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Epidemiological Model and Public Health Sensitization in Mali

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Abstract

In this paper we propose a mathematical model to evaluate the impact of public health sensitization campaign on the spread of HIV-AIDS in Mali. We analyse rigorously this model to get insight into its dynamical features and to obtain associated epidemiological thresholds. If $R_0 < 1$, we show that the disease-free equilibrium of the model is globally asymptotically stable when the public health sensitization program is 100% effective. The impact of public health sensitization strategies is assessed numerically by simulating the model with a reasonable set of parameter values (mostly chosen from the literature) and initial demographic data from Mali.

Keywords

HIV-AIDS, Basic Reproduction Number, Global Stability, Public Health

1. Introduction

AIDS is the most deadly disease caused by a human immunodeficiency virus (HIV). The virus destroys all the immune system and leaves individuals susceptible to any other infections. It multiplies inside lymphocytes and finally destroys them. When the lymphocytes are reduced to a certain numbers, the immune system stops functioning correctly. Therefore, the individual can catch any kind of disease that might kill him easily because of the failure of the immune system. However, there exist drugs that can slow down the evolution of the virus. HIV is usually transmitted in three different ways: sexual contacts, blood transfusion, and exchange between mother and child during pregnancy, childbirth and breastfeeding.

Many mathematical models are used to study the impact of preventive control strategies on the spread of HIV-AIDS in given populations (cf. [1]-[11], etc.). Some of these models showed that a change in risky behaviour was necessary to prevent the spread of HIV even in the presence of a treatment (see for example [12]-[16]). Thus, it is instructive to study models that focus on non-pharmaceutical interventions, such as the use of public

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health sensitization campaign.

The models developed in [15] [17]-[19] study the impact of public health sensitization campaign on the spread of HIV-AIDS. In this paper we propose and study a mathematical model to estimate the impact of public health sensitization campaign on the spread of HIV-AIDS in Mali. We divide for it the population into two classes: "class with high-risk behavioral or class without public health sensitization" and "class with low risk behavioral or class with public health sensitization". Every class consists of susceptible individuals and infected individuals. The class of the individuals at high-risk behavioral is split into susceptibles individuals $\left(S_h\right)$, individuals who are in stage 1 of the infection $\left(I_h^1\right)$, individuals who are in stage 2 of the infection $\left(I_h^2\right)$ and individuals who are in stage AIDS $\left(I_h^3\right)$ while the class of the individuals at low-risk behavioral is split into susceptibles individuals $\left(S_f\right)$, individuals who are in stage 1 of the infection $\left(I_f^1\right)$, individuals who are in stage 2 of the infection $\left(I_f^2\right)$ and individuals who are in stage AIDS $\left(I_f^3\right)$. The total population (**Figure 1**) at time t is denoted by $N\left(t\right)$ and can be expressed as the following sum:

$$N\left(t\right)=S_h\left(t\right)+S_f\left(t\right)+I_h^1\left(t\right)+I_f^1\left(t\right)+I_h^2\left(t\right)+I_f^2\left(t\right)+I_h^3\left(t\right)+I_f^3\left(t\right). \tag{1}$$

Our model is given by the following system of ODEs with constant coefficients:

$$\frac{\mathrm{d}S_h}{\mathrm{d}t}=bN-S_h\left(K_h+K_f\right)-\left(\mu+\theta\right)S_h \tag{2}$$

$$\frac{\mathrm{d}I_h^1}{\mathrm{d}t}=S_h\left(K_h+K_f\right)-\left(\mu+\alpha_1+\gamma_1\right)I_h^1 \tag{3}$$

$$\frac{\mathrm{d}I_h^2}{\mathrm{d}t}=\alpha_1 I_h^1-\left(\mu+\alpha_2+\gamma_2\right)I_h^2 \tag{4}$$

$$\frac{\mathrm{d}I_h^3}{\mathrm{d}t}=\alpha_2 I_h^2-\left(\mu+\gamma_3\right)I_h^3 \tag{5}$$

$$\frac{\mathrm{d}S_f}{\mathrm{d}t}=\theta S_h-S_f\kappa\left(K_h+K_f\right)-\mu S_f \tag{6}$$

$$\frac{\mathrm{d}I_f^1}{\mathrm{d}t}=S_f\kappa\left(K_h+K_f\right)-\left(\mu+\alpha_3\right)I_f^1+\gamma_1 I_h^1 \tag{7}$$

$$\frac{\mathrm{d}I_f^2}{\mathrm{d}t}=\alpha_3 I_f^1-\left(\mu+\alpha_4\right)I_f^2+\gamma_2 I_h^2 \tag{8}$$

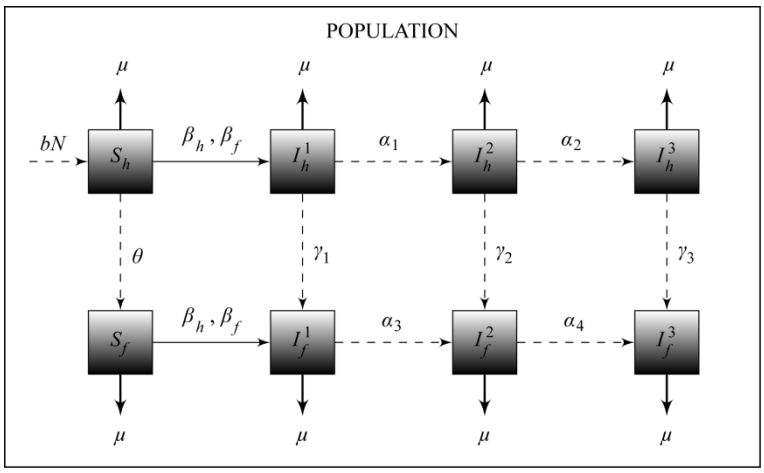


Figure 1. Behavioral representation of the HIV-AIDS model.

$$\frac{\mathrm{d}I_f^3}{\mathrm{d}t} = \alpha_4 I_f^2 - \mu I_f^3 + \gamma_3 I_h^3 \tag{9}$$

with

$$K_h = \beta_h \frac{I_h^1 + I_h^2 + I_h^3}{N} \quad \text{and} \quad K_f = \beta_f \frac{I_f^1 + I_f^2 + I_f^3}{N}. \tag{10}$$

By adding of (2) to (9), we obtain: $\frac{\mathrm{d}N}{\mathrm{d}t} = (b-\mu)N$. where the parameters of the model are defined in **Table 1**.

Our mathematical model is an extension of the models developed in [15] [17]-[19]. In our model, we suppose:

H1: that he mode of transmission of the virus is the horizontal transmission;

H2: that every individual is susceptible at high risk before his recruitment in the compartment S_h and that the rate of mortality induced by the HIV is neglected;

H3: that κ, η_h and η_f are in $[0,1]$, the parameters b, μ, θ, α_1, α_2, α_3, α_4, γ_1, γ_2, γ_3, c_h, c_f are in $\mathbb{R}_+$ and that $\beta_h > \beta_f$.

2. Analysis of the Complete Model

2.1. Existence of Solutions

To show that the model is mathematically and biologically possible, we begin by rewriting it in terms of proportions. So, we introduce the following scalings:

$$s_h = \frac{S_h}{N}, s_f = \frac{S_f}{N}, i_h^1 = \frac{I_h^1}{N}, i_h^2 = \frac{I_h^2}{N}, i_h^3 = \frac{I_h^3}{N}, i_f^1 = \frac{I_f^1}{N}, i_f^2 = \frac{I_f^2}{N}, i_f^3 = \frac{I_f^3}{N}. \tag{11}$$

Consequently:

$$s_h + i_h^1 + i_h^2 + i_h^3 + s_f + i_f^1 + i_f^2 + i_f^3 = 1. \tag{12}$$

By using what precedes, the rates of infection (10) become:

$$k_h = \beta_h \left(i_h^1 + i_h^2 + i_h^3\right) \text{ and } k_f = \beta_f \left(i_f^1 + i_f^2 + i_f^3\right). \tag{13}$$

If we introduce the following parameters:

$$\phi_1 = b + \theta,\ \phi_2 = b + \alpha_1 + \gamma_1,\ \phi_3 = b + \alpha_2 + \gamma_2,\ \phi_4 = b + \gamma_3,\ \phi_5 = b + \alpha_3,\ \phi_6 = b + \alpha_4. \tag{14}$$

In the new variables, (2)-(9) reduces to:

$$\frac{\mathrm{d}s_h}{\mathrm{d}t} = b - s_h\left(k_h + k_f\right) - \phi_1 s_h \tag{15}$$

$$\frac{\mathrm{d}i_h^1}{\mathrm{d}t} = s_h\left(k_h + k_f\right) - \phi_2 i_h^1 \tag{16}$$

Table 1. Model parameters.

