Mathematical model for Covid-19 with “protected susceptible” in the post-lockdown era

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Abstract  Lockdown is one of the drastic measures implemented by governments to curtail the spread of the Covid-19 pandemic and save lives. However, it has caused unprecedented damages to the economy. This paper provides a quantitative approach to assess the impact of a gradual, post-lockdown context concerning the spread of the disease. We propose to create a special class of individuals called “protected” who are risk-free to be infected. Such individuals could also be the vaccinated when an effective vaccine will be available. We developed a mathematical epidemic model for Covid-19 which describes the interactions between susceptible and infected individuals. We investigate the various and optimal strategies to curtail the spread of the infection at a minimum cost. As a case study on South Africa, the sensitivity analysis shows that investing on the special class “protected” is a better approach to reducing new secondary infections as opposed to reducing the contact rate between susceptible and infected individuals, or having more recovered patients. The simulations reveal that the peak could be reached in September 2020. This is consistent with the projection of the South African government as the winter season is expected to be over in mid August. Moreover, if 1 out of 1000 susceptible (cumulatively) join the special class, we project a maximum of 400,000 active cases. The number of infected and deaths could drastically increase as the proportion of individuals joining the special class decreases.

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1. Introduction

Coronavirus disease 2019 (Covid-19) is a respiratory communicable disease caused by the newly-discovered virus strain, SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) [7]. Covid-19 was first identified in Wuhan (in China) in December 2019, and has rapidly spread over four months across 185 nations and territories with more than 2.9 million infected people and 206 thousands deaths [13]. It was declared a pandemic by the World Health Organization on March 11, 2020 [14]. The disease can be propagated primarily from person-to-person through small droplets via coughing, sneezing or talking. Susceptible individuals may also be infected SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) [7]. Covid-19 was first identified in Wuhan (in China) in December 2019, and has rapidly spread over four months across 185 nations and territories with more than 2.9 million infected people and 206 thousands deaths [13]. It was declared a pandemic by the World Health Organization on March 11, 2020 [14]. The disease can be propagated primarily from person-to-person through small droplets via coughing, sneezing or talking. Susceptible individuals may also be infected

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by touching contaminated surfaces. The most common symptoms of Covid-19 are fever, tiredness, dry cough, fatigue, and shortness of breath [15]. Some patients may have aches and pains, nasal congestion, running noses, a sore throat or diarrhea. The symptoms are usually mild, but can progressively worsen. Hand washing, covering of the nose or mouth when sneezing or coughing, avoiding touching the nose, mouth or eyes, and social distancing are recommended preventive measures to avoid infection.

Due to the severity of the Covid-19 pandemic, many governments have taken drastic decisions to curtail the spread and furthermore, to protect healthcare systems. The decisions included the cancellation of public events; the closure of schools, public places and borders; travel bans; lockdown, etc. Countries that have benefited the most from such strategies are those who implemented such strategies earlier than others. Though those strategies have been helpful, they have caused socio-economic damages. In fact, during the lockdown, social disconnection and fear of an uncertain future have fuelled mental health issues, and domestic violence has increased. Many workers have lost their respective jobs. Businesses’ closure disrupted supply chains and lowered productivity. The shutdown of drug-manufacturing plants in China (the second largest exporter of pharmaceutical products) had delayed supplies to factories for producing generic medicines [16]. Tourism, air transport, and oil sectors are visibly impacted. Invisible impacts are also expected regardless of the duration of the pandemic. The global economy is projected by the International Monetary Fund to shrink by 3% in 2020 [18].

To rescue the collapse of the economy, governments are thinking of safety measures to relax the lockdown. Some developed countries are considering issuing an “immunity passport” which indicates immunity to the disease. However, this strategy has been disapproved by the World Health Organization due to a lack of enough scientific evidence that reinfection is not possible using the aforementioned strategy [19]. The South African government implemented a risk balancing approach to gradually lift the lockdown restrictions. Many mathematical models have been developed to study epidemic diseases in general [2,11,21], and Covid-19 in particular [3,6,9,10,12]. Few quantitative studies have been conducted to understand the spread of the infection in the post-lockdown era.

