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A COVID-19 SEIR model for people living with underlying medical conditions in Kenya

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Abstract
In this study we propose a modified SEIR mathematical transmission model with a focus on Kenyans living with underlying medical conditions. The research will rely on reported data from the Kenya Government's Ministry of Health to fit the model parameters. The next generation matrix approach is employed to ascertain the level of infection or the stability condition of infection based on the basic reproduction number R_o that the model will determine. Results obtained will give predictions on the impact of the disease on this group of people which will inform government in relation to prioritization of vaccination and other mitigating measures on policy formulation.
Numerical simulations will be used to generate results that will support arguments put forth in this paper.

Keywords: COVID-19, SEIR model, underlying medical conditions, basic reproduction number

1. Introduction
A novel corona virus outbreak, popularly known as COVID-19 was first documented in Wuhan, Hubec Province, China in December 2019 (@2021 Lab Manager). In 2020 it spread through several countries and Kenya was not spared with the first confirmed case having been reported on 13th March 2020. The case was of a Kenyan citizen who had travelled back to Nairobi from the United States of America via London, United Kingdom. COVID-19 is an infectious disease caused by SARS-COV-2, a member of corona virus family. It is a respiratory disease that affects lungs. It is transmitted through droplets when an infected person coughs or sneezes. This mode of transmission and symptoms are similar with those of other diseases caused by influenza viruses Korobeinikov A 2004 [1].
Since the outbreak COVID-19, there has been untold suffering throughout the world impacting negatively on the economic, social and political sectors of most countries, albeit to varying degrees. Global COVID-19 deaths are estimated at 4.056 million, with Kenya contributing 3,723 deaths as of mid-July 2021.
Studies have shown that COVID-19 does not affect all population groups equally. We are learning more about the risk factors for severe COVID-19 outcomes every day. Age is the strongest risk factor for severe COVID-19 outcomes.
Additionally, some chronic medical conditions occur more frequently in certain population groups and the risk of severe COVID-19 increases as the number of underlying medical conditions increases in an individual. Therefore, old people and those with underlying medical conditions such as cardiovascular disease, diabetes, hypertension, chronic respiratory disease and cancer are more likely to experience serious illness from COVID-19. Severe illness means that a person with COVID-19 may need hospitalization or intensive care.
In Kenya, the Ministry of Health-estimates show that 1 out of 3 people aged 58 years and above are either diabetic or hypertensive or both. This group is at a high risk during this corona virus pandemic. Alongside the frontline health workers, the government has prioritized the individuals aged 58 years and above for vaccination and other intervention measures to mitigate against contracting the disease. It is estimated that bulk of the reported fatalities in Kenya comprise of people living with underlying medical conditions and old age Jayanta Mondal 2020 [2].

Vaccination has made an enormous contribution to global health by greatly reducing the burden of infectious diseases. Two major infections namely smallpox and rinderpest in animals, have been eradicated through vaccination. A number of vaccines for COVID-19 have been developed. Among them are Astra Zeneca, Novavax, Johnson and Johnson which are already being administered. However, there is an emergency of new strains N440K also referred to as the Andhra Pradesh variant as it was first discovered in Kurnool district India, Delta Variant, and B.1.1.28.2 which are at least 15 times more infectious than the earlier virus and highly affect lungs. This new strains seem not to respond to available vaccines and more research is underway.

Since the outbreak of COVID-19, several mathematical models have been formulated to discuss its dynamics. A few among the many researchers who have dealt with this are [2, 3, 4, 5].

In this paper we propose a modified SEIR mathematical transmission model and use reported Kenyan data of cases of COVID-19. The target group is the individuals living with underlying medical conditions mainly diabetes and hypertension. We shall use the next generation matrix to determine the R_o number that provides the quantification of the disease risk.

Assumptions: We assume that all individuals in the population are at risk of infection, and that the recovered population would have developed antibodies and therefore would not be re-infected. We also assume that the incubation period is seven days.

