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To cite this article: J.K. Magani *et al* 2022 *J. Phys.: Conf. Ser.* **2199** 012006

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A numerical technique for solving infectious disease model

J.K. Magani¹, O. P. Ogundile¹ and S. O. Edeki¹

¹Department of Mathematics, Covenant University Ota, Nigeria

Emails: opeyemi.ogundile@covenantuniversityedu.ng, maganijoshua25@gmail.com

Abstract In the medical aspect of life, there are multiple ways of formulating a model that can be used to determine if a disease will become a pandemic or an epidemic. In this research, we discussed how we could use the numerical approach by applying the revised $SEQI_u I_d RF$ (Susceptible, Exposed, Quarantined, Infected undetected, Infected detected, Recovered, and Failed) model to control or contain an infectious disease (COVID-19) by applying the effective contact rate. MATLAB software was used to solve the $SEQI_u I_d RF$ model by considering population growth, mortality rate, infection rate, disease-induced death, failed treatment rate, and recovery rate, which gave pictographic diagrams of the increase and decrease of the infectious disease in the community.

1. Introduction

Coronavirus disease is a viral disease that attacks the lungs and other vital parts of the human body when contracted. The disease is caused by severe acute respiratory syndrome coronavirus 2, A.K.A (SARS-COV2). The sudden outbreak of this deadly disease started in Wuhan, China, in late December, 2019. From the end of 2019 to June 15th, 2021, there have been 177,201,247 million affirmed instances of Coronavirus, 161,607,842 million recuperated cases, and 3,832,356 million death cases around the world [1]. According to [2], the primary source of this pandemic is a live animal and sea food market in Wuhan. This disease can be transmitted majorly when an individual comes in contact with a contaminated surface or via a droplet from an infected person. The disease comes with different signs viz a viz: fever, cough, tiredness, sneezing, pains, sore throats, aches.

Different researchers have worked on the transmission dynamics of COVID-19 using different numerical techniques to the infectious model. In [3], he worked on a deferred SIR plague model that was made by adding an inactive term to a pestilence model, infectious rate, and touchy individual. This new plan sets out freedom for the reasonable situation for the brooding cycle in the SIR model elements. Also, [4] worked on an infectious disease transmission model, SEIQRW. The model partitions the populace into six (6) sections. Consequently, [5] discussed how different non-drug interventions could be utilized to manage and contain the COVID-19 pandemic and lessen the strain on medical services. [6] studied a deterministic model of SIR compartments with non-linear infection flow factors. They provided a study model that is a redesigned version of the original SIR model, useful for disease transmission and compartmental interactions. [7], investigated the mathematical analysis of global covid-19 spread using Nigeria and Spain as a case study, based on the SEIRD model. Other relevant works on covid-19 can be found [8-12]. In this work, a numerical technique called ODE 45 was used to solve a mathematical model called $SEQI_u I_d RF$.



2. Model Formulation and Parameter description

To study the spread rate of Coronavirus disease among humans, we develop a model which separates the total human population into seven (7) compartments at time t .

The compartments are:

- i. The Susceptible population, $S(t)$, are individuals that are being introduced into the society. They may be infected with Coronavirus disease.
- ii. The Exposed population, $E(t)$, are individuals that are infected with the disease but with no signs or symptoms of the virus.
- iii. The Quarantined population, $Q(t)$, are individuals that have been put in isolation or quarantine areas to prevent the spread of the disease.
- iv. The Infected (undetected) population, $I_u(t)$, are individuals that are infected with the disease. They show the signs of being infected with the disease, but it has not been confirmed if they are infected with the disease.
- v. The Infected (confirmed) population, $I_d(t)$, are individuals that have been confirmed to be infected with the disease.
- vi. The Recovered population, $R(t)$, are individuals that have recovered from being infected with the disease.
- vii. The Failed population, $F(t)$, are individuals that were treated with the vaccine but still died from the disease.
- viii. Following [13, 14] we developed the seven-compartmental model for analyzing a system of differential equations. This shows the unique transmission dynamics of COVID-19 infectious disease as:

$$\left. \begin{aligned}
 \frac{dS}{dt} &= \pi + \varpi_s Q - \lambda S - \bar{\mu} S - \varepsilon S \\
 \frac{dE}{dt} &= \varepsilon \lambda S - (1-\theta)k - (2\theta k + \bar{\mu})E \\
 \frac{dQ}{dt} &= \varepsilon S + \theta k E - (\varpi_s + (1-\varpi_d))Q \\
 \frac{dI_u}{dt} &= (1-\varepsilon)\lambda S + (1-\theta)k + (1-\varpi_q)Q - (\gamma_u + \bar{\mu} + \delta_u + \sigma_u)I_u \\
 \frac{dI_d}{dt} &= \theta k E + \gamma_u I_u - (\sigma_d + \tau + \bar{\mu} + \delta_d)I_d \\
 \frac{dR}{dt} &= \sigma_u I_u + \sigma_d I_d + \sigma_f F - \bar{\mu} R \\
 \frac{dF}{dt} &= \tau I_d - (\sigma_f + \bar{\mu} + \delta_f)F
 \end{aligned} \right\} \tag{1}$$

where,

$$\lambda = \frac{\beta(I_u + \eta I_d + \eta fF)}{N}, \tag{2}$$

$$N(t) = S(t) + E(t) + Q(t) + I_u(t) + R(t) + I_d(t) + F(t). \tag{3}$$

subject to the following initial conditions,

$$(S(0), E(0), Q(0), I_u(0), I_d(0), R(0), F(0)) \tag{4}$$

The model disease free equilibrium is given as:

$$DFE = (S^*, E^*, Q^*, I_u^*, I_d^*, R^*, F^*) = \left(\frac{\pi}{\bar{\mu}}, 0, 0, 0, 0, 0, 0 \right) \tag{5}$$

