(t)$ be a trajectory in $\mathbb{D}$ at $t_0 \geq 0$. Suppose that there exists $t > t_0$ such that $X(t) \notin \mathbb{D}$. Notons :

$$t_1 = \inf_{t>t_0} \{X(t) \notin \mathbb{D}\}$$

Hence,

1. If $S_1(t_1) = 0$ then $\dot{S_1}(t_1) = (1-\lambda_1)\Lambda_1 > 0$. Hence there exists $\varepsilon > 0$, we have $S_1(t_1-\varepsilon) < S_1(t_1) = 0$. So $X(t_1-\varepsilon) \notin \mathbb{D}$. Which is absurd.
2. If $S_2(t_1) = 0$ then $\dot{S_2}(t_1) = (1-\lambda_2)\Lambda_2 > 0$. Hence there exists $\varepsilon > 0$, we have $S_2(t_1-\varepsilon) < S_2(t_1) = 0$. Hence $X(t_1-\varepsilon) \notin \mathbb{D}$. Which is absurd.
3. If $I_1(t_1) < 0$ then $\dot{I_1}(t_1) = \beta_1 S_1(t_1) \int_{H_2}^{H_3} \frac{P(t_1-u)}{1+\alpha_1 P(t_1-u)} \varphi_1(u)du - (\mu_1+\delta_1+\eta) I_1(t_1) > 0$. Hence there exists $\varepsilon > 0$, we have $I_1(t_1-\varepsilon) < I_1(t_1) < 0$. So $X(t_1-\varepsilon) \notin \mathbb{D}$. Which is absurd.
4. If $I_2(t_1) < 0$ then $\dot{I_2}(t_1) = \beta_2 S_2(t_1) \int_{H_0}^{H_1} \frac{M(t_1-u)}{M_0+\varepsilon M^2(t_1-u)} \varphi_2(u)du - (\mu_2+\delta_2+\theta) I_2(t_1) > 0$. Hence there exists $\varepsilon > 0$, we have $I_2(t_1-\varepsilon) < I_2(t_1) < 0$. So $X(t_1-\varepsilon) \notin \mathbb{D}$. Which is absurd.
5. If $R_1(t_1) = 0$ then $\dot{R_1}(t_1) = \lambda_1\Lambda_1 + \eta I_1(t_1) > 0$.Hence there exists $\varepsilon > 0$, we have $R_1(t_1-\varepsilon) < R_1(t_1) = 0$. So $X(t_1-\varepsilon) \notin \mathbb{D}$. Which is absurd.
6. If $R_2(t_1) = 0$ then $\dot{R_2}(t_1) = \lambda_2\Lambda_2 > 0$. Hence there exists $\varepsilon > 0$, we have $R_2(t_1-\varepsilon) < R_2(t_1) = 0$. So $X(t_1-\varepsilon) \notin \mathbb{D}$. Which is absurd.
7. If $M(t_1) = 0$ then $\dot{M}(t_1) = k\gamma_1 \int_{H_3}^{H_4} I_1(t_1-u)\varphi_3(u)du > 0$. Hence there exists $\varepsilon > 0$, we have $M(t_1-\varepsilon) < M(t_1) = 0$. So $X(t_1-\varepsilon) \notin \mathbb{D}$. Which is absurd.
8. If $M(t_1) < 0$ then $\dot{M}(t_1) = k\gamma_1 \int_{H_3}^{H_4} I_1(t_1-u)\varphi_3(u)du - \mu_3 M(t_1) > 0$. Hence there exists $\varepsilon > 0$, we have $M(t_1-\varepsilon) < M(t_1) < 0$. So $X(t_1-\varepsilon) \notin \mathbb{D}$. Which is absurd.
9. If $P(t_1) = 0$ then $\dot{P}(t_1) = \gamma_2 \int_{H_1}^{H_2} I_2(t_{1-u})\varphi_4(u)du - (\mu_4+\tau) P(t_1) > 0$. Hence there exists $\varepsilon > 0$, we have $P(t_1-\varepsilon) < P(t_1) = 0$. So $X(t_1-\varepsilon) \notin \mathbb{D}$. Which is absurd.
10. If $P(t_1) < 0$ then $\dot{P}(t_1) = \gamma_2 \int_{H_1}^{H_2} I_2(t_{1-u})\varphi_4(u)du - (\mu_4+\tau) P(t_1) > 0$. Hence there exists $\varepsilon > 0$, we have $P(t_1-\varepsilon) < P(t_1) < 0$. So $X(t_1-\varepsilon) \notin \mathbb{D}$. Which is absurd.
11. If $S_1(t_1)+I_1(t_1)+R_1(t_1) = \frac{\Lambda_1}{\mu_1}$ then $(\dot{S_1}+\dot{I_1}+\dot{R_1})(t_1) = \Lambda_1 - \mu_1(S_1(t_1)+I_1(t_1)+R_1(t_1)) - \delta_1 I_1(t_1) = -\delta_1 I_1(t_1) < 0$. Hence there exists $\varepsilon > 0$, we have $H(t_1-\varepsilon) > H(t_1) = \frac{\Lambda_1}{\mu_1}$. So $X(t_1-\varepsilon) \notin \mathbb{D}$. Which is absurd.
12. If $S_2(t_1)+I_2(t_1)+R_2(t_1) = \frac{\Lambda_2}{\mu_2+\theta}$ then $(\dot{S_2}+\dot{I_2}+\dot{R_2})(t_1) = \Lambda_2 - (\mu_2+\theta)(S_2(t_1)+I_2(t_1)+R_2(t_1)) - \delta_1 I_2(t_1) = -\delta_2 I_2(t_1) < 0$. Hence there exists $\varepsilon > 0$, we have $E(t_1-\varepsilon) > E(t_1) = \frac{\Lambda_2}{\mu_2+\theta}$. So $X(t_1-\varepsilon) \notin \mathbb{D}$.Which is absurd.

As a result, no trajectory leaves $\mathbb{D}$. □

2.4 Disease-free equilibrium DFE : E^0

The disease-free equilibrium point, or DFE, will be found. It is the equilibrium that is reached when neither cercaria nor miracidium are present. Therefore, neither humans nor snails are infected. When we solve $dX(t) = 0$ under these circumstances, we obtain :

$$E^0 = \begin{pmatrix} \frac{(1-\lambda_1)\Lambda_1}{\mu_1} \\ \frac{(1-\lambda_2)\Lambda_2}{\mu_2+\theta} \\ 0 \\ 0 \\ \frac{\lambda_1\Lambda_1}{\mu_1} \\ \frac{\lambda_2\Lambda_2}{\mu_2+\theta} \\ 0 \\ 0 \end{pmatrix}$$

2.5 Basic reproduction number $\mathcal{R}_0$

The approach of VAN DEN DRIESSCHE and WATMOUGH (Driessche & Watmough, 2002) will be applied. Identifying the vectors of newly infected $\mathcal{F}$ and deliveries (dead or recovered from the infection) $\mathcal{V}$ will be our next task.

$\mathcal{F}$ and $\mathcal{V}$ matrices

$$\mathcal{F} = \begin{pmatrix} \beta_1 S_1(t) \int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)} \varphi_3(u)du \\ \beta_2 S_2(t) \int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)} \varphi_1(u)du \end{pmatrix}, \mathcal{V} = \begin{pmatrix} -(\mu_1+\delta_1+\eta)I_1(t) \\ -(\mu_2+\delta_2+\theta)I_2(t) \end{pmatrix}$$

F and V Jacobian matrices

$$\mathcal{F} = \begin{pmatrix} \mathcal{F}_1(I_1,I_2) \\ \mathcal{F}_2(I_1,I_2) \end{pmatrix}, \qquad \mathcal{V} = \begin{pmatrix} \mathcal{V}_1(I_1,I_2) \\ \mathcal{V}_2(I_1,I_2) \end{pmatrix}$$

$$\frac{\partial}{\partial I_1}\mathcal{F}_1(I_1,I_2) = \frac{\partial}{\partial P}\mathcal{F}_1(I_1,I_2) \times \frac{\partial P}{\partial I_1} = 0.$$

$\frac{\partial}{\partial I_2}\mathcal{F}_1(I_1,I_2) = \frac{\partial}{\partial P}\mathcal{F}_1(I_1,I_2) \times \frac{\partial P}{\partial I_2}$.
$\frac{\partial}{\partial P}\mathcal{F}_1(I_1,I_2) = \beta_1 S_1(t)\int_{H_2}^{H_3}\varphi_3(u)\frac{\partial}{\partial P}\left(\frac{P(t-u)}{1+\alpha_1 P(t-u)}\right)du = \beta_1 S_1(t)\int_{H_2}^{H_3}\varphi_3(u)\frac{1}{(1+\alpha_1 P(t-u))^2}du.$
$\frac{\partial}{\partial P}\mathcal{F}_1(I_1,I_2)\mid_{E^0} = \frac{\beta_1(1-\lambda_1)\Lambda_1}{\mu_1}$.
From system (2.3) and $\frac{dP}{dt} = 0$, we take $P(t) = \frac{\gamma_2}{\mu_4+\tau}\int_{H_1}^{H_2} I_2(t-u)\varphi_2(u)du$. Thus $\frac{\partial P}{\partial I_2} = \frac{\gamma_2}{\mu_4+\tau}$

$$\frac{\partial}{\partial I_2}\mathcal{F}_1(I_1,I_2)\mid_{E^0} = \frac{\beta_1(1-\lambda_1)\Lambda_1}{\mu_1} \times \frac{\gamma_2}{\mu_4+\tau} = \frac{\beta_1\gamma_2(1-\lambda_1)\Lambda_1}{\mu_1(\mu_4+\tau)}$$

$$\frac{\partial}{\partial I_1}\mathcal{F}_2(I_1,I_2)=\frac{\partial}{\partial M}\mathcal{F}_2(I_1,I_2)\times\frac{\partial M}{\partial I_1}$$
$$\frac{\partial}{\partial M}\mathcal{F}_2(I_1,I_2)\mid_{E^0}=\beta_2 S_2(t)\int_0^{h_2}\varphi_2(u)\frac{\partial}{\partial M}\left(\frac{M(t-u)}{M_0+\varepsilon M^2(t-u)}\right)du\mid_{E^0}=\frac{\beta_2(1-\lambda_2)\Lambda_2}{M_0(\mu_2+\theta)}.$$

From system (2.3) and $\frac{dM}{dt}=0$, we take $M(t)=\frac{k\gamma_1}{\mu_3}\int_{H_3}^{H_4}I_1(t-u)\varphi_4(u)du$. So $\frac{\partial M}{\partial I_1}=\frac{k\gamma_1}{\mu_3}$

$$\frac{\partial}{\partial I_1}\mathcal{F}_2(I_1,I_2)\mid_{E^0}=\frac{\beta_2(1-\lambda_2)\Lambda_2}{M_0(\mu_2+\theta)}\times\frac{k\gamma_1}{\mu_3}=\frac{k\beta_2\gamma_1(1-\lambda_2)\Lambda_2}{M_0\mu_3(\mu_2+\theta)}$$

$$\frac{\partial}{\partial I_2}\mathcal{F}_2(I_1,I_2)=\frac{\partial}{\partial M}\mathcal{F}_2(I_1,I_2)\times\frac{\partial M}{\partial I_2}=0$$

. Hence the Jacobian F is given by :

$$F=\begin{pmatrix}0 & \frac{\beta_1\gamma_2(1-\lambda_1)\Lambda_1}{\mu_1(\mu_4+\tau)}\\ \frac{k\beta_2\gamma_1(1-\lambda_2)\Lambda_2}{M_0\mu_3(\mu_2+\theta)} & 0\end{pmatrix}$$

$$\frac{\partial}{\partial I_1}\mathcal{V}_1(I_1,I_2)=-(\mu_1+\delta_1+\eta),\qquad \frac{\partial}{\partial I_2}\mathcal{V}_1(I_1,I_2)=0,\qquad \frac{\partial}{\partial I_1}\mathcal{V}_2(I_1,I_2)=0,\qquad \frac{\partial}{\partial I_2}\mathcal{V}_2(I_1,I_2)=-(\mu_2+\delta_2+\theta)$$

Hence the Jacobian V is given by :

$$V=\begin{pmatrix}-(\mu_1+\delta_1+\eta) & 0\\ 0 & -(\mu_2+\delta_2+\theta)\end{pmatrix}$$

Matrice Next Generation $-FV^{-1}$

$$-V^{-1}=\begin{pmatrix}\frac{1}{\mu_1+\delta_1+\eta} & 0\\ 0 & \frac{1}{\mu_2+\delta_2+\theta}\end{pmatrix}$$

$$-FV^{-1}=\begin{pmatrix}0 & \frac{\beta_1\gamma_2(1-\lambda_1)\Lambda_1}{\mu_1(\mu_4+\tau)(\mu_2+\delta_2+\theta)}\\ \frac{k\beta_2\gamma_1(1-\lambda_2)\Lambda_2}{M_0\mu_3(\mu_2+\theta)(\mu_1+\delta_1+\eta)} & 0\end{pmatrix}$$

Definition 2.1. (Spectral radius)

The spectral radius of a square matrix A is the maximum value of the modulus of the eigenvalues of A.

$$\rho(A)=\max_{\lambda\in Sp(A)}|\lambda|$$

Definition 2.2. ($\mathcal{R}_0$)
If the transmission matrix is stable then we define $\mathcal{R}_0$ by :

$$\mathcal{R}_0=\rho(-FV^{-1})$$

Value of $\mathcal{R}_0$

$$\mathcal{R}_0=\sqrt{\frac{k\beta_1\beta_2\gamma_1\gamma_2(1-\lambda_1)(1-\lambda_2)\Lambda_1\Lambda_2}{M_0\mu_1\mu_3(\mu_2+\theta)(\mu_4+\tau)(\mu_1+\delta_1+\eta)(\mu_2+\delta_2+\theta)}}$$

Interpretation of $\mathcal{R}_0$

$$\mathcal{R}_0 = \sqrt{\frac{\beta_1\gamma_2(1-\lambda_1)\Lambda_1}{\mu_1(\mu_4+\tau)(\mu_2+\delta_2+\theta)}} \times \sqrt{\frac{k\beta_2\gamma_1(1-\lambda_2)\Lambda_2}{M_0\mu_3(\mu_1+\delta_1+\eta)(\mu_2+\theta)}}$$

Number of individuals infected with parasites from an infected mollusc during it period of infectiousness immersed in a population of humans susceptible:

$$\mathcal{R}_0^H = \frac{\beta_1\gamma_2(1-\lambda_1)\Lambda_1}{\mu_1(\mu_4+\tau)(\mu_2+\delta_2+\theta)}$$

β_1 : The probability of transmission by contact of a cercariae with a human

$(1-\lambda_1)\Lambda_1$: Number of susceptible humans,

γ_2 : Rate of cercariae released by an infected mollusc,

$\frac{1}{\mu_1}$: lifespan of susceptible human
$\frac{1}{\mu_4+\tau}$: lifespan of cercariae
$\frac{1}{\mu_2+\delta_2+\theta}$: lifespan of infected mollusks.

