

Mathematical Modeling of the effects of gender-based stigmatization on COVID-19 virus transmission in Kenya

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Abstract: Covid-19 has spread throughout the globe, killed millions of people, shattered economies of even the superpower countries and made people to change their way of living since it was discovered in wuhan, china. Covid-19 reached kenya on march 2020 when the ministry of health announced the first positive case in the city of Nairobi from an international traveller. Understanding the transmission dynamics and effective control measures have been crucial for researchers in creating mathematical models and determining the transmission potential of covid-19 in new areas. Our research aims to determine the effect of gender-based stigmatization in the spread of covid-19 and therefore we developed a $(S, E_m, E_f, I_m, I_f, T, Q, R)$ mathematical model of Covid-19 comprising of eight compartments; Susceptible(S), Exposed male (E_m), Exposed female (E_f), Infected male (I_m), Infected female (I_f), Treatment (T), Stigmatized (Q) and Recovered (R). We used the next generation matrix approach to calculate the reproduction number R_0 , explore the occurrence of equilibrium points, both disease-free and endemic, and analyze their stabilities. We used MATLAB to solve and generate the numerical solutions of the model differential equations. After interpretation the results show that increase of stigmatization, increases the infection rate of covid-19 and decrease of stigmatization decreases the infection rate of covid-19 for both male and female. Hence we recommended that the government and relevant authorities should use this report to curb stigmatization through sensitization, awareness, speaking against negative stereotypes and providing the necessary support required by encouraging people to take tests and seek healthcare immediately they start showing covid symptoms.

Keywords: COVID-19 spread dynamics, mathematical modelling, epidemiological modelling, stigmatization.

1. INTRODUCTION

Corona viruses are a large viral species found in humans and a range of animal species which include camels, cattle, cats, and bats. Coronaviruses are most commonly spread through direct contact with respiratory secretions, however other mechanisms of transmission have been discovered. Transmission between people through contact touch is currently the most common form of COVID-19 transmission. covid-19 is a disease created by SARS-CoV-2 virus infection discovered in Dec 2019 in Wuhan, China. SARS-CoV-2 is a part of the corona virus family, which contains viruses that lead to everything from head or chest common cold to more serious infections. [7]

Millions of cases of covid, have been reported in China and other countries since it was first identified. It is very contagious and it has spread quickly throughout the world. The first Covid infection case in Kenya was reported on march 12, 2020 in Nairobi, and since then, virus infections have been reported throughout the country. COVID-19 most commonly produces cold, flu, or pneumonia-like respiratory symptoms.

According to the WHO, the majority of persons infected with the disease experience mild to severe respiratory symptoms and recuperate without the need for special treatment. Some, on the other hand, will become dangerously unwell and will require medical attention. People over the age of 65 are more likely to suffer major illnesses, as are those who have underlying health disorders such as heart disease, diabetes, severe respiratory disease, or cancer. [9]

Individuals with the disease, those displaying similar characteristics to those of covid-19, and those who have simply come into contact with infected or recovered individuals have all faced discrimination as a result of the virus's stigma. More stigma has resulted in group isolation, which has resulted to more severe issues and challenges in the disease control. According to the United Nations, males are more infected than females. For example, according to a report published by the Ministry of Health Kenya (2020) on July 13, 2020, 68 percent of total infections (6951 of 10294) were male, while 32 percent were female (3343 of 10294).

Stigmatization occurs not only among members of society, but also within the health-care system. Stigmatization affects not only the infected and their families, but also health care workers who come into contact with people infected with the virus. Workers in health care have been emotionally and physically abused, had their homes evicted, and have even been separated from their families. These practices are carried out by ordinary citizens who are afraid of the virus and clearly lack the necessary knowledge about covid-19.

In Kenya, male individuals are more infected compared to female, according to all daily covid-19 reports by ministry of health. For instance a report published by the ministry of health Kenya (2020) as per 13th July 2020, it shows that 68% of total infections were male (6951 of 10294) compared to 32% infections of female (3343 of 10294). This study will seek to show how gender based stigmatization have affected the spread of COVID-19, hence it will help the government and various stakeholders tackle stigmatization and discrimination of COVID-19 as a way of controlling the spread of the disease in Kenya.

2. MODEL DESCRIPTION AND FORMULATION

The population model will have a population size $N(t)$ that is divided into eight compartments at any given time (t). Susceptible population, $S(t)$, exposed male population, $E_m(t)$, exposed female population, $E_f(t)$, infected male population, $I_m(t)$, infected female population, $I_f(t)$, stigmatized population, $Q(t)$, population that receives treatment, $T(t)$ and the recovered population, $R(t)$. The population model will be written down as follows:

$$N(t) = S(t) + E_m(t) + E_f(t) + I_m(t) + I_f(t) + Q(t) + T(t) + R(t)$$

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

d -Natural deaths

b - Deaths due to covid

$\frac{I_m}{N}$ -fraction of infected male population that that comes in contact with the susceptible population

$\frac{I_f}{N}$ -fraction of infected female population that comes into contact with the susceptible population

