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Modelling transmission dynamics of coronavirus with infected immigrants in Tanzania

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ABSTRACT

This paper proposes and analyses a compartmental deterministic nonlinear model for coronavirus transmission dynamics in Tanzania. The differential equation of stability theory is used to qualitatively evaluate the mathematical model. The basic reproductive number obtained, which represents the epidemic threshold for coronavirus elimination or persistence. Local stability analysis was performed with parameter values calculated based on data availability and accessibility in Tanzania. The findings revealed that infected immigrants have a greater influence on COVID-19 transmission in a population. Furthermore, it demonstrates that an increase in the number of infected immigrants may result in a high infection rate in the community. Besides that, social interactions among members of the community increase the rate of transmission.

Keywords: Coronavirus, infected immigrants, reproduction number.

INTRODUCTION

Coronaviruses typically affect birds and mammals, including humans in their respiratory tract (Valentina et al. 2020). It was claimed to affect rodents, rats, dogs, cats, turkeys, goats, pigs, and poultry in the last 70 years. Once infected, these animals can spread the virus to human beings. In 2019 a surveillance of the outbreak of a new coronavirus SARS-CoV2 began with the Centers for Disease Control and Prevention (CDC) which is now known as the COVID-19 as officially identified and confirmed in 2019. The virus has since spread to many countries worldwide prompting the World Health Organization (WHO) to announce it as a pandemic (Lin et al. 2020). The virus that causes COVID-19 is transmitted primarily through droplets that are generated when an infected person coughs, sneezes or speaks. Infections with coronavirus occur mainly during the winter months and early spring (Nehemya et al. 2018), although scientists and researchers indicated that high temperature and humidity can minimize transmission (Wang et al. 2020). The reported means of transmission to humans involve contact with an infected person and rapidly spread to humans through the eyes, nose or mouth before washing the contaminated hands. It was later confirmed that the coronavirus can be spreading through the air where community members required protection through masks wearing. The infected person with COVID-19 may show a wide range of signs ranging from mild to serious illness. The typical symptoms include high fever, coughing and breathlessness, shortness of breath, muscle pain, headache, sore throat and possible loss of taste and it can lead to respiratory failure, heart failure, sepsis, and sudden cardiac arrest within a few days (Chen et al., 2020; Huang et al., 2020). Coronavirus affecting many countries worldwide including Tanzania were by Tanzania's Ministry of Health, Community Development, Gender, Elderly and Children led by Minister Ummy Mwalimu announced the first case of COVID-19 on March 16, 2020 (Kombe, 2020). The infected person entered the country from Belgium via Kilimanjaro International Airport (KIA) in Arusha (Citizen, 16 March 2020). Following the first case announcement Prime Minister Kassim Majaliwa declared immediate COVID-19 local transmission control steps including the closure of all school levels and the prohibition of all public or social gatherings which was later extended to colleges and higher education institutions for indefinite closure (Citizen, 17 March 2020).

On other hand, the government announced on 23 March 2020, that all incoming travellers from COVID-19 affected countries will be quarantined for two weeks at their own expense (APO, 2020). Self-isolation at home or in hospitals, as well as wearing face masks in crowded environments was made mandatory for those who suspected COVID-19 symptoms (Ministry, 2020). According to Materu (2020), the number of COVID-19 patients increased from different regions in Tanzania. The trend in infection transmission was declared by the respective Ministers in Tanzania's mainland and Zanzibar. The first COVID-19 death was recorded in Dar es Salaam on 31 March (Citizen, 31 March 2020). More new cases and recovery rates were recorded in Dar es Salaam resulting in a total of 20 cases, 3 recoveries and 1 death (Mirembe, 2020). Until the 10 April 2020, the reported cumulative cases in Tanzania mainland and Zanzibar reached 32 (Owere, 2020) and it was at this point of daily infection increase that President Magufuli asked spirituals to go to their respective churches and mosques to seek help and protection from God against the disease (Bariyo, 2020).

The government through the Tanzania Civil Aviation Authority (TCAA) agreed on April 12 to suspend all foreign passenger planes from landing in Tanzania as an additional measure to combat COVID-19 importation, allowed only cargo planes (Malaga 2020). On April 17th, there were 38 new infection cases in Dar es Salaam and 10 in Zanzibar with the disease spreading to other areas resulting in 147 cases and 5 deaths (Owere, 2020). As of April 19^{th,} 2020, there were 188 recorded cases, with 7 deaths and 11 recoveries. The Tanzania Revenue Authority (TRA) released an order requiring all its officials and clients to wear face masks beginning of 20 April 2020 in all official workstations such as hospitals, government and non-government offices and crowded areas such as markets throughout the country (Citizen, 19 April 2020; Ministry, 2020).

