Scientific Research Publishing

Open Journal of Applied Sciences, 2025, 15(5), 1366-1377
https://www.scirp.org/journal/ojapps
ISSN Online: 2165-3925
ISSN Print: 2165-3917

Mathematical Modelling of Conjunctivitis Viral Disease: Case of Burundi

Vianney Mbazumutima[1], Pascaline Nshimirimana[1], André Dembele[2], Fabiola Ndayiragije[1], Léonard Todjihounde[3]

[1]Ecole Normale Supérieure, Bujumbura, Burundi
[2]Université des Sciences, Techniques et Technologies de Bamako, Bamako, Mali
[3]Institut de Mathématiques et des Sciences Physiques (IMSP), Porto-Novo, Bénin
Email: vianney.mbazumutima@imsp-uac.org, andredembele@ymail.com, nshimirimanapascaline@yahoo.fr, fndayiragije@gmail.com, leonardt@imsp-uac.org

How to cite this paper: Mbazumutima, V., Nshimirimana, P., Dembele, A., Ndayiragije, F. and Todjihounde, L. (2025) Mathematical Modelling of Conjunctivitis Viral Disease: Case of Burundi. *Open Journal of Applied Sciences*, **15**, 1366-1377.
https://doi.org/10.4236/ojapps.2025.155096

Received: December 14, 2024
Accepted: May 25, 2025
Published: May 28, 2025

Abstract

In this paper, an SEIR mathematical model of conjunctivitis viral disease is formulated. The disease free equilibrium (DFE) and the endemic equilibrium points are investigated. The basic reproduction number is computed using the next generation matrix method and the local stability of the disease free equilibrium is investigated. This threshold characterizes the growth rate of an epidemic outbreak and shows that if $R_0 < 1$ the DFE is locally stable and unstable when $R_0 > 1$. We analyze the sensitivity of the model according to its different parameters. Numerical simulations were performed using the defined parameters to support the theoretical results and compared to one from the real data. The results show the suitability of the chosen model of conjunctivitis viral disease that occurred in Burundi for the investigated period of one month.

Keywords

Conjunctivitis, Basic Reproduction Number, Sensitivity Index, Ruth-Hurwitz Criteria

1. Introduction

For a very long time, humankind has been the target of many different kinds of illnesses with a range of causes. To protect themselves against these diseases, human beings have adapted illnesses by taking preventive or curative measures. These diseases attack different parts of the human body and, fortunately thanks to their ingenuity, humans have been able to develop appropriate countermeasures. Viral

conjunctivitis is one of these diseases which have been registered in east Africa region. A lot of research has gone into understanding its origins, its development and how it spreads through the population. Since March 2024, Burundi has faced an epidemic of viral conjunctivitis named also Acute haemorrhagic conjunctivitis (AHC) [1]. But this disease has been around for a long time. It was first detected in Ghana in 1969 [2]. Conjunctivitis is inflammation of the conjunctiva with three causes such as viral, allergic, and bacterial, but most of the cases results from adenovirus [3]. It's a contagious infectious disease characterized by the rapid onset of eye pain, swollen eyelids, foreign body sensation and excessive redness of the eyes [4]. It has been observed that mathematical modeling plays a major role in the understanding of phenomenon. Mathematical modeling, using data, facilitates understanding of how changes can affect results. In combination with data, it helps to explain past behavior, predict and forecast future behavior, and assess how changes may alter these predictions [5]. Since its outbreak, mathematical researchers have developed models to help understand and combat its spread, as well as to help decision-makers take appropriate decisions. Reference [6] applies a mathematical optimal control model of haemorrhagic conjunctivitis disease to understand its transmission by using two control strategies such as efforts to prevent contact and treatment while reference [7] studies the stability of conjunctivitis model with nonlinear incidence term. Authors in [8] study the stability of the model and use isolation and hygiene compliance as control strategies in order to reduce conjunctivitis infection and irritants concentration and the associated cost. Reference [9] uses as strategies the sick leaves considered as isolation and treatment to study the stability conjunctivitis model. The authors in [10] use outbreak data from 2004-2015 in China to estimate the effective reproduction number and assess the efficacy of interventions while the authors in [11] study the propagation in western sub-Sahara Africa especially during the Harmattan period in public schools, and use proper sanitation and training of the educators as mitigating strategies. Also, the educational campaign has been used mathematically to study the transmission of conjunctivitis [12] while [13] proved that if $R_0 \leq 1$ then this disease will be eradicated. Authors in reference [14] applied the effect of under-reporting and behavior changes on the transmission rate to study the transmission dynamics of conjunctivitis in Mexico.