We propose in this paper a mathematical epidemic model for Covid-19 transmission dynamics, which accounts for a safe lockdown restrictions relaxation. We consider a special class of individuals called “protected”. To join this class, individuals must present evidences to be risk-free of being infected. Evidences could be the measures put in place to ensure a risk-free working and/or living environment. Companies can provide temporary shelters for their employees. Immunity passport holders or vaccinated individuals are also be included in this special class. We believe that investing in this group of individuals could significantly curtail the spread while ensuring that some sectors of the economy may be opened.

2. Mathematical model description

Consider a population affected by Covid-19. We classify the population into six compartments: susceptible (S), susceptible protected (SP), asymptomatic infected not in quarantine (IS), symptomatic infected not in quarantine (IA), asymptomatic infected in quarantine (AQ), and recovered (R). We consider the following hypothesis (as per the flow diagram in Fig. 1):

i. A fraction \( z_1 \) (with \( 0 < z_1 < 1 \)) of susceptible are “protected”.

ii. Amongst infected individuals, a fraction \( z_2 \) of asymptomatic (IA) and \( z_3 \) of symptomatic (IS) are neither identified nor tested (with \( 0 < z_2, z_3 < 1 \)) and the remaining fractions are identified and are in quarantine.

iii. Susceptible (not protected) are likely to be infected (if exposed) by unidentified asymptomatic IS at rate \( \eta_1 \), or by unidentified symptomatic IS at rate \( \eta_2 \), or by quarantine Q at rate \( \eta_3 \).

iv. Newly infected are first asymptomatic, and in most cases are not identified.

v. Unidentified asymptomatic can progress to symptomatic stage at rate \( \rho \).

vi. Infected IA and AQ can recover at rates \( r_1, r_2 \) and \( r_3 \) respectively.

vii. A proportion \( \gamma \) of quarantine can be diagnosed negative and join the susceptible compartment.

viii. Symptomatic infected can die due to Covid-19 disease at rate \( \delta \).

ix. No reinfection, constant recruitment \( \Lambda_1 \) of susceptible (for instance due to birth), natural death rate \( \mu \).

The mathematical equations describing our model with the hypothesis above are

\[
\frac{dS}{dt} = \Lambda_1 + \gamma Q - z_1 S - \frac{(1 - z_1)(z_2 \eta_1 I_A + z_3 \eta_2 I_S + \eta_3 Q) S}{S + S_P + I_A + I_S + Q + R} - \mu S, \quad (1)
\]

\[
\frac{dS_P}{dt} = z_1 S - \mu S_P, \quad (2)
\]

\[
\frac{dI_A}{dt} = \frac{(1 - z_1)(z_2 \eta_1 I_A + z_3 \eta_2 I_S + \eta_3 Q) S}{S + S_P + I_A + I_S + Q + R} - (\gamma + r_1 + \mu + \delta) I_A, \quad (3)
\]

\[
\frac{dI_S}{dt} = z_2 \rho I_A - (1 - z_3 + z_1 r_2 + \mu + \delta) I_S, \quad (4)
\]

\[
\frac{dQ}{dt} = (1 - z_2) I_A + (1 - z_3) I_S - (\gamma + r_1 + \mu + \delta) Q, \quad (5)
\]

\[
\frac{dR}{dt} = z_2 r_1 I_A + z_3 r_2 I_S + r_3 Q - \mu R, \quad (6)
\]

associated with the initial conditions

\[
S(0) > 0, S_P(0) \geq 0, I_A > 0, I_S(0) \geq 0, Q(0) \geq 0, R(0) \geq 0. \quad (7)
\]

The meaning of the parameters is given in Table 1.

In the above model, we do not explicitly represent the cases of infections through contaminated surfaces. However, we assume that humans are responsible for the contamination (i.e., indirect human transmission). Our main objective is to evaluate the influence of the “protected” class on the spread of the infection. We will also investigate the various strategies to ensure a low rate of new infections at minimum cost.
In the same manner, we can prove the positivity of $S$, such that (2), (4)–(6) for Proposition 1. For rem [17]. (1)–(6) solution of the system (1), we have provided a given initial condition, we note that the model (1)–3. Model analysis Provided a given initial condition, we note that the model (1)–(6) is mathematically well-posed by the Cauchy-Picard theorem [17].

