An Agent-based Simulation of the SIRD model of COVID-19 Spread

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Abstract: - **The COVID-19 pandemic has resulted in more than a million deaths worldwide and wreaked havoc on world economies. SARS-CoV-2, the virus that causes COVID-19, belongs to a family of coronaviruses that have appeared in the past; however, this virus has been proven to be more lethal and have a much higher infection rate than coronaviruses that have previously emerged. Vaccines for COVID-19 are still in development phases, with limited deployment, and the most effective response to the pandemic has been to adopt social distancing and, in extreme cases, complete lockdown. This paper adopts a modified SIRD (Susceptible, Infectious, Recovered, Deaths) disease spread model for COVID-19 and utilizes agent-based simulation to obtain the number of infections in four different scenarios. The simulated scenarios utilized different contact rates in order to identify their effects on disease spread. Our results confirmed that not taking strict precautionary procedures to prohibit human interactions will lead to increased infections and deaths, adversely affecting countries' healthcare infrastructure. The model is flexible, and other studies can use it to measure other parameters discovered in the future.**

Key-Words: - **Agent-based simulation, SIR Model, SIRD model, COVID-19, Modeling and simulation, Mathematical model**

I. INTRODUCTION

COVID-19 is an infectious disease that spread according to populations density and social interactions. Detecting these viruses spread between people on later stages is costly and can lead to huge pressure on healthcare sector and consequently increase number of deaths over the time.

Medical professionals and healthcare services need to know how one patient's infection can be transmitted to other patients in order to reduce outbreaks. They must determine how many patients are likely to be infected, how rapidly the infection could spread, and what types of contact spread the infections throughout society. To this end, simulation techniques can be used to examine various scenarios and understand the effects of changing one or more parameters in each scenario [1].

COVID-19 is a new disease that appeared for the first time in Wuhan City, Hubei Province of China, at an animal and seafood market. Its spread was announced on January 7, 2020, by the Chinese authorities. SARS-CoV-2, the virus that causes COVID-19, belongs to the coronavirus (CoV) family, the members of which cause different illnesses ranging from moderate to severe. It is particularly dangerous for older people and those suffering from chronic diseases. In addition, there is currently no vaccine or effective treatment for it. Due to the nature of this virus, it is spread very quickly between humans as social interactions increase [2].

In epidemiology, compartmental models, which simplify the mathematical modeling of infectious diseases, have been used to study the spread of infectious diseases. One of the most commonly used models is SIR (Susceptible, Infectious, Recovered). A number of variants of the SIR model have been developed to take other factors into account. One such model is SIRD (Susceptible, Infectious, Recovered, Deaths), which incorporates the number of deaths from the disease into the model.

Both the standard SIR and SIRD models assume long-lasting immunity such that a recovered person will not become susceptible again. We adopted the modified SIRD model, which introduces a parameter ν that represents the mean time until immunity wanes. After recovery, a person may become susceptible again after a time ν. We used an agent-based simulation to simulate the proposed SIRD model for COVID-19 spread. The simulation incorporated four scenarios to investigate the effect of different contact rates on the spread of the disease using the proposed model. The contributions of this paper are as follows:

1. Application of the modified SIRD disease spread model that takes waning immunity into account.
2. An agent-based simulation of the modified SIRD model to investigate the effect of different contact rates on COVID-19 spread.
3. The sharing of the model through a web-based interface on which different what-if scenarios can be investigated interactively.

The rest of the paper is arranged as follows: Section 2 presents a brief review of the literature related to COVID-19 infection simulation. Section 3 introduces the research model and its variables, parameters, and relationships between them, and explains the simulation methodology in detail. Section 4 presents the results of the study and discussion. The last section concludes the paper by proposing future studies.

II. LITERATURE REVIEW

The COVID-19 pandemic has motivated many researchers to conduct modeling and analysis techniques in order to help control the disease spread. The majority of studies use modified SIR models that include parameters that are not included in the standard model [3]. One of the studies used a modified SIR model for disease spread that was based on official data about the spread of COVID-19 in Italy up to the end of March 2020 in order to identify parameters for the model [4]. The nonstandard part of their solution was that they considered the initial number of susceptible people as model parameters, as well as including a proportion factor related to the reported number of positive individuals and the approximate and unknown number of infected individuals. The main limitation of the study was that they did not run an appropriate analysis for the parameters and predictions of the model. The SIR model was also adopted by the authors of [5], in which the main control factors were human interaction, transmission, health treatment, and initial infection. The results of the simulation showed the effects of these factors and their roles in the spread of COVID-19. However, the analysis included the treatment factor, which is based on a noncredible data resource.