The paper is organized as follows. In Section 0, we establish a mathematical model for conjunctivitis viral. In Section 1, we investigate the dynamics of our model while Section 1 computes the basic reproduction number. Stability and sensitivity of the model are analyzed in Section 1 while Section 2 studies numerically the model by using its estimate parameters and the collected real data and also make discussion of the different schema. Finally, We give the conclusion and future perspectives.

2. Mathematical Model Formulation

This section describes compartmental model of conjunctivitis viral and, identify

the parameters used in numerical simulations. The human population at time is assumed to be constant because birth rate and death rate of human population are approximately equal. From Figure 1, the population is partitioned into four compartments: susceptible individuals S, exposed human E, Infected individuals I, and recovered individuals R. The total population at any given time is $N(t)=S(t)+E(t)+I(t)+R(t)$. The following schema was adapted from [11].

The parameters are defined in Table 1.

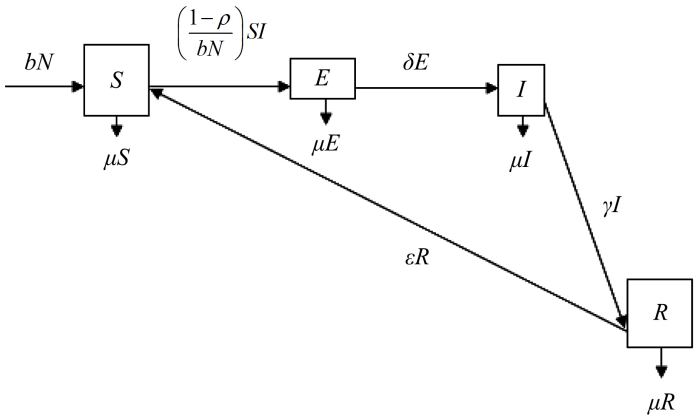

Figure 1. Conjunctivitis viral scheme.

Table 1. Baseline parameters used in the model.

Parameters	Interpretation	Values	Units	Reference
b	Birth rate of human population	0.000456	day^{-1}	[12]
ρ	Transmission rate of infection	0.02	day^{-1}	[7]
μ	Natural death rate	0.04	day^{-1}	[12]
δ	Outflow rate of exposed subjects to infectious compartment	0.3	day^{-1}	Assumed
γ	Recovery rate	0.08	day^{-1}	[15]
ϵ	Rate of imminity after recovery which is lost and individuals become susceptible again	0.01	day^{-1}	[12]

The resulting explicit equations are as follows

$$\begin{aligned}
\frac{\mathrm{d}S}{\mathrm{d}t} &= bN-\left(\frac{1-\rho}{bN}\right)SI-\mu S+\epsilon R,\\
\frac{\mathrm{d}E}{\mathrm{d}t} &= \left(\frac{1-\rho}{bN}\right)SI-(\mu+\delta)E,\\
\frac{\mathrm{d}I}{\mathrm{d}t} &= \delta E-(\gamma+\mu)I,\\
\frac{\mathrm{d}R}{\mathrm{d}t} &= \gamma I-(\mu+\epsilon)R.
\end{aligned} \tag{1}$$

By normalization, we obtain

$$\begin{aligned}
\frac{\mathrm{d}S}{\mathrm{d}t} &= b - \frac{(1-\rho)}{b} SI - \mu S + \epsilon R, \\
\frac{\mathrm{d}E}{\mathrm{d}t} &= \frac{(1-\rho)}{b} SI - (\mu + \delta) E, \\
\frac{\mathrm{d}I}{\mathrm{d}t} &= \delta E - (\gamma + \mu) I, \\
\frac{\mathrm{d}R}{\mathrm{d}t} &= \gamma I - (\mu + \epsilon) R.
\end{aligned} \tag{2}$$

3. Analysis of the Dynamical Model

This section determines the boundary of solutions of the System (2). It also computes the disease free equilibrium and the endemic equilibrium point of the same system.