**Proposition 1.** For $\gamma = 0$, the functions $S, S_P, I_A, I_S, Q$ and $R$ solution of the system (1)–(6) are nonnegative and bounded.

**Proof.** Since $S(0) > 0$, by contradiction assume there is $t_1 > 0$ such that $S(t_1) = 0, S(t_1) < 0$ and $S(t) > 0$ for all $t < t_1$ (i.e., $t_1$ is the first time from which $S$ changes its sign). Then from (1), we have $S(t_1) = \Lambda_1 > 0$ which is a contradiction. Hence $S(t)$ will never change its sign and will be positive at all time.

In the same manner, we can prove the positivity of $I_A$. Solving (2), (4)–(6) for $S_P, I_S, Q$ and $R$ respectively, we obtain

\[
S_P(t) = e^{-\mu t}S_P(0) + \int_0^t e^{\mu(t-s)}\frac{\partial S}{\partial t}(s) \, ds \
I_A(t) = e^{-\mu t}I_A(0) + \int_0^t e^{\mu(t-s)}\frac{\partial I_A}{\partial t}(s) \, ds \
Q(t) = e^{-\mu t}Q(t_0) + \int_0^t e^{\mu(t-s)}(1 - \gamma)I_A(s) + (1 - \delta)I_S(s) \frac{\partial Q}{\partial t}(s) \, ds \
R(t) = e^{-\mu t}R(0) + \int_0^t e^{\mu(t-s)}(\mu + \delta)Q(s) + r_3Q(s) \frac{\partial R}{\partial t}(s) \, ds
\]

where $\alpha_2 = 1 - \gamma_3 + \gamma r_3 + \mu + \delta$ and $\alpha_3 = \gamma + r_3 + \mu + \delta$.

To prove the boundedness, it suffices to show that $N = S + S_P + I_A + I_S + Q + R$ is bounded. Clearly $N(t) \geq 0$ for all $t \geq 0$. From (1)–(6), we get

\[
\frac{dN}{dt} = -\Lambda_1 - \mu N - \delta(I_S + Q) \leq -\Lambda_1 - \mu N.
\]

This implies that

\[
N(t) \leq \frac{\Lambda_1}{\mu} + \left(\frac{\Lambda_1}{\mu} - N(0)\right) e^{-\mu t} \leq \max \left(\frac{\Lambda_1}{\mu}, N(0)\right) \tag{10}
\]

which is bounded. □

We note that the study of the positivity and boundedness is to ensure that the population will not be negative and blow up at any time in our model.

3.1. Steady states and basic reproduction number

Steady states are time-independent solutions of the system (1)–(6), that is, satisfying

\[
\frac{dS}{dt} = \frac{dS_P}{dt} = \frac{dI_A}{dt} = \frac{dI_S}{dt} = \frac{dQ}{dt} = \frac{dR}{dt} = 0
\]

There are two steady states: the disease free equilibrium and the endemic equilibrium.

3.1.1. The disease free equilibrium

It is given by

\[
E_0 = \left(\Lambda_1, \frac{\Lambda_1}{\mu} + \frac{\gamma_3 \Lambda_1}{\mu(\gamma_3 + \mu)}, 0, 0, 0, 0\right).
\]

3.1.2. The basic reproduction number

It is defined as the average number of secondary infections caused by a single infected individual in a population of purely susceptible. It is computed using the next generation matrix approach [23]. Denoting by $\mathcal{F}$ the vector for the newly
infected and $\mathcal{F}$ the vector for transfer and death into the disease compartments, then we get from (1)-(6)

$$
\mathcal{F} = \begin{pmatrix}
-\frac{(1-a_1)(1-a_2)+\frac{1}{C_0}}{\mu (1-a_1) a_2} \\
0 \\
0
\end{pmatrix}
$$

where $a_1 = 2z_2 + 2z_1 r_1 + 1 - z_2 + \mu, a_2 = 1 - z_3 + 2z_2 r_2 + \mu + \delta$ and $a_2 = \gamma + r_4 + \mu + \delta$. The Jacobian matrices $\mathcal{F}$ and $V$ of $\mathcal{F}$ and $V$ with respect to the disease variable $I_1, I_2, Q$ at $E_0$ are

$$
F = \begin{pmatrix}
\frac{1}{\mu + z_1} \\
0 \\
0
\end{pmatrix},
V = \begin{pmatrix}
\frac{1}{\mu + z_1} \\
0 \\
0
\end{pmatrix}
$$

