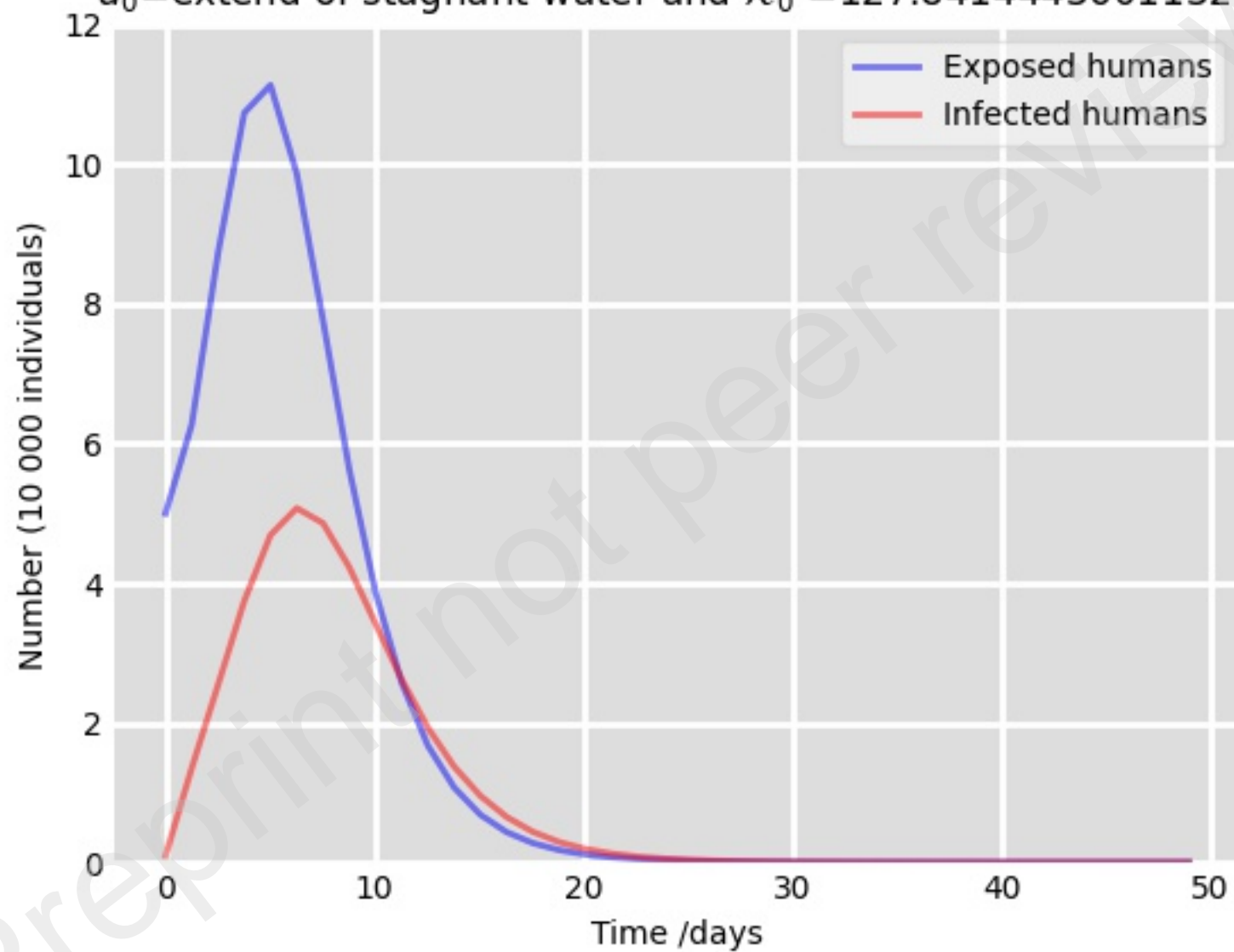
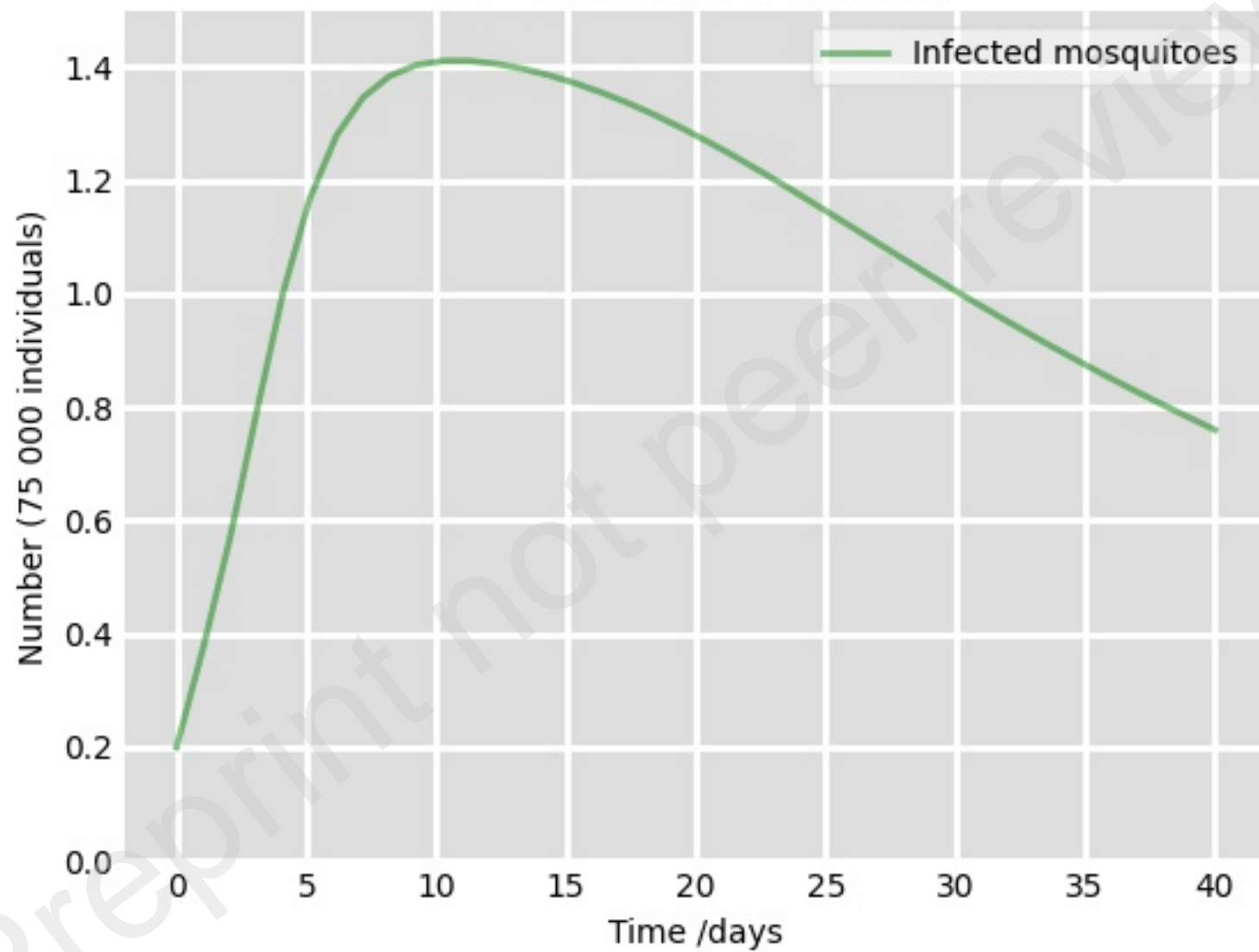


