MODELLING THE IMPACT OF AWARENESS PROGRAM ON THE TRANSMISSION DYNAMICS OF COVID-19

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Abstract: Corona virus is an infectious disease that became a pandemic in 2020 and has killed many people around the world. This study modifies the work of mugisha *et al*., 2021 by introducing "awareness factor" to quantify the influence of the awareness programs in the dynamics of the disease. The existence and stability of the disease free equilibrium state of the modified model is also established and is found to be locally asymptotically stable. The next generation method is used to compute the effective reproduction number. Our results demonstrate that well-timed and adequately implemented awareness campaigns can lead to a significant reduction in reproduction number and effectively curtail the spread of the disease.

Key words: awareness program, covid-19

Introduction

Corona-virus disease is an infectious disease caused by the SARS-CoV-2 virus. The virus is known to cause illness ranging from the common cold to more severe disease such as Middle East Respiratory Syndrome (MERS) and severe acute respiratory syndrome (SARS).

There is currently no cure for COVID-19 but medications have been approved to treat infected people. Two pills taken by mouth can treat COVID-19 in some people. One pill molnupiravir, is produced by Merck. The other, paxlovid (nirmatrelvir and ritonavir tablets, co-packaged for oral use) is made by Pfizer. Both medications were granted an emergency use authorization (EUA) by U.S. Food and Drug Administration. (FDA) in December 2021.

COVID-19 continues to spread around the world and can be found in both vaccinated and unvaccinated individuals. COVID-19 control measures include vaccination, screening of blood and treatment and public awareness. Increased public awareness also helps to find new cases of the disease early (Seung*et al*., 2021)

Public awareness is critically important in preventing the spread of the infectious disease (Guo*et al*., 2015). It is possible to significantly reduce the spread of infectious diseases by pre-emptively disseminating knowledge about how widely infectious diseases are spreading and how severe the outbreaks will be and educating the public of precautionary measures (funk *et al*., 2009; Wang *et al*., 2019).

Method

The Existing Model

Mugisha *et al*. (2021) presented a mathematical model for COVID-19 transmission dynamics. We state the assumptions, parameter and the equation of the existing model below.

Assumptions of the Existing Model By Mugisha et al. (2021)

The following are assumptions of the existing model by Mugisha *et al*. (2021)

a. For the relatively short-term dynamics, an epidemic model in which the vital dynamics (i.e., birth and natural mortality) is opted for.
b. Upon infection, some latently infected individuals can be identified (e.g. through contact tracing) subsequently individually isolated under high bio-security conditions leading to their eventual upon testing positive (i.e. completing their latent period), thereby denying them a chance of ever infecting other individuals in the community, while others may remain in the community and become infectious up until when they are identified and hospitalized.
c. In relation to the disease transmission potential, like the hospitalized individuals, individuals in institutional quarantine such as the traced contacts that later turn out to be latently infected at the moment of their quarantine are assumed not to participate in disease transmission while in supervised quarantine centers.
d. Asymptomatically infected individuals are assumed to be less likely to succumb to the disease but are still being debated globally, with initial studies indicating cases of lung damage development in such individuals.
e. On disease recovery, the model parameter (τ) can varied to capture situations of varying duration of disease-induced immunity, ranging from no immunity to temporary and to life-long immunity at simulation level.
f. The arriving individuals (i.e. truck drivers, returnees and refugees etc.) comprise of susceptible, latently infected and asymptomatic infectious individuals while those exiting are susceptible and perhaps (later) the recovered.
g. The hospitalized individuals have potential of spreading the disease. (i.e. hospital-acquired infections) albeit at a lower rate than the free-leaving infectious individuals.

Variables and Parameters of the Existing Model

The existing model has the following variables and parameters:

a(t) percentage of arrivals that are asymptomatic.

e(t) percentage of arrivals that are latently infected.

λ Per capita recruitment rate.

β Disease transmission rate.

b Percentage of susceptible individuals that is available.

g Infectivity factor for hospitalized individuals.

q Infectivity factor among asymptomatic individuals.

α Recovery rate of hospitalized individuals.

τ Waning rate of disease-induced immunity.

ρ Progression rate from latent stage to infectious stage.

r Percentage of latently infected individuals in community that becomes asymptotical.

σ_s Disease induced mortality rate in symptomatic non-hospitalized individuals.