β - rate at which treated individuals recovers

α_1 -rate at which exposed male population is infected

α_2 -rate at which exposed female population is infected

μ_1 -rate at which infected male population gets treatment

μ_2 -rate at which infected female population gets treatment

δ_1 - male contact rate

δ_2 - female contact rate

ρ_1 -rate at which infected male population is stigmatized

ρ_2 -rate at which infected female population is stigmatized

ϵ -rate at which stigmatized population recovers

θ -rate at which recovered population becomes susceptible

2.2 Model diagram

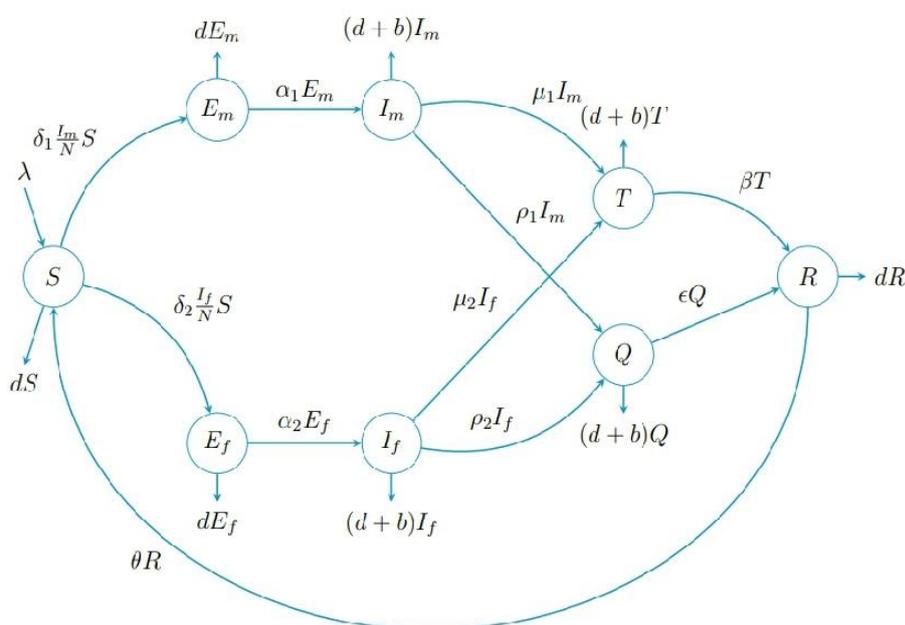


Figure 1: Stigmatized gender based model of COVID-19

The following system of equations represents the model:

$$\frac{dS}{dt} = \lambda + \theta R - dS - \delta_1 \frac{I_m}{N} S - \delta_2 \frac{I_f}{N} S \tag{2.1}$$

$$\frac{dE_m}{dt} = \delta_1 \frac{I_m}{N} S - \alpha_1 E_m - dE_m \tag{2.2}$$

$$\frac{dE_f}{dt} = \delta_2 \frac{I_f}{N} S - \alpha_2 E_f - dE_f \tag{2.3}$$

$$\frac{dI_m}{dt} = \alpha_1 E_m - (d + b + \mu_1 + \rho_1) I_m \tag{2.4}$$

$$\frac{dI_f}{dt} = \alpha_2 E_f - (d + b + \mu_2 + \rho_2) I_f \tag{2.5}$$

$$\frac{dT}{dt} = \mu_1 I_m + \mu_2 I_f - (d + b + \beta) T \tag{2.6}$$

$$\frac{dQ}{dt} = \rho_1 I_m + \rho_2 I_f - (d + b + \epsilon) Q \tag{2.7}$$

$$\frac{dR}{dt} = \beta T + \epsilon Q - (d + \theta) R \tag{2.8}$$

Let $\frac{I_m}{N} = I_m, \frac{I_f}{N} = I_f$. Then the simplified model equations becomes;

$$\frac{dS}{dt} = \lambda + \theta R - (d + \delta_1 I_m + \delta_2 I_f)S \tag{2.9}$$

$$\frac{dE_m}{dt} = \delta_1 I_m S - (\alpha_1 + d)E_m \tag{2.10}$$

$$\frac{dE_f}{dt} = \delta_2 I_f S - (\alpha_2 + d)E_f \tag{2.11}$$

$$\frac{dI_m}{dt} = \alpha_1 E_m - (d + b + \mu_1 + \rho_1)I_m \tag{2.12}$$

$$\frac{dI_f}{dt} = \alpha_2 E_f - (d + b + \mu_2 + \rho_2)I_f \tag{2.13}$$

$$\frac{dT}{dt} = \mu_1 I_m + \mu_2 I_f - (d + b + \beta)T \tag{2.14}$$

$$\frac{dQ}{dt} = \rho_1 I_m + \rho_2 I_f - (d + b + \varepsilon)Q \tag{2.15}$$

$$\frac{dR}{dt} = \beta T + \varepsilon Q - (d + \theta)R \tag{2.16}$$

Subject to the initial conditions below:

$$S(0) \geq 0, E_m(0) \geq 0, E_f(0) \geq 0, I_m(0) \geq 0, I_f(0) \geq 0, T(0) \geq 0, Q(0) \geq 0, R(0) \geq 0.$$

2.3 Assumptions of the Model

The following assumptions will accompany the mathematical model;

1. Everyone in the population has the same chance of contracting covid.
2. Stigmatized population does not seek treatment
3. Recruitment rate(Newborns) are taken to be susceptible.
4. Natural death occurs at the same rate in all compartments.