Number of mollusks infected with parasites from eggs rejected by an infected human immersed in a population of susceptible mollusks:

$$\mathcal{R}_0^E = \frac{k\beta_2\gamma_1(1-\lambda_2)\Lambda_2}{M_0\mu_3(\mu_1+\delta_1+\eta)(\mu_2+\theta)}$$

β_2 the probability of transmission by contact between $S_2 - M$
$(1-\lambda_2)\Lambda_2$: Number of susceptible mollusks,
γ_1 : Rate of miracidium released by a hatched egg,

$\frac{k}{M_0}$: Egg rate
$\frac{1}{\mu_3}$: lifespan of miracidia
$\frac{1}{\mu_1+\delta_1+\eta}$: lifespan of infected human
$\frac{1}{\mu_2+\theta}$: lifespan of susceptible mollusks.

$\mathcal{R}_0$ is the geometric mean of $\mathcal{R}_0^H$ and $\mathcal{R}_0^E$

2.6 Endemic equilibrium point $E^\star$

Let determine the endemic equilibrium point, denoted EE. It is the point of equilibrium obtained by solving $dX(t) = 0$, we obtain :

$$I_1^\star = I_1(t^\star) \quad , \quad S_1^\star = S_1(t^\star) = S_1(I_1^\star) = \frac{(1-\lambda_1)\Lambda_1 - (\mu_1+\delta_1+\eta)I_1^\star}{\mu_1}$$

$$S_2^\star = S_2(t^\star) = S_2(I_1^\star) = \frac{\beta_1\gamma_2(1-\lambda_1)\Lambda_1(1-\lambda_2)\Lambda_2 - [\gamma_2(\beta_1+\alpha_1\mu_1)(1-\lambda_2)\Lambda_2 + \mu_1(\mu_4+\tau)(\mu_2+\delta_2+\theta)](\mu_1+\delta_1+\eta)I_1^\star}{\gamma_2(\mu_2+\theta)\left[\beta_1(1-\lambda_1)\Lambda_1 - (\mu_1+\delta_1+\eta)(\beta_1+\alpha_1\mu_1)I_1^\star\right]} \quad ,$$

$$I_2^\star = I_2(t^\star) = I_2(I_1^\star) = \frac{\mu_1(\mu_4+\tau)(\mu_1+\delta_1+\eta)I_1^\star}{\gamma_2\left[\beta_1(1-\lambda_1)\Lambda_1 - (\beta_1+\alpha_1\mu_1)(\mu_1+\delta_1+\eta)I_1^\star\right]} \quad , \quad R_1^\star = R_1(t^\star) = R_1(I_1^\star) = \frac{\lambda_1\Lambda_1 + \eta I_1^\star}{\mu_1}$$

$$R_2^\star = R_2(t^\star) = R_2(I_1^\star) = \frac{\lambda_2\Lambda_2}{\mu_2} \quad , \quad M^\star = M(t^\star) = M(I_1^\star) = \frac{k\gamma_1 I_1^\star}{\mu_3} \quad ,$$

$$P^\star = P(t^\star) = P(I_1^\star) = \frac{\mu_1(\mu_1+\delta_1+\eta)I_1^\star}{\beta_1(1-\lambda_1)\Lambda_1 - (\beta_1+\alpha_1\mu_1)(\mu_1+\delta_1+\eta)I_1^\star}$$

Now, from the equation $dI_2dt(t^\star) = 0$ let's substitute $S_2^\star$, $M^\star$ and $I_2^\star$ by their respective expressions in $I_1^\star$. We have the following equation

$$\begin{aligned} & I_1^\star\Big(\mu_3(k\beta_1\beta_2\gamma_1\gamma_2(1-\lambda_1)(1-\lambda_2)\Lambda_1\Lambda_2 - M_0\mu_1\mu_3(\mu_2+\theta)(\mu_4+\tau)(\mu_1+\delta_1+\eta)(\mu_2+\delta_2+\theta)) \\ & -k\gamma_1\beta_2\mu_3(\mu_1+\delta_1+\eta)\Big(\gamma_2(1-\lambda_2)\Lambda_2(\beta_1+\alpha_1\mu_1) + \mu_1(\mu_2+\delta_2+\theta)(\mu_4+\tau)\Big)I_1^\star \\ & -\mu_1(\mu_2+\theta)(\mu_4+\tau)(\mu_1+\delta_1+\eta)(\mu_2+\delta_2+\theta)\varepsilon k^2\gamma_1^2 I_1^{\star 2}\Big) \\ & = 0 \end{aligned} \tag{2.5}$$

Let's pose

$$\begin{aligned} c_1 &= \mu_3(k\beta_1\beta_2\gamma_1\gamma_2(1-\lambda_1)(1-\lambda_2)\Lambda_1\Lambda_2 - M_0\mu_1\mu_3(\mu_2+\theta)(\mu_4+\tau)(\mu_1+\delta_1+\eta)(\mu_2+\delta_2+\theta)) \\ &= \mu_1 M_0\mu_1\mu_3(\mu_2+\theta)(\mu_4+\tau)(\mu_1+\delta_1+\eta)(\mu_2+\delta_2+\theta)(\mathcal{R}_0^2-1) \\ c_2 &= -k\gamma_1\beta_2\mu_3(\mu_1+\delta_1+\eta)\Big(\gamma_2(1-\lambda_2)\Lambda_2(\beta_1+\alpha_1\mu_1) + \mu_1(\mu_2+\delta_2+\theta)(\mu_4+\tau)\Big)I_1^\star \\ c_3 &= -\mu_1(\mu_2+\theta)(\mu_4+\tau)(\mu_1+\delta_1+\eta)(\mu_2+\delta_2+\theta)\varepsilon k^2\gamma_1^2 I_1^{\star 2} \end{aligned}$$

Hence c_2 and c_3 are negative and c_1 is positive for $\mathcal{R}_0 > 1$.

Equation (2.5) can be rewritten as

$$I_1^\star\left(c_1 + c_2 I_1^\star + c_3 I_1^{\star 2}\right) = 0 \tag{2.6}$$

By solving the equation (2.6) of unknown I, we obtain a null solution corresponding to the free-disease equilibrium which exists in the conditions of endemic equilibrium.

Let's solve the second factor equal to zero. For $\mathcal{R}_0 > 1$, c_1 is positive and c_3 negative, hence the equation admits a unique positive solution.

The endemic equilibrium point is $E^\star$

$$E^\star = \begin{pmatrix} \frac{(1-\lambda_1)\Lambda_1 - (\mu_1+\delta_1+\eta)I_1^\star}{\mu_1} \\ \frac{\beta_1\gamma_2(1-\lambda_1)\Lambda_1(1-\lambda_2)\Lambda_2 - [\gamma_2(\beta_1+\alpha_1\mu_1)(1-\lambda_2)\Lambda_2 + \mu_1(\mu_4+\tau)(\mu_2+\delta_2+\theta)](\mu_1+\delta_1+\eta)I_1^\star}{\gamma_2(\mu_2+\theta)\left[\beta_1(1-\lambda_1)\Lambda_1 - (\mu_1+\delta_1+\eta)(\beta_1+\alpha_1\mu_1)I_1^\star\right]} \\ I_1^\star \\ \frac{\mu_1(\mu_4+\tau)(\mu_1+\delta_1+\eta)I_1^\star}{\gamma_2\left[\beta_1(1-\lambda_1)\Lambda_1 - (\beta_1+\alpha_1\mu_1)(\mu_1+\delta_1+\eta)I_1^\star\right]} \\ \frac{\lambda_1\Lambda_1+\eta I_1^\star}{\mu_1} \\ \frac{\lambda_2\Lambda_2}{\mu_2} \\ \frac{k\gamma_1 I_1^\star}{\mu_3} \\ \frac{\mu_1(\mu_1+\delta_1+\eta)I_1^\star}{\beta_1(1-\lambda_1)\Lambda_1 - (\beta_1+\alpha_1\mu_1)(\mu_1+\delta_1+\eta)I_1^\star} \end{pmatrix}$$

Theorem 2.4.

The system (2.3) *always has the disease-free equilibrium point (DFE)* E^0

- *When* $\mathcal{R}_0 \leq 1$ *, the disease-free equilibrium point* E^0 *is the only equilibrium point of the system* (2.3) *and* E^0 *is globally asymptotically stable in* $\mathbb{D}$*.*
- *When* $\mathcal{R}_0 > 1$*, the disease-free equilibrium point* E^0 *is unstable.*

Proof of Theorem 2.4. .

Let us determine the Jacobian matrix of the system (2.3) at point E^0

$\frac{\partial}{\partial X_1}F_1(E^0) = -\mu_1$	$\frac{\partial}{\partial X_i}F_1(E^0) = 0 \ \forall\, i \in \{2,...,7\}$	$\frac{\partial}{\partial X_8}F_1(E^0) = -\frac{\beta_1(1-\lambda_1)\Lambda_1}{\mu_1}$
$\frac{\partial}{\partial X_2}F_2(E^0) = -(\mu_2+\theta)$	$\frac{\partial}{\partial X_i}F_2(E^0) = 0 \ \forall\, i \in \{1,3,...,6,8\}$	$\frac{\partial}{\partial X_7}F_2(E^0) = -\frac{\beta_2(1-\lambda_2)\Lambda_2}{M_0(\mu_2+\theta)}$
$\frac{\partial}{\partial X_3}F_3(E^0) = -(\mu_1+\delta_1+\eta)$	$\frac{\partial}{\partial X_i}F_3(E^0) = 0 \ \forall\, i \in \{1,2,4,...,7\}$	$\frac{\partial}{\partial X_8}F_3(E^0) = \frac{\beta_1(1-\lambda_1)\Lambda_1}{\mu_1}$
$\frac{\partial}{\partial X_4}F_4(E^0) = -(\mu_2+\delta_2+\theta)$	$\frac{\partial}{\partial X_i}F_4(E^0) = 0 \ \forall\, i \in \{1,2,3,5,6,8\}$	$\frac{\partial}{\partial X_7}F_4(E^0) = \frac{\beta_2(1-\lambda_2)\Lambda_2}{M_0(\mu_2+\theta)}$
$\frac{\partial}{\partial X_3}F_5(E^0) = \eta$	$\frac{\partial}{\partial X_5}F_5(E^0) = -\mu_1$	$\frac{\partial}{\partial X_i}F_5(E^0) = 0 \ \forall\, i \in \{1,2,4,6,7,8\}$
$\frac{\partial}{\partial X_6}F_6(E^0) = -(\mu_2+\theta)$	$\frac{\partial}{\partial X_i}F_6(E^0) = 0 \ \forall\, i \in \{1,...,5,7,8\}$	
$\frac{\partial}{\partial X_3}F_7(E^0) = k\gamma_1$	$\frac{\partial}{\partial X_i}F_7(E^0) = 0 \ \forall\, i \in \{1,2,4,...,6,8\}$	$\frac{\partial}{\partial X_7}F_7(E^0) = -\mu_3$
$\frac{\partial}{\partial X_4}F_8(E^0) = \gamma_2$	$\frac{\partial}{\partial X_i}F_8(E^0) = 0 \ \forall\, i \in \{1,2,3,5,6,7\}$	$\frac{\partial}{\partial X_8}F_8(E^0) = -(\mu_4+\tau)$

$$J_F(E^0) = \begin{pmatrix} -\mu_1 & 0 & 0 & 0 & 0 & 0 & 0 & -\frac{\beta_1(1-\lambda_1)\Lambda_1}{\mu_1} \\ 0 & -(\mu_2+\theta) & 0 & 0 & 0 & 0 & -\frac{\beta_2(1-\lambda_2)\Lambda_2}{M_0(\mu_2+\theta)} & 0 \\ 0 & 0 & -(\mu_1+\delta_1+\eta) & 0 & 0 & 0 & 0 & \frac{\beta_1(1-\lambda_1)\Lambda_1}{\mu_1} \\ 0 & 0 & 0 & -(\mu_2+\delta_2+\theta) & 0 & 0 & \frac{\beta_2(1-\lambda_2)\Lambda_2}{M_0(\mu_2+\theta)} & 0 \\ 0 & 0 & \eta & 0 & -\mu_1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -(\mu_2+\theta) & 0 & 0 \\ 0 & 0 & k\gamma_1 & 0 & 0 & 0 & -\mu_3 & 0 \\ 0 & 0 & 0 & \gamma_2 & 0 & 0 & 0 & -(\mu_4+\tau) \end{pmatrix}$$

Let λ be a scalar, study the eigenvalues of the Jacobian matrice at point E^0
$det(J_F(E^0) - \lambda I_8)$

$$= \begin{pmatrix} -\mu_1-\lambda & 0 & 0 & 0 & 0 & 0 & 0 & -\frac{\beta_1(1-\lambda_1)\Lambda_1}{\mu_1} \\ 0 & -(\mu_2+\theta)-\lambda & 0 & 0 & 0 & 0 & -\frac{\beta_2(1-\lambda_2)\Lambda_2}{M_0(\mu_2+\theta)} & 0 \\ 0 & 0 & -(\mu_1+\delta_1+\eta)-\lambda & 0 & 0 & 0 & 0 & \frac{\beta_1(1-\lambda_1)\Lambda_1}{\mu_1} \\ 0 & 0 & 0 & -(\mu_2+\delta_2+\theta)-\lambda & 0 & 0 & \frac{\beta_2(1-\lambda_2)\Lambda_2}{M_0(\mu_2+\theta)} & 0 \\ 0 & 0 & \eta & 0 & -\mu_1-\lambda & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -(\mu_2+\theta)-\lambda & 0 & 0 \\ 0 & 0 & k\gamma_1 & 0 & 0 & 0 & -\mu_3-\lambda & 0 \\ 0 & 0 & 0 & \gamma_2 & 0 & 0 & 0 & -(\mu_4+\tau)-\lambda \end{pmatrix}$$

$$= (\mu_1+\lambda)^2(\mu_2+\theta+\lambda)^2\left(-\mathcal{R}_0^2\mu_3(\mu_4+\tau)(\mu_1+\delta_1+\eta)(\mu_2+\delta_2+\theta)+(\mu_3+\lambda)(\mu_1+\delta_1+\eta+\lambda)(\mu_2+\delta_2+\theta+\lambda)(\mu_4+\tau+\lambda)\right)$$

$det(J_F(E^0) - \lambda I_8) = 0$ is equivalent to

- $(\mu_1+\lambda)^2 = 0$. Hence $-\mu_1 < 0$ is a double eigenvalue.
- $(\mu_2+\theta+\lambda)^2 = 0$. Hence $-(\mu_2+\theta) < 0$ is a double eigenvalue.
- $-\mathcal{R}_0^2\mu_3(\mu_4+\tau)(\mu_1+\delta_1+\eta)(\mu_2+\delta_2+\theta)+(\mu_3+\lambda)(\mu_1+\delta_1+\eta+\lambda)(\mu_2+\delta_2+\theta+\lambda)(\mu_4+\tau+\lambda)$ $= 0$. Hence $\mathcal{R}_0^2\mu_3(\mu_4+\tau)(\mu_1+\delta_1+\eta)(\mu_2+\delta_2+\theta) = (\mu_3+\lambda)(\mu_1+\delta_1+\eta+\lambda)(\mu_2+\delta_2+\theta+\lambda)(\mu_4+\tau+\lambda)$

Write λ in the algebraic form where a and b are reals numbers such that $\lambda = a+ib$.

Let us calculate the squares of the modulus in the previous equality.