Theorem 2.1:

There exists a region \mathfrak{R} in which the set $\{S, E, Q, I_u, I_d, R, F\}$ is bounded and contained set. The region

is given by: $\mathfrak{R} = \left\{ (S, E, Q, I_u, I_d, R, F) \in \mathbb{R}^7 \leq \frac{\pi}{\bar{\mu}} \right\}$

2.1 The Key Characteristics of the Model

See Table 1 for Parameters Description, Symbol and Value, and the hints below.

- (i) The model provides for disease transmission via infected undetected I_u and infected detected people I_d ;
- (ii) the model allows for spontaneous reactivation of exposed people (at a rate of k);

Table 1: Parameters Description, Symbol, and Value

Description	Symbol	Value	Source
Population growth	π	4000 (per 100000 individuals)	[4]
Total Human Population	N	$200 \times e^6$	[4]
Fraction of newly-infected individuals	ε	0.7000	Assumed
Recovery rate of individuals that are infected from the Infected undetected class	σ_u	0.0667	[5]
Recovery rate of individuals that are infected from the Infected detected class	σ_d	0.0667	[5]
Recovery rate of individuals that are infected from the Failed class	σ_f	0.0667	[5]
Mortality rate of the population	$\bar{\mu}$	0.782	Assumed
COVID-19 induced death from Infected detected class	δ_d	0.022	[5]
COVID-19 induced death from Infected undetected class	δ_u	0.022	[5]
COVID-19 induced death from Failed class	δ_f	0.022	[5]
Rate of quarantined individuals return back to the Susceptible class	ϖ_s	0.8667	[5]
Rate at which quarantined individuals move to the infected undetected class	ϖ_u	0.1333	[5]
Rate of re-activation rate for exposed individuals	k	0.552	Assumed
Rate of treatment failure	τ	0.925	Assumed
Rate of exposed individuals detected	θ	0.725	[4]
Effective contact rate for COVID-19 infection	β	1, 3, 5, 7	Assumed
Rate for undetected individuals to detected class	γ_u	0.626	[5]
Modification parameters	η_d, η_f	0.001, 0.7	Assumed

3. Numerical Solution

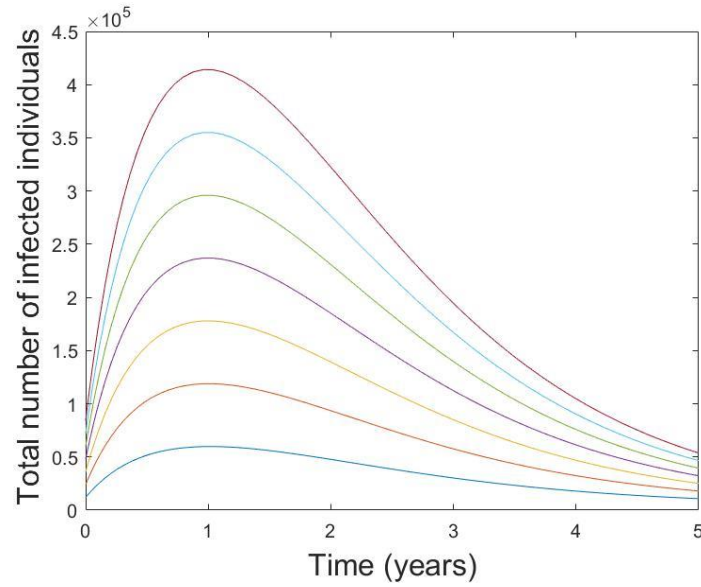


Figure 1: Model running simulation for $\beta = 1, t = 5$

Figure 1 shows the result of running a simulation of the model displaying the total number of new Covid-19 infected people as a function with respect to time (t) for different values of $\beta = 3$. Other parameter values used are as in Table 1.