Several studies have been developed to minimize COVID-19 transmission (Jewell, 2020) such as victim isolation, handwashing with soap and water, hand sanitizer, social distancing, shutting down all official gatherings such as schools, colleges, universities, sports club matches and prohibiting all unnecessary gatherings in many territories but the virus continues to spread. Mathematically, the transmission dynamics of the disease can be evaluated using mathematical methods especially differential equations (Chen et al., 2018; Mann et al., 2020). Chen et al. (2020) developed a mathematical model for the transmission network of Bats-Hosts-Reservoir-People (BHRP) with the source of infection (probably bats) to the human population. The results showed that it was difficult for the Bats-Hosts-Reservoir network to investigate the transmissions because public worries centered on the transmission to people from the Huanan seafood wholesale market (reservoir). On other hand, its reproduction number $\left(R_0\right)$ was estimated as 2.30 from reservoir to person and 3.58 from person to person.

Okhuese (2020) presented the SEIRUS model and obtained the basic reproductive number ($R_0 < 1$) shows that there is an opportunity of minimizing infections as the ratio between population incidence rate and the total number of infected populations quarantined by observatory procedure decreases. Besides, Zhao et al. (2020) worked on time series to predict the trend and short-term prediction of COVID-19 transmission. Results based on time series and kinetic model show that in mainland China the cumulative diagnosis of COVID-19 can reach 36,343 after a week (February 8, 2020). On the other hand, on March 15, 2020, the cumulative confirmed cases were 87,701, while in Wuhan the cumulative number was 76,982 on 3rd March 2020. Kucharski et al. (2020) combined a stochastic transmission model with data on Wuhan 2019 cases of coronavirus disease (COVID-19) and foreign cases originating in Wuhan to estimate how transmission varied over time between January 2020 and February 2020. Based on the estimates, outbreaks are highly likely to occur in many areas or countries. Besides, Prem et al. (2020) studied the model with distancing as the measure of control to mitigate the outbreak. The results show the transmission can be reduced by several physical distancing measures.

Therefore, the goal of this research is to formulate and analyze a mathematical model for COVID-19 transmission that focuses on the effect of infected immigrants while taking into account the Tanzanian context.

Model Formulation

In this paper, a non-linear mathematical model of COVID 19 is proposed and analyzed. The epidemiological model comprises five subclasses namely: a susceptible human population which is likely to be infected denoted by $S(t)$, exposed human populations $E(t)$. The infected classes were classified into two subclasses basing on infectiousness; that is highly infected individuals denoted as $I_H(t)$ and mildly infected individuals, $I_U(t)$. Individuals in a mild class of infection can easily recover if proper care and treatment are effectively provided. Finally, total recovered individuals are represented by $R(t)$.

The immigrants joined the populations at a rate $\Pi = q\left(1-\pi_1-\pi_2-\pi_3\right)$, where π_i for $i=1,2,3$ are the rates of immigrants enter to exposed class $E(t)$, highly infected individuals $I_H(t)$, and mildly infected individuals $I_U(t)$ respectively. The infection rate $B = \frac{\beta_1 I_H + \beta_2 I_U}{N}$, where $N = S(t) + E(t) + I_H(t) + I_U(t) + R(t)$ denotes the total populations at the time (t). We assume that individuals under a high infection rate may transmit disease more than mild infection that is to say $\beta_1 > \beta_2$. The disease is primarily transmitted through contact and merely by air, with the fraction of infected individuals detected through government screening denoted by θ whereas $(1-\theta)$ represents people with low or minimum symptoms and not detected by authorities. Furthermore, σ represents the transition rate per day to classes $I_H(t)$ and $I_U(t)$. The individuals in the compartment $I_U(t)$ may naturally recover at the rate τ_2 while individuals in class $I_H(t)$ may recover through treatment (hospitalized) by the rate τ_1. All individuals that are gain immunity and recover are moved to susceptible class by the rate ω. The individuals with a mild infection may move to a high infection class $I_H(t)$ by the rate ρ. The population decreases by the mortality rate μ and disease-induced death rate α_i, $i = 1, 2$. It is also assumed that individuals under high infection class have a high probability of death rate that is $\alpha_1 > \alpha_2$. Figure 1 presents a summary of the model formulation.