a_0 =extend of stagnant water and $\mathcal{R}_0 = 127.84144436011326$



$$\mathcal{R}_0 = 1.2784144436011327$$



Highlights

Mathematical modelling of dengue fever incorporating the extent of stagnant water*

Gerard Kanga, Jacques Tano, Mohamed Coulibaly, Eric N'Zi

- In the mathematical model of dengue transmission, we introduce the fact that some individuals infected by the mosquito are asymptomatic and recover on their own.
- We take into account the fact that the mosquito recruitment rate depends on the extent of stagnant water in urban areas. The basic reproduction number is strongly dependent on this extent.

Mathematical modelling of dengue fever incorporating the extent of stagnant water

Gerard Kanga¹, Jacques Tano¹, Mohamed Coulibaly^{1,*}, Eric N'Zi¹

Abstract

Dengue fever is a viral infection caused by the dengue virus (DENV) and transmitted to humans by infected female mosquitoes, primarily of the species *Aedes aegypti*. About half of the world's population is now at risk of contracting dengue (PLNP (2023)). The number of infections each year is estimated at 100-200 millions. In Abidjan, the city where we live, the dengue epidemic is fairly persistent, and the disease can cause very severe symptoms that can lead to death. For all these reasons, we propose solutions for controlling the epidemic in an urban area through mathematical modelling. We develop an improved SEIR-SEI model inspired by the contributions of other researchers in the fight against dengue fever. Our model takes certain entomological realities into account. We consider that the mosquito recruitment rate is not constant and depends on the extent of stagnant water in the city. We prove that the system of ordinary differential equations translating our model has a positive solution with biological meaning. We compute the basic reproduction number \mathcal{R}_0 . A sensitivity analysis shows the strong dependence of \mathcal{R}_0 on certain parameters of the model, mainly the extent of stagnant water. These results enable us to propose efficient and effective solutions in the fight against dengue fever. We carry out numerical simulations that support our conclusions.

Keywords: Mathematical model, Dengue fever, Basic reproduction number, Sensitivity analysis, Numerical simulation

*corresponding author

Email addresses: gerardkanga@yahoo.fr (Gerard Kanga), jaktanoy@yahoo.fr (Jacques Tano), coulmo@yahoo.fr (Mohamed Coulibaly), nzieric@yahoo.fr (Eric N'Zi)

¹Mathematical Research Institute, Felix Houphouët-Boigny university, Abidjan, Côte d'Ivoire

Preprint submitted to Scientific African

December 25, 2024

1. Introduction

Dengue fever has been a persistent public health problem for several decades. Côte d'Ivoire has been experiencing recurrent epidemics of dengue fever since 2017. In Abidjan, from 28 April 2017 to 2020, 4729 new suspected cases including 594 confirmed cases of serotypes DEN 1, 2 and 3 were reported (see A.K.M.N (2022)). All of Abidjan's health districts reported suspected and confirmed cases. We observed major outbreaks during the rainy season.

An entomological study carried out in Côte d'Ivoire (see A.K.M.N (2022)) showed a strong correlation between the presence of numerous areas of stagnant water (abandoned containers, tyres and other breeding grounds) and the alarming development of mosquitoes spreading dengue fever in Abidjan. Most of these mosquitoes belong to the genus *Aedes*, with the only representative being the species *Aedes aegypti* (97.9%). Overall, since the start of 2024, 80 006 dengue cases (11 718 confirmed, 12 129 probable and 56 159 suspected) and 90 deaths (case-fatality rate : 0.11 per cent) have been reported by 15 African Union countries: Burkina Faso, Cameroon, Cape Verde, Côte d'Ivoire, Ethiopia, Ghana, Kenya, Mali, Mauritius, Central African Republic, Sao Tome and Principe, Senegal, Sudan, Chad and Togo (AfricaCDC (2024)).

The following information provided by the Programme National de Lutte contre le Paludisme (PNLP) of Côte d'Ivoire (PLNP (2023)) corroborates the above information . The virus is transmitted to humans by the bite of infected female mosquitoes, mainly of the *Aedes aegypti* species. Other species of the *Aedes* genus can also act as vectors. But, their contribution is secondary to that of *Aedes aegypti*. Once a mosquito has fed on the blood of a dengue-infected person, the virus replicates in the midgut before spreading to secondary tissues, including the salivary glands. The time between ingestion of the virus and transmission to a new host is known as the "extrinsic incubation period" (EIP). The EIP lasts approximately 8 to 12 days at ambient temperatures between 25°C and 28°C. Most persons infected by the virus have mild or no symptoms and recover within 1-2 weeks. Infection is asymptomatic in 50 – 90% of cases. In rare cases, dengue fever can be severe, leading to death. If symptoms do appear, they usually begin 4 to 10 days after infection. Symptoms include high fever (40°C), intense headache,

retro-orbital pain, muscle and joint pain, nausea, vomiting, swollen glands, rash, fatigue, rapid breathing, etc. (WHO (2024)).