Theorem 1. Let (S, E, I, R) be the solution of the model System (2) with initial conditions $S > 0$, $E \geq 0$, $I \geq 0$, $R \geq 0$. The region of epidemiological relevance in the sense of conjunctivitis transmission is given by the set

$$\Gamma = \left\{ (S, E, I, R) \in \mathbb{R}_+^4, N \leq \frac{b}{\mu} \right\}.$$

Proof. The total population of the model is $N = S + E + I + R$, therefore we have

$$\frac{\mathrm{d}N}{\mathrm{d}t} = b - \mu N. \tag{3}$$

Solving this equation gives

$$N(t) = \frac{b}{\mu} - \left[\frac{b}{\mu} - N_0 \right] \mathrm{e}^{-\mu t}. \tag{4}$$

When $t \to \infty$, $N(t) \to \frac{b}{\mu}$ which implies that $0 < N \leq \frac{b}{\mu}$. Hence all solutions of the model (2) are bounded and enter the region

$\Gamma = \left\{ (S, E, I, R) \in \mathbb{R}_+^4, N \leq \frac{b}{\mu} \right\}$. Therefore, Γ is a positively invariant region. We conclude that every solution of our model remains within the region for all $t > 0$.

Equating System (2) by zero and solve, we obtain the steady point

$$\begin{aligned}
S^* &= \frac{b + \epsilon R}{\left(\frac{1-\rho}{b} \right) I + \mu}, \\
E^* &= \frac{1}{\mu + \delta} \left[\frac{(1-\rho) b}{b\mu + (1-\rho) I} \right], \\
I^* &= \frac{\delta E}{\gamma + \mu} = \frac{\delta b (1-\rho) - b\mu (\gamma + \mu)(\delta + \mu)}{(\gamma + \mu)(\delta + \mu)(1-\rho)}, \\
R^* &= \frac{\gamma I}{\mu + \epsilon} = \frac{\gamma}{\mu + \epsilon} \left[\frac{\delta b - (1-\rho) - b\mu (\gamma + \mu)(\delta + \mu)}{(\gamma + \mu)(\delta + \mu)(1-\rho)} \right].
\end{aligned} \tag{5}$$

In the absence of the disease, meaning when $I=0$, we have the following expression

$$E_0\left(S^*,E^*,I^*,R^*\right)=E_0\left(\frac{b}{\mu},0,0,0\right). \tag{6}$$

In the case where $I\neq 0$, we have the endemic disease steady state $E_1\left(S^*,E^*,I^*,R^*\right)$ where S^*,E^*,I^*,R^* are defined in System (5).

4. Basic Reproduction Number

This section computes the basic reproduction number (R_0) defined as the average number of secondary infections produced by a typical case of an infection in a population where everyone is susceptible. Using the next generation matrix defined in [16] (see also [17]), we calculate R_0 for the System (2). Considering X and X' as the vectors representing infected and uninfected compartments respectively, we have

$$\frac{\mathrm{d}X}{\mathrm{d}t}=\mathcal{F}\left(\mathbb{X}\right)-\mathcal{V}\left(\mathbb{X}\right), \tag{7}$$

$$\frac{\mathrm{d}X'}{\mathrm{d}t}=\mathcal{W}\left(\mathbb{X}\right), \tag{8}$$

where $\mathbb{X}=\left(X,X'\right)$, $\mathcal{F}\left(\mathbb{X}\right)$ represents the vector of in-flows into infected compartments (including new infections) and $\mathcal{V}\left(\mathbb{X}\right)$ is the vector of out-flows. The functions $\mathcal{F}$ and $\mathcal{V}$ are chosen so that $\mathcal{F}\left(\mathbb{X}\right)\geq 0$ and $\mathcal{V}\left(\mathbb{X}\right)\geq 0$. We denote the disease free equilibrium by $\left(0,\bar{X}'\right)$. Replacing in Equation (7), we have $\mathcal{F}\left(0,\bar{X}'\right)=0$ and $\mathcal{V}\left(0,\bar{X}'\right)=0$.