Parameters	Biological description
b, μ	Recruitment rate, natural mortality rate.
θ, γ_1, γ_2, γ_3	Sensitization rates.
α_1, α_2, α_3, α_4	Transfer rates.
κ	Reduction probability of the susceptible contamination S_f.
β_h, β_f	Transmission rates.

$$\frac{\mathrm{d}i_h^2}{\mathrm{d}t} = \alpha_1 i_h^1 - \phi_3 i_h^2 \tag{17}$$

$$\frac{\mathrm{d}i_h^3}{\mathrm{d}t} = \alpha_2 i_h^2 - \phi_4 i_h^3 \tag{18}$$

$$\frac{\mathrm{d}s_f}{\mathrm{d}t} = \theta s_h - s_f \kappa\left(k_h + k_f\right) - b s_f \tag{19}$$

$$\frac{\mathrm{d}i_f^1}{\mathrm{d}t} = s_f \kappa\left(k_h + k_f\right) - \phi_5 i_f^1 + \gamma_1 i_h^1 \tag{20}$$

$$\frac{\mathrm{d}i_f^2}{\mathrm{d}t} = \alpha_3 i_f^1 - \phi_6 i_f^2 + \gamma_2 i_h^2 \tag{21}$$

$$\frac{\mathrm{d}i_f^3}{\mathrm{d}t} = \alpha_4 i_f^2 - b i_f^3 + \gamma_3 i_h^3 \tag{22}$$

We suppose that the initial conditions belong in Ω where

$$\Omega = \left\{\left(s_h, i_h^1, i_h^2, i_h^3, s_f, i_f^1, i_f^2, i_f^3\right) \in [0,1]^8 \,\middle|\, 0 \le s_h + i_h^1 + i_h^2 + i_h^3 + s_f + i_f^1 + i_f^2 + i_f^3 \le 1\right\}. \tag{23}$$

Now we can enounce the following result:

Theorem 1. *For any initial condition in* Ω, *the system has a unique solution globally defined and which stays in* Ω *for any time* $t \ge 0$.

Before giving the proof of this theorem, we give at first a technical result which we shall use after.

Lemma 1. *Let a*(*t*) *and y*(*t*) *be n X n matrices of bounded measurable functions on* $[0,\infty)$, *if*

$$\frac{\mathrm{d}}{\mathrm{d}t}x(t) + a(t)x(t) = y(t) \tag{24}$$

with $y(t) \ge 0$ for $0 \le t < t_0$ and $x(0) \ge 0$ then $x(t) \ge 0$ for all $0 \le t < t_0$.

Proof. Indeed, this follows from the integrated form of the differential Equation (24),

$$x(t) = x(0)\mathrm{e}^{-\int_0^t a(x)\mathrm{d}x} + \mathrm{e}^{-\int_0^t a(x)\mathrm{d}x}\int_0^t y(z)\mathrm{e}^{\int_0^t a(x)\mathrm{d}x}\mathrm{d}z. \qquad \square$$

We rewrite the system (15)-(22) in the form

$$\frac{\mathrm{d}x_i}{\mathrm{d}t} = f_i(x), \quad i = 1,\cdots,8. \tag{25}$$

Now we can give the proof of the theorem 1.

Proof. **Step 1: Local existence of the solutions.**

The local existence of the solutions ensues directly from the regularity of the function $f = (f_1,\cdots,f_8)$ which is of class C^1 in Ω.

Step 2: We show that Ω is positively invariant.

A. $s_h(t) \ge 0$, $i_h^1(t) \ge 0$, $i_h^2(t) \ge 0$, $i_h^3(t) \ge 0$, $s_f(t) \ge 0$, $i_f^1(t) \ge 0$, $i_f^2(t) \ge 0$, $i_f^3(t) \ge 0$, $\forall t \ge 0$. Let's suppose that it exists $t_0 \in [0,T]$ such $\forall 0 \le t < t_0$, $i_h^1(t) \ge 0$ and $i_f^1(t) \ge 0$ and let's rewrite the Equations (15), (17)-(22) in the form:

$$\frac{\mathrm{d}s_h}{\mathrm{d}t} + s_h\left(k_h + k_f + \phi_1\right) = b \tag{26}$$

$$\frac{\mathrm{d}i_h^2}{\mathrm{d}t} + \phi_3 i_h^2 = \alpha_1 i_h^1 \tag{27}$$

$$\frac{\mathrm{d}i_h^3}{\mathrm{d}t} + \phi_4 i_h^3 = \alpha_2 i_h^2 \tag{28}$$

$$\frac{\mathrm{d}s_f}{\mathrm{d}t}+s_f\left(k_h+k_f+b\right)=\theta s_h \tag{29}$$

$$\frac{\mathrm{d}i_f^2}{\mathrm{d}t}+\phi_6 i_f^2=\gamma_2 i_h^2+\alpha_3 i_f^1 \tag{30}$$

$$\frac{\mathrm{d}i_f^3}{\mathrm{d}t}+bi_f^3=\gamma_3 i_h^3+\alpha_4 i_f^2 \tag{31}$$

By Lemma 1, $i_h^2(t)\geq 0$, $i_h^3(t)\geq 0$, $i_f^2(t)\geq 0$, $i_f^3(t)\geq 0$, $s_h(t)\geq 0$ et $s_f(t)\geq 0$ for $0\leq t<t_0$.
We next show that $i_h^1(t)$ and $i_f^1(t)$ remains positive for all $t>0$.
Proceding by contradiction:
We suppose that $i_h^1(t)>0$ and $i_f^1(t)>0$ for $0\leq t<t_0$ and $i_h^1(t_0)=i_f^1(t_0)=0$.
Then, $\frac{\mathrm{d}}{\mathrm{d}t}i_h^1(t_0)\leq 0$ and $\frac{\mathrm{d}}{\mathrm{d}t}i_f^1(t_0)\leq 0$. By considering the Equation (26) in time $t=t_0$, we have:

$$\frac{\mathrm{d}i_h^2(t_0)}{\mathrm{d}t}+\phi_3 i_h^2(t_0)=0 \tag{32}$$

$$\frac{\mathrm{d}i_h^3(t_0)}{\mathrm{d}t}+\phi_4 i_h^3(t_0)=\alpha_2 i_h^2(t_0) \tag{33}$$

$$\frac{\mathrm{d}i_f^2(t_0)}{\mathrm{d}t}+\phi_6 i_f^2(t_0)=\gamma_2 i_h^2(t_0) \tag{34}$$

$$\frac{\mathrm{d}i_f^3(t_0)}{\mathrm{d}t}+bi_f^3(t_0)=\gamma_3 i_h^3(t_0)+\alpha_4 i_f^2(t_0) \tag{35}$$

$$\frac{\mathrm{d}s_h(t_0)}{\mathrm{d}t}+s_h(t_0)\left(k_h(t_0)+k_f(t_0)+\phi_1\right)=b \tag{36}$$

$$\frac{\mathrm{d}s_f(t_0)}{\mathrm{d}t}+s_f(t_0)\left(k_h(t_0)+k_f(t_0)+b\right)=\theta s_h(t_0). \tag{37}$$

By Lemma 1, $i_h^2(t)\geq 0$, $i_h^3(t)\geq 0$, $i_f^2(t)\geq 0$, $i_f^3(t)\geq 0$, $s_h(t)\geq 0$ and $s_f(t)\geq 0$ for $t=t_0$.
Now we consider the Equations (16) and (20) in time $t=t_0$

$$\frac{\mathrm{d}i_h^1(t_0)}{\mathrm{d}t}=s_h(t_0)\left(k_h(t_0)+k_f(t_0)\right)\geq 0 \tag{38}$$

$$\frac{\mathrm{d}i_f^1(t_0)}{\mathrm{d}t}=s_f(t_0)\left(k_h(t_0)+k_f(t_0)\right)\geq 0 \tag{39}$$

which is a contradiction, Consequently i_h^1 and i_f^1 remains positive for all $t>0$.