In [6], the estimates of basic reproductive number (R0) and the rates of recovery, mortality, and infections per day were given. The study attempts to predict the outbreak evolution at the epicenter three weeks in advance by resetting the parameters of the SIRD model to the data available. Their analysis showed a substantial decrease in the case-fatality ratio for the specified duration to which different variables, such as strict control measures, may have contributed. The main limitation of the study is that it did not take into account the heterogeneous transmission by contact, which affects the measures taken to resist the pandemic.

Another analysis initially relied on a mean field model that helped gather a quantitative image of the spread of the disease in three countries (France, Italy, and China) and, in particular, the time and height of the peak of the number of recorded infected people. The use of the same reported data in a simple SIRD model showed that, regardless of the region, the kinetic factor that describes the recovery rate seems to be the same [7]. The analysis updated the forecast of the SIRD model with the expected results caused by fading infectivity due to lockdown. However, declines in the pandemic peak and the rate of mortality were also noted. The limitation of the study is that it relied on the simple SIRD model, which does not consider further critical parameters such as waning rate of immunity and infection period.

By adopting the user-defined SEIR (Susceptible, Exposed, Infectious, Recovered) model, a study simulated the distribution dynamics of the COVID-19 outbreak and the impact of various control mechanisms. The authors of this study conducted a sensitivity analysis to identify the main factor, traced the trend graph of potential reproduction number, and obtained data fits after the simulation [8]. The model revealed the highest confirmed current cases of 50,000 arriving on February 15, 2020, via simulation and data fitting, with the determination coefficient close to 01, indicating high accuracy of data-fitting performance. The SEIR model does not consider a long-lasting immunity such that a recovered person will not become susceptible again. This reduces its reliability for predicting the disease spread curve.

A regenerated SEIR model that takes into account a new infected state, the impact of preventive interventions, and the main infection parameters for COVID-19, including latent period, quarantine period, and the specific replication number, evaluated these factors in a fairly reliable manner [9]. The frequently interested point of inflection, stopping time and maximum cases of infection in hot regions are forecast and confirmed by both directly and indirectly evidences. In addition, the starting date of this outbreak is calculated at 3 estimation points via inverse reasoning. A new infected state, along with the state of recovery, replaces the original R state in the SEIR model and accurately accounts for the identified cases and recovered cases reported daily. The study was limited by the incomplete data reported, as its proposed model depends on multiple and complicated parameters.

Another study developed a model of stochastic distribution with parameters specific for the COVID-19 pandemic [10]. It used the model to measure the possible efficacy of contact tracing and case isolation in managing SARS-CoV-2. Its scenario assumed that the number of preliminary cases, the simple replication number, the period from the onset of symptoms to isolation, the likelihood that contacts were identified, the proportion of infection that existed before the onset of symptoms, and the proportion of clinically significant infections were discovered. Isolation is presumed to prevent any further distribution in the model. The main limitation of the study was that they did not rely on a mathematical model and only considered the isolation parameter in order to relax their assumptions.

Another study fitted a reported serial duration (standard deviation and mean) with a regression distribution and applied the 'recent R' programming package in R to measure the initial number of infections early in the COVID-19 epidemic [11]. The study used the "projections" module in R to estimate realistic cumulative disease trajectories and expected daily infection by fitting current daily incidence data, serial distribution intervals, and the approximate initial number of infections into a model based on the fact that daily infections approximately obey the average Poisson distribution of infections. As the study based on data-driven analysis, it is limited by the reported data, in which the number of infected individuals increases and the portion of susceptible individuals decreases rapidly. Their results are thus restricted to a limited time frame, and this could affect the outcome.

Another study was based on linear regression models, a popular technique for predicting the effect of certain variables on the COVID-19 pandemic. Data from March 31 to May 29, 2020, were collected from the website of the Nigeria Centre for Disease Control. In this analysis, to assess the effect of contacts and travel history on the spread of the disease in Nigeria, the researchers adopted the ordinary least-square estimator and made a prediction [12]. The study was based on the invalid assumption that travel history is not highly correlated with confirmed cases. Thus, the regression predictions are not accurate.