Our aim in this study is to use mathematical tools to design a realistic mathematical model of the dynamics of dengue transmission. Some researchers have built fairly satisfactory deterministic compartmental SEIR-SEI models which describe the dynamics between human and mosquito populations. We are using these to develop a new deterministic model. In 2018, Ganga Ram Phaijool et al. (Phaijool (2018)) studied a SEIR-SEI model taking into account different latency periods in both humans and mosquitoes by using two compartments of exposed individuals (humans who have contracted the virus and haven't symptom or mosquitoes that have contracted the virus and cannot transmit it). In their model, the force of infection comes from contact between susceptible humans and infected mosquitoes or between susceptible mosquitoes and infected humans. They carried out an analytical study of the model parameters after on the determination of the basic reproduction number of the entire model. They concluded that the prevalence of dengue fever could be reduced by decreasing the number of bites and increasing the mortality rate of mosquitoes.

In 2024, Harshit et al., based on previous work, proposed an other SEIR-SEI model (Harshit (2024)). They compute two basic reproduction numbers : one for humans and one for mosquitoes. An analytical study of the model parameters based on these two reproduction numbers enabled them to show the major importance in the spread of dengue of the infection transmission rates.

Taking into account the previous advances, we propose in section 2 a SEIR-SEI model of dengue in which we introduce two major realities stated above:

- a large proportion of the exposed humans remain asymptomatic and recover naturally ;
- in urban areas, recruitment of susceptible mosquitoes is highly dependent on the extent of standing water because of the low presence of natural factors that are favorable to mosquito reproduction.

We therefore consider that the number of mosquitoes recruited per day is linearly dependent on the extent of stagnant water. In section 3, we establish classical results such as the positivity of the solution of our model, the calculation of the basic reproduction number R_0 and the locally asymptotic

stability of the disease-free equilibrium point. Section 4 presents an analytical sensitivity of \mathcal{R}_0 with respect to the extent of standing water surfaces and different transmission rates in humans and mosquitoes. In the fight against dengue fever, the results obtained show the relevance of reducing the extent of standing water in relation to the reduction of other model parameters. In Section 5, we carry out numerical simulations that corroborate our results.

2. A new model for urban areas

Based on the mathematical models of dengue transmission dynamics developed in Phaijoo (2018) and Harshit (2024), we establish a seven-compartment deterministic SEIR-SEI compartmental model. This model corresponds to urban areas and describes the dynamics between populations whose numbers at time t are as follows. t is expressed in days.

In humans :

$S_h(t)$: **Susceptible humans** composed of humans who may contract the disease at t ,

$E_h(t)$: **Exposed humans** i.e. people who have contracted the disease but are not infectious at t ,

$I_h(t)$: **Infected humans** humans i.e. people who have contracted the disease and are infectious at t ,

$R_h(t)$: **Recovered humans** i.e. healed humans at t .

In mosquitoes :

$S_m(t)$: **Susceptible mosquitoes** i.e. mosquitoes that can contract the disease at t ,

$E_m(t)$: **Exposed mosquitoes** i.e. mosquitoes that have contracted the disease but are unable to transmit it at t ,

$I_m(t)$: **Infected mosquitoes** i.e. mosquitoes that can transmit the virus at t .

We consider that the total populations of humans and mosquitoes are respectively non-constant. We take into account the fact that a large proportion of exposed humans will not show symptoms, will heal naturally and will exit the disease dynamic (WHO (2024)). The second contribution takes account of the urban environment. In urban areas, almost all larval breeding sites are made up of stagnant water produced by human activities. Natural breeding factors for mosquitoes are almost non-existent due to urbanization. The work

in (Huaiyu (2016)) confirms this. An event in the town of Tortiya (Côte d'Ivoire) in June 2024 corroborates this choice. In this town, where artisanal mining activities are carried out, there was an outbreak of dengue fever in June 2024 (AIP (June 14th, 2024) and AIP (June 7th, 2024)). Previously this disease was non-existent. An epidemic was quickly averted. Dengue fever is suspected to originate from the many areas of stagnant water created by illegal mining.

Larvae can be found in all water collections : polluted ditches, septic tanks, tree hollows, used tires, except in running water. The development of larvae in breeding sites depends on environmental conditions (temperature, chemical or biological composition of the water, etc.) (Benhissen (2018)). Development of larvae is therefore not the same in all larval habitats. The larvae occupy the water surface. We use the simplifying hypothesis that larval density is uniform across all sites, which assumes that environmental conditions are the same in the urban area we consider. On the other hand, the mosquito responsible for dengue fever flies poorly and has a range of around 100 meters. We can therefore consider it urban. For all these reasons, we consider that the number of susceptible mosquitoes recruited per day is a linear function of the extent a of stagnant water surfaces caused by human activity.

We obtain a number of susceptible mosquitoes recruited per day defined by :

$$\Lambda(a) = k_1 a + k_2 \quad (1)$$

where k_1 and k_2 are strictly positive constants. k_1 is the number of susceptible mosquitoes generated by day and by a unit area of stagnant water surfaces created by human activity. k_2 is the number of susceptible mosquitoes recruited by day naturally without taking into account the effect of human action. k_2 is very small due to urbanization.

The dynamics of dengue transmission in urban areas are shown in the following graph whose parameters are defined below.

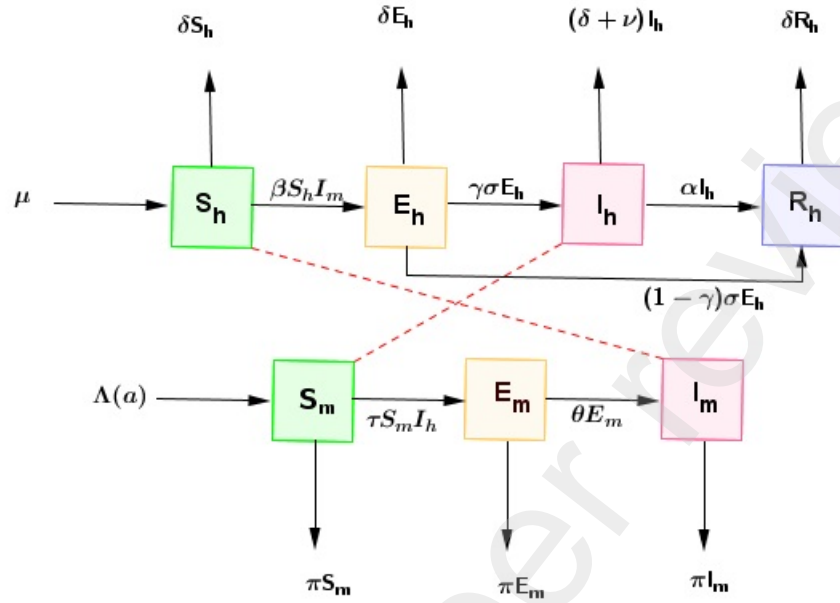


Figure 1: the model graph

μ : the number of susceptible humans births per day,
 β : the rate at which an infected transmits the virus to a human,
 σ : the rate at which an exposed human cures or becomes ill,
 γ : the proportion of exposed humans who develop the disease,
 ν : death rate from dengue in infected humans,
 α : the cure rate among infected humans,
 δ : the natural death rate for humans,
 $\Lambda(a)$: the number of susceptible mosquitoes births per day,
 τ : the rate at which a susceptible mosquito bites and becomes exposed through contact with an infected human,
 θ : the rate at which a susceptible mosquito becomes an infected mosquito,
 π : the natural death rate for mosquitoes.