The next generation matrix is given by FV^{-1}, where

$$F=\left(\frac{\partial\mathcal{F}}{\partial X}\right)\Big|_{\left(0,\bar{X}'\right)} \text{ and } V=\left(\frac{\partial\mathcal{V}}{\partial X}\right)\Big|_{\left(0,\bar{X}'\right)}.$$

The basic reproduction number R_0 is the spectral radius of the matrix FV^{-1}. From System of equations (2), we define matrices F and V as follows:

$$F=\begin{pmatrix}0 & 0 & 0\\ 0 & 0 & \dfrac{1-\rho}{\mu}\\ 0 & 0 & 0\end{pmatrix} \tag{9}$$

and

$$V=\begin{pmatrix}\mu & 0 & \dfrac{1-\rho}{\mu}\\ 0 & \mu+\delta & 0\\ 0 & -\delta & \gamma+\mu\end{pmatrix}. \tag{10}$$

Computing V^{-1}, we obtain

$$V^{-1}=\frac{1}{(\mu+\delta)(\gamma+\mu)}\begin{pmatrix}\dfrac{(\mu+\delta)(\gamma+\mu)}{\mu} & -\dfrac{\delta(1-\delta)}{\mu^2} & -\dfrac{(1-\rho)(\mu+\delta)}{\mu^2}\\ 0 & \gamma+\mu & 0\\ 0 & \delta & \mu+\delta\end{pmatrix}. \tag{11}$$

The next generation matrix is then given by

$$FV^{-1}=\begin{pmatrix}0 & 0 & 0\\ 0 & \dfrac{\delta(1-\rho)}{\mu(\gamma+\mu)(\mu+\delta)} & \dfrac{(1-\rho)}{\mu(\gamma+\mu)}\\ 0 & 0 & 0\end{pmatrix}. \tag{12}$$

From Equation (12), we calculate the basic reproduction number given by

$$R_0=\rho\left(FV^{-1}\right)=\frac{\delta(1-\rho)}{\mu(\mu+\gamma)(\mu+\delta)}. \tag{13}$$

5. Stability and Sensitivity of the Model

In this section, the stability of the model is treated and the sensitivity of the basic reproduction number is analyzed.

5.1. Stability Analysis of the Model

This subsection treats the stability of the model (2) using the disease-free equilibrium and endemic equilibrium point. It computes the eigenvalues of the Jacobian matrix J_0 at each steady point and analyze their signs.

First, we use the DFE defined in Equation (6) to show that the system of Equations (2) is locally asymptotically stable. The eigenvalues are the solutions of the characteristic equation

$$\left|J(E_i)-\lambda I\right|=0, \tag{14}$$

with $J(E_i)$ the Jacobian matrix at a given steady state $E_i, i=0,1$ and I is defined as the identity matrix of dimension 3×3.

Theorem 2. The disease free equilibrium (DFE) is locally stable if $R_0<1$ and unstable if $R_0>1$

- Consider the DFE $E_0\left(\frac{b}{\mu},0,0,0\right)$, the Jacobian matrix at this steady point is given by

$$J(E_0)=\begin{pmatrix}-\mu & 0 & -\dfrac{1-\rho}{\mu}\\ 0 & -(\mu+\delta) & \dfrac{1-\rho}{\mu}\\ 0 & \delta & -(\gamma+\mu)\end{pmatrix}. \tag{15}$$

Its characteristic equation is defined as follows:

$$\left|J(E_0)-\lambda I\right|=\begin{vmatrix}-\mu-\lambda & 0 & -\dfrac{1-\rho}{\mu}\\ 0 & -(\mu+\delta)-\lambda & \dfrac{1-\rho}{\mu}\\ 0 & \delta & -(\gamma+\mu)-\lambda\end{vmatrix}=0. \tag{16}$$

After some algebraic calculations, we obtain

$$(\lambda+\mu)\left[\lambda^2+(\delta+2\mu+\gamma)\lambda+(\delta+\mu)(\gamma+\mu)-\frac{\delta(1-\rho)}{\mu}\right]=0. \quad (17)$$

Thus, $\lambda_1=-\mu<0$ and $\lambda^2+(\delta+2\mu+\gamma)\lambda+(\delta+\mu)(\gamma+\mu)-\frac{\delta(1-\rho)}{\mu}=0$. Let $\lambda^2+a_1\lambda+a_2=0$ with $a_1=\delta+2\mu+\gamma$ and $a_2=(\delta+\mu)(\gamma+\mu)-\frac{\delta(1-\rho)}{\mu}$. Writing a_2 in term of R_0, we have $a_2=(\delta+\mu)(\gamma+\mu)(1-R_0)$.

