A mathematical model for the prediction of the impact of coronavirus(COVID-19) and social distancing effect

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Abstract: - The spread of coronavirus across the world has become a major pandemic following the Spanish flu of 1918. A mathematical model of the spread of the coronavirus with social distancing effect is studied. A mathematical model of the spread of the virus form Wuhan in China to the rest of the world is suggested and analyzed. Another mathematical model with quarantine and social distancing factors is proposed and analyzed. Stability analysis for both models were carried out and data fitting was performed to predict the possible extinction of the disease. The disease free equilibria of both models were locally and globally asymptotically stable. The models suggest that with interventions such as lock downs and social distancing the extinction of the coronavirus can be achieved. Increasing social distancing could reduce the number of new cases by up to 30%. The paper presents a unique style of considering both theoretical and data analysis which is rarely studied in the literature. Questions arising from this study for further research include the right time to apply interventions and the state of preparedness in case of similar pandemics.

Key-Words: - Coronavirus, migration, quarantine, social distancing.

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1 Introduction

Coronaviruses fall under the coronaviradae family which consist of the alpha (α), beta (β), gamma(γ) and delta (δ) subgroups. Corona is the veil that appears around the sun or star. The virus looks much like the corona of the star with spikes around it. The viruses include the Severe Acute Respiratory Syndrome (SARS-Cov), N1H1 2009, H5N1 influenza, Middle-East Respiratory Syndrome (MERS-Cov) ([1, 2]). The coronavirus was discovered in the 1960s as common cold, SARS was first discovered in 2002-2003 in China. It affected over 8000 people and had case fatality rate of 10% and only affected seventeen countries and the disease cleared out by 2004. The disease is much like the Spanish flu of 1918 although the two diseases are different. This flu killed over 500 million people with a case fatality rate of 2,5%. The number of deaths and the case fatality of the Spanish flu is debatable and not accurate.

Other types of coronaviruses such as the MERS-Cov originated in Middle-East and came from camels, it affected between 30-40% of the population, the outbreak started in 2012 and by late 2019 it had caused 851 deaths of the confirmed 2468 accounting for a case fatality rate of 35% in Saudi Arabia ([3, 4, 5]). This coronavirus MERS-Cov could be detected by X-ray and CT scans making it easier to identify cases ([6]). There is also Bovine coronavirus (BCV) and Bovine syncytial virus (BRSV) which affects animals like cattle and pigs, cases of this disease were reported in Sweden ([7]).

The novel coronavirus is caused by SARS-Cov 2 or COVID'19 which started in China in the city of Wuhan, genetic analysis show that SARS-Cov 2 is related to SARS bat and pangolin viruses. Its transmission from bats to humans is not known ([1, 8]). [9] suggested that there is a connection between bats and civets which were consumed in Asia. This places the relationship between humans and animals at risk. The genetic investigation of the coronavirus shows that its origin from bats is most probable ([10, 11]). The disease is now in humans and is spread when a person coughs, sneezes or talks. The virus is lands on surfaces and can be transmitted to other people who touch the same surfaces.

The outbreak of the coronavirus began in Wuhan in China, by 20 February 2020 75000 cases 2000 deaths had been confirmed in China, it spread to other parts of the world due to movement of people ([9]). In Singapore 117 cases had been reported by 5 March 2020, fights from Wuhan to Singapore were being screened [12] showing the rapid transportation of the virus. By 28 March 2020, Italy recorded a total of more than 86 000 total cases and over 9000 total deaths. Spain recoded a total of over 64 000 cases and total deaths of 4500. The USA recorded more than 104 000 cases and total deaths of 1700. At this time the world had recorded total cases of more than 591 000 and total deaths of more than 27 000 ([13]). Many cases of this disease remain undetected due to the fail-

ure of getting more tests, the delay in testing and feedback of results assist in spreading of the disease more rapidly [14]. The rate at which the disease spreads shows that it could remain endemic for a longer period [15]. The main method of reducing the spread of the virus across the globe is isolation or quarantine [16].

Coronavirus affects people of all ages and there is no evidence that children are more vulnerable than any other age group.([17]). People with blood group A are at higher risk compared to non-A groups. The O-group has lower risk than non-O groups ([18]). People at risk include those with chronic illnesses and medical staff. Since the disease was declared "Public Health Emergence of International Concern" by the World Health Organization (WHO) it has now become imperative to protect medical staff ([19]). Due to its effect across of all people, it has caused post-traumatic stress symptoms in health workers and families especially during quarantines, lock downs and social distancing ([20]).

The novel coronavirus cannot be treated and so far people are using preventative measures to avoid it ([1]). Now vaccines are being developed and this takes a long time. Other coronaviruses have vaccines that have been tried using nanoparticles; examples include SARS-Cov particles known as sVLPs ([21]). The paper discusses both theoretical and data analysis of the problem of control of the novel coronavirus. The paper is organised as follows; the introduction covering comparative analysis, mathematical formulation, model analysis, model with quarantine and social distancing, data analysis and conclusion.

2 Mathematical formulation

In this section a mathematical model for the spread of coronavirus from the epicentre in Wuhan is proposed. It consist of two main populations, the population of the people of Wuhan and the population of the rest of the world. Coronavirus is believed to have come from the bats and pangolin populations. It found its way into the human population by consumption of these species. Each of these two groups is divided into four sub-populations, the susceptible, exposed, infected and the immune populations of Wuhan residents S_w, E_w, I_w, R_w respectively and the population of the rest of the world for susceptible, exposed, infected and immune S_r, E_r, I_r, R_r and I_v respectively.