2.3.1 Disease Free Equilibrium

This is the state whereby no any human being is infected with the disease,therefore the population is free from the virus.[26]

Then;

$$E_m = E_f = I_f = I_m = T = Q = R = 0$$

$$\frac{dS}{dt} = \lambda + \theta R - dS - \delta_1 I_m S - \delta_2 I_f S = 0$$

$$\lambda + \theta R - dS - \delta_1 I_m S - \delta_2 I_f S = 0$$

$$\text{But, } R = I_m = I_f = 0$$

$$\lambda - dS = 0$$

$$S = \frac{\lambda}{d}$$

As a result, the disease-free equilibrium is given by;

$$(S^*, E_m^*, E_f^*, I_m^*, I_f^*, T^*, Q^*, R^*)$$

$$= \left(\frac{\lambda}{d}, 0, 0, 0, 0, 0, 0, 0\right)$$

2.3.2 Endemic Equilibrium

There is an endemic equilibrium if and only if the value of S provided by this condition is less than N, which is equivalent to $R_0 > 1$. [24]

The point at which the disease exists within the susceptible population is referred to as drug endemic equilibrium. We set the equations resulting from our model to zero.

$$\text{From } \frac{dI_m}{dt} = \alpha_1 E_m - (d + b + \mu_1 + \rho_1) I_m,$$

We make I_m the subject of the equation by equating the above equation to zero as follows;

$$\alpha_1 E_m - (d + b + \mu_1 + \rho_1) I_m = 0$$

$$I_m^* = \frac{\alpha_1 E_m}{(d+b+\mu_1+\rho_1)}.$$

$$\text{From } \frac{dI_f}{dt} = \alpha_2 E_f - (d + b + \mu_2 + \rho_2) I_f,$$

We make I_f the subject of the equation by equating the above equation to zero;

$$\alpha_2 E_f - (d + b + \mu_2 + \rho_2) I_f = 0$$

In simplifying the equation ;

$$I_f^* = \frac{\alpha_2 E_f}{(d+b+\mu_2+\rho_2)}.$$

$$\text{From } \frac{dT}{dt} = \mu_1 I_m + \mu_2 I_f - (d + b + \beta) T,$$

Making T the subject of the equation we get;

$$T = \frac{\mu_1 I_m + \mu_2 I_f}{(d+b+\beta)}.$$

Replacing I_m and I_f in the equation of T above, we get a simplified form of T as follows;

$$T^* = \frac{\mu_1 \alpha_1 E_m (d+b+\mu_2+\rho_2) + \mu_2 \alpha_2 E_f (d+b+\mu_1+\rho_1)}{(d+b+\mu_1+\rho_1)(d+b+\mu_2+\rho_2)(d+b+\beta)}.$$

$$\text{From } \frac{dQ}{dt} = \rho_1 I_m + \rho_2 I_f - (d + b + \varepsilon) Q,$$

Making Q the subject of the equation we get;

$$Q = \frac{\rho_1 I_m + \rho_2 I_f}{(d+b+\varepsilon)}.$$

Replacing I_m and I_f in the equation of Q above we get a simplified form of Q as follows;

$$Q^* = \frac{\rho_1 \alpha_1 E_m (d+b+\mu_2+\rho_2) + \rho_2 \alpha_2 E_f (d+b+\mu_1+\rho_1)}{(d+b+\mu_1+\rho_1)(d+b+\mu_2+\rho_2)(d+b+\varepsilon)}.$$

$$\text{From } \frac{dR}{dt} = \beta T + \varepsilon Q - (d + \theta) R, \text{ Making R the subject of the equation we get;}$$

$$R = \frac{\beta T + \varepsilon Q}{(d+\theta)}.$$

Replacing T and Q in the equation above we get a simplified form of R as follows;

$$R^* = \beta \frac{\mu_1 \alpha_1 E_m (d+b+\mu_2+\rho_2) + \mu_2 \alpha_2 E_f (d+b+\mu_1+\rho_1)}{(d+b+\mu_1+\rho_1)(d+b+\mu_2+\rho_2)(d+b+\beta)(d+\theta)} + \varepsilon \frac{\rho_1 \alpha_1 E_m (d+b+\mu_2+\rho_2) + \rho_2 \alpha_2 E_f (d+b+\mu_1+\rho_1)}{(d+b+\mu_1+\rho_1)(d+b+\mu_2+\rho_2)(d+b+\varepsilon)(d+\theta)}.$$

From $\frac{dS}{dt} = \lambda + \theta R - dS - \delta_1 I_m S - \delta_2 I_f S,$

Equating the equation to zero and making S the subject of the equation we get;

$$S = \frac{\lambda + \theta R}{d + \delta_1 I_m + \delta_2 I_f}.$$

Replacing R, $I_m, I_f,$ in the equation above, we get a simplified form of S as follows;

$$S^* = \frac{\lambda + \theta \beta \frac{\mu_1 \alpha_1 E_m (d + b + \mu_2 + \rho_2) + \mu_2 \alpha_2 E_f (d + b + \mu_1 + \rho_1)}{(d + b + \mu_1 + \rho_1)(d + b + \mu_2 + \rho_2)(d + b + \beta)(d + \theta)} + \theta \varepsilon \frac{\rho_1 \alpha_1 E_m (d + b + \mu_2 + \rho_2) + \rho_2 \alpha_2 E_f (d + b + \mu_1 + \rho_1)}{(d + b + \mu_1 + \rho_1)(d + b + \mu_2 + \rho_2)(d + b + \varepsilon)(d + \theta)}}{d + \delta_1 \frac{\alpha_1 E_m}{(d + b + \mu_1 + \rho_1)} + \delta_2 \frac{\alpha_2 E_f}{(d + b + \mu_2 + \rho_2)}}$$

