Novelty Journals

ISSN 2394-9651

International Journal of Novel Research in Physics Chemistry & Mathematics
Vol. 9, Issue 2, pp: (29-39), Month: May - August 2022, Available at: www.noveltyjournals.com

Mathematical Model Incorporating Screening of International Travellers using RT-PCR Test As A Control against the Spread Of Covid -19

Anne Ndunge Mutinda – SR[1*], Joseph Oloo[2], George Kimathi[3]

[1*,2,3] Department of Mathematics and Actuarial Science, Catholic University of Eastern Africa, Box 62157-00200, Nairobi-Kenya.

DOI: https://doi.org/10.5281/zenodo.6976332

Published Date: 09-August-2022

Abstract: **A worldwide pandemic called COVID-19 has afflicted humanity in various aspects of life.There exists,several mathematical models aimed at limiting the transference of COVID-19.This research brings in, the intervention of RT-PCR screening of international travelers seeking to identify the infected at the beginning phases of infection,to lower the rate of its spread led by high mobility of human beings,therefore,the novelty is on RT-PCR screening as a control measure.We create and examine a SPEIR model for COVID 19 dynamics incorporating RT-PCR screening and apply the results to explore COVID-19 dynamics in the presence of screening of international travelers.The model includes five time dependent compartments Susceptible(S),Screened(P), Exposed(E), Infected(I) and Recovered (R).We developed the basic reproduction number (R_0) and investigated the existence of all the equilibrium points;the disease free equilibrium and endemic equilibrium and determined their stabilities.The epidemic model's system of differential equations was subjected to numerical simulations by use of Matlab.The interpretation and comparison to the qualitative solutions was done and the outcome after the analysis is that RT-PCR screening revealed a clear picture of the evolution and spread of COVID-19,with its infections having fallen off significantly. This study shows that RT-PCR screening of travelers is paramount in preventing the spread of COVID-19.**

Keywords: **COVID-19 spread dynamics, mathematical modelling, epidemiological modelling, RT-PCR screening modelling.**

1. INTRODUCTION

Severe acute respiratory syndrome corona virus 2 is a new corona virus that causes the disease known as corona virus disease 2019 (COVID-19).[11, 6, 8, 4] which was discovered on December 31,2019 in Wuhan,China.The outbreak later infected more than 200 countries, and the World Health Organization (WHO) declared COVID-19 a global pandemic on January 30, 2020. (WHO,2020a,2020b; CDC, 2020).According to a World Health Organization report released on June 5,2022, over 529 million confirmed cases and over six million deaths have been reported globally [12].

Current evidence suggests that the virus spreads primarily through close contact between people,Nonetheless, it can also spread in crowded or poorly ventilated indoor spaces,where people frequently spend extended amounts of time. [1, 8]According to a report published by Statista Research Department on June 7,2022, the number of international tourist arrivals globally totals approximately 427 million, with travel and tourism contributing 5.81 trillion US dollars to the global economy.As a result, in the absence of international traveler screening for COVID-19, the threat of international spread of this highly infectious and fatal disease is evident due to the large number of travelers recorded globally [12].

The International Civil Aviation Organization(ICAO) issued takeoff guidance, which is the global standard for governments to follow when it comes to connecting their people and economies by air. As of the 5th June 2020, all international travelers must present a digitally -verified negative COVID-19 RT-PCR swab test using Trusted Travel (TT) electronic verification system in order to board a flight. This will help passengers travel safely and halt the Covid-19 epidemic [2]

Since its onset, the Covid-19 epidemic has caused a shocking loss of life globally.The world has seen significant economic fallout, significant hardship, and disruptions in the education system, among other things. According to a WHO statement issued on October 13, 2020,With ten million individuals at danger of living in extreme poverty and a daily rise in the number of undernourished people, the pandemic has had a devastating impact on the economy and society. In addition, roughly half of the 3.3 billion people employed globally face employment insecurity. The spread is associated with, among other things, open economies, globalization, increasing travel and trade, and urbanization.[2].

Due to the complexity of the COVID-19 pandemic, which necessitates the creation of medicines and medical services, prevention and global initiatives cannot be fully grasped by biology and healthcare tools alone. Key transmission factors and pandemic countermeasures must be estimated using mathematical models, which are crucial.With the threat of such a highly infectious disease spreading internationally,RT-PCR screening of international travelers is critical if its spread is to be contained.This study focused on raising scientific awareness about RT-PCR screening.