With Gaussian models, COVID-19 spread could be predicted using field mean to collect quantitative data on disease spread, including fatality, recovery, and infection rates. The regression Gaussian model expected that in the USA, the epidemic would exceed saturation in July 2020 [13]. The findings indicate that new containment actions could be effective with further restrictions on prevention techniques introduced in the USA, but it could cause a high rate of infections and deaths in the following two months. The study was restricted, as the analysis relied on the total number of cases reported by timely short-term forecasts.

A simulation of the COVID-19 transmission cycle on a tour ship, determining the number of infections among approximately 3700 passengers, was conducted in [14]. The virus spread rule between passengers was developed based on the crowd flowing model and was used to analyse the spread of infection caused by close contact during the regular activities of passengers on a tour ship. Three situations were simulated, with the main scenario emphasizing the function of virus transmission triggered by a virus transporter and the impact of personal preventive measures against the virus. Control conditions were designed to simulate the influence of compulsory or recommended steps on virus spread. The study was limited by a lack of data availability (103 out of 300 records) and may thus be affected by a downward bias. However, their transmission potential estimates pointed to the high potential for SARS-CoV-2 to be transmitted in restricted settings.

III. METHODOLOGY

As the aim of the study was to investigate the effect of contact rate on the number of infections, we proposed the following null and alternative hypotheses:

H0: There is no relationship between c, the contact rate, and I, the number of infected individuals in the population.

H1: There is a relationship between c, the contact rate, and I, the number of infected individuals in the population.

To test the null hypothesis, we developed a modified SIRD model and used agent-based simulation to manipulate the independent variable c and investigate its effect on the dependent variable I. The following subsections explain the SIRD model and the agent-based simulation in detail.

A. Modified SIRD Model

The modified SIRD compartmental model divides the population into four compartments (stocks). The block diagram in Fig. 1 depicts these four stocks and their relationship in the proposed model.

Susceptible (S): The number of susceptible individuals in the population. When a susceptible person comes in contact with and infected person, he/she becomes infected with a probability p.

Infectious (I): The number of infected individuals in the population. These individuals are capable of infecting susceptible individuals. An infected individual may recover with a recovery rate γ or die with a fatality rate μ

Recovered (R): The number of recovered individuals. These are individuals who were infected and are recovered from their infection.

Deceased (D): The number of individuals who died after becoming infected.

The SIRD model is a dynamic model; thus, the above population stocks can be represented as S(t), I(t), R(t), and D(t), indicating the number of Susceptible, Infectious, Recovered, and Deceased individuals, respectively, at time t. The proposed SIRD model can be represented with the following set of differential equations:

$$\frac{dS}{dt} = \frac{-\beta\, I\, S}{N} \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta\, I\, S}{N} - \gamma I - \mu I \tag{2}$$

$$\frac{dR}{dt} = \gamma I - \nu R \tag{3}$$

$$\frac{dD}{dt} = \mu I \tag{4}$$

Where

$$\beta = c \times p \tag{5}$$

And

β is the infection rate
c is the contact rate
p is the probability of disease transmission
γ is the recovery rate
ν is the waning rate
N is the population size
Note that

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} + \frac{dD}{dt} = 0 \tag{6}$$

