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# Compartmental mathematical modelling of dynamic transmission of COVID-19 in Rwanda

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ABSTRACT

*Objectives:* Mathematical modelling is of interest to study the dynamics of coronavirus disease 2019 (COVID-19), and models such as SEIR (Susceptible–Exposed–Infected–Recovered) have been considered. This article describes the development of a compartmental transmission network model – Susceptible–Exposed–Quarantine–Infectious–Infectious, undetected–Infectious, home-based care–Hospitalized–Vaccinated–Recovered–Dead – to simulate the dynamics of COVID-19 in order to account for specific measures put into place by the Government of Rwanda to prevent further spread of the disease.

*Methods:* The compartments of this model are connected by parameters, some of which are known from the literature, and others are estimated from available data using the least squares method. For the stability of the model, equilibrium points were determined and the basic reproduction number $R_0$ was studied; $R_0$ is an indicator for contagiousness.

*Results:* The model showed that secondary infections are generated from the exposed group, the asymptomatic group, the infected (symptomatic) group, the infected (undetected) group, the infected (home-based care) group and the hospitalized group. The formulated model was reliable and fit the data. Furthermore, the estimated $R_0$of 2.16 shows that COVID-19 will persist without the application of control measures.

*Conclusions:* This article presents results regarding predicted spread of COVID-19 in Rwanda.

## Introduction

Since the beginning of the 21st century, the world has experienced several epidemic diseases which have caused global public health problems. These include severe acute respiratory syndrome (SARS) in 2002, which caused 800 deaths among the 8000 documented cases [1]; swine-origin influenza A (H1N1) in 2009, which caused 18,500 registered deaths [2]; Middle East Respiratory Syndrome (MERS) in 2012, which caused 800 deaths among 2500 registered cases [3]; and an Ebola outbreak in West Africa in 2014, which resulted in 11,310 deaths among 28,616 cases [4]. Coronavirus disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), emerged in 2019.

Coronaviruses (CoVs) are single-stranded RNA viruses that belong to Nidovirales, in the Coronaviridae family and Orthocoronavirinae subfamily. There are four genera of CoVs: alpha, beta, delta and gamma

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[5]. Alpha CoVs and beta CoVs originate from bats and rodents, while delta CoVs and gamma CoVs originate from avian species [6]. SARS-CoV-1 is a beta CoV, and the first case was isolated from bats in 1992, with civet cats as the intermediary host. MERS-CoV was isolated from dormitory camels in 2003. SARS-CoV-2 was first detected in China in late 2019 at the South China Seafood Market in Wuhan [7], and a global pandemic was declared by the World Health Organization on 11 March 2020. COVID-19 can be transmitted by human-to-human by respiratory droplets from sneezing, coughing and aerosols, with symptomatic people being the major source of transmission [8]. The incubation period for COVID-19 is approximately 7–14 days [9].

According to Worldometer Coronavirus [10], as of 18 March 2022, COVID-19 was affecting 227 countries. The number of recorded cases in accordance with the applied case definition and testing strategies was 466,544,318, including at least 6,088,220 deaths and 398,168,581 recovered cases. On 18 March 2022, the country with the highest COVID-19 burden was the USA, with 81,350,883 total cases, 996,072 deaths and 56,822,580 recovered cases. COVID-19 has affected all African countries, and despite the basic preventative measures adopted to stop its spread, the number of infected cases has increased significantly. On 18 March 2022, the Centre for Disease Control of African Union reported 11,291,388 cases, 250,437 deaths and 10,565,882 recovered cases. On the same date, the most affected African country was South Africa, with 3,700,484 cases, 99,829 deaths and 3,585,603 recovered cases. The East Africa Community (EAC) reported 703,290 cases, 11,640 deaths and 691,650 recovered cases. Kenya was the EAC country most affected by COVID-19, with 323,237 cases, 5647 deaths, 317,527 recovered cases and 63 active cases, whereas the least affected EAC country was Tanzania with 33,778 cases and 800 deaths.

In Rwanda, as of 18 March 2022, there were 129,623 cases, 128,112 recovered cases, 1459 deaths and 52 active cases. However, the above statistics may be biased due to the lack of reporting facilities, such as poor reporting systems, poor reporting knowledge and poor understanding of health policies. More developed countries have higher reporting capability, which may lead to higher numbers of reported cases and deaths.

Globally, all countries have focusing on making decisions about measures to fight the COVID-19 pandemic. These measures differ between countries, but common preventive control measures adopted by the Government of Rwanda include social distancing, washing hands regularly using soap or hand sanitizer, and wearing facemasks in public. Rwandan citizens and residents returning to the country and visitors to Rwanda have been subjected to a mandatory 14-day quarantine period at designated locations. These measures continue to be monitored and updated according to the current situation of disease burden and transmission in the population.

To slow down the spread of COVID-19, countries and health organizations have developed different vaccines. COVID-19 vaccines provide strong protection against severe illness, and have been proven to be safe and effective as a clear path to bring the pandemic to an end [11]. However, in some low-income countries, particularly in Africa, vaccination rates have been insufficient to prevent the spread of COVID-19. As of 17 March 2022, 63.8% of the population worldwide had received at least one dose of a COVID-19 vaccine. The country with the highest rate of vaccination was the United Arab Emirates, with 98.99% of the population vaccinated (95.85% had received the complete initial protocol, 3.17% were partially vaccinated) [12]. In Africa, 19.76% of the population were partially vaccinated, 14.99% were fully vaccinated, and only 1.16% had received a booster dose [12]. Rwanda is a good model for COVID-19 vaccination in Africa as, by 17 March 2022, 66.37% of the population had been vaccinated (58.81% had received the complete initial protocol, and only 7.56% were partially vaccinated).

Mathematical modelling and simulation are very important tools to control human and animal diseases [13]. They can provide projections of the likely future, provide descriptions of the natural history of infections at population and individual levels, and provide insights into the impact of possible interventions.

