

# Epidemic Testing Strategies: SARS-CoV-2

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## Abstract

In this project, the evolution of a virus such as the SARS-CoV-2 within a society was studied with the introduction of different testing and containment strategies. A number of models were introduced to contain the spread of the virus, such as lockdown policies or methods of identifying individuals who were spreading the virus to prevent further dissemination. The spread of a virus is simulated with an agent-based extended SIR model to account for the greater number of stages an agent could possess. This approach describes a society of agents more precisely than the standard SIR model. Furthermore, a contact-tracing element that could track the agents' location was tested against standard symptomatic detection and full societal lockdown. The contact tracing procedure is based on the Test-Track-Treat methodology, in which cases are identified based on previous contacts with detected agents, and then they are quarantined. The results are discussed in terms of their practical applicability and evaluated based on the final number of recovered agents  $R_{\text{inf}}$  and ideally the evolution of the effective case reproductive number  $R_c(t)$ . Based on the parameters of each containment strategy, we calculate the results achieved by the simulations and draw conclusions.

## 1 Introduction

The COVID-19 pandemic is considered the worst pandemic mankind has ever faced, after the Spanish flu. There are still millions of people all over the world who have become infected and the spread is still ongoing. Around 269 million people are affected by the disease as of 11th December 2021, and approximately 5 million have lost their lives as a result of the pandemic[2]. There is a lack of knowledge about how to treat the disease, as well as the need for a large quantity of medicinal remedies. These factors have led to various economic and social strains around the world with countries imposing prolonged lockdowns.

The world's countries have tried various methods to prevent the spread of the virus. From the basic methods of wearing masks and avoiding large crowd gatherings to strict methods like complete lockdowns and severe quarantine of the affected.

It requires mathematical models to compute calculated measures concerning the control of the pandemic, as well as disease transmission, recovery, deaths, and other significant parameters separately for each country, that is for the areas where COVID-19 is reported in high and low numbers. Various countries have already taken precise and differentiated steps to combat the disease. The existence of important factors such as population density, uncertainty regarding the symptoms, transmission mechanisms, and the lack of

a reliable vaccine make it difficult to deal with such a deadly and infectious disease, especially in countries with high population densities like India. There have been many recent research articles[2][7][8] that have used real data from affected countries and have analyzed different characteristics of outbreaks based on different parameters as well as the effects of intervention strategies in different countries according to their current circumstances.

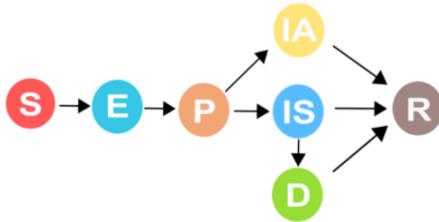
SIR(Susceptible-Infected-Recovered) is a model commonly used to analyze the spread of disease. Based on the model, the population is categorized into three groups: Susceptible (high probability of developing the disease), Infected (affected by the disease), and Recovered (cured of the disease). There are however many assumptions in this model and it does not factor in some real-life parameters.

In our project, we aim to create a more realistic and complex agent-based model with seven stages, that include Susceptible (S), Exposed (E)(active in the region where the spread is seen), Pre-Symptomatic (P)(infected agents who have not yet developed symptoms but are already contagious), Infectious Asymptomatic (IA)(infected agents without symptoms), Infectious Symptomatic (IS)(Infected agents with symptoms), Detected (D)(people detected with the help of certain tests), and Recovered (agents who have recovered and gained immunity). The model does not only include the simulation of these seven stages, but also the implementation of the methods to fight

against the pandemic, which includes lockdown and symptomatic tests. The lockdown is the implementation of a widespread strict lockdown over the entire model for a particular amount of days to stop the spread to a certain level. Symptomatic tests include the consideration of testing the people with symptoms and doing the necessary post-actions. Apart from this, the model also includes the contact tracing implemented in it. It is the process of detecting individuals with symptoms, isolating them, and tracing the contacts that they had in the recent past as they represent potential infections that may have occurred before the case was detected. Contact tracing has the real purpose of reducing the spread of the virus by preventing the spread of secondary cases, which reduces the rate of infection and therefore the ability to reproduce.

## 2 Models and Parameters

To incorporate testing dynamics, symptomatic detection and contact tracing into the study of the transmission of SARS-CoV-2, we first construct an epidemic model including 7 compartments (states): Susceptible, Exposed, Pre-symptomatic, Infectious asymptomatic , Infectious symptomatic, Detected, and Recovered. The model has 250 individuals(N) in it and the lattice size(L) being considered for the model is 50. The initial infection rate taken is 0.01. The expected number of moves of an individual in a day lies in the range [6,8]. The transitions between these states are shown in Fig.1 and explained as follows.