Migrations from Wuhan m_w and from the rest of the world into Wuhan m_r are considered. The rate of recruitment from the main populations of Wuhan and the rest if the world are give as Π_w and Π_r respectively. Only migration of the exposed is considered, it is assumed that those infected show symptoms and are not allowed to migrate. The natural mortality rates of humans is assumed to be the same across the world

μ. The population from the rest of the world is infected by those migrating from Wuhan who will have become infectious before the end if the period $1/\epsilon_w$. The force of infection in Wuhan $\lambda_w = \beta_w I_w / N_w$ is the new infections caused by other infected individuals in Wuhan. The force of infection in the rest of the world $\lambda_r = \beta_r I_r / N_r$ is the new infections caused by other infected individuals in the rest of the world. The force of infection $\lambda_{wr} = \beta_{wr} I_w / N_r$, these are new cases caused by migration of exposed individuals from Wuhan to the rest of the world. The compartmental model is shown in Figure 1.
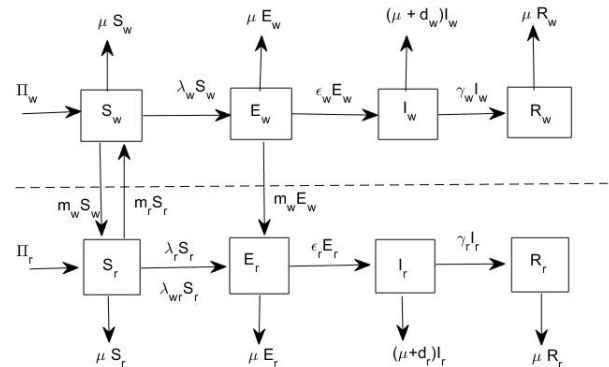

Figure 1: Compartmental model for the transmission of coronavirus

The system of equations describing the spread of corona virus is given by

$$\frac{dS_w}{dt} = \Pi_w + m_r S_r - (m_w + \mu)S_w$$
$$- \frac{\beta_w S_w I_w}{N_w}, \quad (1)$$

$$\frac{dE_w}{dt} = \frac{\beta_w S_w I_w}{N_w} - (m_w + \mu + \epsilon_w)E_w, \quad (2)$$

$$\frac{dI_w}{dt} = \epsilon_w E_w - (\mu + d_w + \gamma_w)I_w, \quad (3)$$

$$\frac{dR_w}{dt} = \gamma_w I_w - \mu R_w, \quad (4)$$

$$\frac{dS_r}{dt} = \Pi_r + m_w S_w - (m_r + \mu)S_r$$
$$- \frac{\beta_{wr} S_r I_w}{N_r} - \frac{\beta_r S_r I_r}{N_r}, \quad (5)$$

$$\frac{dE_r}{dt} = \frac{\beta_{wr} S_r I_w}{N_r} + \frac{\beta_r S_r I_r}{N_r} + m_w E_w$$
$$- (\epsilon_r + \mu)E_r, \quad (6)$$

$$\frac{dI_r}{dt} = \epsilon_r E_r - (\mu + d_r + \gamma_r)I_r, \quad (7)$$

$$\frac{dR_r}{dt} = \gamma_r I_r - \mu R_r, \quad (8)$$

subject to

$$S_w(0) \geq 0, E_w(0) \geq 0, I_w(0) \geq 0,$$
$$R_w(0) \geq 0,$$
$$S_r(0) \geq 0, E_r(0) \geq 0, I_r(0) \geq 0,$$
$$R_r(0) \geq 0, \quad (9)$$

3 Basic Model Analysis

The model system is studied in the region given by

$$\Omega = \Big[(S_w, E_w, I_w, R_w, S_r, E_r, I_r, R_r) \in \mathcal{R}^8$$
$$N(t) \leq \frac{\Pi_w + \Pi_r}{\mu}, \text{ if } d_w = d_r \approx 0. \Big] \quad (10)$$

For brevity the we will denote the expressions as follows;

$$\xi_w = \Pi_w(m_r + \mu) + m_r \Pi_r, \quad (11)$$
$$\xi_r = \Pi_r(m_w + \mu) + m_w \Pi_w, \quad (12)$$
$$\xi_{wr} = (m_r + m_w + \mu), \quad (13)$$
$$\eta_{w1} = (m_w + \mu), \quad (14)$$
$$\eta_{w2} = (m_w + \epsilon_w + \mu), \quad (15)$$
$$\eta_{w3} = (d_w + \mu + \gamma_w), \quad (16)$$
$$\eta_{r1} = (m_r + \mu), \quad (17)$$
$$\eta_{r2} = (\mu + \epsilon_r), \eta_{r3} = (\gamma_r + d_r + \mu), \quad (18)$$

The disease-free equilibrium point E_0 is given as

$$E_0 = \left(\frac{\xi_w}{\mu \xi_{wr}}, 0, 0, 0, \frac{\xi_r}{\mu \xi_{wr}}, 0, 0, 0 \right), \quad (19)$$

3.1 Basic Reproduction Number

At this stage it is important to calculate the basic reproduction number. The basic reproduction number is the number of secondary cases produced by one infective case introduced in a naive population. The Basic reproduction number as described in ([22]) and ([23]) is calculated as follows;