The inverse of the matrix $V$ is given by

$$
V^{-1} = \frac{1}{a_1 a_2 a_3} \begin{pmatrix}
0 & 0 & 0 \\
-2z_2 & a_3 a_1 & 0 \\
0 & 0 & a_1 a_2
\end{pmatrix}
$$

Hence the next generation matrix $FV^{-1}$ is given by

$$
FV^{-1} = \frac{(1-z_1)\mu}{\mu + z_1} \begin{pmatrix}
\frac{\alpha_1 a_1 a_2 a_3}{\alpha_1 a_1 a_2 a_3} \\
0 \\
0
\end{pmatrix}
$$

The basic reproduction number which is the spectral radius of the matrix $FV^{-1}$ is given by

$$
R_0 = \frac{(1-z_1)\mu}{\mu + z_1} \left( \frac{a_2 \eta_1 a_3}{a_1 a_2 a_3} + \eta_2 (a_2 (1-z_2) + \rho z_2 (1-z_3)) \right).
$$

We note that the basic reproduction number $R_0$ is an important epidemiological parameter used to understand and predict the spread of infection. For example, $R_0 > 1$ means that each infected will infect at least one individual in average and the disease may remain in the population forever.

3.1.3. Endemic equilibrium

This steady state has disease components. Solving (11), we obtain

$$
S' = \frac{\alpha_1 a_1 a_2 a_3}{\alpha_1 a_1 a_2 a_3}
$$

$$
S' = \frac{a_2 \rho (1-z_1) a_2}{a_1 a_2},
$$

$$
S' = \frac{a_2 \rho (1-z_1) a_2}{a_1 a_2}
$$

$$
S' = \frac{a_2 \rho (1-z_1) a_2}{a_1 a_2}
$$

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$$

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$$

$$
S' = \frac{a_2 \rho (1-z_1) a_2}{a_1 a_2}
$$

The value $\lambda = 0$ leads to the disease free equilibrium $E_0$.

The endemic equilibrium is $E_1 = \left( S', S''_1, I'_{l_1}, I''_{l_1}, Q', Q'' \right)$, where $S', S''_1, I'_{l_1}, I''_{l_1}, Q'$ and $Q''$ are given in (13), with $\lambda = \lambda_2$.

We note that $E_1$ exists when $R_0 > 1$ (otherwise its components will be negative). The stability of the equilibrium $E_1$ indicates that the disease will become endemic. This is consistent with the condition $R_0 > 1$ for the existence of $E_1$.

3.2. Stability of the disease free equilibrium

Theorem 1. The disease free equilibrium $E_0$ is asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

Proof. The Jacobian matrix evaluated at $E_0$ is given by

$$
J = \begin{pmatrix}
\frac{1}{\mu + \alpha_1} & 0 & -\frac{1}{\mu + \alpha_1} & 0 & -\frac{1}{\mu + \alpha_1} & 0 & 0 & 0 \\
0 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0
\end{pmatrix}
$$

The matrix $J$ can be regarded as an upper triangular block matrix. Its eigenvalues are $\lambda_1 = -\mu, \lambda_2 = \mu, \lambda_3, \lambda_4, \lambda_5, \lambda_6$ and $\lambda_7 = -\mu$, where $\lambda_3, \lambda_4, \lambda_5$ are the eigenvalues of the block matrix

$$
A = \begin{pmatrix}
\frac{1}{\mu + \alpha_1} - \mu & -a_1 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & -a_1 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0
\end{pmatrix}
$$