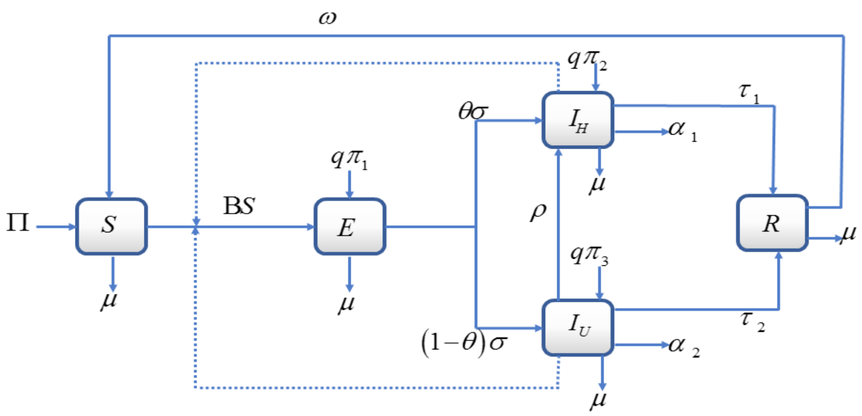

Figure 1: Model flow diagram for COVID 2019 transmission

Based on these assumptions we come up with the following system of the model equations:

$$\frac{dS}{dt} = q(1-\pi_1-\pi_2-\pi_3) - BS + \omega R - \mu S$$
$$\frac{dE}{dt} = BS + q\pi_1 - \theta\sigma E - (1-\theta)\sigma E - \mu E$$
$$\frac{dI_H}{dt} = \theta\sigma E + q\pi_2 + \rho I_U - \tau_1 I_H - (\mu+\alpha_1) I_H$$
$$\frac{dI_U}{dt} = (1-\theta)\sigma E + q\pi_3 - \rho I_U - \tau_2 I_U - (\mu+\alpha_2) I_U$$
$$\frac{dR}{dt} = \tau_1 I_H + \tau_2 I_U - \omega R - \mu R \qquad (1)$$

such that $S(t) > 0, E(t) > 0, I_H(t) > 0, I_U(t) > 0, R(t) > 0$

Boundedness of the Solution

Lemma 1: *All solutions of the system* (1) *which start in* $\mathbb{R}_+^5$ *are uniformly bounded.*

Proof:

Let

$$N(t) = S(t) + E(t) + I_H(t) + I_V(t) + R(t) \tag{2}$$

Differentiating and solving (2) we get

$$0 \le N(t) \le \frac{\Pi}{\mu}(1 - e^{-\mu t}) + W(S(0), E(0), I_H(0), I_U(0), R(0))e^{-\mu t} \tag{3}$$

Consequently, as $t \to \infty$, we observe $0 \le N(t) \le \frac{\Pi}{\mu}$.

Implying that all solutions of the system (1) are uniformly bounded in the interior of $\mathbb{R}_5^+$ then,

$$\Gamma = \{(S, E, I_H, I_U, R) \in \mathbb{R}_+^5 : N \le \frac{\Pi}{\mu} + \varepsilon\}$$ for any $\varepsilon > 0$ is bounded.

Disease Free Equilibrium (DFE)

The disease-free equilibrium point denoted as P_0 for the system of equation (1) is obtained by setting the equations of the system to zero and solving with $E = I_H = I_U = R = 0$ to obtain

$$P_0\left(S^*, E^*, I_H^*, I_U^*, R^*\right) = \left(\frac{q(1 - \pi_1 - \pi_2 - \pi_3)}{\mu}, 0, 0, 0, 0\right) \tag{4}$$

The Basic Reproduction Number (R_0)

The essence of disease transmission is often studied by epidemiologists with reproduction numbers, this is a threshold parameter that informs researchers whether a disease will die out or persist in the community. This is a crucial epidemiological quantity as it defines the scale and length of epidemics and is an important factor in deciding the target of coverage of intervention as reported in Grais et al. (2006). By using the next generation method as used by Driessche et al. (2002), the basic reproduction number of the system (1) is given as:

$$R_0 = \frac{\Pi\sigma\left[\theta\beta_1\left(\mu + \alpha_2 + \tau_2 + \rho\right) + \left(1 - \theta_2\right)\left(\mu + \alpha_1 + \tau_1\right)\beta_2\right]}{\mu(\mu + \sigma)(\mu + \alpha_1 + \tau_1)(\mu + \rho + \alpha_2 + \tau_2)} \tag{5}$$

The value R_0 depends on transmission rates β_1 and β_2 without changing other parameters.

