

Mathematical Modelling Of The Impact Of Misinformation On The Spread Of Covid-19

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Abstract

In order to understand how misinformation affects the spread of COVID-19, this research project is developing a mathematical model. Every continent has been affected by the respiratory disease COVID-19, which is brought on by the SARS-CoV-2 virus. The virus swiftly spread because of the unprecedented speed at which information, particularly false information, has spread in this century. A mathematical model will be put forth in this study to examine the effect of incorrect information on COVID-19 dissemination. The reproduction (RO) which is the average number of new infections caused by infected person, will be obtained in order to assess the illness's contagiousness. In addition, the model's equilibrium point stability conditions will be established, giving new information about how the disease will behave over the long term. In order to solve the model, the Runge-Kutta method will be used. This will enable the investigation of the effects of changing parameters as well as the simulation of various scenarios. Understanding how misinformation affects the spread of COVID-19 will help researchers develop strategies that will effectively combat misinformation and limit the disease's spread, thereby reducing the overall impact of the disease.

Date of Submission: 13-05-2024

Date of Acceptance: 23-05-2024

I. Introduction

Background Information

The history of coronavirus disease 2019 (COVID-19 or SARS-CoV-2) dates back from discoveries of Tyrrell and Bynoe (1966) and Hamre and Procknow (1966). The coronavirus was first cultivated from the rhinoviruses (viruses that cause common cold) and some of the early strains of the coronavirus are B814 and 229E. These viruses were found to have some similar traits to the ones present in animals such as rats, bats, and pigs. There have been two major outbreaks of coronavirus in the history of the world and the outbreaks emanated from China each time. In 2002, coronavirus outbreak emanated from Southern China and the spread was experienced in 29 countries. The second outbreak of the coronavirus was in 2019 (from which the virus was named coronavirus disease in 2019, COVID-19) from Wuhan in China (Gross, 2020). COVID-19 cases have been recorded by all non-island countries except North Korea (although there are speculations that North Korea might be withholding some information). The origin of the COVID-19 outbreak remains unknown; some speculate it is from the consumption of live animals, while others speculate it is from some laboratories (Wu *et al.*, 2020). One thing that is known is that the predominant way that COVID-19 spreads is from person to person. In an attempt to contain the illness's dissemination, a lot of efforts have been placed on the sensitisation of the populace on the necessary precautions to prevent getting infected.

The ongoing efforts to contain the spread of COVID-19 include the global sensitisation. Government, non-governmental organisations and individuals have invested a lot of funding to create awareness. Unfortunately, many individuals still have some wrong perspectives about the spread of COVID-19. Misinformation from religious perspectives, unverified information on social media, conspiracy theories, and popular misinformation beliefs have been argued by Barua *et al.* (2020) to carry dangerous consequences on the spread of COVID-19. It is on this premise that this study is based; to mathematically investigate the effects of misinformation on the spread of COVID-19 dynamics.

Statement of the Problem

The rate of COVID-19 transmission is very low compared with the rate at which information is disseminated through social media. Also, the rate of acceptance of facts has been found to be low compared with the spontaneity with which religious beliefs are imbibed. These and many other reasons are responsible for misinformation about the transmission of COVID-19 from an infected individual to a susceptible individual. This subtle factor requires attention so that all governmental and non-governmental efforts do not continue to go to waste. It has been claimed that misinformation has dangerous consequences for COVID-19 transmission. This study is carried out to mathematically investigate the impact of misinformation on the transmission of

COVID-19.

Objectives

General objective

The general objective of this study is to investigate the effects of misinformation on the transmission of COVID-19.

Specific objectives

Specific objectives of this study are to:

1. formulate a mathematical model that captures the effect of misinformation on the transmission of COVID-19.
2. obtain the reproduction number, and establish the stability region and the positivity of the model.
3. determine the effects of misinformation on the transmission of COVID-19.

Significance of the Study

The results from this study shall provide a detailed explanation of the impact of misinformation on the spread of COVID-19. This study shall be useful for the health workers in discharging their duties during their sensitisation programs. Finally, this study shall serve as a basis for further research on COVID-19 transmission.

Justification of the Study

Barua et al. (2020) has laid claim that misinformation can lead to a grave consequence on the COVID-19 transmissions; the claim which has not been validated by any scientific means. Hence, this study shall propose and analyse a mathematical model that investigates the effect of misinformation on the transmission of COVID-19

Definition of Keywords

SARS: Severe Acute Respiratory Syndrome.