The system (1)-(6) is arranged starting with the infective classes and is given as

$$\frac{dE_w}{dt} = \frac{\beta_w S_w I_w}{N_w} - (m_w + \mu + \epsilon_w)E_w, (20)$$

$$\frac{dE_r}{dt} = \frac{\beta_{wr} S_r I_w}{N_r} + \frac{\beta_r S_r I_r}{N_r} + m_w E_w$$
$$- (\epsilon_r + \mu)E_r \quad (21)$$

$$\frac{dI_w}{dt} = \epsilon_w E_w - (\mu + d_w + \gamma_w)I_w, \quad (22)$$

$$\frac{dI_r}{dt} = \epsilon_r E_r - (\mu + d_r + \gamma_r)I_r, \quad (23)$$

By using the method described by ([?]) we have the following matrices from (20)-(23), $\mathcal{F}$ and $\mathcal{V}$ are define as

$$\mathcal{F} = \begin{pmatrix} 0 & 0 & \frac{\beta_w S_w}{N_w} & 0 \\ 0 & 0 & \frac{\beta_{wr} S_r}{N_r} & \frac{\beta_{wr} S_r}{N_r} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

$$\mathcal{V} = \begin{pmatrix} \eta_{w2} & 0 & 0 & 0 \\ -m_w & \eta_{r2} & 0 & 0 \\ -\epsilon_w & 0 & \eta_{w3} & 0 \\ 0 & -\epsilon_r & 0 & \eta_{r3} \end{pmatrix}.$$

The Basic Reproduction number is defined as the dominant eigenvalue of $G = \mathcal{F}\mathcal{V}^{-1}$

$$R_0 = \frac{\epsilon_w \beta_w \xi_w}{\mu N_w \eta_{w2} \eta_{w3} \xi_{wr}} + \frac{\epsilon_r \beta_r \xi_r}{\mu N_r \eta_{r2} \eta_{r3} \xi_{wr}} \quad (24)$$

$$R_0 = R_1 + R_2, \quad (25)$$

where

$$R_1 = \frac{\epsilon_w \beta_w \xi_w}{\mu N_w \eta_{w2} \eta_{w3} \xi_{wr}}, R_2 = \frac{\epsilon_r \beta_r \xi_r}{\mu N_r \eta_{r2} \eta_{r3} \xi_{wr}} \quad (26)$$

From the work of ([23]), the Theorem 3.1

Theorem 3.1. *The disease-free equilibrium, E_0 is locally asymptotically stable when $R_1 < 1$, $R_2 < 1$ and unstable when $R_1 > 1$, $R_2 > 1$.*

The Jacobian matrix evaluated at the disease-free equilibrium point is given by

$$J(E_0) = \begin{pmatrix} -\eta_{w1} & 0 & -\frac{\beta_w S_w^*}{N_w} & 0 & m_r & 0 & 0 & 0 \\ 0 & -\eta_{w2} & \frac{\beta_w S_w^*}{N_w} & 0 & 0 & 0 & 0 & 0 \\ 0 & \epsilon_w & -\eta_{w3} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \gamma_w & -\mu & 0 & 0 & 0 & 0 \\ m_w & 0 & -\frac{\beta_{wr} S_r^*}{N_r} & 0 & -\eta_{r1} & 0 & -\frac{\beta_r S_r^*}{N_r} & 0 \\ 0 & m_w & \frac{\beta_{wr} S_r^*}{N_r} & 0 & 0 & -\eta_{r2} & \frac{\beta_r S_r^*}{N_r} & 0 \\ 0 & 0 & 0 & 0 & 0 & \epsilon_r & -\eta_{r3} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \gamma_r & -\mu \end{pmatrix}$$

To investigate the stability of the disease-free equilibrium point. The two eigenvalues of the matrix are clearly $-\mu$ twice, The other six eigenvalues are given by

$$\lambda_1 = -\frac{1}{2}\left[\eta_{w2} + \eta_{w3} + \sqrt{(\eta_{w2} + \eta_{w3})^2 - 4\eta_{w2}\eta_{w3}(1 - R_1)}\right], \tag{27}$$

$$\lambda_2 = -\frac{1}{2}\left[\eta_{w2} + \eta_{w3} - \sqrt{(\eta_{w2} + \eta_{w3})^2 - 4\eta_{w2}\eta_{w3}(1 - R_1)}\right], \tag{28}$$

$$\lambda_3 = -\frac{1}{2}\left[\eta_{w1} + \eta_{r1} + \sqrt{\eta_{w1}^2 + \eta_{r1}^2 + 4m_r m_w - 2\eta_{w1}\eta_{r1}}\right], \tag{29}$$

$$\lambda_4 = -\frac{1}{2}\left[\eta_{w1} + \eta_{r1} - \sqrt{\eta_{w1}^2 + \eta_{r1}^2 + 4m_r m_w - 2\eta_{w1}\eta_{r1}}\right], \tag{30}$$

$$\lambda_5 = -\frac{1}{2}\left[\eta_{r2} + \eta_{r3} + \sqrt{(\eta_{r2} + \eta_{r3})^2 - 4\eta_{r2}\eta_{r3}(1 - R_2)}\right], \tag{31}$$

$$\lambda_6 = -\frac{1}{2}\left[\eta_{r2} + \eta_{r3} - \sqrt{(\eta_{r2} + \eta_{r3})^2 - 4\eta_{r2}\eta_{r3}(1 - R_2)}\right], \tag{32}$$

$$\tag{33}$$

The eigenvalues of the matrix are all negative when $R_1 < 1$ and $R_2 < 1$, the disease-free equilibrium point is asymptotically stable.