From the criteria of Ruth-Hurwitz [18] for the stability of the systems, if $a_1>0$ and $a_2>0$, then the eigenvalues are negative. It is obvious that $a_1>0$ and $a_2>0$ if $R_0<1$. Therefore, the DFE is asymptotically stable.

- For this case, consider the Jacobian matrix at the endemic equilibrium point given by Expression (5), we have

$$J(E_1)=\begin{pmatrix} -\mu-\frac{1-\rho}{b}I^* & 0 & -\frac{1-\rho}{b}S^* \\ \frac{1-\rho}{b}I^* & -(\mu+\delta) & \frac{1-\rho}{b}S^* \\ 0 & \delta & -(\gamma+\mu) \end{pmatrix}. \quad (18)$$

Computing the eigenvalues associated to $J(E_1)$, we have

$$|J(E_1)-\lambda I|=\begin{vmatrix} -\mu-\frac{1-\rho}{b}I^*-\lambda & 0 & -\frac{1-\rho}{b}S^* \\ \frac{1-\rho}{b}I^* & -(\mu+\delta)-\lambda & \frac{1-\rho}{b}S^* \\ 0 & \delta & -(\gamma+\mu)-\lambda \end{vmatrix}=0$$

$$\Leftrightarrow \lambda^3+c_1\lambda^2+c_2\lambda+c_3=0,$$

where

$$c_1=2\mu+\gamma+\delta+\mu R_0,$$

$$c_2=\mu R_0\left[(\delta+\mu)+\mu R_0(\delta+\mu)\right]-\delta(1-\rho),$$

$$c_3=(\mu R_0)^2(\delta+\mu)(\gamma+\mu)-\mu\delta(1-\rho).$$

The above eigenvalues are negative in the case where $c_i, i=1,2,3$ fulfill the conditions of Routh-Hurwitz. One can verify that:

- $c_1>0$,
- $c_2>0$,
- $c_1c_2-c_3>0$.

It is clear that c_1 is positive. For having $c_2>0$, it must satisfy $\mu R_0\left[(\delta+\mu)+\mu R_0(\delta+\mu)\right]>\delta(1-\rho)$. For $c_1c_2-c_3>0$ to be verified, we have $(\mu R_0)^2(\delta+\mu)(\gamma+\mu)>\mu\delta(1-\rho)$. Therefore the Routh-Hurwitz criteria is satisfied and the endemic equilibrium point is locally asymptotically stable.

5.2. Parameter Sensitivity Analysis

Sensitivity analysis shows how changing values of independent variables have an

impact on particular dependent variables [19]. It helps to distinguish different parameters that have a high effect on the basic reproduction number R_0 when they are changed, and should be taken in consideration when intervention strategies are applied.

Definition 5.1. We defined the normalized forward sensitivity index of R_0 [8] which is differentiable with respect to a given parameter Φ, by

$$\Upsilon_{\Phi}^{R_0} = \frac{\partial R_0}{\partial \Phi}\frac{\Phi}{R_0}. \tag{19}$$

Using Definition 5.1, we have

$$\begin{aligned}
\Upsilon_{\delta}^{R_0} &= 1 - \frac{\delta}{(\mu+\delta)(1-\rho)},\\
\Upsilon_{\rho}^{R_0} &= -\frac{\rho}{1-\rho},\\
\Upsilon_{\gamma}^{R_0} &= -\frac{\gamma}{\mu+\gamma},\\
\Upsilon_{\mu}^{R_0} &= -\frac{2\mu+\gamma}{\mu(\mu+\gamma)} - \frac{1}{\mu+\delta}.
\end{aligned} \tag{20}$$

From Table 2, the positive sign means that R_0 will increase as the parameters increase while the negative signs indicate the decrease in R_0 as the parameters decrease. Furthermore, parameter with positive sign index means that an increase or decrease in the values of this parameter will lead to an increase or decrease in R_0. Also, the parameters with negative sign indices indicate that increasing or decreasing the values will decrease (or increase) R_0. We can see from Table 2 the parameters that have the most effect on R_0, and consequently on the entire model, are: δ, γ and μ.