From the above it follows that

$$S(t) + I(t) + R(t) + D(t) = N \tag{7}$$

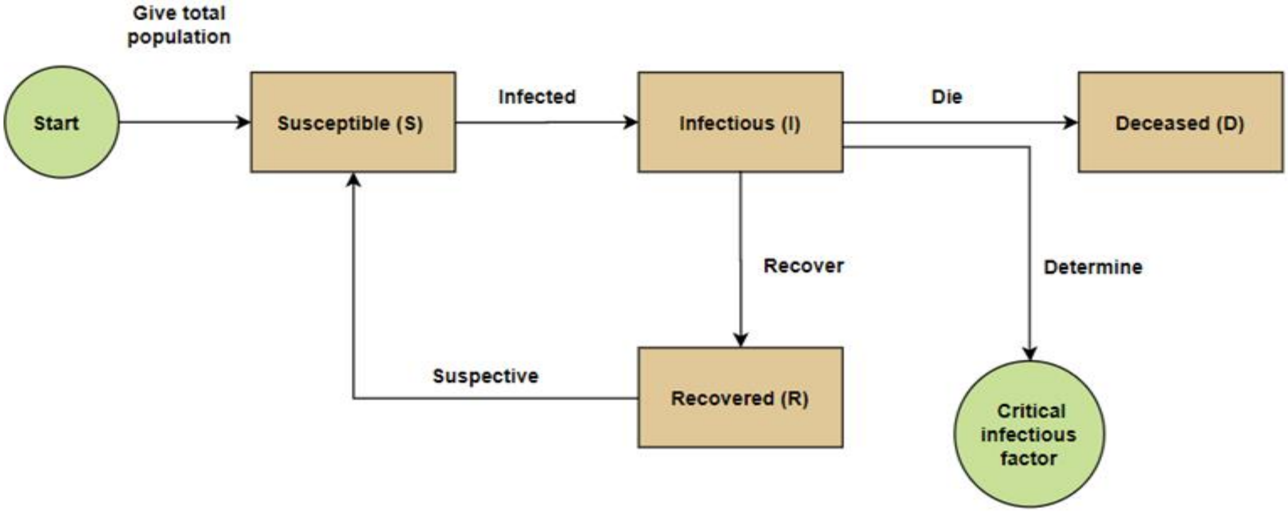

Fig. 1: Block diagram of the modified SIRD model

To solve the above system of differential equations, we employed agent-based simulation. The pseudocode below shows the loop for the specified stocks in the modified model:

```
INITIALIZE total population
INITIALIZE Infectious cases
SET mean infection period = 14
SET mean time until of wining immunity = 100
SET fatality rate = 0.01
START LOOP
    IF individual contacts with Infectious THEN
        COMPUTE infectious
        PRINT the number of infected cases
    END IF
    IF infected individual recovered THEN
        COMPUTE recovery
        PRINT the number of recovered cases
        COMPUTE susceptible
        PRINT susceptible cases
    ELSE
        COMPUTE death
        PRINT the number of deceased
    END IF
END LOOP
```

B. Agent-based Simulation

Modeling based on agents reflects the different active entities of a situation. This differs from both the theoretical approaches to system processes and the discrete approach of events focused on the flow. Active components, defined as agents, can only be described with agent-based modeling and their specified activity. Agents can be individuals, families, cars, machinery, goods, or businesses, as relevant to the situation. Connections are formed between them; contextual variables are set and simulations are run. Thus, the system's overall dynamics arise from the associations of many agents' behaviors.

This paper uses the COVID-19 data repository from Johns Hopkins [15] to investigate parameters that affect the spread of COVID-19. They developed an interactive dashboard to visualize and track reported cases in real time. Reports are released from the dashboard to present daily of infections, deaths, and recovered patients. These numbers are updated frequently in a time-series manner in order to reflect current numbers.

The model was implemented in AnyLogic, a multimethod simulation modeling tool that supports agent-based, discrete event, and system dynamics simulation. We used AnyLogic Cloud, which enables users to store, access, run, and share simulation models online, as well as analyze experiment results. The four population stocks are represented as agents, and to solve the system of equations, their interactions are represented as flows from one type of agent to the other. These flows define the quantities on the right-hand sides of the equations. These flows are as follows:

(1) infection (flow between susceptible & infectious) = $\beta * I/N * S$
(2) recovery (flow between infectious & recovered) = $\gamma * I$
(3) waningImmunity (flow between recovered & susceptible) = $\nu * R$
(4) death (flow between infectious & deceased) = $\mu * I$

The proposed model has four agents which are displayed as squares and the four flows are depicted as double-lined arrows. A number of intermediate variables were used to facilitate the computation. Following is the full list of variables used in the model.

- forceOfInfection: $F = \beta * I/N$
- contactRate: c
- probabilityOfTransmission: p
- infectionRate: $\beta = c * p$
- prevalenceOfInfection: I/N
- meanInfectiousPeriod: P
- recoveryRate: $\gamma = 1/P$
- fatalityRate: μ
- meanTimeUntilWaningImmunity: W
- waningRate = ν
- population: N

The COVID-19 model is available at the AnyLogic Cloud[1].

C. Experiment Settings

The AnyLogic application was used to run the model to simulate 30 days of SARS-CoV-2 infection, which is the critical duration for infection spread [7], [14]. Since the goal was to investigate the effect of contact rate on disease spread, we kept all other parameters constant and manipulated c, the contact rate. The simulation was run in four scenarios: in the initial

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[1] https://cloud.anylogic.com/model/4d546172-12b4-4d0599ed2d3f60155698?mode=SETTINGS&tab=GENERAL

scenario, the contact rate was 100% among people in the population; the second decreased the contact rate to 50%; the third set the contact rate equal to 25%; and the last allowed only 10% contact among people in the population.

