A C++ based simulation study of SARS-CoV-2 progression using SIR epidemiological modeling

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Abstract

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), a global pandemic, resulted in more than 6 million deaths worldwide, and caused more than 1 million deaths in the USA alone. Lack of prior information about the disease made the management and control of the disease very difficult at its initial phase. Disease modeling was the only way to get insight and prediction about the disease progression. Susceptible Infected Recovered(SIR) modeling consists of compartmental and stochastic systems to monitor population dynamics in three compartments:Susceptible, Infected, Recovered.Increase in Reproduction Number(Ro), rate of transmission(beta) and decrease in doubling time is the indicator of disease spread feasibility. Our observation was that change in population size did not bring change in progression dynamics, and increase in contact number and days of infection have negative contributions to the likelihood of disease progression. Further, studies are needed in the area where unusual observations were seen, and in the area of interaction between progression determinants.

1.Introduction

1.1. Background

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), a very contagious viral infectious disease, declared as global pandemic by World Health Organization on March 11 2020, originated in Wuhan, Hubei Province 2019, affecting societies, economies and the medical sector throughout the world(Šušteršič T et al, 2021 ;Cooper I et al, 2020). People around the world suffered mortality, morbidity, isolation and lockdown.More than 6 million people died worldwide with the USA alone accounting for more than 1 million deaths(Cascella M et al, 2022).

As a means of study of infectious disease transmission, the mathematical model provides valuable understanding of the dynamics of transmission and causality in/across population, region, and countries, and may offer predictions that helps in effective management and control of the disease(Šušteršič T et al, 2018). The puzzle and lack of anticipation of disease progression

at its initial phase may lead to crisis to control and management of the disease.A purpose of a disease progression model is to serve as a predictive tool, as well as to help to extract key insight about the dynamics of disease, making prior anticipation of disease transmission and causality possible(Cooper I et al, 2020).

1.2. Motivation of the study

The project is exciting in a sense, since SIR is one of the most common ways of modeling disease progression in the field of epidemiology, yet very simple, can serve as a prototype to develop a more complex model of the disease progression, or may be applied to the other infectious disease setting current or future. Similarly, these models enable prior prediction, and provide control capabilities as they are based on parameters in which a usual disease would have progressed in real time. Another motivation is that it fits within scope of the project deliverable, can be developed and computed within a short period of time, and there are a lot of areas for update or reinforcement. For example, we can adopt monte carlo simulation, similar to a stochastic point process model, treating each individual as a random point, on top of SIR, to make it more realistic and intuitive(Xie G, 2020).

The objective of the study is to create a simulation algorithm that will mimic the SIR model of Covid 19 progression, so that the effect of different conditions and parameters on disease progression dynamics could be studied.

2. Method

2.1. SIR model

Susceptible-infected-removed (SIR) model may be appropriate to model disease propagation statistically as it has been utilized, in different forms, in various studies(Amaro JE et al, 2021;Ndaïrou F et al, 2020). SIR is a very common and simple epidemiological method of studying spread of infectious disease in a population. SIR incorporates compartmental and stochastic systems. It has three compartments: Susceptible(S), Infected(I), and Removed(R). Susceptible(S) represents the section of the population who are susceptible to the infection but has not been infected yet, infected are the ones who are infected and have the potential to transmit the disease, and removed compartment comprises of the people who have recovered, developed immunity against the disease or faced death(Salimipour, 2023). At any given point of time, S, I, R represents the number of people in susceptible, infectious, and recovered

compartments. S(t), I(t), and R(t) measures the change of population in these compartments over a period of time. s(t), i(t), and r(t) are the proportion of the population who are susceptible, recovered and infected (Salimipour A et al, 2023).

2.2. Basic assumptions of the model

- Population divided into three groups: Susceptible, infected and recovered
- Total population remains constant
- Rate of transmission is proportional to infected and susceptible
- Duration of infection rate is same for all individual
- Time scale of SIR should be short enough so that birth and death can be neglected

2.3. Pertinent equations and figures

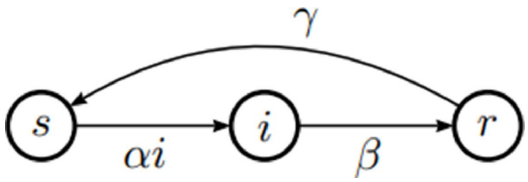

Figure 1: SIR compartment model taken from Salimipour A et al(2023)

As represented in the flow chart each individual migrates from the susceptible to removed in linear fashion, such that a system of ordinary differential equations(ODEs) is applied.