Finally, the dengue dynamic transmission is modeled by the following nonlinear system of ordinary differential equations :

$$\left\{ \begin{array}{l} \frac{dS_h(t)}{dt} = \mu - \delta S_h(t) - \beta S_h(t)I_m(t) \\ \frac{dE_h(t)}{dt} = \beta S_h(t)I_m(t) - (\sigma + \delta)E_h(t) \\ \frac{dI_h(t)}{dt} = \gamma\sigma E_h(t) - (\alpha + \delta + \nu)I_h(t) \\ \frac{dR_h(t)}{dt} = \alpha I_h(t) - \delta R_h(t) + (1 - \gamma)\sigma E_h(t) \\ \frac{dS_m(t)}{dt} = \Lambda(a) - \pi S_m(t) - \tau S_m(t)I_h(t) \\ \frac{dE_m(t)}{dt} = \tau S_m(t)I_h(t) - (\theta + \pi)E_m(t) \\ \frac{dI_m(t)}{dt} = \theta E_m(t) - \pi I_m(t) \end{array} \right. \quad (2)$$

3. Mathematical properties of the model

3.1. The positivity and uniqueness of the solution

For our system (2) to have biological significance, it is essential that for $(S_h(0), E_h(0), I_h(0), R_h(0), S_m(0), E_m(0), I_m(0)) \in \mathbb{R}_+^7$, this system admits a unique positive solution. The existence and uniqueness of its solution are guaranteed by the fact that the coefficients of this system are Lipschitzian. The positivity of the solution is shown by the following result.

Theorem 1. *For any initial value $(S_h(0), E_h(0), I_h(0), R_h(0), S_m(0), E_m(0), I_m(0)) \in \mathbb{R}_+^7$, the set \mathbb{R}_+^7 is positively invariant for the system 2.*

Proof. Note that $\frac{dS_h(t)}{dt}|_{S_h(t)=0}$ is the expression of the derivative of S_h when $S_h(t)$ equals 0. Analogously, we define $\frac{dE_h(t)}{dt}|_{E_h(t)=0}$, $\frac{dI_h(t)}{dt}|_{I_h(t)=0}$, $\frac{dR_h(t)}{dt}|_{R_h(t)=0}$, $\frac{dS_m(t)}{dt}|_{S_m(t)=0}$, $\frac{dE_m(t)}{dt}|_{E_m(t)=0}$ and $\frac{dI_m(t)}{dt}|_{I_m(t)=0}$. Let's prove that \mathbb{R}_+^7 is positively invariant for the system 2.

From an analytical result seen in Brice (2020) and Stephen (2003), it suffices to show that if $(S_h(t), E_h(t), I_h(t), R_h(t), S_m(t), E_m(t), I_m(t)) \in \mathbb{R}_+^7$ then $\frac{dE_h(t)}{dt}|_{E_h(t)=0} \geq 0$, $\frac{dI_h(t)}{dt}|_{I_h(t)=0} \geq 0$, $\frac{dR_h(t)}{dt}|_{R_h(t)=0} \geq 0$, $\frac{dS_m(t)}{dt}|_{S_m(t)=0} \geq 0$, $\frac{dE_m(t)}{dt}|_{E_m(t)=0} \geq 0$ and $\frac{dI_m(t)}{dt}|_{I_m(t)=0} \geq 0$.

If $(S_h(t), E_h(t), I_h(t), R_h(t), S_m(t), E_m(t), I_m(t)) \in \mathbb{R}_+^7$ then the system 2 gives us that

$$\begin{aligned} \frac{dS_h(t)}{dt}|_{S_h(t)=0} &= \mu \geq 0, \frac{dE_h(t)}{dt}|_{E_h(t)=0} = \beta S_h(t)I_m(t) \geq 0, \frac{dI_h(t)}{dt}|_{I_h(t)=0} = \\ \gamma\sigma E_h(t) &\geq 0, \frac{dR_h(t)}{dt}|_{R_h(t)=0} = \alpha I_h(t) + (1-\gamma)\sigma E_h(t) \geq 0, \frac{dS_m(t)}{dt}|_{S_m(t)=0} = \\ \Lambda(a) &\geq 0, \frac{dE_m(t)}{dt}|_{E_m(t)=0} = \tau S_m(t)I_h(t) \geq 0 \text{ and } \frac{dI_m(t)}{dt}|_{I_m(t)=0} = \theta E_m(t) \geq 0. \end{aligned}$$

This proves (Brice (2020) and Stephen (2003)) that \mathbb{R}_+^7 is positively invariant for the system 2. Initialized in \mathbb{R}_+ , S_h , E_h , I_h , R_h , S_m , E_m and I_m remain in \mathbb{R}_+ . □

3.2. The Basic reproduction number

To better understand the dynamics of our model, it is essential to determine the basic reproduction number \mathcal{R}_0 . This number indicates the average number of new cases of the disease that a single infected and contagious individual (human or mosquito) will generate on average in the population with no immunity (individuals with no immunity are referred to as susceptible human or mosquito).

Obviously, our system only admits a single disease free equilibrium $E^0 = \left(\frac{\mu}{\delta}, 0, 0, 0, \frac{\Lambda(a)}{\pi}, 0, 0\right)$. Using Next Generation matrix method [Driessche (2002) and Sallet (2010)], we compute basic reproduction number \mathcal{R}_0 as the spectral radius of the matrix FV^{-1} .