In the literature, several papers on mathematical modelling have described the dynamics of the evolution of COVID-19, with general purpose models such as SIR, SEIR (Susceptible–Infected–Recovered; Susceptible–Exposed–Infected–Recovered) etc. To develop a mathematical model for COVID-19, it is important to consider the known specific characteristics of this new disease [8, 9, 14]. Roosa et al. [15] presented three phenomenological models that can be applied to the outbreak of diseases other than COVID-19. Kucharski et al. [16] presented SEIR-type models with little variation, some of which incorporated stochastic components. Several authors have reported mathematical modelling of the COVID-19 pandemic, but many focused on the dynamics of COVID-19 in China [17–19]. An extended Susceptible–Exposed–Quarantined–Asymptomatic–Non-hospitalized, asymptomatic–Hospitalized–Recovery mathematical model which captured the dynamic transmission of COVID-19 in Ethiopia was developed and analysed by Kifle and Obsu [20]. They found that $R_0 = 1.0029$, and stated that the infected and asymptomatic contact transmission rates should be decreased as they were found to be positively sensitive to $R_0$, and both the quarantined rate and the treatment rate should be increased to reduce the value of $R_0$ to <1. Wamalwa and Tonnang [21] summarized the COVID-19 situation in the Eastern African region (Rwanda, Kenya, Burundi, South Sudan, Ethiopia, Tanzania and Uganda), and, more specifically, in Rwanda and its neighbouring countries such as Kenya, Burundi, Tanzania and Uganda, with $R_0 = 1.32$, 8.52, 2.84, 2.57 and 2.34, respectively. However, the results were based on outbreak data, and extended and simplified SIR and SEIR models that are not thought to have captured all COVID-19 dynamic behaviours and government measures in these countries. Furthermore, due to under-reporting in some of these countries, the $R_0$ results presented may be biased. There is a need, therefore, to develop models that, in addition to considering known specific epidemiological characteristics of COVID-19, also consider specific control measures that governments have put in place in order to control the spread of the disease. As such, this article reports the development of a model of dynamic transmission of COVID-19 in Rwanda. This model can be applied elsewhere where similar strategies are implemented, especially in the East African region.

An extended SEIR mathematical model was developed by incorporating compartments for quarantined patients, patients with undetected infection, infected patients receiving home-based care, hospitalized patients, deaths and vaccinated patients. This resulted in a Susceptible–Exposed–Quarantine–Infectious (detected, undetected and home-based care)–Hospitalized–Vaccinated–Recovered–Dead ($SEQII_uI_hHVRD$) transmission network model to simulate the dynamics of transmission of COVID-19. This mathematical model was built by considering the special characteristics of the pandemic in Rwanda.

## Materials and methods

### *Data source*

This study used the official data reported by the Rwanda Ministry of Health (MoH), recorded by Rwanda Biomedical Centre (RBC). As reported by the MoH, the onset date for the first case of COVID-19 in Rwanda was 14 March 2020. Since then, the MoH has reported the COVID-19 situation (i.e. total cases, number of tests, number of recoveries and deaths, total active cases and total number of vaccinated patients) on a daily basis. This data set can be downloaded from the geographic distribution of COVID-19 cases worldwide [22].

### *Methods and techniques*

Based on the compartmental model presented in Fig. 1, a set of nonlinear differential equations was formulated. To analyse the stability of

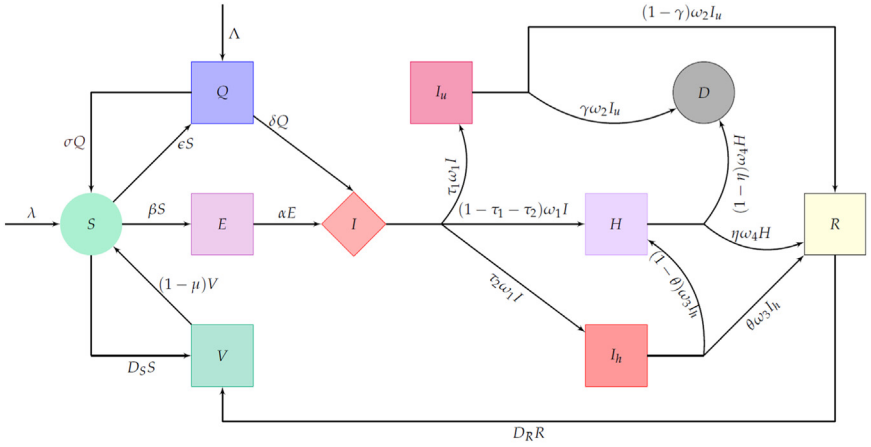


**Fig. 1.** The mathematical model.

the model, equilibrium points were computed and a next-generation matrix was used to compute the basic reproduction number ($R_0$). The least squares method was used to estimate the model parameters. The classical logistic formula was used for prediction. The reader is referred to Appendix B (see online supplementary material) for further information.

## Model equations

The compartments of the SEQII$_u$I$_h$HVRD model are as follows:

- Susceptible ($S$) : people who are not infected by the disease pathogen but who may be infected.
- Exposed ($E$) : people who are in the incubation period after being infected by the disease pathogen, but are without the typical symptoms of infection. People in this compartment could infect susceptible people with a slightly lower probability than people in the infectious compartment. After the incubation period, the people in this compartment pass to the infectious compartment.
- Infectious ($I$) : people infected with the virus and who are highly infectious but not quarantined. There are three scenarios, listed below.
  - Infectious but undetected ($I_u$) : a fraction of infectious people will not be reported. People in this compartment pass to the recovered compartment or may die due to the disease.
  - Infectious and receiving home-based care ($I_h$): people infected with the virus, but followed remotely by the medical team; these people may recover without medical care. However, in the case of complications, these people will be taken to the nearest health facility.
  - Hospitalized ($H$) : infectious people who are hospitalized (or isolated) and can still infect other people, especially healthcare professionals. At the end of treatment, these people can recover from the disease or die.
- Quarantine ($Q$) : Susceptible people suspected or identified through contact tracing to have been in contact with infected people will be subjected to mandatory quarantine either at home or at designated locations. Moreover, all people, including Rwandan citizens and residents returning to Rwanda from abroad, are subjected to quarantine. After the quarantine period, those with a negative test result can return home, and those with a positive test result are hospitalized/isolated.
- Recovered ($R$) : people who were previously detected as infectious, who survived the disease through healthcare treatment at hospital or natural antibodies, and who have developed natural immunity to the virus and are no longer infectious.
- Dead ($D$) : people who succumbed to COVID-19.
- Vaccinated individuals ($V$) : the measure of protection against the disease for vaccinated people depends on vaccine efficacy. In this paper, vaccinated individuals were considered as those who had received more than two doses of the Pfizer, Moderna or Johnson and Johnson vaccines.