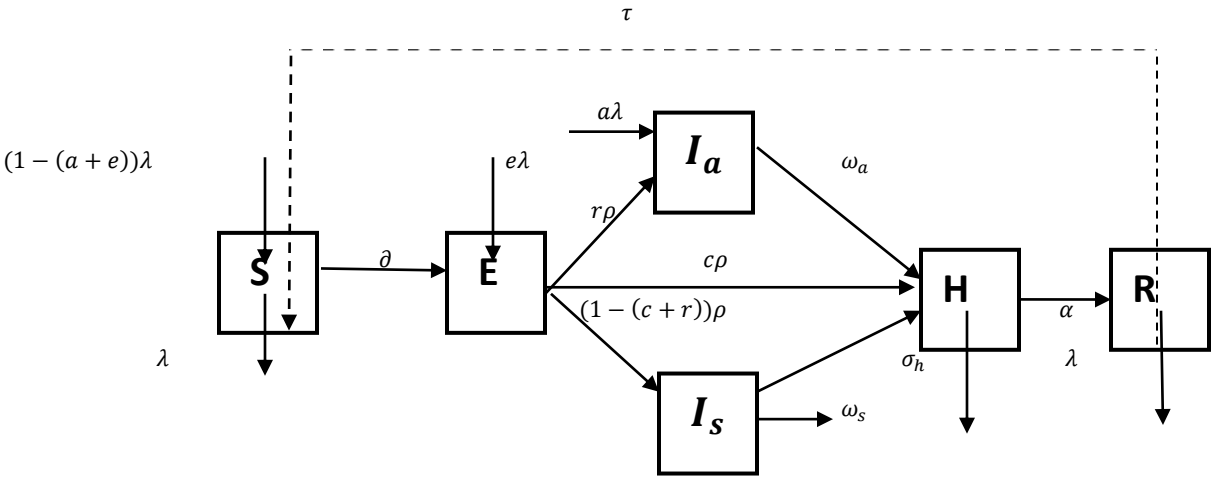
σ_h Disease induced mortality rate in hospitalized individuals.

ω_a Hospitalization rate of asymptomatic infectious

ω_s Hospitalization rate of asymptomatic infectious

c Percentage of latently infected individuals that is traced and isolated immediately.

The following is the flow diagram for existing model



The Existing Model Equation

With the above assumptions, parameters and flow diagram by Mugisha*et al*, (2021), the following model equations where derived.

Let $\partial = \frac{\beta bS(qI_a+I_s+gH)}{N}$

$$\frac{dS}{dt} = (1-(a+e))\lambda N - \frac{\beta bS(qI_a + I_s + gH)}{N} + \tau R - \lambda S$$

$$\frac{dE}{dt} = e\lambda N + \frac{\beta bS(qI_a + I_s + gH)}{N} - \rho E$$

$$\frac{dI_a}{dt} = a\lambda N + r\rho E - \omega_a I_a \qquad (1)$$

$$\frac{dI_s}{dt} = (1-(c+r))\rho E - \sigma_s I_s - \omega_s I_s$$

$$\frac{dH}{dt} = c\rho E + \omega_a I_a + \omega_s I_s - \sigma_h H - \alpha H$$

$$\frac{dR}{dt} = \alpha H - \tau R - \lambda R$$

Where $N(t) = S(t) + E(t) + I_a(t) + I_s(t) + H(t) + R(t)$.

In equation (5.1), the term $(1-(a+e))\lambda N$represents the number of arriving susceptible individuals per day, $\frac{\beta bS(qI_a+I_s+gH)}{N}$represents the number of susceptible individuals that becomes latently.

The Modified Model

An infectious disease may spread in a complex manner when having different interacting variables. Mathematically models are among the tools used to analyse and predict the disease spread and its severity. To have a deeper insight on the impact of awareness programs on the transmission of COVID-19, this study introduces a new parameter called

the individuals that are aware (Θ) into the existing model. The new parameters are shown in the table below.

Table 1: Modified Model Parameters and Descriptions

Parameters	**Descriptions**
a(t)	percentage of arrivals that are asymptomatic
e(t)	percentage of arrivals that are latently infected
λ	Per capita recruitment rate
θ	Percentage of aware individuals in the susceptible class
β	Disease transmission rate
B	Percentage of susceptible individuals that is available.
G	Infectivity factor for hospitalized individuals
Q	Infectivity factor among asymptomatic individuals
α	Recovery rate of hospitalized individuals
τ	Waning rate of disease-induced immunity
ρ	Progression rate from latent stage to infectious stage
R	Percentage of latently infected individuals in community that becomes asymptomatic
δ_s	Disease induced morality rate for symptomatic non-hospitalized individuals
δ_H	Disease induced morality rate for hospitalized individuals
δ_a	Disease induced morality rate for asymptomatic non-hospitalized individuals
λ_s	Natural death of symptomatic individuals per day
λ_a	Natural death of asymptomatic individuals per day
λ_H	Natural death of hospitalized individuals per day
ω_a	Hospitalization rate of asymptomatic infectious
ω_s	Hospitalization rate of asymptomatic infectious
c	Percentage of latently infected individuals that is traced and isolated immediately