F is the matrix of transmission terms and V is the matrix of transition terms. We obtains

$$F = \begin{pmatrix} 0 & 0 & 0 & \frac{\beta\mu}{\delta} \\ 0 & 0 & \frac{\tau\Lambda(a)}{\pi} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} \sigma + \delta & 0 & 0 & 0 \\ 0 & \theta + \pi & 0 & 0 \\ -\gamma\sigma & 0 & \alpha + \delta + \mu & 0 \\ 0 & -\theta & 0 & \pi \end{pmatrix}$$

This means that

$$\mathcal{R}_0 = \sqrt{\frac{\gamma\sigma\theta\beta\mu\tau\Lambda(a)}{\delta(\sigma + \delta)(\theta + \pi)(\alpha + \delta + \nu)\pi^2}} \quad (3)$$

3.3. The local asymptotically stability of the disease-free equilibrium point

The local asymptotically stability of the disease-free equilibrium point is very important in that it gives our model the prospect of eradicating the disease under certain conditions. Indeed, moving towards E^0 means that the disease disappears from the population.

This stability is provided by the following result as in (Coddington (1995)).

Theorem 2. *The disease-free equilibrium $\left(\frac{\mu}{\delta}, 0, 0, 0, \frac{\Lambda(a)}{\pi}, 0, 0\right)$ is locally asymptotically stable.*

Proof. The Jacobian matrix of the system 2 at the state $\left(\frac{\mu}{\delta}, 0, 0, 0, \frac{\Lambda(a)}{\pi}, 0, 0\right)$ is

$$J = \begin{pmatrix} -\delta & 0 & 0 & 0 & 0 & 0 & -\frac{\beta\mu}{\delta} \\ 0 & -(\delta + \sigma) & 0 & 0 & 0 & 0 & \frac{\beta\mu}{\delta} \\ 0 & \sigma_1 & -(\alpha + \delta + \nu) & 0 & 0 & 0 & 0 \\ 0 & \sigma_2 & \alpha & -\delta & 0 & 0 & 0 \\ 0 & 0 & -\frac{\tau\Lambda(a)}{\pi} & 0 & -\pi & 0 & 0 \\ 0 & 0 & \frac{\tau\Lambda(a)}{\pi} & 0 & 0 & -(\theta + \pi) & 0 \\ 0 & 0 & 0 & 0 & 0 & \theta & -\pi \end{pmatrix}$$

It is easy to see that $-\pi$ et $-\delta$ are the eigenvalues of this matrix. There are all negatives so we get our result.

□

4. Sensitivity analysis

Sensitivity analysis of the basic reproduction number \mathcal{R}_0 with respect to a parameter in its expression shows how the value of this parameter influences \mathcal{R}_0 . The quality of the parameter's influence on \mathcal{R}_0 could thus help public authorities make the right decisions in the fight against dengue fever. This sensitivity analysis is based on the determination of a sensitivity index of \mathcal{R}_0 with respect to a parameter.

The normalized sensitivity index of \mathcal{R}_0 which depends differentiably on a parameter ζ , is defined by Chitnis (2008)

$$\gamma_{\zeta}^{\mathcal{R}_0} = \frac{\partial \mathcal{R}_0}{\partial \zeta} * \frac{\zeta}{\mathcal{R}_0} \quad (4)$$

The sensitivity index can be a non-constant expression depending on the model parameters, or it can be a constant value. The latter case is easier

to interpret. $\gamma_{\zeta}^{\mathcal{R}_0} = +0.3$ means if parameter ζ increases (respectively decreases) by 10%, \mathcal{R}_0 increases (respectively decreases) by 3%. In the case of our study, a large sensitivity index would be a good contribution, as it would mean that a small variation in the parameter concerned would lead to a large variation in \mathcal{R}_0 .

Λ is derivable with respect to a , then we have:

$$\gamma_a^{\mathcal{R}_0} = \frac{\partial \mathcal{R}_0}{\partial a} * \frac{a}{\mathcal{R}_a} = \frac{a\Lambda'(a)}{2\Lambda(a)} = \frac{k_1 a}{2(k_1 a + k_2)} \quad (5)$$

We also obtain the following sensitivity indexes :

Parameters	Sensitivity Indices of \mathcal{R}_0
a	$\frac{k_1 a}{2(k_1 a + k_2)}$
β, τ, μ, γ	0.5
σ	$\frac{1}{2} \times \frac{\delta}{\delta + \sigma}$
θ	$\frac{1}{2} \times \frac{\pi}{\pi + \theta}$
α	$-\frac{1}{2} \times \frac{\alpha}{(\alpha + \delta + \nu)}$
ν	$-\frac{1}{2} \times \frac{\nu}{(\alpha + \delta + \nu)}$
π	$-\frac{1}{2} \times \frac{2\theta + 3\pi}{\theta + \pi}$
δ	$-\frac{1}{2} \times \frac{3\delta^2 + 2(\sigma + \alpha + \nu)\delta + \sigma(\alpha + \nu)}{\delta^2 + (\sigma + \alpha + \nu)\delta + \sigma(\alpha + \nu)}$

Table 1: Sensitivity index values of the model parameters.

In previous studies (Rodrigues (2013), Phaijoo (2018) and Harshit (2024)), the analytical sensitivity of the basic reproduction rate to model parameters led to the conclusion that virus transmission and mosquito mortality rates were highly influential, with indices of 0.5. The strategies to be implemented to reduce transmission or death rates are costly or environmentally damaging: distribution of insecticide-impregnated mosquito nets, spraying of areas with insecticides, etc. In our model, k_2 is very small, so we have :

$$\gamma_a^{\mathcal{R}_0} = \frac{k_1 a}{2(k_1 a + k_2)} \approx 0.5 \quad (6)$$

Equal variations in the extent of standing water, the transmission rate or the mortality rate of mosquitoes have the same effect on the basic reproduction number \mathcal{R}_0 . Reducing the extent of stagnant water is inexpensive and ecological. Education campaigns can be a solution.

5. Numerical simulation

The female tiger mosquito responsible for transmitting dengue fever can live for 4 to 6 weeks. It is active during the day and feeds on human blood or flower nectar. The male, on the other hand, feeds only on flower nectar (see ARS Auvergne-Rhône-Alpes (2024)). For all these reasons, this mosquito thrives in Cocody a municipality of Abidjan. This municipality has many villas with gardens offering stagnant water and nectar to mosquitoes. Cocody is one of the main centres of the dengue epidemic. We run simulations that are supposed to correspond to Cocody.