$\left((\mu_3+a)^2+b^2\right)\left((\mu_1+\delta_1+\eta+a)^2+b^2\right)\left((\mu_2+\delta_2+\theta+a)^2+b^2\right)\left((\mu_4+\tau+a)^2+b^2\right)$
$= \mathcal{R}_0^4\mu_3^2(\mu_4+\tau)^2(\mu_1+\delta_1+\eta)^2(\mu_2+\delta_2+\theta)^2$
As $\mathcal{R}_0 \leq 1$ then
$\left((\mu_3+a)^2+b^2\right)\left((\mu_1+\delta_1+\eta+a)^2+b^2\right)\left((\mu_2+\delta_2+\theta+a)^2+b^2\right)\left((\mu_4+\tau+a)^2+b^2\right)$
$\leq \mu_3^2(\mu_4+\tau)^2(\mu_1+\delta_1+\eta)^2(\mu_2+\delta_2+\theta)^2$

To obtain $(\mu_3+a)^2+b^2 \leq \mu_3^2$, a must be negative.
So in each of the three cases the eigenvalues have negative real part. Hence E^0 is asymptotically stable.
By using the Theorem 2.2, we can deduce that E^0 is globally asymptotically stable.

For $a > 0$, It is impossible that $(\mu_3+a)^2+b^2 \leq \mu_3^2$, $(\mu_1+\delta_1+\eta+a)^2+b^2 \leq (\mu_1+\delta_1+\eta)^2$
, $(\mu_4+\tau+a)^2+b^2 \leq (\mu_4+\tau)^2$, nor $(\mu_2+\delta_2+\theta+a)^2+b^2 \leq (\mu_2+\delta_2+\theta)^2$.
Which means that $a > 0$ for $\mathcal{R}_0 > 1$.

For $\mathcal{R}_0 > 1$ a eigenvalue has its strictly positive real part. We deduce that for $\mathcal{R}_0 > 1$, the disease-free equilibrium point E^0 is unstable. □

Theorem 2.5.

The system (2.3) *has an endemic equilibrium point(EE),* $E^\star$ *when* $\mathcal{R}_0 > 1$. $E^\star$ *is globally asymptotically stable in* $\mathbb{D}$.

Lemma 2.6.
Let f *the definite function of* $]0;+\infty[$ *in* $[0;+\infty[$
by $\forall x > 0$ $f(x) = x - 1 - ln(x)$ f *is strictly decreasing over* $]0;1[$ *and is strictly increasing over* $]1;+\infty[$.
$f(1) = 0$ *and* $\forall x \in]\,0;1[\cup]1;+\infty[$, $f(x) > 0$.

Proof of Theorem 2.5. .

Suppose that $\mathcal{R}_0 > 1$, and let prove that $E^\star$ is globally asymptotically stable
We define the following functions :
For all $t \geq 0$ and $X(t)$ in $\mathbb{D}$, we have $X(t) = (S_1(t);S_2(t);I_1(t);I_2(t);R_1(t);R_2(t);M(t);P(t))^\intercal$

$$\begin{aligned}
V_H(t) =& S_1(t) + I_1(t) + R_1(t) - (S_1^\star + I_1^\star + R_1^\star) - (S_1^\star + I_1^\star + R_1^\star)\ln\left(\frac{S_1(t)+I_1(t)+R_1(t)}{S_1^\star + I_1^\star + R_1^\star}\right)\\
=& H(t^\star)\left(\frac{H(t)}{H(t^\star)} - 1 - ln\left(\frac{H(t)}{H(t^\star)}\right)\right)\\
=& H(t^\star)\, f\left(\frac{H(t)}{H(t^\star)}\right)
\end{aligned}$$

$$\begin{aligned}
V_E(t) =& S_2(t) + I_2(t) + R_2(t) - (S_2^\star + I_2^\star + R_2^\star) - (S_2^\star + I_2^\star + R_2^\star)\ln\left(\frac{S_2(t)+I_2(t)+R_2(t)}{S_2^\star + I_2^\star + R_2^\star}\right)\\
=& E(t^\star)\left(\frac{E(t)}{E(t^\star)} - 1 - ln\left(\frac{E(t)}{E(t^\star)}\right)\right)\\
=& E(t^\star)\, f\left(\frac{E(t)}{E(t^\star)}\right)
\end{aligned}$$

$$V_M(t) = M(t) - M^\star - M^\star \ln\left(\frac{M(t)}{M^\star}\right) = M^\star\left(\frac{M(t)}{M^\star} - 1 - ln\left(\frac{M(t)}{M^\star}\right)\right) = M^\star f\left(\frac{M(t)}{M^\star}\right)$$

$$V_P(t) = P(t) - P^\star - P^\star \ln\left(\frac{P(t)}{P^\star}\right) = P^\star\left(\frac{P(t)}{P^\star} - 1 - ln\left(\frac{P(t)}{P^\star}\right)\right) = P^\star f\left(\frac{P(t)}{P^\star}\right).$$

Let $V(t) = V_H(t) + V_E(t) + V_M(t) + V_P(t)$
$\forall i \in \{1;...;8\}$, $\dfrac{X_i(t)}{X_i(t^\star)} \neq 1$ for all positive $t$and different from $t^\star$
Hence $f\left(\dfrac{X_i(t)}{X_i(t^\star)}\right) > 0$.
For any positive t , different from $t^\star$, $V(t) > 0$ and $V(t^\star) = 0$.
As a result, V is a positive definite function and now let us verify that $\dfrac{dV}{dt}$ is definite negative.

$$\frac{dV_H(t)}{dt} = H(t^\star)\left(\frac{1}{H(t^\star)}\frac{dH(t)}{dt} - \frac{1}{H(t)}\frac{dH(t)}{dt}\right) = \frac{dH(t)}{dt}\left(1 - \frac{H(t^\star)}{H(t)}\right)$$

$$\frac{dV_H(t)}{dt} = \Big(\Lambda_1 - \mu_1 H(t) - \delta_1 I_1(t)\Big)\left(\frac{H(t) - H(t^\star)}{H(t)}\right)$$

$$Yet \quad \frac{dH(t^\star)}{dt} = \Lambda_1 - \mu_1 H(t^\star) - \delta_1 I_1(t^\star) = 0$$

$$\frac{dH(t)}{dt} = \frac{dH(t)}{dt} - \frac{dH(t^\star)}{dt} = -\mu_1\left(H(t) - H(t^\star)\right) - \delta_1\left(I_1(t) - I_1(t^\star)\right)$$

Hence, $\frac{dH(t)}{dt}$, $-H(t)$ *and* $-I_1(t)$ have the same direction of variation from t to $t^\star$
So $H(t)-H(t^\star)$ and $I_1(t)-I_1(t^\star)$ have the same sign.

$$\begin{aligned}\frac{dV_H(t)}{dt} &= \left(\mu_1 H(t^\star)+\delta_1 I_1(t^\star)-\mu_1 H(t)-\delta_1 I_1(t)\right)\left(\frac{H(t)-H(t^\star)}{H(t)}\right)\\ &= \left(\mu_1\left(H(t^\star)-H(t)\right)+\delta_1\left(I_1(t^\star)-I_1(t)\right)\right)\left(\frac{H(t)-H(t^\star)}{H(t)}\right)\\ &= -\frac{\mu_1}{H(t)}\left(H(t)-H(t^\star)\right)^2-\frac{\delta_1 I_1(t)}{H(t)}\left(1-\frac{I_1(t^\star)}{I_1(t)}\right)\left(1-\frac{H(t^\star)}{H(t)}\right)\end{aligned}$$

Now let's expand,

$$\begin{aligned}\left(1-\frac{I_1(t^\star)}{I_1(t)}\right)\left(1-\frac{H(t^\star)}{H(t)}\right) &= 1-\frac{I_1(t^\star)}{I_1(t)}-\frac{H(t^\star)}{H(t)}+\frac{I_1(t^\star)}{I_1(t)}\frac{H(t^\star)}{H(t)}\\ &= -\left(\frac{I_1(t^\star)}{I_1(t)}-1-LN\left(\frac{I_1(t^\star)}{I_1(t)}\right)\right)-\left(\frac{H(t^\star)}{H(t)}-1-LN\left(\frac{H(t^\star)}{H(t)}\right)\right)\\ &+\left(\frac{I_1(t^\star)}{I_1(t)}\frac{H(t^\star)}{H(t)}-1-LN\left(\frac{I_1(t^\star)}{I_1(t)}\frac{H(t^\star)}{H(t)}\right)\right)\\ &= -f\left(\frac{I_1(t^\star)}{I_1(t)}\right)-f\left(\frac{H(t^\star)}{H(t)}\right)+f\left(\frac{I_1(t^\star)}{I_1(t)}\frac{H(t^\star)}{H(t)}\right)\end{aligned}$$

As $H(t)-H(t^\star)$ and $I_1(t)-I_1(t^\star)$ have the same sign then $\left(1-\frac{I_1(t^\star)}{I_1(t)}\right)$ and $\left(1-\frac{H(t^\star)}{H(t)}\right)$ have also the same sign.

Consequently $\forall t\neq t^\star$, $f\left(\frac{I_1(t^\star)}{I_1(t)}\frac{H(t^\star)}{H(t)}\right) > f\left(\frac{I_1(t^\star)}{I_1(t)}\right)+f\left(\frac{H(t^\star)}{H(t)}\right)$.

$\forall \neq t^\star$ $\frac{dV_H(t)}{dt} < 0$ and $\frac{dV_H(t^\star)}{dt} = 0$

As a result $\frac{dV_H}{dt}$ is definite negative.

$$\frac{dV_E(t)}{dt} = E(t^\star)\left(\frac{1}{E(t^\star)}\frac{dE(t)}{dt}-\frac{1}{E(t)}\frac{dE(t)}{dt}\right) = \frac{dE(t)}{dt}\left(1-\frac{E(t^\star)}{E(t)}\right)$$

$\frac{dE(t)}{dt} = \Lambda_2-(\mu_2+\theta)E(t)-\delta_2 I_2(t)$

Yet $\frac{dE(t^\star)}{dt} = \Lambda_2-(\mu_2+\theta)E(t^\star)-\delta_2 I_2(t^\star) = 0$

$$\frac{dE(t)}{dt} = \frac{dE(t)}{dt}-\frac{dE(t^\star)}{dt} = -(\mu_2+\theta)\left(E(t)-E(t^\star)\right)-\delta_2\left(I_2(t)-I_2(t^\star)\right)$$

Thus $\frac{dE(t)}{dt} = -(\mu_2+\theta)\left(E(t)-E(t^\star)\right)-\delta_2\left(I_2(t)-I_2(t^\star)\right)$

Hence,

$$\begin{aligned}\frac{dV_E(t)}{dt} &= \left(-(\mu_2+\theta)\left(E(t)-E(t^\star)\right)-\delta_2\left(I_2(t)-I_2(t^\star)\right)\right)\left(\frac{E(t)-E(t^\star)}{E(t)}\right)\\ &= -\frac{\mu_2+\theta}{E(t)}\left(E(t)-E(t^\star)\right)^2-\frac{\delta_2}{E(t)}\left(I_2(t)-I_2(t^\star)\right)\left(E(t)-E(t^\star)\right)\end{aligned}$$

$\frac{\delta_2}{E(t)}\left(I_2(t)-I_2(t^\star)\right)\left(E(t)-E(t^\star)\right) = \delta_2 I_2(t)\left(1-\frac{I_2(t^\star)}{I_2(t)}\right)\left(1-\frac{E(t^\star)}{E(t)}\right)$

Let expand and let transform as before.

$$\left(1-\frac{I_2(t^\star)}{I_2(t)}\right)\left(1-\frac{E(t^\star)}{E(t)}\right)=1-\frac{I_2(t^\star)}{I_2(t)}-\frac{E(t^\star)}{E(t)}+\frac{I_2(t^\star)}{I_2(t)}\frac{E(t^\star)}{E(t)}=-\left(\frac{I_2(t^\star)}{I_2(t)}-1-\ln\left(\frac{I_2(t^\star)}{I_2(t)}\right)\right)$$
$$-\left(\frac{E(t^\star)}{E(t)}-1-\ln\left(\frac{E(t^\star)}{E(t)}\right)\right)+\left(\frac{I_2(t^\star)}{I_2(t)}\frac{E(t^\star)}{E(t)}-1-\ln\left(\frac{I_2(t^\star)}{I_2(t)}\frac{E(t^\star)}{E(t)}\right)\right)$$
$$=-f\left(\frac{I_2(t^\star)}{I_2(t)}\right)-f\left(\frac{E(t^\star)}{E(t)}\right)+f\left(\frac{I_2(t^\star)}{I_2(t)}\frac{E(t^\star)}{E(t)}\right)$$

By a justification similar to that seen, we get:

$$f\left(\frac{I_2(t^\star)}{I_2(t)}\right)+f\left(\frac{E(t^\star)}{E(t)}\right)<f\left(\frac{I_2(t^\star)}{I_2(t)}\frac{E(t^\star)}{E(t)}\right)$$

Hence,
$\forall\ t\neq t^\star,\ \frac{dV_E(t)}{dt}<0$ and for $t=t^\star\ \frac{dV_E(t)}{dt}=0$
From the above $\frac{dV_E}{dt}$ is negative definite.

$$\frac{dV_M(t)}{dt}=M(t^\star)\left(\frac{1}{M(t^\star)}\frac{dM(t)}{dt}-\frac{1}{M(t)}\frac{dM(t)}{dt}\right)=\frac{dM(t)}{dt}\left(1-\frac{M(t^\star)}{M(t)}\right)$$
$$=\left(k\gamma_1\phi_4(t)-\mu_3M(t)\right)\frac{M(t)-M(t^\star)}{M(t)}$$

As $\frac{dM(t^\star)}{dt}=k\gamma_1\phi_4(t^\star)-\mu_3M(t^\star)=0$ then, $\frac{dM(t)}{dt}-\frac{dM(t^\star)}{dt}=k\gamma_1\left(\phi_4(t)-\phi_4(t^\star)\right)-\mu_3\left(M(t)-M(t^\star)\right)$
Hence, $\frac{dM(t)}{dt}$, $\phi_4(t)$ *and* $-M(t)$ have the same direction of variation from t to $t^\star$
So $\phi_4(t)-\phi_4(t^\star)$ and $-(M(t)-M(t^\star))$ have the same sign.

$$\frac{dV_M(t)}{dt}=\left(k\gamma_1\left(\phi_4(t)-\phi_4(t^\star)\right)-\mu_3\left(M(t)-M(t^\star)\right)\right)\frac{M(t)-M(t^\star)}{M(t)}$$
$$=-\frac{\mu_3}{M(t)}\left(M(t)-M(t^\star)\right)^2+\frac{k\gamma_1}{M(t)}\left(\phi_4(t)-\phi_4(t^\star)\right)\left(M(t)-M(t^\star)\right)$$
$$=-\frac{\mu_3}{M(t)}\left(M(t)-M(t^\star)\right)^2+\frac{k\gamma_1}{\phi_4(t)}\left(1-\frac{\phi_4(t^\star)}{\phi_4(t)}\right)\left(1-\frac{M(t^\star)}{M(t)}\right)$$