Model Assumptions

The following are the assumptions of the modified COVID-19 model (1):

i. The members of the population are mixed homogeneously
ii. Transmission is from human-to-human
iii. Individuals that are aware use personal preventive measure like: wearing masks, sanitation, hygiene and physical distancing.
iv. The awareness program reduce the rate of transmission and eradicate the disease when it's full, i.e. $\theta = 1$
v. Asymptomatically infectious individuals are assumed to be less likely to transmit the disease since they cannot cough or sneeze asymptomatic but this is still being debuted globally (Mugishal*et al*., 2021)
vi. The hospitalized individuals have potential of spreading the disease (i.e. hospital-acquired infections) at a lower rate than free-leaving infectious individual.

Model flow diagram of modified model equations

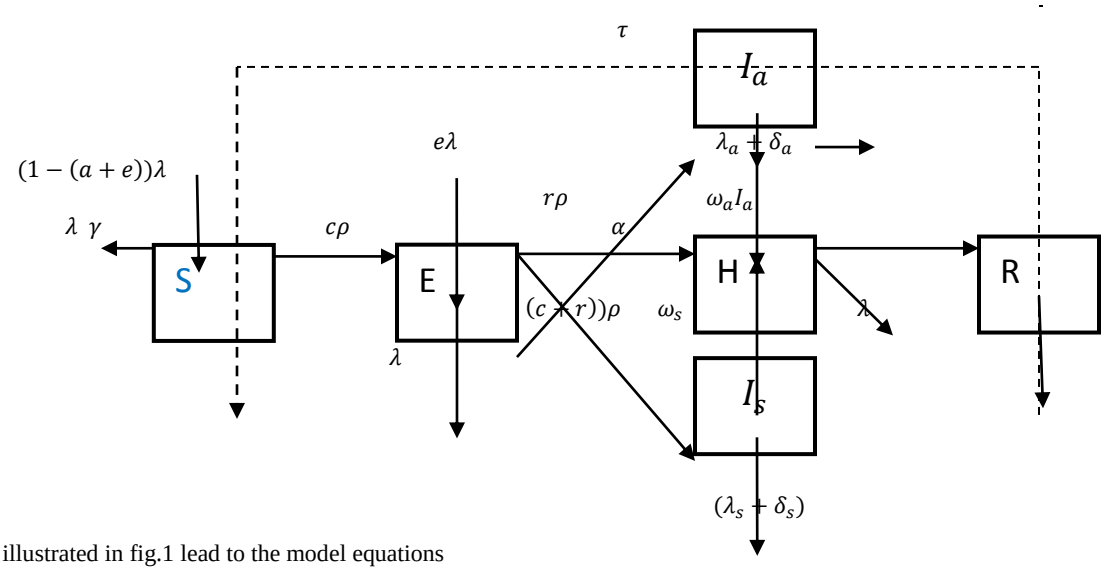


Figure 1

The flow diagram illustrated in fig.1 lead to the model equations

Let $\gamma = \frac{(1-\Theta)\beta bS(qI_a+I_s+gH)}{N}$

$$\frac{dS}{dt} = \big(1-(a+e)\big)\lambda N - \frac{(1-\Theta)\beta bS(qI_a+I_s+gH)}{N} + \tau R - \lambda S$$

$$\frac{dE}{dt} = e\lambda N + \frac{(1-\Theta)\beta bS(qI_a+I_s+gH)}{N} - \lambda E - \big(1-(c+r)\big)\rho E$$

$$\frac{dI_a}{dt} = a\lambda N + r\rho E - \omega_a I_a - (\lambda_a + \delta_a)I_a$$

$\frac{dI_s}{dt} = \big(1-(c+r)\big)\rho E - \omega_s I_s - (\lambda_s + \delta_s)I_s$ (2) $\frac{dH}{dt} = c\rho E + \omega_a I_a + \omega_s I_s - (\lambda_H + \delta_H)H - \alpha H$

$$\frac{dR}{dt} = \alpha H - \tau R - \lambda R$$

For the disease free equilibrium, we know that

$$\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI_a}{dt} = \frac{dI_s}{dt} = \frac{dH}{dt} = \frac{dR}{dt} = 0$$

Form equation (2) (the susceptible class)

$$\big(1-(a+e)\big)\lambda N - \lambda S = 0$$

$$S = \frac{\big(1-(a+e)\big)\lambda N}{\lambda}$$

$S = 1-(a+e)N(2.1)$

Therefore, the disease free equilibrium will be;