**Figure 1: Flow diagram of the Extended-SIR Model.**

The states considered are: Susceptible (S), Exposed (E), Pre-symptomatic (P), Infected Asymptomatic (IA), Infected Symptomatic (IS), Detected (D) and Recovered (R). Arrows represent the possible transitions between the different states.

Healthy individuals are susceptible (S) to infection with a probability  $\beta = 0.5$ . As soon as an S agent is infected, they turn into Exposed (E) meaning that they show no symptoms and cannot spread the infection. The average duration of this state is  $\eta^{-1}$  days, where  $\eta$  is 2.5. As agents pass from (E) to (P) state, they become pre-symptomatic. There is no visible symptom in this state, but the individual is already contagious. Individuals last an average of  $\alpha^{-1}$  days during this (P) stage, without detection. The value of  $\alpha$  considered for this model is 2.5[1]

Following (P) stage, individuals may remain asymptomatic(IA) with a certain probability  $1-p$ ,where p is taken as 0.65, based on the fraction of fully asymptomatic infections. The remaining agents are symptomatic infectious(IS), with a probability p. During this time, an individual lasts an average of  $\gamma^{-1}$  days without being detected before entering the Recovered state (R). The value of  $\gamma$  is taken as 10.

From the above model, we can see that the extended-SIR model seems to be more specific in the stages that the epidemic undergoes in a real-time environment, with the inclusion of P, IS, and IA stages after the P stage. This model is now further used to examine the spreading of SARS-CoV-2 with the inclusion of containment stages such as symptomatic detection, lockdown and contact tracing.

In order to describe and quantify the impact of the different control policies on the spread of transmissible diseases the effective reproductive number is often looked at as a function of time,  $R(t)$ , which measures the average number of contagions that an agent, infected at time t, makes during its infectious period and can be expressed as:

$$R(t) = \tau * k * \beta * \pi_S(t) \quad (1)$$

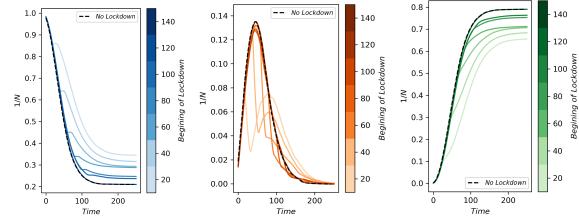
where  $\tau$  is the average duration of the infectious period,  $k$  the average number of contacts per unit time,  $\beta$  the probability of infection per contact,  $\pi_S(t)$  fraction of susceptible individuals in the population at time t. By analysing the value of this number, we can study the trend of the new infections: when  $R(t) > 1$  the number of new infections grow in time. Otherwise, when the reproductive number takes values below the epidemic threshold,  $R(t) < 1$ , the disease is on decline and the new infections will decrease until it becomes zero. This becomes particularly important when there is a chance of losing immunity, although immunity is permanent in our model. Thus, one of the major goals when facing an epidemic outbreak is to decrease the reproductive number to values below 1 via either pharmaceutical (like masks or vaccines) or non-pharmaceutical interventions. In this project we are going to focus on the use of non-pharmaceutical interventions with the aim of reducing the social contacts  $k$  and the disease transmissibility  $\beta$  by the use of social distancing measures (quarantine and lockdown). If during some time all the individuals are frozen, they don't interact and transmit the disease anymore and the epidemic outbreak is easily extinguished. However, this is sort of an ideal lockdown which means that it is a very effective strategy but it is not possible in large scale outbreaks, and the economy would be very negatively affected. For this reason, we introduce different strategies where we test the individuals in order to know if they are infectious or not, but limited testing resources are available, so therefore is crucial how this test are used to affect the epidemic development.

### 3 Results for the Implemented Containment Strategies

A common way to describe and quantify the epidemic outbreak is by looking at the fraction of the population in each of the model categories as a function of time. Since an agent-based model is being applied, the simulation is performed numerous times and all values are averaged to obtain a quantifiable trend and minimize the influence of outliers. The fraction of the population that was susceptible, infected and recovered (including exposed, presymptomatic, etc.) was tracked as the virus spread and plotted below for all three individual containment strategies.

#### 3.1 Full lockdown

The first containment strategy considered is the full lockdown. The epidemic outbreak is easily extinguished with this measure as the individuals are frozen, they don't interact and transmit the disease anymore. However, this is sort of an ideal lockdown which means that is a very effective strategy but it is not possible in large scale outbreaks, that's why a full spread lockdown is introduced into the model for a certain number of days.