If $(\beta_1 + \beta_2) > (\mu + \alpha_1 + \tau_1)(\mu + \rho + \alpha_2 + \tau_2)$ (6)

then $R_0 > 1$ and infection invades and the disease grows in the human population.

If $(\beta_1 + \beta_2) < (\mu + \alpha_1 + \tau_1)(\mu + \rho + \alpha_2 + \tau_2)$, then $R_0 < 1$ and the population remains free from the disease invasion.

Model Stability Analysis

The analysis of the model carried out using Jaccobian Matrix. To simplify the analysis of the model equation (1), the system of the equation can be reduced by setting $R = \left(\frac{\tau_1 I_H + \tau_2 I_U}{\omega + \mu}\right)$ and $E = B\left(\frac{(\beta_1 I_H + \beta_2 I_U)}{\sigma + \mu}\right)$ from the model (1) and re-write the remaining model of three equations as:

$$\frac{dS}{dt}=q(1-\pi_1-\pi_2-\pi_3)-BS+\omega\left(\frac{\tau_1 I_H+\tau_2 I_U}{\omega+\mu}\right)-\mu S$$
$$\frac{dI_H}{dt}=\theta\sigma\left(\frac{B(\beta_1 I_H+\beta_2 I_U)}{\sigma+\mu}\right)+q\pi_2+\rho I_U-\tau_1 I_H-(\mu+\alpha_1)I_H \tag{7}$$
$$\frac{dI_U}{dt}=(1-\theta)\sigma\left(\frac{B(\beta_1 I_H+\beta_2 I_U)}{\sigma+\mu}\right)+q\pi_3-\left(\rho+\tau_2+\mu+\alpha_2\right)I_U$$

Using the system of equations (7), we obtain the Jacobian matrix (8) at the disease-free equilibrium point

$P_0(S^*,I_H^*,I_U^*)=(\frac{\Pi}{\mu},0,0)$.

$$Df|_{P_0}=\begin{bmatrix}-\mu & -\beta_1+\frac{\omega\tau_1}{\mu+\omega} & -\beta_2+\frac{\omega\tau_2}{\mu+\omega}\\ 0 & -\mu-\alpha_1+\frac{\theta\sigma\beta_1}{\mu+\sigma}-\tau_1 & \rho+\frac{\theta\sigma\beta_2}{\mu+\sigma}\\ 0 & \frac{(1-\theta)\sigma\beta_1}{\mu+\sigma} & -\mu-\rho-\alpha_2+\frac{(1-\theta)\sigma\beta_2}{\mu+\sigma}-\tau_2\end{bmatrix} \tag{8}$$

From matrix (8) we find that eigenvalue $\lambda_1=-\mu$ and the rest of eigenvalues λ_2,λ_3 are obtained from block matrix (9) with characteristic equation (10)

$$\begin{vmatrix}-a_2+\frac{\theta\sigma\beta_1}{a_3}-\lambda & \rho+\frac{\theta\sigma\beta_2}{a_3}\\ \frac{(1-\theta)\sigma\beta_1}{a_3} & -a_1+\frac{(1-\theta)\sigma\beta_2}{a_3}-\lambda\end{vmatrix}=0 \tag{9}$$

$$\lambda^2+\lambda\left(a_1+a_2-\sigma\left(\frac{\theta\beta_1-\beta_2+\theta\beta_2}{a_3}\right)\right)-\left(\frac{\beta_1\rho\sigma(1-\theta)}{a_3}+a_1a_2(1-\mu R_0)\right)=0 \tag{10}$$

where $a_1=\mu+\rho+\alpha_2+\tau_2$, $a_2=\mu+\alpha_1+\tau_1$, $a_3=\mu+\sigma$ and $\mu a_1a_2a_3R_0=\theta\sigma a_1\beta_1+(1-\theta)\sigma a_2\beta_2$

$$\lambda_{2,3}=\frac{\theta\sigma(\beta_1+\beta_2)-(a_1a_3+a_2a_3+\sigma\beta_2)\pm\sqrt{(a_1a_3+a_2a_3+4a_3\rho\sigma\beta_1+4a_3a_1a_2a_3(1-\mu R_0)-\theta\sigma\beta_1-(1-\theta)\sigma\beta_2)^2-4a_3\rho\sigma\beta_1\theta}}{2} \tag{11}$$

The $R_0<1$ if $\lambda_{2,3}<0$ and hence the disease-free equilibrium is stable, otherwise, it will be unstable.