$. E_0 = (S, E, I_a, I_s, H, R) = \ \big(\big(1-(a+e)\big)N, 0, 0, 0, 0, 0\big)$

The Effective Reproduction Number, R_e

The effective reproduction number R_e measures the average number of new infections generated by a single infected person during his or her infectious period in a population that is fully susceptible Diekmann*et al*(1990). One can easily predict if an infection will spread in exponential progression, die off after some time or remain constant with no further spread judging from the value of the reproduction number. When $R_e < 1$, the disease will die out because every infected person will transmits the disease to less than one person in the transmittable period. When $R_e = 1$, the disease will become endemic and will stay with each

infected person transmitting to one new person. When $R_e > 1$, a disease will spread and the infected people will grow exponentially which will in the end lead to a pandemic. Using next generation method, the Effective Reproduction Number (R_e) is given as $R_e = \rho(FV^{-1})$ where ρ is the spectral radius.

Given the matrices F and V below,

$$F = \begin{bmatrix} 0 & (1-\theta)\cdot\beta\cdot q & (1-\theta)\cdot\beta\cdot b & (1-\theta)\cdot\beta\cdot b\cdot g \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, V = \begin{bmatrix} \lambda + k_1 & 0 & 0 & 0 \\ -r\rho & k_2 & 0 & 0 \\ -k_1 & 0 & k_3 & 0 \\ -c\rho & -\omega_a & -\omega_s & k_4 \end{bmatrix}$$

From *V*above ,

$$V^{-1} = \begin{bmatrix} \frac{1}{\lambda + k_1} & 0 & 0 & 0 \\ \frac{r\rho}{(\lambda + k_1)k_2} & \frac{1}{k_2} & 0 & 0 \\ \frac{k_1}{(\lambda + k_1)k_3} & 0 & \frac{1}{k_3} & 0 \\ \frac{c k_2 k_3 \rho + k_3 r\rho\,\omega_a + k_1 k_2 \omega_a}{(\lambda + k_1)k_2 k_3 k_4} & \frac{\omega_a}{k_2 k_4} & \frac{\omega_s}{k_3 k_4} & \frac{1}{k_4} \end{bmatrix}$$

$$\rho(FV^{-1}) = \begin{bmatrix} 0 & (1-\theta)\beta q & (1-\theta)\beta b & (1-\theta)\beta bg \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} * \begin{bmatrix} \frac{1}{\lambda + k_1} & 0 & 0 & 0 \\ \frac{r\rho}{(\lambda + k_1)k_2} & \frac{1}{k_2} & 0 & 0 \\ \frac{k_1}{(\lambda + k_1)k_3} & 0 & \frac{1}{k_3} & 0 \\ \frac{c k_2 k_3 \rho + k_3 r\rho\,\omega_a + k_1 k_2 \omega_a}{(\lambda + k_1)k_2 k_3 k_4} & \frac{\omega_a}{k_2 k_4} & \frac{\omega_s}{k_3 k_4} & \frac{1}{k_4} \end{bmatrix}$$

$$\left[\left[-\frac{\beta(b(k_3cg\rho+k_1(g\,\omega_s+k_4))k_2+k_3r\rho(bg\,\omega_a+k_4q))(-1+\theta)}{(\lambda+k_1)k_2k_3k_4},\right.\right.$$
$$\left.-\frac{(-1+\theta)\beta(bg\,\omega_a+k_4q)}{k_2k_4},-\frac{(-1+\theta)\beta b(g\,\omega_s+k_4)}{k_3k_4},\frac{(1-\theta)\beta bg}{k_4}\right].$$
$$[0,0,0,0],$$
$$[0,0,0,0],$$
$$\left.[0,0,0,0]\right]$$

Solving for the eigen values we have

$$\begin{bmatrix}0\\0\\0\\-\frac{\beta(b(k_3cg\rho+k_1(g\,\omega_s+k_4))k_2+k_3r\rho(bg\,\omega_a+k_4q))(-1+\theta)}{(\lambda+k_1)k_2k_3k_4}\end{bmatrix}$$

Therefore, the desired reproduction number will be;

$$R_e=\frac{(b(k_3cg\rho+k_1(g\,\omega_s+k_4))k_2+r\rho k_3(bg\,\omega_a+k_4q))(-1+\theta)\beta}{(-\lambda-k_1)k_2k_3k_4}$$

Where

$k_1=(1-c-r)\rho$

$k_2=\omega_a+\lambda_a+\delta_a$

$k_3=\omega_s+\lambda_s+\delta_s$

$k_4=+\lambda_H+\delta_H+\alpha$

Local Stability of Disease Free Equilibrium

Theorem 1: The disease free equilibrium of the modified model equation is locally stable if $R_e<1$ and unstable if $R_e>1$.

