

Comprehensive analysis of the COVID-19 pandemic through the SIR model

Xiaorui Bao

Bard College at Simon's Rock MA 01230

xbao19@simons-rock.edu

Abstract. In the study of infectious disease transmission, understanding the dynamics of disease spread and the impact of population-wide preventive measures is crucial. This study is conducted with the overarching goal of investigating how a comprehensive set of protective measures affects the spread of infectious diseases, while simultaneously creating a mathematical model that can accurately describe the dynamics of disease transmission within a population. By utilizing a mathematical modeling approach, this study aims to unravel the intricate relationship between key variables, including the overall protection coefficient, the daily contact rate of infected individuals, and the size of the total population. Furthermore, the model is subjected to a rigorous refinement process to explore the conditions under which disease transmission comes to a halt. The findings of this research shed light on the paramount importance of implementing broad-scale protective measures at the population level in order to effectively control and mitigate the spread of infectious diseases. These insights not only inform the development of robust disease prevention strategies but also provide a foundation for evidence-based policymaking to safeguard public health and well-being.

Keywords: Infectious disease transmission, Population-wide protective measures, SIR model, Disease spread, COVID-19.

1. Introduction

Coronavirus disease, also known as COVID-19, is an acute respiratory infectious disease caused by the SARS-CoV-2 virus. Common symptoms of infection include fever, dry cough, fatigue, loss of appetite, and shortness of breath. The first identification and description of COVID-19 occurred in Wuhan, China on December 8, 2019. Due to its rapid spread to other countries and continents, on March 11, 2020, the World Health Organization classified COVID-19 as a pandemic [1]. In terms of mortality rate and infectivity, COVID-19 is considered the most serious pandemic since the influenza pandemic of the early 20th century. The mathematical modeling theory of infectious disease transmission dynamics has attracted significant research interest, as the global impact of the COVID-19 epidemic has drawn researchers from various fields to study this issue.

This study is grounded in the mathematical modeling theory of infectious disease transmission dynamics. This methodology is chosen due to its capacity to provide valuable insights into how infectious diseases spread within populations. The analysis involves examining various factors, including the overall protection coefficient, daily contact rate of infected individuals, and the total population, to create a comprehensive model. We also incorporate refined modeling techniques to

identify the conditions under which disease transmission ceases. Specifically, this paper seek to unravel the intricate relationships that exist between these key variables, which include the overall protection coefficient, the daily contact rate of infected individuals, and the size of the total population. Additionally, the integration of infectious disease models with smart city development and other technological advancements has the potential to enhance urban emergency management, making it a crucial component of urban construction and development.

2. Development of SIR Model

2.1. Origin of SIR Model

About 3 years ago, all countries around the world were facing a complex situation with the COVID-19 pandemic. It is crucial to effectively control the pandemic from its root cause, and understanding the process and influencing factors of disease transmission is the primary task to achieve this ultimate goal. Therefore, in order to study the impact of infectious diseases, many researchers use mathematical models to simulate the transmission process of infectious diseases, some of which are improved based on the original models to obtain better research results. As early as 1760, Bernoulli used mathematical models to study smallpox [2]. In the 1920s and 1930s, Kermack respectively established the classic SIR and SIS infectious disease models [3]. Subsequently, mathematical models of infectious diseases have received widespread attention from scientists. Under the assumption that the total population size N is constant, the following improved SIR infectious disease model has been established.

$$\begin{aligned}\frac{di}{dt} &= \lambda si - \mu i - mi \\ \frac{ds}{dt} &= -\lambda si \\ \frac{dr}{dt} &= \mu i \\ \frac{dq}{dt} &= mi\end{aligned}$$

In this model, i , s , r , and q represent the number of infected, uninfected, recovered, and deceased individuals, respectively, while λ , μ , and m represent the daily contact rate, recovery rate, and mortality rate. By analyzing this model, the conditions for preventing the spread of COVID-19 can be obtained is $s_0 < \frac{(\mu+m)}{\lambda}$.

In the past few years of epidemic prevention and control, with the increase in vaccination rates and the development of medical technology, the mortality rate of COVID-19 has been greatly reduced[1]. However, whether people take protective measures still directly or indirectly affects the spread of infectious diseases. In some countries, inadequate protective measures or lack of awareness have led to the rampant spread of the disease. By excluding the impact of deaths from the disease, a new SIR infectious disease model considering overall protective factors is established to analyze the impact of overall protection on the spread of the virus[4]. In addition, it is noted that the assumption in the model that the total population N is constant is not quite consistent with reality. In order to better reflect the actual situation, factors such as natural birth and death rates will also be considered to improve the established model, and the influence of overall protection on the stability of the equilibrium point of the improved model will be analyzed to demonstrate the role of overall protection in epidemic prevention and control.