RESULTS AND DISCUSSION

Numerical Simulation of COVID 19 Model

In this section, we quantitatively evaluate the model to explain the empirical calculations. The following parameter values were considered in carrying out this function as shown in table 1.

Table 1: Parameter values for numerical simulations

Parameter	Description	Value (per day)
π_i for $i=1,2,3$	The proportion of immigrants entering class $E(t)$, $I_H(t)$ and $I_U(t)$ respectively	$\pi_1 = 0.4-0.6$, $\pi_2 = 0.2$, $\pi_3 = 0.03$
$\Pi = q(1-\pi_1-\pi_2-\pi_3)$	Recruitment rate of $S(t)$	1
β_i for $i=1,2$	The transmission rate of classes $I_H(t)$ and $I_U(t)$ respectively, whereby $\beta_1 > \beta_2$	$\beta_1 = 0.5$, $\beta_2 = 0.3$
$B = \dfrac{\beta_1 I_H + \beta_2 I_U}{N}$	The force of infection	0.5
τ_i for $i=1,2$	The recovery rate of classes $I_H(t)$ and $I_U(t)$ respectively	$\tau_1 = 0.2$, $\tau_2 = 0.5$
α_i for $i=1,2$	Disease induced death rate for classes $I_H(t)$ and $I_U(t)$ respectively	$\alpha_1 = \frac{21}{509} = 0.041257$, $\alpha_2 = 0.002$
μ	Natural mortality rate	0.0001-0.09
σ	Transition rate between classes $I_H(t)$ and $I_U(t)$	0.1
ρ	Transition rate from class $I_U(t)$ to class $I_H(t)$	0.3
θ	The fraction of people infected and detected by authorities	0.008
ω	Transition rate from class $R(t)$ to class $S(t)$	186/509=0.365422 (Mumbu, 2020)

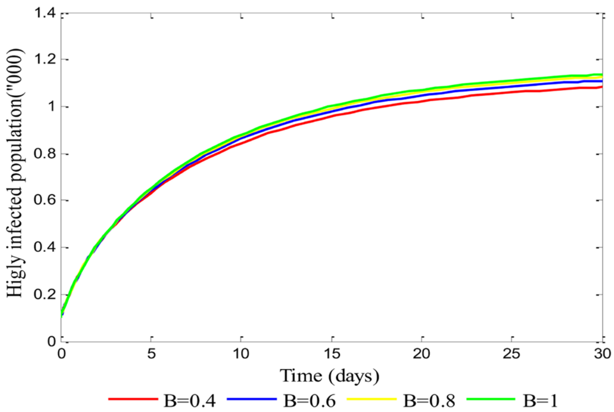

Figure 2: Proportion of highly infected individuals varying infection rates

Figure 2 shows that the highly infected population increases as the rate of infection increases and the disease become widespread within society.

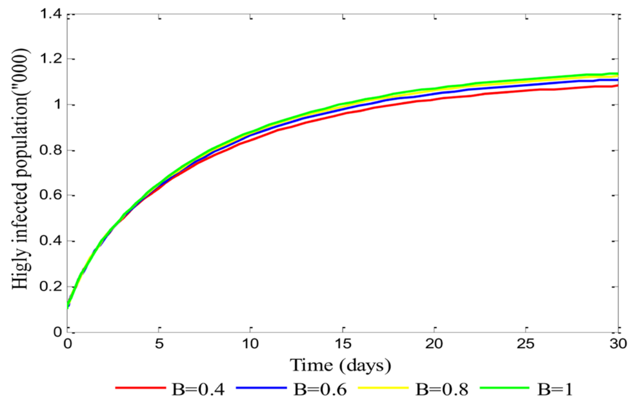

Figure 3: Proportion of highly infected individuals varying immigrants entering class $I_H(t)$

Looking at the findings of Figure 3 we can see that the rise in contaminated immigrants joining the population contributes to a rise in society's COVID-19 infection.