As $\phi_4(t)-\phi_4(t^\star)$ and $M(t)-M(t^\star)$ have opposite signs then $\left(1-\frac{\phi_4(t^\star)}{\phi_4(t)}\right)$ and $\left(1-\frac{M(t^\star)}{M(t)}\right)$ also have opposite signs.
Let's develop $\left(1-\frac{\phi_4(t^\star)}{\phi_4(t)}\right)\left(1-\frac{M(t^\star)}{M(t)}\right)$

$$\left(1-\frac{\phi_4(t^\star)}{\phi_4(t)}\right)\left(1-\frac{M(t^\star)}{M(t)}\right)=1-\frac{\phi_4(t^\star)}{\phi_4(t)}-\frac{M(t^\star)}{M(t)}+\frac{\phi_4(t^\star)}{\phi_4(t)}\frac{M(t^\star)}{M(t)}$$
$$=-\left(\frac{\phi_4(t^\star)}{\phi_4(t)}-1-ln\left(\frac{\phi_4(t^\star)}{\phi_4(t)}\right)\right)-\left(\frac{M(t^\star)}{M(t)}-1-ln\left(\frac{M(t^\star)}{M(t)}\right)\right)$$
$$+\left(\frac{\phi_4(t^\star)}{\phi_4(t)}\frac{M(t^\star)}{M(t)}-1-ln\left(\frac{\phi_4(t^\star)}{\phi_4(t)}\frac{M(t^\star)}{M(t)}\right)\right)$$
$$=-f\left(\frac{\phi_4(t^\star)}{\phi_4(t)}\right)-f\left(\frac{M(t^\star)}{M(t)}\right)+f\left(\frac{\phi_4(t^\star)}{\phi_4(t)}\frac{M(t^\star)}{M(t)}\right)$$

Yet $f\left(\frac{\phi_4(t^\star)}{\phi_4(t)}\right)+f\left(\frac{M(t^\star)}{M(t)}\right)>f\left(\frac{\phi_4(t^\star)}{\phi_4(t)}\frac{M(t^\star)}{M(t)}\right)$
Hence,

$\forall t \neq t^\star \ \dfrac{dV_M(t)}{dt} < 0$ and $\dfrac{dV_M(t)}{dt} = 0$ for $t = t^\star$
Hence $\dfrac{dV_M(t)}{dt}$ is definite negative.

$$\begin{aligned}\frac{dV_P(t)}{dt} =& P(t^\star)\left(\frac{1}{P(t^\star)}\frac{dP(t)}{dt} - \frac{1}{P(t)}\frac{dP(t)}{dt}\right) = \frac{dP(t)}{dt}\left(1 - \frac{P(t^\star)}{P(t)}\right)\\ =& \left(\gamma_2\phi_2(t) - (\mu_4+\tau)P(t)\right)\frac{P(t)-P(t^\star)}{P(t)}\end{aligned}$$

As $\dfrac{dP(t^\star)}{dt} = \gamma_2\phi_2(t^\star) - (\mu_4+\tau)P(t^\star) = 0$
Then $\dfrac{dP(t)}{dt} = \dfrac{dP(t)}{dt} - \dfrac{dP(t^\star)}{dt} = \gamma_2\left(\phi_2(t) - \phi_2(t^\star)\right) - (\mu_4+\tau)\left(P(t) - P(t^\star)\right)$
It can be deduced that $\left(\phi_2(t) - \phi_2(t^\star)\right)$ and $\left(P(t) - P(t^\star)\right)$ have opposite signs.

$$\begin{aligned}\frac{dV_P(t)}{dt} =& \left(\gamma_2\left(\phi_2(t) - \phi_2(t^\star)\right) - (\mu_4+\tau)\left(P(t) - P(t^\star)\right)\right)\frac{P(t)-P(t^\star)}{P(t)}\\ =& -\frac{\mu_4+\tau}{P(t)}\left(P(t) - P(t^\star)\right)^2 + \gamma_2\phi_2(t)\left(1 - \frac{P(t^\star)}{P(t)}\right)\left(1 - \frac{\phi_2(t^\star)}{\phi_2(t)}\right)\end{aligned}$$

In a similar way as before

$$\left(1 - \frac{P(t^\star)}{P(t)}\right)\left(1 - \frac{\phi_2(t^\star)}{\phi_2(t)}\right) = -f\left(\frac{P(t^\star)}{P(t)}\right) - f\left(\frac{\phi_2(t^\star)}{\phi_2(t)}\right) + f\left(\frac{P(t^\star)}{P(t)}\frac{\phi_2(t^\star)}{\phi_2(t)}\right)$$

Yet $f\left(\dfrac{P(t^\star)}{P(t)}\right) + f\left(\dfrac{\phi_2(t^\star)}{\phi_2(t)}\right) > f\left(\dfrac{P(t^\star)}{P(t)}\dfrac{\phi_2(t^\star)}{\phi_2(t)}\right)$
Hence,
$\forall t \neq t^\star \ \dfrac{dV_P(t)}{dt} < 0$ and $\dfrac{dV_P(t)}{dt} = 0$ pour $t = t^\star$
Hence $\dfrac{dV_P(t)}{dt}$ is definite negative.
So, $\dfrac{dV}{dt}$ is definite negative.

Additionally, by referring to the chapter on stability in (Mullhaupt, 2009), we can affirm that the endemic equilibrium point $E^\star$ is asymptotically stable in $\mathbb{D}$ when $\mathcal{R}_0 > 1$. □

3 Formulation and Analysis of the Stochastic Model

3.1 From ordinary differential equation to stochastic differential equation

We will retain all of the previous section's annotations in this section. The females deposit their eggs in the fine venous branches of the bladder or the intestine, depending on the species. The eggs break and enter the organ's cavity and are then expelled by the stool or urine (S. haematobium). In the event that the eggs become embolized within the tissues, a histological section containing the fixed and calcified eggs will have an eosinophilic granuloma encircling it. Extra-intestinal locations result from either random parasite migration or, more frequently, from the Portocave anastomoses' massive embolization of live eggs. These are typically neurological and cardiovascular sites with three different kinds of complications. (Professeur Aubri & Docteur Gauzère, 2021) If the patient is not attended to promptly, he may develop complications that are not treatable with praziquantel.

Let us examine the changes in the vector $Z(t) = (S_1(t); S_2(t); I_1(t); I_2(t); R_1(t); R_2(t); M(t); P(t))^{\mathsf{T}}$ between times t and $t+\Delta t$, where Δt represents a very small time variation.

If Δt is sufficiently small, then $\Delta S_1(t)$ changes either by 0 or by 1. An increase by 1 corresponds to a new birth with a probability of $(1-\lambda_1)\Lambda_1\Delta t$. A decrease by 1 occurs either due to a new infection with the probability $\beta_1 S_1(t)\int_{H_2}^{H_3}\frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du\Delta t$, or due to a natural death with the probability $\mu_1 S_1(t)\Delta t$. The probability that $\Delta S_1(t)$ remains unchanged (varies by 0) is given by: $1-\left((1-\lambda_1)\Lambda_1\Delta t+\beta_1 S_1(t)\int_{H_2}^{H_3}\frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du\Delta t+\mu_1 S_1(t)\Delta t\right)$

Hence $\Delta S_1(t) = (1-\lambda_1)\Lambda_1\Delta t-\beta_1 S_1(t)\int_{H_2}^{H_3}\frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du\Delta t-\mu_1 S_1(t)\Delta t$

Similarly, $\Delta S_2(t) = (1-\lambda_2)\Lambda_2\Delta t-\beta_2 S_2(t)\int_{H_0}^{H_1}\frac{M(t-u)}{M_0+\varepsilon M^2(t-u)}\varphi_1(u)du\Delta t-(\mu_2+\theta)S_2(t)\Delta t$

$\Delta I_1(t)$ increases by 1 due to a new infection with the probability $\beta_1 S_1(t)\int_{H_2}^{H_3}\frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du\Delta t$ and decreases by 1 due to death or recovery with the probability $(\mu_1+\delta_1+\eta)I_1(t)\Delta t$.

$\Delta I_1(t)$ remains unchanged with the probability: $1-\left(\beta_1 S_1(t)\int_{H_2}^{H_3}\frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du\Delta t+(\mu_1+\delta_1+\eta)I_1(t)\Delta t\right)$

Therefore, $\Delta I_1(t) = \beta_1 S_1(t)\int_{H_2}^{H_3}\frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du\Delta t-(\mu_1+\delta_1+\eta)I_1(t)\Delta t$.

Similarly, $\Delta I_2(t) = \beta_2 S_2(t)\int_{H_0}^{H_1}\frac{M(t-u)}{M_0+\varepsilon M^2(t-u)}\varphi_1(u)du\Delta t-(\mu_2+\delta_2+\theta)I_2(t)\Delta t$

For $\Delta R_1(t)$

- Increase:
  - The probability of $\Delta R_1(t)$ increasing by 1 due to new vaccinations is $\lambda_1\Lambda_1\Delta t$.
  - The probability of $\Delta R_1(t)$ increasing by 1 due to new healed individuals is $\eta I_1(t)\Delta t$.
- Decrease:
  - The probability of $\Delta R_1(t)$ decreasing by 1 due to deaths is $\mu_1 R_1(t)\Delta t$.
- No Change:
  - The probability that $\Delta R_1(t)$ does not change is: $1-(\lambda_1\Lambda_1\Delta t+\eta I_1(t)\Delta t+\mu_1 R_1(t)\Delta t)$.

Combining these effects, the net change in $\Delta R_1(t)$ is:

$\Delta R_1(t) = \lambda_1\Lambda_1\Delta t+\eta I_1(t)\Delta t-\mu_1 R_1(t)\Delta t$.
Similarly, $\Delta R_2(t) = \lambda_2\Lambda_2\Delta t-(\mu_2+\theta)R_2(t)\Delta t$.
$\Delta M(t) = k\gamma_1\int_{H_3}^{H_4} I_1(t-u)\varphi_r(u)du\Delta t-\mu_3 M(t)\Delta t$
$\Delta P(t) = \gamma_2\int_{H_1}^{H_2} I_2(t-u)\varphi_2(u)du\Delta t-(\mu_4+\tau)P(t)\Delta t$
Let us determine the mean of $\Delta Z(t)$

States	Probabilities
$z_1 = (1;0;0;0;0;0;0;0)^\intercal$	$p_1 = (1-\lambda_1)\Lambda_1\Delta t$
$z_2 = (-1;0;0;0;0;0;0;0)^\intercal$	$p_2 = \mu_1 S_1(t)\Delta t$
$z_3 = (-1;0;1;0;0;0;0;0)^\intercal$	$p_3 = \beta_1 S_1(t)\int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du\Delta t$
$z_4 = (0;1;0;0;0;0;0;0)^\intercal$	$p_4 = (1-\lambda_2)\Lambda_2\Delta t$
$z_5 = (0;-1;0;0;0;0;0;0)^\intercal$	$p_5 = (\mu_2+\theta)S_2(t)\Delta t$
$z_6 = (0;-1;0;1;0;0;0;0)^\intercal$	$p_6 = \beta_2 S_2(t)\int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)}\varphi_1(u)du\Delta t$
$z_7 = (0;0;-1;0;0;0;0;0)^\intercal$	$p_7 = (\mu_1+\delta_1)I_1(t)\Delta t$
$z_8 = (0;0;-1;0;1;0;0;0)^\intercal$	$p_8 = \eta I_1(t)\Delta t$
$z_{10} = (0;0;0;0;1;0;0;0)^\intercal$	$p_{10} = \lambda_1\Lambda_1\Delta t$
$z_{11} = (0;0;0;0;-1;0;0;0)^\intercal$	$p_{11} = \mu_1 R_1(t)\Delta t$
$z_{12} = (0;0;0;0;0;1;0;0)^\intercal$	$p_{12} = \lambda_2\Lambda_2\Delta t$
$z_{13} = (0;0;0;0;0;-1;0;0)^\intercal$	$p_{13} = (\mu_2+\theta)R_2(t)\Delta t$
$z_{14} = (0;0;0;0;0;0;1;0)^\intercal$	$p_{14} = k\gamma_1\int_{H_3}^{H_4} I_1(t-u)\varphi_4(u)du\Delta t$
$z_{15} = (0;0;0;0;0;0;-1;0)^\intercal$	$p_{15} = \mu_3 M(t)\Delta t$
$z_{16} = (0;0;0;0;0;0;0;1)^\intercal$	$p_{16} = \gamma_2\int_{H_1}^{H_2} I_2(t-u)\varphi_2(u)du\Delta t$
$z_{17} = (0;0;0;0;0;0;0;-1)^\intercal$	$p_{17} = (\mu_4+\tau)P(t)\Delta t$
$z_{18} = (0;0;0;0;0;0;0;0)^\intercal$	$p_{18} = 1-\sum_{i=1}^{17} p_i$

$$\mathbb{E}(\Delta Z(t)) = \sum_{i=1}^{18} p_i z_i = \begin{pmatrix} (1-\lambda_1)\Lambda_1 - \beta_1 S_1(t)\int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du - \mu_1 S_1(t) \\ (1-\lambda_2)\Lambda_2 - \beta_2 S_2(t)\int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)}\varphi_1(u)du - (\mu_2+\theta)S_2(t) \\ \beta_1 S_1(t)\int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du - (\mu_1+\delta_1+\eta)I_1(t) \\ \beta_2 S_2(t)\int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)}\varphi_1(u)du - (\mu_2+\delta_2+\theta)I_2(t) \\ \lambda_1\Lambda_1 + \eta I_1(t) - \mu_1 R_1(t) \\ \lambda_2\Lambda_2 - (\mu_2+\theta)R_2(t) \\ k\gamma_1\int_{H_3}^{H_4} I_1(t-u)\varphi_4(u)du - \mu_3 M(t) \\ \gamma_2\int_{H_1}^{H_2} I_2(t-u)\varphi_2(u)du - (\mu_4+\tau)P(t) \end{pmatrix}\Delta t$$

$$\text{Let's note } \kappa = \begin{pmatrix} (1-\lambda_1)\Lambda_1 - \beta_1 S_1(t)\int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du - \mu_1 S_1(t) \\ (1-\lambda_2)\Lambda_2 - \beta_2 S_2(t)\int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)}\varphi_1(u)du - (\mu_2+\theta)S_2(t) \\ \beta_1 S_1(t)\int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du - (\mu_1+\delta_1+\eta)I_1(t) \\ \beta_2 S_2(t)\int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)}\varphi_1(u)du - (\mu_2+\delta_2+\theta)I_2(t) \\ \lambda_1\Lambda_1 + \eta I_1(t) - \mu_1 R_1(t) \\ \lambda_2\Lambda_2 - (\mu_2+\theta)R_2(t) \\ k\gamma_1\int_{H_3}^{H_4} I_1(t-u)\varphi_4(u)du - \mu_3 M(t) \\ \gamma_2\int_{H_1}^{H_2} I_2(t-u)\varphi_2(u)du - (\mu_4+\tau)P(t) \end{pmatrix}$$

Thus $\mathbb{E}(\Delta Z(t)) = \kappa\Delta t$

Let us determine the covariance matrix of $\Delta Z(t)$

$$\mathbb{V}(\Delta Z(t)) = \left(\mathbb{E}(\Delta Z(t))(\Delta Z(t))^\intercal\right) - \left(\mathbb{E}(\Delta Z(t))\right)\left(\mathbb{E}(\Delta Z(t))\right)^\intercal = \left(\mathbb{E}(\Delta Z(t))(\Delta Z(t))^\intercal\right) - \kappa\kappa^\intercal(\Delta t)^2$$

As Δt is small enough then $(\Delta t)^2$ is negligible hence

$$\mathbb{V}(\Delta Z(t)) = \mathbb{E}\left((\Delta Z(t))(\Delta Z(t))^\intercal\right) = \sum_{i=1}^{18} p_i z_i z_i^\intercal =$$

$$= \begin{pmatrix} A_{11} & 0 & A_{13} & 0 & 0 & 0 & 0 & 0 \\ 0 & A_{22} & 0 & A_{24} & 0 & 0 & 0 & 0 \\ A_{31} & 0 & A_{33} & 0 & A_{35} & 0 & 0 & 0 \\ 0 & A_{42} & 0 & A_{44} & 0 & 0 & 0 & 0 \\ 0 & 0 & A_{53} & 0 & A_{55} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & A_{66} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & A_{77} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & A_{88} \end{pmatrix} \Delta t$$