2. MODEL DESCRIPTION AND FORMULATION

Epidemiological studies seek to determine whether there is a connection between a risk factor and a certain ailment [11]. In this study, the RT-PCR is included into a modified version of the SEIR model.A SPEIR Model is developed.The population size N(t) is divided into five compartments at any given moment(t). The susceptible class is represented in the diagram by S(t). These people frequently travel internationally and are at risk of contracting the corona virus.A group of international visitors who undergo screening using an RT-PCR test is represented by the P(t) compartment.The E(t) represents the exposed class,this is part of the traveling population who have been infected but are not yet infectious.This group has the disease but cannot infect anyone.The I(t) is the infectious class,this is the class that has been tested and confirmed to be infected with Covid-19 and are capable of spreading the disease.R(t) is the recovery compartment,this are the individuals that have totally recovered from the disease,though they acquire temporal immunity still they can be reinfected with the disease.We utilize the arrows to denote the rates entering and exiting the compartments in order to construct our differential equations for the compartments.The rate is positive when an arrow is entering the compartment and negative as the arrow leaves a compartment.

The the entire population (N) at time t is represented by;

$$N(t) = S(t) + P(t) + E(t) + I(t) + R(t)$$

2.1 Description of the model's parameters

The definitions of the parameters that will be used in the model are as follows:

Λ - Recruitment rate

μ - Natural death

σ - Rate at which Susceptible individuals get to be screened

κ - Rate of screened to susceptible

β - Per-contact likelihood of disease transmission

ω -Rate of those who undergone through R.T PCR test get to the Exposed compartment

γ -Rate at which exposed people enter the infectious compartment

Ψ - Rate at which the Screened get into the Infectious compartment

Novelty Journals

ISSN 2394-9651

International Journal of Novel Research in Physics Chemistry & Mathematics
Vol. 9, Issue 2, pp: (29-39), Month: May - August 2022, Available at: www.noveltyjournals.com

τ - death due to the disease

ϕ - Rate of the Infected individuals to Recovery

δ - Rate at which the recovered get into Susceptible class due to temporal immunity

S - Susceptible

P - Screened

E - Exposed

I -Infectious humans

R - Recovered

2.2 Model diagram

The diagram in fig1 below illustrates how the aforementioned model can be presented.

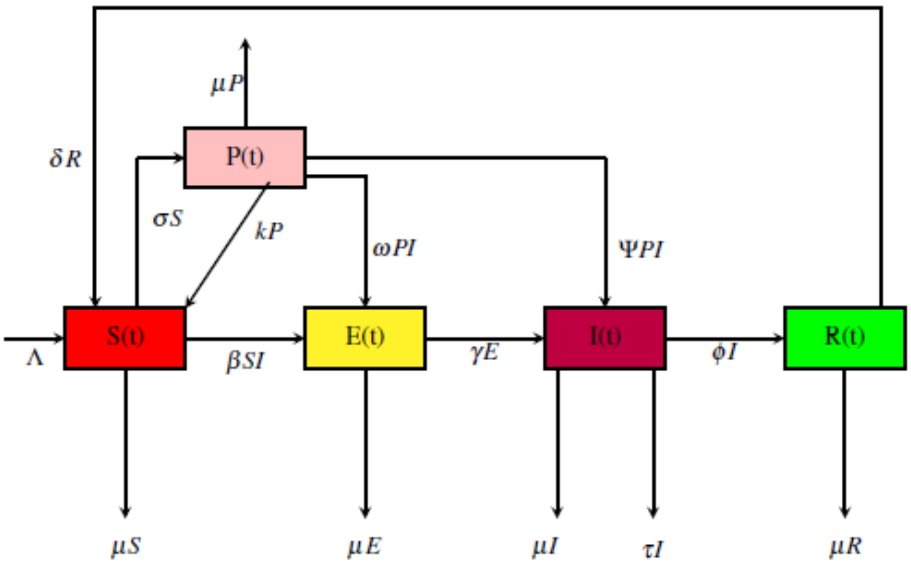

Figure 1: SPEIR Model flow diagram

A system of nonlinear differential equations is generated and presented below using the schematic diagram shown in 1

$$\frac{dS}{dt} = \Lambda + \delta R + kP - (\beta I + \mu + \sigma)S \tag{2.1}$$