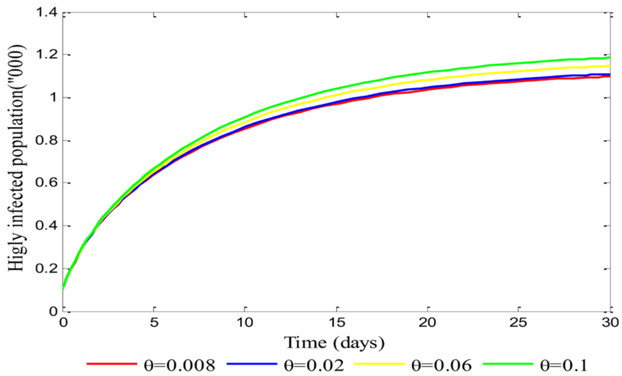

Figure 4: Proportion of highly infected individuals varying fraction of people infected and detected by authorities

In Figure 4 we noted the decreases in the proportion of infected individuals as the percentage of people infected and identified by authorities.

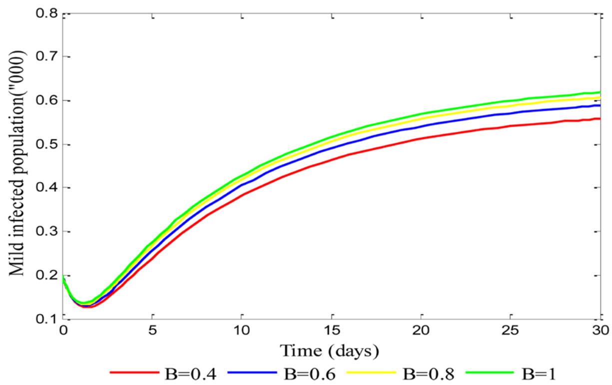

Figure 5: Proportion of mild infected individuals varying force of infection

In Figure 5 we observed that the mildly infected population increases as the infection force increases, resulting in the disease persisting in the population as these individuals are difficult to detect.

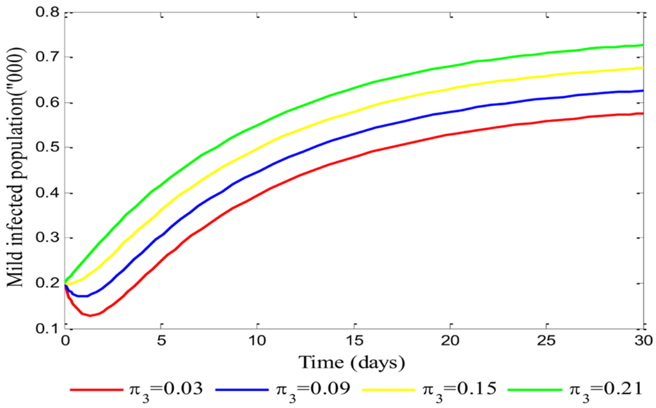

Figure 6: Proportion of mildly infected individuals varying immigrants entering class $I_V(t)$

Figure 6 shows a drastic rise in mild infections as immigrants with mild infections are permitted to reach the population.

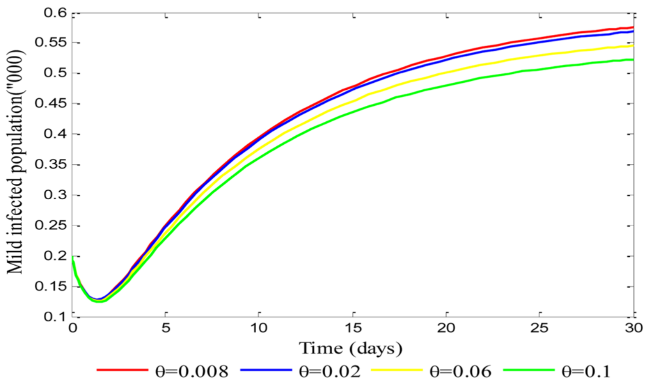

Figure 7: Proportion of mildly infected individuals varying fraction of people infected and detected by authorities

Detection of infected individuals as seen in Figure 7 helps to decrease mild contagious individuals within the population.