B. The following inequalities hold:

$$s_h(t)+i_h^1(t)+i_h^2(t)+i_h^3(t)+s_f(t)+i_f^1(t)+i_f^2(t)+i_f^3(t)=1, \quad \text{for all } t>0.$$

Adding all the equations of (15), we obtain:

$$\frac{\mathrm{d}}{\mathrm{d}t}\left[s_h(t)+i_h^1(t)+i_h^2(t)+i_h^3(t)+s_f(t)+i_f^1(t)+i_f^2(t)+i_f^3(t)\right]=0. \tag{40}$$

By integrating (40) between 0 and *t*, we have:

$$\left[s_h(t)+i_h^1(t)+i_h^2(t)+i_h^3(t)+s_f(t)+i_f^1(t)+i_2^2(t)+i_f^3(t)\right]$$
$$-\left[s_h(0)+i_h^1(0)+i_h^2(0)+i_h^3(0)+s_f(0)+i_f^1(0)+i_2^2(0)+i_f^3(0)\right]=0.$$

So if the initial condition verifies

$$s_h(0)+i_h^1(0)+i_h^2(0)+i_h^3(0)+s_f(0)+i_f^1(0)+i_2^2(0)+i_f^3(0)=1,$$

then the relation

$$s_h(t)+i_h^1(t)+i_h^2(t)+i_h^3(t)+s_f(t)+i_f^1(t)+i_2^2(t)+i_f^3(t)=1,$$

will be verified for all $t>0$.

This second stage shows that the solutions are limited for everything $t\geq 0$. We can conclude that the solutions of the model exist globally in Ω. □

2.2. Desease Free Equilibruim

There will be absence of desease in the population if the proportions i_h^1, i_h^2, i_h^3, i_f^1, i_f^2 et i_f^3 are nil. Let be x_{dfe} (resp. X_{dfe}) a desease free equilibruim of the model (15)-(22) (resp. (2)-(9)). The following theorem gives us the existence and the uniqueness of this desease free equilibruim. Given that the models (2)-(9) and (15)-(22) are equivalent, then x_{dfe} and X_{dfe} are also equivalent.

Theorem 2. *The model of HIV-SIDA* (2)-(9) *or* (15)-(22) *possesses a unique desease free equilibruim in* Ω *where*

$$x_{dfe}=\left(s_h^*,0,0,0,s_f^*,0,0,0\right) \tag{41}$$

$$X_{dfe}=\left(S_h^*,0,0,0,S_f^*,0,0,0\right) \tag{42}$$

and

$$s_h^*=\frac{b}{\phi_1},\quad s_f^*=\frac{\theta}{\phi_1} \tag{43}$$

$$S_h^*=s_h^*N^*,\quad S_f^*=s_f^*N^*. \tag{44}$$

Proof. Let be x_{dfe} a desease free equilibruim of the model (15)-(22). There will be absence of desease in the population if $i_h^1=i_h^2=i_h^3=i_f^1=i_f^2=i_f^3=0$. If we substitute these useless values in $f_i=0$, $i=1,\cdots,8$, we find that the unique free equilibruim for s_h in Ω from (15) is s_h^*, the unique free equilibruim for s_f in Ω from (19) is s_f^*. Consequently the unique desease free equilibruim in Ω is x_{dfe}.

Let be X_{dfe} desease free equilibruim for the model (2)-(9). By substituting x_{dfe} in (11), we obtain:

$$X_{dfe}=\left(S_h,I_h^1,I_h^2,I_h^3,S_f,I_f^1,I_f^2,I_f^3\right)=\left(S_h^*,0,0,0,S_f^*,0,0,0\right),$$

where

$$S_h^*=s_h^*N^*,\quad \text{et}\quad S_f^*=s_f^*N^*.$$ □

2.3. Local Stability of Disease Free Equilibrium

By using the method of Van den Drissche and Watmough, we denote by *F* the rate of appearance of new infections in compartments of the infectious, and by *V*s the rate of transfer of individuals in and out the compartments of the infectious by all other means. Then

$$F=\begin{bmatrix}\beta_h s_h^* & \beta_h s_h^* & \beta_h s_h^* & \beta_f s_h^* & \beta_f s_h^* & \beta_f s_h^*\\ 0&0&0&0&0&0\\ 0&0&0&0&0&0\\ \beta_h s_f^* & \beta_h s_f^* & \beta_h s_f^* & \beta_f s_f^* & \beta_f s_f^* & \beta_f s_f^*\\ 0&0&0&0&0&0\\ 0&0&0&0&0&0\end{bmatrix} \text{ and } V=\begin{bmatrix}\phi_2&0&0&0&0&0\\ -\alpha_1&\phi_3&0&0&0&0\\ 0&-\alpha_2&\phi_4&0&0&0\\ -\gamma_1&0&0&\phi_5&0&0\\ 0&-\gamma_2&0&-\alpha_3&\phi_6&0\\ 0&0&-\gamma_3&0&-\alpha_4&b\end{bmatrix}.$$

The next-generation matrix is defined by:

$$K = FV^{-1} = \frac{1}{M_7}\begin{bmatrix} M_1 b & M_2 b & M_3 b & M_4 b & M_5 b & M_6 b \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ M_1\kappa\theta & M_2\kappa\theta & M_3\kappa\theta & M_4\kappa\theta & M_5\kappa\theta & M_6\kappa\theta \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

where M_1, M_2, M_3, M_4, M_5, M_6 and M_7 are defined by the equations of (45) to (51).

$$\begin{aligned} M_1 = {} & \beta_h b\phi_3\phi_4\phi_5\phi_6 + \alpha_1\beta_h b\phi_4\phi_5\phi_6 + \beta_h\alpha_1\alpha_2 b\phi_5\phi_6 + \beta_f\gamma_1 b\phi_3\phi_4\phi_6 + \beta_f\gamma_2\alpha_1 b\phi_4\phi_5 \\ & + \beta_f\alpha_3\gamma_1 b\phi_3\phi_4 + \beta_f\gamma_3\alpha_2\alpha_1\phi_5\phi_6 + \beta_f\alpha_4\alpha_1\gamma_2\phi_4\phi_5 + \beta_f\alpha_4\alpha_3\gamma_1\phi_3\phi_4 \end{aligned} \tag{45}$$

$$M_2 = \beta_h b\phi_2\phi_4\phi_5\phi_6 + \beta_h\alpha_2 b\phi_2\phi_5\phi_6 + \beta_f\gamma_2 b\phi_2\phi_4\phi_5 + \beta_f\gamma_3\alpha_2\phi_2\phi_5\phi_6 + \beta_f\alpha_4\gamma_2\phi_2\phi_4\phi_5 \tag{46}$$

$$M_3 = \beta_h b\phi_2\phi_3\phi_5\phi_6 + \beta_f\gamma_3\phi_2\phi_3\phi_5\phi_6 \tag{47}$$

$$M_4 = \beta_f b\phi_2\phi_3\phi_4\phi_6 + \beta_f\alpha_3 b\phi_2\phi_3\phi_4 + \beta_f\alpha_3\alpha_4\phi_2\phi_3\phi_4 \tag{48}$$

$$M_5 = \beta_f b\phi_2\phi_3\phi_4\phi_5 + \beta_f\alpha_4\phi_2\phi_3\phi_4\phi_5 \tag{49}$$

$$M_6 = \beta_f\phi_2\phi_3\phi_4\phi_5\phi_6 \tag{50}$$

$$M_7 = b\phi_1\phi_2\phi_3\phi_4\phi_5\phi_6 \tag{51}$$

Proposition 3. *The basic reproduction ratio for HIV-SIDA model* (15)-(22) *is explicitly given by the formula* (52) *where* M_1, M_4 *and* M_7 *are explicitly defined by equations* (45), (48) *and* (51):

$$R_0 = \rho(K) = \frac{bM_1 + \kappa\theta M_4}{M_7} \tag{52}$$

Theorem 4. *The disease free equilibrium* x_{dfe} *of the model* (15) *is locally-asymptotically stable if* $R_0 < 1$ *and unstable if* $R_0 > 1$.