3.2 Global stability of the disease-free equilibrium

In this section we consider two conditions such that if met, global asymptotic stability is guaranteed. We rewrite the system of equations (1)-(9) in the form

$$\frac{dX}{dt} = F(X, Z), \tag{34}$$

$$\frac{dZ}{dt} = G(X, Z), G(X, 0) = 0, \tag{35}$$

where $X = (S_w, R_w, S_r, R_r)$, and $Z = (E_w, I_w, E_r, I_r)$, X denotes the uninfected individuals and Z denotes the infected classes. The disease-free equilibrium is expressed as $E_0 = (X^*, 0)$ where $X^* = (S_w, 0, S_r, 0)$. The following conditions (36)-(37) must be met to guarantee global asymptotic stability;

$$\frac{dX}{dt} = F(X, 0), X^*$$
is globally asymptotically stable, (36)

$$G(X, Z) = AZ - \hat{G}(X, Z),$$

$$\hat{G}(X, Z) \geq 0, \tag{37}$$

for $(X, Z) \in \mathcal{R}^2,$

where $A = D_Z G(X^*, 0)$ is a matrix whose diagonal elements are non-negative. If the system (34)-(35) satisfies the condition (36)-(37) then Theorem 3.2 holds The eigenvalues of the Jacobian matrix are negative for $R_1 < 1$ and $R_2 < 1$. The disease free equilibrium point E_0 is asymptotically stable.

Theorem 3.2. *The fixed point $E_0 = (X^*, 0)$ is globally asymptotically stable equilibrium of the system (34)-(35) provided that $R_1 < 1$, $R_2 < 1$ and that the assumptions in (36)-(37) are satisfied.*

3.3 Stability of endemic equilibria

In this section we study the stability of the endemic equilibrium point. The endemic equilibrium points are given as follows

$$S_w^* = \frac{\xi_w}{\mu \xi_{wr} R_1}, \tag{38}$$

$$E_w^* = \frac{\eta_{w3} I_w^*}{\epsilon_w}, \tag{39}$$

$$I_w^* = \frac{N_w}{\beta_w} \left[\frac{\Pi_w R_1}{\xi_w} \left(\mu \xi_{wr} \right.\right.$$
$$\left.\left. + \frac{m_w m_r}{R_2} \right) + \eta_{w1} \left(\frac{m_r \Pi_r R_1}{\xi_1 R_2} - 1 \right) \right], \tag{40}$$

$$R_w^* = \frac{\gamma_w I_w^*}{\mu}, \tag{41}$$

$$S_r^* = \frac{\xi_r}{\mu \xi_{wr} R_2}, \tag{42}$$

$$E_r^* = \frac{\beta_r S_r^* I_r^*}{N_r \eta_{r2}} + \frac{\beta_{wr} S_r^* I_w^*}{N_r \eta_{r2}} + \frac{m_w E_w^*}{\eta_{r2}}, \tag{43}$$

$$I_r^* = \frac{\epsilon_r E_r^*}{\eta_{r3}}, \tag{44}$$

$$R_r^* = \frac{\gamma_r I_r^*}{\mu}, \tag{45}$$

All the endemic equilibrium points are strictly positive whenever $R_1 > 1$ and $R_2 > 1$. The disease persists under these conditions. In the next section an analysis of the impact of the outbreak of corona virus is investigated. The respective values of R_0 are calculated to indicate the level of transmission.

The effect of migrations from Wuhan to the rest of the world m_w and migration from the rest of the world to Wuhan is investigated for this model.
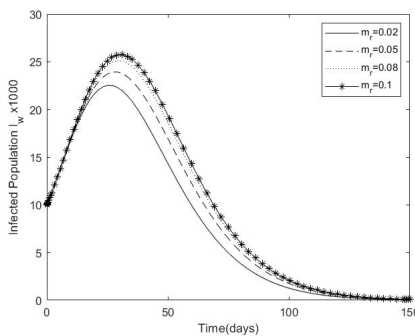

Figure 2: Effect of migration from the rest of the world into Wuhan on infected population I_w

Movement from the rest of the world to Wuhan had an increase in the infective population in Wuhan. This increase the susceptible population resulting in the increase of infected individuals in Wuhan. The reduction in migrations result in the significant reduction of infected population as shown in Figure 2
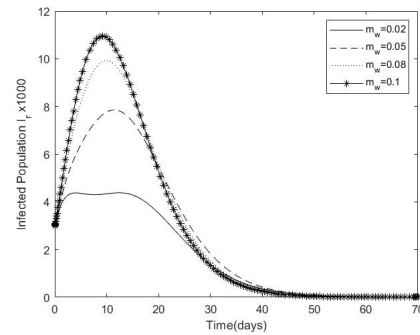

Figure 3: Effect of migration from Wuhan to the rest of the world on infected populations I_r

The effect of increasing the migration of susceptible and exposed individuals from Wuhan to the rest of the world had an effect of increasing infective population in the rest of the world. Limiting migrations have a significant effect in reducing infective populations. The increase of infective population in the rest of the world was more enhanced due to migrations from Wuhan than the movement from the rest of the world to Wuhan.

4 Model with quarantine and social distancing factor

When the outbreak of coronavirus intensified most countries used quarantine methods to slow down the spread of the virus. In this section we investigate to what extent does quarantine and social distancing methods work and at what stage does quarantine need to be started? Quarantine methods involve isolating different groups of individuals in the affected population. This may be in the form of isolating exposed and infected individuals. It may involve isolating the susceptible population as well. In the case of the coronavirus all these methods have been applied. Most countries have applied lock-downs for up to $21 - 60$ days. In this section we investigate how effective are these quarantines.