$$s(t) + i(t) + r(t) = 1$$

$$\frac{ds(t)}{dt} = -\alpha s\,(t)\,i\,(t) + \gamma r\,(t)$$
$$\frac{di(t)}{dt} = \alpha s\,(t)\,i\,(t) - \beta i\,(t)$$
$$\frac{dr(t)}{dt} = \beta i\,(t) - \gamma r\,(t)$$

Figure 2: Equation to calculate population dynamics in the system,from Salimipour A et al(2023)

A representative diagram that represents the changes in each compartment is as follows:

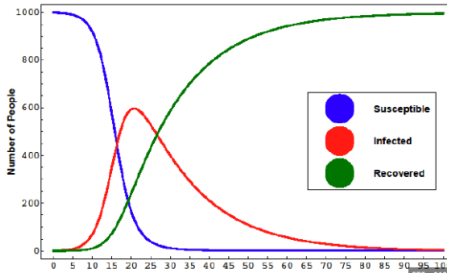

Figure 3. Figure showing growth/decline of infected, susceptible and recovered over the period of time.

At peak, point of inflection, $di(t)/dt=0$, such $1/Ro=\gamma/\beta=s(t)$. Reproduction number(Ro) is the average number of new infections caused by an infected person in a population of susceptibles. Doubling time(TD) is time required for the infectious population to double. Transmission rate or contact rate(β) is the likelihood of a susceptible individual who becomes infected when coming into contact with an infected person. γ is reciprocal of the infectious period of the disease. Higher the value of Ro, γ, β, the disease is likely to spread.

2.4. C++ implementation

The simulation was written and implemented in C++ using Visual studio code. There are two classes: Person and Population with its own operations. Person class has two fields: Days of infection and status of a person. It comprises the methods:currenState(), which gives current states of the person; infect(n), which can infect the person for n days;and two boolean checks(isStable, and isInfected), which checks whether the person is infected or not. Population class has a field for each compartment counts, probability of disease transfer, size of the population, and number of contacts an infectious disease can make, and days of infection. It has methods: infectRandomPersons(), which randomly selects the person from the population container, and infects for n days; setter method to set the probability of disease transfer, infection days, and number of contacts to be made; currentState(), which initializes all counts, newly_infected container,checks whether each person in the population is sick, susceptible or recovered, and if sick, pushed to interact with n number of people,which is contact number, and contacted person likelihood to get infection is determined by a contract(), which based upon the probability of disease transfer.

3. Results and Discussion

The main purpose of the study was to establish the SIR model, based upon its assumption, to mimic SARS-COVID-2 progression.Simulation was successful to generate the expected growth/decline trend for infected, susceptible and recovered. Different factors/parameters were enforced against the model to see if that changes the dynamics of the disease progression.

3.1. Different population size

Simulations were run for 1000, 10000, 100000 and 1000000 population size. It showed reproduction number (Ro), doubling time(TD), and rate of transmission(β) remained stagnant across all population sizes. It may be because all these parameters are interdependent to each

other, and related to the susceptible population at a peak time of infection normalized to the total population only.