Where

$$A_{11} = (1-\lambda_1)\Lambda_1 + \mu_1 S_1(t) + \beta_1 S_1(t) \int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)} \varphi_3(u) du$$

$$A_{13} = -\beta_1 S_1(t) \int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)} \varphi_3(u) du$$

$$A_{22} = (1-\lambda_2)\Lambda_2 + (\mu_2+\theta) S_2(t) + \beta_2 S_2(t) \int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)} \varphi_1(u) du$$

$$A_{24} = -\beta_2 S_2(t) \int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)} \varphi_1(u) du$$

$$A_{31} = -\beta_1 S_1(t) \int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)} \varphi_3(u) du$$

$$A_{33} = \beta_1 S_1(t) \int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)} \varphi_3(u) du + (\mu_1+\delta_1) I_1(t) + \eta I_1(t)$$

$$A_{35} = -\eta I_1(t)$$

$$A_{42} = -\beta_2 S_2(t) \int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)} \varphi_1(u) du$$

$$A_{44} = \beta_2 S_2(t) \int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M^2(t-u)} \varphi_1(u) du + (\mu_2+\delta_2+\theta) I_2(t)$$

$$A_{53} = -\eta I_1(t)$$

$$A_{55} = \eta I_1(t) + \lambda_1 \Lambda_1 + \mu_1 R_1(t)$$

$$A_{66} = \lambda_2 \Lambda_2 + (\mu_2+\theta) R_2(t)$$

$$A_{77} = k\gamma_1 \int_{H_3}^{H_4} I_1(t-u)\varphi_4(u) du + \mu_3 M(t)$$

$$A_{88} = \gamma_2 \int_{H_1}^{H_2} I_2(t-u)\varphi_2(u) du + (\mu_4+\tau) P(t)$$

Let $A = \begin{pmatrix} A_{11} & 0 & A_{13} & 0 & 0 & 0 & 0 & 0 \\ 0 & A_{22} & 0 & A_{24} & 0 & 0 & 0 & 0 \\ A_{31} & 0 & A_{33} & 0 & A_{35} & 0 & 0 & 0 \\ 0 & A_{42} & 0 & A_{44} & 0 & 0 & 0 & 0 \\ 0 & 0 & A_{53} & 0 & A_{55} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & A_{66} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & A_{77} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & A_{88} \end{pmatrix}$

As A is a symmetrical and positive definite square matrix then there exists a unique symmetrical and positive difinite square matrix B such that $B^2 = A$. So $B = (A)^{\frac{1}{2}} = \frac{1}{\sqrt{\Delta t}} (\mathbb{V}(\Delta Z(t)))^{\frac{1}{2}}$. Thus, $(\mathbb{V}(\Delta Z(t)))^{\frac{1}{2}} = B\sqrt{\Delta t}$

Consider the following Euler scheme:

$$x(t+\Delta t) = x(t) + \kappa \Delta t + B\sqrt{\Delta t}\varepsilon \tag{3.1}$$

$$\Delta x(t) = \kappa \Delta t + B\sqrt{\Delta t}\varepsilon \tag{3.2}$$

Let's determine the mean and covariance of $\Delta x(t)$

$$\mathbb{E}(\Delta x(t)) = \kappa \Delta t$$

$\mathbb{V}(\Delta x(t)) = B^2\Delta t$
It follows that $\Delta Z(t)$ satisfies equation (2.2). $\Delta Z(t)$ follows gaussian law $\mathcal{N}\left(\kappa\Delta t; B^2\Delta t\right)$.

We can say by E. J. Allen in (Allen, 1999), that $\Delta Z(t)$ by doing $\Delta t \to 0$, $dZ(t)$ strongly converges to the solution of the stochastic differential equation :

$$dZ(t) = \kappa dt + BdW(t) \tag{3.3}$$

with $Z(0) = X_0$ and $W(t)$ is a Brownisn process of this form $W(t) = (W_1(t), W_2(t), ..., W_8(t))$ and $W_i(\Delta t) - W_i(0) \rightsquigarrow \mathcal{N}(0; \Delta t)$ for $i = 1, ..., 8$

Determination of the matrix B

$$det(A) = \begin{vmatrix} A_{11} & 0 & A_{13} & 0 & 0 & 0 & 0 & 0 \\ 0 & A_{22} & 0 & A_{24} & 0 & 0 & 0 & 0 \\ A_{31} & 0 & A_{33} & 0 & A_{35} & 0 & 0 & 0 \\ 0 & A_{42} & 0 & A_{44} & 0 & 0 & 0 & 0 \\ 0 & 0 & A_{53} & 0 & A_{55} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & A_{66} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & A_{77} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & A_{88} \end{vmatrix}$$

$$= A_{66}A_{77}A_{88}\left(A_{22}A_{44} - A_{24}^2\right)\left(A_{11}A_{33}A_{55} - A_{11}A_{13}^2 - A_{55}A_{35}^2\right)$$

characteristic polynomial equation
$P(x) = det(A - xI)$

$$= \begin{vmatrix} A_{11}-x & 0 & A_{13} & 0 & 0 & 0 & 0 & 0 \\ 0 & A_{22}-x & 0 & A_{24} & 0 & 0 & 0 & 0 \\ A_{31} & 0 & A_{33}-x & 0 & A_{35} & 0 & 0 & 0 \\ 0 & A_{42} & 0 & A_{44}-x & 0 & 0 & 0 & 0 \\ 0 & 0 & A_{53} & 0 & A_{55}-x & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & A_{66}-x & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & A_{77}-x & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & A_{88}-x \end{vmatrix}$$

$$= (A_{66}-x)(A_{77}-x)(A_{88}-x)\left(A_{22}A_{44} - A_{22}x - A_{44}x - A_{24}^2 + x^2\right)(A_{11}x^2 - A_{13}^2A_{55} - A_{11}A_{35}^2 + A_{13}^2x + A_{33}x^2 + A_{35}^2x + A_{55}^2x$$

$$-x^3 + A_{11}A_{33}A_{55} - A_{11}A_{33}x - A_{11}A_{55}x - A_{33}A_{55}x)$$

The eigenvalues of A ;

$$\lambda_1 = \frac{A_{22}}{2} + \frac{A_{44}}{2} - \frac{\sqrt{A_{22}^2 - 2A_{22}A_{44} + 4A_{24}^2 + A_{44}^2}}{2}$$

$$\lambda_2 = \frac{A_{11}}{3} + \frac{A_{33}}{3} + \frac{A_{55}}{3} + \sqrt[3]{\sqrt{\frac{A_{11}A_{35}^2}{2} + \frac{A_{13}^2A_{55}}{2} - \frac{(A_{11}+A_{33}+A_{55})^3}{27} + \frac{(A_{11}+A_{33}+A_{55})(-A_{13}^2 - A_{35}^2 + A_{11}A_{33} + A_{11}A_{55} + A_{33}A_{55})}{6}}}...$$

The complexity of the eigenvalues lets show through the complexity of B which is therefore not very malleable therefore difficult to use. In the following, we will use $\tilde{B}$ instead of B, taking into account the biological constraints.

3.2 Equivalent stochastic differential equation

$\tilde{B}$ is an (8×18)-dimensional matrix. The relation between the matrix B and $\tilde{B}$ was determined by Allen & Al. in (Allen, Allen, Arciniega, & Greenwood, 2008).

$$dX(t) = \kappa(t,X(t))dt + \tilde{B}(t,X(t))dW(t) \tag{3.4}$$

with $X(0) = X_0$ and $W(t)$ is a Brownian processus of the form $W(t) = (W_1(t), W_2(t), ..., W_{18}(t))$ and $W_i(\Delta t) - W_i(0) \rightsquigarrow \mathcal{N}(0;\Delta t)$ for $i = 1, ..., 18$

Thus

$$\tilde{B} = \begin{array}{c} \\ L_1 \\ \vdots \\ L_8 \end{array} \begin{array}{c} \begin{array}{cccccc} 1 & \cdots & \cdots & 6 & \end{array} \\ \left(\begin{array}{c|c|c} \tilde{B}_A & \tilde{B}_B & \tilde{B}_C \end{array}\right) \\ \begin{array}{cccccc} C_1 & \cdots & \cdots & C_6 & \end{array} \end{array} \begin{array}{c} \\ L_1 \\ \vdots \\ L_8 \end{array}$$

Where $\tilde{B_A} =$

$$\begin{pmatrix}
\sqrt{(1-\lambda_1)\Lambda_1} & -\sqrt{\mu_1 S_1(t)} & -\sqrt{\beta_1 S_1(t)\int_{H_2}^{H_3}\frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du} & 0 & 0 & 0 \\
0 & 0 & 0 & \sqrt{(1-\lambda_2)\Lambda_2} & -\sqrt{(\mu_2+\theta)S_2(t)} & -\sqrt{\beta_2 S_2(t)\int_{H_0}^{H_1}\frac{M(t-u)}{M_0+\varepsilon M(t-u)^2}\varphi_1(u)du} \\
0 & 0 & \sqrt{\beta_1 S_1(t)\int_{H_2}^{H_3}\frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)du} & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & \sqrt{\beta_2 S_2(t)\int_{H_0}^{H_1}\frac{M(t-u)}{M_0+\varepsilon M(t-u)^2}\varphi_1(u)du} \\
0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0
\end{pmatrix}$$

$$\tilde{B_B} = \begin{pmatrix}
ccccc0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
-\sqrt{(\delta_1+\mu_1)I_1(t)} & -\sqrt{\eta I_1(t)} & 0 & 0 & 0 & 0 \\
0 & 0 & -\sqrt{(\mu_2+\delta_2+\theta)I_2(t)} & 0 & 0 & 0 \\
0 & 0 & 0 & \sqrt{\eta I_1(t)}dW_8(t)+\sqrt{\lambda_1\Lambda_1} & -\sqrt{\mu_1 R_1(t)} & 0 \\
0 & 0 & 0 & 0 & 0 & \sqrt{\lambda_2\Lambda_2} \\
0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0
\end{pmatrix}$$

$$\tilde{B_C} = \begin{pmatrix}
0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
-\sqrt{(\mu_2+\theta)R_2(t)} & 0 & 0 & 0 & 0 & 0 \\
0 & \sqrt{k\gamma_1\int_{H_3}^{H_4} I_1(t-u)\varphi_4(u)du} & -\sqrt{\mu_3 M(t)} & 0 & 0 & 0 \\
0 & 0 & 0 & \sqrt{\mu_3 M(t)} & -\sqrt{(\mu_4+\tau)P(t)} & 0
\end{pmatrix}$$

By calculating this matrix product, we obtain that $\tilde{B}(t,X(t))\tilde{B}(t,X(t))^\intercal = A$

Hence the following system

$$
\begin{cases}
dS_1(t) = (1-\lambda_1)\Lambda_1 dt - \beta_1 S_1(t)\displaystyle\int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)dudt - \mu_1 S_1(t)dt \\
\qquad + \sqrt{(1-\lambda_1)\Lambda_1}dW_1(t) - \sqrt{\mu_1 S_1(t)}dW_2(t) \\
\qquad - \sqrt{\beta_1 S_1(t)\displaystyle\int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)dudW_3(t)} \\
dS_2(t) = (1-\lambda_2)\Lambda_2 dt - \beta_2 S_2(t)\displaystyle\int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M(t-u)^2}\varphi_1(u)dudt - (\mu_2+\theta)S_2(t)dt \\
\qquad + \sqrt{(1-\lambda_2)\Lambda_2}dW_4(t) - \sqrt{(\mu_2+\theta)S_2(t)}dW_5(t) \\
\qquad - \sqrt{\beta_2 S_2(t)\displaystyle\int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M(t-u)^2}\varphi_1(u)dudW_6(t)} \\
dI_1(t) = \beta_1 S_1(t)\displaystyle\int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)dudt - (\mu_1+\delta_1+\eta)I_1(t)dt \\
\qquad + \sqrt{\beta_1 S_1(t)\displaystyle\int_{H_2}^{H_3} \frac{P(t-u)}{1+\alpha_1 P(t-u)}\varphi_3(u)dudW_3(t)} - \sqrt{(\delta_1+\mu_1)I_1(t)}dW_7(t) \\
\qquad - \sqrt{\eta I_1(t)}dW_8(t) \\
dI_2(t) = \beta_2 S_2(t)\displaystyle\int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M(t-u)^2}\varphi_1(u)dudt - (\mu_2+\delta_2+\theta)I_2(t)dt \\
\qquad + \sqrt{\beta_2 S_2(t)\displaystyle\int_{H_0}^{H_1} \frac{M(t-u)}{M_0+\varepsilon M(t-u)^2}\varphi_1(u)dudW_6(t)} - \sqrt{(\mu_2+\delta_2+\theta)I_2(t)}dW_9(t) \\
dR_1(t) = \lambda_1\Lambda_1 dt - \mu_1 R_1(t)dt + \eta I_1(t)d(t) + \sqrt{\eta I_1(t)}dW_8(t) + \sqrt{\lambda_1\Lambda_1}dW_{10}(t) \\
\qquad - \sqrt{\mu_1 R_1(t)}dW_{11}(t) \\
dR_2(t) = \lambda_2\Lambda_2 dt - (\mu_2+\theta)R_2(t)dt + \sqrt{\lambda_2\Lambda_2}dW_{12}(t) - \sqrt{(\mu_2+\theta)R_2(t)}dW_{13}(t) \\
dM(t) = k\gamma_1\displaystyle\int_{H_3}^{H_4} I_1(t-u)\varphi_4(u)dudt - \mu_3 M(t)dt + \sqrt{k\gamma_1\int_{H_3}^{H_4} I_1(t-u)\varphi_4(u)dudW_{14}(t)} \\
\qquad - \sqrt{\mu_3 M(t)}dW_{15}(t) \\
dP(t) = \gamma_2\displaystyle\int_{H_1}^{H_2} I_2(t-u)\varphi_2(u)dudt - (\mu_4+\tau)P(t)dt + \sqrt{\gamma_2\int_{H_1}^{H_2} I_2(t-u)\varphi_2(u)dudW_{16}(t)} \\
\qquad - \sqrt{(\mu_4+\tau)P(t)}dW_{17}(t)
\end{cases}
\tag{3.5}
$$

4 Numerical Simulations

In this section, we propose numerical simulations of the systems (2.3) and (3.5) to attest to our results and to have a better understanding of the spread of the disease.

Our simulations will be done with the Julia language with its $Differential Equations.jl$ packages and complements. Our parameters will be those used by Gao et al. in article (Gao et al., 2011) in large parts, the demographic parameters of Ivory Coast and we will estimate some to meet the requirements of the model.

4.1 Simulation of the deterministic model

Due to the coronavirus disease (COVID-19) scare, neglected tropical diseases have gained momentum. The basic reproduction rate $\mathcal{R}_0 = \sqrt{\mathcal{R}_0^H} \times \sqrt{\mathcal{R}_0^E} = 364.60374791677896 \times 6.243917507264464 = 321.9535981555265$, in our model. Which produces the following graphic representations.