Table 2. Sensitivity of R_0 evaluated to its parameter values given in Expression (13).

Parameters	Sensitivity index
δ	+0.099
ρ	−0.02
μ	−0.416
γ	−0.66

6. Numerical Simulations and Discussion

We carry out numerical simulations to compare our model with the results of the real data obtained from Kamenge University Hospital Center (CHUK). The data were collected from February 13th, 2024 which corresponds to the starting point of our simulations (day 0), when the CHUK alerts the new virus with already 9 confirmed cases in one day up to March 25th, 2024. During our survey, 310 new cases have been reported in one month (30 days). Note that, according to the spe-

cialist, the conjunctivitis viral doesn't cause any death but destabilizes the eye capacity of seeing.

We show that our conjunctivitis model describes well the real data of daily confirmed cases during one month outbreak. The following list is the number of infected cases who went to consult the ophthalmologist at Kamenge University Hospital Center per day: [9, 2, 10, 3, 11, 19, 29, 16, 26, 16, 14, 17, 9, 19, 10, 8, 11, 7, 20, 14, 11, 5, 6, 2, 2, 4, 3, 2, 3, 2] represented by the blue line on **Figure 2** and **Figure 3**.

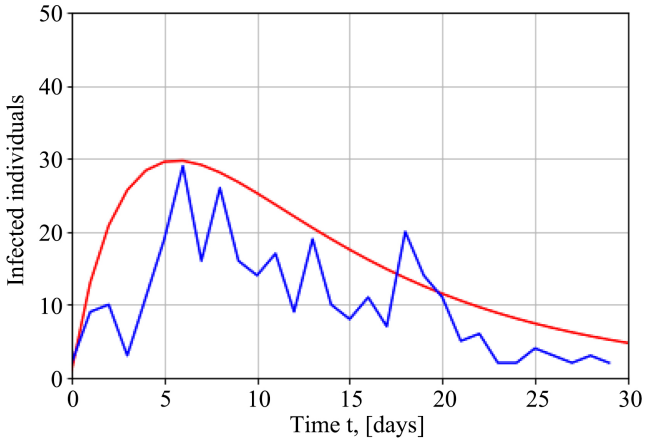

Figure 2. Number of confirmed cases per day. The blue line corresponds to the real data obtained from CHUK while the red line has been obtained by solving numerically the System of equations (2) where the parameters are taken from **Table 1**.