Table 1: Below gives the definitions of the symbols used in the model.

Ω	Recruitment rate
β	Contact rate between susceptible individuals and exposed individuals (transmission rate)
μ	Natural mortality rate
η	Transfer rate from exposed individuals to quarantine
β_1	Rate of transfer of individuals from exposed class to symptomatic infected individuals class with underlying medical conditions
δ_1	Rate of transfer of individuals from exposed class to symptomatic infected individuals class without underlying medical conditions
d_u	Mortality rate due to COVID-19 in symptomatic infected individuals class with underlying medical condition
d_n	Mortality rate due to COVID-19 in symptomatic infected individuals class without underlying medical condition
β_2	Rate of transfer of individuals from quarantine class to symptomatic infected individuals class with underlying medical conditions
δ_2	Rate of transfer of individuals from quarantine class to symptomatic infected individuals class without underlying medical conditions
γ_3	Transfer rate from quarantine class to class of recovered individuals
γ_1, γ_2	Recovery rate from symptomatic infected classes I_u, I_n

2. Model Description

This is a SEIR model that comprises of four classes, namely; Susceptible (S), Exposed (E), Infected (I), and Recovered (R). Further, we make some modifications to the basic model by including Quarantine isolations and divided I into two compartments I_u and I_n where I_u are the infected individuals living with underlying medical conditions and I_n are those infected but without underlying medical conditions. Based on these considerations, the total population is:

$$N(t) = S(t) + E(t) + I_u(t) + I_n(t) + Q(t) + R(t) \tag{2.1}$$

Individuals in the infected classes I_u and I_n have fully developed disease symptoms and can infect other people. People in the exposed class are in the incubation period .They do not show symptoms but can infect others.

The COVID-19 transmission model is illustrated in figure 1 below

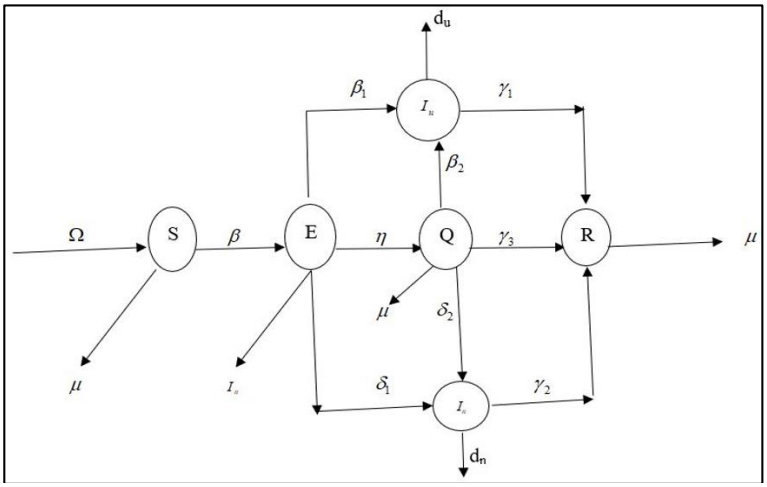

Fig 1: Transmission pattern of COVID-19

The newly established COVID-19 modified $SEIR$ model is defined by a system of first order ordinary differential equations:

$$\frac{dS}{dt} = \Omega - \beta SE - \mu S$$

$$\frac{dE}{dt} = \beta SE - (\beta_1 + \delta_1 + \eta + \mu) E$$

$$\frac{dQ}{dt} = \eta E - (\mu + \beta_2 + \delta_2 + \gamma_3) Q$$

$$\frac{dI_u}{dt} = \beta_1 E + \beta_2 Q - (\gamma_1 + d_u) I_u$$

$$\frac{dI_n}{dt} = \delta_1 E + \delta_2 Q - (\gamma_2 + d_n) I_n \quad (2.2)$$

$$\frac{dR}{dt} = \gamma_1 I_u + \gamma_2 I_n + \gamma_3 Q - \mu R$$

Subject to the following initial conditions:

$$S(0) > 0,\ E(0) \geq 0,\ Q(0) \geq 0,\ I_u(0) \geq 0, I_n(0) \geq 0, R(0) \geq 0 \text{ For all } t \geq 0. \quad (2.3)$$

The epidemic data used in this paper comes from the raw epidemic notification data published on the official website 'Coronavirus-Kenya: COVID-19 update (*http://www.africanews.com*)'.