Cocody has 692,583 inhabitants with a density of 5,247 inhabitants per km² (RCI (2021)). These figures are highly favourable to the spread of dengue fever. Based on (Maíra (2022)) and for the reasons given, we assume that : $S_h(0) = 690000$, $E_h(0) = 50000$, $I_h(0) = 1000$, $R_h(0) = 0$, $S_m(0) = 10000$, $E_m(0) = 4000$, $I_m(0) = 2000$.

We don't have enough epidemiological data on dengue fever in our country because of the poor attendance at hospitals. So, we consider the following data which permit to compute a high basic reproduction number which seems to suit the situation at Cocody. .

Table 2: Values of parameters of the model

Parameters	Values	References
μ (per day)	100 (new residents by day in Cocody)	an extrapolation
β (per day)	0.25	(Maíra, 2022)
σ (per day)	0.5	(Maíra, 2022)
γ (per day)	0.5	(WHO, 2024)
ν (per day)	0.25	(Maíra, 2022)
α (per day)	0.2081	(Maíra, 2022)
δ (per day)	0.017	(Maíra, 2022)
$\Lambda(a_0)$ (per day)	400 (corresponds to a value a_0 of a)	an extrapolation
θ (per day)	0.5	(Maíra, 2022)
π (per day)	0.02941	(Phaijoo, 2018)
τ (per day)	0.25	(Maíra, 2022)

Programs implemented in Python give us initial simulations that could correspond to reality in Cocody. A large basic reproduction number, reflecting a high number of infected individuals that can be generated by an infected mosquito or an infected human.

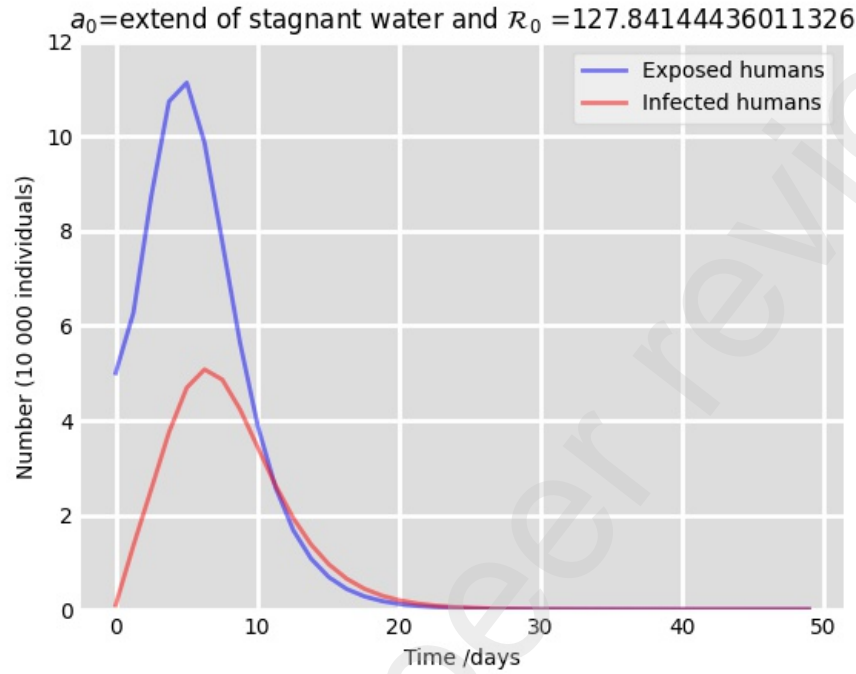


Figure 2: An example of the evolution of compartments of infected humans in Cocody

If we reduce the x-axis scale and show the phenomenon over more than 2 years, the numbers infected appear to become constant. This would seem to indicate a point of endemic equilibrium.

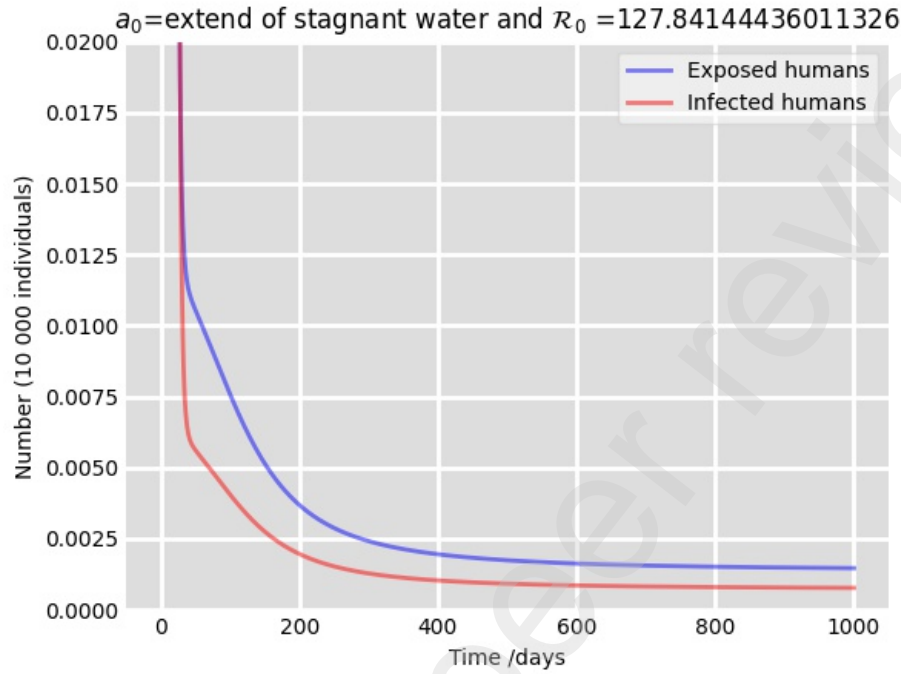


Figure 3: A stabilisation in the infected compartments of humans in an endemic situation in Cocody

