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Mathematical Modelling of the Impact of stigmatization on Vaccination and on the Spread of COVID -19 in Kenya

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Abstract: **In this study, a $SEIR$ mathematical model incoporating stigmatization and vaccination is developed to asses the effect of stigma on vaccination and transmission dynamics of COVID-19. Unlike several earlier model studies on this condition, we took into account the impact of stigma on vaccination and transmission on COVID-19 .The disease free equilibrium is calculated and its stability proven using the jacobian method,The endemic equilibrium is also evaluated and stablity proven by Hurwitz criteria.The parameters are estimated using available data from the ministry of health and available lierature review.Finally numerical analysis validate the prediction of the model.**

Keywords: **COVID-19 spread dynamics, mathematical modelling, vaccination.**

1. INTRODUCTION

Corona Virus (COVID-19) is a communicable respiratory disease caused by severe acute respiratory syndro (SARS-CoV-2). The virus spreads among people and affects people all over the world through direct and indirect physical contact. The 1^st case of COVID-19 disease was identified in the Chinese city of Wuhan at the end of December 2019. The outbreak quickly spread throughout China and then worldwide, with nearly 237 counties reporting confirmed cases. According to the WHO, there are 259, 502, 031 global confirmed cases and 5, 183, 003 global confirmed deaths by November 29, 2021. It is noteworthy that the WHO reported 611,528 new infected cases, with 7,881 deaths (data source: GAV/WHO, November 29 2021).

The first case of Corona virus disease in Kenya was reported in March 2020. COVID-19 disease was declared by World Health Organization major health hazard at the end of 2019. (WHO). At the moment, this disease is rapidly spreading in many countries, and the global number of COVID-19 cases is rapidly increasing.

Since the outbreak of novel corona viruses, a great variety of scientific modeling techniques have been published, each targeting a different aim in terms of forecasting and regulating pandemic progression (2019-nCoV). One commonly debated subject is ideal authoritarian intervention tactics, which should limit infection numbers in order to avoid future exponential expansion while not placing unnecessary restrictions on economies and people's lives.

Finding and executing an adequate mathematical model that contains specific real-world transmission and transition dynamics is a difficulty in infectious illness modeling. To fit the model to available data such as infection and death numbers and make prediction, suitable and preferably exact algorithms and estimation methods must be chosen and applied.

In this study, an SEIR model incorporating vaccination and stigmatization is developed. The model's development is supported by current information on the incidence, symptomatology, disease progression, and governmental measures.

2. MODEL DESCRIPTION AND FORMULATION

2.1. Model formulation

The proposed model will comprise of a population size $N(t)$ which is then subdivide into 9 classes at any time (t). $S(t)$, susceptible population, exposed individuals $E(t)$, stigmatized population $M(t)$, Susceptible vaccinated individuals $V_s(t)$, Stigmatized vaccinated individualsV_m, Stigmatized vaccinated individuals who are infectious $I_v$individuals with the disease and can infect others $I_s(t)$, Individuals who have gained herd immunity $R_v$and individuals that have recovered/removed from COVID-19 $R(t)$.

Based on this development , the tot. population is

$$N(t) = S(t) + E(t) + M(t) + V_s(t) + V_m(t) + I_v(t) + I_s(t) + R_v(t) + R(t).$$

subject to the following initial conditions:

$S(0) \geq 0,\ E(0) \geq 0,\ M(0) \geq 0,\ V_s(0) \geq 0,\ V_m(0) \geq 0,\ I_v(0) \geq 0,\ I_s(0) \geq 0,\ R_v(0) \geq 0\ R(0) \geq 0.$

2.2 Model Assumptions

1. Everyone in the population has an equal chance of contracting a COVID-19 disease.

2. All vaccinated susceptible individuals acquire herd immunity

3. Recovery rate of vaccinated individiuls is higher than that of unvaccinated individuals

4. Exposed individuals are being stigmatized

2.3 The Model

The figure 1 below depicts the schematic diagram showing the spread of COVID-19.