3. The Invariant Region

We have to show that the state parameters $S(t), E(t), Q(t),\ I_u(t),\ I_n(t), R(t)$ are all positive for all $t \geq 0$.

From equation (2.1) and the system (2.2)-(2.3) we see that

$$\frac{dN}{dt} = \Omega - \mu N \quad (3.1)$$

since all μ and d_u, d_n represent death.

On integration, we obtain;

$$N(t) = \frac{\Omega}{\mu} + \left(N_0 - \frac{\Omega}{\mu} \right) e^{-\mu t}$$

Now, $\lim_{t \to +\infty} N(t) = \frac{\Omega}{\mu}$ showing that solutions with positive initial data remain positive for all $t \geq 0$ and are bounded Thus we study the system (2.2)-(2.3) in the feasible region

$$\Omega = \left\{ S(t), E(t), Q(t),\ I_u(t), I_n(t), R(t) \in \mathbb{R}^6_+ : 0 \leq N(t) \leq \frac{\Omega}{\mu} \right\} \quad (3.2)$$

Hence the system (2.2)-(2.3) is epidemiologically well posed.

The Disease Free Equilibrium point (DFE) is determined to be

$$DFE = \left(\frac{\Omega}{\mu}, 0, 0, 0, 0, 0 \right). \quad (3.3)$$

We use the next generation matrix to find the basic reproduction number of the model (2.2)-(2.3).

The infection compartments in the model are $E, \mathrm{Q}, \mathrm{I}_u, \mathrm{I}_n$. We wish to determine the basic reproduction number R_o which provides the quantification of the disease risk.

The Jacobian matrices for infection matrix F and transition matrix V at the DFE are:

$$F_{DFE} = \begin{pmatrix} \beta S & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \quad V_{DFE} = \begin{pmatrix} A & 0 & 0 & 0 \\ -\eta & B & 0 & 0 \\ -\beta_1 & -\beta_2 & C & 0 \\ -\delta_1 & -\delta_2 & 0 & D \end{pmatrix}$$

$$V_{DFE}^{-1} = \begin{pmatrix} \frac{1}{A} & 0 & 0 & 0 \\ \frac{\eta}{AB} & \frac{1}{B} & 0 & 0 \\ \frac{\beta_2}{AC}\left(\frac{\eta}{B}+\frac{\beta_1}{\beta_2}\right) & \frac{\beta_2}{BC} & \frac{1}{C} & 0 \\ \frac{\delta_2}{AD}\left(\frac{\eta}{B}+\frac{\delta_1}{\delta_2}\right) & \frac{\delta_2}{BD} & 0 & \frac{1}{D} \end{pmatrix}$$

From which we determine the R_o number as the spectral radius of the next generation matrix:

$$R_o = \rho\left(FV^{-1}\right) = \frac{\beta S}{A} = \frac{\beta\Omega}{\mu\left(\mu+\eta+\delta_1+\beta_1\right)}$$

Where $A = \mu+\eta+\delta_1+\beta_1$, $B = \mu+\gamma_3+\delta_2+\beta_2$, $C = \gamma_1+d_u$, $D = \gamma_2+d_n$ and FV^{-1} is the next generation matrix of the model that comprises of $E, \mathrm{Q}, \mathrm{I}_u, \mathrm{I}_n$ as the unknowns.