Proof: The Jacobian matrix of the system modified model at disease free equilibrium point E_0 is obtained as follow.

$$J(E_0)=\begin{bmatrix}-\lambda & 0 & (1-\theta)\beta bq & (1-\theta)\beta b & (1-\theta)\beta bg & \tau\\ 0 & -\lambda-(1-c-r)\rho & (1-\theta)\beta bq & (1-\theta)\beta b & -(1-\theta)g & 0\\ 0 & r\rho & -\omega_a-\lambda_a-\delta_a & 0 & 0 & 0\\ 0 & (1-c-r)\rho & 0 & -\omega_s-\lambda_s-\delta_s & 0 & 0\\ 0 & \rho c & \omega_a & \omega_s & -\lambda_H-\delta_H-\alpha & 0\\ 0 & 0 & 0 & 0 & \alpha & -\lambda-\tau\end{bmatrix}$$

We need to show that all the eigenvalues of $J(E_0)$ are negative. As the first and fifth columns contain only the diagonal terms which form the two negative eigenvalues, $-\mu h$ and $-\mu m$, the other five eigenvalues can be obtained from the sub-matrix, $J_1(E_0)$, formed by excluding the first and fifth rows and columns of $J(E_0)$. Hence we have

$$J=\begin{bmatrix} -\lambda & 0 & (1-\theta)\beta bq & (1-\theta)\beta b & (1-\theta)\beta bg & \tau \\ 0 & -\lambda-k_1 & (1-\theta)\beta bq & (1-\theta)\beta b & -(1-\theta)g & 0 \\ 0 & r\rho & -k_2 & 0 & 0 & 0 \\ 0 & k_1 & 0 & -k_3 & 0 & 0 \\ 0 & \rho c & \omega_a & \omega_s & -k_4 & 0 \\ 0 & 0 & 0 & 0 & \alpha & -k_5 \end{bmatrix}$$

Since the first and six column of the equation (2) have only the diagonal terms that form the first two negative Eigen values that is $-\lambda$ and k_5, hence we have;

$$J_1(E_0)=\begin{bmatrix} -\lambda-k_1 & (1-\theta)\beta bq & (1-\theta)\beta b & -(1-\theta)g \\ r\rho & -k_2 & 0 & 0 \\ k_1 & 0 & -k_3 & 0 \\ \rho c & \omega_a & \omega_a & -k_4 \end{bmatrix}=0$$

The eigenvalues of the matrix $J1(E_0)$ are the roots of the characteristic

$$\lambda^4+(k_4+k_3+k_2+\lambda_i+k_1)\lambda^3+((+k_3+k_4+\lambda_i+k_1)k_2+(k_4+\lambda_i+k_1)k_3+(b\beta\theta-b\beta+k_4)k_1$$
$$+k_4\lambda_i+\rho(-1+\theta)(b\beta qr-cg))\lambda^2+(((k_4+\lambda_i+k_1)k_3+(b\beta\theta-b\beta+k_4)k_1+k_4\lambda_i-cg\rho(-1+\theta)k_2$$
$$+(k_1k_4+k_4\lambda_i+\rho(-1+\theta)(b\beta qr-cg))k_3+((b\beta k_4-g\omega_s)k_1+r\rho(b\beta k_4q-g\omega_a))(-1+\theta))\lambda+$$
$$((k_1k_4+k_4\lambda_i-cg\rho(-1+\theta)k_3+k_1(-1+\theta)(b\beta k_4-g\omega_s))k_2+k_3r\rho(-1+\theta)(b\beta k_4q-g\omega_a)$$

$$A_4\lambda^4+A_3\lambda^3+A_2\lambda^2+A_1\lambda+A_0=0$$

Where

$$A_4=1$$
$$A_3=(k_4+k_3+k_2+\lambda_i+k_1)$$
$$A_2=((+k_3+k_4+\lambda_i+k_1)k_2+(k_4+\lambda_i+k_1)k_3+(b\beta\theta-b\beta+k_4)k_1$$
$$+k_4\lambda_i+\rho(-1+\theta)(b\beta qr-cg))$$

$$A_1=(((k_4+\lambda_i+k_1)k_3+(b\beta\theta-b\beta+k_4)k_1+k_4\lambda_i-cg\rho(-1+\theta)k_2$$
$$+(k_1k_4+k_4\lambda_i+\rho(-1+\theta)(b\beta qr-cg))k_3+((b\beta k_4-g\omega_s)k_1+r\rho(b\beta k_4q-g\omega_a))(-1+\theta))$$

$$A_0=((k_1k_4+k_4\lambda_i-cg\rho(-1+\theta)k_3+k_1(-1+\theta)(b\beta k_4-g\omega_s))k_2+k_3r\rho(-1+\theta)(b\beta k_4q-g\omega_a)$$

We employ the Routh-Hurwitz criterion, which states that all roots of the polynomial have negative real parts if and only if the coefficients A_i (i=0,1,2,3) are positive and matrices $H_i > 0$, for(i = 0, 1, 2, 3, 4). Clearly, $A_4>0, A_3>0, A_2>0, A_1>0$ and $A_0>0$ if $R_e<1$.