2.4. Global Stability of the Disease Free Equilibrium

We have the following theorem.

Theorem 5. *For the system* (15)-(22), *if* $R_0 < 1$ *then the disease free equilibrium is globally asymptotically stable.*

Proof. We begin by rewriting the system (15)-(22) in the form:

$$\frac{\mathrm{d}x_1}{\mathrm{d}t} = -b + \left(b\phi_1^{-1} - x_1\right)\left(k_h + k_f\right) + \phi_1\left(b\phi_1^{-1} - x_1\right) \tag{53}$$

$$\frac{\mathrm{d}i_h^1}{\mathrm{d}t} = \left(b\phi_1^{-1} - x_1\right)\left(k_h + k_f\right) - \phi_2 i_h^1 \tag{54}$$

$$\frac{\mathrm{d}i_h^2}{\mathrm{d}t} = \alpha_1 i_h^1 - \phi_3 i_h^2 \tag{55}$$

$$\frac{\mathrm{d}i_h^3}{\mathrm{d}t} = \alpha_2 i_h^2 - \phi_4 i_h^3 \tag{56}$$

$$\frac{\mathrm{d}x_2}{\mathrm{d}t} = -\theta\left(b\phi_1^{-1} - x_1\right) + \kappa\left(\theta\phi_1^{-1} - x_2\right)\left(k_h + k_f\right) + b\left(\theta\phi_1^{-1} - x_2\right) \tag{57}$$

$$\frac{\mathrm{d}i_f^1}{\mathrm{d}t} = \kappa\left(\theta\phi_1^{-1} - x_2\right)\left(k_h + k_f\right) - \phi_5 i_f^1 + \gamma_1 i_h^1 \tag{58}$$

$$\frac{\mathrm{d}i_f^2}{\mathrm{d}t} = \alpha_3 i_f^1 - \phi_6 i_f^2 + \gamma_2 i_h^2 \tag{59}$$

$$\frac{\mathrm{d}i_f^3}{\mathrm{d}t} = \alpha_4 i_f^2 - b i_f^3 + \gamma_3 i_h^3 \tag{60}$$

where $x_1 = b\phi_1^{-1} - s_h$ and $x_2 = \theta\phi_2^{-1} - s_f$, the disease free equilibrium x_{dfe} for the system (53)-(60) corresponds to the point $(0,0,0,0,0,0,0,0)$.

Now, let us consider the following function:

$$\begin{aligned} V = {} & \phi_2^{-1}\left(M_7 - \kappa\theta M_4\right) i_h^1 + b\phi_2^{-1} M_2 i_h^2 + b\phi_2^{-1} M_3 \left(x_1 + x_2 - i_h^1 - i_h^2 - i_f^1 - i_f^2 - i_f^3\right) \\ & + b\phi_2^{-1} M_4 i_f^1 + b\phi_2^{-1} M_5 i_f^2 + b\phi_2^{-1} M_6 \left(x_1 + x_2 - i_h^1 - i_h^2 - i_h^3 - i_f^1 - i_f^2\right). \end{aligned}$$

If $R_0 < 1$, $M_7 - \kappa\theta M_4$, M_2, M_3, M_4, M_5 and M_6 are positives. Consequently the function V is positive, and it nulle at the disease free equilibrium. The derivative of this Lyapunov function V along the trajectories of the ordinary differentiel system is:

$$\begin{aligned} \dot{V} = {} & \phi_2^{-1}\left(M_7 - \kappa\theta M_4\right)\left[\left(b\phi_1^{-1} - x_1\right)\left(k_h + k_f\right) - \phi_2 i_h^1\right] + b\phi_2^{-1} M_2 \left(\alpha_1 i_h^1 - \phi_3 i_h^2\right) \\ & + b\phi_2^{-1} M_3 \left(\alpha_2 i_h^2 - \phi_4 i_h^3\right) + b\phi_2^{-1} M_4 \left[\kappa\left(\theta\phi_1^{-1} - x_2\right)\left(k_h + k_f\right) - \phi_5 i_f^1 + \gamma_1 i_h^1\right] \\ & + b\phi_2^{-1} M_5 \left(\alpha_3 i_f^1 - \phi_6 i_f^2 + \gamma_2 i_h^2\right) + b\phi_2^{-1} M_6 \left(\alpha_4 i_f^2 - b i_f^3 + \gamma_3 i_h^3\right). \end{aligned}$$

We can also write

$$\begin{aligned} \dot{V} = {} & \phi_2^{-1}\left(M_7 - \kappa\theta M_4\right)\frac{b}{\phi_1}\left(k_h + k_f\right) - \phi_2^{-1}\left(M_7 - \kappa\theta M_4\right)\left(k_h + k_f\right) x_1 \\ & - \left(M_7 - \kappa\theta M_4\right) i_h^1 + b\phi_2^{-1} M_2 \alpha_1 i_h^1 - b\phi_2^{-1} M_2 \phi_3 i_h^2 + b\phi_2^{-1} M_3 \alpha_2 i_h^2 \\ & - b\phi_2^{-1} M_3 \phi_4 i_h^3 + b\phi_2^{-1} \kappa\theta M_4 \phi_1^{-1}\left(k_h + k_f\right) - b\phi_2^{-1} \kappa M_4 \left(k_h + k_f\right) x_2 \\ & - b\phi_2^{-1} M_4 \phi_5 i_f^1 + b\phi_2^{-1} M_4 \gamma_1 i_h^1 + b\phi_2^{-1} M_5 \alpha_3 i_f^1 - b\phi_2^{-1} M_5 \phi_6 i_f^2 \\ & + b\phi_2^{-1} M_5 \gamma_2 i_h^2 + b\phi_2^{-1} M_6 \alpha_4 i_f^2 - b\phi_2^{-1} M_6 b i_f^3 + b\phi_2^{-1} M_6 \gamma_3 i_h^3. \end{aligned}$$

Algebraic manipulations give

$$\begin{aligned} \dot{V} = {} & -\phi_2^{-1}\left(M_7 - \theta\kappa M_4\right)\left(k_h + k_f\right) x_1 - b\phi_2^{-1} \kappa M_4 \left(k_h + k_f\right) x_2 \\ & + \left(-M_7 + \theta\kappa M_4 + b\phi_2^{-1} M_2 \alpha_1 + b\phi_2^{-1} M_4 \gamma_1 + \beta_h b\phi_1^{-1}\phi_2^{-1} M_7\right) i_h^1 \end{aligned}$$

or

$$\dot{V} = -\phi_2^{-1}\left(M_7 - \kappa\theta M_4\right)\left(k_h + k_f\right) x_1 - b\phi_2^{-1} \kappa M_4 \left(k_h + k_f\right) x_2 - \left(M_7 - \kappa\theta M_4 - b M_1\right) i_h^1.$$

If $R_0 < 1$, $M_7 - \kappa\theta M_4$ and $M_7 - \kappa\theta M_4 - b M_1$ are positives, consequently $\dot{V}$ is negative definite along the trajectories. This ends the proof of the theorem. □

2.5. Numerical Simulations

Before closing this section, we verify numerically the theoretical results obtained in subsections 2, 2 and 2 for an initial condition $s_h = 0.96104$, $i_h^1 = 0.01872$, $i_h^2 = 0.00374$, $i_h^3 = 0.00094$, $s_f = 0.0091$, $i_f^1 = 0.00468$, $i_f^2 = 0.00094$, $i_f^3 = 0.00023$. For numerical simulations, the system (15) (22) is discretized with a Runge-Kutta's method (ODE45). We collect a set of values of biological parameters for the model corresponding to the data on the spread of the HIV-SIDA in two cases:

First case: the disease goes extinct in the population (see **Figure 2**).