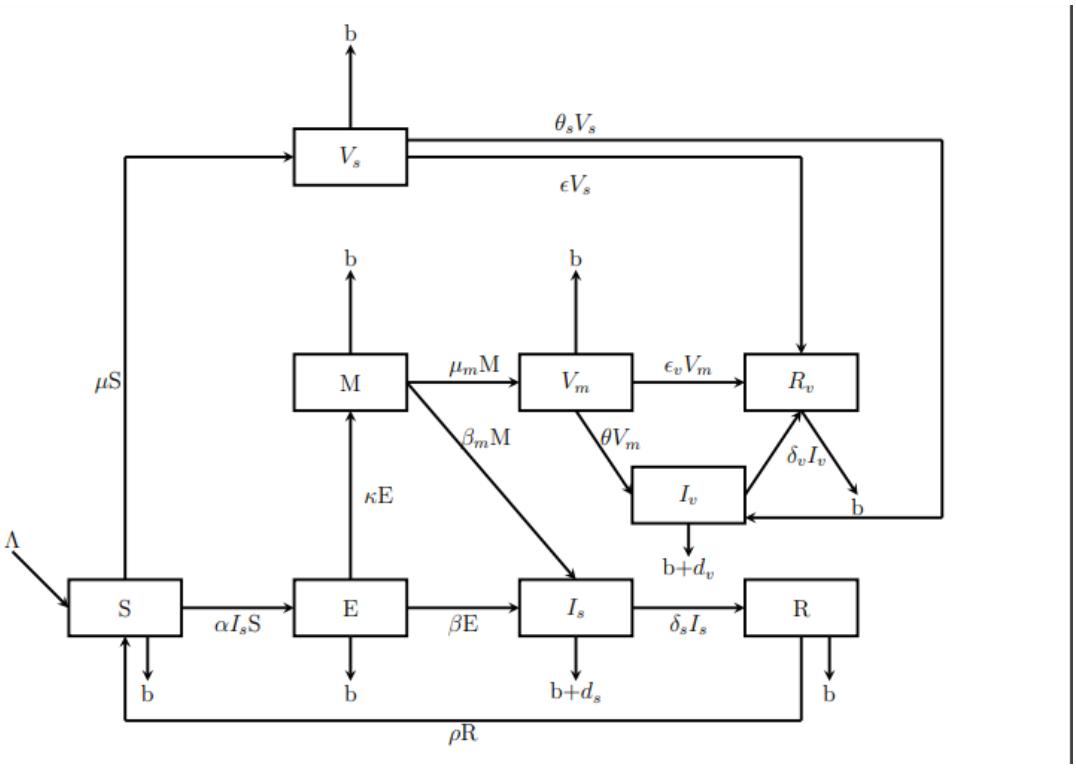


Figure 1: Transmission sequence of COVID-19

Model Compartments and Dynamics

Table 2 describes the model parameters found in Equation 3.1 . The transmission phases are as follows when considering the $SEMVsVmIvIsRvR$ model with six compartments in 1:

The Susceptible class, $S(t)$, grows as a result of the addition of a recruitment rate, Λ and re-infection of recovered individuals at the rate of ρ. It also decreases by infection, which is caused by contact rate of α and natural death rate of b

After having direct contact with an infected person, an individual joins the Exposed class $E(t)$with an infection rate of α. It decreases at the rate of κ by individuals being stigmatized and by the individuals getting infected with the disease at the rate β, then it diminishes by a leaving rate of natural death b.

The stigmatized class $M(t)$ compises of people who progressed from exposed at the rate κ and decreases by vaccination at the rate μ_m and infection rate (β_m) .This class also diminishes by natural death(b).

The vaccinated susceptible individuals $V_s(t)$ class was formed by people who moved from susceptible population at the rate (μ),it decreased by individuals who gained herd immunity at the rate, (ϵ) and individuals who get infected at the rate,θ_s.The class $V_s(t)$ also diminishes by natural death b.

The vaccinated stigmatised individuals V_m was formed by stigmatized people who moved from stigmatized at the rate (μ_m) it decreased by individuals who become infectious at the rate $(\theta)$and also by individuals who gained herd immunity at the rate ϵ_v,This class also diminishes by natural death b.

The infected vaccinated class $I_v(t)$ are people who moved from Vaccinated stigmatized class at the rate θ and from vaccinated susceptible class at the rate θ_s and decreases by acquiring herd immunity at the rateδ_v.It also reduced the natural death rate, b, and disease-related death, dv.

The Infectious class, $I_s(t)$, are those who progress from being exposed at the rateβ and also from stigmatized at the rate of β_m and then this class decreases by recovered at the rateδ_s and also by leaving the rates of natural death, b, and disease-related death, dv.

vaccinated Recovered class$R_v(t)$ are people who moved from vaccinated susceptible at the rate ϵ,vaccinated stigmatized at the rate of ϵ_v and also from infected vaccinated at the rate of δ_v.This class diminishes by natural death b.

The Recovered class,$R(t)$, consists of people who progress from the infectious susceptible at the rate of δs and recovered individuals who return to the susceptible population ρ, who are subsequently followed by the leaving rate of b.

Table 1: Model Variables description

Variables	Description
$S(t)$	Number of susceptible population at time t
$E(t)$	Number of exposed population at time t
$M(t)$	Number of stigmatized population at time t
$V_s(t)$	Number of vaccinated susceptible population at time t
$V_m(t)$	Number of stigmatized vaccinated population at time t
$I_v(t)$	Number of infected vaccinated population at time t
$I_s(t)$	Number of infected population at time t
$R_v(t)$	Number of recovered vaccinated population at time t
$R(t)$	Number of recovered population at time t

Table 2: Model parameter description

parameters	Description
Λ	Recruitment rate
α	Contact rate (effective transmission rate)
β	rate of transmission from E to I_s
d_s	death due to the disease
δ_s	Recovery rate of infectious individuals.
μ	vaccination rate of susceptible individuals
ϵ	rate at which vaccinated susceptible individuals become immune
d_v	death due to the disease of vaccinated individuals
θ_s	infection rate of vaccinated individuals
κ	rate of stigmatization
δ_v	Recovery rate of infectious vaccinated individuals.
β_m	Rate at which stigmatized individuals get vaccinated.