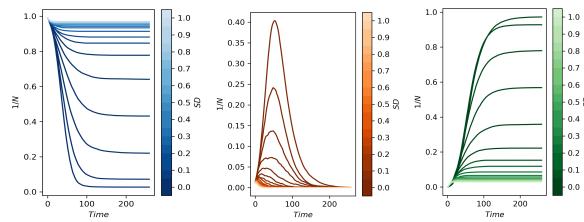
**Figure 2:** From left to right: Susceptible a), Infected b), Recovered c). Time evolution for SIR agents in the Lockdown Model.

This allows the model to restrict the movement of the individuals and stop the infected individuals from spreading the virus further for a certain period of time.

Perfect lockdowns are unrealistic and impossible, therefore an effectiveness parameter  $\lambda$  was introduced which takes up a value between 0 and 1. It reduces the probability of movement for an individual at each time step by a factor of  $1 - \lambda$ . In our model  $\lambda$  is taken as 0.95. When looking at the implementation of a full lockdown it becomes noticeable, that lockdowns implemented early on lead to a quick decline in infected agents, yet result in a secondary wave that can surpass the intensity of the original number(Figure 2 b). As the introduction time of a lockdown is increased, the model starts to resemble the free evolution (no lockdown) line, especially if the lockdown is implemented at or shortly after the peak of infected agents.

#### 3.2 Symptomatic Detection (SD)

Symptomatic detection is the process of detecting the individuals who are infected symptomatically and recovering them. This process includes the detection of symptomatically infected individuals with a certain probability. With this, it helps the process of recovery to accelerate as it is easy for the detected individual to take the necessary steps faster in order to get recovered from the disease and also stop them from further spreading the disease. The true accuracy of each testing method is nuanced and unclear[10], so for our model we have assumed a 95% testing precision.

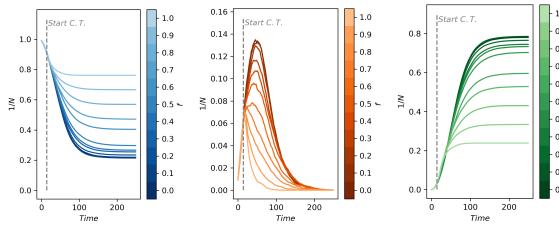


**Figure 3:** From left to right: Susceptible a), Infected b), Recovered c). Time evolution for SIR agents in the Symptomatic Detection Model.

Symptomatic detection cases are clearly very dependent on the rate of detection  $SD$ . For very high, yet unrealistic values the infected cases can be kept at a minimum, leading to rapid extermination of the virus. Yet this would imply near perfect detection of symptomatic cases at every time step. For lower values of  $SD$  the model starts to resemble free evolution again. This can be minimized by introducing contact tracing, since the two work together as containment strategies.

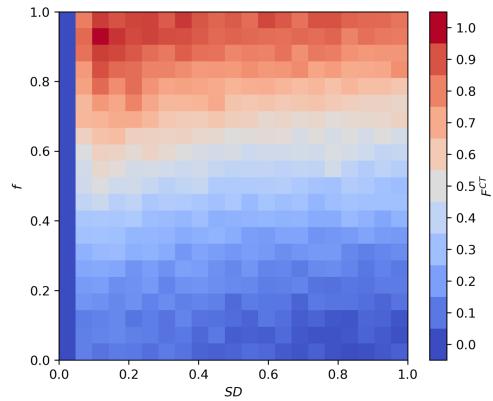
#### 3.3 Contact Tracing (CT)

The third containment strategy is contact tracing. This strategy starts with the consideration of symptomatically infected individuals. The symptomatically infected individuals who are detected are identified. Then individuals around the detected that could be tracked are identified and are labeled immediately. Further, in this, there are a fraction of individuals(which is determined by the accessibility of the app or an effective tracking method) who are in contact with the detected are simultaneously traced. In the next step, these agents are detected. With contact tracing, the tracing of the infected individuals around the detected agent is determined effectively.



**Figure 4:** From left to right: Susceptible a), Infected b), Recovered c). Time evolution for SIR agents in the CT Model.

The graphs in contract tracing are run with a symptomatic detection rate of 0.2, which can be seen as the peak on the infection curve of CT, where 0% of initial agents have tracking capabilities. To mimic the reaction to a real epidemic CT is only introduced 10 days into the pandemic, which is why a peak number of infected cases still appears initially. Yet as soon as CT is introduced, for all values of  $f > 0.2$  the slope of infected cases immediately decreases and the spread of the virus is slowed. The variable  $f$  denotes the fraction of agents that will have contact tracing capabilities. As a complementary side effect of the reduction of infected cases is of course a reduction of recovered agents. In real life applications this may lead to a larger susceptible population should the virus spread again before alternatives, such as a vaccine, are developed.