The characteristic polynomial associated with $A$ is

$$
p(\lambda) = \det(A - \lambda I) = -\lambda^3 + b_1 \lambda^2 + b_3 \lambda + b_0,
$$

where

$$
b_2 = \frac{(1-z_1)\mu}{\mu + z_1} \left( \frac{\alpha_2 a_2 \rho}{a_1 a_2} + \eta_2 (a_2 (1-z_2) + \rho z_2 (1-z_3)) \right) + \alpha_3 a_1 (1 - R_0),
$$

$$
b_1 = \frac{(1-z_1)\mu}{a_1 (\mu + z_1)} \left( a_2 \eta_1 (1-z_2) + 2z_2 \rho (1-z_3) - a_1 (a_2 a_3 \eta_1 + \eta_3 (1-z_2)) + a_1 a_2 (1 - R_0) + a_1 a_2 \right),
$$

$$
b_0 = a_1 a_2 a_3 (1 - R_0).
$$

Moreover,

$$
b_2 b_1 - b_0 = b_2 (b_1 - a_1 a_2 (1 - R_0)) + a_1 a_2 (1 - R_0) (b_2 - a_0).
$$

If $R_0 > 1$, then $\det(A) > 0$ and at least one of the eigenvalues of $A$ is positive (since $\det(A) = \lambda_3 \lambda_4 \lambda_5 = -b_0$). As a result, $E_0$ is
unstable. Assuming $R_0 < 1$, $b_0, b_1, b_2$ and $b_2b_1 - b_0$ are positive. In this case, by Routh-Hurwitz criteria [1] the disease free equilibrium $E_0$ is locally asymptotically stable.

The stability results in Theorem 1 indicate that if $R_0 < 1$ (i.e., each infected individual infects at most one individual in average) then over time the population could be disease free. Moreover, secondary infections are low as the basic reproduction number $R_0$ is small. We will investigate the strategies to reduce $R_0$. It is expected that the endemic equilibrium $E_1$ is stable when $R_0 > 1$. In what follows, we will investigate the strategies to reduce $R_0$ (including the impact of $x_1$ on $R_0$) by studying how $R_0$ is sensitivity with respect to some parameters. We overlooked the compartment $I_3$ by assuming that when asymptomatic infected are not in quarantine and they become symptomatic, they are immediately placed in quarantine.

3.3. Sensitivity analysis

Sensitivity analysis is used to investigate the effect of parameters on a given quantity.

i. The absolute sensitivity of $R_0$ with respect to $\eta_1, \eta_2$ and $\eta_1$

$$\frac{\partial R_0}{\partial \eta_1} = \frac{(1 - x_1)\mu_1}{(x_1 + \mu)a_1} > 0, \quad \frac{\partial R_0}{\partial \eta_2} = \frac{(1 - x_1)\mu_2}{(x_1 + \mu)a_1a_2} > 0$$

$$\frac{\partial R_0}{\partial \eta_3} = \frac{(1 - x_1)\mu_1\mu_2}{(x_1 + \mu)a_1a_2a_3} > 0.$$  

We observe that the basic reproduction number $R_0$ decreases as $\eta_1, \eta_2$ or $\eta_1$ decreases. Therefore, to reduce new secondary infections, one can decrease the contact rates between susceptible and infected $I_4, I_5$ or $Q$. This can be done through massive testing of the population every day to identify infected individuals for quarantine, reinforcing the protection of medical personnel and close family members (in the case of self-quarantine). It is difficult to monitor contact between susceptible and unidentified infected individuals $I_4$ or $I_5$. Social distancing or lockdown can be implemented, but will involve serious costs.

ii. The absolute sensitivity of $R_0$ with respect to $r_1, r_2$ and $r_3$

$$\frac{\partial R_0}{\partial r_1} = \frac{\mu_1}{a_1} R_0 < 0,$$

$$\frac{\partial R_0}{\partial r_2} = \frac{(1 - x_1)\mu_1\mu_2}{(x_1 + \mu)a_1a_2a_3} < 0,$$

$$\frac{\partial R_0}{\partial r_3} = \frac{(1 - x_1)\mu_1\mu_2}{(x_1 + \mu)a_1a_2a_3} < 0.$$  

The basic reproduction number $R_0$ decreases as $r_1, r_2$ or $r_3$ increases. As a result, to reduce new secondary infections one can increase the recovery rate. This strategy requires investment on an effective treatment (accessible to everyone so that unidentified infected individuals might access it). Some challenges with this strategy are the duration to develop an effective treatment or the financial burden due to the mass testing involved as it has been observed that early diagnoses are more easily treated [8].