ρ	Recovered population rate back to susceptible class
b	Human natural death rate
ϵ_v	rate at which stigmatized vaccinated individuals become immune
θ	infection rate of vaccinated stigmatized
μ_m	vaccination rate of stigmatized individuals

Model equations

$$\frac{dS}{dt} = \Lambda + \rho R - (\mu + \alpha I_s + b)S$$

$$\frac{dE}{dt} = \alpha I_s S - (\kappa + \beta + b)E$$

$$\frac{dM}{dt} = \kappa E - (\mu_m + \beta_m + b)M$$

$$\frac{dV_s}{dt} = \mu_S - (\theta_s + \epsilon + b)V_s$$

$$\frac{dV_m}{dt} = \mu_m M - (\epsilon_v + \theta + b)V_m \quad (3.1)$$

$$\frac{dI_v}{dt} = \theta V_m + \theta_s V_s - (\delta_v + b + d_v)I_v$$

$$\frac{dI_s}{dt} = \beta E + \beta_m M - (\delta_s + b + d_s)I_s$$

$$\frac{dR_v}{dt} = \epsilon_v V_m + \delta_v I_v + \epsilon V_s - bR_v$$

$$\frac{dR}{dt} = \delta_s I_s - \rho R - bR$$

Disease Free Equilibrium(DFE)

Disease free equilibrium is a state where there is no any human infected.Therefore the population is free from the virus.

To determine the equilibria of this model , we set the right hand side of equations 3.1 to 0 and solve the system.This system D.F.E is obtained by setting $E = I_s = I_v = M = V_m = V_s = R_v = R = 0$

To solve for DFE this model , we set the derivatives of equations 3.1 to 0 and solve the system.This system D.F.E is obtained by setting $E = I_s = I_v = M = V_m = V_s = R_v = R = 0$ The system of equation simplifies to:

$\frac{dS}{dt} = \Lambda + \rho R + (\mu + \alpha + b)S$

$$S^* = \frac{\Lambda}{\mu + b} \quad (3.2)$$

Therefore the D.F.E is given by ;

$(S^*, E^*, M^*, V_s^*, V_m^*, I_v^*, I_s^*, R_v^*, R^*) = (\frac{\Lambda}{(\mu+b)}, 0,0,0,0,0,0,0,0)$

Endemic Equillibrium

In this section we are going to to look at at the existence of endemic equilibrium

let $\varepsilon^*=(S^*, E^*, M^*, V_s^*, V_m^*, I_v^*, R_v^*, R^*)$ be the endemic equilibrium of model 3.1 ,One can find the ε^* of equation 3.1 by setting the left-hand expressions to zero and then solving tin terms of the number of infectives I_s^*.

The equations of endemic equilibrium are then given by :

$$0 = \Lambda + \rho R - (\mu + \alpha I_s + b)S$$

$$0 = \alpha I_s S - (\kappa + \beta + b)E$$

$$0 = \alpha I_s S - (\kappa + \beta + b)E$$

$$0 = \kappa E - (\mu_m + \beta_m + b)M$$

$$0 = \mu_S - (\theta_s + \epsilon + b)V_s$$

$$0 = \mu_m M - (\epsilon_v + \theta + b)V_m \qquad (3.3)$$

$$0 = \theta V_m + \theta_s V_s - (\delta_v + b + d_v)I_v$$

$$0 = \beta E + \beta_m M - (\delta_s + b + d_s)I_s$$

$$0 = \epsilon_v V_m + \delta_v I_v + \epsilon V_s - bR_v$$

$$0 = \delta_s I_s - \rho R - bR$$

solving to find$(S^*, E^*, M^*, V_s^*, V_m^*, I_v^*, R_v^*, R^*)$in terms of the number of infectives I_s^* we obtain :

$$S^* = \frac{\Lambda(b+\rho) + \rho\delta_s I_s}{(\mu + \alpha I_s + b)(b+\rho)}$$

$$E^* = \frac{\alpha I_s^*(\Lambda(b+\rho) + \rho\delta_s I_s)}{(\mu + \alpha I_s^* + b)(b+\rho)(\kappa+\beta+b)}$$

$$M^* = \frac{\kappa\alpha I_s^*(\Lambda(b+\rho) + \rho\delta_s I_s)}{(\mu + \alpha I_s^* + b)(b+\rho)(\kappa+\beta+b)(\mu_m+\beta_m+b)}$$

$$V_s^* = \frac{mu(\Lambda(b+\rho) + \rho\delta_s I_s^*)}{(\mu + \alpha I_s^* + b)(b+\rho)(\theta_s+\epsilon+b)}$$

$$V_m^* = \frac{\mu_m\kappa\alpha I_s(\Lambda(b+\rho) + \rho\delta_s I_s^*)}{(\mu + \alpha I_s^* + b)(b+\rho)(\kappa+\beta+b)(\mu_m+\beta_m+b)(\epsilon_v+\theta+b)}$$

$$I_v^* = \frac{\theta\mu_m\kappa\alpha I_s^*(\Lambda(b+\rho)+\rho\delta_s I_s^*)}{(\mu+\alpha I_s^*+b)(b+\rho)(\kappa+\beta+b)(\mu_m+\beta_m+b)(\epsilon_v+\theta+b(\delta_v+b+d_v)} + \frac{\theta_s\mu(\Lambda(b+\rho)+\rho\delta_s I_s^*)}{(\mu+\alpha I_s^*+b)(b+\rho)(\theta_s+\epsilon+b)(\delta_v+b+d_v)}$$