From $\frac{dE_m}{dt} = \delta_1 I_m S - \alpha_1 E_m - dE_m,$

Equating the equation to zero and making E_m the subject of the equation we get;

$$E_m = \frac{\delta_1 I_m S}{\alpha_1 + d};$$

Replacing I_m in the equation above, we get a simplified form of E_m as follows;

$$E_m = \frac{\delta_1 \alpha_1 E_m S}{(\alpha_1 + d)(d + b + \mu_1 + \rho_1)};$$

cross-multiplying and putting like terms together we get;

$$E_m [(\alpha_1 + d)(d + b + \mu_1 + \rho_1) - \delta_1 \alpha_1 S] = 0;$$

Hence, $E_m^* = 0.$

From $\frac{dE_f}{dt} = \delta_2 I_f S - \alpha_2 E_f - dE_f,$

Equating the equation to zero and making E_f the subject of the equation we get;

$$E_f = \frac{\delta_2 I_f S}{\alpha_2 + d};$$

Replacing I_f in the equation above, we get a simplified form of E_f as follows;

$$E_f = \frac{\delta_1 \alpha_2 E_f S}{(\alpha_2 + d)(d + b + \mu_2 + \rho_2)};$$

cross-multiplying and putting like terms together we get;

$$E_f [(\alpha_2 + d)(d + b + \mu_2 + \rho_2) - \delta_2 \alpha_2 S] = 0;$$

Hence, $E_f^* = 0.$

Hence the endemic equilibrium $(S^*; E_m^*; E_f^*; I_m^*; I_f^*; T^*; Q^*; R^*)$ is given by;

$$\frac{\lambda + \theta \beta \frac{\mu_1 \alpha_1 E_m (d + b + \mu_2 + \rho_2) + \mu_2 \alpha_2 E_f (d + b + \mu_1 + \rho_1)}{(d + b + \mu_1 + \rho_1)(d + b + \mu_2 + \rho_2)(d + b + \beta)(d + \theta)} + \theta \varepsilon \frac{\rho_1 \alpha_1 E_m (d + b + \mu_2 + \rho_2) + \rho_2 \alpha_2 E_f (d + b + \mu_1 + \rho_1)}{(d + b + \mu_1 + \rho_1)(d + b + \mu_2 + \rho_2)(d + b + \varepsilon)(d + \theta)}}{d + \delta_1 \frac{\alpha_1 E_m}{(d + b + \mu_1 + \rho_1)} + \delta_2 \frac{\alpha_2 E_f}{(d + b + \mu_2 + \rho_2)}};$$

0;

0;

$$\frac{\alpha_1 E_m}{(d + b + \mu_1 + \rho_1)};$$

$$\frac{\alpha_2 E_f}{(d+b+\mu_2+\rho_2)};$$

$$\frac{\mu_1 \alpha_1 E_m (d+b+\mu_2+\rho_2) + \mu_2 \alpha_2 E_f (d+b+\mu_1+\rho_1)}{(d+b+\mu_1+\rho_1)(d+b+\mu_2+\rho_2)(d+b+\beta)};$$

$$\frac{\rho_1 \alpha_1 E_m (d+b+\mu_2+\rho_2) + \rho_2 \alpha_2 E_f (d+b+\mu_1+\rho_1)}{(d+b+\mu_1+\rho_1)(d+b+\mu_2+\rho_2)(d+b+\varepsilon)};$$

$$\beta \frac{\mu_1 \alpha_1 E_m (d+b+\mu_2+\rho_2) + \mu_2 \alpha_2 E_f (d+b+\mu_1+\rho_1)}{(d+b+\mu_1+\rho_1)(d+b+\mu_2+\rho_2)(d+b+\beta)(d+\theta)} + \varepsilon \frac{\rho_1 \alpha_1 E_m (d+b+\mu_2+\rho_2) + \rho_2 \alpha_2 E_f (d+b+\mu_1+\rho_1)}{(d+b+\mu_1+\rho_1)(d+b+\mu_2+\rho_2)(d+b+\varepsilon)(d+\theta)}.$$

2.3.3 Basic reproductive number R_0

we are going to identify the infectious classes of our model and then calculate (R_0) using the next generation matrix.

The infectious classes are E_m, E_f, I_m, I_f . Hence we will calculate the R_0 using the next generation method (NGM).

We let $x = (S, E_m, E_f, I_m, I_f, T, Q, R)^T$, $F(x)$ be the number of new infections coming into the system and $V(x)$ be the number of infections coming out of the system, then the model will be:

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

The above infectious classes E_m, E_f, I_m, I_f , can be expressed as a matrix from their equations below:

$$\frac{dE_m}{dt} = \delta_1 I_m S - (\alpha_1 + d) E_m$$

$$\frac{dE_f}{dt} = \delta_2 I_f S - (\alpha_2 + d) E_f$$

$$\frac{dI_m}{dt} = \alpha_1 E_m - (d + b + \mu_1 + \rho_1) I_m$$

$$\frac{dI_f}{dt} = \alpha_2 E_f - (d + b + \mu_2 + \rho_2) I_f$$

The next generation matrix (NGM) is defined as ; $K = FV^{-1}$ and $R_0 = \rho(FV^{-1})$ whereby ρ is the spectral radius.

$$F(x) = \begin{bmatrix} \delta_1 I_m S \\ \delta_2 I_f S \\ \alpha_1 E_m \\ \alpha_2 E_f \end{bmatrix} \quad V(x) = \begin{bmatrix} (\alpha_1 + d) E_m \\ (\alpha_2 + d) E_f \\ (d + b + \mu_1 + \rho_1) I_m \\ (d + b + \mu_2 + \rho_2) I_f \end{bmatrix}$$