iii. The absolute sensitivity of $R_0$ with respect to $x_1$, $x_2$ and $x_3$

$$\frac{\partial R_0}{\partial x_1} = \frac{(1 + \mu)R_0}{(1 - x_1)(x_1 + \mu)} < 0,$$

$$\frac{\partial R_0}{\partial x_2} = \frac{1 + \mu}{a_1x_2}(R_0 - R_1), \quad \frac{\partial R_0}{\partial x_3} = \frac{(1 - x_1)\mu}{x_1 + \mu}(R_2 - R_3),$$

where $R_1 = \frac{\mu_1(1-x_1)}{(1+x_1)\mu_1} + \frac{\mu_2(1-x_1)}{\mu_2}$ and $R_3 = \frac{\mu_1(1-x_1)}{(1+x_1)\mu_1} + \frac{\mu_2(1-x_1)}{\mu_2}$.

Since $\frac{\partial R_0}{\partial x_1} < 0$, increasing the fraction of “protected” will decrease secondary new infections. If $R_0 < R_1$ or $R_2 < R_3$, then the identification of newly infected individuals as a strategy will have no effect. However, if $R_1 < R_0$ or $R_1 < R_3$, then the increase in identifying newly infected individuals can reduce the number of secondary infections.

Though the absolute sensitivity analysis suggests strategies to reduce secondary infections, it is not the most efficient. We have computed the sensitivity index (SI) of $R_0$ with respect to the above parameters (that is, $\frac{\partial R_0}{\partial \eta_i}$) and displayed the results in Tables 2–5. Unless specified, we have used in the computations (including Figs. 2 and 3) the numerical values $x_1 = 0.008, x_2 = 0.1, \eta_1 = 0.25, \eta_2 = 0.385, r_1 = r_3 = 0.02976, \mu = 0.00236/90, \delta = 0.017/90, z_1 = 1, \rho = \gamma = \eta_1 = 0$ and $A_1 = 296425.875/90$. The parameters $r_1, r_3, \mu, \delta, A_1$ have been estimated from the Covid-19 data of South Africa between March 05 to April 18, 2020 [20,22]. We estimated $z_2, \eta_1, \eta_2$ to fit our model prediction with exact data (as per the Fig. 3 (c)). We overlooked the compartment $I_4$ by assuming that asymptomatic infected go to quarantine immediately when they become symptomatic (i.e., $r_2 = \rho = \eta_2 = 0$).

From Table 2, we observe that a 10% decrease of the contact rates with infected $\eta_1, \eta_2$ will decrease the number of new infections ($R_0$) to respectively 0.21%, 9.78%. Likewise, a 10% increase of $r_1, r_3, z_1$, will result to 0.32%, 9.72%, 10.04% respective decrease of new secondary infections. Therefore, encouraging more individuals to join the “protected” class, or reducing contact between quarantined and susceptible individuals, or having recovered patients, are better strategies to reduce secondary new infections. In Tables 3–5 we computed the sensitivity index (based on the output resulting from Table 2) and we observe that $z_1$ is the parameter that reduces the number of new infections the most.

4. Optimal control problem

We assume in this section that $x_1$ is not constant. We investigate the optimal value of $x_1$ that minimizes both the number of infected and the cost of getting more individuals to be “protected”. We consider the objective functional

$$J(u) = \int_0^T \left( c_1I_4(t) + c_2I_5(t) + c_3Q(t) + \frac{c_4}{2}u^2(t) \right),$$