2.2. Establish Model

Assume that the population is composed of uninfected individuals, infected individuals, and recovered individuals, that is

$$s(t) + i(t) + r(t) = N(t)$$

Assume that there is a relationship between the overall protective coefficient and the daily contact rate of infected individuals, that is

$$\lambda(\alpha) = \lambda(1 - \alpha)$$

Assume that N remains constant and do not consider the effect of birth and death rates on the total population.

* List of notations

t means time

$s(t)$ means numbers of uninfected individuals

$i(t)$ means numbers of infected individuals

$r(t)$ means numbers of recovered individuals

$\alpha(0 < \alpha < 1)$ means overall protection coefficient

λ means daily contact rate of infected individuals

$\lambda(\alpha) = \lambda(1 - \alpha)$ means daily contact rate of infected individuals under overall protective measures

μ means recovery rate

N means the total population

When the time changes from t to $t + \Delta t$, consider the number of newly infected people, the number of decreased uninfected people, and the number of cured people within Δt . Without considering the effects of natural birth and death rates, assume that the number of decreased uninfected people within Δt is:

$$s(t + \Delta t) - s(t) = -\lambda(\alpha)s(t)i(t)\Delta t \quad (1)$$

The number of recovered added to Δt is directly proportional to the number of infected individuals:

$$r(t + \Delta t) - r(t) = \mu i(t)\Delta t \quad (2)$$

The number of infected individuals added to Δt would be:

$$i(t + \Delta t) - i(t) = \lambda(\alpha)s(t)i(t)\Delta t - \mu i(t)\Delta t \quad (3)$$

Combine (1) to (3), we get the equation set (4):

$$\begin{aligned} \frac{ds}{dt} &= -\lambda(\alpha)si \\ \frac{di}{dt} &= \lambda(\alpha)si - \mu i \\ \frac{dr}{dt} &= \mu i \end{aligned}$$

Suppose the initial condition is $s(0) = s_0, i(0) = i_0, r(0) = r_0, s_0 + i_0 \approx N$, so the analytical solution of model (4) cannot be calculated until. Therefore, only the relationship between $s(t), i(t), r(t)$ with time t is analyzed here.

From $\frac{dr}{dt} = \mu i$ in equation set (4) we know, $r(t)$ increases monotonically with t , and $r(t) < N$, hence there is a limit to the increase of $r(t)$ with time, i.e. there is $r_\infty, \lim_{t \rightarrow \infty} r(t) = r_\infty$.

From $\frac{ds}{dt} = -\lambda(\alpha)si$ in equation set (4) we know, $s(t)$ decreases monotonically with t , and $s(0) = s_0 \geq 0$, therefore there is a limit to the increase of $s(t)$ with t , i.e. there is $s_\infty, \lim_{t \rightarrow \infty} s(t) = s_\infty$.

Based on the two previous conclusions and assumption (1), it can be inferred that over time, the number of uninfected, infected, and cured individuals in the population will eventually stabilize. Next, the overall impact of prevention measures on this model will be analyzed.

Theorem 1: The condition for the infectious disease to no longer spread (i.e., i no longer increases) in Model (4) is $\lambda(\alpha) \leq \frac{\mu}{s_0}$.

Proof:

Assume $D(s, i) = \{(s, i) | s \geq 0, i \geq 0, s + i \leq N\}$, analyze the trend of $i(t)$ with respect to $s(t)$ on $D(s, i)$. Dividing the first two equations in equation set (4) gives

$$\frac{di}{ds} = -1 + \frac{\mu}{\lambda(\alpha)s} \quad (5)$$

$$i(s) = -s + \frac{\mu}{\lambda(\alpha)} \ln(s) - \frac{\mu}{\lambda(\alpha)} \ln(s_0) + i_0 + s_0 = -s + \frac{\mu}{\lambda(\alpha)} \ln\left(\frac{s}{s_0}\right) + i_0 + s_0 \quad (6)$$

Take the derivative on both side of (6):

$$i'(s) = -1 + \frac{\mu}{\lambda(\alpha)s} \quad (7)$$

From now, $\lambda(\alpha) = \frac{\mu}{s}$ can be obtained. So based on the initial condition $s(0) = s_0$, we get:

(1). If $\lambda(\alpha) > \frac{\mu}{s_0}$, from the first equation of the equation set (4) and equation (7), it can be concluded that as t increases, $s(t)$ gradually decreases from s_0 , and $i(t)$ increases as $s(t)$ decreases; When $s(t)$ decreases to satisfy $\lambda(\alpha) < \frac{\mu}{s}$, $i(t)$ decreases as $s(t)$ decreases, and at $\lambda(\alpha) = \frac{\mu}{s}$, the proportion of infected individuals, $i(t)$, reaches its maximum value. After a period of time of disease spread in this scenario, the spread is eventually controlled with the improvement of overall preventive measures.