Fig. 1 summarizes the structure of the proposed mathematical model. If $N(t)$ is the total population at time $t$, then:

$$N(t) = S(t) + E(t) + I(t) + Q(t) + I_u(t) + I_h(t) + H(t) + R(t) + D(t) + V(t).$$

The dynamics of COVID-19 are modelled by the following system of ordinary differential equations:

$$\begin{aligned}
\frac{dS}{dt} &= \lambda + \sigma Q - \left(\frac{\beta_E E+\beta_{I_u} I_u+\beta_I I+\beta_{I_h} I_h+\beta_H H}{N} + \varepsilon + D_S\right)S + (1-\mu)V;\\
\frac{dE}{dt} &= \left(\frac{\beta_E E+\beta_{I_u} I_u+\beta_I I+\beta_{I_h} I_h+\beta_H H}{N}\right)S - \alpha E;\\
\frac{dI}{dt} &= \alpha E + \delta Q - \omega_1 I;\\
\frac{dQ}{dt} &= \Lambda + \varepsilon S - (\delta+\sigma)Q;\\
\frac{dI_u}{dt} &= \tau_1\omega_1 I - \omega_2 I_u;\\
\frac{dI_h}{dt} &= \tau_2\omega_1 I - \omega_3 I_h;\\
\frac{dH}{dt} &= (1-\tau_1-\tau_2)\omega_1 I + (1-\theta)\omega_3 I_h - \omega_4 H;\\
\frac{dR}{dt} &= (1-\gamma)\omega_2 I_u + \eta\omega_4 H + \theta\omega_3 I_h - D_R R;\\
\frac{dD}{dt} &= \gamma\omega_2 I_u + (1-\eta)\omega_4 H;\\
\frac{dV}{dt} &= D_S S + D_R R - (1-\mu)V.
\end{aligned} \tag{1}$$

where the initial conditions of the model are $S(0) = 13,210,031$, $E(0) = 100$, $I(0) = 1$, $Q(0) = 1$, $I_u(0) = 3$, $I_h(0) = 0$, $H(0) = 1$, $R(0) = 0$, $D(0) = 0$ and $V(0) = 0$.

The model parameters are described below:

- Assume that the population is introduced to the susceptible compartment at rate $\lambda$.
- The entrance rate to the quarantine compartment is $\Lambda$.
- $\beta_E$, $\beta_{I_u}$, $\beta_I$, $\beta_{I_h}$ and $\beta_H$ are the transmissibility rate parameters due to exposed, undocumented infected, infected, infected and receiving home-based care, and hospitalized individuals, respectively. Fig. 1 shows the force of infection $\frac{\beta_E E+\beta_{I_u} I_u+\beta_I I+\beta_{I_h} I_h+\beta_H H}{N}$, which is the transition rate from susceptible to infectious.
- $\varepsilon$ estimates the rate of movement of the susceptible population into the quarantined population.
- $\sigma$ denotes the rate of non-infection in the quarantined population.
- $\delta$ denotes the rate of infection in the quarantined population.
- $\tau_1$ and $\tau_2$ are the fractions of infected individuals who are undocumented and followed at home, respectively.
- Assume that $\frac{1}{\alpha}$ days is the mean latent period, so $\alpha$ is the rate at which exposed individuals become infectious.
- Assume that $\frac{1}{\eta}$, $\frac{1}{\theta}$ and $\frac{1}{\gamma}$ days are the average durations of infection for infected individuals in $H$, $I_h$ and $I_u$, respectively.
- $\omega_1$, $\omega_2$, $\omega_3$ and $\omega_4$ are the transition rates (in days) from compartments, $I_u$, $I_h$ and $H$, respectively.

**Table 1**
Durations for various compartments.

| Symbol | Description |
|---|---|
| $d_E$ | Mean duration in $E$ |
| $d_I$ | Mean duration in $I$ |
| $d_Q$ | Mean duration in $Q$ |
| $d_{I_h}$ | Mean duration in $I_h$ |
| $d_H$ | Mean duration in $H$ |
| $d_g$ | Reduction of duration in $I$ due to control measures |

$E$, exposed; $I$, infectious; $Q$, quarantine; $I_h$, infectious, receiving home-based care; $H$, hospitalized.

- Assume that vaccines are rolled out gradually. The fraction of total susceptible (recovered) vaccinated patients each day is $D_S$ ($D_R$), with efficacy of $\mu$.

## Qualitative study

The qualitative analysis of this model requires stability analysis of the equilibrium point through computation of the basic reproduction number $R_0 = \rho(FV^{-1})$; that is, the spectral radius of the next-generation matrix, where $F$ and $V$ are, respectively, Jacobian matrices of the source of infection and progressions in model compartments evaluated at the disease-free equilibrium point. If $R_0 < 1$, COVID-19 will not persist in the Rwandan population. On the other hand, if $R_0 > 1$, COVID-19 will persist in the Rwanda population. Calculations from the model lead to $R_0 = 2.16$; for more details on how this value was obtained, the reader is referred to Appendix A (see online supplementary material).

## Estimation of parameters

The least squares method was used to estimate unknown parameters in this model. The objective function was defined based on minimization of the relative errors between the cumulative number of diagnosed cases and deaths reported by RBC (i.e. $CC_r$ and $CD_r$) and the cumulative number of cases and deaths estimated by the model when considering a particular set of values of $\varphi$, denoted by $CC^{\varphi}$ and $CD^{\varphi}$. For more details, the reader is referred to Appendix B (see online supplementary material) (Table 1).