Second case: the disease persists in the population (see **Figure 3**).

These parameters are obtained in the literature and are summarized in the **Table 2**.

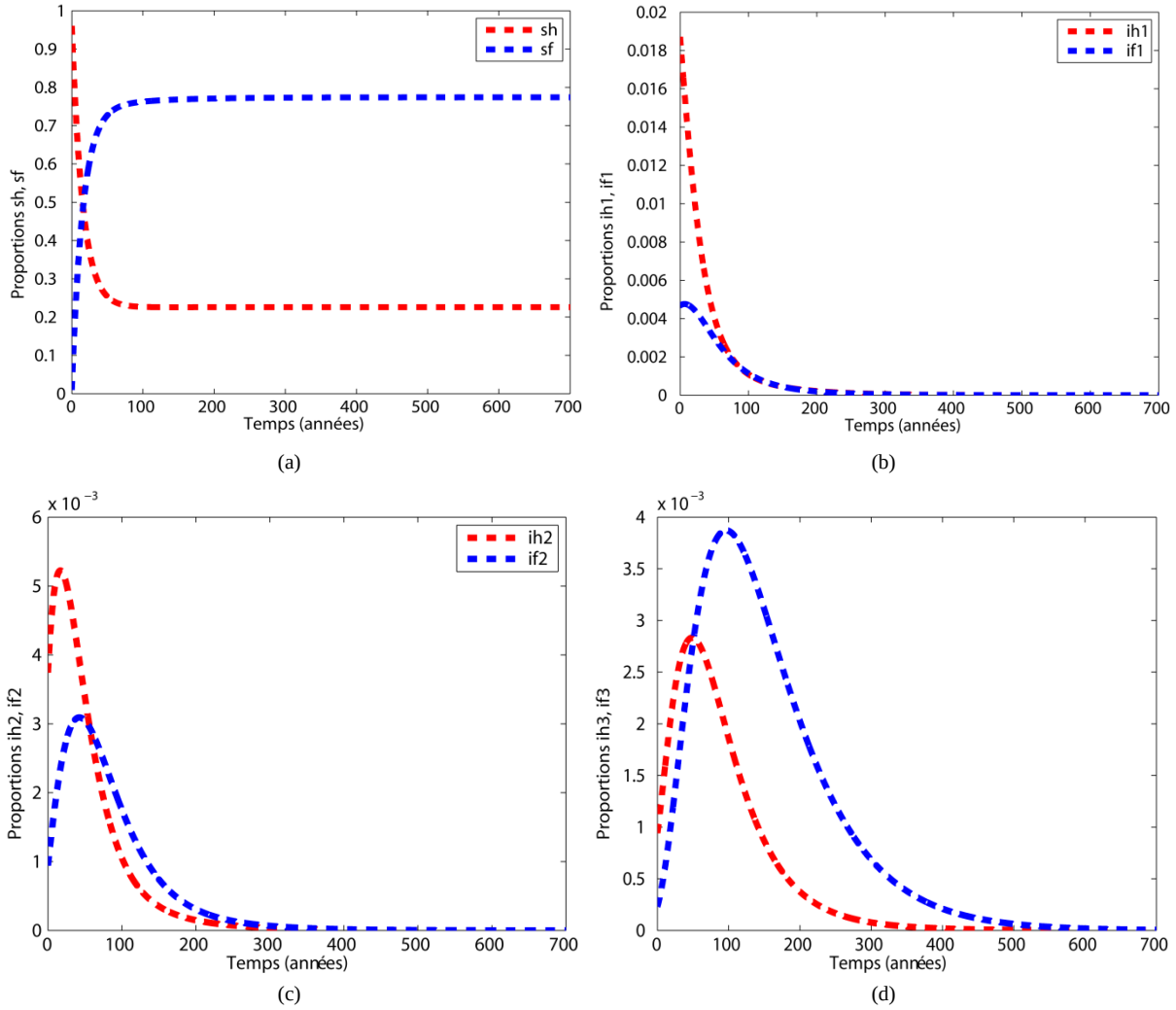


Figure 2. Dynamics of the system (15)-(22) in case where the disease goes extinct in the population. With the parameters of the **Table 2** (first case), we have $R_0 = 0.5826$. **Figure 2(a)** shows the evolution of susceptibles individuals, whereas **Figures 2(b)-(d)** show the evolution of infected individuals. The system converges towards the desease free equilibruim (0.226, 0, 0, 0, 0.774, 0, 0, 0). The simulation was realized with the MATLAB logiciel.

3. Model without Public Health Sensitization

In this section all sensitization-related parameters and variables are fixed to zero in order to understand the dynamic behavior of the population without public health sensitization campaign.

So, we pose $s_f = i_f^1 = i_f^2 = i_f^3 = \theta = \gamma_1 = \gamma_2 = \gamma_3 = \kappa = 0$. the model (15)-(22) reduces to:

$$\frac{\mathrm{d}s_h}{\mathrm{d}t} = b - s_h k_h - \phi_1 s_h \tag{61}$$

$$\frac{\mathrm{d}i_h^1}{\mathrm{d}t} = s_h k_h - \phi_2 i_h^1 \tag{62}$$

$$\frac{\mathrm{d}i_h^2}{\mathrm{d}t} = \alpha_1 i_h^1 - \phi_3 i_h^2 \tag{63}$$

$$\frac{\mathrm{d}i_h^3}{\mathrm{d}t} = \alpha_2 i_h^2 - \phi_4 i_h^3 \tag{64}$$

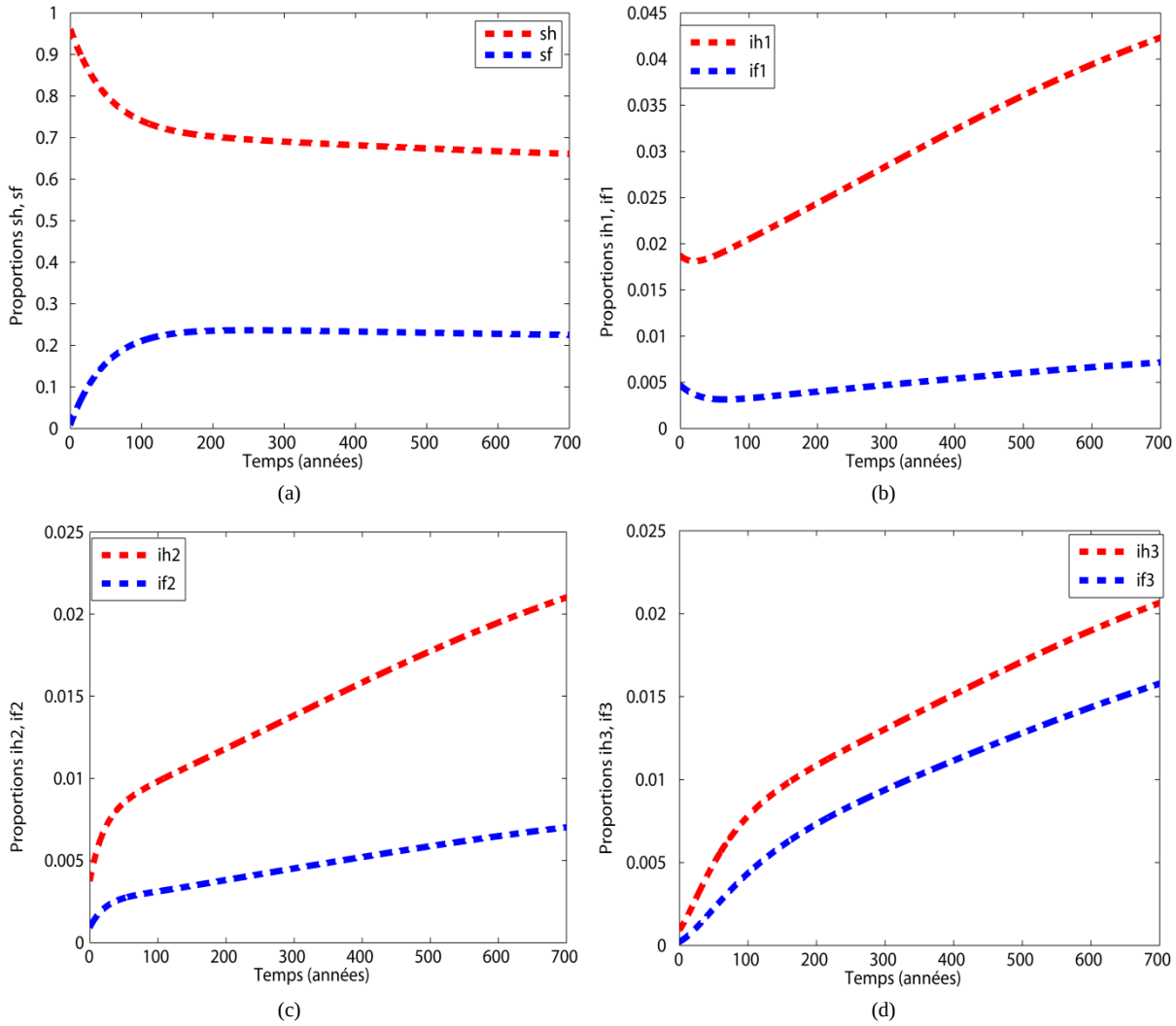


Figure 3. Dynamics of the system (15)-(22) in case where the disease persists in the population. With the parameters of the **Table 2** (second case), we have R_0 = 1.2928. **Figure 3(a)** shows the evolution of susceptibles individuals, whereas **Figures 3(b)-(d)** show the evolution of infected individuals. The system converges towards the endemic equilibrium (0.6609, 0.0423, 0.021, 0.0206, 0.2251, 0.0072, 0.007, 0.0158). The simulation was realized with the MATLAB logiciel.

Table 2. Biological parameters.

Parameters	First case	Second case
b ; μ	0.0146; 0.014	0.0146; 0.014
θ ; κ	0.05; 0.07	0.005; 0.007
α_1 ; α_2	0.02; 0.02	0.02; 0.02
α_3 ; α_4	0.02; 0.02	0.02; 0.02
γ_1 ; γ_2	0.01; 0.01	0.005; 0.005
γ_3	0.01	0.005
β_h ; β_f	0.015; 0.0075	0.028; 0.0075

where

$$\phi_1 = \phi_4 = b, \quad \phi_2 = b + \alpha_1, \quad \phi_3 = b + \alpha_2$$

with $s_h + i_h^1 + i_h^2 + i_h^3 = 1$. For this sub-model by using the same reasoning in the theorem 1, we demonstrate that for any initial condition in Ω_h, the system has a unique solution globally defined and which stays in Ω_h for any time $t \geq 0$ where

$$\Omega_h = \left\{ \left(s_h, i_h^1, i_h^2, i_h^3 \right) \in [0,1]^4 \,\middle|\, 0 \leq s_h + i_h^1 + i_h^2 + i_h^3 \leq 1 \right\}. \tag{65}$$

3.1. Local Stability of Disease Free Equilibrium

The desease free equilibruim x_{dfe} of the sub-model (61)-(64) is:

$$x_{dfe} = \left(s_h^*, i_h^{1*}, i_h^{2*}, i_h^{1*} \right) = (1,0,0,0).$$

By using the method of Van den Drissche and Watmough, we denote by F the rate of appearance of new infections in compartments of the infectious, and by Vs the rate of transfer of individuals in and out the compartments of the infectious by all other means. Then:

$$F = \begin{bmatrix} \beta_h & \beta_h & \beta_h \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \quad \text{and} \quad V = \begin{bmatrix} \phi_2 & 0 & 0 \\ -\alpha_1 & \phi_3 & 0 \\ 0 & -\alpha_2 & \phi_4 \end{bmatrix}.$$

the next-generation matrix is defined by:

$$K = FV^{-1} = \begin{bmatrix} \dfrac{\beta_h \left(\phi_3\phi_4 + \alpha_1\phi_4 + \alpha_1\alpha_2 \right)}{\phi_2\phi_3\phi_4} & \dfrac{\beta_h \left(\alpha_2 + \phi_4 \right)}{\phi_3\phi_4} & \dfrac{\beta_h}{\phi_4} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}.$$

Proposition 6. *The basic reproduction ratio for the sub-model* (61)-(64) *is given by the formula* (66):

$$R_{h0} = \rho\left(FV^{-1} \right) = \frac{\beta_h \left(\phi_3\phi_4 + \alpha_1\phi_4 + \alpha_1\alpha_2 \right)}{\phi_2\phi_3\phi_4} \tag{66}$$

Theorem 7. *The disease free equilibrium* x_{dfe} *of the sub-model* (61)-(64) *is locally-asymptotically stable if* R_{h0} *and unstable if* $R_{h0} > 1$.

3.2. Global Stability of the Disease Free Equilibrium

Theorem 8. *For the system* (61)-(64), *if* $R_{h0} < 1$ *then the disease free equilibrium* x_{dfe} *is globally asymptotically stable.*

Proof. We begin by rewriting the system (61)-(64) in the form:

$$\frac{\mathrm{d}x_h}{\mathrm{d}t} = -b + \left(1 - x_h\right) k_h + \phi_1 \left(1 - x_h\right) \tag{67}$$

$$\frac{\mathrm{d}i_h^1}{\mathrm{d}t} = \left(1 - x_h\right) k_h - \phi_2 i_h^1 \tag{68}$$

$$\frac{\mathrm{d}i_h^2}{\mathrm{d}t} = \alpha_1 i_h^1 - \phi_3 i_h^2 \tag{69}$$

$$\frac{\mathrm{d}i_h^3}{\mathrm{d}t} = \alpha_2 i_h^2 - \phi_4 i_h^3 \tag{70}$$

where $x_h = b\phi_1^{-1} - s_h$.

The disease free equilibrium x_{dfe} for the system (67)-(70) corresponds to the point $(0,0,0,0)$.

Now, let us consider the following function:

$$V = \phi_3\phi_4 i_h^1 + \beta_h(\phi_4 + \alpha_2)\left(x - i_h^1 - i_h^3\right) + \beta_h\phi_3\left(x - i_h^1 - i_h^2\right).$$

The function V is positive, and it nulle at the disease free equilibrium. The derivative of this Lyapunov function V along the trajectories of the ordinary differentiel system is:

$$\dot{V} = \phi_3\phi_4\left[(1-x_h)k_h - \phi_2 i_h^1\right] + \beta_h(\phi_4 + \alpha_2)\left(\alpha_1 i_h^1 - \phi_3 i_h^2\right) + \beta_h\phi_3\left(\alpha_2 i_h^2 - \phi_4 i_h^3\right).$$

We can also write

$$\begin{aligned}\dot{V} = &-\phi_3\phi_4 k_h x_h + \left(-\phi_2\phi_3\phi_4 + \beta_h\alpha_1\phi_4 + \beta_h\alpha_1\alpha_2 + \beta_h\phi_3\phi_4\right) i_h^1 \\ &- \beta_h\left(\phi_3\phi_4 + \alpha_2\phi_3 - \phi_3\phi_4 - \alpha_2\phi_3\right) i_h^2 + \beta_h\left(\phi_3\phi_4 - \phi_3\phi_4\right) i_h^3.\end{aligned}$$

Algebraic manipulations give

$$\dot{V} = -\phi_3\phi_4 k_h x_h + \left(\beta_h\alpha_1\phi_4 + \beta_h\alpha_1\alpha_2 + \beta_h\phi_3\phi_4 - \phi_2\phi_3\phi_4\right) i_h^1$$

or

$$\dot{V} = -\phi_3\phi_4 k_h x_h + \left(R_{h0} - 1\right) i_h^1.$$

If $R_{h0} < 1$, then $\dot{V}$ is negative along the trajectories. This ends the proof of the theorem. □