(2). If $\lambda(\alpha) < \frac{\mu}{s_0}$, when $i(t)$ decreases as $s(t)$ decreases, the infectious disease will not spread in this scenario.

(3). If $\lambda(\alpha) = \frac{\mu}{s_0}$, as t increases, $s(t)$ decreases, and the decrease in $s(t)$ leads to $\lambda(\alpha) < \frac{\mu}{s}$. At this point, similar to scenario (2), the infectious disease will not spread.

Under the condition $\lambda(\alpha) \leq \frac{\mu}{s_0}$ that prevents the spread of infectious diseases, there are several ways to control the spread of infectious diseases: 1) Increase the overall protection coefficient α and enhance overall protection efforts to reduce $\lambda(\alpha)$; 2) Increase s_0 , that is, each individual should take personal protective measures, public places should be cleaned and disinfected in a timely manner, and the probability of the transmission of infectious diseases from an individual, a certain medium, or certain places to uninfected individuals should be reduced.

2.3. Improvement of the Model

Model (4) only considers the changes in the number of susceptible, infected, and recovered individuals under the influence of contact rate and cure rate. In order to better reflect the actual situation, natural birth rate, death rate, and other factors are added to the model, and the inhibitory effect of natural resources and environmental carrying capacity on population in growth is taken into account, and a new improved model that satisfies the logistic law of population growth is established:

$$\begin{aligned} \frac{dS(t)}{dt} &= (b - \frac{rN(t)}{K})N(t) - \lambda(\alpha)S(t)I(t) - \beta S(t) \\ \frac{dI(t)}{dt} &= \lambda(\alpha)S(t)I(t) - (\mu + \beta)I(t) \\ \frac{dR(t)}{dt} &= \mu I(t) - \beta R(t) \end{aligned} \quad (8)$$

$S(t)$, $I(t)$, and $R(t)$ respectively represent the number of susceptible, infected, and recovered individuals at time t . $N(t) = I(t) + R(t) + S(t)$ represents the total population at time t . b is the natural birth rate, and β is the natural death rate. $r = b - \beta$ represent intrinsic growth rate. K represents the environmental carrying capacity, and all parameters are positive constants.

By adding 3 equations in set (8), we obtain:

$$\begin{aligned} \frac{dN(t)}{dt} &= (b - \frac{rN(t)}{K})N(t) - \beta[S(t) + I(t) + R(t)] = (b - \frac{rN(t)}{K})N(t) - \beta N(t) \\ &= r(1 - \frac{N(t)}{K})N(t) \end{aligned}$$

That is, the total population at time t satisfies the logistic law.

Because $S(t) = N(t) - I(t) - R(t)$, the equation set (8) equals to

$$\begin{aligned} \frac{dS(t)}{dt} &= r(1 - \frac{N(t)}{K})N(t) \\ \frac{dI(t)}{dt} &= \lambda(\alpha)(N(t) - I(t) - R(t))I(t) - (\mu + \beta)I(t) \end{aligned} \quad (9)$$

$$\frac{dR(t)}{dt} = \mu I(t) - \beta R(t)$$

Based on biological significance, this thesis only discusses the essence of model (9) within the scope of $G = \{N(t), R(t), I(t) | N(t) \geq 0, R(t) \geq 0, I(t) \geq 0\}$.

Due to the relative complexity of model (9) compared to model (4), it is not possible to analyze and discuss it using the proof method of Theorem 1. Therefore, by analyzing the stability of the equilibrium points of the model, we can explore the impact of overall protection on the spread of infectious diseases.

3. SIR Model's Role in the COVID-19

During the initial phases of the COVID-19 pandemic, characterized by a lack of comprehensive understanding about the novel virus, the application of SIR models proved to be an invaluable tool for epidemiologists, healthcare professionals, and policymakers alike. The model offered crucial insights and predictive capabilities that played a significant role in guiding decision-making processes. SIR models, which compartmentalize the population into categories of susceptible individuals, infectious cases, and recovered individuals, provided a structured framework for analyzing the spread of the virus[5]. This framework enabled researchers and policymakers to make data-informed assessments of the potential impacts on the healthcare system and the broader community. By adapting the parameters of the SIR model, such as the transmission rate and the recovery rate, to align with real-time data, it became possible to fine-tune the model's predictions, enhancing its accuracy and relevance.