Differentiating the above matrices with respect to E_m, E_f, I_m, I_f , gives;

$$F = \begin{bmatrix} 0 & 0 & \delta_1 S & 0 \\ 0 & 0 & 0 & \delta_2 S \\ \alpha_1 & 0 & 0 & 0 \\ 0 & \alpha_2 & 0 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} \alpha_1 + d & 0 & 0 & 0 \\ 0 & \alpha_2 + d & 0 & 0 \\ 0 & 0 & d + b + \mu_1 + \rho_1 & 0 \\ 0 & 0 & 0 & d + b + \mu_2 + \rho_2 \end{bmatrix}$$

$$V^{-1} = \begin{bmatrix} \frac{1}{\alpha_1 + d} & 0 & 0 & 0 \\ 0 & \frac{1}{\alpha_2 + d} & 0 & 0 \\ 0 & 0 & \frac{1}{d + b + \mu_1 + \rho_1} & 0 \\ 0 & 0 & 0 & \frac{1}{d + b + \mu_2 + \rho_2} \end{bmatrix}$$

$$FV^{-1} = \begin{bmatrix} 0 & 0 & \delta_1 S & 0 \\ 0 & 0 & 0 & \delta_2 S \\ \alpha_1 & 0 & 0 & 0 \\ 0 & \alpha_2 & 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{\alpha_1 + d} & 0 & 0 & 0 \\ 0 & \frac{1}{\alpha_2 + d} & 0 & 0 \\ 0 & 0 & \frac{1}{d + b + \mu_1 + \rho_1} & 0 \\ 0 & 0 & 0 & \frac{1}{d + b + \mu_2 + \rho_2} \end{bmatrix}$$

$$FV^{-1} = \begin{bmatrix} 0 & 0 & \frac{\delta_1 S}{d + b + \mu_1 + \rho_1} & 0 \\ 0 & 0 & 0 & \frac{\delta_2 S}{d + b + \mu_2 + \rho_2} \\ \frac{\alpha_1}{\alpha_1 + d} & 0 & 0 & 0 \\ 0 & \frac{\alpha_2}{\alpha_2 + d} & 0 & 0 \end{bmatrix}$$

Hence the eigenvalues are $0, 0, \frac{\delta_1 \alpha_1 S}{(d + b + \mu_1 + \rho_1)(\alpha_1 + d)}, \frac{\delta_2 \alpha_2 S}{(d + b + \mu_2 + \rho_2)(\alpha_2 + d)}$.

Therefore;

$$R_0(m) = \frac{\delta_1 \alpha_1 S}{(d + b + \mu_1 + \rho_1)(\alpha_1 + d)}$$

$$R_0(f) = \frac{\delta_2 \alpha_2 S}{(d + b + \mu_2 + \rho_2)(\alpha_2 + d)}$$

Replacing S with $\frac{\lambda}{d}$, our two reproduction numbers simplifies to;

$$R_0(m) = \frac{\delta_1 \alpha_1 \lambda}{d(d + b + \mu_1 + \rho_1)(\alpha_1 + d)}$$

$$R_0(f) = \frac{\delta_2 \alpha_2 \lambda}{d(d + b + \mu_2 + \rho_2)(\alpha_2 + d)}$$

The two reproduction numbers are positive. when $\delta = 0$, the reproduction numbers becomes 0

implying that there is no transmission in the model.

$\frac{\lambda}{d}$, is the number of susceptible people in a disease-free state.

$\frac{\lambda\delta}{d(d+b+\mu+\rho)}$, is the total number of secondary cases caused by a single sick individual.

$\frac{\alpha}{\alpha+d}$, is the proportion of new infections that survive and become infectious after being exposed.

Here R_0 is the sum of two terms, one for each of the two infectious classes' average new infections.

Hence R_0 of the system is given by;

$$R_0 = R_0(m) + R_0(f).$$

2.4 Stability of the system

2.4.1 Local Stability of Disease Free Equilibrium

If $R_0 < 1$, the disease free equilibrium is locally asymptotically stable otherwise unstable if $R_0 > 1$.

The jacobian Matrix of the model is given by;

$$J = \begin{bmatrix} -(d + \delta_1 I_m + \delta_2 I_f) & 0 & 0 & -\delta_1 S & -\delta_2 S & 0 & 0 & \theta \\ \delta_1 I_m & -(\alpha_1 + d) & 0 & \delta_1 S & 0 & 0 & 0 & 0 \\ \delta_2 I_f & 0 & -(\alpha_2 + d) & 0 & \delta_2 S & 0 & 0 & 0 \\ 0 & \alpha_1 & 0 & -(d + b + \mu_1 + \rho_1) & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_2 & 0 & -(d + b + \mu_2 + \rho_2) & 0 & 0 & 0 \\ 0 & 0 & 0 & \mu_1 & \mu_2 & -(d + b + \beta) & 0 & 0 \\ 0 & 0 & 0 & \rho_1 & \rho_2 & 0 & -(d + b + \varepsilon) & 0 \\ 0 & 0 & 0 & 0 & 0 & \beta & \varepsilon & -(d + \theta) \end{bmatrix}$$