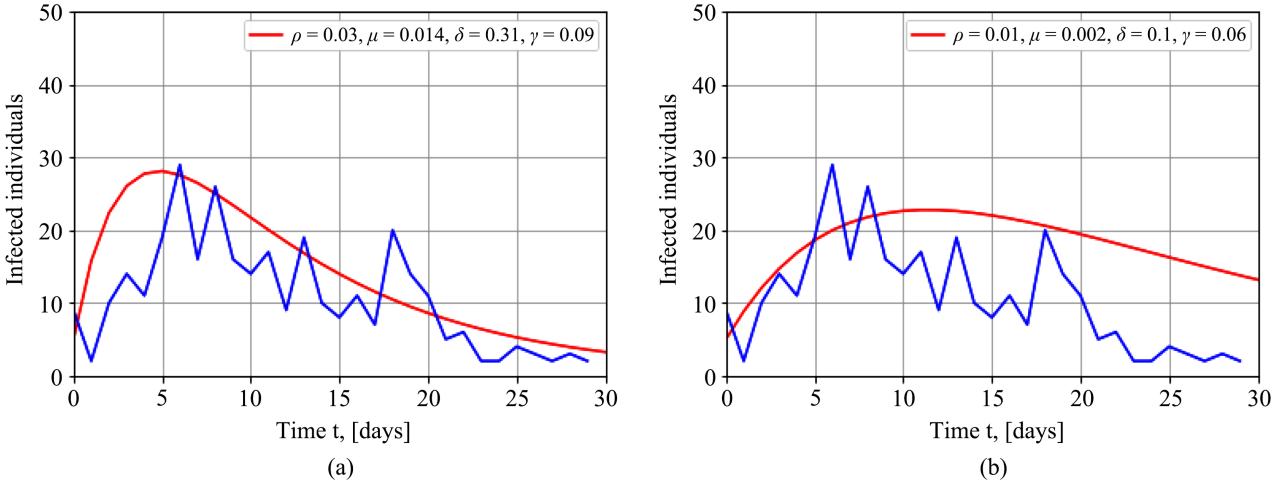

Figure 3. Infected cases per day (a) obtained by increasing of 0.01 at each parameter that appears into Expression (13) of R_0 or by decreasing those parameters (b) where the original values are in **Table 1**.

Figure 3(a), **Figure 3(b)** have been obtained by adjusting the most sensitive parameters to the basic reproduction number *i.e.*: δ, γ, μ and ρ while keeping fixed the others parameters that do not appear in the R_0 expression. Those figures shows that not only their change has the effect on the reproduction number but

also the impact is evident and detected on the infected red curve.

By increasing the parameters influencing the number of basic reproduction by 0.01, we can see on **Figure 3(a)** that the red curve representing the number of infected cases per day found numerically reaches its maximum on the fifth day, with the maximum number around 28 cases lower than that shown in **Figure 2**, which is estimated at 30 infected cases. Moreover, between days 25 and 30, the curve found by the real data and that found numerically are very close to each other and tend to converge on the time axis, indicating the immediate extinction of the disease. In **Figure 3(b)**, by reducing the parameters influencing the basic reproduction number, we can see that the maximum number of infection is found on the tenth day, estimated at 22 cases. Between days 25 and 30, there is a remarkable gap, which means that in this situation, the number of infected will be under control beyond 30 days, hence the persistence of the disease.

7. Conclusion

In this paper, an SEIR mathematical model of conjunctivitis viral disease has been formulated. The basic reproduction number for the model has been calculated and explored as a key parameter in understanding the dynamics of disease. Stability of the model has been studied and the sensitivity analysis was performed, which showed that R_0 is highly sensitive to the infected rate of E class δ, recovery rate γ, death rate μ and the transmission rate of infection ρ. Numerical results are performed in Section 2 where estimated parameters have been confronted with the real data. These results show that our model fits enough the real data of daily infected cases from conjunctivitis viral disease as shown in **Figure 2**, which reflects the reality in Burundi, especially in Bujumbura town. These results would be useful for the decision-makers and to the health NGO or health authorities to know better the parameters that need to be controlled than others in order to mitigate the transmission of the disease. Our model can also be adjusted and used to study the transmission of the conjunctivitis viral disease in other regional countries where the outbreaks have been noted. In the future, this model can be improved by including control measures and the compartment of the infected cases who have taken treatment without a medical prescription.

Acknowledgements

The authors would like to thank the anonymous reviewers and the Kamenge University Teaching Hospital for authorizing access to data on conjunctivitis patient.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

References

[1] (2024) Le Renouveau du Burundi. MINISANTE: Déclaration sur l'épidémie de conjonctivité virale.

http://lerenouveau.bi/minisante-declaration-sur-lepidemie-de-conjonctivite-virale/

[2] Chatterjee, S., Quarcoopome, C.O. and Apenteng, A. (1970) Unusual Type of Epidemic Conjunctivitis in Ghana. *British Journal of Ophthalmology*, **54**, 628-630. https://doi.org/10.1136/bjo.54.9.628

[3] Solano, D., Fu, L.X. and Czyz, C.N. (2017) Viral Conjunctivitis. Treasure island (FL): Statpearls Publishing. https://www.ncbi.nlm.nih.gov/books/NBK470271/

[4] Wright, P.W., Strauss, G.H. and Langford, R.M. (1992) Acute Hemorrhagic Conjunctivitis. *American Family Physician*, **45**, 173-178.