For estimating the model parameters, $N = 13,210,137$ was taken as an approximation of the population of Rwanda in 2020 [23], and $\mu = 0.85$ was taken as the efficacy of the vaccine [24]. The cumulative numbers of infected cases ($CC_r$) and deaths ($CD_r$) used were those reported daily by the Rwanda MoH from 14 March 2020 to 28 February 2022. The cumulative number was calculated weekly for a total of 100 weeks. The solution for Equation (1) was obtained using Matlab R2018a. The model fitting curve with the cumulative number of infected cases and deaths against reported cases is shown in Fig. 2. Table 2 shows the estimated parameters. The dynamics for different population groups are shown in Figs. 3–5. According to the estimated parameter values in Table 2, the disease contact rates $\beta_I, \beta_E, \beta_{I_u}, \beta_{I_h}$ and $\beta_H$ make a total contribution to disease transmission of 10.21%. There was a large fraction of undocumented infected people (64.74% of all people infected with COVID-19 were undetected); this could represent a major source of spread of the pandemic in the Rwandan population. It appears that 34.74% of all infected people are treated at home. From these results, it appears that 0.05% of undetected infected people died from COVID-19. Another significant result obtained from parameter estimation was that a high number (93%) of Rwandan citizens and residents were suspected to have COVID-19 and placed in quarantine. Many of them (approximately 97% of those placed in quarantine) tested negative, and 3% of quarantined people were found to be infected. The results show that it takes almost 5 days to develop COVID-19 symptoms, and move from the exposed group to the infectious group. While 99.5% of infected people who are treated in hospital recover, 93.21% of those who are treated at home recover. It is likely that 98% of infections, if not from patients with undetected COVID-19, are from hospitalized individuals. The estimated probability that undetected infected people die from COVID-19 is 94.74%, and the probability that hospitalized individuals recover from COVID-19 is estimated at 91.14%. Referring to the study findings, approximately 10% of the uninfected Rwandan population is vaccinated each day. Recovered individuals develop immunity against COVID-19, and it takes time to vaccinate them. As a result, the number of recovered individuals who receive their vaccination shot each day is low, and is estimated to be 0.086%. It was found that the average number of people placed in quarantine (susceptible) was 347 (66) per day.

Table 3 compares the total numbers of reported cases of infection, deaths and vaccinated individuals on 28 February 2022 with the numbers simulated from the mathematical model.

Fig. 3(a) shows that 133,229 people were infected with COVID-19 in Rwanda during the outbreak. The numbers of undetected infectious patients and home-based-care patients were almost $8.5 \times 10^4$ and $4.8 \times 10^4$, respectively [Fig. 3(b,c)]. Fig. 3(d) shows that the number of patients hospitalized with COVID-19 increased to almost $10.8 \times 10^4$. The overall observation in Fig. 3 is that, as the numbers of infected, infected but undetected, and home-care-based infected individuals increase, a fraction of them are hospitalized, others die and others recover. This decreases the curves of $I$, $I_u$ and $I_h$.

The numerical results in Fig. 4(a) show that the number of deaths from COVID-19 increased to 1358 individuals, and the number of exposed individuals decreased to 100, as shown in Fig. 4(b). According to the results displayed in Fig. 4(c), there were almost $5.2 \times 10^6$ quarantined individuals in Rwanda due to intensive tracing activities and the return of Rwandan citizens during the outbreak. However, the number of quarantined individuals has declined because of relaxation of these activities. As Rwanda enforced the vaccination process, the number of vaccinated people increased to almost $8.7 \times 10^6$ [Fig. 4(d)]. The number of susceptible individuals, considered as the total Rwandan population, declined as individuals moved from the susceptible group to other model compartments [Fig. 5(a)]. The number of recovered individuals in Fig. 5(b) increased from 0 to almost $2.9 \times 10^6$ due to enhancement of the Rwandan healthcare service. The number of recovered individuals observed exceeded the total number of cases obtained from RBC because it combined both detected individuals (hospitalized and home-based care) and undetected, recovered individuals ($I_u$ group).

## Prediction of the COVID-19 pandemic

First, it was considered if the Riccati equation [25] satisfied the following ordinary differential Equation (9):

$$\frac{dM(t)}{dt} = \rho(t)\left(M(t) - \frac{[M(t)]^2}{M_f}\right) \tag{9}$$

where $M(t)$ refers to function modelling the cumulative number of individuals reported to be infected with a viral epidemic disease at time $t$, $\rho(t)$ denotes the time-dependent function, and $M_f$ is a constant parameter. $\rho(t)$ and $M_f$ depend on the basic characteristics of COVID-19, and on the cumulative effect of the control measures taken in Rwanda to prevent transmission. The time dependence of $\rho(t)$ reflects different time-dependent factors, including the effect of different control measures taken by the Government of Rwanda, dependent on time $t$. Solving non-linear Equation (9) yields the following classical logistic formula:

$$M(t) = \frac{M_f}{1 + ae^{-\tau}}, \ \tau = \int \rho(t)dt \tag{10}$$

The prediction of model calibration is performed by considering a particular case of $\rho(t)$ taken as constant $b$, such that Equation (10) becomes:

$$M(t) = \frac{M_f}{1 + ae^{-bt}} \tag{11}$$

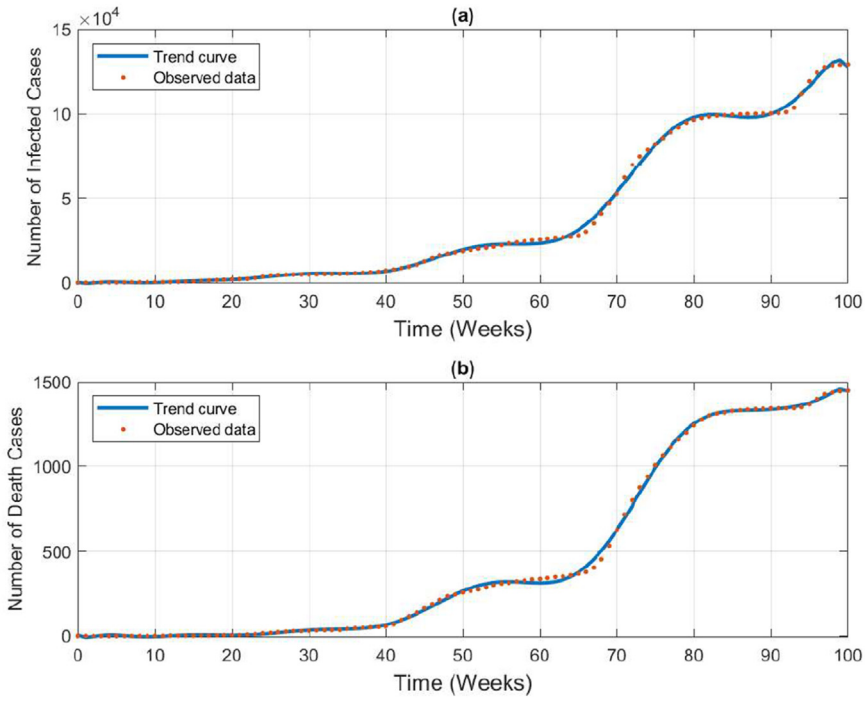


**Fig. 2.** Evolution of the cumulative reported (dotted line) and trend curves (solid line) for infected cases (a) and deaths (b) from the occurrence of the first case in Rwanda (14 March 2019) to 28 February 2022.

**Table 2**
Estimated parameters of the model.

| Symbol | Description | Value | Source |
|---|---|---|---|
| $\beta_I$ | Disease contact rate of infected people | 0.0405 | Estimated |
| $\beta_E$ | Disease contact rate of exposed people | 0.0251 | Estimated |
| $\beta_{I_u}$ | Disease contact rate of undocumented infected people | 0.0140 | Estimated |
| $\beta_{I\_h}$ | Disease contact rate of infected people receiving home-based care | 0.0175 | Estimated |
| $\beta_{I_u}$ | Disease contact rate of hospitalized people | 0.0050 | Estimated |
| $\tau_1$ | Fraction of undocumented infected people | 0.6474 | Estimated |
| $\tau_2$ | Fraction of infected people receiving home-based care | 0.3474 | Estimated |
| $\gamma$ | Fraction of deaths among undocumented infected people | $5 \times 10^{-4}$ | Estimated |
| $\Lambda$ | Recruitment rate in $Q$ | $2.6256 \times 10^{-5}$ | Data |
| $\lambda$ | Recruitment rate in $S$ | $5.0513 \times 10^{-6}$ | Data |
| $\sigma$ | Transition rate from $Q$ to $S$ | 0.9662 | Data |
| $\varepsilon$ | Transition rate from $S$ to $Q$ | 0.9265 | Data |
| $\alpha$(days) | Transition rate (mean latent period) from $E$ to $I$ | 0.1850 (5 days) | [11] |
| $\theta$ | Fraction of infected patients who recovered while receiving home-based care | 0.9321 | Estimated |
| $\delta$ | Transition rate to $I$ in $Q$ | 0.0273 | Estimated |
| $\eta$ | Fraction of infected patients who recovered while hospitalized | 0.9950 | Assumed |
| $\omega_1$ | Transition rate from $I$ to $I_u$ or $I_h$ | 0.9800 | Estimated |
| $\omega_2$ | Transition rate from $I_u$ to $D$ | 0.9474 | Estimated |
| $\omega_3$ | Transition rate from $I_h$ to $R$ | 0.9114 | Estimated |
| $\omega_4$ | Transition rate from $H$ to $R$ | 0.0015 | Estimated |
| $D_s$ | Fraction of total susceptible people vaccinated each day | 0.0974 | Data |
| $D_r$ | Fraction of recovered people vaccinated each day | $8.5538 \times 10^{-4}$ | Data |

$S$, susceptible; $E$, exposed; $I$, infectious; $Q$, quarantine; $I_h$, infectious, receiving home-based care; $H$, hospitalized; $I_u$, infectious, undetected; $R$, recovered.

**Table 3**
Estimated state variables for infectious cases ($I$), deaths ($D$) and vaccinated cases ($V$).

| | $I$ | $D$ | $V$ |
|---|---|---|---|
| Reported | 129,502 | 1457 | 8,815,573 |
| Model | 133,229 | 1358 | 8,653,110 |

Equation (11) is adequate to predict the evolution of COVID-19 after determining the three constants $M_f$, $a$ and $b$ using the observed data. The built-in function *ftnlm* available in Matlab R2018a which creates a non-linear regression model by fitting to data is used to calculate these constants. Table 4 gives the relevant constants specifying the logistic Equation (11) for infectious ($I$), exposed ($E$), infectious but undetected ($I_u$), infectious and receiving home-based care ($I_h$), quarantined ($Q$), hospitalized ($H$), vaccinated ($V$) and death ($D$).

Fig. 6(a), (b), (c) and (d) indicates that the numbers of individuals who were infected, infected but undocumented, infected and receiving home-based care, and hospitalized were predicted to be almost 1200, 28,000, 16,000 and 440,000, respectively, for the 6-month infection period. In total, there were almost 89,200 individuals with COVID-19 in Rwanda over the 6-month period.

Fig. 7(a) predicts that the number of deaths will increase as a consequence of the increase in the number of infected people. The number of