The deaths d_u, d_n in compartments I_u and I_n are assumed to be purely due to COVID-19.

The model (2.2)-(2.3) has two equilibrium states namely: a disease free equilibrium (DFE) with coordinates $\left(\frac{\Omega}{\mu}, 0, 0, 0, 0, 0\right)$ and an endemic equilibrium (EE) $\left(S^*, \mathrm{E}^*, \mathrm{Q}^*, \mathrm{I}_u^*, \mathrm{I}_n^*, \mathrm{R}^*\right)$

4. Stability of the equilibrium states

Theorem 1

The DFE is locally asymptotically stable if R_o <1 and unstable if $R_0 > 1$.

Proof:

We only need to show that the Jacobian matrix of the system (2.2)-(2.3) has all the eigenvalues real and negative at DFE point.

The Jacobian matrix at DFE point of the system (2.2)-(2.3) is

$$J_{DFE} = \begin{pmatrix} -\mu & -\beta S & 0 & 0 & 0 & 0 \\ 0 & \beta S - A & 0 & 0 & 0 & 0 \\ 0 & \eta & -B & 0 & 0 & 0 \\ 0 & \beta_1 & \beta_2 & -C & 0 & 0 \\ 0 & \delta_1 & \delta_2 & 0 & -D & 0 \\ 0 & 0 & \gamma_3 & \gamma_2 & \gamma_2 & -\mu \end{pmatrix} \quad 4.1$$

The characteristic equation of J_{DFE} corresponding to the eigenvalue λ is the determinant

$$\mathrm{Det}\left(J_{DFE}-I\lambda\right)=\begin{vmatrix}-\mu-\lambda & -\beta S & 0 & 0 & 0 & 0\\ 0 & \beta S-A-\lambda & 0 & 0 & 0 & 0\\ 0 & \eta & -B-\lambda & 0 & 0 & 0\\ 0 & \beta_1 & \beta_2 & -C-\lambda & 0 & 0\\ 0 & \delta_1 & \delta_2 & 0 & -D-\lambda & 0\\ 0 & 0 & \gamma_3 & \gamma_2 & \gamma_2 & -\mu-\lambda\end{vmatrix}=0$$

i.e.

$$\left(\mu+\lambda\right)^2\left(B+\lambda\right)\left(C+\lambda\right)\left(D+\lambda\right)\left(1-R_o+\lambda\right)=0. \qquad 4.2$$

Thus

$\lambda_{1,2}=-\mu<0,\ \lambda_3=-B<0,\ \lambda_4=-C<0,\ \lambda_5=-D<0,\ \lambda_6=R_o-1<0$ only if $R_o<1$, thus the claim.

Theorem 2

The endemic equilibrium point for the model (2.2)-(2.3) exists and it is locally asymptotically stable if $R_0>1$.

Proof

We set:

$$\begin{aligned}\Omega-\mu S-\beta SE &= 0\\ \beta SE-AE &= 0\\ \eta E-BQ &= 0\\ \beta_1 E-\beta_2 Q-CI_u &= 0\\ \delta_1 E+\delta_2 Q-DI_n &= 0\\ \gamma_3 Q+\gamma_1 I_u+\gamma_2 I_n+-\mu R &= 0\end{aligned} \qquad 4.3$$

Solving, we get

$$S^*=\frac{A}{\beta},\ E^*=\frac{\mu}{\beta}\left(R_o-1\right),\ Q^*=\frac{\mu\eta}{\beta B}\left(R_o-1\right),\ I_u^*=\frac{\beta_1\Omega}{AC}+\frac{\mu\eta\beta_2}{\beta BC}\left(R_o-1\right)$$

$$I_n^*=\frac{\delta_1\Omega}{AD}+\frac{\mu\eta\delta_2}{\beta BD}\left(R_o-1\right),\ R^*=\frac{\gamma_1\beta_1\Omega}{\mu AC}+\left(\frac{\gamma_1\beta_1\eta}{\beta BC}+\frac{\gamma_2\delta_2}{D}\left(\Omega+\frac{\eta}{\beta B}\right)+\frac{\gamma_3\eta}{\beta}\right)\left(R_o-1\right)$$

Hence the endemic equilibrium point exists and is unique given by $\left(S^*,\mathrm{E}^*,\mathrm{Q}^*,\mathrm{I}_u^*,\mathrm{I}_n^*,\mathrm{R}^*\right)$.