Therefore, the reproduction number is less than one which signifies that the disease free equilibrium is locally asymptotically stable. Also, the Routh-Hurwitz matrix H_i is all positive which are given below;

$$H_1 = A_3>0\ , H_2 = \begin{bmatrix} A_3 & A_4 \\ A_1 & A_2 \end{bmatrix} > 0\ , H_3 = \begin{bmatrix} A_3 & A_4 & 0 \\ A_3 & A_3 & A_3 \\ 0 & A_0 & A_1 \end{bmatrix} > 0 \text{ and } H_3 = \begin{bmatrix} A_3 & A_4 & 0 & 0 \\ A_1 & A_2 & A_3 & A_4 \\ 0 & A_0 & A_1 & A_2 \\ 0 & 0 & 0 & A_0 \end{bmatrix} > 0$$

Therefore, all the eigenvalues of the Jacobian matrix J(E0) have negative real parts when $R_e<1$ and the disease-free equilibrium point is locally asymptotically stable.

Sensitivity Analysis

The sensitivity analysis is used to investigate or determine how sensitive the threshold quantity Effective Reproduction number R_e is with respect to its parameters, through this investigation, we will know which of the parameter causes highest reduction in Effective Reproduction Number R_e and also parameters that have high impact on R_e. These should be targeted by intervention strategies so as to find the most effective control of the disease. The analysis tells us how crucial and important each parameter is to disease transmission.

The normalized forward sensitivity index of the reproduction number with respect to natural recovery and the incorporated vector reduction will be computed below.

Definition: supposing a variable 'P' which is differentiable depends on a parameter 'w', then, normalized forward sensitivity index of 'p' with respect to 'w' is denoted by Xp, which is defined as

$$Xp = \frac{p}{w}\frac{\partial w}{\partial p}$$

As we have explicit for R_e, we derive an analytical expression for the sensitivity of R_e as

$$X_w^{R_e} = \frac{d\,R_e}{dW}\frac{W}{R_e}$$

For each parameter involved in R_C, the results of the sensitivity indicesof R_e are as shown in the table below;

Table 1: Numerical values of sensitivity Analysis of the parameters

Parameter	Descriptions	Sensitivity Values
R_0	Reproduction number	0.1770189273
Θ	Percentage of aware individuals in the susceptible class	1.000000000
ρ	Progression rate from latent stage to infectious stage	−0.002355539430
g	Infectivity factor for hospitalize individuals	0.000006985
ω_s	Hospitalization rate of symptomatic infectious	0.0008695024863
λ_s	Natural death of symptomatic individuals per day	−0.01869475738
δ_s	Disease induced mortality rate for symptomatic non hospitalized	−0.8634607790

	individuals	
c	Percentage of latently infected individuals that is traced and isolated immediately	$1.975810560\,10^{-7}$
β	Disease transmission rate	1
r	Percentage of latently infected individuals in community that become asymptomatic	−0.002355737013
α	Recovery rate of hospitalized individuals	$-4.301119581\,10^{-8}$
δ_H	Disease induced mortality rate of hospitalized individuals	−0.000006179769507
λ_H	Natural death of hospitalized individuals per day	$-7.625835576\,10^{-7}$
b	Percentage of susceptible individuals that is available	1.000000000
ω_a	Hospitalization rate of asymptomatic infectious	0.03385191078
λ_a	Natural death of asymptomatic individuals per day	−0.0003177934483
δ_a	Disease induced mortality rate for asymptomatic non hospitalized individuals	−0.03108848950
q	Infectivity factor among asymptomatic	−0.002445562630
	individuals	
λ	Per capita recruitment rate	−0.05115168531

Numerical Simulation

The numerical behavior of the modified model equation is studied using MAPLE 18 software with parameters values presented in the table below;