We reduce the surface area of stagnant water. a_0 is divided by

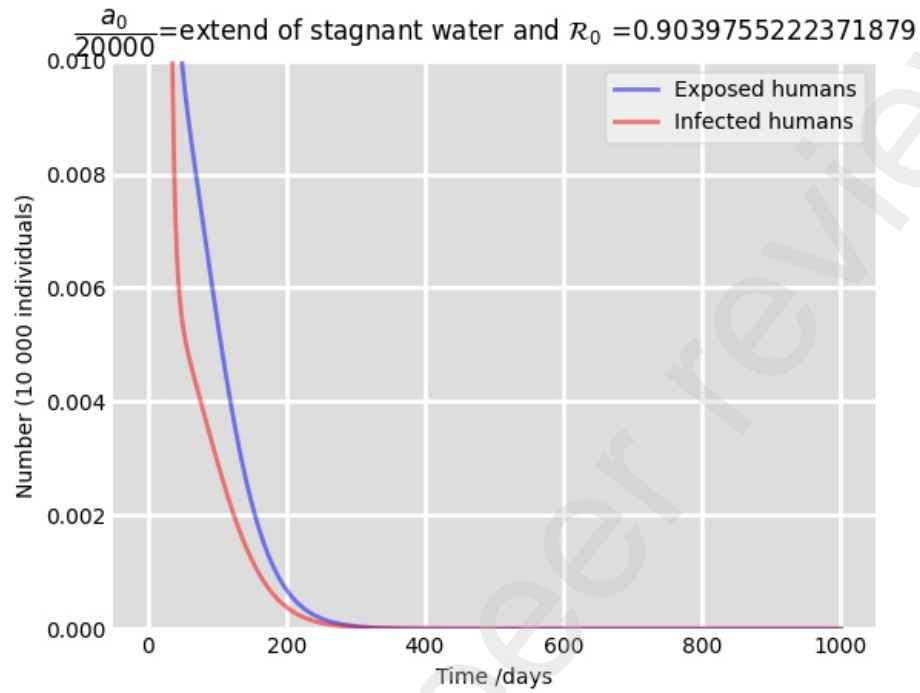


Figure 4: A major reduction in the extent of stagnant water, leading to the disappearance of dengue fever in Cocody

In fact, we are seeing a sharp fall in the population of susceptible mosquitoes, and even their disappearance.

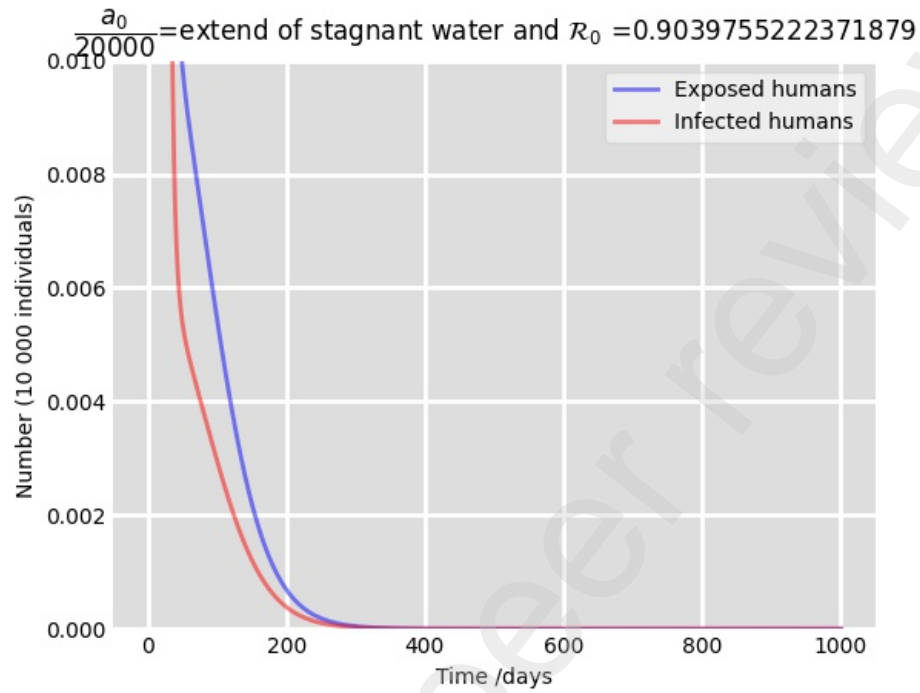


Figure 5: A major reduction in the extent of stagnant water, leading to the disappearance of dengue fever in Cocody

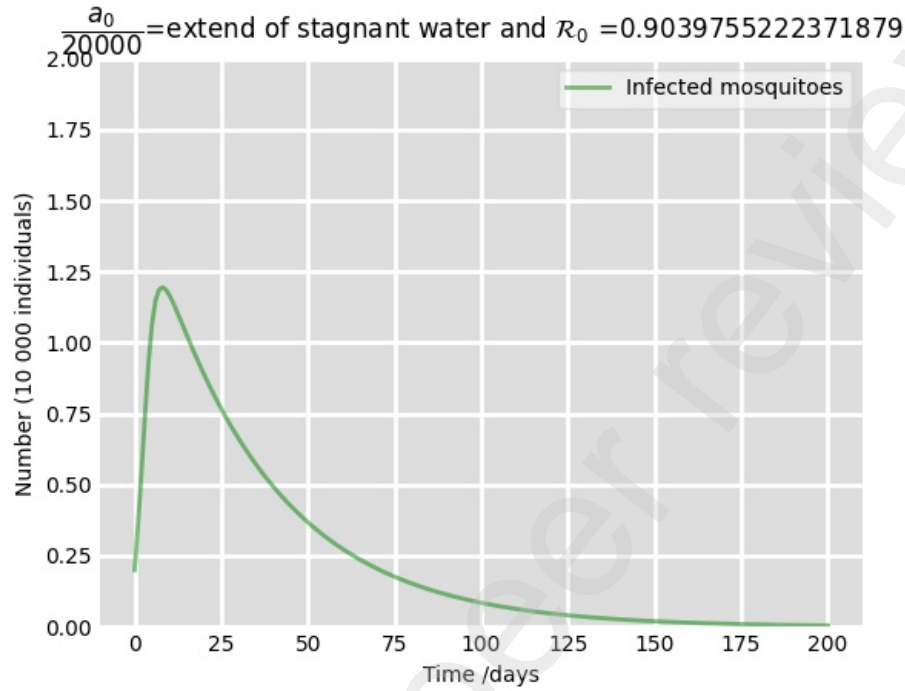


Figure 6: A large reduction in the population of infected mosquitoes due to the reduction in the extent of stagnant water in Cocody

6. Conclusion

In this survey, we have created a mathematical model which translates the dynamics of the spreading the dengue fever in a urban aera. This model takes into account two major realities. First, the fact that a large part of the exposed humans remain asymptomatic and heal naturally. Second, the fact the proliferation of tiger mosquitoes is highly dependant on the extent of stagnant water made by human activities.