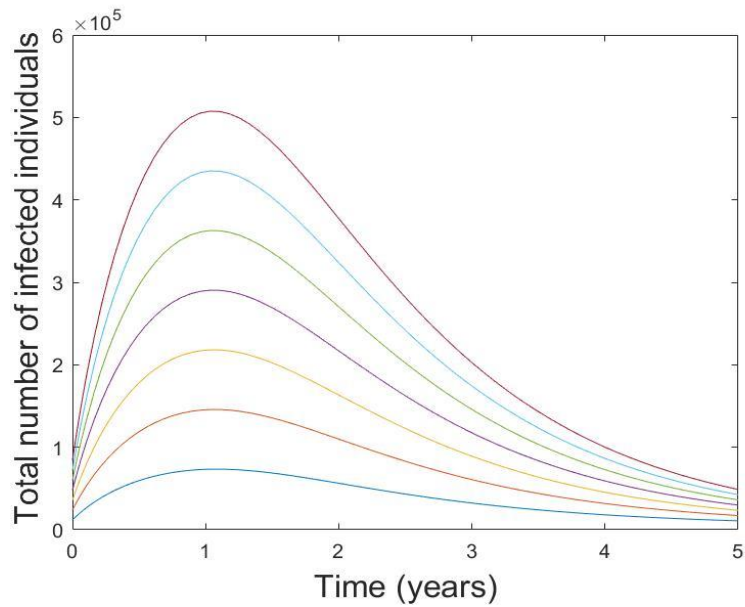


Figure 2: Model running simulation for $\beta = 3, t = 5$

Figure 2 shows the result of running a simulation of the model displaying the total number of new Covid-19 infected people as a function with respect to time (t) for different values of $\beta = 5$. Other parameter values used are as in Table 1.

3.1: Model Simulation when the time rate is 10 years

When the time rate is 10 years, we ran three simulations where the effective rates were: 1,3.

Figure 3 shows the result of running a simulation of the model displaying the total number of new Covid-19 infected people as a function with respect to time (t) for different values of $\beta = 1$. Other parameter values used are as in Table 1.

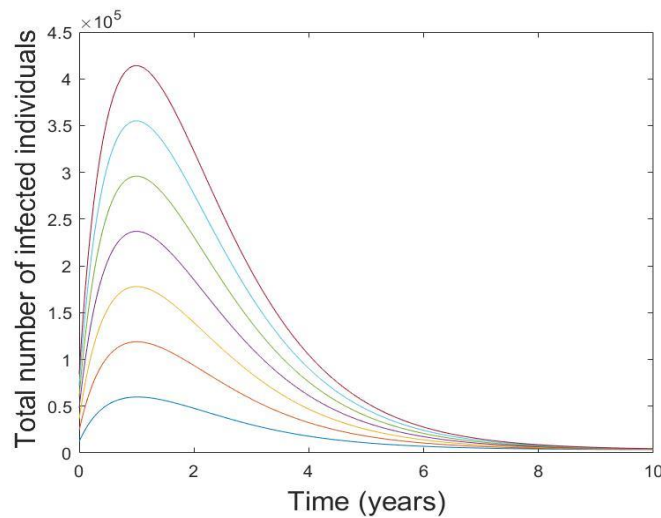


Figure 3: Model running simulation for $\beta = 1, t = 10$

Figure 4 shows the result of running a simulation of the model displaying the total number of new Covid-19 infected people as a function with respect to time (t) for different values of $\beta = 3$. Other parameter values used are as in Table 1.

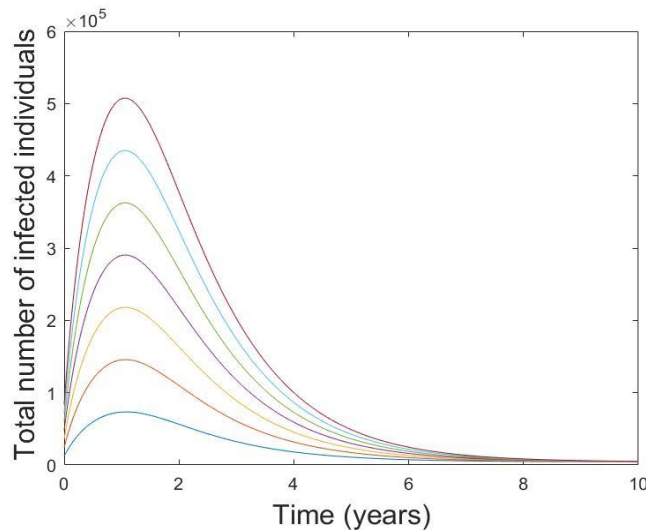


Figure 4: Model running simulation for $\beta = 3, t = 10$

4. Concluding remarks

A six compartmental mathematical model to investigate the transmission dynamics of COVID-19 was formulated. We also propose a method for reducing disease propagation in the community using four hypothetical instances, and a simulation was performed using MATLAB to determine the influence of the effective contact rate for the COVID-19 infectives. Figure 1 depicts the rise and decrease in the number of infected people when $\beta = 1$ and when $t = 5$. Figure 2 depicts the rise and decrease in the number of infected people when $\beta = 3$ and when $t = 5$. Figure 3 depicts the rise and decrease in the number of infected people when $\beta = 1$ and when $t = 10$. Figure 4 depicts the rise and decrease in the number of infected people when $\beta = 3$ and when $t = 10$. Finally, the model study indicates that when the effective contact (β) rate grows, so does the overall number of infected persons. This demonstrates that once there is widespread contact with sick persons, the illness may take a long time to croak in the population.

Acknowledgment

The authors thank Covenant University Centre for Research, Innovation, and Development for supporting this research.

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