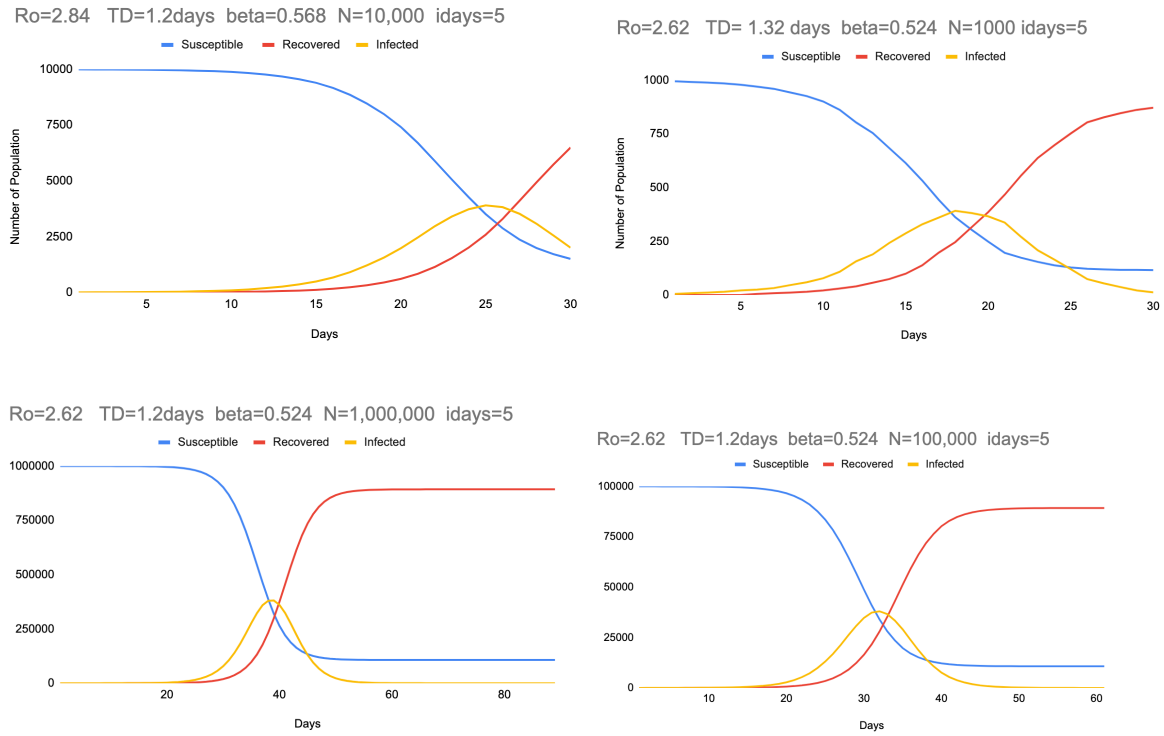

Figure 4. Graphical representation of disease progression dynamics for population size 1000, 10000, 100000, and 1000000.

3.2. Different days of infection with contact ratio(1:1 and 1:5)

An unexpected behavior was observed. The general expected behavior was that increase in infection days, which makes the person available for infection for more days, would have increased the parameters that ensured the disease spread. Ro showed biphasic growth as the number of infection days increased. There was an increase in doubling time with increase in infection days, and value of β also decreased, meaning that the disease likelihood of spreading decreases with increase in infection days(see figure 5). A strong possibility could be that there might be interaction between parameters, such that an optimal combination of parameters would be required to obtain expected behavior. Keeping in mind, I ran the simulation for an increased number of infection days with contact number of 5, but a similar observation was obtained; only the biphasic progression of Ro transformed into path to decrement(see figure 6).

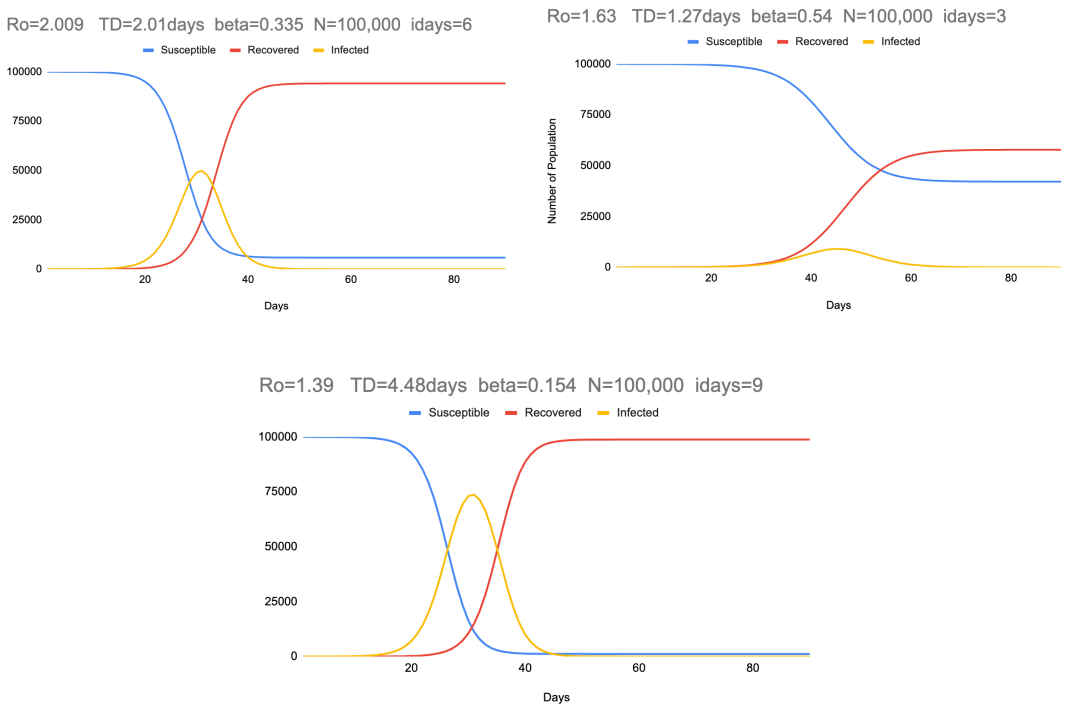

Figure 4. Graphical representation of disease progression dynamics for different infection days and for contact ratio of 1:1