Table 2: Description of Parameters with Values

Parameter	**Descriptions**	Numerical Values/ Data
θ	Percentage of aware individuals in the susceptible class	0-1
ρ	Progression rate from latent stage to infectious stage	0.007
G	Infectivity factor for hospitalize individuals	$\frac{1}{65.356}$
ω_a	Hospitalization rate of asymptomatic infectious	0.0003454
δ_s	Disease induced mortality rate for symptomatic non hospitalized individuals	0.343
C	Percentage of latently infected individuals that is traced and isolated immediately	0.0005275
β	Disease transmission rate	0-1
R	Percentage of latently infected individuals in community that become asymptomatic	0.24
α	Recovery rate of hospitalized individuals	0.0696

ω_s	Hospitalization rate of symptomatic infectious	0.84
δ_H	Disease induced mortality rate of hospitalized individuals	0.254
λ_H	Natural death of hospitalized individuals per day	0.234
B	Percentage of susceptible individuals that is available	2.32
τ	Waning rate of disease induced immunity	0.98
λ_a	Natural death of asymptotic individuals per day	0.0092
δ_a	Disease induced mortality rate of asymptotic non-hospitalized individuals	0.900
Q	Infectivity factor among asymptotic individuals	0.6
λ	Per capita recruitment rate	0.054
E	Percentage of arrivals that are latently infected	0.56
A	Percentage of arrivals that are asymptomatic	0.00025

4.3 Graphical Representation of Numerical Simulation

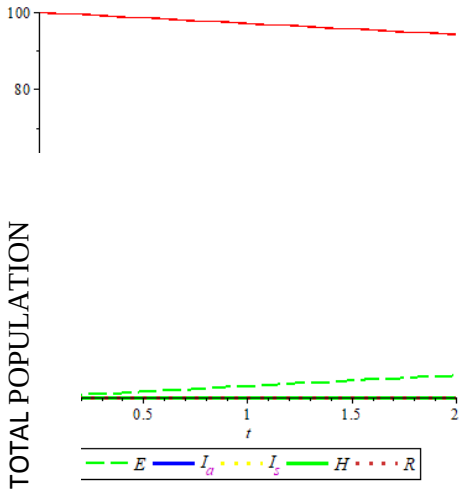


Fig.4.1: Graph for the total population at disease free equilibrium state (DFE)

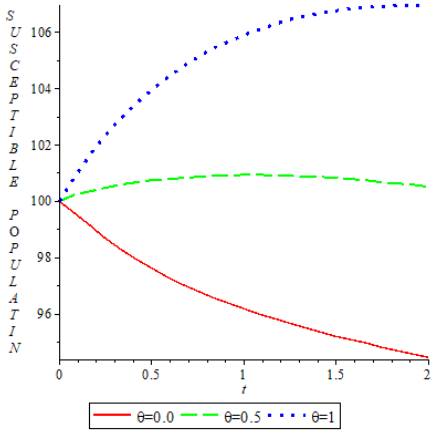


Fig. 4.2: Graph showing the impact of awareness at different rate (0.0, 0.5, and 1.0) on the susceptible human population

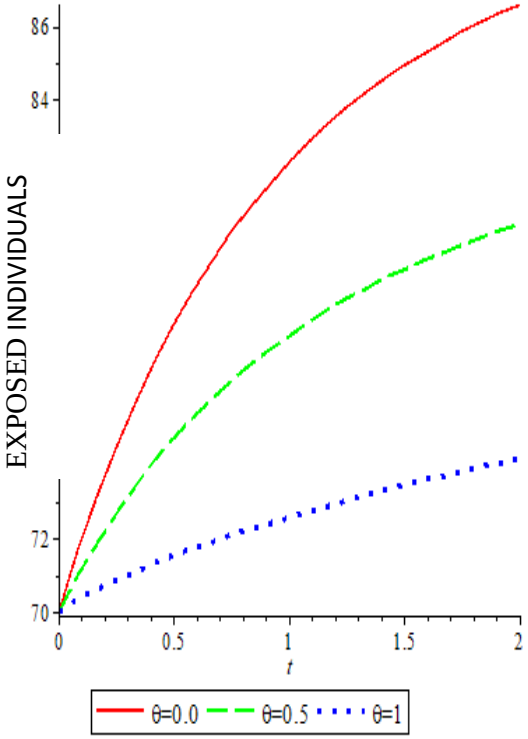


Fig. 4.3: Graph showing the impact of awareness at different rate (0.0, 0.5, and 1.0) on the Expose human population