$$\frac{dP}{dt} = \sigma S - (k + \omega I + \Psi I + \mu)P \tag{2.2}$$

$$\frac{dE}{dt} = \beta SI + \omega PI - (\gamma + \mu)E \tag{2.3}$$

$$\frac{dI}{dt} = \gamma E + \Psi IP - (\phi + \mu + \tau)I \tag{2.4}$$

$$\frac{dR}{dt} = \phi I - (\mu + \delta)R \tag{2.5}$$

subject to the initial conditions enlisted below:

$$S(0) \geq 0,\ P(0) \geq 0,\ E(0) \geq 0,\ I(0) \geq 0,\ R(0) \geq 0$$

Then the derivative of N(t) with respect to t is given by:

$$\frac{dN(t)}{dt} = \frac{dS(t)}{dt} + \frac{dP(t)}{dt} + \frac{dE(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt} \tag{2.6}$$

2.3 Assumptions of the Model

The following assumptions will accompany the mathematical model

(i)Any person intending to travel internationally is Susceptible

(ii)The Recovered individuals acquire temporal immunity and can be reinfected.

(iii) Recruitment takes place at the constant rate Λ .

2.3.1 Disease Free Equillibrium

The disease free equilibrium (DFE) is described as the stage point at which no disease is present in the population.At equilibrium point all differentials are equal to zero.A system has equilibrium point if there is no change in the system at all the time [3, 9].Therefore,equilibrium for the differential equations can be found by by zeroing off the right sides of each of the five differential equations.This is gives the nonlinear system.

$$0 = \Lambda + \delta R + kP - (\beta I + \mu + \sigma)S$$

$$0 = \sigma S - (k + \omega I + \Psi I + \mu)P$$

$$0 = \beta SI + \omega PI - (\gamma + \mu)E$$

$$0 = \gamma E + \Psi IP - (\phi + \mu + \tau)I$$

$$0 = \phi I - (\mu + \delta)R$$

At Disease free equilibrium;

$$P^* = 0,\ E^* = 0,\ I^* = 0, R^* = 0$$

since there is no disease in the community.This implies that,

$$0 = \Lambda - (\mu + \sigma)S$$

$$0 = \sigma S$$

simplifying equation

$$0 = \Lambda - (\mu + \sigma)S \tag{2.7}$$

we get

$$S^* = \frac{\Lambda}{(\mu + \sigma)} \tag{2.8}$$

Novelty Journals

ISSN 2394-9651

International Journal of Novel Research in Physics Chemistry & Mathematics
Vol. 9, Issue 2, pp: (29-39), Month: May - August 2022, Available at: www.noveltyjournals.com

From the equation, $0 = \sigma S$

we get either $\sigma = 0$ or $s = 0$

however $S \neq 0$ Therefore $\sigma = 0$

Thus the DFE will be given by $\frac{\Lambda}{\mu}$ thus,

$$(S^*, P^*, E^*, I^*, R^*) = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0\right) \tag{2.9}$$

2.3.2 Endemic Equillibrium

The endemic equilibrium state is the state where the disease cannot be completely eliminated but still has a controllable presence in the population.[5].For the disease to continue to affect people,the susceptible class,the Screened,the Exposed,the Infectious class and the recovered class must not be empty at equilibrium state.That is,if EE = (S*,P*,E* ,1*,R*) is the endemic equilibrium state,then (S,P,E,I,R) $\neq$ (0,0,0,0,0) The endemic equilibrium point of the formulated model is obtained by equating the derivatives to zero and solving for the variables S*,P*,E* ,1*,R*.from the model equations. Therefore;

$$0 = \Lambda + \delta R + kP - (\beta I + \mu + \sigma)S$$

$$0 = \sigma S - (k + \omega I + \Psi I + \mu)P$$

$$0 = \beta SI + \omega PI - (\gamma + \mu)E$$

$$0 = \gamma E + \Psi IP - (\phi + \mu + \tau)I$$

$$0 = \phi I - (\mu + \delta)R$$

From equation $0 = \phi I - (\mu + \delta)R$ and making I the subject of the formula we get;

$$I^* = \frac{(\mu + \delta)R}{\phi} \tag{2.10}$$

From the equation $0 = \Lambda + \delta R + kP - (\beta I + \mu + \sigma)S$,replacing I and making P the subject of the formula we get;

$$P^* = \frac{\left((\sigma + \mu)S - \delta R - \Lambda\right)\phi + \beta S(\mu + \delta)R}{\phi\kappa} \tag{2.11}$$