The mathematical model is divided into five sub-populations, the susceptible S, the exposed E; these include those individuals that that are infected and not yet infectious and those that are in the asymptomatic stage (not showing symptoms). These individuals transform from being exposed to the infected group I, the sub-group R are those that recover from the disease and those that are immune to the disease. Q are those that will have been quarantined. μ is the natural death rate, Π is the rate of recruitment form

the main population, $\beta I/N$ is the force of infection, q_1 is the rate of quarantining exposed individuals, q_2 is the rate of quarantining infected individuals, ϵ is the rate of transformation from exposed to infected individuals, $1/\epsilon$ is referred to as the latent period. γ and α are the recovery rates. The compartmental model is shown in Figure 4. The basic reproduction number can be written as $R_0 = pc(T_1 - T_0)$, p is the probability of infection, c is the contact rate, $(T_1 - T_0)$ is the infectious period. the probability of infection is given as

$$ p = \begin{cases} 0 & if \ \tau < T_0 \\ e^{-s_d} & if \ T_0 < \tau < T_1 \\ 0 & if \ \tau > T_1 \end{cases} $$

where s_d is the social distancing parameter, if $s_d = 0$, then $p = 1$, the probability of infection decrease as s_d increases.

In the proposed model

$$ R_0 = e^{-s_d}c(T_1 - T_0) \tag{46} $$
$$ R_0 = e^{-s_d}e^{\alpha_0}(T_1 - T_0) $$
$$ = e^{\alpha_0 - s_d}(T_1 - T_0, \tag{47} $$

α_0 is the contact rate index. In the Figure 4 the infection rate $\beta = e^{\alpha_0 - s_d}$.
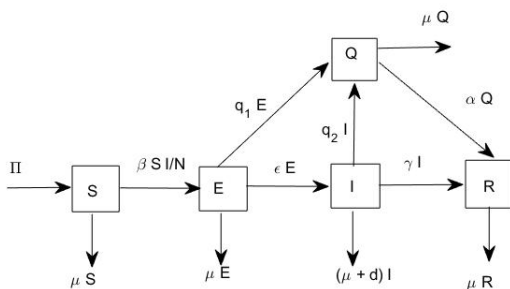

Figure 4: Effect of quarantining only the exposed group

The mathematical model with quarantine factor is given below

$$ \frac{dS}{dt} = \Pi - \mu S - \frac{e^{\alpha_0 - s_d}SI}{N}, \tag{48} $$
$$ \frac{dE}{dt} = \frac{e^{\alpha_0 - s_d}SI}{N} - (\mu + \epsilon + q_1)E, \tag{49} $$
$$ \frac{dI}{dt} = \epsilon E - (\mu + d_1 + \gamma + q_2), \tag{50} $$
$$ \frac{dQ}{dt} = q_1 E + q_2 I - (\alpha + \mu)Q, \tag{51} $$
$$ \frac{dR}{dt} = \gamma I + \alpha Q - \mu R, \tag{52} $$

with initial conditions

$$ S(0) = S_0, E(0) = E_0, I(0) = I_0, $$
$$ Q(0) = Q_0, R(0) = R0. \tag{53} $$

The problem will be considered in the following region

$$ \Omega_1 = \left[(S, E, I, Q, R \in \mathcal{R}^5, N(t) \leq \frac{\Pi}{\mu}. \right]. \tag{54} $$

4.1 Stability analysis of the model with quarantine factor

The disease-free equilibrium point is $E_0 \left(\frac{\Pi}{\mu}, 0, 0, 0, 0 \right)$ The basic reproduction number is calculated as discussed in the previous section and is obtained as

By denoting $\eta_1 = (\mu + \epsilon + q_1), \eta_2 = (\mu + d_1 + q_2 + \gamma), \eta_3 = (\alpha + \mu)$

$$ R_0 = \frac{\epsilon e^{\alpha_0 - s_d}\Pi}{\mu N \eta_1 \eta_2}. \tag{55} $$

The Jacobian matrix of the system (48)-(53) evaluated at the disease-free equilibrium point is given by

$$ J(E_0) = \begin{pmatrix} -\mu & 0 & -\frac{e^{\alpha_0 - s_d}\Pi}{\mu N} & 0 & 0 \\ 0 & -\eta_1 & \frac{e^{\alpha_0 - s_d}\Pi}{\mu N} & 0 & 0 \\ 0 & \epsilon & -\eta_2 & 0 & 0 \\ 0 & q_1 & q_2 & -\eta_3 & 0 \\ 0 & 0 & \gamma & \alpha & -\mu \end{pmatrix} $$

The eigenvalues of the above matrix are

$$\lambda_{1,2} = -\mu, \tag{56}$$

$$\lambda_3 = -\frac{1}{2}[\eta_1 + \eta_2 \tag{57}$$

$$+\sqrt{(\eta_1 + \eta_2)^2 - 4\eta_1\eta_2(1 - R_0)}], \tag{58}$$

$$\lambda_4 = -\frac{1}{2}[\eta_1 + \eta_2 \tag{59}$$

$$-\sqrt{(\eta_1 + \eta_2)^2 - 4\eta_1\eta_2(1 - R_0)}], \tag{60}$$

$$\lambda_5 = -\eta_3. \tag{61}$$

where $\eta_1 = (\mu + \epsilon + q_1), \eta_2 = (\mu + d_1 + q_2 + \gamma), \eta_3 = (\alpha + \mu)$ The disease-free equilibrium is asymptotically stable if $R_0 < 1$.