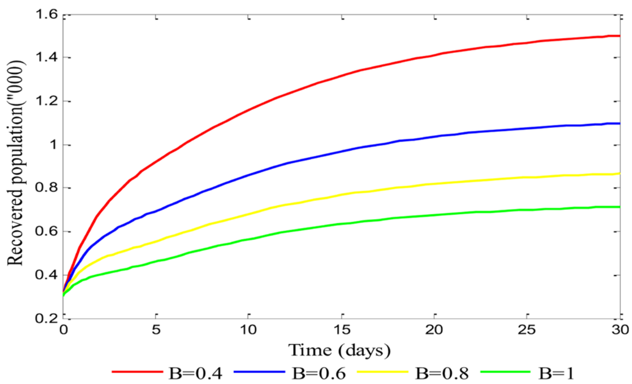

Figure 8: Proportion of recovered individuals varying force of infection

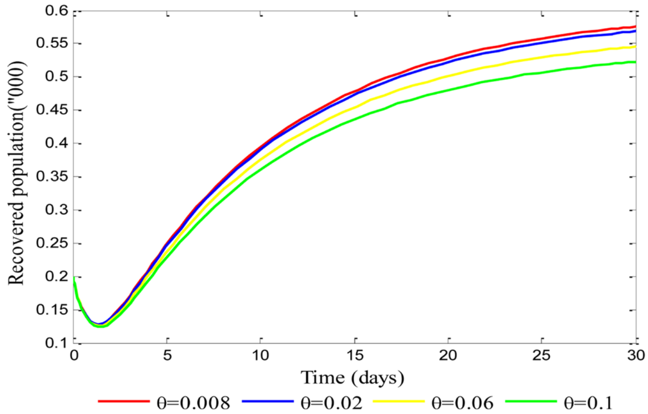

Figure 9: Proportion of recovered individuals varying fraction of people infected and detected by authorities

Figure 8 shows that the population is declining as the infection increases. Figure 9 shows that there is a decrease in infected people who have been identified by the authorities as a result of natural recovery and hospitalization. The global challenge continues to be to prevent infectious diseases such as COVID-19. As a result, the affected country must battle the disease's spread by quarantine vigorously to reduce COVID-19 socioeconomic consequences. It is prudent to advise the Tanzanian government to reduce the number of immigrants in the area and to impose quarantine based on the results of all immigrants. Both immigrants must be checked for their status to be recognized. The effect of the transmission parameters determined by the reproduction number is shown in Figure 10 which shows that the reproduction number increases as the infection rate increases. Reducing the number of infected immigrants leads to the 0.6115 basic reproduction number. To minimize the spread of COVID 19, the government should track all immigrants and take all required COVID 19 precautions.

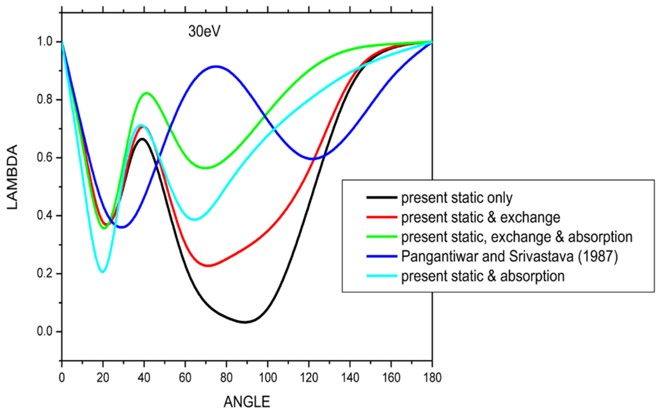

Figure 10: Variation of reproduction number as the impact of transmitting parameters

CONCLUSION

The model demonstrated the impact of contaminated immigrants in a population on COVID-19 transmission. As the number of infected immigrants grows, the number of individuals infected grows as well as shown in Figures 3 and 6 which reflect the real-life scenario of COVID 19 first case in Tanzania. Furthermore, the findings revealed that both congested areas and moisture sites in the region can contribute to COVID 19 rapid spread. The basic reproduction number obtained as 0.6115 which reflect the result of minimization and control of all immigrants through quarantine. This necessitates the government's attention in monitoring all immigrants in order to reduce community risk. The recovered individuals, on the other hand, provide more relief and reduce tension among community members, which is one of the major threats. This helps to reduce disease transmission and its consequences in the community. Furthermore, urgent assistance for the affected country recommends quarantine of immigrants and hospitalization to combat the disease's spread and improve socio-economic and community welfare. Based on the findings, the government should monitor and test all immigrants before allowing them to join the community and should keep track of all immigrants in order to prevent the spread of COVID 19.

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