From the equation $0 = \sigma S - (k + \omega I + \Psi I + \mu)P$,replacing I and P and making S the subject of the formula we get;

$$S^* = \frac{\phi(\delta R + \Lambda)\left((\psi + \omega)(\mu + \delta)R + \phi(\mu + \kappa)\right)}{\beta(\mu + \delta)^2(\psi + \omega)R^2 + \phi\left((\psi + \beta + \omega)\mu + \beta\kappa + \sigma(\psi + \omega)\right)(\mu + \delta)R + \mu\phi^2(\mu + \kappa + \sigma)} \tag{2.12}$$

From the equation $0 = \beta SI + \omega PI - (\gamma + \mu)E$,replacing I,P and S,and making E the subject of the formula we get;

$$E^* = \frac{(\delta R + \Lambda) R(\mu + \delta)\left(\beta(\psi + \omega)(\mu + \delta) R + \phi(\beta\kappa + \mu\beta + \omega\sigma)\right)}{\left(\beta(\mu + \delta)^2 (\psi + \omega) R^2 + \phi\left((\psi + \beta + \omega)\mu + \beta\kappa + \sigma(\psi + \omega)\right)(\mu + \delta) R + \mu\phi^2 (\mu + \kappa + \sigma)\right)(\mu + \gamma)}$$

(2.13)

From the equation $0 = \gamma E + \Psi IP - (\phi + \mu + \tau)I$,replacing I,P, S,and E and making R the subject of the formula we get;

$$R^* = 0 \tag{2.14}$$

2.3.3 Basic reproductive number R_0

The number of secondary infections that result from infected persons is the basic reproductive number.[3].In this section the Next Generation Matrix will be used to ascertain the R_0 . Considering the compartments with infectious and non - infectious Compartments denoted as vectors X and Y respectively, we have:

$$X = \begin{bmatrix} E \\ I \end{bmatrix} \text{and } Y = \begin{bmatrix} S \\ P \\ R \end{bmatrix} \tag{2.15}$$

The next generation matrix FV^{-1} yields the expected number of secondary infections.

Therefore

$$FV^{-1} = \begin{bmatrix} \frac{\beta\Lambda\gamma}{\mu(\gamma + \mu)(\phi + \mu + \tau)} & \frac{\beta\Lambda}{\mu(\phi + \mu + \tau)} \\ 0 & 0 \end{bmatrix}$$

is the next generation matrix.

The spectral radius ρ of the next generation matrix FV^{-1} gives us the Basic reproduction number [7]. Thus FV^{-1} is the Next Generation Matrix $R_0 = \rho(FV^{-1})$ .We now determine the eigenvalues and find the one that is most dominating.

Therefore,

$$R_0 = \frac{\beta\Lambda\gamma}{\mu(\gamma + \mu)(\phi + \mu + \tau)} \tag{2.16}$$

2.4 Stability of the system

The stability of a system refers to the behaviour and error propagation.Any given system is considered to be stable if the eigenvalues of the Jacobian matrix lie within the stability region of the system [3].

2.4.1 Local Stability of Disease Free Equilibrium

The DFE is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.The Jacobian matrix of the model system equations at J(SPEIR) is given by:

$$J=\begin{bmatrix} -(\beta I+\mu+\sigma) & k & 0 & -(\beta S) & \delta \\ \sigma & -(k+\omega I+\Psi I+\mu) & 0 & -(\omega P+\Psi P) & 0 \\ \beta I & \omega I & -(\gamma+\mu) & (\beta S+\omega P) & 0 \\ 0 & \Psi I & \gamma & \Psi P-(\phi+\mu+\tau) & 0 \\ 0 & 0 & 0 & \phi & -(\mu+\delta) \end{bmatrix}$$

At DFE the jacobian reduces to;

$$J=\begin{bmatrix} -(\mu+\sigma)-\lambda & k & 0 & -(\beta S) & \delta \\ \sigma & -(k+\mu)-\lambda & 0 & 0 & 0 \\ 0 & 0 & -(\gamma+\mu)-\lambda & (\beta S & 0 \\ 0 & 0 & \gamma & (\phi+\mu+\tau)-\lambda & 0 \\ 0 & 0 & 0 & \phi & -(\mu+\delta)-\lambda \end{bmatrix}$$