For the EE point to be asymptotically stable, we only need to show that the eigenvalues of the Jacobian matrix of the model (2.2) – (2.3) are all real and negative.

Hence

$$J_{EE}=\begin{pmatrix}-\mu R_o & -A & 0 & 0 & 0 & 0\\ \mu\left(R_o-1\right) & 0 & 0 & 0 & 0 & 0\\ 0 & \eta & -B & 0 & 0 & 0\\ 0 & \beta_1 & \beta_2 & -C & 0 & 0\\ 0 & \delta_1 & \delta_2 & 0 & -D & 0\\ 0 & 0 & \gamma_3 & \gamma_1 & \gamma_2 & -\mu\end{pmatrix} \qquad 4.4$$

The characteristic polynomial corresponding to the eigenvalue λ is:

$$\begin{vmatrix} -\mu R_o - \lambda & -A & 0 & 0 & 0 & 0 \\ \mu(R_o - 1) & 0 - \lambda & 0 & 0 & 0 & 0 \\ 0 & \eta & -B - \lambda & 0 & 0 & 0 \\ 0 & \beta_1 & \beta_2 & -C - \lambda & 0 & 0 \\ 0 & \delta_1 & \delta_2 & 0 & -D - \lambda & 0 \\ 0 & 0 & \gamma_3 & \gamma_1 & \gamma_2 & -\mu - \lambda \end{vmatrix} = 0$$

Solving

$$(B+\lambda)(C+\lambda)(D+\lambda)(\mu+\lambda)\left(\lambda^2 + \lambda\mu R_o + A\mu(R_o - 1)\right) = 0 \quad 4.5$$

we obtain the first four roots as
$\lambda_1 = -\mu < 0,\ \lambda_2 = -B < 0,\ \lambda_3 = -C < 0,\ \lambda_4 = -D < 0$ and for the quadratic part $\lambda^2 + \lambda\mu R_o + A\mu(R_o - 1) = 0$ all coefficients positive, and hence the corresponding roots must be negative. This brings us to the conclusion that EE point is locally asymptotically stable.

Theorem 3

The endemic equilibrium point $(S^*, E,^* Q^*, I^*)$ of the model (2.2)-(2.3) is globally asymptotically stable if $R_o > 1$

Proof

We use the Lyapunov function due to [1] of the form $V(t) = t - 1 - \ln t$. We only need to show that $\dot{V}(t) \le 0$ i.e. is negative definite for all $S, E, Q, I > 0$ where equality holds only at the equilibrium point $(S^*, E,^* Q^*, I^*)$.

Without lose of generality, we temporarily dispense with the last equation involving R and let $I = I_u + I_n$ so that the model (2.2)-(2.3) becomes:

$$\begin{aligned} \frac{dS}{dt} &= \Omega - \beta SE - \mu s \\ \frac{dE}{dt} &= \beta SE - AE \\ \frac{dQ}{dt} &= \eta E - BQ \\ \frac{dI}{dt} &= aE + bQ - cI \end{aligned} \quad 4.6$$

Where $a = \delta_1 + \beta_1,\ b = \delta_2 + \beta_2,\ c = \gamma_1 + \gamma_2 + d_u + d_n$

The endemic equilibrium point is at

$$S^* = \frac{A}{\beta},\ E^* = \frac{\mu}{\beta}(R_o - 1),\ Q^* = \frac{\eta\mu}{\beta B}(R_o - 1),\ I^* = \frac{\mu}{\beta B}\left\{B(\beta_1 + \delta_1) + \eta(\beta_2 + \delta_2)\right\}(R_o - 1)$$