The endemic equilibrium points are given as

$$S^* = \frac{\Pi}{\mu R_0}, \tag{62}$$

$$E^* = \frac{\Pi}{\eta_1}\left(\frac{R_0 - 1}{R_0}\right), \tag{63}$$

$$I^* = \frac{N\mu}{e^{\alpha_0 - s_d}}(R_0 - 1), \tag{64}$$

$$Q^* = \frac{(R_0 - 1)}{\eta_3}\left[\frac{q_1\Pi}{R_0(\eta_1) + \frac{q_2 N\mu}{e^{\alpha_0 - s_d}}}\right], \tag{65}$$

$$R^* = \frac{(R_0 - 1)}{\mu}\left[\frac{\alpha q_1\Pi}{R_0\eta_3\eta_1}\right. \tag{66}$$

$$\left. + \frac{\alpha q_2 N\mu}{e^{\alpha_0 - s_d}(\alpha + \mu)} + \frac{\gamma N\mu}{\beta}\right]. \tag{67}$$

The Jacobian matrix of the system (48)-(53) evaluated at the endemic equilibrium point is given by

$$J(E_0) = \begin{pmatrix} -A_0 & 0 & -\frac{\beta\Pi}{\mu N R_0} & 0 & 0 \\ B_0 & -\eta_1 & \frac{\beta\Pi}{\mu N R_0} & 0 & 0 \\ 0 & \epsilon & -\eta_2 & 0 & 0 \\ 0 & q_1 & q_2 & -\eta_3 & 0 \\ 0 & 0 & \gamma & \alpha & -\mu \end{pmatrix}$$

where $A_0 = \mu[1 + (R_0 - 1)], B_0 = \mu(R_0 - 1), \beta = e^{\alpha_0 - s_d}$, by applying Descates' Rule of Signs, the characteristic polynomial of the above matrix is given by

$$P(\lambda) = \lambda^5 + \zeta_1\lambda^4 + \zeta_2\lambda^3 + \zeta_3\lambda^2 + \zeta_4\lambda + \zeta_5. \tag{68}$$

where

$$\zeta_1 = A_0 + \eta_1 + \eta_2 + \eta_3 + \mu, \tag{69}$$

$$\zeta_2 = A_0[\eta_1 + \eta_2 + \eta_3 + \mu]$$
$$+ \eta_1[\eta_2 + \eta_3 + \mu] + \eta_2[(\alpha + \mu) + \mu]$$
$$+ \eta_3\mu - \frac{\beta\Pi\epsilon}{\mu R_0 N}, \tag{70}$$

$$\zeta_3 = A_0\eta_1[\eta_2 + \eta_3 + \mu] + \eta_1 + \eta_2$$
$$+ (\eta_3 + \mu)A_0\eta_2 + \eta_1\eta_2)$$
$$+ \eta_3 A_0 - \frac{\beta\Pi\epsilon}{\mu R_0 N}(3\mu + \alpha), \tag{71}$$

$$\zeta_4 = A_0\eta_1\eta_2[\eta_3 + \mu] - \frac{\beta\Pi\epsilon}{N R_0}(\alpha + 2\mu)$$
$$+ A_0\eta_3\mu[\eta_1 + \eta_2]$$
$$+ \eta_3\mu\left[\eta_1\eta_2 + \frac{\beta\Pi\epsilon}{\mu N R_0}\right], \tag{72}$$

$$\zeta_5 = \eta_3\mu\left(A_0\eta_1\eta_2 + \frac{\beta\Pi\epsilon}{\mu N R_0}\right). \tag{73}$$

The coefficients of the polynomial $P(\lambda)$ are all positive, the quantity $\beta\Pi/(\mu N R_0) \to 0$, as $N \to \infty$. By replacing λ by $-\lambda$ in (68) we obtain five sign changes. This shows that the Jacobian matrix evaluated at the endemic equilibrium point has five negative eigenvalues. The endemic equilibrium point is stable if $R_0 > 1$.

4.2 Results for the model with quarantine factors

The effects of quarantining different sub-populations in an infected population is shown in the figures below.
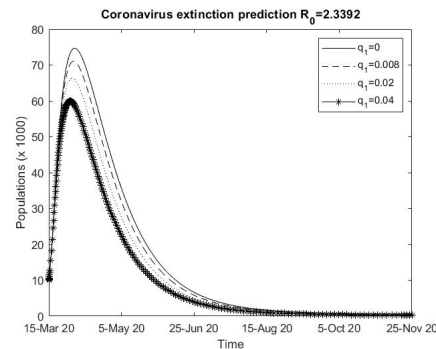

Figure 5: Effect of quarantining only the exposed group

With the value of $R_0 \approx 3$, meaning that every infected person infects three people and so on. The effect of quarantining only those exposed individuals is shown in Figure 5. This does not have substantial effect in reducing the number of new cases. The effect

of quarantining only the infected individuals would have the same effect. The prediction is that if only exposed or infected individuals are quarantined it requires about six months before the virus could clear out.
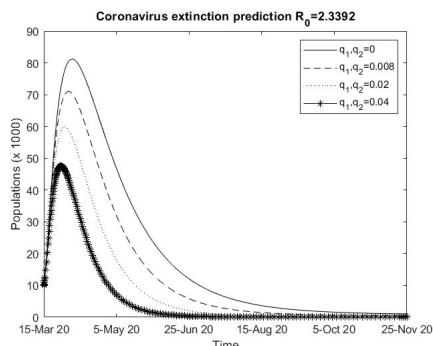

Figure 6: Effect of quarantining both exposed and infected groups

The effect of quarantining both exposed and infected groups has a better effect of reducing new cases as shown in Figure 6. The prediction is that with an initial approximately 10 000 new cases, effective quarantines of these both groups could require a peak of about 50 000 new cases before the they start declining, this requires approximately two months. The prediction shows that if these quarantines are not effective the clearing out of the coronavirus requires up to eight months.
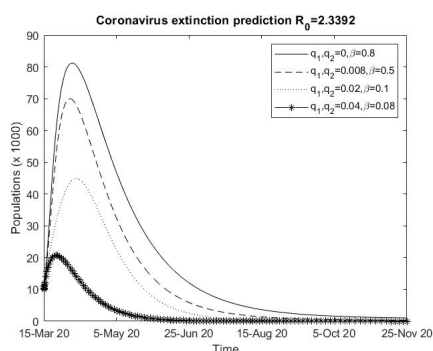
Figure 7: Effect of quarantining susceptible individuals, exposed and infected groups