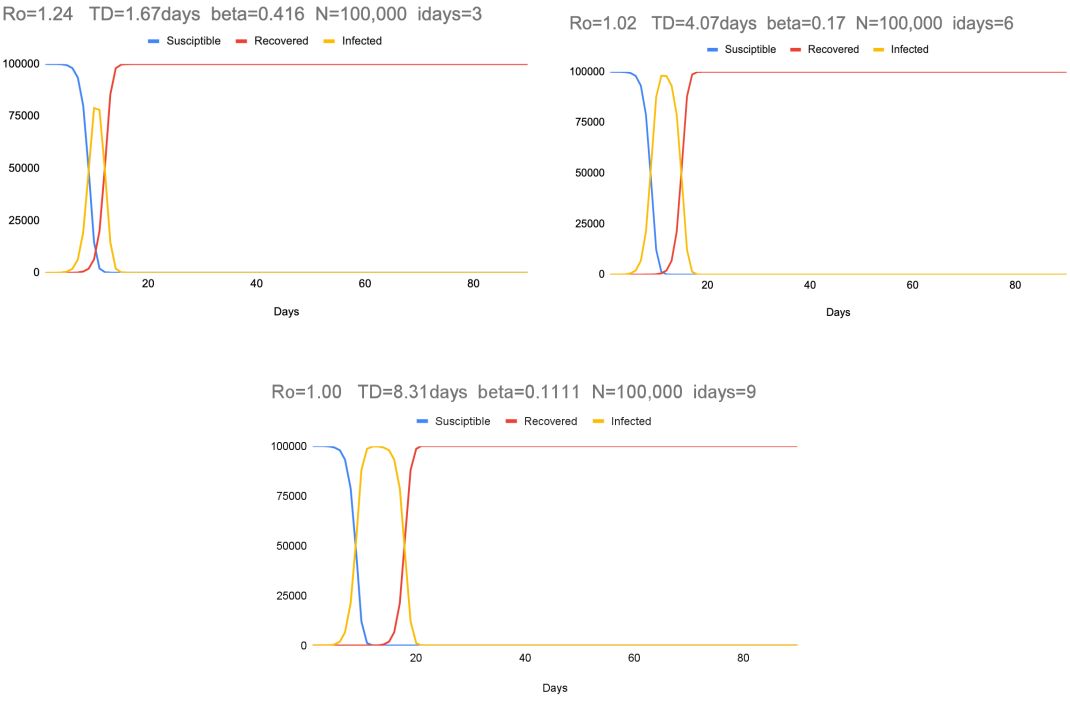

Figure 5. Graphical representation of disease progression dynamics for different infection days and for contact ratio of 1:5

3.3. Different contact number

For further investigation of abnormal behavior mentioned above, the contact number is only changed with days of infection intact. Nevertheless, a similar observation was observed as above. The reproduction number(Ro) and transmission rate (Ro) both decreased as the contact number increased, whereas doubling time has increased(see Figure 6).However, all changes were just slight. So, the possibility of interaction between contact number and days of infection may be ruled out. This unusual nature of simulation may be attributed to the stochastic nature of simulation, or rapid conversion of susceptible individuals to infection and recovery, such that, in almost all conditions, the number of susceptible almost decreased to zero and total population transitioned to recovery within a short period of time.