Thus for the bilinear incidence βSE, we let

$$V_{EE}(S, E, Q, I) = (S - S^* \ln S) + (E - E^* \ln E) + (Q - Q^* \ln Q) + (I - I^* \ln I) \quad 4.7$$

Then

$$\dot{V} = \left(1 - \frac{S^*}{S}\right)\dot{S} + \left(1 - \frac{E^*}{E}\right)\dot{E} + \left(1 - \frac{Q^*}{Q}\right)\dot{Q} + \left(1 - \frac{I^*}{I}\right)\dot{I}$$

Or

$$\dot{V}(t)=\mu S^*\left(2-\frac{S^*}{S}-\frac{S}{S^*}\right)+\beta S^*E^*\left(1-\frac{S^*}{S}-\frac{S}{S^*}\frac{E}{E^*}+\frac{E}{E^*}\right)+\beta SE\left(1-\frac{S^*}{S}-\frac{E^*}{E}+\frac{E^*}{E}\frac{S^*}{S}\right)$$

$$+\eta E\left(1-\frac{Q^*}{Q}-\frac{E^*}{E}.\frac{Q}{Q^*}+\frac{E^*}{E}\right)+R\left(1-\frac{I^*}{I}-\frac{I}{I^*}\frac{R^*}{R}+\frac{R^*}{R}\right) \text{ Where } R=aE+bQ,\ R^*=aE^*+bQ^*$$

Since the arithmetical mean is greater than or equal to the geometrical mean, we

$$1-\frac{S^*}{S}-\frac{S}{S^*}\frac{E}{E^*}+\frac{E}{E^*}\le 0 \text{ for } S,S^*,E,E^*>0 \text{ and}$$

$$1-\frac{S^*}{S}-\frac{S}{S^*}\frac{E}{E^*}+\frac{E}{E^*}=0 \text{ if } S=S^*=E=E^*=1.$$

Similar argument is done to the rest and hence $\dot{V}(t)\le 0$ for $S,S^*,E,E^*,Q,Q^*,I,I^*>0$ and $\dot{V}(t)=0$ if and only if $S=S^*=E=E^*=Q=Q^*=I=I^*=1$, the maximum invariant set of the model (4.6) on the set $\left\{S,E,Q,I:V(\dot{t})=0\right\}$ is $(1,1,1,1)$. By LaSalle Invariance Principle [7], the endemic equilibrium point $\left(S^*,E,^*Q^*,I^*\right)$ is globally asymptotically stable if $R_o>1$.

5. Numerical Results

We have calibrated our modified SEIR model system (2.2) for the novel corona virus diseases to the daily newly infected cases for the Republic of Kenya.

We used ODE45 in MATLAB to estimate the parameter values of best fit for the modified SEIR model.

The parameter values obtained from data-fit for Kenya were used to compute the reproduction number,

$$R_o=5.434$$

Which shows that the corona virus disease will not be eliminated from Kenya if preventive measures like vaccination, wearing of masks and social distancing are not practiced.

5.1 Application of the model to COVID-19 data in Kenya

The data used was collected from May 10th to June 30th 2021 Coronavirus-Kenya: COVID-19 update (http://www.africanews.com). Therefore our time zero in the figures below is May 10th 2021.