The model parameters were fixed in order to observe the changes caused by the desired variable (the contact rate). The parameters are set as follows: probability of transmission (p) = 0.04, fatality rate (μ) = 0.01, mean time until waning immunity (W) = 100 days, and mean infection period (P) = 14 days [16].

The initial numbers were: susceptible people (N) = 1,000,000, infectious (I) = 3, recovered (R) = 0, and deceased (D) = 0. The simulation model was validated by comparing the result of the proposed model and a data-driven model established in [17]; the comparison process revealed that both results were almost the same; thus, our simulation model is valid.

IV. FINDINGS AND DISCUSSIONS

Running the COVID-19 simulation model resulted in the following scenarios: In the first scenario, in which the contact rate is 100%, the entire population became infectious, with only 1641 susceptible individuals remaining at the end of the simulation (30 days). Of the infectious population, 43,272 recovered and 8,182 had died by the end of the simulation. The number of infectious individuals at the end of simulation was 46,903. This represents the situation in which no precautionary measures are taken. The results are depicted in Fig. 2 (a).

By adjusting the contact rate value to be 50%, with some assumed preventive procedures, it is clear from Fig. 2 (b) that the result obtained in the first scenario will still be true. This means that most of the population will be infected by day 30. The only difference is in the number of susceptible individuals, which stood at 3194 at the end of the second scenario. The number of recoveries was 46,943, the number of deaths was 7,382, and the number of infectious individuals was 46,943 at the end of the 30-day simulation.

In the third scenario, shown in Fig. 2 (c), in which the contact rate is 25%, the number of susceptible individuals was increased to 5516 and the number of deaths was decreased to 5726. The number of infectious individuals was 48,364, and there were 40,115 recoveries at the end of the simulation.

The final scenario, displayed in Fig. 2 (d), confirms the result obtained in the previous scenario. In this case, when the contact rate is 10%, with strict precautionary procedures and quarantine, the number of susceptible people remained at 82,048 and only 256 deaths were reported. The number of infectious individuals was 14,933, and there were 2,761 recoveries at the end of the simulation.

It is important to note that recovered individuals can be infected again if they contact infected individuals. This is clear from the third scenario, in which the number of infected people increased compared to the first and second scenarios. Based on the results obtained from these four scenarios, we reject the null hypothesis that there is no relationship between contact rate and the number of infections and conclude in favor of the alternative hypothesis. It is important to note that the relationship was not obvious in the first three scenarios, and it was only the fourth scenario that described the inverse nature of the relationship between contact rate and number of infections. It follows from the above that even a 25% contact rate among individuals in the population resulted in a higher number of infections and deaths than when the contact rate is only 10%. The 10% contact rate represents a lockdown situation in which only individuals who are crucial to support the country's infrastructure services are allowed to go outside.

The result of the COVID-19 spread model simulation confirms that not taking strict precautionary procedures to prohibit human interactions at a critical time leads to increased infections and deaths. This means that without a lockdown, the number of infections and deaths is higher than there would be with one. These high numbers may lead to a breakdown of the healthcare infrastructure of a country.

We compared our work with four other COVID-19 spread studies and the results are summarized in Table 1. The authors in [4] used two-dimensional grid search instead of a simulation to estimate the model parameters and reported a 78% uncertainty in the reported infections. Our model used an agent-based simulation approach and hence is more capable of answering what-if scenarios. The second study [6] also reported high uncertainty in the simulation results due to the large differences between the lower and upper bounds of infected cases, recovered population, and deaths. Moreover, it did not consider a variable contact rate, which is an important