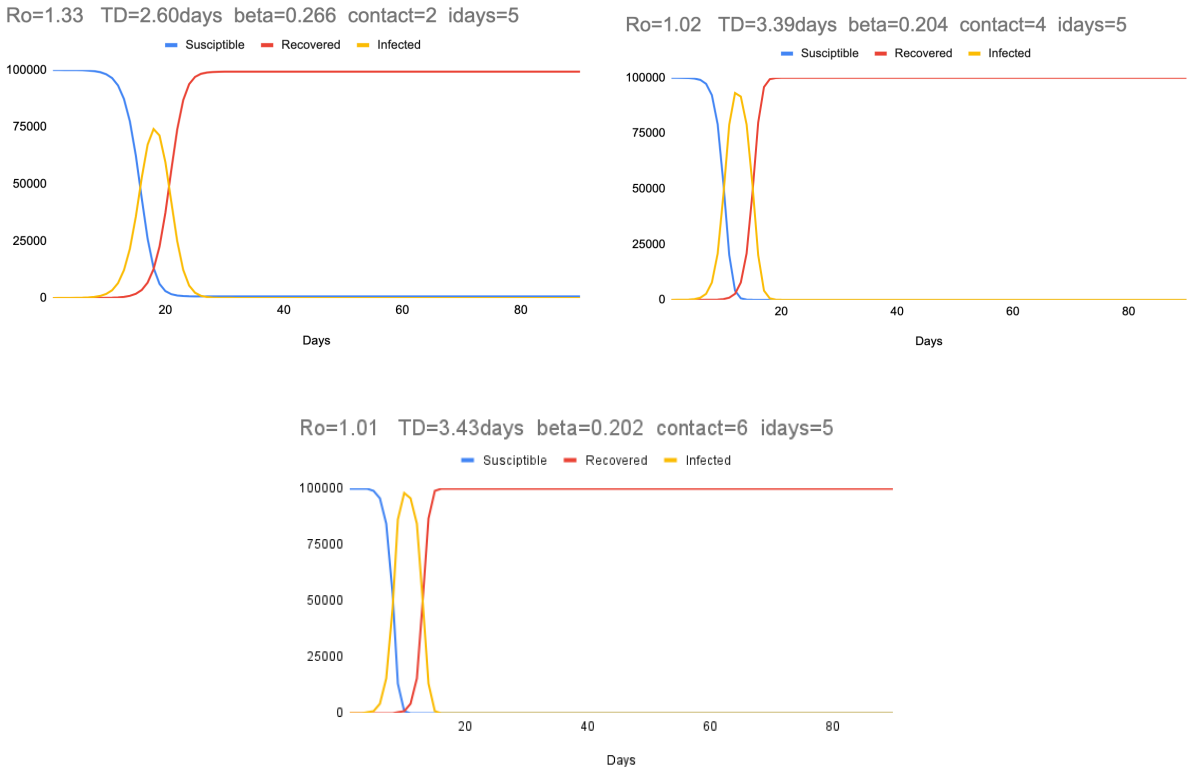

Figure 6. Graphical representation of disease progression dynamics for different contact numbers

4. Conclusion

The simulation was successful in mimicking expected disease progression dynamics. Size of the population did not change the behavior of the disease progression dynamics. Unusual behavior was seen when contact number and duration of infection was changed in incremental manner. Reproduction number(Ro),and rate of transmission(beta) decreased with increase in contact number and duration of infection, however doubling time increased. These are negative indicators of disease spread. Further investigation is needed to find out possible reasons for such deviation from expected behavior. Also, investigation may be done on possible interaction of dynamics parameters on disease progression behavior.

References

Amaro, J.E., Dudouet, J. and Orce, J.N., 2021. Global analysis of the COVID-19 pandemic using simple epidemiological models. *Applied Mathematical Modelling*, *90*, pp.995-1008.

Cascella, M., Rajnik, M., Aleem, A., Dulebohn, S.C. and Di Napoli, R., 2022. Features, evaluation, and treatment of coronavirus (COVID-19). *Statpearls [internet]*.

Cooper, I., Mondal, A. and Antonopoulos, C.G., 2020. A SIR model assumption for the spread of COVID-19 in different communities. *Chaos, Solitons & Fractals*, *139*, p.110057.

Salimipour, A., Mehraban, T., Ghafour, H.S., Arshad, N.I. and Ebadi, M.J., 2023. SIR model for the spread of COVID-19: a case study. *Operations Research Perspectives*, *10*, p.100265.

Šušteršič, T., Blagojević, A., Cvetković, D., Cvetković, A., Lorencin, I., Šegota, S.B., Milovanović, D., Baskić, D., Car, Z. and Filipović, N., 2021. Epidemiological predictive modeling of COVID-19 infection: development, testing, and implementation on the population of the Benelux union. *Frontiers in public health*, p.1567.

Xie, G., 2020. A novel Monte Carlo simulation procedure for modelling COVID-19 spread over time. *Scientific reports*, *10*(1), p.13120.

Ndaïrou, F., Area, I., Nieto, J.J. and Torres, D.F., 2020. Mathematical modeling of COVID-19 transmission dynamics with a case study of Wuhan. *Chaos, Solitons & Fractals*, *135*, p.109846.