4.1.1 Deterministic model code in Julia Language

```
#Declaration
import Pkg
Pkg.add("DifferentialEquations")
Pkg.add("MTH229")
Pkg.add("CalculusWithJulia")
Pkg.add("QuadGK")
Pkg.add("Roots")
Pkg.add("GraphPlot")
Pkg.add("Plots")
using CalculusWithJulia
using QuadGK
using Roots
using MTH229
using Plots
using DifferentialEquations
using GraphPlot
# Functions of infectuositises
\Phi (x,b1,b2)=(exp((b2-x)/(b2-b1)))/((b2-b1)*(exp(1)-1))
# Function of the model
function sirmpf(du, u, h, p, t)
H00, H01, H02, H03, H04, \Lambda_{01}, \Lambda_{02}, \lambda_{1}, \lambda_{2}, \mu_{1}, \mu_{2},
\mu_3, \mu_4, \beta_1 , \beta_2, \delta_1, \delta_2, \gamma_1, \gamma_2, k, \alpha_1, M0, \epsilon,
\eta, \theta, \tau = p
S1, S2, I1, I2, R1, R2, M, PP = u
# Produit de convolution
@syms x101,x102
function fhist(x1,x2, j1,f_1,f_2)
f_1(h(p,x1 - x2)[j1])*f_2(x2)
end
fp(x) = x / (1+ ?1 * x)
\phi_1(x) = \phi(x,H02,H03)
fcp(x) = fhist(t,x,8,fp,\phi_1)
fm(x) = x / (M0 + \epsilon * x^2)
\phi_2(x) = \phi(x,H00,H01)
fcm(x) = fhist(t,x,7,fm,\phi_2)
fi(x) = x
\phi_3(x) = \phi(x,H03,H04)
fci1(x) = fhist(t,x,3,fi,\phi_3)
\phi_4(x) = \phi(x,H01,H02)
fci2(x) = fhist(t,x,4,fi,\phi_4)
elt1 = quadgk(fcp,H02,H03)[1]
elt2 = quadgk(fcm,H00,H01)[1]
elt3 = quadgk(fci1,H03,H04)[1]
```

```
elt4 = quadgk(fci2,H01,H02)[1]
if elt1<0
elt1=0
end
if elt2< 0
elt2=0
end
if elt3<0
elt3=0
end
if elt4<0
elt4=0
end

dS1 = du[1] = (1 - \lambda_1)* \Lambda_01 - \beta_1* S1* elt1  - \mu_1*S1
dS2 = du[2] = (1 - \lambda_2)* \Lambda_02 - \beta_2* S2* elt2  - (\mu_2 + \theta)*S2
#Initialization
if t < H03
dI1 = du[3] = \beta_1* S1*elt1
else
dI1 = du[3] = \beta_1* S1*elt1 - (\mu_1 + \delta_1 + \eta)*I1
end
if t < H01
dI2 = du[4] = \beta_2* S2* elt2- (\mu_2 )*I2
else
dI2 = du[4] = \beta_2* S2* elt2- (\mu_2 +\delta_2 + \theta)*I2
end
if t < H03
dR1 = du[5] = \lambda_1* \Lambda_01 - \mu_1*R1
else
dR1 = du[5] = \lambda_1* \Lambda_01 + \eta*I1 - \mu_1*R1
end
if t < H01
dR2 = du[6] = ?2* ?02 - ?2 *R2
else
dR2 = du[6] = \lambda_2* \Lambda_02 - (\mu_2 + \theta)*R2
end
dM =  du[7] = k * \gamma_1*elt3 - \mu_3 *M
if t < H03
dP =  du[8] =0
else
dP =  du[8] = \gamma_2*elt4 - (\mu_4 +\tau)*PP
end
println("Fonction F  ",round(100*t/156,digits=2),"  % ",elt2)
end
# Initialisation de la fonction historique
#h(p,t)=ones(8)
#h(p, t) = [0.8*10^6, 0.9*190000.0, 1, 0, 0.2*10^6, 19000, 0, 0]
# Definition de la sparse matrice A
h(p,t) = ones(8)
# Parameters of model
```

```
h0 = 9 # Duree minimale pour l'apparution des 1er Oeufs rejetes dans les selles et les urines
h1 = 1/20 # Duree d'infectuosite des miracidums
h2 = 6 # Duree de la transformation de miraciiu, en cercaires
h3 = 0.2 # Duree d'infectuosite des cercaires
H00 = h0
H01 = H00 + h1
H02 = H01 + h2
H03 = H02 + h3
H04 = H03 + h0
\Lambda_01 = 200 # Nbre de nouveuax-nes par semaine
\lambda_1 = 0.6 # Taux de Chimioprophylaxie + Taux d'humains de la zone a risque
\Lambda_02 = 52 # Nbre de mollusques nes par semaine
\lambda_2 = 0.3 # Taux de mollusques porteges
\mu_1 = 0.000384 # Taux de deces des hommes par jour
\mu_2 = 0.00569 # Taux de mort des mollusques par jour
\mu_3= 6.3 # Taux de mort des miracidums par semaine
\mu_4 = 0.028 # Taux de mort des cercaires par jour
\beta_1 = 3*10^(-4) # Probabilite de contact S_1 et p par jour
\beta_2 = 0.815e+2 # Nombre de M en contact avec S_2 par semain
\delta_1 = 0.0039 # Taux de deces du a la maladie pae jour
\delta_2 = 0.004012 # Taux de deces du a la maladie par jour
\gamma_1 = 0.02 # Taux de miracidums liberes par Oeuf par jour
\gamma_2 = 18.2 # Taux de cercaires liberees par mollusques par jour
k = 300 # Nbre d'Oeufs evacues par homme infecte par jour
\alpha_1 = 0.3*10^(-8) # Coefficient
M0 = 1*10^6 # Saturation constante pour les miracidums
\epsilon = 0.3 # Limitation de la vitesse de croissance
\eta = 0.03 # Taux de traitement de malades par jour
\theta = 0.1 # Taux de mollusques elimines par jour
\tau = 0.05 # Taux de cercaires eliminees par jour
lags = [H00]
p = (H00, H01, H02, H03, H04, \Lambda_01, \Lambda_02, \lambda_1, \lambda_2, \mu_1, \mu_2,
\mu_3, \mu_4, \beta_1 , \beta_2, \delta_1, \delta_2, \gamma_1, \gamma_2, k, \alpha_1, M0,
\epsilon, \eta, \theta, \tau)
tspan = (0, 156)
u0 = [0.4*5e+3, 0.7*2e+2, 1, 0, 0.6*5e+3, 0.3*2e+2, 00, 00]
R0 = sqrt((k*\beta_1*\beta_2*\gamma_1*\gamma_2*(1-\lambda_1)*(1-\lambda_2)*\Lambda_01*\Lambda_02)/
(M0*\mu_1*\mu_3*(\mu_2+\theta)*(\mu_4+\tau)*(\mu_1+\delta_1+\eta)*(\mu2+\delta_2+\theta)))
R01 = sqrt((\beta_1*\gamma2*(1-\lambda_1)*\Lambda_01)/(\mu_1*(\mu_4+\tau)*(\mu_2+\delta_2+\theta)))
R02 = sqrt((k*\beta_2*(1-\lambda_2)*\Lambda_02)/(M0*\mu_3*(\mu_2+\theta)*(\mu_1+\delta_1+\eta)))

# Modelisation du probleme
# Modelisation du probleme
prob = DDEProblem(sirmpf, u0, h, tspan, p)
#; constant_lags = lags)
# La methode resolution du probleme
alg = MethodOfSteps(Tsit5())
alg1 =MethodOfSteps(BS3())
alg2 = MethodOfSteps(DP8())
alg3 = MethodOfSteps(Vern6())
# Resolution du probleme
```

```
sol = solve(prob, alg)
temps = sol.t
sol1 = sol.u
S1=Vector{Float64}(undef,length(sol))
S2=Vector{Float64}(undef,length(sol))
I1=Vector{Float64}(undef,length(sol))
I2=Vector{Float64}(undef,length(sol))
R1=Vector{Float64}(undef,length(sol))
R2=Vector{Float64}(undef,length(sol))
M=Vector{Float64}(undef,length(sol))
P=Vector{Float64}(undef,length(sol))
for j in 1:length(sol)
S1[j] = sol1[j][1]
S2[j] = sol1[j][2]
I1[j] = sol1[j][3]
I2[j] = sol1[j][4]
R1[j] = sol1[j][5]
R2[j] = sol1[j][6]
M[j] = sol1[j][7]
P[j] = sol1[j][8]
end
using Plots
#
C_S1 = Plots.plot(temps, S1,
title="Susceptible humans",
label="S1", linecolor=:blue, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_S1,"S1.png")
#
C_SIR1 = Plots.plot(temps, [S1 I1 R1],
title="SIR humans",
label=["S1" "I1" "R1"], linecolor=[:blue :red :purple ], linewidth=[3 3 3])
xlabel!("Weeks"); ylabel!("Size")
savefig(C_SIR1,"SIR1.png")

C_SI1 = Plots.plot(temps, [S1 I1 ],
title="Susceptible and Infected humans",
label=["S1" "I1" ], linecolor=[:blue :red ], linewidth=[3 3])
xlabel!("Weeks"); ylabel!("Size")
savefig(C_SI1,"SI1.png")

C_S2 = Plots.plot(temps, S2,
title="Susceptible molluscs",
label="S2", linecolor=:green, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_S2,"S2.png")
#
C_SIR2 = Plots.plot(temps, [S2 I2 R2],
title="SIR molluscs",
label=["S2" "I2" "R2"], linecolor=[:green :pink :orange]
, linewidth=[3 3 3])
```

```
xlabel!("Weeks"); ylabel!("Size")
savefig(C_SIR2,"SIR2.png")

C_SI2 = Plots.plot(temps, [S2 I2 ],
title="Susceptible and Infected molluscs",
label=["S2" "I2" ], linecolor=[:green :pink]
, linewidth=[3 3])
xlabel!("Weeks"); ylabel!("Size")
savefig(C_SI2,"SI2.png")

C_I1 = Plots.plot(temps, I1,
title="Infected humans",
label="I1", linecolor=:red, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_I1,"I1.png")
#
C_I2 = Plots.plot(temps, I2,
title="Infected molluscs",
label="I2", linecolor=:pink, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_I2,"I2.png")
#
C_R1 = Plots.plot(temps, R1,
title="Recovered humans",
label="R1", linecolor=:purple, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_R1,"R1.png")
#
C_R2 = Plots.plot(temps, R2,
title="Recovered molluscs",
label="R2", linecolor=:orange, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_R2,"R2.png")
#
C_M = Plots.plot(temps, M,
title="Miracidia",
label="M", linecolor=:blue, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_M,"M.png")
#
C_P = Plots.plot(temps, P,
title="Cercariae",
label="P", linecolor=:green, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_P,"P.png")
SIR_1=Plots.plot!(C_SI1,C_R1)
SIR_2 =Plots.plot!(C_SI2,C_R2)
M_P=Plots.plot!(C_M,C_P)
savefig(SIR_1,"SIR_1.png")
savefig(SIR_2,"SIR_2.png")
savefig(M_P,"M_P.png")
```

4.1.2 Graphic illustrations

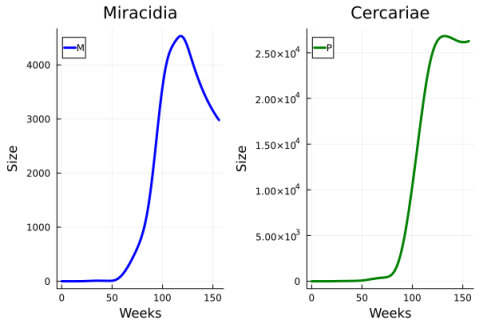

Fig. 4. Miracidium and Cercaria evolution curve

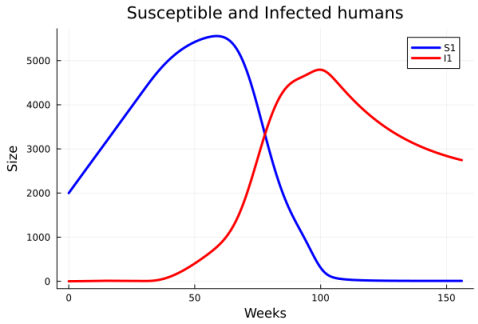

Fig. 5. Evolutionary curve for susceptible and infected humans

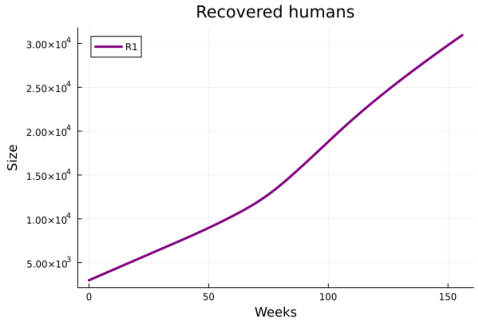

Fig. 6. Evolution curve of recovered humans

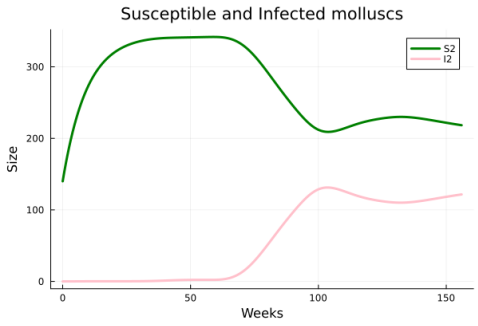

Fig. 7. Evolution curve of susceptible and infected molluscs

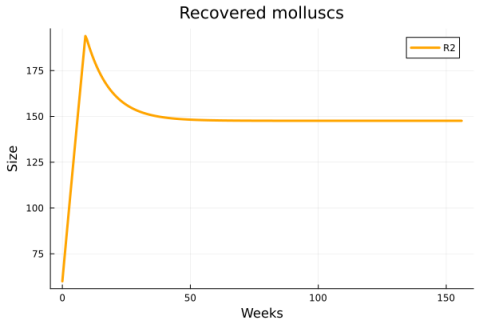

Fig. 8. Evolution curve of recovered molluscs

4.1.3 Illustration analysis

For the initial conditions of the model, the initial population of humans and that of molluscs are healthy. There is only one infected human who just became infected. There is no miracidium egg, no miracidium, no cercaria. The first miracidiums appear after more than 9 weeks from the initial date. They then start looking for compatible molluscs. It is after this period that infected molluscs will appear.These infected molluscs will produce cercariae which will infect susceptible humans.And the cycle begins again. As $\mathcal{R}_0^H$ and $\mathcal{R}_0^E$ are greater than 1, the infection grows.