$$R_v^* = \frac{\epsilon_v \mu_m \kappa \alpha I_s^* (\Lambda(b+\rho)+\rho\delta_s I_s^*)+\delta_v \theta \mu_m \kappa \alpha I_s^* (\Lambda(b+\rho)+\rho\delta_s I_s+\theta_s \mu(\Lambda(b+\rho)+\rho\delta_s I_s^*)+\epsilon\mu(\Lambda(b+\rho)+\rho\delta_s I_s)}{(\mu+\alpha I_s^*+b)(b+\rho)(\kappa+\beta+b)(\mu_m+\beta_m+b)(\epsilon_v+\theta+b)(\theta_s+\epsilon+b)(b)}$$

$$R^* = \frac{\delta_s I_s^*}{b+\rho}$$

where;

$$f(I_s^*) = c_2 {I_s^*}^2 + c_1 I_s^* + c_o = 0 \tag{3.4}$$

To do this we consider the 7th equation in equation3.1 and solve it

$$\beta E + \beta_m M - (\delta_s + b + d_s) I_s = 0$$

$$\beta E + \beta_m M = (\delta_s + b + d_s) I_s$$

Dividing both sides by $(\delta_s + b + d_s) I_s$

$$\frac{\beta E + \beta_m M}{(\delta_s + b + d_s) I_s} = 1$$

$$= \frac{\beta \alpha I_s^* (\Lambda(b+\rho)+\rho\delta_s I_s)}{(\mu+\alpha I_s^*+b)(b+\rho)(\kappa+\beta+b)} + \frac{\kappa \alpha I_s^* (\Lambda(b+\rho)+\rho\delta_s I_s)}{(\mu+\alpha I_s^*+b)(b+\rho)(\kappa+\beta+b)(\mu_m+\beta_m+b)}$$

$$= \frac{\beta(\alpha I_s^* (\Lambda(b+\rho)+\rho\delta_s I_s)((\mu_m+\beta_m+b)+\kappa\alpha I_s^* (\Lambda(b+\rho)+\rho\delta_s I_s)}{(\mu+\alpha I_s^*+b)(b+\rho)(\kappa+\beta+b)((\delta_s+b+d_s)I_s)}$$

Recall R_0 can be simplified as ; $R_0 = \frac{\beta_m \alpha \Lambda \kappa + \alpha \Lambda \beta (\mu_m+\beta_m+b}{(\kappa+\beta+b)((\delta_s+b+d_s)(\mu_m+\beta_m+b)(\mu+b)}$

Multiplying both sides by $\frac{(\mu+\alpha I_s^*+b)}{\mu+b}$ to obtain:

$$\frac{\beta(\alpha I_s^* (\Lambda(b+\rho)+\rho\delta_s I_s)((\mu_m+\beta_m+b)+\kappa\alpha I_s^* (\Lambda(b+\rho)+\rho\delta_s I_s)}{(\mu+b)(b+\rho)(\kappa+\beta+b)((\delta_s+b+d_s)I_s)} = \frac{(\mu+\alpha I_s^*+b)}{\mu+b}$$

$$= R_o + \frac{\alpha I_s^* (\beta\rho\delta_s I_s^* + \beta_m \rho \delta_s I_s^*}{(b+\rho)(\kappa+\beta+b)(\delta_s+b+d_s)I_s(\mu+b)} = 1 + \frac{\alpha I_s}{\mu+b}$$

This can be simplified as

$$(\alpha((b+\rho)(\kappa+\beta+b)(\delta_s+b+d_s))I_s^2 * - \frac{(\alpha(\beta\rho\delta_s + \beta_m\rho\delta_s)I_s^*}{(b+\rho)(\kappa+\beta+b)(\delta_s+b+d_s)(\mu+b)} + 1 - R_o$$

Where:

$$c_2 = (\alpha\big((b+\rho)(\kappa+\beta+b)(\delta_s+b+d_s)\big)$$

$$c_1 = (\alpha(\beta\rho\delta_s + \beta_m\rho\delta_s)I_s^*(b+\rho)(\kappa+\beta+b)(\delta_s+b+d_s)(\mu+b)$$

$$c_0 = 1 - R_o$$

We can summarize the endemic equilibria of model equation 3.1 through the following theorem:

1. A unique endemic equilibrium if$c_1 < 0 and c_0 = 0$or the discriminant $\Delta = c_1^2 - 4c_2c_0 = 0$,
2. A unique endemic equilibrium if $c_0 < 0$,
3. Two endemic equilibria if $c_1 < 0, c_0 > 0$ and $\Delta = c_1^2 - 4c2c_0 > 0$
4. No endemic equilibrium if $c_1 > 0$and $c_0 > 0$.

Basic Reproduction Number R_0

R_0 represents the average number of new infections that a single infected person will spread during their illness. It is used to foretell how an illness will progress (i.e., whether it will spread, die, or remain stable): If R_0 is greater than 1, the disease will spread; if $R0$ is less than 1, the disease will die out; and if R_0 is equal to 1, the disease will become endemic, meaning it will migrate across the population but not increase or diminish.