where $u = x_1$ is the control variable and the $c_i (i = 1, \ldots, 5)$ are positive constants. The quadratic (scaled) term $\frac{c_4}{2}u^2$ represents the cost for being “protected”. We aim to find $\bar{u}$ such that
Theorem 2. \( u^* \) is a solution of the system of equations (1)–(6) if and only if it minimizes the Hamiltonian
\[
H = c_1 I_1 + c_2 I_5 + c_3 Q + \frac{c_4}{2} u^2 + \lambda_1 f_1 + \lambda_2 f_2 + \lambda_3 f_3 + \lambda_4 f_4 + \lambda_5 f_5,
\]
subject to the transversality conditions and the control variable \( u \). With the transversality conditions \( \lambda_i(t_f) = 0 \), \( i = 1, \ldots, 5 \), we have the existence of the optimal control \( u^* \) [5]. The Pontryagin's Maximum Principle leads to the adjoint equations
\[
\begin{align*}
\frac{d\lambda_1}{dt} &= -\frac{\partial H}{\partial S_1}, \\
\frac{d\lambda_2}{dt} &= -\frac{\partial H}{\partial S_2}, \\
\frac{d\lambda_3}{dt} &= -\frac{\partial H}{\partial S_3}, \\
\frac{d\lambda_4}{dt} &= -\frac{\partial H}{\partial S_4}, \\
\frac{d\lambda_5}{dt} &= -\frac{\partial H}{\partial S_5},
\end{align*}
\]
with the terminal condition \( \lambda_i(t_f) = 0 \), \( i = 1, \ldots, 5 \), which gives (27) at the control \( u^* \) and the corresponding state solutions \((S^*, S_{p^*}, I_{p^*}, I_{B^*}, Q^*)\). Within \( \Omega \) (i.e., for \( 0 < u < 1 \)), we have
\[
\frac{\partial H}{\partial u}|_{u=u^*} = 0.
\]

Solving (29) for \( u^* \), we get (26). \( \square \)

5. Numerical Simulation

We have computed the numerical solutions of the system (1)–(6) to illustrate the theoretical results (see Figs. 2 and 3).
Fig. 2 Illustration of the evolution of the epidemic in South Africa over time. The initial time \( t = 0 \) is the date April 18, 2020. We observe that the total number of infected decreases as more people join the “protected” class, and the epidemic reach its peak earlier.

Fig. 3 Evolution of the total number of deaths due to Covid-19 for the case South Africa. At the initial time \( t = 0 \) (that is April 18, 2020) there were 52 deaths.
We used the initial conditions: $S(0) = 59300000$, $S_I(0) = 2079$, and $R(0) = 903$. The initial time $t = 0$ corresponds to April 18 and the unit of time is the day.

From Fig. 2, we observe that if 1 out of 1000 susceptible individuals are (cumulatively) “protected”, then the pandemic in South Africa will reach its peak approximately after 150 days (that is around September 10, 2020) and there will be about 400,000 active case (see Fig. 2(a)]. After some days, most of the susceptible will be “protected” and less will be likely infected. As a result, the population could be disease free over time (see Fig. 2(a)]). If 1 out of 2000 susceptible are (cumulatively) “protected”, the total number of active case will rise up to one million (see Fig. 2(c)). If 1 out of 5000 susceptible are (cumulatively) “protected”, the total active cases will increase more up to 1.2 million (see Fig. 2(e)). We also observe in general in Fig. 3 that less people will die as $x_t$ increases (i.e., more individuals are “protected”).

6. Conclusion

In this paper, we proposed a mathematical compartmental model which describes the transmission dynamics of Covid-19 in a population. As an attempt to address the economic crisis due to the lockdown restrictions imposed by government to curtail the spread of the infection, we propose to consider a special class of individuals called “protected”. Such individuals must provide sufficient evidences that their environment is risk-free from the infection. We investigated in our model the impact of that special class of individuals on the transmission dynamics of the disease, and also other strategies to ensure low infections. Our results reveal that encouraging more individuals to join the special class, or reducing contact between quarantined and susceptible individuals, or having more recovered patients are better strategies to reduce secondary new infections. However, the latter strategies involve serious costs in supplying protective equipment to the medical personnel (and family members of infected individuals in the case of self-quarantine), or in treatment (including gravity and supply of ventilators and vaccine when available). Considering the case study of South Africa, we observe that investing in the “protected” class is the best strategy since it reduces the most the number of new infections. Moreover, new infections could significantly decrease as more individuals commit to the special class. Doungmo Goufo et al. [4] predicted in their model a shifting of the Covid-19 epicenters to the southern hemisphere countries (such as South Africa) during the winter period. Our results indicate that the peak of the infection could be reached within 150 days (that is, in September 2020). This is consistent with the projection of the South African government as the winter is expected to be over in mid August. However, the total number of infections could vary from low to very high depending on the fraction of people joining the special class.

Our model can be used as a scientific tool to assess and monitor the potential impact of the spread of the disease after the lockdown. It can also be used to control and understand the spread when an effective vaccine (or immunity passport) will be made available. In this case, the “protected” class will be regarded as a vaccinated class (provided that vaccination induced immunity).

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References