**Figure 5:** The fraction of detected agents that were identified using CT. The function is defined as the ratio between agents detected by CT and all agents detected. The first column is completely zero as without symptomatic detection, neither SD nor CT can occur, as such no cases are detected

Evidently it is of interest to identify infected agents as quickly as possible, which is attempted with symptomatic detection and contact tracing. This allows quick isolation of infected individuals and reduces the spread of the virus. To further visualize their respective ef-

fectivity in identifying infected agents, the fraction of detected agents are compared based on the method of detection. Within the same society, the fraction of detected agents that were detected via contact tracing is plotted as a function of different symptomatic detection rates and tracked agents in figure 5.

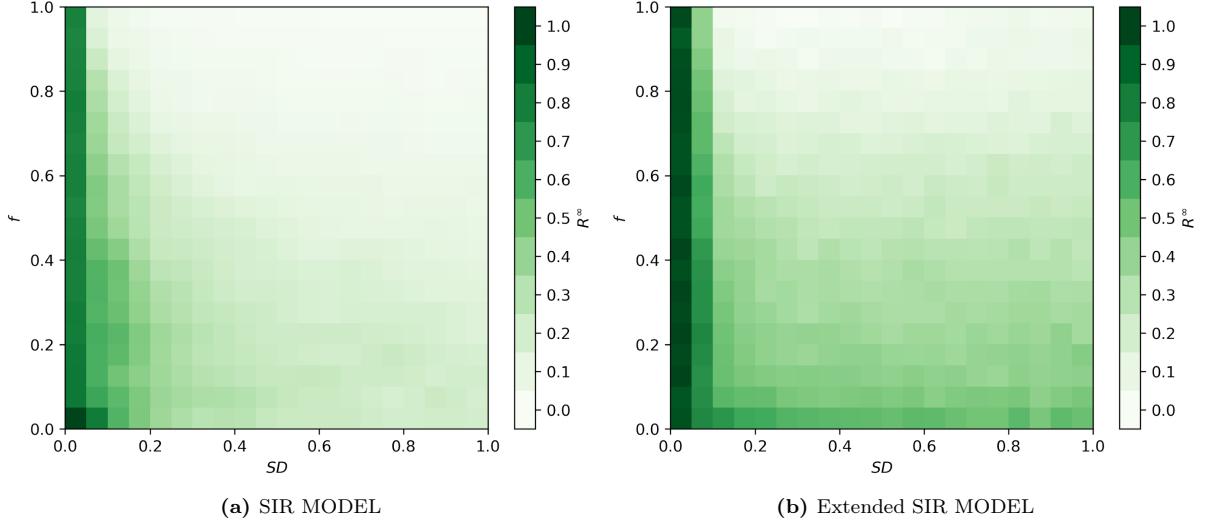
The role that CT plays in detecting infected individuals becomes evident, as the trend shows a sharp increase along the axis increasing the fraction of tracking-capable agents, opposed to the axis of increased SD. Although the line of 0.5, where CT generates half of the detected results slightly increases as SD grows, the rate of change at specific values of  $f$  is not significant. This points towards CT being possibly the most influential factor in our agent-based model, when it comes to detecting individuals and isolating these cases.

Finally we want to study the importance of CT when implemented in a more complex model as opposed to the basic SIR model. We utilize the same ranges of  $f$  and SD and map the final number of recovered agents, meaning the fraction of agents that have recovered from the virus once the maximum time has been reached or no more infectious agents are present in the population, effectively stopping the spread. The final number of recovered agents, denoted by  $R_{\text{inf}}$ , is used here for comparison since it is a direct result of the number of detected agents. It can be seen that the effectiveness of CT becomes more evident when more stages are introduced to the system. This can be proven in the plot (Figure 6) by the increasing gradient of  $R_{\text{inf}}$  as the fraction of CT capable agents is reduced. The SIR model possesses only one state for symptomatic detection, the infected state, similar to our extended model. Yet once CT is implemented the extended model additionally allows detection of pre-symptomatic and asymptomatic individuals, resulting in more detections, since these are less prone to get tested for the virus. Although these detections directly lead to recovery, it is effective in reducing the spread of the virus as seen by the fact that there are less recovered agents at higher values of  $f$ .