3.3. Existence and Uniqueness of an Endemic Equilibrium

It is found that an unique endemic equilibrium of (61)-(64) for $R_{h0} > 1$. Thus, we solve the system:

$$b - s_h^* k_h^* - \phi_1 s_h^* = 0 \tag{71}$$

$$s_h^* k_h^* - \phi_2 i_h^{1*} = 0 \tag{72}$$

$$\alpha_1 i_h^{1*} - \phi_3 i_h^{2*} = 0 \tag{73}$$

$$\alpha_2 i_h^{2*} - \phi_4 i_h^3 = 0. \tag{74}$$

From (72), we have:

$$s_h^* = \frac{\phi_2 i_h^{1*}}{k_h^*}. \tag{75}$$

From (73), we have:

$$i_h^{2*} = \frac{\alpha_1 i_h^{1*}}{\phi_3}. \tag{76}$$

From (74) et (76), we have:

$$i_h^{3*} = \frac{\alpha_1\alpha_2 i_h^{1*}}{\phi_3\phi_4}. \tag{77}$$

From (75), (76) and (77), we have:

$$s_h^* = \frac{\phi_2\phi_3\phi_4}{\beta_h\left(\phi_3\phi_4 + \alpha_1\alpha_2 + \alpha_1\phi_4\right)} = \frac{1}{R_{h0}}. \tag{78}$$

(76), (77) and (78) in (71) give:

$$i_h^{1*} = \frac{\phi_1\phi_3\phi_4\left(R_{h0} - 1\right)}{\beta_h\left(\phi_3\phi_4 + \alpha_1\alpha_2 + \alpha_1\phi_4\right)}; \tag{79}$$

(79) dans (76) give:

$$i_h^{2*} = \frac{\alpha_1\phi_1\phi_3\phi_4\left(R_{h0}-1\right)}{\beta_h\phi_3\left(\phi_3\phi_4+\alpha_1\alpha_2+\alpha_1\phi_4\right)}; \tag{80}$$

(79) in (77) give

$$i_h^{3*} = \frac{\alpha_1\alpha_2\phi_1\phi_3\phi_4\left(R_{h0}-1\right)}{\beta_h\phi_3\phi_4\left(\phi_3\phi_4+\alpha_1\alpha_2+\alpha_1\phi_4\right)}. \tag{81}$$

If $R_{h0}>1$, the system (61)-(64) admits a unique endemic equilibrium.

3.4. Numerical Simulations

Before closing this section, we verify numerically the theoretical results obtained in this section for an initial condition $s_h = 0.97075$, $i_h^1 = 0.0232$, $i_h^2 = 0.00468$, $i_h^3 = 0.00137$. For numerical simulations, the system (61)-(64) is discretized with a Runge-Kutta's method (ODE45). We collect a set of values of biological parameters for the sub-model (61)-(64) corresponding to the data on the spread of the HIV-SIDA in two cases:

First case: the disease goes extinct in the population (see **Figure 4**).

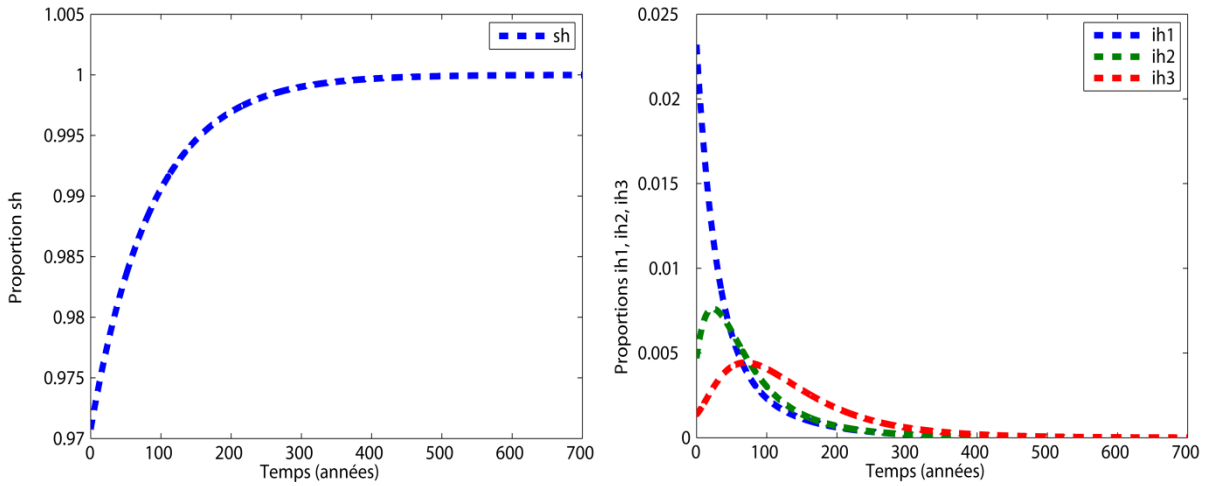
Second case: the disease persists in the population (see **Figure 5**).

These parameters are obtained in the literature and are summarized in the **Table 3**.

4. Evaluation of Impact of Public Health Sensitization

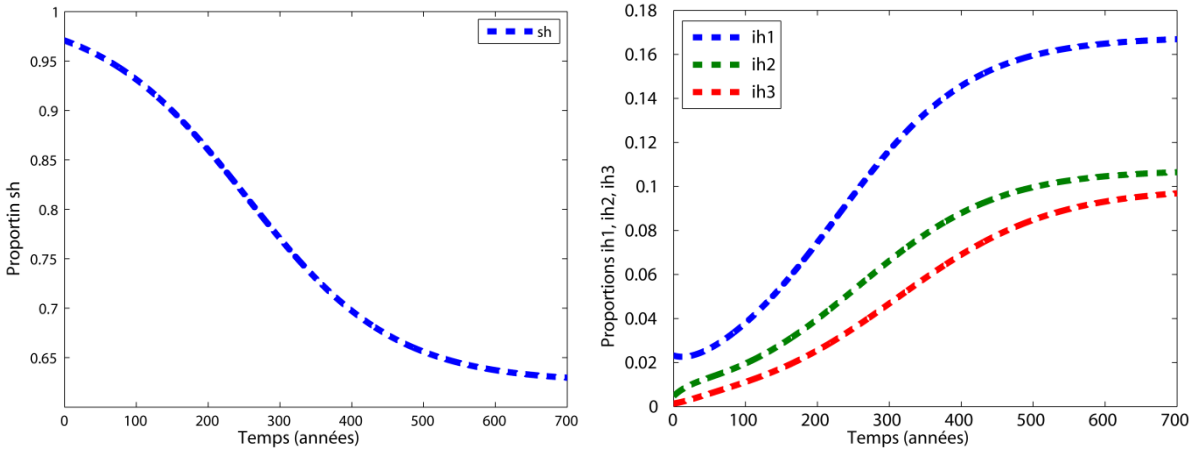
Before using the model (15)-(22) to evaluate the impact of public health sensitization in combatting HIV-AIDS spread in a population, it is instructive to evaluate the behaviour of the model under the worst case scenario (*i.e.*, the case where no public health sensitization is provided in the population). By setting all sensitization related parameters to zero (*i.e.*, $\theta = \gamma_1 = \gamma_2 = \gamma_3 = 0$) and using the data in **Table 4** and **Table 5**, simulations of the model (15)-(22) show that in Mali the proportion of infected individuals would reach approximately 0.0686 (let 499550 cas) in 9 years from 2001 (**Figure 6(b)**). These projections of the model are compatible with the EDSM III projections over the year 2010 which predicted that by the year 2010 in Mali, if measures are not taken to control the epidemic of the HIV-AIDS, about 50000 people could be infected by the virus (see **Figure 6**).

We resume in **Table 4** and **Table 5**, data of Mali concerning the spread of the HIV-AIDS.



(a) (b)

Figure 4. Dynamics of the system (61)-(64) in case where the disease goes extinct in the population. With the parameters of the **Table 3** (first case), we have R_{h0} = 0.3077. **Figure 4(a)** shows the evolution of susceptibles individuals, whereas **Figures 4(b)-(d)** show the evolution of infected individuals. The system converges towards the desease free equilibruim (1, 0, 0, 0). The simulation was realized with the MATLAB logiciel.



(a) (b)

Figure 5. Dynamics of the system (61)-(64) in case where the disease persists in the populationn. With the parameters of the **Table 3** (second case), we have R_{h0} = 1.6. **Figure 5(a)** shows the evolution of susceptibles individuals, whereas **Figures 5(b)-(d)** show the evolution of infected individuals. The system converges towards the endemic equilibrium (0.6298, 0.038, 0.0195, 0.0111). The simulation was realized with the MATLAB logiciel.