COVID-19: A strain of the Severe Acute Respiratory Syndrome coronavirus that broke out in 2019.

Misinformation: An inaccurate or false piece of information about a certain subject.

Infected individual: This is an individual who is infected with the disease and is capable of transmitting such to a non-infected individual.

Exposed Individual: An individual who has contracted the disease but is going through the incubation period of the disease and is unable to transmit the disease.

Recovered Individual: An individual who was infected but has recovered from the disease and therefore has tested negative.

II. Literature Review

Rhinoviruses, coronaviruses, influenza A and B viruses, and parainfluenza are responsible for about 75% of the common cold (Mäkeä et al., 1998; Bada et al., 2021) while the causes of the remaining 25% remain unknown. In an attempt to identify and understand the cold viruses, Hamre and Procknow (1966) and Tyrrell and Bynoe (1966) independently researched the nasal washing of mostly adult human beings who have been infected with the common cold. The B814 and 229E strains of coronaviruses were cultivated from the common cold viruses and were found to be genetically different from the known influenzas and myxoviruses. Additional research on the B814 and 229E viruses showed that human-to-human and animal-to-animal transmission is possible for other coronavirus strains. The viruses attack the respiratory system and eventually lead to difficulty in breathing. Rats, mice and bats are some of the animals in which these coronaviruses have been found (Kahn and McIntosh, 2005). The coronavirus has the most prominent RNA of all known viruses. The structure of the coronavirus keeps changing because when two different strains of coronaviruses attack the cytoplasm of the same host cell, their genes can recombine to produce another strain of coronavirus. Figure (3.1) shows the structure of the coronavirus.

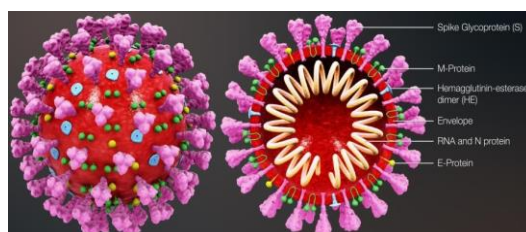


Figure 3.1: Structure of coronavirus

LeDuc and Barry (2004) identified the first pandemic in the third millennium as the SARS pandemic. SARS is a distinct variant of coronavirus caused by the SARS-CoV viral agent. Animals or some laboratory mishaps were thought to be the source of SARS-CoV. The pandemic started in Southern China in 2002 and spread rapidly across 29 countries causing eight hundred deaths after infecting about eight thousand individuals. As of March 2003, SARS has been recognised as a threat to the global community. A more deadly strain of the coronavirus broke out in 2019 in Wuhan city in China. The strain was called COVID-19 which was caused by the SARS-CoV-2 viral agent. The SARS-CoV-2 possesses 96% genome identity as the Bat-CoV-RatG13 viruses found in bats; and for this reason, many scientists believe that the virus must have been transmitted from bats to the first human. It is important to point out that although there are many insinuations about the origin of SARS-CoV-2, none of the claims have been verified as the correct one (Oke et al., 2021). The mode of transmission of COVID-19 includes direct transmission (directly from an infected individual to a non-infected individual) and indirect transmission (a case where an infected individual leaves some droplets on a surface and a non-infected individual contracts the disease by touching the same surface). Since the pandemic, five variant viral agents whose RNA stems from the SARS-CoV-2 virus have been discovered. The Beta variant, Alpha variant, Delta variant, Gamma variant, and Lambda variant are the variants of SARS-CoV-2 which are of major concern to the global community. Other variants include the Mu variant and the Omicron variant.

Mathematical modelling of infectious diseases has gained ground in the science community for predicting the future damage possible by a disease spread, simulation of possible measures to contain the spread, and studying the effects of certain factors on the disease's dissemination. Ever since the arrival of COVID-19, numerous mathematical models have been established to investigate the dynamics of the disease. Shahrear et al. (2021) used the SEQIR model to predict a downward trend population of individuals infected with COVID-19 in Bangladesh. In the same manner, Ndairou and Torres (2021) developed a fractional-time derivative model to examine the dynamics of COVID-19 in Spain, Portugal and Wuhan.