Solving for eigenvalues $\lambda_1,\lambda_2,\lambda_3,\lambda_4,\lambda_5$ we get Respectively;

$$\begin{bmatrix} -\mu \\ -\mu-\sigma \\ -\mu-\delta \\ \frac{1}{2}\frac{-2\mu^2+(-\phi-\tau-\gamma)\mu+\sqrt{\mu\left((\phi+\tau-\gamma)^2\mu+4\Lambda\beta\gamma\right)}}{\mu} \\ \frac{1}{2}\frac{-2\mu^2+(-\phi-\tau-\gamma)\mu-\sqrt{\mu\left((\phi+\tau-\gamma)^2\mu+4\Lambda\beta\gamma\right)}}{\mu} \end{bmatrix} \quad (2.17)$$

Because all the eigenvalues are negative,the Disease Free Equilibrium is locally asymptotically stable.

2.4.2 Global Stability of Endemic Equillibrium

If $R_0>1$,then disease endemic equilibrium is globally asymptotically stable [3][10]. We shall prove this using lyapunov function as shown below:

$$L(S^*,P^*,E^*,I^*,R^*,)=(S-S^*-S^*\ln\left(\frac{S^*}{S}\right)+(P-P^*-P^*\ln\left(\frac{P^*}{P}\right)+(E-E^*-E^*\ln\left(\frac{E^*}{E}\right)$$

$$+(I-I^*-I^*\ln\left(\frac{I^*}{I}\right)+(R-R^*-R^*\ln\left(\frac{R^*}{R}\right)$$

Novelty Journals

ISSN 2394-9651

International Journal of Novel Research in Physics Chemistry & Mathematics
Vol. 9, Issue 2, pp: (29-39), Month: May - August 2022, Available at: www.noveltyjournals.com

By computing the derivative of L:

$$\frac{dL}{dt}=\left(\frac{S-S^*}{S}\right)\frac{dS}{dt}+\left(\frac{P-P^*}{P}\right)\frac{dP}{dt}+\left(\frac{E-E^*}{E}\right)\frac{dE}{dt}+\left(\frac{I-I^*}{I}\right)\frac{dI}{dt}+\left(\frac{R-R^*}{R}\right)\frac{dR}{dt}$$

Substituting the system model ODE's in the above equation we get;

$$\frac{dL}{dt}=\left(\frac{S-S^*}{S}\right)[\Lambda+\delta R+kP-(\beta I+\mu+\sigma)S]+\left(\frac{P-P^*}{P}\right)[\sigma S-(k+\omega I+\Psi I+\mu)P]+$$
$$\left(\frac{E-E^*}{E}\right)[\beta SI+\omega PI-(\gamma+\mu)E]+\left(\frac{I-I^*}{I}\right)[\gamma E+\Psi IP-(\phi+\mu+\tau)I]+\left(\frac{R-R^*}{R}\right)[\phi I-(\mu+\delta)R]$$

This reduces down to;

$$\Lambda+\delta R+kP-(\beta I+\mu+\sigma)S-\Lambda S^*-\delta RS^*-kPS^*+(\beta I+\mu+\sigma)S^*+\sigma S-(k+\omega I+\Psi I+\mu)P$$
$$-\sigma SP^*+(k+\omega I+\Psi I+\mu)P^*+\beta SI+\omega PI-(\gamma+\mu)E-\beta SIE^*-\omega PIE^*+(\gamma+\mu)E^*+\gamma E$$
$$+\Psi IP-(\phi+\mu+\tau)I-\gamma EI^*+\Psi IPI^*+(\phi+\mu+\tau)I^*+\phi I-(\mu+\delta)R-\phi IR^*+(\mu+\delta)R^*$$

We let X to be the positive terms and Y to be the negative terms

$$X=\Lambda+\delta R+kP+(\beta I+\mu+\sigma)S^*+\sigma S+(k+\omega I+\Psi I+\mu)P^*+\beta SI+\omega PI+(\gamma+\mu)E^*+$$
$$\gamma E+\Psi IP+\Psi IPI^*+(\phi+\mu+\tau)I^*+\phi I+(\mu+\delta)R^*$$

$$Y=(\beta I+\mu+\sigma)S+\Lambda S^*+\delta RS^*+kPS^*+(k+\omega I+\Psi I+\mu)P+\sigma SP^*+(\gamma+\mu)E+\beta SIE^*+\omega PIE^*$$
$$+(\phi+\mu+\tau)I+\gamma EI^*+(\mu+\delta)R+\phi IR^*$$