In this section we derive R_0 using next generation matrix approach .We consider the infectious classes in our model

To calculate R_0 we consider the following infectious classes $E(t), M(t), V_m(t), I_s(t)$and $I_v(t)$

$$\frac{dE}{dt} = \alpha I_s S - (\kappa + \beta + b)E$$

$$\frac{dM}{dt} = \kappa E - (\mu_m + \beta_m + b)M$$

$$\frac{dV_m}{dt} = \mu_m M - (\epsilon_v + \lambda + b)V_m \qquad (3.5)$$

$$\frac{dI_v}{dt} = \theta V_m + \theta_s V_s - (\epsilon_v + \lambda + b)I_v$$

$$\frac{dI_s}{dt} = \beta E - (\delta_s + b + d)I_s$$

Let $x = (S, E, M, V_s, V_m, I_s, I_v, R_v, R)^T$, F(x) be the no of new infection coming into the system and V(x) coming out of the system,the equation can be written as

$\frac{dx}{dt} = F(x) - V(x)$.

The next gen approach is defined as ; $K = FV^{-1}$ and R_0=$\rho(FV^{-1})$ F(x)= $\begin{bmatrix} \alpha I_s S \\ \kappa E \\ \mu_m M \\ \theta V_m + \theta_s V_s \\ \beta E + \beta_m M \end{bmatrix}$

V(x)= $\begin{bmatrix} (\kappa + \beta)E \\ (\mu_m + \beta_m + b)M \\ (\epsilon_v + \theta + b)V_m \\ \delta_v I_v \\ \delta_s I_s \end{bmatrix}$

$$F = \begin{bmatrix} 0 & 0 & 0 & 0 & \alpha S_o \\ \kappa & 0 & 0 & 0 & 0 \\ 0 & \mu_m & 0 & 0 & 0 \\ 0 & 0 & \theta & 0 & 0 \\ \beta & \beta_m & 0 & 0 & 0 \end{bmatrix}$$

The partial derivatives of equation 3.5 in respect to E, M, V_m, I_v, I_s

$$V = \begin{bmatrix} (\kappa+\beta+b) & 0 & 0 & 0 & 0 \\ 0 & (\mu_m+\beta_m+b) & 0 & 0 & 0 \\ 0 & 0 & (\epsilon_v+b+\theta & 0 & 0 \\ 0 & 0 & 0 & (\delta_v+b+d) & 0 \\ 0 & 0 & 0 & 0 & (\delta_s+b+d) \end{bmatrix}$$

$$FV^{-1} = \begin{bmatrix} 0 & 0 & 0 & 0 & \alpha S_o \\ \kappa & 0 & 0 & 0 & 0 \\ 0 & \mu_m & 0 & 0 & 0 \\ 0 & 0 & \lambda & 0 & 0 \\ \beta & \beta_m & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{(\kappa+\beta+b)} & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{(\mu_m+\beta_m+b)} & 0 & 0 & 0 \\ 0 & 0 & \frac{1}{(\epsilon_v+b+\theta)} & 0 & 0 \\ 0 & 0 & 0 & \frac{1}{\delta_v+b+d} & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{\delta_s+b+d} \end{bmatrix} =$$

$$\begin{bmatrix} 0 & 0 & 0 & 0 & \alpha S_0 \\ \frac{\kappa}{\kappa+\beta+b} & 0 & 0 & 0 & 0 \\ 0 & \frac{\mu_m}{\mu_m+\beta_m+b} & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{\theta}{\epsilon+\beta+\theta} & 0 \\ \frac{\beta}{\kappa+\beta+b} & \frac{\beta_m}{\mu_m+\beta_m+b} & 0 & 0 & 0 \end{bmatrix}$$

The eigenvalues of matrix product FV^{-1} are:

0, 0,0,$\frac{\alpha S_o \beta_m}{(\kappa+\beta+b)(\delta_s+b+d)}$ and $\frac{\beta \alpha S_o \kappa}{(\kappa+\beta+b)(\delta_s+b+d)(\mu_m+\beta_m+b}$

Thus, reproduction number is given by :

$$R_o = \frac{\beta_m \alpha S_o \kappa}{(\kappa+\beta+b)(\delta_s+b+d)(\mu_m+\beta+b} + \frac{\alpha S_o \beta}{(\kappa+\beta+b)(\delta_s+b+d)}$$

But we know that $S_0 = \frac{\Lambda}{\mu+b}$ Therefore;

$$R_o = \frac{\beta_m \alpha \Lambda \kappa}{(\kappa+\beta+b)(\delta_s+b+d)(\mu_m+\beta+b)(\mu+b)} + \frac{\alpha \Lambda \beta}{(\kappa+\beta+b)(\delta_s+b+d)(\mu+b)} \quad (3.6)$$