In their study, Barua et al. (2020) stated that false information's impact on the dynamics of COVID-19 is dangerous and can have lethal consequences. The claims in the study were only substantiated by taking people's opinions. It will be of value to validate the claims by proposing a mathematical model for such a situation and establishing that the claims are true. Hence, this study proposes an SEIR model for the study. The model shall be analysed to verify the plausibility of the claims.

III. Methodology

Model Formulation

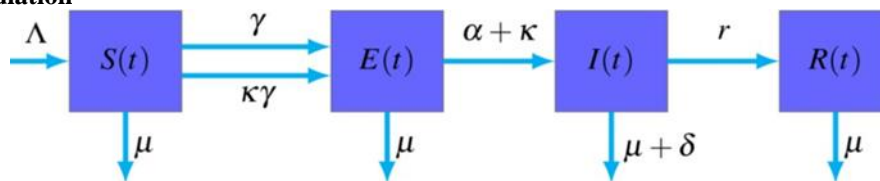


Figure 3.1: Flowchart for the model

Figure (1) is the flowchart showing the dynamics of COVID-19 with misinformation parameters factored into the model. Every individual in the population can only belong to only one of the four compartments, namely; Susceptible $S(t)$, Exposed $E(t)$, Infected $I(t)$ or Recovered $R(t)$. A population Λ is born into the susceptible population at any time t . Susceptible individuals interact with the infected population and get infected at the rate γ , meanwhile, the proportion of the susceptible population that gets infected due to misinformation is $\kappa\gamma$. An infected individual stays in the Exposed class $E(t)$ for the 14-day incubation period, after which the individual migrates to the infected class $I(t)$. Infected individuals recover at the rate β and disease-related death occurs at the rate δ . Natural death occurs at the rate μ . The models are formulated based on the following assumptions;

1. Healthy individuals give birth to healthy children.
2. COVID-19 can only be contracted by susceptible individuals when they interact with some infected individuals.
3. The natural death rate is constant at μ .

IV. Analysis And Discussion Of Results

The equations governing the spread of COVID-19 is shown in equation (3.1) – (3.4). On solving the equations using the RK4 method, and varying the parameters, the resulting graphs are shown in Figures (4.1) – (4.4). Figure (4.1) shows the response of the four subpopulations to the varying infection rates γ . The susceptible class reduces with increases in infection rate. The Exposed class increases at the outbreak of the COVID-19 disease, reaches its peak and then gradually reduces over time. The Infected class also increases

with increasing infection rate as expected. The recovered class also increases with increasing infection rate α . Figure (4.2) shows the response of each sub-population to increasing rate of infection-related death. Both the susceptible subpopulation and exposed subpopulation increase with increasing infection-related death rates while the Recovered and Infected subpopulations decrease with increasing rates of infection-related death. Figure (4.3) shows the behaviour of the subpopulations as the rate of migration from the Exposed to the Infected class increases. The susceptible subpopulation increases while the Exposed class reduces. The Recovered and the Infected class increases with increasing migration from the Exposed to the Infected class. Figure (4.4) displays the behaviour of the subpopulations when misinformation increases. The susceptible class, the infected class and the recovered classes rise significantly.