The adaptability of the SIR model is a critical feature that makes it an indispensable tool for public health officials and policymakers. As the pandemic evolved and more information became available, the ability to adjust these parameters in real-time allowed for a more precise and dynamic assessment of the situation. This adaptability was particularly crucial in developing strategies to contain the virus, allocate resources effectively, and plan for healthcare system capacity. In essence, the SIR model's capacity to accommodate real-world data and reflect the changing dynamics of COVID-19 transmission enabled a responsive and evidence-based approach to pandemic management. This adaptability remains a fundamental aspect of the ongoing efforts to combat COVID-19, serving as a vital tool for policymakers and healthcare professionals in their quest to mitigate the impact of the virus on public health and society.

4. Disucssion

4.1. *The Impact of the SIR Model on Society*

The advent of the COVID-19 pandemic has underscored the pivotal role that mathematical models like the SIR model play in shaping society's response to infectious diseases. The pandemic has ignited a surge of interest in epidemiology and statistics among students and researchers [6]. As they delve into these fields, they bridge the gap between theoretical knowledge and real-world applications. This educational focus equips the next generation with a deeper understanding of disease dynamics and the tools to confront similar crises. The SIR model has emerged as a fundamental teaching and learning tool, fostering a generation better prepared to navigate future health challenges.

Also, individuals are increasingly cognizant of concepts like herd immunity and the substantial consequences of their actions on community health. This heightened awareness fosters a sense of collective responsibility, driving individuals to participate actively in preventive measures and health-promoting behaviors. The SIR model has become a powerful educational and communication tool, empowering communities to protect themselves and one another.

4.2. *The Need for Interdisciplinary Cooperation*

The COVID-19 pandemic has highlighted the imperative for interdisciplinary cooperation in the face of complex global challenges [7]. Firstly, mathematicians and epidemiologists collaborate closely to develop and refine disease models like the SIR model. Their joint efforts produce models that are not only scientifically robust but also practical and adaptable, allowing for real-time decision-making.

Secondly, healthcare professionals, including doctors, nurses, and public health experts, work alongside mathematicians and epidemiologists to translate mathematical models into actionable healthcare strategies. Their clinical insights help validate model predictions and ensure that healthcare systems are adequately prepared to meet the demands of a pandemic. Besides, policymakers rely on the expertise of mathematicians, epidemiologists, and healthcare professionals to design effective public health policies. The input of these diverse experts is invaluable in crafting strategies that balance public health protection with societal and economic well-being.

4.3. Technological Innovation

The pressing need for accurate modeling in the face of the COVID-19 pandemic has spurred significant technological innovation. Advanced computing and data science techniques have played a central role in continuously improving disease models like the SIR model. High-quality data collection and analysis have become critical for monitoring the virus's progression, refining models, and providing more accurate predictions. These advancements empower decision-makers with real-time information to guide their responses. Technological innovation has not only informed modeling but has also expedited vaccine and treatment development. New technologies like mRNA vaccines have emerged as a result of interdisciplinary collaboration and advancements in biotechnology. These innovations offer promising solutions for controlling the pandemic and protecting global health [8].

5. Conclusion

In conclusion, the study of infectious disease transmission plays a pivotal role in safeguarding public health and well-being. Through the development and refinement of mathematical models, such as the SIR model, we gain valuable insights into the dynamics of disease spread and the impact of population-wide preventive measures. This research underscores the significance of implementing comprehensive protective measures at the population level to effectively control and mitigate the spread of infectious diseases.

The development of the SIR model has proven to be an invaluable tool in understanding the spread of infectious diseases. The SIR model has had a profound impact on society by aiding in the formulation of effective strategies for disease control and highlighting the need for interdisciplinary cooperation between mathematical modelers, epidemiologists, and policymakers. As people continue to face new challenges in the realm of infectious diseases, the SIR model, alongside technological innovation, will remain essential in our efforts to protect public health and well-being. However, mathematical models, including the SIR model, often simplify the complex dynamics of real-world disease transmission. They make assumptions that may not fully capture all aspects of a particular infectious disease, such as variations in transmission rates, population movement, and behavior changes in response to outbreaks. In future studies, developing models that consider variations in contact patterns, demographics, and behaviors within a population to better reflect the complexities of infectious disease spread.

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