In disease free equilibrium, $E_m = E_f = I_f = I_m = T = Q = R = 0$, then the jacobian matrix of disease free equilibrium, $J(\varepsilon_0)$ will be given by;

$$J(\varepsilon_0) = \begin{bmatrix} -d & 0 & 0 & -\delta_1 S & -\delta_2 S & 0 & 0 & \theta \\ 0 & -(\alpha_1 + d) & 0 & \delta_1 S & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\alpha_2 + d) & 0 & \delta_2 S & 0 & 0 & 0 \\ 0 & \alpha_1 & 0 & -(d + b + \mu_1 + \rho_1) & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_2 & 0 & -(d + b + \mu_2 + \rho_2) & 0 & 0 & 0 \\ 0 & 0 & 0 & \mu_1 & \mu_2 & -(d + b + \beta) & 0 & 0 \\ 0 & 0 & 0 & \rho_1 & \rho_2 & 0 & -(d + b + \varepsilon) & 0 \\ 0 & 0 & 0 & 0 & 0 & \beta & \varepsilon & -(d + \theta) \end{bmatrix}$$

Finding the determinant of the disease free equilibrium's jacobian matrix yields;

$|J(\varepsilon_0) - \lambda I| = 0$, where λ is the eigen values.

$$|J(\varepsilon_0) - \lambda I| = \begin{vmatrix} -d - \lambda & 0 & 0 & -\delta_1 S & -\delta_2 S & 0 & 0 & \theta \\ 0 & -(\alpha_1 + d) - \lambda & 0 & \delta_1 S & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\alpha_2 + d) - \lambda & 0 & \delta_2 S & 0 & 0 & 0 \\ 0 & \alpha_1 & 0 & -(d + b + \mu_1 + \rho_1) - \lambda & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_2 & 0 & -(d + b + \mu_2 + \rho_2) - \lambda & 0 & 0 & 0 \\ 0 & 0 & 0 & \mu_1 & \mu_2 & -(d + b + \beta) - \lambda & 0 & 0 \\ 0 & 0 & 0 & \rho_1 & \rho_2 & 0 & -(d + b + \varepsilon) - \lambda & 0 \\ 0 & 0 & 0 & 0 & 0 & \beta & \varepsilon & -(d + \theta) - \lambda \end{vmatrix}$$

The matrix clearly shows that all eigenvalues are negative. Because all eigenvalues are negative, the DFE is locally asymptotically stable.

2.4.2 Global Stability of Endemic Equilibrium

If $R_0 > 1$, the disease endemic equilibrium will thereafter be asymptotically stable.[27].

We will prove using the lypunov function as follows;

$$L(S^*, E_m^*, E_f^*, I_m^*, I_f^*, T^*, Q^*, R^*) = [(S - S^* - S^* \ln \frac{S^*}{S}) + (E_m - E_m^* - E_m^* \ln \frac{E_m^*}{E_m}) + (E_f - E_f^* - E_f^* \ln \frac{E_f^*}{E_f}) + (I_m - I_m^* - I_m^* \ln \frac{I_m^*}{I_m}) + (I_f - I_f^* - I_f^* \ln \frac{I_f^*}{I_f}) + (Q - Q^* - Q^* \ln \frac{Q^*}{Q}) + (T - T^* - T^* \ln \frac{T^*}{T}) + (R - R^* - R^* \ln \frac{R^*}{R})].$$

Computing the derivative of L we get;

$$\frac{dL}{dt} = [(\frac{S-S^*}{S}) \frac{dS}{dt} + (\frac{E_m-E_m^*}{E_m}) \frac{dE_m}{dt} + (\frac{E_f-E_f^*}{E_f}) \frac{dE_f}{dt} + (\frac{I_m-I_m^*}{I_m}) \frac{dI_m}{dt} + (\frac{I_f-I_f^*}{I_f}) \frac{dI_f}{dt} + (\frac{Q-Q^*}{Q}) \frac{dQ}{dt} + (\frac{T-T^*}{T}) \frac{dT}{dt} + (\frac{R-R^*}{R}) \frac{dR}{dt}].$$

Substituting our model equations in $\frac{dL}{dt}$ above we get;

$$\begin{aligned} \frac{dL}{dt} = & [(\frac{S-S^*}{S})(\lambda + \theta R - (d + \delta_1 I_m + \delta_2 I_f)S) + (\frac{E_m-E_m^*}{E_m})(-(\alpha_1 + d)E_m) + (\frac{E_f-E_f^*}{E_f})(\delta_2 I_f S - (\alpha_2 + d)E_f) + \\ & (\frac{I_m-I_m^*}{I_m})(\alpha_1 E_m - (d + b + \mu_1 + \rho_1)I_m) + (\frac{I_f-I_f^*}{I_f})(\alpha_2 E_f - (d + b + \mu_2 + \rho_2)I_f) + (\frac{Q-Q^*}{Q})(\rho_1 I_m + \rho_2 I_f - (d + b + \\ & \epsilon)Q) + (\frac{T-T^*}{T})(\mu_1 I_m + \mu_2 I_f - (d + b + \beta)T) + (\frac{R-R^*}{R})(\beta T + \epsilon Q - (d + \theta)R)]. \end{aligned}$$

After expanding and simplifying the above equation,

we let A be the positive terms and B the negative terms. Then $\frac{dL}{dt} = A - B$.

Where;

$$A = (d + \delta_1 I_m + \delta_2 I_f)S^* + (\alpha_1 + d)E_m^* + (\alpha_2 + d)E_f^* + (d + b + \mu_1 + \rho_1)I_m^* + (d + b + \mu_2 + \rho_2)I_f^* + (d + b + \epsilon)Q^* + (d + b + \beta)T^* + (d + \theta)R^*.$$

and

$$B = (\lambda + \theta R) \frac{S^*}{S} + (\delta_1 I_m S) \frac{E_m^*}{E_m} + (\delta_2 I_f S) \frac{E_f^*}{E_f} + (\alpha_1 E_m) \frac{I_m^*}{I_m} + (\alpha_2 E_f) \frac{I_f^*}{I_f} + (\rho_1 I_m + \rho_2 I_f) \frac{Q^*}{Q} + (\mu_1 I_m + \mu_2 I_f) \frac{T^*}{T} + (\beta T + \epsilon Q) \frac{R^*}{R}.$$

If $A < B$, then $\frac{dL}{dt} \leq 0$.