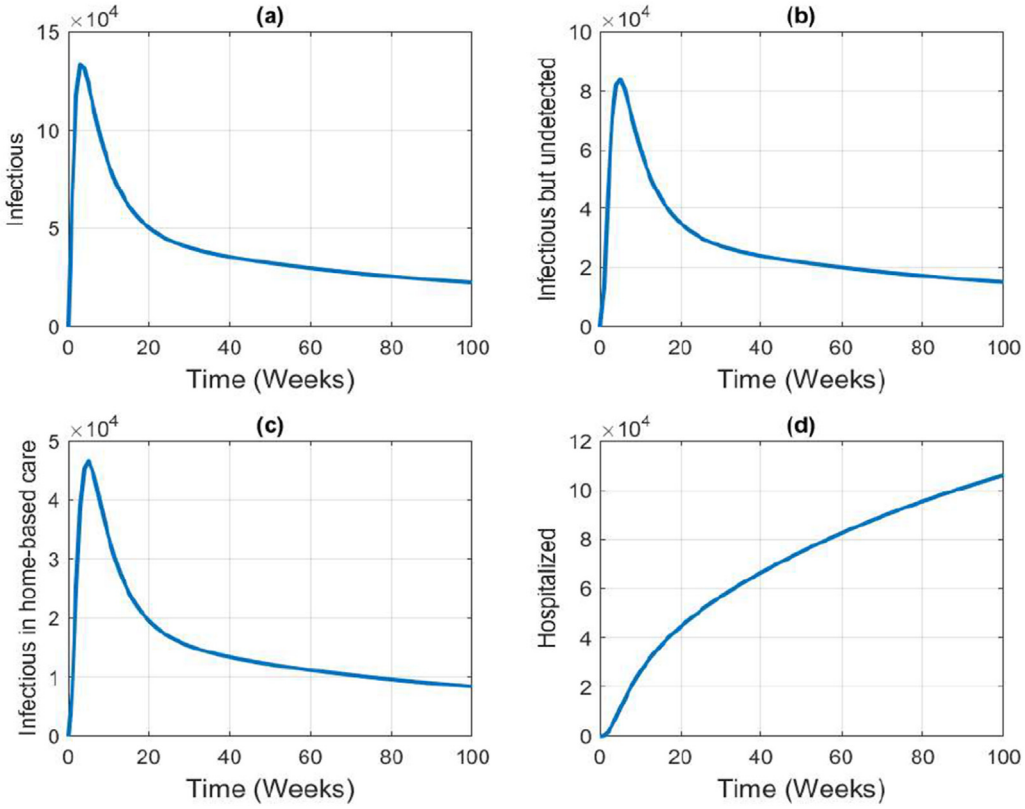


**Fig. 3.** Computational numerical simulations for the mathematical model (1). Model dynamics of infectious cases (a), infectious, undetected cases (b), infectious cases receiving home-based care (c) and hospitalized cases (d). Simulations from the occurrence of the first case in Rwanda (14 March 2019) to 28 February 2022.

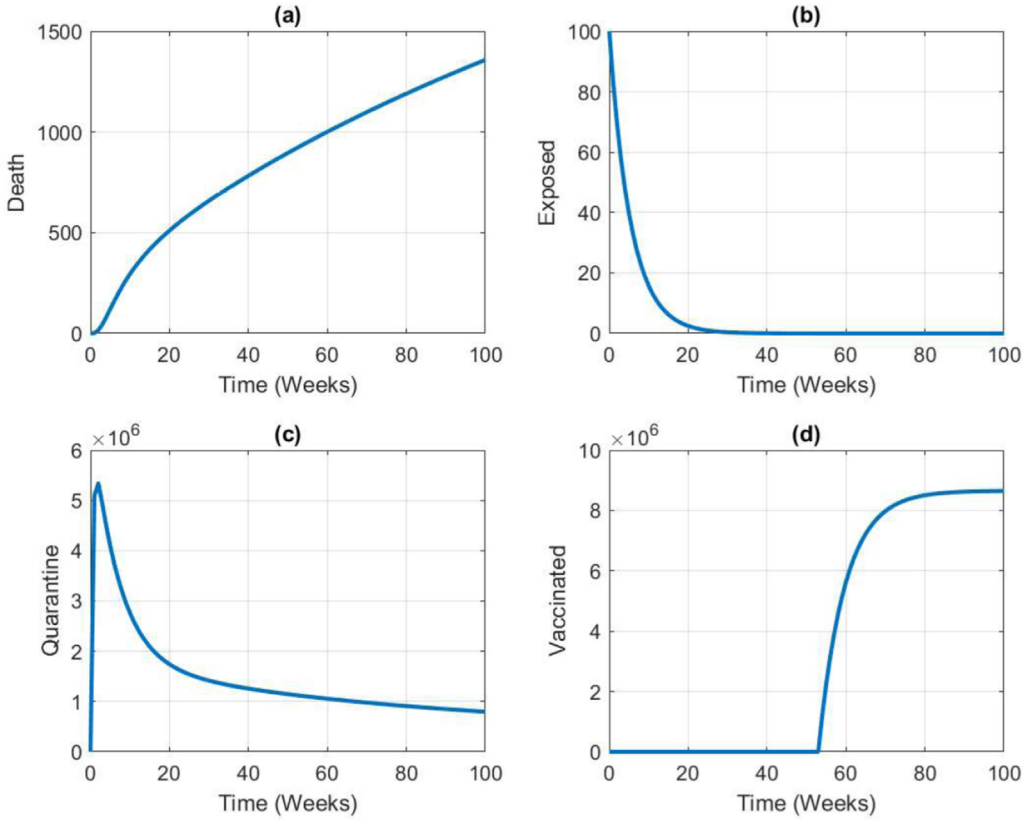


**Fig. 4.** Computational numerical simulations for the mathematical model (1). Model dynamics of deaths (a), exposed cases (b), quarantined cases (c) and vaccinated cases (d). Simulations from the occurrence of the first case in Rwanda (14 March 2019) to 28 February 2022; vaccines were administered from 9 March 2021.