Let $\frac{dL}{dt}=X-Y$

If we introduce the condition $X<Y$, we find out that, $\frac{dL}{dt}\le 0$

Hence, $\frac{dL}{dt}=0$, if and only if;

$$S=S^*,P=P^*,E=E^*I=I^*andR=R^*$$

Therefore,highest or largest invariant set in ; S^*,P^*,E^*,I^*,R^* $\frac{dL}{dt}=0$ is E^*,where E^* is the endemic point. At this point we proof that the endemic equilibrium is asymptotically stable [3]

3. NUMERICAL SOLUTIONS

3.1 Covid-19 in relation to the Entire population with time

Figure 2 below shows the dynamics of Covid-19 in the entire population comprising of the Susceptible (S),ScreenedP,Exposed(E),Infectious(I),and Recovered(R) is analyzed.An increase in the number of the Screened population leads to the decrease of those who are at the risk of being infected.This is because through RT-PCR screening

Novelty Journals

ISSN 2394-9651

International Journal of Novel Research in Physics Chemistry & Mathematics
Vol. 9, Issue 2, pp: (29-39), Month: May - August 2022, Available at: www.noveltyjournals.com

those who are infected are identified and restricted to travel hence the rate of infection is minimal.Initially the graph of the infectious takes time to rise.After a minimal rise it stabilizes and this is as a result of Screening.We also note that the number of the Recovered is higher than the Exposed.Relatively,the number of Infectious is directly proportional to the Recovered.The Susceptible Decrease with time ,this is due to natural death and the effect of the RT-PCR screening ,meaning screening regulates the number of travelers to avoid new Covid-19 infections.

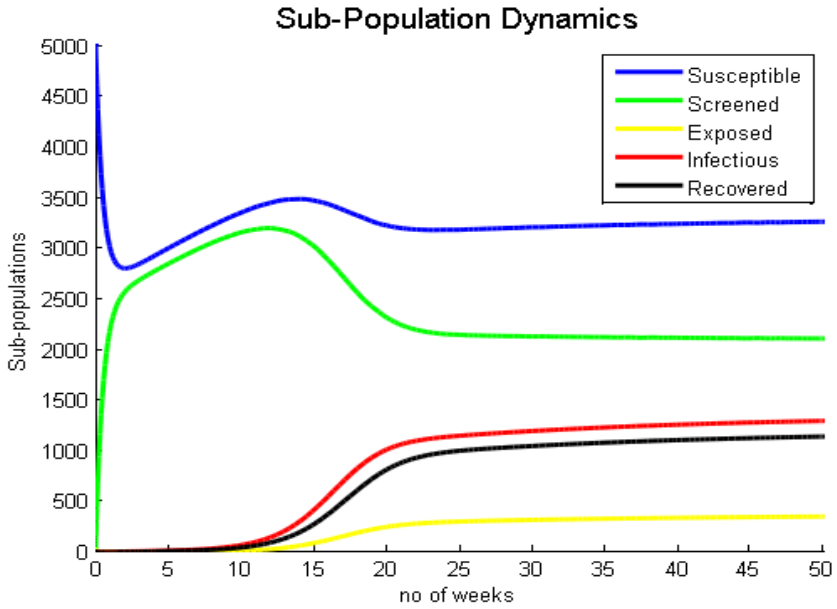

Figure 2: Covid-19 dynamics graph

3.1.1 Screened Population Dynamics

Figure 3 shows the graph of the dynamics of the screened population.At any given time as we increase the number of the people screened the graph increases.The increase in the population being screened causes a decrease in the rate of infection.From the graph we confidently conclude that the rate of Screening of the Susceptible has a significant effect on the transmission of the disease.Hence, we can reduce COVID-19 infections by increasing the rate at which the susceptible population is screened.The more we use RT-PCR in screening the more we will have less people being infected with Covid-19.