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

$$S = S^*, E_m = E_m^*, E_f = E_f^*, I_m = I_m^*, I_f = I_f^*, Q = Q^*, T = T^* \text{ and } R = R^*.$$

The largest invariant set in $(S, E_m, E_f, I_m, I_f, T, Q, R) \in \infty : \frac{dL}{dt} = 0$, is E^* , whereby E^*

is the disease endemic point. As a result, the endemic equilibrium is asymptotically stable.[26]

3. NUMERICAL SOLUTIONS

3.1 Parameters Estimation

The following parameters are obtained from the existing literature reviews, others through estimation and others we assumed them. we used the data from the ministry of health from the start of the pandemic up to july 2020 [34] to calculate some of the parameters. At the start of covid in kenya after the first infection case was reported we assumed that the disease was

already spreading and hence we set the initial conditions as follows; $S = 5000, E_m = 50, E_f = 50, I_m = 1, I_f = 1, Q = 0, T = 0, R = 0$. Then we entered the parameters into our system of differential equations and then used MATLAB together with the initial conditions to generate the respective figures.

Parameter	Value	Source
λ	0.027	Estimated
d	0.013	[31]
b	0.038	[31]
δ_1	0.587	Calculated
δ_2	0.276	Calculated
α_1	0.029	Calculated
α_2	0.014	Calculated
μ_1	0.13	[32]
μ_2	0.13	[32]
ρ_1	0.5	Estimated
ρ_2	0.5	Estimated
θ	0.0032	[31]
β	0.2904	[30]
ε	0.2	Estimated

3.2 Covid-19 in relation to SEIR population dynamics

Figure 1 below illustrates the population dynamics comprising of susceptible(s), exposed male population (E_m), exposed female population (E_f), infected male population (I_m), infected female population (I_f) and recovered population (R). The results show that, the number of susceptible population decreases with respect to time. The number of exposed population increases within the early months but it stabilizes and then starts to decrease gradually for both male and female. Infected population rises with respect to time for both male and female though at different rates. Exposed population is higher compared to infected population for both male and female because of intervention measures like maintaining physical distance, use of masks and general body hygiene. The recovered population dynamics increases gradually with respect to time because of intervention of treatment measures.

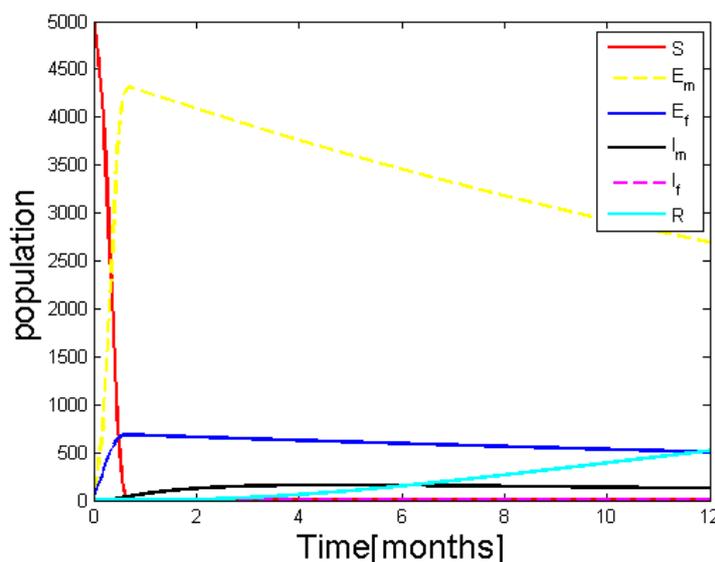


Figure 2: SEIR population dynamics with respect to time

3.3 Covid-19 in relation to the infected Population with time

During the Covid-19 pandemic, great attention was placed initially on the aged or those with underlying health issues such as high blood pressure as being at high risk of getting or dying from Covid-19. However, it is now obvious that being masculine is also a determinant.

The figure 2 below shows number of infected individuals with respect to time. Male individuals are highly infected compared to their female counterparts. Male individuals are more infected because of their bad habits and lifestyle factors such as increased smoking and drinking which inturn increases physical contact. Also men had an irressponsible attitude compared to women towards preventive measures such as handwashing, social distance and wearing of masks.[33]

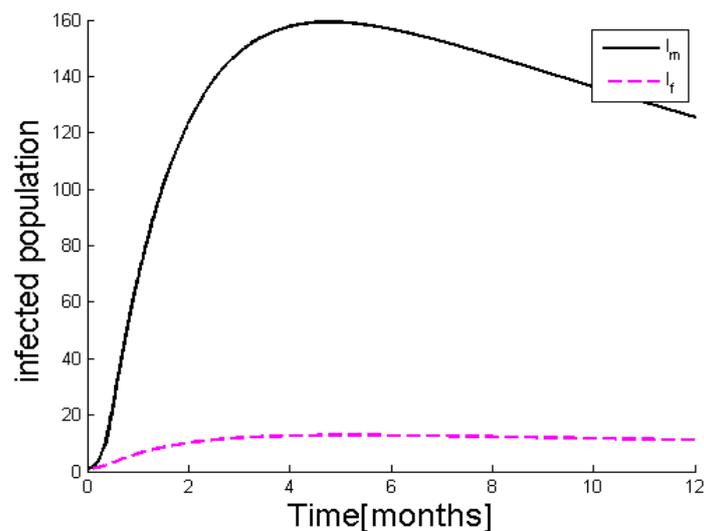


Figure 3: Infected population with respect to time

3.4 infected male dynamics

The figure below shows the graph of infected male population varying the rate of stigmatization. From the graph as the rate of stigmatization of male increases it inturn increases the male infections. At the beginning of the graph the rate of infection is high compared to the latter stages because at the latter stages there is stigmatization awareness hence decreasing the rate of infection compared to the early stages of the pandemic.