In Figure 7, it is shown that quarantining all three groups reduce the infected population significantly, this is a complete lock down. Lock downs prevent the spread of the disease, but they are not always desirable as they are detrimental to economic growth.
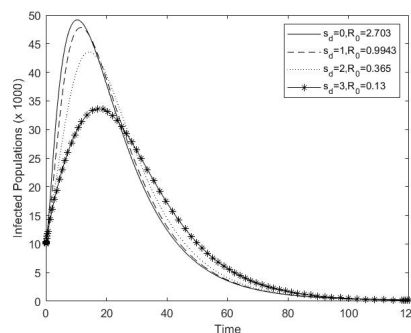

Figure 8: Effect of increasing social distancing on infected populations

In Figure 8 the effect of social distancing on infected population is shown. Increasing social distance reduce the infected population. It is clear from the illustrations that in the absence of quarantine, social distancing alone can lead to 50% decline in the infected population. The value of the basic reproduction number declines as the social distance increase. The value of R_0 declines significantly. This is one of the tools that can be used before a cure or vaccine is developed.

5 Data analysis of the outbreak of coronavirus from Wuhan

5.1 Theoretical prediction of the Coronavirus waves

Theoretically a disease outbreak is characterised by waves, the first outbreak invades a naive population. This means that the population is unaware of the disease and invades it quickly resulting in increased cases of the disease. In the case of the novel Coronavirus that originated in China, mostly in other parts of the world thought that it would just be same as MERS-Cov and SARS-Cov. The outbreak of coronavirus was known as far back as November 2019, very little was known about human to human transmission. The basic reproduction number of the previous coronavirus diseases was much lower that the novel coronavirus which made people not to take it serious [?]. This time it took the world by surprise. A theoretical prediction of the novel coronavirus Covid'19 is shown in Figure 9
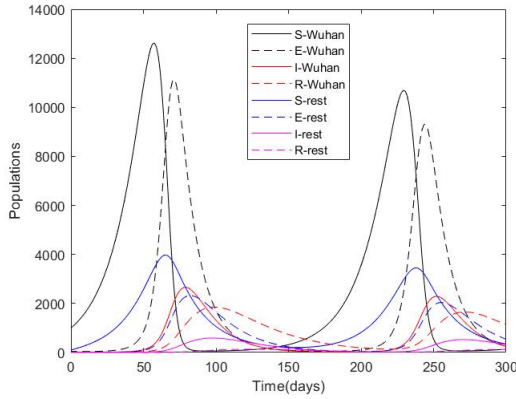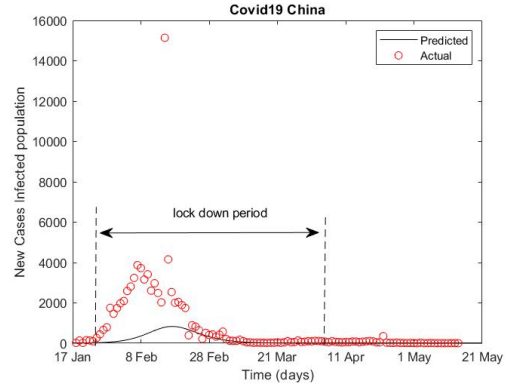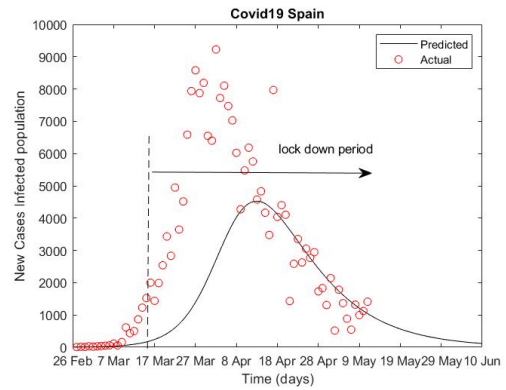
Figure 9: Theoretical pandemic predictions $m_w = 0.02, m_r = 0.01, \beta_w = 0.08, \beta_r = 0.02, \beta_{wr} = 0.04, d_w = d_r = 0.02$

(a) New cases in China $R_0 = 1.03, \beta_w = 8.68, \gamma_w = 8.53$.

(b) Coronavirus New cases in Spain $R_0 = 1.14, \beta = 0.97, \gamma = 0.9$.

Figure 10: Prediction of new cases China and Spain.

Naturally without intervention, the first epidemic wave reaches a peak. The drop in new cases is as a result of running in short of susceptible population. The population recovers and the second wave occurs. With interventions such as social distancing and quarantines the peaks can be much smaller. In most cases the disease need to infect a certain number of people before the curve flatten or tails off. If there are recoveries, if a certain number of people recover, the disease runs in short of people to infect (herd immunity).

The early statistics recorded from the epicentre of the outbreak in Wuhan in China can be traced as far back as 21 January 2020 ([13]).The first case was detected in November 2019. The recorded data shows the increase in the number of cases in China,by the 17th of February 2020 there were 19461 cases recorded in China and 1772 deaths. On the 22 of February 2020, China recorded the first decrease in new cases. At this time movement of people was not very restricted and this migration of people in and out of China resulted in the infection of people in the rest of the world. The hardest hit were among others Italy, France, Germany, USA,Spain and South Africa. The impact of the spread of coronavirus is shown the figures below

The outbreak of coronavirus started in Wuhan in China with new cases rising rapidly with the basic reproduction number $R_0 = 1.03$ indicating that the disease could persist to infect many people. According to the data obtained from ([13]), new cases in China rose to 15141 on the on the 13th of February 2020, the numbers started decreasing from the that peak. This could be attributed to the implementation of lock downs and social distancing that they imposed. The predictions that are shown in the Figure 10a are the possible extinction of the virus should lock downs and social distancing had applied earlier. In Figure 10b, Spain was one of the European countries that recorded a large number of cases. The prediction shows that with social distancing and lock downs implemented, virus extinction could have been achieved much earlier. The actual data shows that even when lock down was implemented, the number of cases kept on increasing, this could mean that the regulations were not followed as perfectly as in the prediction. Generally lock downs and social distancing had positive effects in reducing the number of new cases.