The basic reproduction number being fundamental in a epidemiologic survey, a sensivity analysis of this number with respect of the parameters of this model allowed the note that equal variations of transmission rate, death rate or of stagnat water extent, have the same impact on the basic reproduction number. The cost of these variations depend on the different parameters. In the fight against dengue fever, we urge public authorities to emphasize their actions on the reduction of stagnant water which can be done by means

of awareness campaigns which are cheaper and more ecological than other strategies (insecticides spreading, impregnated mosquito nets, ...)

Numerical simulations allowed us to corroborate our results. Our simulations tried to describe the epidemiological situation in Cocody, a municipality of Abidjan. when all the data corresponding to this place will be available, we will be able to improve the control of epidemic in Cocody with our simulations. In the future our mathematical model could be bettered by taking into account all the types of contamination by dengue fever.

References

- Programme National de Lutte contre le Paludisme, *Epidémie de dengue à Abidjan*, <https://www.pnlpcotedivoire.org/article-detail/8/158/epidemie-de-dengue-abidjan>, 2023.
- Africa CDC, *Africa CDC Epidemic Intelligence Weekly Report*, <https://africacdc.org/fr/download/africa-cdc-weekly-event-based-surveillance-report-september-2024/>, september 2024.
- World Health Organization (WHO), *Report on dengue fever*, <https://www.who.int/fr/news-room/fact-sheets/detail/dengue-and-severe-dengue>, April 23, 2024.
- Phaijoo GR, Gurung DB., *Sensitivity analysis of SEIR-SEI model of dengue disease*, GAMS Journal of Mathematics and Mathematical Bioscience, 6 (2018) 41-50.
- Harshit et al., *Mathematical Modelling and Analysis of Dengue Transmission Dynamics*, Procedia Computer Science, 235 (2024) 539–5480.
- A.K.M.N. Ano, D. Coulibaly, V.J. Béné, B.C. Akani, A. Douba, E.M. Ahoussou, N.S. Dagnan, *Situation épidémiologique de la dengue en Côte d'Ivoire de 2017 à 2020*, Revue d'Épidémiologie et de Santé Publique, Volume 70, Supplement 3, 2022, Page S146, ISSN 0398-7620, <https://doi.org/10.1016/j.respe.2022.06.048>.
- N. Guindo-Coulibaly, M.D.S Kpan, A.M. Adja, K.R.M. Azongnibo, A.M.N. Kouadio, K.F. Assouho, D.D. Zoh, A. Yapi, F. Remoué, F. Fournet, *La dengue en Côte d'Ivoire : évaluation des indices de risque entomologique à Abidjan*, Revue d'Épidémiologie et de Santé

Publique, Volume 70, Supplement 3, 2022, Page S233,ISSN 0398-7620,
<https://doi.org/10.1016/j.respe.2022.06.252>.

Agence Ivoirienne de Presse, *Côte d'Ivoire-AIP/ Le sous-préfet de Tortiya appelle à une mobilisation générale contre la dengue et le paludisme*, <https://www.aip.ci/72486/cote-divoire-aip-le-sous-prefet-de-tortiya-appelle-a-une-mobilisation-generale-contre-la-dengue-et-le-paludisme/>

Agence Ivoirienne de Presse, *Côte d'Ivoire-AIP/Le ministère de la Santé initie une opération de démoustication de la ville de Tortiya*, <https://www.aip.ci/70364/cote-divoire-aip-le-ministere-de-la-sante-lance-une-operation-de-demoustication-de-la-ville-de-tortiya/>

Brice Girol, *Dynamical systems, Invariance Conditions and Applications*, FernUniversität in Hagen, Fakultät für Mathematik und Informatik, Lehrgebiet Analysis, Master Thesis Course. March 22, 2020.

Stephen Wiggins, *Introduction to Applied Nonlinear Dynamical Systems and Chaos*, Springer, 2003, Volume 2.

P. Van Den Driessche and J. Watmough, *Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission*, Math. Biosci., (2002), 121-142.

G. Sallet, *R0*, INRIA et IRD EPICASA09,avril 2010.

Huaiyu Tian, Shanqian Huang, Sen Zhou, Peng Bi, Zhicong Yang, Xiujun Li, Lifan Chen, Bernard Cazelles, Jing Yang, Lei Luo, Qinlong Jing, Wenping Yuan, Yao Pei, Zhe Sun, Tianxiang Yue, Mei-Po Kwan, Qiyong Liu, Ming Wang, Shilu Tong, John S. Brownstein, Bing Xu, *Surface water areas significantly impacted 2014 dengue outbreaks in Guangzhou, China*, Environmental Research, Volume 150, 2016, Pages 299-305.

BENHISSEN Saliha, HABBACHI Wafa, REBBAS Khellaf, MASNA Fatiha, *Entomological and typological studies of larval breeding sites of mosquitoes (Diptera: Culicidae) in Bousaâda area (Algeria)*, Bulletin de la Société Royale des Sciences de Liège, Vol. 87, article, 2018; p. 112 - 120.

E.A. Coddington, N. Levinson, *Theory of Ordinary Differential Equations*, McGraw-Hill, New York (1995).

Chitnis N, Hyman JM, Cushing JM, *Determining important parameters in the spread of malaria through the sensitivity analysis of a mathematical model*, Bull Math Biol. 2008 Jul;70(5):1272-96.

Rodrigues, Helena Sofia, Monteiro, M. Teresa T., Torres, Delfim F. M., *Sensitivity Analysis in a Dengue Epidemiological Model*, Conference Papers in Science, 2013, 721406, 7 pages, 2013.

Maíra Aguiar, Vizda Anam, Konstantin B. Blyuss, Carlo Delfin S. Estadilla, Bruno V. Guerrero, Damián Knopoff, Bob W. Kooi, Akhil Kumar Srivastav, Vanessa Steindorf, Nico Stollenwerk, *Mathematical models for dengue fever epidemiology : A 10-year systematic review*, Physics of Life Reviews. Volume 40. Pages 65-92. ISSN 1571-0645 (2022).

République de Côte d'Ivoire, Ministère de l'intérieur et de la sécurité, *Annuaire statistique d'état civil 2021*, https://www.despse.ci/fichiers_uploades/files_Annuaire_EC21_VF.pdf

Agence Régionale de Santé Auvergne-Rhône-Alpes, *Moustique tigre : ce qu'il faut savoir sur lui*, 31 juillet 2024, <https://www.auvergne-rhone-alpes.ars.sante.fr/moustique-tigre-ce-qu'il-faut-savoir-sur-lui>