Table 3. Biological parameters.

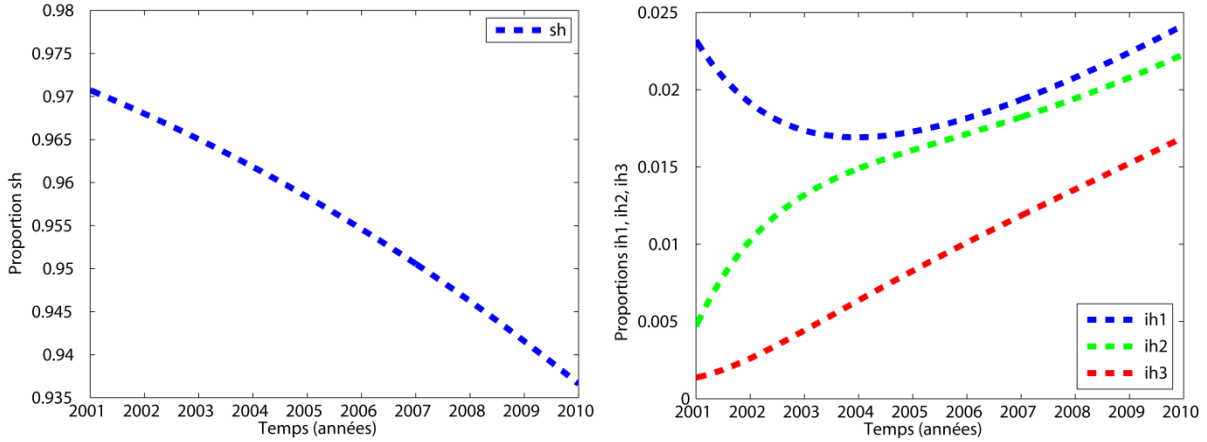
Parameters	First case	Second case
b	0.01625	0.01625
μ	0.014	0.014
α_1	0.02	0.02
α_2	0.015	0.015
β_h	0.005	0.026

Table 4. Mali epidemiological data for the model (15).

Parameters	Values
θ, κ	0.05, 0.7
α_1, α_2, α_3, α_4	0.04, 0.02, 0.04, 0.02
γ_1, γ_2, γ_3	0.05, 0.05, 0.05
β_h, β_f	0.0026 0.00718

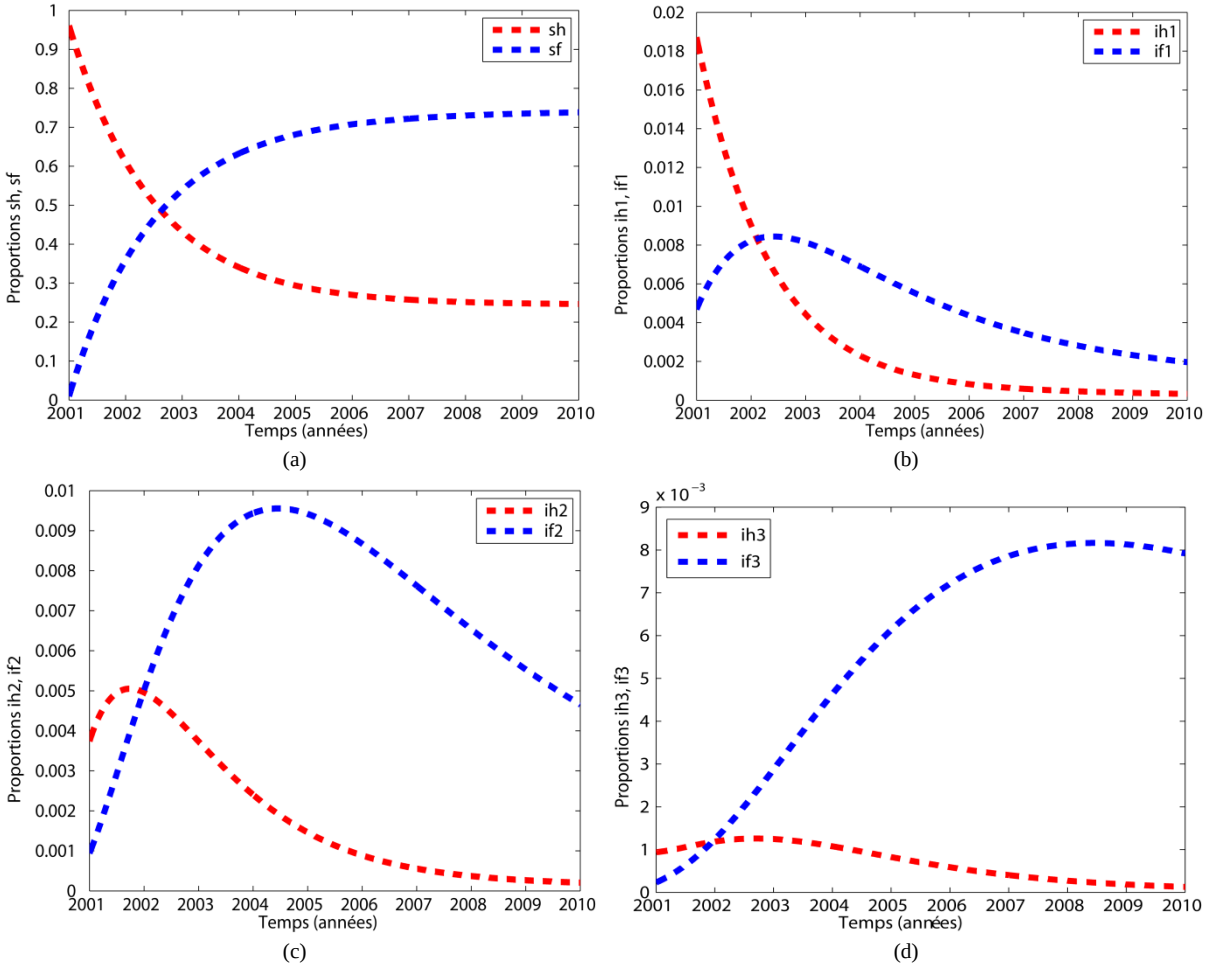
Table 5. Mali demographic data of 2001 used as initial conditions.

Demographic data	Values
$N(0)$, μ	5812498, 0.014
$i(0)$, b	170000, 0.0146
$s_h(0)$, $s_f(0)$	0.96104, 0.00971
$i_h^1(0)$, $i_f^1(0)$	0.01872, 0.00468
$i_h^2(0)$, $i_f^2(0)$	0.00374, 0.00094
$i_h^3(0)$, $i_f^3(0)$	0.00094, 0.00023



(a) (b)

Figure 6. Dynamics of the system (15)-(22) in the nose of the cases, R_{h0} = 1.6. **Figure 6(a)** shows the evolution of susceptibles individuals, whereas **Figure 6(b)** shows the evolution of infected individuals. We use the parameters of the **Table 4**. The simulation was realized with the MATLAB logiciel.



(a) (b) (c) (d)

Figure 7. Dynamics of the system (15) in case the population of Mali is submitted to Public Health sensitization compaign on the spread of HIV-AIDS, R_0 = 0.5109. **Figure 7(a)** shows the evolution of susceptibles individuals, whereas **Figures 7(b)-(d)** show the evolution of infected individuals. We use the parameters of the **Table 4**. The simulation was realized with the MATLAB logiciel.

We evaluate now the behavior of the model (15)-(22) by considering the impact of Public Health sensitization compaign on the spread of HIV-AIDS in Mali. Using the data in **Table 4** and **Table 5**, simulations of the model (15)-(22) show that in Mali the proportion of infected individuals would reach approximately 0.0137 (soit 100020 cas) in 9 years from 2001 (**Figure 6(b)**). These projections of the model are compatible with the data found in the literature (Source CIA factbook). According to this source, in Mali the individuals infected by the HIV-AIDS in 2010 were 100000 (see **Figure 7**).

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