Denoting the basic reproduction numbers for stigmatized individuals R_m and for non stigmatized individuals R_s, we make the following deductions:

$$R_m = \frac{\beta_m \alpha \Lambda \kappa}{(\kappa+\beta+b)(\delta_s+b+d)(\mu_m+\beta+b)(\mu+b)}$$

$$R_s = \frac{\alpha \Lambda \beta}{(\kappa+\beta+b)(\delta_s+b+d)(\mu+b)}$$

$R_0 = R_s + R_m$

Local Stability of Disease Free Equilibrium

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

The jacobian matrix of the model equation $J(S, E, M, V_s, V_m, I_v, I_s, R_v, R)$

$$= \begin{bmatrix} -(\mu+\alpha I_s+b) & 0 & 0 & 0 & 0 & 0 & -\alpha S & 0 & \rho \\ \alpha I_s & -(\kappa+\beta+b) & 0 & 0 & 0 & 0 & \alpha S & 0 & 0 \\ 0 & \kappa & -(\mu_m+\beta_m+b) & 0 & 0 & 0 & 0 & 0 & 0 \\ \mu & 0 & 0 & -(\theta_s+\epsilon+b) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \mu_m & 0 & -(\epsilon_v+\theta+b) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta_s & \theta & -(\delta_v+b+d) & 0 & 0 & 0 \\ 0 & \beta & 0 & 0 & 0 & 0 & -(\delta_s+b+d) & 0 & 0 \\ 0 & 0 & 0 & \epsilon & \epsilon_v & \delta_v & 0 & -b & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \delta_s & 0 & -(\rho+b) \end{bmatrix}$$

At DFE S=$\frac{\Lambda}{\mu+b}$, I=0

$$J(\epsilon^o) = \begin{bmatrix} -(\mu+b) & 0 & 0 & 0 & 0 & 0 & -\alpha & \frac{\Lambda}{\mu+b} & \rho \\ 0 & -(\kappa+\beta+b) & 0 & 0 & 0 & 0 & \alpha\frac{\Lambda}{\mu+b} & 0 & 0 \\ 0 & \kappa & -(\mu_m+\beta_m+b) & 0 & 0 & 0 & 0 & 0 & 0 \\ \mu & 0 & 0 & -(\epsilon+b) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \mu_m & 0 & -(\epsilon_v+\theta+b) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \theta & -(\delta_v+b+d) & 0 & 0 & 0 \\ 0 & \beta & 0 & 0 & 0 & 0 & -(\delta_s+b+d) & 0 & 0 \\ 0 & 0 & 0 & \epsilon & \epsilon_v & \delta_v & 0 & -b & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \delta_s & 0 & -(\rho+b) \end{bmatrix}$$

Finding the determinant of the jacobian matrix of DFE gives:

$$\begin{bmatrix} -(\mu+b)-\lambda & 0 & 0 & 0 & 0 & 0 & -\alpha & \frac{\Lambda}{\mu+b} & \rho \\ 0 & -(\kappa+\beta+b)-\lambda & 0 & 0 & 0 & 0 & \alpha\frac{\Lambda}{\mu+b} & 0 & 0 \\ 0 & \kappa & -(\mu_m+\beta_m+b)-\lambda & 0 & 0 & 0 & 0 & 0 & 0 \\ \mu & 0 & 0 & -(\theta_s+\epsilon+b)-\lambda & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \mu_m & 0 & -(\epsilon_v+\theta+b)-\lambda & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta_s & \theta & -(\delta_v+b+d)-\lambda & 0 & 0 & 0 \\ 0 & \beta & 0 & 0 & 0 & 0 & -(\delta_s+b+d)-\lambda & 0 & 0 \\ 0 & 0 & 0 & \epsilon & \epsilon_v & \delta_v & 0 & -b-\lambda & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \delta_s & 0 & -(\rho+b)-\lambda \end{bmatrix}$$

Where λ is the eigen values

Since all the eigen values are negative . Then the DFE is locally assymptotically stable.

stability of endemic equilibrium

We consider the local stability of the endemic equilibrium point $\varepsilon^* = (S^*, E^*, M^*, V_s^*, V_m^*, I_v^*, R_v^*, R^*)$ by analyzing the

eigenvalues of the Jacobian matrices of 1 at the endemic equilibrium point using the Routh Hurwitz Criterion.

The jacobian matrix of the model equation $J(S^*, E^*, M^*, V_s^*, V_m^*, I_v^*, R_v^*, R^*)$

$J(\varepsilon^*) =$

$$\begin{bmatrix} -(\mu+\alpha I_s^*+b) & 0 & 0 & 0 & 0 & 0 & -\alpha S^* & 0 & \rho \\ \alpha I_s^* & -(\kappa+\beta+b) & 0 & 0 & 0 & 0 & \alpha S^* & 0 & 0 \\ 0 & \kappa & -(\mu_m+\beta_m+b) & 0 & 0 & 0 & 0 & 0 & 0 \\ \mu & 0 & 0 & -(\theta_s+\epsilon+b) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \mu_m & 0 & -(\epsilon_v+\theta+b) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta_s & \theta & -(\delta_v+b+d) & 0 & 0 & 0 \\ 0 & \beta & 0 & 0 & 0 & 0 & -(\delta_s+b+d) & 0 & 0 \\ 0 & 0 & 0 & \epsilon & \epsilon_v & \delta_v & 0 & -b & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \delta_s & 0 & -(\rho+b) \end{bmatrix}$$

Expanding the ramaining part we obtain five roots equation equal that is $\lambda_1 = -(\mu_m + \beta_m + b)$,$\lambda_2 = -(\theta_s + \epsilon + b)$, $\lambda_3 = -(\delta_v + b + d)$,$\lambda_4 = -b$ and $\lambda_5 = -(\epsilon_v + \theta + b)$.