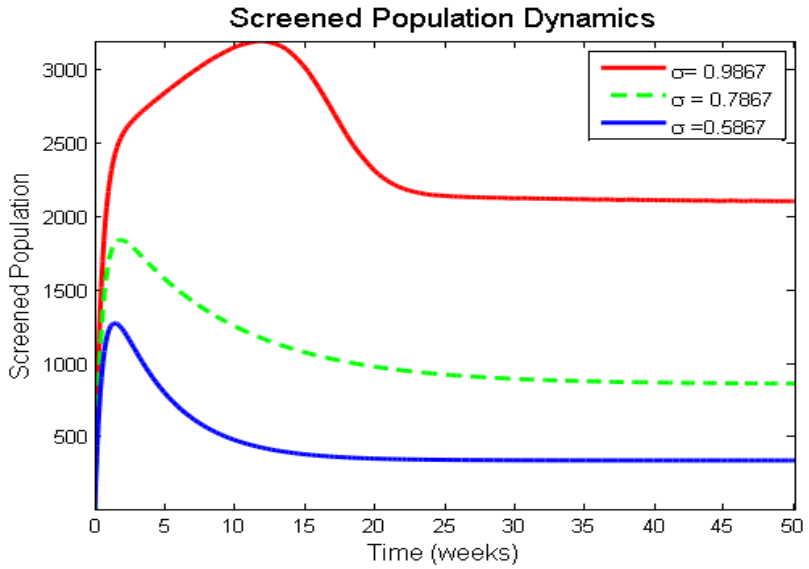

Figure 3: Varying the rate of Screening graph

Novelty Journals

ISSN 2394-9651

International Journal of Novel Research in Physics Chemistry & Mathematics
Vol. 9, Issue 2, pp: (29-39), Month: May - August 2022, Available at: www.noveltyjournals.com

3.2 Infectious Population Dynamics

Figure 4 shows the rate of infectious as we vary the rate of the screening. With time,the infectious population increases due to increase in the rate of screening. The more peeople are screened the more the infectious are identified hence screening exposes the infected among the travelers ,hence the restriction and control of the spread of Covid-19.It can be seen from the graph that screening exposes those who are infected hence screening helps in the management of Covid -19.

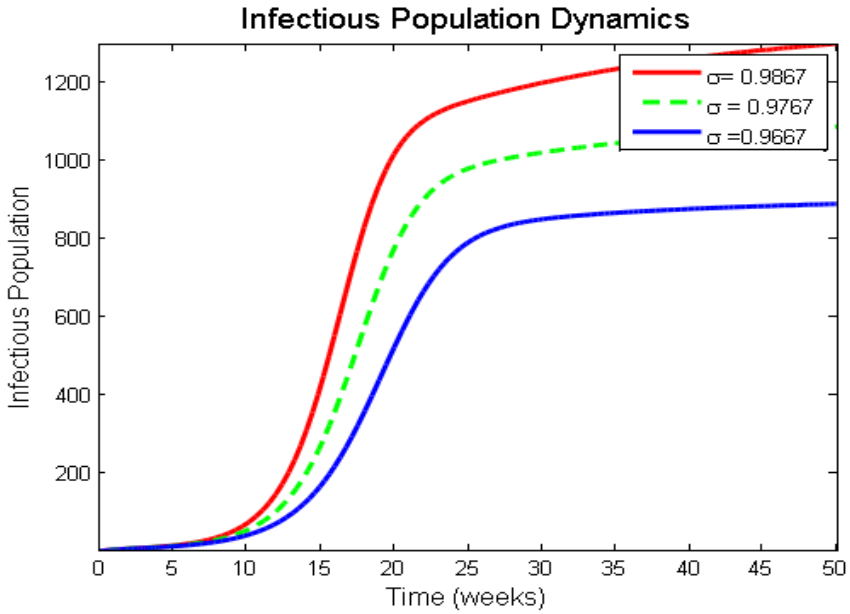

Figure 4: Varying the rate of Screening graph

4. CONCLUSIONS AND RECOMMENDATIONS

4.1 Conclusion

In our study, we created and examined an RT-PCR-integrated deterministic model for the dynamics of Covid 19 among foreign travelers. We determined the model's Basic reproduction number R_0 , which is the anticipated number of secondary infections.The research demonstrates that both globally and locally,the model's disease-free equilibrium is asymptotically stable.

We have also demonstrated that as we increase the number of those who are screened, the number of the susceptible decreases, therefore significantly reducing the number of the people prone to Covid-19 .