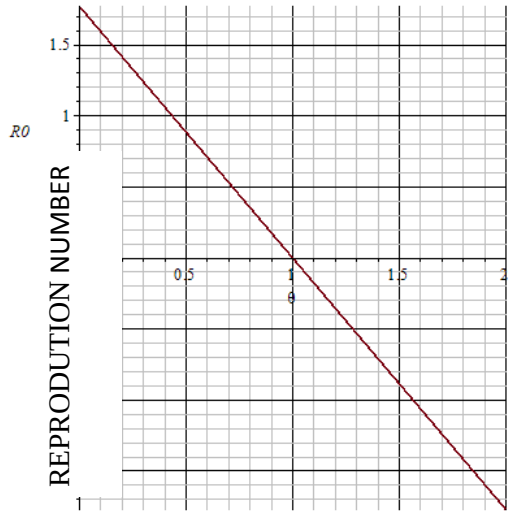
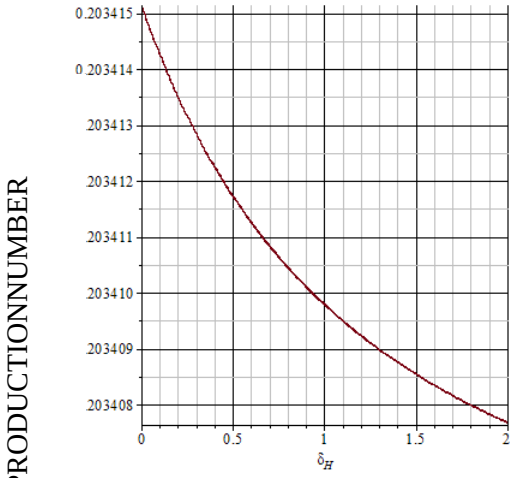


Fig. 4.4: Graph showing the impact of awareness on the spread of COVID19



4.5: Graph showing the impact of disease induced ı on the spread of COVID19

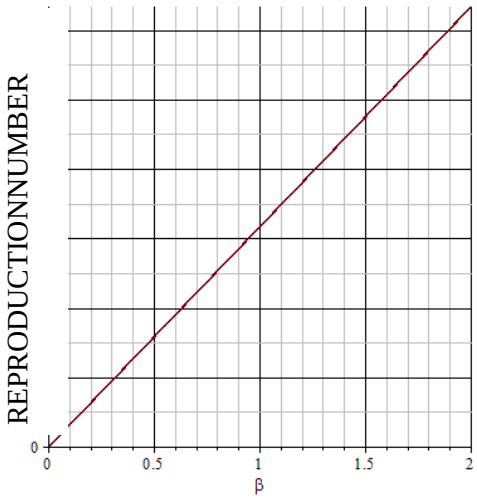


Fig. 4.6: Graph showing the impact of disease transmission rate on the spread of COVID19

Discussion of Results

In this research, we studied the impact of awareness program on transmission dynamics of COVID-19. We derived the basic reproduction number and discussed the existence and local stability of Disease Free Equilibrium (DFE) of the modified model using linearization method.

Our analysis shows that if the reproduction number is less than one then the (DFE) is locally asymptotically stable, this implies that only the susceptible human will be present and other populations reduces to zero, and the disease dies out. And if the reproduction number is greater than one, then Disease Free Equilibrium (DFE) for the modified model equation is unstable. This has been verified numerically by simulations in Figs.4.1- 4.6,and if the effective reproduction number is greater than one then the Disease Free Equilibrium is unstable, this implies that all the populations exist, for the modified model.

In figure 4.2 we inspect the susceptible population at different point of θ. When θ=0 the susceptible population is very low. The people are still not aware of the disease and its preventive measures so the disease spreads at a high rate, implying there is a high rate of infected individuals. When θ=0.5, we can see an increase in the susceptible population but the disease is still spreading at a low rate, there are still people who aren't aware of the disease and the preventive measure and there is still a high rate of infected individuals. When θ=1, there is a very high number of susceptible individuals implying people are fully aware of the disease and they are adhering to all the prevention measures of the disease. This will further lead to the eradication of the virus. In fig 4.3, as people become aware of the disease, the infection reduces thereby reducing the population of the expose class. Also fig 4.4 and 4.5 simply means that infection classes (symptomatic and asymptomatic) will reduce showing the disease will surely die out as people become fully aware.

Conclusion and Recommendation

In this research work, we modify a six deterministic compartmental model of Mugisha*et al*., (2020) by incorporating the proportion of "awareness factor" to quantify the influence of the awareness programs on the transmission dynamics of COVID-19. We studied the modified model to examine the effect of awareness program on the dynamics of the infection. First we obtained the effective reproduction number (R_e) for the model using the next generation method. The disease-free equilibrium is locally asymptotically stable for R_e<1 and unstable otherwise. Some inferences have been drawn regarding the spread of the disease by way of establishing stability and numerical results. It is found that well-timed and adequately implemented awareness campaigns can lead to a significant reduction in reproduction number and effectively curtail the spread of the disease. The study can be extended to include the cost-effectiveness of the treatment strategy.

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