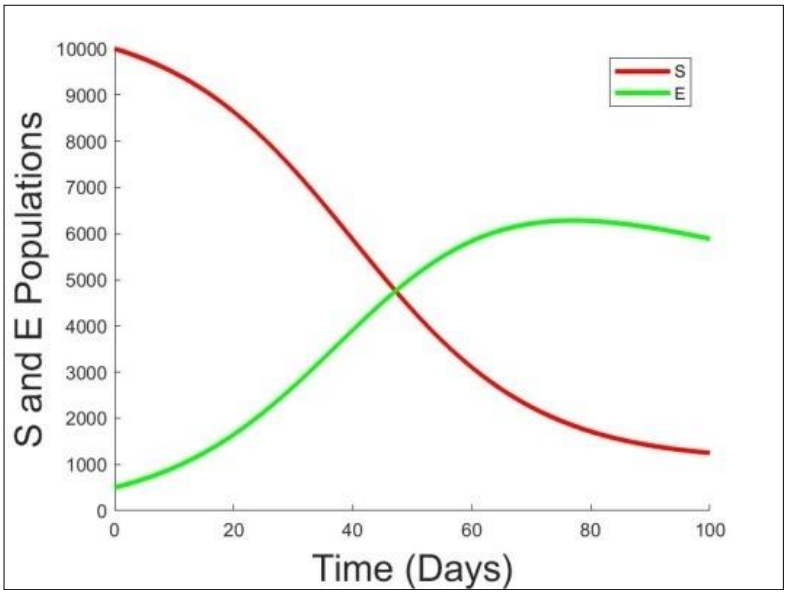

Fig 2: shows how the susceptible and the exposed populations relate over the specific time period.

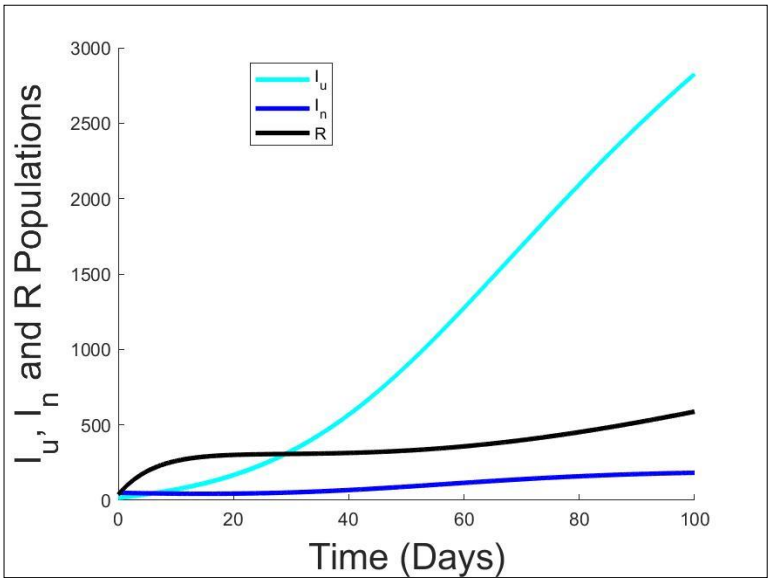

Fig 3: above shows that individuals living with underlying medical conditions have very high rate of infection by COVID-19 once they get exposed, and hence the fatality rate for this group due to the infection is high compared to that of those infected with COVID-19 but do not have underlying medical conditions.

The remedy could be for the Kenyan Government to carry out mass tests awareness for underlying medical conditions and to do vaccination of all these individuals to induce resistance against this pneumonia.

6. Discussion

We have proposed a mathematical model to investigate the effect of novel coronavirus pandemic to the people above 58 years old and those leaving with underlying medical conditions in Kenya. We used the data from the ministry of Health of Kenya to carry out the analysis.

We have shown that the local asymptotic stability of the disease free and endemic equilibria when $R_o < 1$ and $R_o > 1$ respectively. Also, the global asymptotic stability for endemic equilibrium occurs when $R_o > 1$.

Through data fitting, we obtain $R_o = 5.434$. The numerical analysis and simulation results show that individuals living with underlying medical conditions have very high rate of infection by COVID-19 once they are exposed.

The high R_o number shows that the disease would persist in Kenya and become endemic. Among other intervention strategis, vaccination has to be done in mass to eradicate this disease.

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