The numerical simulations also demonstrate the critical role that RT-PCR traveler screening plays in halting the spread of Covid-19.We can conclude that screening of international travelers using RT-PCR test significantly reduces the rate of the spread of covid -19 among travelers and should be enhanced by policy makers and the international community for the effective management of covid-19 from the results that have been presented because it is clear that there is a significant decrease in the number of Covid -19 infections with an increase in the rate of RT-PCR screening.

4.2 Recommendations

In order to wrap up,we offer the list of suggestions below, the majority of which are directly drawn from the simulation findings presented in this study.

1. According to the results of this investigation,there is a definite correlation between increased screening rates and a large drop in the number of Covid-19 infectives.In order to effectively manage and control the spread of Covid -19, we advise that the use of RT-PCR in screening foreign passengers be used as a control mechanism.

2. Further research can be done whereby the use of RT-PCR screening can be effected for mass testing globally.

3. As we have demonstrated in this study, we recommend that governments should put strict measures to ensure that the use of RT-PCR test is mandatory in testing Covid 19.Other agencies such as faith based institutions and non governmental organizations can also use the findings of this research to sensitize the community.

REFERENCES

[1] Al-Tameemi, Afrah KS and Naji, Raid K. The Impact of Media Coverage and Curfew on the Outbreak of Coronavirus Disease 2019 Model: Stability and Bifurcation. *International Journal of Differential Equations*, 2021, 2021.

[2] Anteneh, Alemzewde Ayalew and Bazezew, Yezbalem Molla and Palanisamy, Shanmugasundaram. Mathematical Model and Analysis on the Impact of Awareness Campaign and Asymptomatic Human Immigrants in the Transmission of COVID-19. *BioMed Research International*, 2022, 2022.

[3] Bolster, Carl H and Hornberger, George M. On the use of linearized Langmuir equations. *Soil Science Society of America Journal*, 71(6):1796–1806, 2007.

[4] Brooks, Heather Z and Kanjanasaratool, Unchitta and Kureh, Yacoub H and Porter, Mason A. Disease detectives: using mathematics to forecast the spread of infectious diseases. *SocArXiv. June*, 30, 2020.

[5] Carpenter, Mark H and Kennedy, Christopher A. Fourth-order 2N-storage Runge-Kutta schemes. Technical report, 1994.

[6] Mbogo, Rachel Waema and Orwa, Titus Okello. SARS-COV-2 outbreak and control in Kenya-Mathematical model analysis. *Infectious Disease Modelling*, 6:370–380, 2021.

[7] Michel, Barath Roy and Lokre, Piyusha and Subramanian, Aarthi Rajam and Kannan, Manivannan and Alvarado, Gianfranco Molfino. A Study on Skills Gap Beyond COVID. *Journal of Innovation in Polytechnic Education*, 4(1):57–61, 2022.

[8] Mwalili, Samuel and Kimathi, Mark and Ojiambo, Viona and Gathungu, Duncan and Mbogo, Rachel. SEIR model for COVID-19 dynamics incorporating the environment and social distancing. *BMC Research Notes*, 13(1):1–5, 2020.

[9] Nda1̆3053′f rou, Fa1̆3053′f çal and Area, Iván and Nieto, Juan J and Torres, Delfim FM. Mathematical modeling of COVID-19 transmission dynamics with a case study of Wuhan. *Chaos, Solitons & Fractals*, 135:109846, 2020.

[10] Onsongo, Winnie Mokeira and Mwini, Enoch Deyaka and Nyanaro, Brian Nyasagare and Osman, Shaibu. The dynamics of psittacosis in human and poultry populations: a mathematical modelling perspective. *J. Math. Comput. Sci.*, 11(6):8472–8505, 2021.

[11] Riyapan, Pakwan and Shuaib, Sherif Eneye and Intarasit, Arthit. A mathematical model of COVID-19 pandemic: a case study of Bangkok, Thailand. *Computational and Mathematical Methods in Medicine*, 2021, 2021.

[12] Russell, Timothy W and Wu, Joseph T and Clifford, Sam and Edmunds, W John and Kucharski, Adam J and Jit, Mark and others. Effect of internationally imported cases on internal spread of COVID-19: a mathematical modelling study. *The Lancet Public Health*, 6(1):e12–e20, 2021.