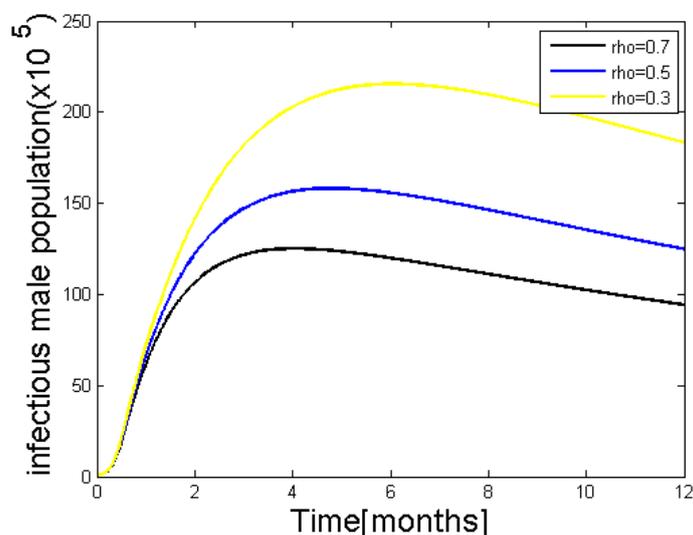


Figure 4: Male infected population varying stigmatization

3.5 infected female dynamics

The figure below shows the infected female population varying the rate of stigmatization. From the figure below, as the rate of stigmatization increases it also increases the female infection rate. At the start the rate of infection is high but as time goes by it starts to stabilize because of the intervention of sensitization and stigmatization awareness.[31]

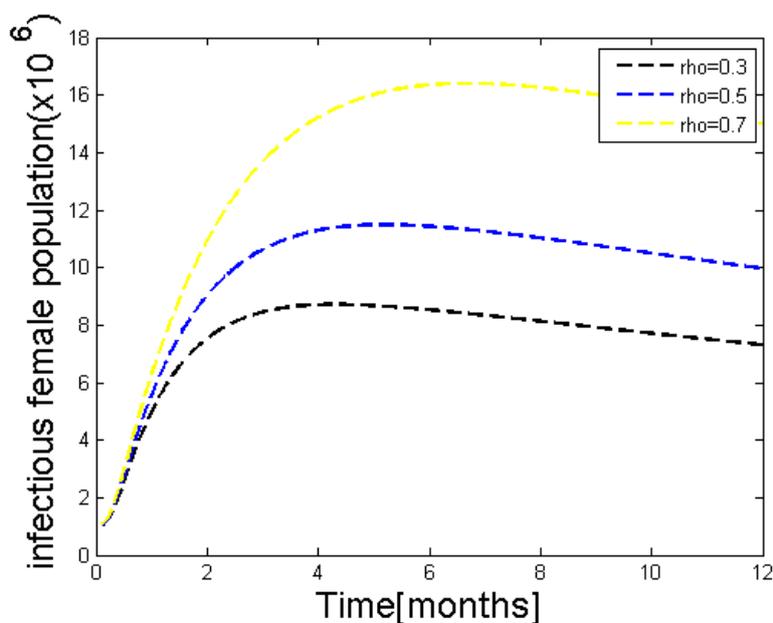


Figure 5: Female infected population varying stigmatization

4. CONCLUSIONS AND RECOMMENDATIONS

4.1 Conclusion

In our research we created a gender-based stigmatization covid-19 model. From figures 4 and 5 we found out that as the rate of stigmatization increases it also increases the infection rate, also as the rate of stigmatization decreases it also returns to decrease the rate of infection for both male and female. From our figures above, male population were more stigmatized compared to female because of their bad habits and irresponsible attitude compared to women towards preventive measures such as handwashing, social distance and wearing of masks.[33]. Amid covid-19 pandemic, physical contact with an infected person was the cause of rise of covid-19 infections, but clearly from our study stigmatization plays an important part in the transmission of the covid-19. Stigma is linked to lack of information, myths and fears over the disease. Clearly if we curb stigmatization it will return to reduce the infection rate. In summary, curbing stigmatization should be enhanced by relevant organizations fighting covid-19 because reducing stigmatization returns to reduce the spread of covid-19.

4.2 Recommendations

From our study we recommend that;

1. The government and relevant authorities should use this report to curb stigmatization through awareness by speaking against negative stereotypes and providing the necessary support required by encouraging people to take tests and seek healthcare immediately they start showing covid symptoms.
2. More research should be done on covid-19 stigmatization in order to allow fully understanding of this menace.
3. The government other stakeholders can use the media to stop stigmatization through education and adverts against stigmatization.
4. Further studies should be done on effects of stigmatization of covid-19 control strategies.

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