4.2 Simulation of the stochasstic model

4.2.1 Stochastic model code in Julia Language

```
#Declaration
import Pkg
Pkg.add("DifferentialEquations")
Pkg.add("BoundaryValueDiffEq")
Pkg.add("MTH229")
Pkg.add("CalculusWithJulia")
Pkg.add("QuadGK")
Pkg.add("Roots")
Pkg.add("StochasticDelayDiffEq")
Pkg.add("SparseArrays")
```

```
Pkg.add("RandomProcesses")
Pkg.add("GraphPlot")
Pkg.add("Plots")
Pkg.add("SparseDiffTools")
Pkg.add("BandedMatrices")
# Pkg.add("ArrayInterfaceBandedMatrices")
# Pkg.add("ArrayInterfaceBlockBandedMatrices")
Pkg.add("FiniteDifferences")
Pkg.add("IterativeSolvers")
Pkg.add("Zygote")
Pkg.add("MultiScaleArrays")
using RandomProcesses
using CalculusWithJulia
using StochasticDelayDiffEq
using QuadGK
using Roots
using MTH229
using Plots
using BoundaryValueDiffEq
using DifferentialEquations
using Zygote
using IterativeSolvers
using SparseArrays
using GraphPlot
using SparseDiffTools
using BandedMatrices
# using ArrayInterfaceBandedMatrices
# using ArrayInterfaceBlockBandedMatrices
using FiniteDifferences
using Printf
using MultiScaleArrays
# Fonctions infectuosites
\phi(x,b1,b2)=(exp((b2-x)/(b2-b1)))/((b2-b1)*(exp(1)-1))
# Fonction du modele
function sirmpf(du, u, h, p, t)
H00, H01, H02, H03, H04, \Lambda_01, \Lambda_02, \lambda_1, \lambda2, \mu_1, \mu_2,
\mu_3, \mu_4, \beta_1 , \beta_2, \delta_1, \delta_2, \gamma_1, \gamma_2, k, \alpha_1, M0,
\epsilon, \eta, \theta, \tau = p
S1, S2, I1, I2, R1, R2, M, PP = u
# Produit de convolution
@syms x101,x102
function fhist(x1,x2, j1,f_1,f_2)
f_1(h(p,x1 - x2)[j1])*f_2(x2)
end

fp(x) = x / (1+ \alpha_1 * x)
\phi_1(x) = \phi(x,H02,H03)
fcp(x) = fhist(t,x,8,fp,\phi_1)
fm(x) = x / (M0 + \epsilon * x^2)
\phi_2(x) = \phi(x,H00,H01)
fcm(x) = fhist(t,x,7,fm,\phi_2)
```

```
fi(x) = x
\phi_3(x) = \phi(x,H03,H04)
fci1(x) = fhist(t,x,3,fi,\phi_3)
\phi_4(x) = \phi(x,H01,H02)
fci2(x) = fhist(t,x,4,fi,\phi_4)
elt1 = quadgk(fcp,H02,H03)[1]
elt2 = quadgk(fcm,H00,H01)[1]
elt3 = quadgk(fci1,H03,H04)[1]
elt4 = quadgk(fci2,H01,H02)[1]
if elt1<0
elt1=0
end
if elt2< 0
elt2=0
end
if elt3<0
elt3=0
end
if elt4<0
elt4=0
end

dS1 = du[1] = (1 - \lambda_1)* \Lambda_01 - \beta_1* S1* elt1 -
\mu_1*S1
dS2 = du[2] = (1 - \lambda_2)* \Lambda_02 - \beta_2* S2* elt2-
(\mu_2 + \theta)*S2
#Initialization
if t < H03
dI1 = du[3] = \beta_1* S1*elt1
else
dI1 = du[3] = \beta_1* S1*elt1 - (\mu_1 + \delta_1 + \eta)*I1
end
if t < H01
dI2 = du[4] = \beta_2* S2* elt2 - (\mu_2 )*I2
else
dI2 = du[4] = \beta_2* S2* elt2- (\mu_2 +\delta_2 + \theta)*I2
end
if t < H03
dR1 = du[5] = \lambda_1* \Lambda_01 - \mu_1*R1
else
dR1 = du[5] = \lambda_1* \Lambda_01 + \eta*I1 - \mu_1*R1
end
dR2 = du[6] = \lambda_2* \Lambda_02 - (\mu_2 + \theta)*R2
dM =  du[7] = k * \gamma_1*elt3 - \mu_3 *M
#if t < H03
#   dP =  du[8] = 0
#   else
dP =  du[8] = \gamma_2*elt4- (\mu_4 +\tau)*PP
#end
@printf("Pourcentage F =%0.2f", 100*t/10);println(" ")
# println("Fonction F  ",round(100*t/52,digits=2),"  % ",elt2)
```

```
end

function sirmpg(du, u, h, p, t)
H00, H01, H02, H03, H04, \Lambda_01, \Lambda_02, \lambda_1, \lambda_2, \mu_1, \mu_2,
\mu_3, \mu_4, \beta_1 , \beta_2, \delta_1, \delta_2, \gamma_1, \gamma_2, k, \alpha_1,
M0, \epsilon, \eta, \theta, \tau = p
S1, S2, I1, I2, R1, R2, M, P = u
# Produit de convolution
@syms x101,x102
function fhist(x1,x2, j1,f_1,f_2)
f_1(h(p,x1 - x2)[j1])*f_2(x2)
end

fp(x) = x / (1+ ?1 * x)
\phi_1(x) = \phi(x,H02,H03)
fcp(x) = fhist(t,x,8,fp,\phi_1)
fm(x) = x / (M0 + \epsilon * x^2)
\phi_2(x) = \phi(x,H00,H01)
fcm(x) = fhist(t,x,7,fm,\phi_2)
fi(x) = x
\phi_3(x) = \phi(x,H03,H04)
fci1(x) = fhist(t,x,3,fi,\phi_3)
\phi_4(x) = \phi(x,H01,H02)
fci2(x) = fhist(t,x,4,fi,\phi_4)
elt1 = quadgk(fcp,H02,H03)[1]
elt2 = quadgk(fcm,H00,H01)[1]
elt3 = quadgk(fci1,H03,H04)[1]
elt4 = quadgk(fci2,H01,H02)[1]
if elt1<0
elt1=0
end
if elt2<0
elt2=0
end
if elt3<0
elt3=0
end
if elt4<0
elt4=0
end
du[1,1] = sqrt(abs((1 - \lambda_1)* \Lambda_01))
du[1,2] = - sqrt(abs(?1*S1))
du[1,3] = - sqrt(abs(\beta_1* S1* elt1))
du[2,1] = sqrt(abs((1 - \lambda_2)* \Lambda_02))
du[2,2] = - sqrt(abs(\beta_2* S2* elt2))
du[2,3] = - sqrt(abs((\mu_2 + \theta)*S2))
du[3,1] =sqrt(abs(\beta_1* S1*elt1))
du[3,2] =-sqrt(abs((\mu_1 + \delta_1)*I1))
du[3,3] = -sqrt(abs(\eta*I1))
#if t<H03
#    du[3,2] =-0
```

```
#   du[3,3] = 0
# else
#   du[3,2] =-sqrt(abs((\mu_1 + \delta_1)*I1))
#{}    du[3,3] = -sqrt(abs(\eta*I1))
#end
#if t<H02
#    du[4,1] =sqrt(abs(\beta_2* S2* elt2))
#    du[4,2] = 0
# else
#    du[4,1] =sqrt(abs(\beta_2* S2* elt2))
#   du[4,2] =-sqrt(abs((\mu_2 +\delta_2 + \theta)*I2))
#end

du[4,1] =sqrt(abs(\beta_2* S2* elt2))
du[4,2] =-sqrt(abs((\mu_2 +\delta_2 + \theta)*I2))
du[4,3] = 0
du[5,1] =sqrt(abs(\eta*I1))
du[5,2] =sqrt(abs(\lambda_1*\Lambda_01))
du[5,3] = -sqrt(abs(\mu_1*R1))
du[6,1] = sqrt(abs(\lambda_2*\Lambda_02))
du[6,2] = -sqrt(abs((\mu_2 + \theta)*R2))
du[6,3] = 0
du[7,1] =sqrt(abs(k * \gamma_1*elt3))
du[7,2] =-sqrt(abs(\mu_3 *M))
du[7,3] = 0
du[8,1] =sqrt(abs(\gamma_2*elt4))
du[8,2] =-sqrt(abs((\mu4 + \tau)*P))
du[8,3] = 0
@printf("Pourcentage G =%0.2f", 100*t/10); println(" ")
# println("Fonction G  ",round(100*t/156,digits=2),"  %")
end

# Initialisation de la fonction historique
#h(p,t)=ones(8)
#h(p, t) = [0.8*10^6, 0.9*190000.0, 1, 0, 0.2*10^6, 19000, 0, 0]
# Definition de la sparse matrice A
A = zeros(8,3)
for j in 1:3
A[1,j] = 1
end
for j in 1:3
A[2,j] = 1
end
for j in 1:3
A[3,j] = 1
end
#A[3,3] = 1
#A[3,7] = 1
#A[3,8] = 1
for j in 1:2
A[4,j] = 1
```

```
end
#A[4,6] = 1
#A[4,9] = 1
for j in 1:3
A[5,j] = 1
end
#A[5,8] = 1
#A[5,10] = 1
#A[5,11] = 1
for j in 1:2
A[6,j] = 1
end
for j in 1:2
A[7,j] = 1
end
for j in 1:2
A[8,j] = 1
end
A = sparse(A)
h(p,t) = ones(8)
# Les parametres du modele
h0 = 9 # Duree minimale pour l'apparution des 1er Oeufs rejetes dans les selles et les urines
h1 = 1/20 # Duree d'infectuosite des miracidums
h2 = 6 # Duree de la transformation de miraciiu, en cercaires
h3 = 0.2 # Duree d'infectuosite des cercaires
H00 = h0
H01 = H00 + h1
H02 = H01 + h2
H03 = H02 + h3
H04 = H03 + h0
\Lambda_01 = 200 # Nbre de nouveuax-nes par semaine
\lambda_1 = 0.6 # Taux de Chimioprophylaxie + Taux d'humains de la zone a risque
\Lambda_02 = 52 # Nbre de mollusques nes par semaine
\lambda_2 = 0.3 # Taux de mollusques porteges
\mu_1 = 0.000384 # Taux de deces des hommes par jour
\mu_2 = 0.00569 # Taux de mort des mollusques par jour
\mu_3= 6.3 # Taux de mort des miracidums par semaine
\mu_4 = 0.028 # Taux de mort des cercaires par jour
\beta_1 = 3*10^(-4) # Probabilite de contact S_1 et p par jour
\beta_2 = 0.815e+2 # Nombre de M en contact avec S_2 par semain
\delta_1 = 0.0039 # Taux de deces du a la maladie pae jour
\delta_2 = 0.004012 # Taux de deces du a la maladie par jour
\gamma_1 = 0.02 # Taux de miracidums liberes par Oeuf par jour
\gamma_2 = 18.2 # Taux de cercaires liberees par mollusques par jour
k = 300 # Nbre d'Oeufs evacues par homme infecte par jour
\alpha_1 = 0.3*10^(-8) # Coefficient
M0 = 1*10^6 # Saturation constante pour les miracidums
\epsilon = 0.3 # Limitation de la vitesse de croissance
\eta = 0.03 # Taux de traitement de malades par jour
\theta = 0.1 # Taux de mollusques elimines par jour
\tau = 0.05 # Taux de cercaires eliminees par jour
```

```
lags = [H00]
p = (H00, H01, H02, H03, H04, \Lambda_01, \Lambda_02, \lambda_1, \lambda_2, \mu_1, \mu_2,
\mu_3, \mu_4, \beta_1 , \beta_2, \delta_1, \delta_2, \gamma_1, \gamma_2, k, \alpha_1,
M0, \epsilon, \eta, \theta, \tau)
tspan = (0, 10)
u0 = [0.4*5e+3, 0.7*2e+2, 1, 0, 0.6*5e+3, 0.3*2e+2, 00, 00]
R0 = sqrt((k*\beta_1*\beta_2*\gamma_1*\gamma_2*(1-\lambda_1)*(1-\lambda_2)*\Lambda_01*\Lambda_02)/
(M0*\mu_1*\mu_3*(\mu_2+\theta)*(\mu_4+\tau)*(\mu_1+\delta_1+\eta)*(\mu_2+\delta_2+\theta)))
R01 = sqrt((\beta_1*\gamma_2*(1-\lambda_1)*\Lambda_01)/(\mu_1*(\mu_4+\tau)*(\mu_2+\delta_2+\theta)))
R02 = sqrt((k*\beta_2*(1-\lambda_2)*\Lambda_02)/(M0*\mu_3*(\mu_2+\theta)*(\mu_1+\delta_1+\eta)))


# Modelisation du probleme
prob = SDDEProblem(sirmpf,sirmpg,
u0, h, tspan, p,
#noise_rate_prototype = zeros(8,3))
noise_rate_prototype = A)
#; constant_lags = lags)
# La methode resolution du probleme
alg = ISSEM()
alg1 = ISSEulerHeun()
alg2 = LambaEulerHeun()
alg3 = EM()
alg5 = EulerHeun()
alg4 = RKMil()
alg6 = LambaEM()
alg7 = SKenCarp()
alg8 = SimplifiedEM()
alg9 = SOSRA2()
alg10 = SOSRA()
alg11 = DRI1()
alg01 = EulerHeun()
choice_function(integrator) = (Int(integrator.dt < 1e-20) + 1)
alg12= StochasticCompositeAlgorithm((alg1, alg2), choice_function)
alg13= StochasticCompositeAlgorithm((alg2, alg2), choice_function)
alg14= StochasticCompositeAlgorithm((alg, alg), choice_function)
# Resolution du probleme
sol = solve(prob, alg01,dt = 1/1000)
temps = sol.t
sol1 = sol.u
S1=Vector{Float64}(undef,length(sol))
S2=Vector{Float64}(undef,length(sol))
I1=Vector{Float64}(undef,length(sol))
I2=Vector{Float64}(undef,length(sol))
R1=Vector{Float64}(undef,length(sol))
R2=Vector{Float64}(undef,length(sol))
M=Vector{Float64}(undef,length(sol))
P=Vector{Float64}(undef,length(sol))
for j in 1:length(sol)
S1[j] = sol1[j][1]
S2[j] = sol1[j][2]
```

```
I1[j] = sol1[j][3]
I2[j] = sol1[j][4]
R1[j] = sol1[j][5]
R2[j] = sol1[j][6]
M[j] = sol1[j][7]
P[j] = sol1[j][8]
end
# Extraction de vecteurs
function Rech_i(a,b,v)
l=length(v)
ind_1=15
ind_2=17
for i in 1:l
if v[i]< a
ind_1= i
end
if v[i]< b
ind_2= i
end
end
return ind_1, ind_2
end
function ext_vec(a,b,v)
l1=length(v)
l2=b-a+1
v2=zeros(l2)
for i in 1:l2
v2[i]=v[i+a-1]
end
return v2
end
(ind_d1,ind_f1)=Rech_i(20,21,temps)
(ind_d2,ind_f2)=Rech_i(20,20.1,temps)
tps = ext_vec(ind_d1,ind_f1,temps)
tps2 = ext_vec(ind_d2,ind_f2,temps)
ext_S1 = ext_vec(ind_d2,ind_f2,S1)
ext_S2 = ext_vec(ind_d1,ind_f1,S2)
ext_I1 = ext_vec(ind_d2,ind_f2,I1)
ext_I2 = ext_vec(ind_d1,ind_f1,I2)
ext_R1 = ext_vec(ind_d2,ind_f2,R1)
ext_R2 = ext_vec(ind_d2,ind_f2,R2)
ext_M = ext_vec(ind_d1,ind_f1,M)
ext_P = ext_vec(ind_d2,ind_f2,P)
using Plots
# Susceptible Humains
C_SS1 = Plots.plot(temps, S1,
title="Susceptible humans",
label="S1", linecolor=:blue, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_SS1,"SS1.png")
C_ESS1 = Plots.plot(tps2, ext_S1,
```

```
title="Susceptible humans",
label="S1", linecolor=:blue, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_ESS1,"ESS1.png")
C_S1_ES1 = Plots.plot(C_SS1,C_ESS1)
savefig(C_S1_ES1,"S1_ES1.png")
# SI1 Humains
C_SSII1 = Plots.plot(temps, [S1 I1],
title="Susceptible and infected humans",
label=["S1" "I1"], linecolor=[:blue :red], linewidth=[3 3])
xlabel!("Weeks"); ylabel!("Size")
savefig(C_SSII1,"SSII1.png")
# SIR1 Humains
C_SSIIRR1 = Plots.plot(temps, [S1 I1 R1],
title="SIR humans",
label=["S1" "I1" "R1"], linecolor=[:blue :red :purple],
linewidth=[3 3 3])
xlabel!("Weeks"); ylabel!("Size")
savefig(C_SSIIRR1,"SSIIRR1.png")
# Susceptible Mollusques
C_SS2 = Plots.plot(temps, S2,
title="Susceptible molluscs",
label="S2", linecolor=:green, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_SS2,"SS2.png")
C_ESS2 = Plots.plot(tps, ext_S2,
title="Susceptible molluscs",
label="S2", linecolor=:green, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_ESS2,"ESS2.png")
C_S2_ES2 = Plots.plot(C_SS2,C_ESS2)
savefig(C_S2_ES2,"S2_ES2.png")
# Susceptible et Infectes Mollusques
C_SSII2 = Plots.plot(temps, [S2 I2],
title="Susceptible and infected molluscs",
label=["S2" "I2"], linecolor=[:green :pink],
linewidth=[3 3])
xlabel!("Weeks"); ylabel!("Size")
savefig(C_SSII2,"SSII2.png")
# SIR2 Mollusques
C_SSIIRR2 = Plots.plot(temps, [S2 I2 R2],
title="SIR molluscs",
label=["S2" "I2" "R2"], linecolor=[:green :pink :orange],
linewidth=[3 3 3])
xlabel!("Weeks"); ylabel!("Size")
savefig(C_SSIIRR2,"SSIIRR2.png")
# humains infectes
C_II1 = Plots.plot(temps, I1,
title="Infected humans",
label="I1", linecolor=:red, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
```

```
savefig(C_II1,"II1.png")
C_EII1 = Plots.plot(tps2, ext_I1,
title="Infected humans",
label="I1", llinecolor=:red, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_EII1,"EII1.png")
C_I1_EI1 = Plots.plot(C_II1,C_EII1)
savefig(C_I1_EI1,"I1_EI1.png")
# Mollusaques infectes
C_II2 = Plots.plot(temps, I2,
title="Infected molluscs",
label="I2", linecolor=:pink, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_II2,"II2.png")
C_EII2 = Plots.plot(tps, ext_I2,
title="Infected molluscs",
label="I2",  linecolor=:pink, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_EII2,"EII2.png")
C_I2_EI2 = Plots.plot(C_II2,C_EII2)
savefig(C_I2_EI2,"I2_EI2.png")
# Humains recuperes
C_RR1 = Plots.plot(temps, R1,
title="Recovered humans",
label="R1", linecolor=:purple, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_RR1,"RR1.png")
C_ERR1 = Plots.plot(tps2, ext_R1,
title="Recovered humans",
label="R1", linecolor=:purple, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_ERR1,"ERR1.png")
C_R1_ER1 = Plots.plot(C_RR1,C_ERR1)
savefig(C_R1_ER1,"R1_ER1.png")
# Mollusques recuperew
C_RR2 = Plots.plot(temps, R2,
title="Recovered molluscs",
label="R2", linecolor=:orange, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_RR2,"RR2.png")
C_ERR2 = Plots.plot(tps2, ext_R2,
title="Recovered molluscs",
label="R2", linecolor=:orange, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_ERR2,"ERR2.png")
C_R2_ER2 = Plots.plot(C_RR2,C_ERR2)
2savefig(C_R2_ER2,"R2_ER2.png")
#Miracidiums
C_MM = Plots.plot(temps, M,
title="Miracidia",
label="M", linecolor=:blue, linewidth=3)
```

```
xlabel!("Weeks"); ylabel!("Size")
savefig(C_MM,"MM.png")
C_EMM = Plots.plot(tps, ext_M,
title="Miracidia",
label="M", linecolor=:blue, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_EMM,"EMM.png")
C_M_EM = Plots.plot(C_MM,C_EMM)
savefig(C_M_EM,"M_EM.png")
# Cercaires
C_PP = Plots.plot(temps, P,
title="Cercariae",
label="P", linecolor=:green, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_PP,"PP.png")
C_EPP = Plots.plot(tps2, ext_P,
title="Cercariae",
label="P", linecolor=:green, linewidth=3)
xlabel!("Weeks"); ylabel!("Size")
savefig(C_EPP,"EPP.png")
C_P_EP = Plots.plot(C_PP,C_EPP)
savefig(C_P_EP,"P_EP.png")
#
C_SSIIRR_1=Plots.plot!(C_SS1,C_II1,C_RR1)
C_SSIIRR_2=Plots.plot!(C_SS2,C_II2,C_RR2)
C_MMPP=Plots.plot!(C_MM,C_PP)
savefig(C_SSIIRR_1,"SSIIRR_1.png")
savefig(C_SSIIRR_2,"SSIIRR_2.png")
savefig(C_MMPP,"MM_PP.png")
```