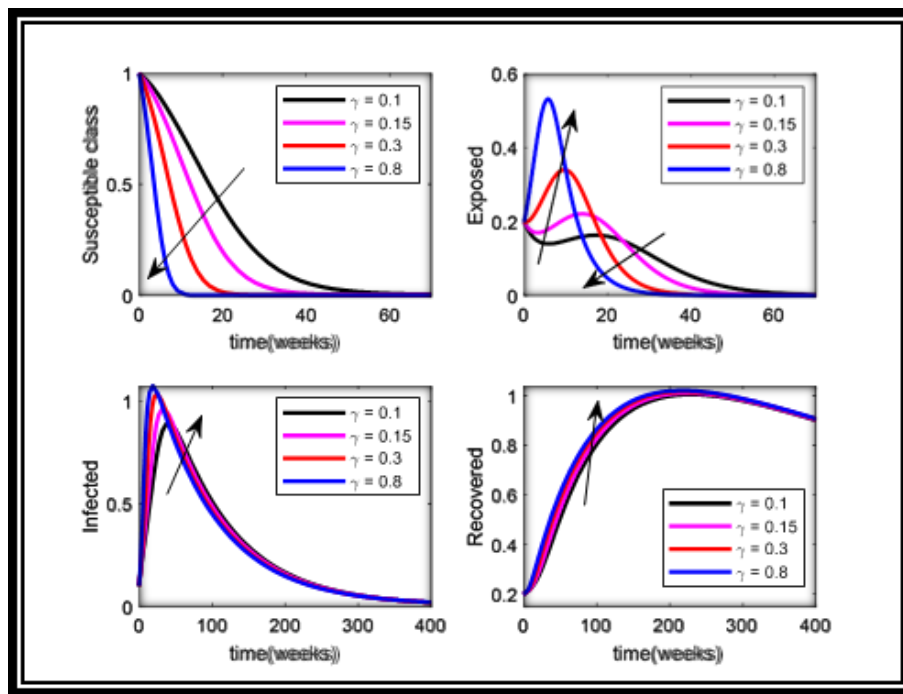


Figure 4.1: Response of the population to varying infection rate

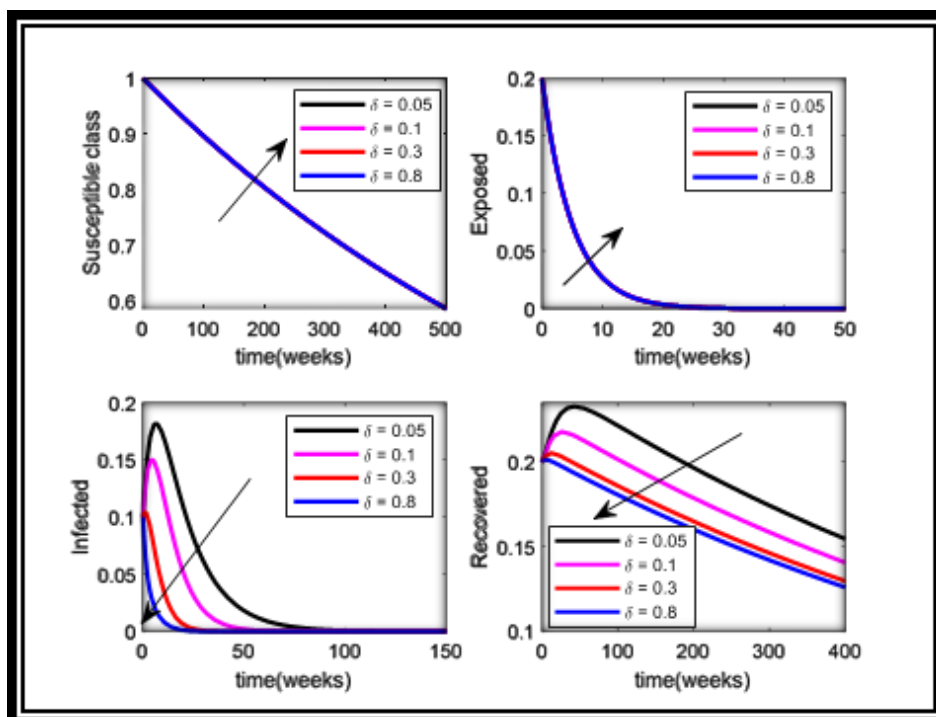


Figure 4.2: Response of the population to varying infection-related death rate

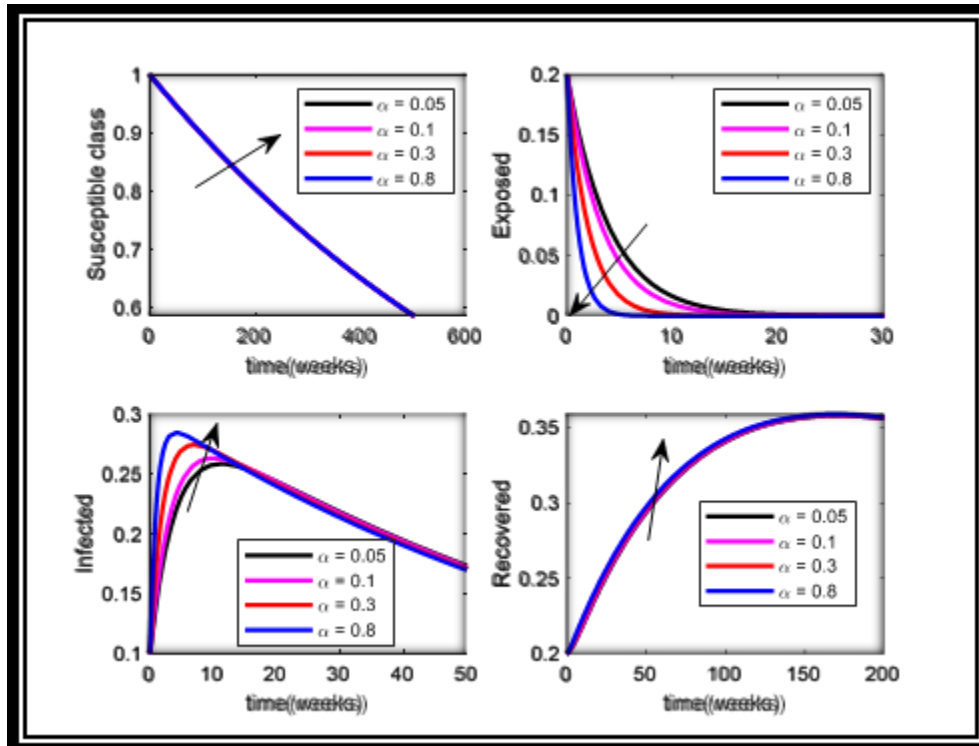


Figure 4.3: Response of the population to varying migration from Exposed to Infected class

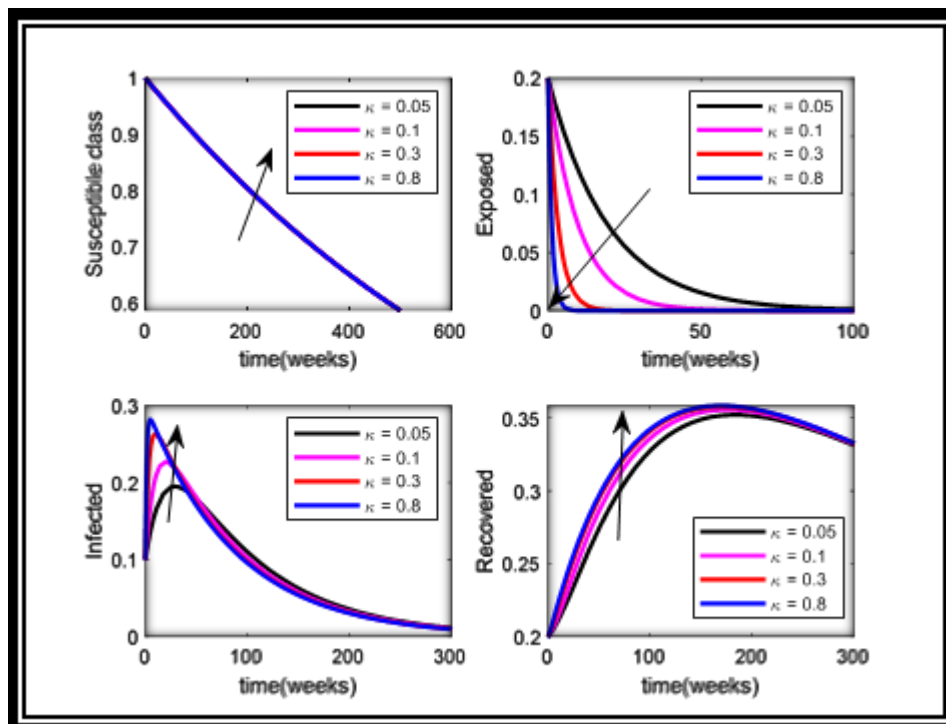


Figure 4.4: Response of the population to varying misinformation rate

V. Summary –

The dynamics of COVID-19 are investigated by factoring in the influence of misinformation. The model for the dynamics is developed with the assumption that healthy individuals only give birth to healthy children and COVID-19 can only be contracted by susceptible individuals when they interact with some infected individual. The model is given in equation (3.1) – (3.4). Two equilibrium points are obtained as the DFE $E_0 = (\hat{N}, 0, 0, 0)$ and the point of equilibrium μ

There is a significant rise in the infected class as the rate of misinformation increases.

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