Italy and Germany also recorded large numbers of

coronavirus cases in Europe.
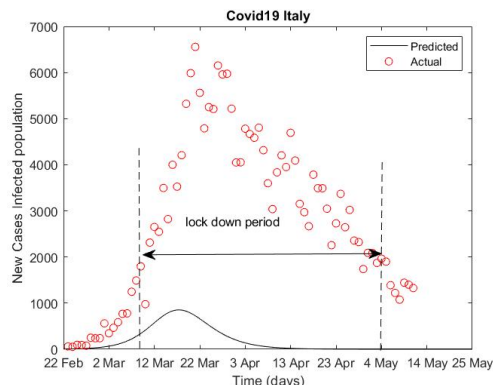
(a) New cases in Italy $R_0 = 1.15, \beta = 2.23, \gamma = 1.94$.
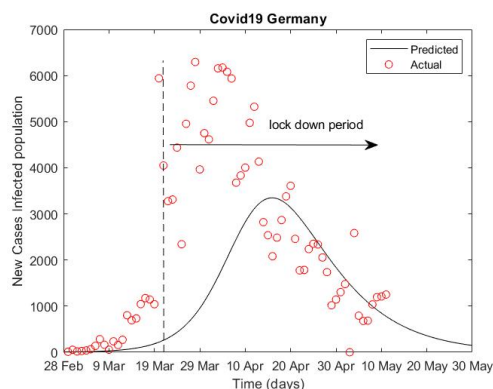
(b) New cases in Germany $R_0 = 1.5, \beta = 1.15, \gamma = 0.76$.

Figure 11: New cases in Italy and Germany.

In Figures 11a and 11b the prediction for the virus extinction should the lock downs and social distancing have been applied perfectly. In the case of Italy, there is large difference between the actual and prediction, this can be attributed to two reasons; firstly it is possible that lock down and social distancing rules were not seriously observed and secondly the model did not consider other factors such as underlying illnesses and age factors.
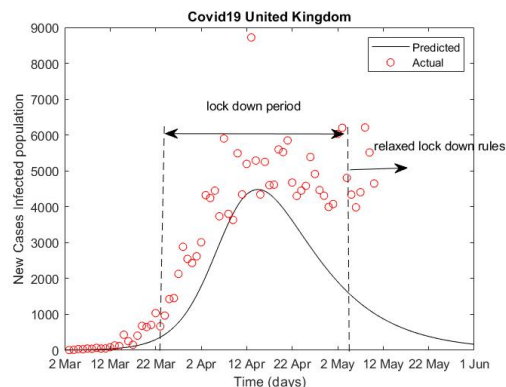
(a) New cases in the Unite Kingdom $R_0 = 1.15, \beta = 2.46, \gamma = 2.13$.
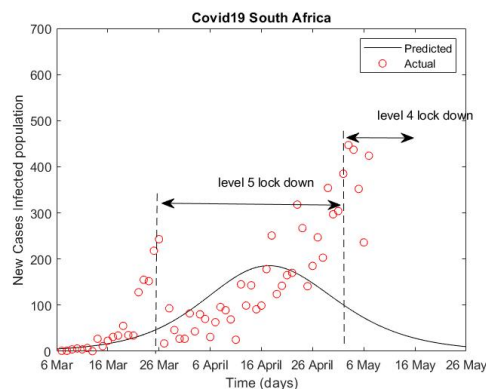
(b) New cases in South Africa $R_0 = 1.22, \beta = 2.75, \gamma = 2.26$.

Figure 12: New cases in United Kingdom and South Africa.

The United Kingdom recorded a high number of cases, the lock down and social distancing was introduced and the number of new cases started decreasing as shown in Figure 12a.

African countries were least affected as of the 28th of March 2020. At this time South Africa had total cases of 1170 of coronavirus infections. In Figure 12b South African cases decreased when lock down rules were announced and started increasing again when they moved to level 4 in which the rules were relaxed. One observation is that the United Kingdom could have reached its peak while South Africa still had to reach its peak. The number of people infected in South Africa are still very few as compared to its total population, this could mean that the virus still need to infect enough number of people for country to start experiencing a peak.

6 Conclusion

The study of the impact of the novel coronavirus (COVID'19) was performed using the SEIR model describing the outbreak of the disease in the city of

Wuhan in China with migrations to the rest of the world. Another model with quarantine and social distancing factors was considered. Conditions under which the disease persist and clears out were mathematically shown. The disease-free equilibrium for both models is asymptotically stable. The predictions for the extinction of the novel coronavirus was done, the predictions are based on factors such as effective quarantines and social distancing being practised effectively. The theoretical model also showed that quarantining both the exposed and infected is more effective that only quarantining the infected individuals. Increasing social distancing could decrease number of new cases by up to 30%.The spread of the coronavirus became rapid because it was believed to be the same as the previous MERS-Cov and SARS-Cov. During its outbreak in China little was known about human to human transmission. Travelling continued to happen in and outside Wuhan. Future research need to investigate issues such as when is the right time to apply interventions and what is the state of preparedness in future pandemics.

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