[5] Panovska-Griffiths, J., Kerr, C.C., Waites, W. and Stuart, R.M. (2021) Mathematical Modeling as a Tool for Policy Decision Making: Applications to the COVID-19 Pandemic. *Handbook of Statistics*, **44**, 291-326. https://doi.org/10.1016/bs.host.2020.12.001

[6] Nana-Kyere, S., Desmond Titus, B., After Boateng, F. and Jonathan, P. (2018) Optimal Control Model of Haemorhagic Conjunctivitis Disease. *Advances in Computer Sciences*, **1**, Article 108. https://doi.org/10.31021/acs.20181108

[7] Unyong, B. and Naowarat, S. (2014) Stability Analysis of Conjunctivitis Model with Nonlinear Incidence Term. *Australian Journal of Basic and Applied Sciences*, **8**, 52-58.

[8] Ogunmiloro, O.M. (2020) Stability Analysis and Optimal Control Strategies of Direct and Indirect Transmission Dynamics of Conjunctivitis. *Mathematical Methods in the Applied Sciences*, **43**, 10619-10636. https://doi.org/10.1002/mma.6756

[9] Viriyapong, R. and Khedwan, N. (2019) Effects of Isolation by Taking Sick Leaves of Conjunctivitis Infected Individuals and Treatment Control on Stability of Mathematical Modeling of Conjunctivitis. *Science, Engineering and Health Studies*, **13**, 20-28.

[10] Chen, S.L., Liu, R.C., Chen, F.M., Zhang, X.X., Zhao, J. and Chen, T.M. (2016) Dynamic Modelling of Strategies for the Control of Acute Haemorrhagic Conjunctivitis Outbreaks in Schools in Changsha, China (2004-2015). *Epidemiology and Infection*, **145**, 368-378. https://doi.org/10.1017/s0950268816002338

[11] Uchenna, M. (2019) Control Model on Transmission Dynamic of Conjunctivitis during Harmattan in Public Schools. *Applied and Computational Mathematics*, **8**, 29-36. https://doi.org/10.11648/j.acm.20190802.11

[12] Sangthongjeen, S., Sudchumnong, A. and Naowarat, S. (2015) Effect of Education Campaign on Transmission Model of Conjunctivitis. *Australia Journal of Basis and Applied Science*, **9**, 811-815.

[13] Sangsawang, S., Tanutpanit, T., Mumtong, W. and Pongsumpun, P. (2012) Local Stability Analysis of Mathematical Model for Hemorrhagic Conjunctivitis Disease. *KMITL Science and Technology Journal*, **12**, 189-197.

[14] Chowell, G., Shim, E., Brauer, F., Diaz-Dueñas, P., Hyman, J.M. and Castillo-Chavez, C. (2006) Modelling the Transmission Dynamics of Acute Haemorrhagic Conjunctivitis: Application to the 2003 Outbreak in Mexico. *Statistics in Medicine*, **25**, 1840-1857. https://doi.org/10.1002/sim.2352

[15] Suksawat, J. and Naowarat, S. (2014) Effect of Rainfall on the Transmission Model of Conjunctivitis. *Advances in Environmental Biology*, **8**, 99-104.

[16] van den Driessche, P. and Watmough, J. (2002) Reproduction Numbers and Sub-Threshold Endemic Equilibria for Compartmental Models of Disease Transmission. *Mathematical Biosciences*, **180**, 29-48. https://doi.org/10.1016/s0025-5564(02)00108-6

[17] van den Driessche, P. (2017) Reproduction Numbers of Infectious Disease Models.

Infectious Disease Modelling, **2**, 288-303. https://doi.org/10.1016/j.idm.2017.06.002

[18] Erawaty, N., Kasbawati, and Amir, A.K. (2019) Stability Analysis for Routh-Hurwitz Conditions Using Partial Pivot. *Journal of Physics*: *Conference Series*, **1341**, Article ID: 062017. https://doi.org/10.1088/1742-6596/1341/6/062017

[19] Thabane, L., Mbuagbaw, L., Zhang, S., Samaan, Z., Marcucci, M., Ye, C., et al. (2013) A Tutorial on Sensitivity Analyses in Clinical Trials: The What, Why, When and How. *BMC Medical Research Methodology*, **13**, Article No. 92. https://doi.org/10.1186/1471-2288-13-92