The remaining roots are solutions to the following equation:

$$\begin{bmatrix} -(\mu+\alpha I_s^*+b) & 0 & -\alpha S^* & \rho \\ \alpha I_s^* & -(\kappa+\beta+b) & \alpha S^* & 0 \\ 0 & \beta & -(\delta_s+b+d) & 0 \\ 0 & 0 & \delta_s & -(\rho+b) \end{bmatrix}$$

from which we obtain the characteristic equation

$$\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a^4 = 0 \qquad (3.7)$$

where:

$$a_1 = (\mu + \alpha I_s^* + b) + (\kappa + \beta + b) + (\delta_s + b + d) + (\rho + b)$$

$$a_2 = (\mu + \alpha I_s^* + b)((\kappa + \beta + b) + (\delta_s + b + d) + (\rho + b)) + (\kappa + \beta + b)((\delta_s + b + d) + (\rho + b)) + (\rho + b)(\delta_s + b + d) - \beta(\alpha S^*)$$

$$a_3 = (\mu + \alpha I_s^* + b)((\kappa + \beta + b)(\delta_s + b + d)) + (\rho + b)((\mu + \alpha I_s^* + b)(\delta_s + b + d)) + \beta(\alpha S^*)((\alpha I_s^*) - (\mu + \alpha I_s^* + b) - (\rho + b)) \qquad (3.8)$$

$$a_4 = (\rho + b)(\mu + \alpha I_s^* + b)((\kappa + \beta + b)(\delta_s + b + d) - \beta(\alpha S^*)) + \beta(\alpha I_s^*)((\rho + b)(\alpha S^*) - \rho\delta_s))$$

Notice that a_1 is always positive. Thus, by the Routh-Hurwitz criterion, we have that the endemic equilibrium of (1) is locally asymptotically stable if and only if $a_3 > 0, a_4 > 0 and a_1a_2a_3 > a_3^2 + a_1^2a_4$. Hence, the theorem follows.

4. NUMERICAL SOLUTIONS

Parameters Estimation

In this section, we fit the COVID-19 model to data from ministry of health. We chose the initial conditions based on the assumption that COVID-19 affects nearly the entire Kenyan population. The preliminary data indicate that there were three cases of COVID-19 as of March 3, 2020, but we believe the disease had been spreading undetected for some time within the Kenyan population. As a result, we start with $S = 47000000, E = 0, M = 0, Vs = 0, Vm = 0, Is = 100, Iv = 0, Rv = 0, R = 0$. The COVID-19 literature is used to obtain the baseline parameters.

Parameter	Value	Source
Λ	9.8	[23]
α	0.8633	[20]
β	0.1857	[20]
d_s	0.015	estimated
δ_s	0.0518	estimated
μ	0.03	[21]
ϵ	0.01	[21]
d_v	0.01	[21]
θ_s	0.1	[21]
κ	0.45	estimated
δ_v	0.2	[22]
β_m	0.25	Assumed
ρ	0.0032	[23]
b	0.013	[23]
ϵ_v	0.018	assumed
θ	0.51	assumed
β_m	0.72	assumed
μ_m	0.083	assumed

5. THE DYNAMICAL BEHAVIOR OF THE MODEL SYSTEM

Here, we analyze the population's biological trend in the presence of vaccination and stigmatization by analyzing the dynamical behavior of model 3.1 .

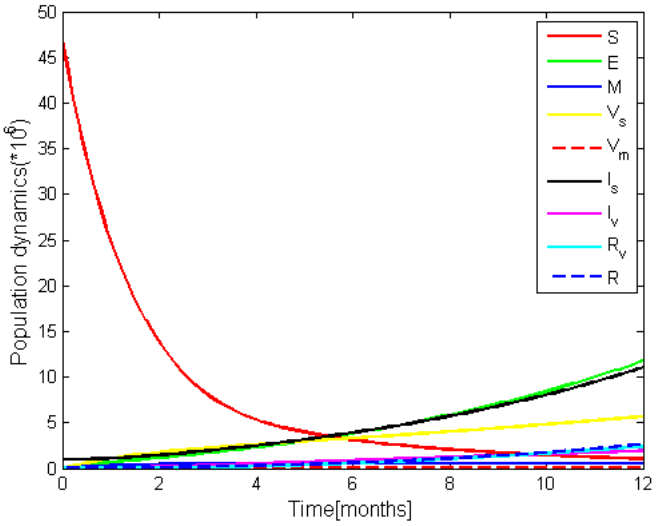


Figure 2: The The dynamical behavior of the model system

Figure 2 shows the dynamic behaviour of susceptible, Exposed, stigmatized ,vaccinated susceptible, Vaccinated stigmatized,infected vaccinated,infected susceptible,Infected susceptible,Recovered vaccinated and Recovered classes.

MATLAB generates the plot above using the parameter values shown in section 5.11. The susceptible population decreases. On the other hand exposed population increases with time to their carrying capacities.