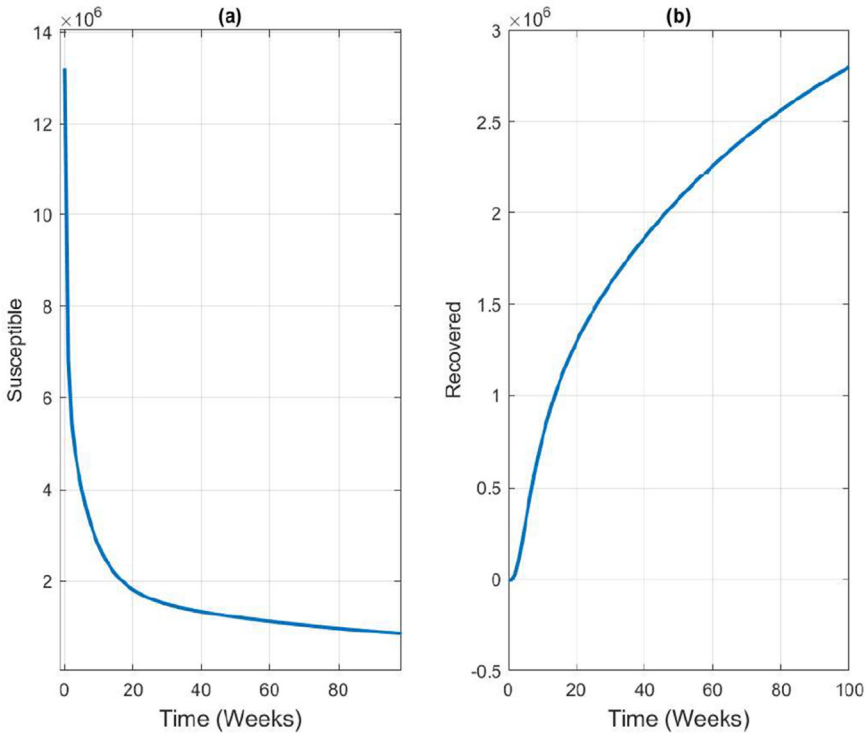


**Fig. 5.** Computational numerical simulations for the mathematical model (1). Models for susceptible cases (a) and recovered cases (b). Simulations from the occurrence of the first case in Rwanda (14 March 2019) to 28 February 2022.

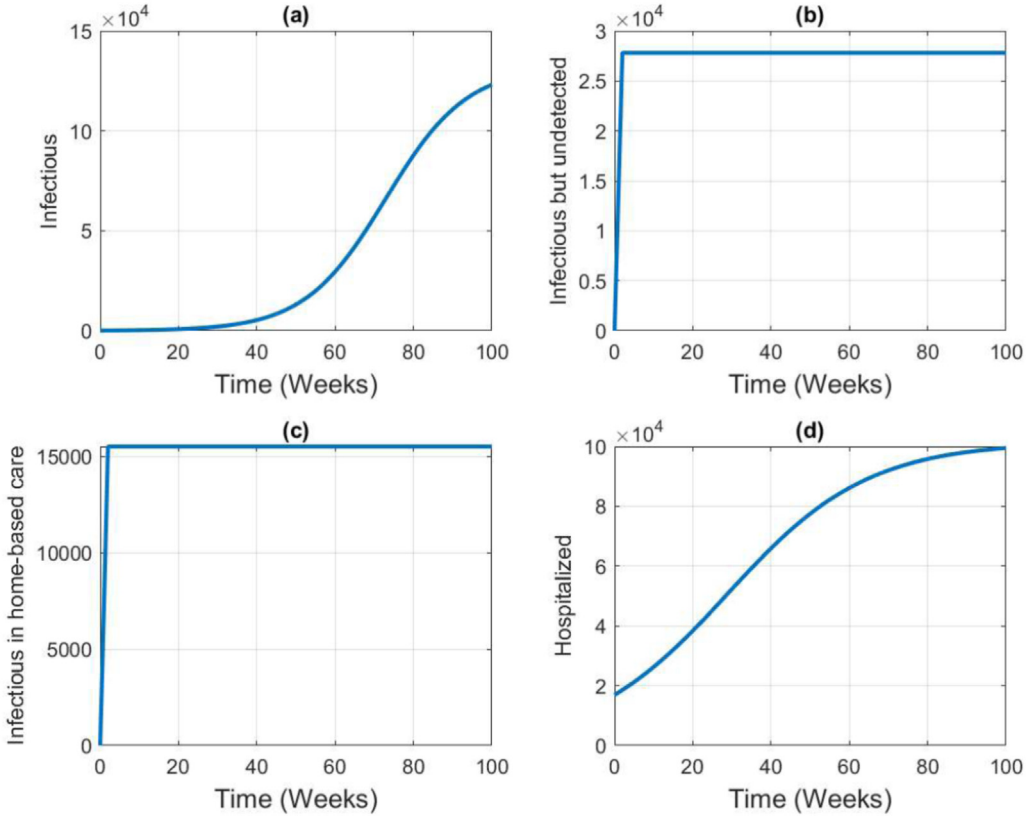


**Fig. 6.** Predictions of cumulative numbers of infectious cases (a), infectious, undetected cases (b), infectious cases receiving home-based care (c) and hospitalized cases (d) for 100 weeks. Simulations from the occurrence of the first case in Rwanda (14 March 2019) to 28 February 2022.