4.2.2 Graphic illustrations

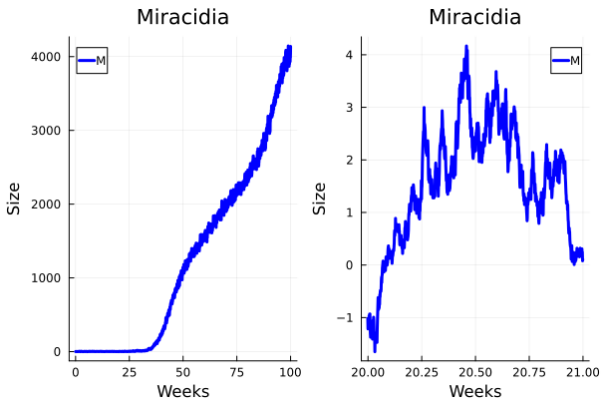

Fig. 9. Miracidium evolution curve

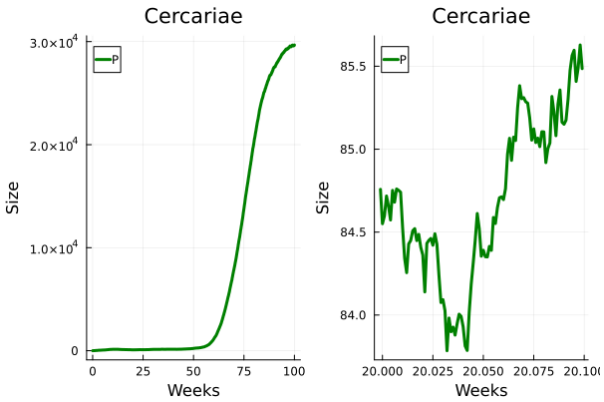

Fig. 10. Cercaria evolution curve

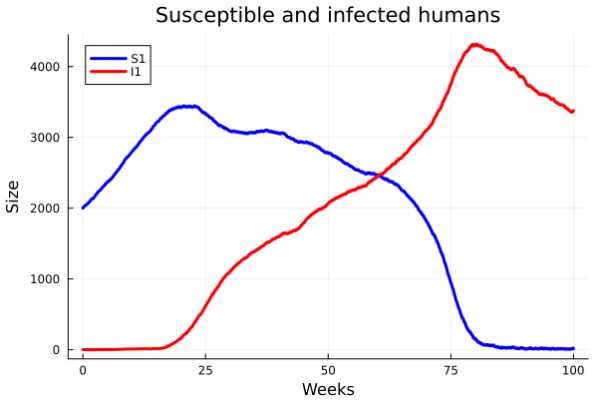

Fig. 11. Evolutionary curve for susceptible infected humans

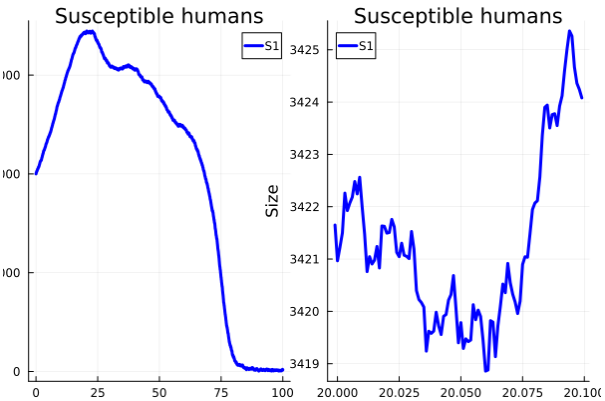

Fig. 12. Evolution curve of susceptible humans

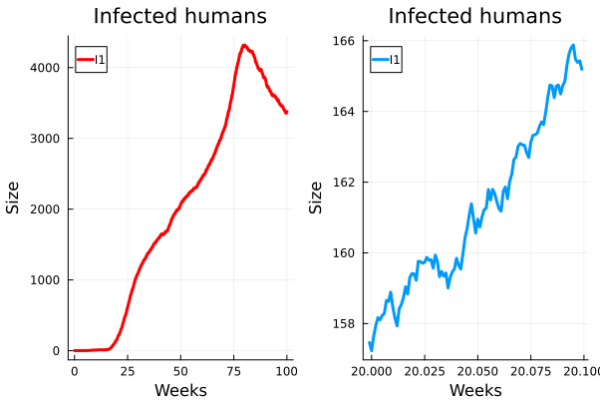

Fig. 13. Evolution curve of infected humans

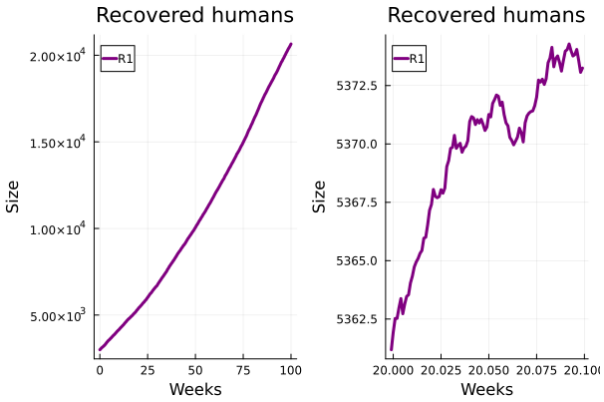

Fig. 14. Evolution curve of recovered humans

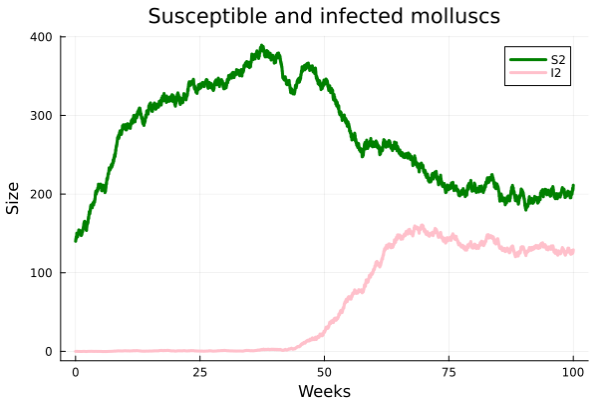

Fig. 15. Evolution curve of susceptible and infected molluscs

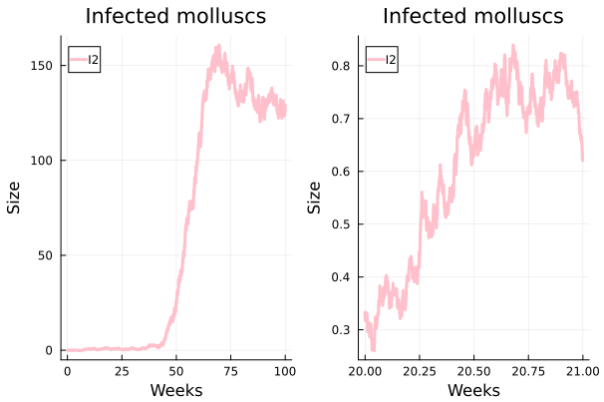

Fig. 16. Evolution curve of infected molluscs

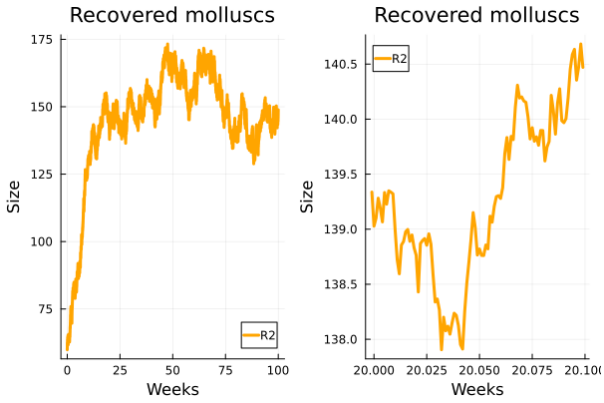

Fig. 17. Evolution curve of recovered molluscs

4.2.3 Illustration analysis

The evolution curves of stochastic processes have the same appearance as those of deterministic processes. We just notice that disturbances

4.2.4 Analysis of the Results of Deterministic and Stochastic Model Simulations

The deterministic model simulations (section 4.1) illustrate the progression of schistosomiasis under controlled conditions, where outcomes strictly follow the governing differential equations without randomness. Figures 4 through 8 reveal the population dynamics of miracidium, cercariae, humans, and molluscs across susceptible, infected, and recovered states. These curves show a predictable increase in infected populations following the initial exposure and the eventual stabilization or decrease due to recovery or death.

In contrast, the stochastic model (section 4.2) introduces randomness to simulate real-world variability, where the outcomes deviate slightly around the deterministic trends due to unpredictable events, such as fluctuations in infection rates. Figs. 9 to 17 show this variability, particularly noticeable in smaller populations where chance plays a more significant role. For example,

while deterministic curves present a steady progression, stochastic simulations display fluctuations around this progression, highlighting the effect of random events on disease spread.

The stochastic model, therefore, provides a more nuanced understanding of schistosomiasis transmission, accounting for real-world unpredictability that is absent in the deterministic approach. This distinction is crucial for accurately assessing intervention strategies, especially in populations where random factors can significantly impact disease dynamics.

5 Conclusion

In this study, we developed both deterministic and stochastic models with delays to analyze the dynamics of schistosomiasis transmission between humans and molluscs. By integrating vaccination and control strategies, we highlighted the essential role of preventive measures in curbing the spread of the disease. Utilizing Lyapunov functions enabled us to establish necessary and sufficient conditions for the global stability of both disease-free and endemic equilibrium states.

Our results underscore that effective schistosomiasis control necessitates a comprehensive approach that combines medical treatment, enhanced sanitation, and vaccination initiatives. The stochastic model reveals the inherent unpredictability of disease transmission, indicating that additional interventions may be needed under specific circumstances. Moreover, incorporating delays in parasite transmission provides a more accurate representation of disease dynamics, which is crucial for formulating effective public health policies.

Future research could aim to refine the model by incorporating spatial variables or examining the implications of drug resistance, which are becoming increasingly significant in the context of schistosomiasis management. Overall, this work enhances our understanding of schistosomiasis transmission mechanisms and lays the groundwork for developing more robust strategies to mitigate its global impact.

Disclaimer (Artificial Intelligence)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

1. Reformulation of the comparison between deterministic and stochastic simulations.
2. Assistance in refining the conclusion of the manuscript.
3. Translation of texts from French to English.

Competing Interests

Authors have declared that no competing interests exist.

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