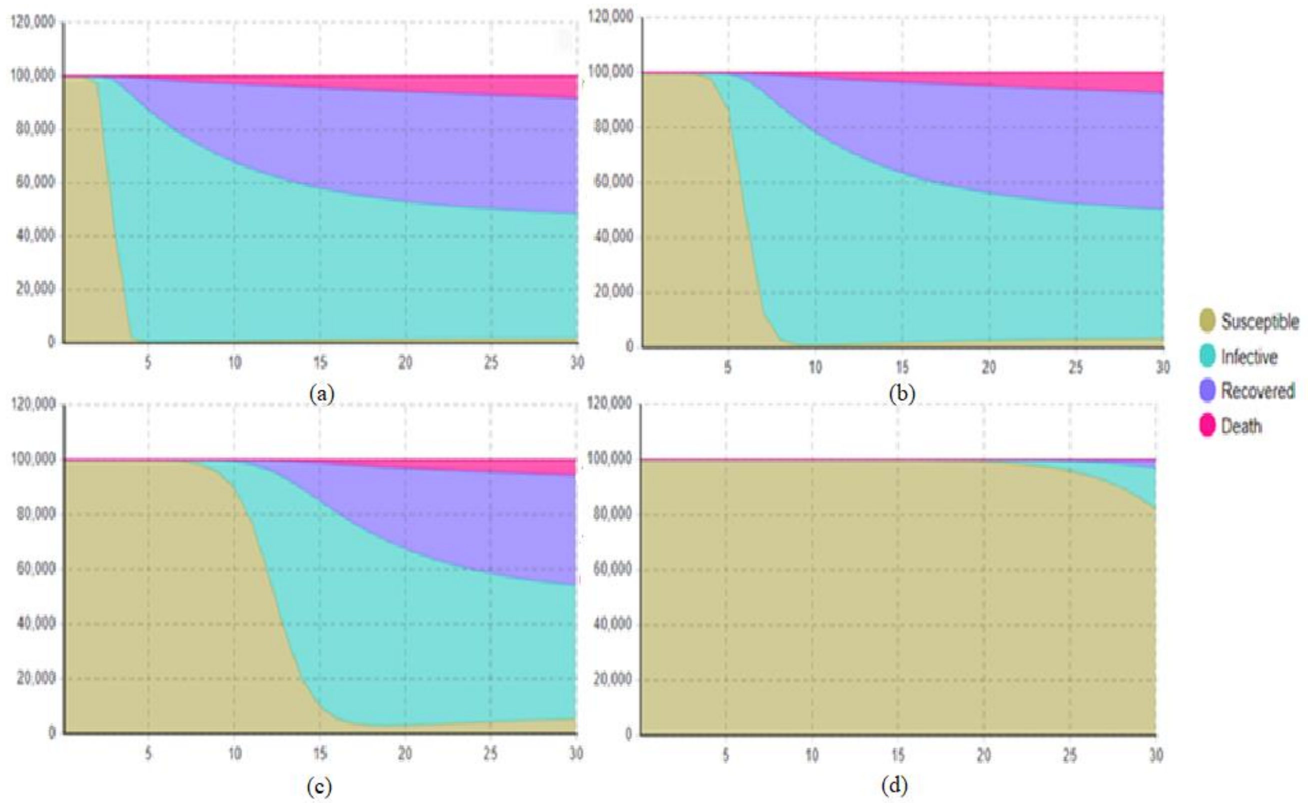

Fig. 2: (a) first scenario with 100% contact rate, (b) second scenario with 50% contact rate, (c) third scenario with 25% contact rate, (d) fourth scenario with 10% contact rate

parameter in our proposed model to measure the spread of COVID-19. The third study in our comparison [18] used a fixed contact rate which limits the model's capability as it is an important factor to determine a suitable lockdown strategy. Further, the use of the SIR model (without calculating the number of deaths) is a limitation in the fourth study [19] that is resolved in our agent-based modified SIRD model.

Table 1: Comparison of similar studies

Ref.	Approach	Results
[4]	Modified SIR model	78% uncertainty in reported infections
[6]	Linear regression and SIRD simulation	High uncertainty in reported infections and the effect of contact rate not considered
[18]	Modified SIRD Model	Considered a fixed transmission rate
[19]	SIR Model	High uncertainty in reported infections

V. Conclusion

COVID-19 is an infectious disease that has spread internationally. The developed model confirmed that contact rate is the primary factor for the rapid increase in the number of infected and dead individuals. By minimizing contact rate, the number of infected people and deaths decreased. Because there is not yet a vaccine for COVID-19 and effective treatment for this disease remains unknown, curfews and other strict procedures must be enacted in order to reduce the number of contacts between humans. Those who have recovered are assumed to be susceptible to reinfection unless clinical tests show the opposite. For future work, adding more parameters obtained from future medical studies is encouraged in order to further develop the model, as is building a dashboard to provide up-to-date information about disease spread, which will be helpful for future research.

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