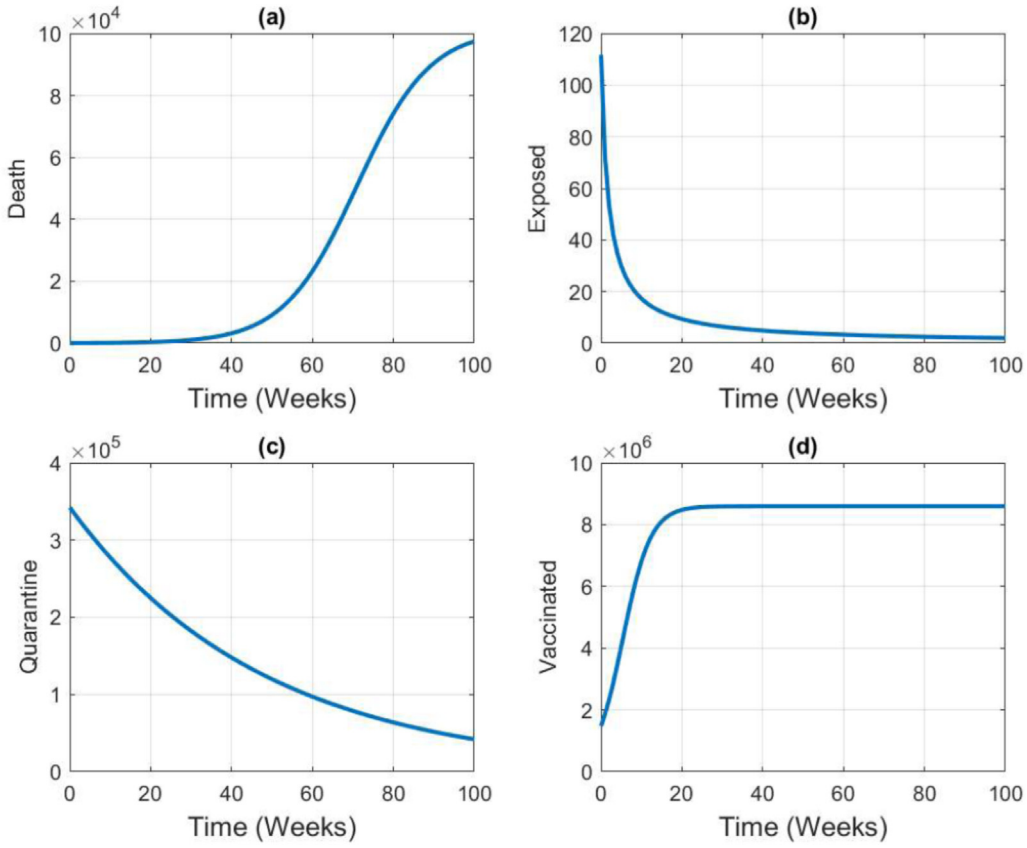


**Fig. 7.** Predicted cumulative numbers of deaths (a), exposed cases (b), quarantined cases (c) and vaccinated cases (d) for 100 weeks. Simulations from the first case in Rwanda (14 March 2019) to 28 February 2022.

**Table 4**
Estimated parameters.

| | | Estimate | SE | tStat | *P*-value |
|---|---|---|---|---|---|
| | $M_f$ | $1.3223 \times 10^{5}$ | 3864.9 | 34.212 | $2.7011 \times 10^{-56}$ |
| $I$ | $a$ | 1124.1 | 350.31 | 3.2089 | 0.0018013 |
| | $b$ | 0.096317 | 0.0050885 | 18.928 | $1.6763 \times 10^{-34}$ |
| | $M_f$ | 0.039097 | 1.0468 | 0.037348 | 0.97028 |
| $E$ | $a$ | -0.99965 | 0.0092213 | -108.41 | $7.3272 \times 10^{-104}$ |
| | $b$ | 0.0001922 | 0.0051763 | 0.03713 | 0.97046 |
| | $M_f$ | 27808 | 1632.6 | 17.033 | $3.4718 \times 10^{-31}$ |
| $I_u$ | $a$ | 48790 | $2.6528 \times 10^{-3}$ | $1.8392 \times 10^{8}$ | 0 |
| | $b$ | 10.779 | 2.3399 | 4.6068 | $1.2194 \times 10^{-5}$ |
| | $M_f$ | 15512 | 908.45 | 17.075 | $2.8873 \times 10^{-31}$ |
| $I_h$ | $a$ | 51967 | $9.5964 \times 10^{-5}$ | $5.4152 \times 10^{8}$ | 0 |
| | $b$ | 10.784 | 2.3374 | 4.6136 | $1.1866 \times 10^{-5}$ |
| | $M_f$ | $2.2082 \times 10^{9}$ | $9.6704 \times 10^{-6}$ | $2.2834 \times 10^{14}$ | 0 |
| $Q$ | $a$ | 6450.51 | 32.996 | 19.563 | $8.6534 \times 10^{-36}$ |
| | $b$ | -0.020997 | $1.6996 \times 10^{-3}$ | -12.354 | $9.0465 \times 10^{-22}$ |
| | $M_f$ | $1.0138 \times 10^{5}$ | 1453.4 | 69.752 | $2.4348 \times 10^{-95}$ |
| $H$ | $a$ | 4.9907 | 0.33013 | 15.117 | $2.3362 \times 10^{-27}$ |
| | $b$ | 0.055677 | 0.0026394 | 21.095 | $3.2539 \times 10^{-38}$ |
| | $M_f$ | $8.5966 \times 10^{6}$ | 24689 | 348.2 | $2.2878 \times 10^{-153}$ |
| $V$ | $a$ | 4.8129 | 0.34386 | 13.997 | $4.1605 \times 10^{-25}$ |
| | $b$ | 0.29169 | 0.010738 | 27.165 | $2.07 \times 10^{-47}$ |
| | $M_f$ | 1536.2 | 35.013 | 43.874 | $3.1109 \times 10^{-66}$ |
| $D$ | $a$ | 2571.9 | 924.33 | 2.7824 | $6.4738 \times 10^{-2}$ |
| | $b$ | 0.11069 | 0.005699 | 19.423 | $2.2673 \times 10^{-35}$ |

*E*, exposed; *I*, infectious; *Q*, quarantine; $I_h$, infectious, receiving home-based care; *H*, hospitalized; $I_u$, infectious, undetected; *R*, recovered; *V*, vaccinated; D, death.
The estimated parameters in Table 4 were used in Figs. 6 and 7, and show the predicted cumulative cases based on the logistic equation.

exposed people is predicted to decline due to the fact that individuals in the incubation period develop symptoms after 5 days and become infectious, according to the results in Fig. 7(b). The number of quarantined people is predicted to decrease linearly towards zero [Fig. 7(c)], and the number of vaccinated individuals in Fig. 7(d) for the 6-month period is projected to be at least 9,000,000 in Rwanda.

## Concluding remarks

This article presents a compartmental $SEQII_uI_hHVRD$ transmission network model of the dynamics of transmission of COVID-19. The compartments are connected by parameters. To describe the dynamics of the people in different compartments, a system of non-linear differential equations has been formulated [3]. Qualitative analysis of the model was conducted. Some of the model parameters were estimated using the least squares method with observed data, while others were taken from existing literature. The findings show that secondary infections are generated from the exposed group by asymptomatic individuals, infected (symptomatic) patients, infected (undetected) patients, infected patients receiving home-based care, and hospitalized cases, and they all contribute to $R_0$. The model fits the Rwandan COVID-19 data well, and can be used for future predictions as differences between observed and predicted data (cumulative cases, cumulative deaths and vaccinated) are not significant. Based on the finding that $R_0$ was 2.16, it is recommended that the Government of Rwanda should reinforce the control measures to reduce $R_0$ to <1. In the future, the authors intend to carry out a sensitivity analysis for this compartmental model to predict the impact of control measures in Rwanda.

## Conflict of interest statement

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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## Ethical approval

Ethical approval was issued by the Institutional Review Board of the College of Medicine and Health Science at the University of Rwanda.

## Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.ijregi.2023.01.003.

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