Stigmatized population also increases with time.Vaccinated susceptible population and vaccinated stigmatized also increases with time. It should be noted that vaccinated susceptible population increases with high rate as compared to vaccinated stigmatized population. Susceptible infected individuals increase and vaccinated infected individuals also increases with time. Vaccinated infected individuals increases with a lower rate as compared to the unvaccinated individuals,This is because of vaccination which decreases infection rate. The recovered population individuals and recovered vaccinated also increased with time.

Impact of stigma on the vaccine intake of Covid-19

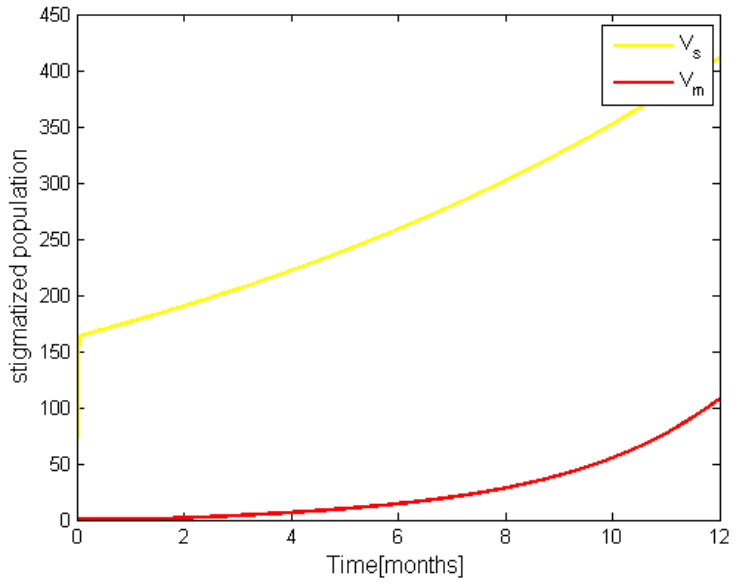
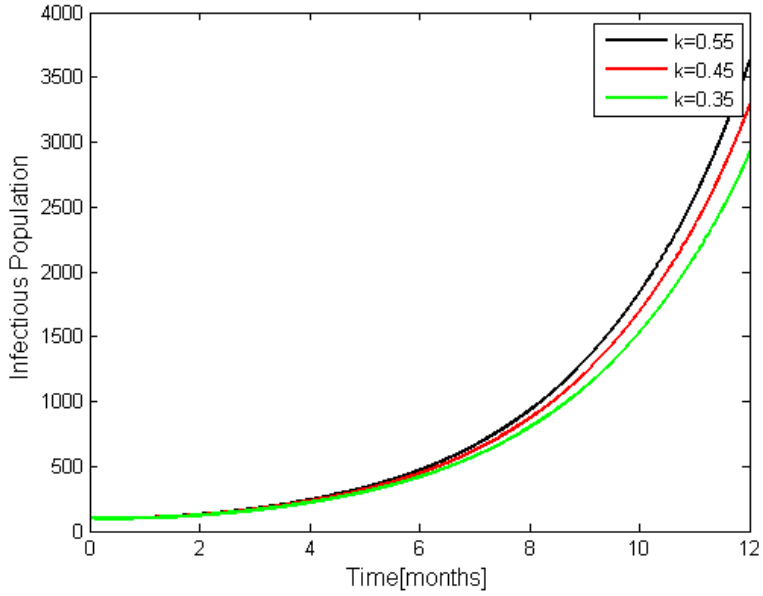


Figure 3: The impact of stigma on the vaccine intake of Covid-19

Fig 3 shows the impact of stigmatization on vaccine intake of covid 19 where V_s is the vaccinated susceptible individuals and V_m are the vaccinated stigmatized population

From figure3 ,unstigmatized individualsV_s has high vaccine intake as compared to the stigmatized individuals V_m.This is true to say that stigmatization has negative impact on vaccine intake.In this case

Impact of stigma on infection of the disease



The effect of stigma on infection of the disease

Fig4.4 displays the impact of stigmatization on the infection of covid 19 as stigmatization rate vary (κ = 0.55,0.45 and 0.35)

From fig 4.4 ,stigma increases the infection of covid 19, When stigma increases, especially among the infected population, the disease spreads quicker than when stigma levels are low.In this instance, intervention techniques that aim to decrease the spread of covid 19 by lowering stigma among afflicted persons are required.

limitation of the study

The following limitations were found in this study:

1. There was no data available for stigmatization of Covid 19.
2. Absence of comparable research in the same field

6. CONCLUSION AND RECOMMENDATIONS

conclusion

In this thesis we formulated a $SEMV_sV_mI_vI_sR_vR$ model to assess the effect of stigma on on COVID-19 vaccination intake and on the spread ofCOVID-19.

T Numerical analysis suggested that stigma increases the rate of infection of COVID-19 among the infected individuals. It also pointed out that stigma decreases the rate of vaccine intake among the population. We also noted that vaccination had a positive impact in controlling the spread of COVID-19 as it decreased the infection rate.

Recommendations

1. There is need to educate the community on the dangers of COVID-19 stigma.
2. More research need to be done on COVID -19 related stigma.
3. More efforts should be made to encourage people to get the COVID-19 vaccine.
4. Institutions working on COVID-19 prevention should deal with the problem of COVID-19 and its associated stigma.

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