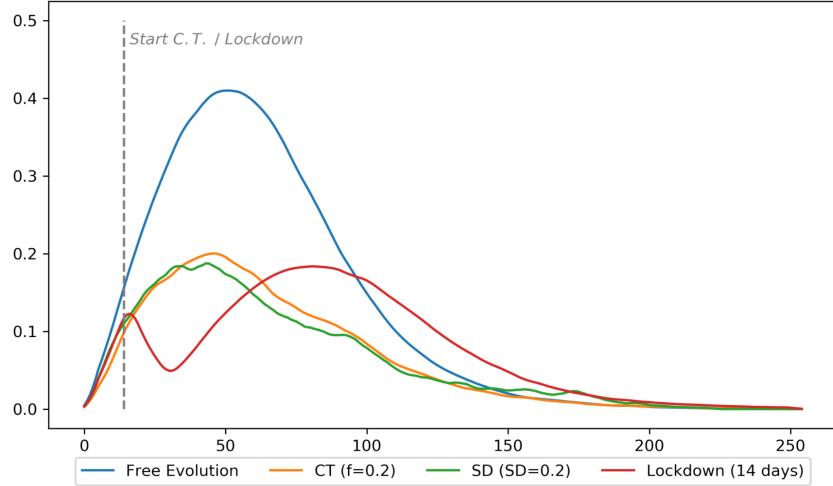
When the SIR model is extended to reflect asymptomatic cases as are present in a real pandemic, CT becomes more relevant. Since asymptomatic cases still account for transmissions, CT works at undercutting the spread through these otherwise non-identifiable cases.

## 4 Discussion

The continuous surge of waves during this pandemic have deepened the discussion not only for conquering this virus, but possibly preparing for any pandemic of the sort. The severity and frequency of spillover infectious diseases and viruses from wildlife to humans has been steadily increasing in recent decades [5] and the development of vaccines are time demanding and not guaranteed when such an outbreak occurs again.



**Figure 6: Final number of recovered individuals (with quarantine of detected individuals)**



**Figure 7: Time evolution of infected agents for all cases** The number of infected agents is shown for specific parameters of each containment strategy. It shows that straight comparison between the methods can be difficult to quantify due to the importance of their parameters.

To better understand the spread of these diseases and how to combat them, agent based SIR models are vital and employ basic concepts to easily predict the spread. The extension of the SIR model was a necessity in our case (ref. figure 5), as it allows a more precise implementation of containment strategies, especially in the case of contact tracing. We analyzed the effectiveness of the three different containment strategies independent of each other which are displayed in figures 2, 3 and 4. The lockdown model is deemed rather ineffective since an early implementation leads to a second wave where as later implementations occur either at the peak number of infections or shortly afterwards, where the infections are already on the decline. Ideally a lockdown could be extended and thus completely halt the spread of the virus, yet the economic repercussions of an extended lockdown quickly reflect on the

production index and national GDP [6]. As such other methods of containment that tried to maximize individual mobility were studied. The number of infectious agents for the different cases can be displayed together as shown in figure 7. The figure can be modeled with different parameters for  $SD$  and  $f$ , allowing the peak of infectious cases to be minimized. Here it was assumed that 20% of agents are capable of CT. Germany is a good example of a country that implemented CT by means of a smartphone application. A study[9] showed that 36% of the countries population had downloaded the app and that 72% of these individuals had downloaded the app out of concern for their own health, which compares well to the 20% value assumed above. Symptomatic detection was shown to be very effective at containing the outbreak when very high rates of detectability were simulated. Yet the question re-

mains how realistic such a simulation is. This easily turns into a question out of our reach, because the probability of getting tested depends on the strength of the symptoms and the ability to get tested, which differs from individual to individual and is often only applicable at later stages in the disease. In our model we assumed the possibility of symptomatic detection from the beginning, which often isn't the case since it takes time for tests or other methods of detection to become available. We found CT tracing to be a relatively non-invasive and effective method of combating the spread of the virus. It allows detection not only of symptomatic individuals, but of other asymptomatic or pre-symptomatic agents who are far less likely to get tested otherwise. Furthermore CT can be implemented in a number of ways independent of the disease characteristics, making the societal reaction to the epidemic rather simple. This way individuals are quarantined and the majority of individuals can still act as functioning members of society.

## 5 Conclusion

Even though our model has extended the boundaries of the basic SIR model, it does fall short to some limitations. It does not take death tolls into account nor temporal immunity. In reality failing immunity will result in an emerging endemic after a while. In that case,  $R_{\text{inf}}$  is not a reasonable metric as most of the population will become infected with a high probability after some time. Temporal immunity can be assumed on a short timescale as some countries grant recovered certificates which are equal to vaccine passports or covid tests for a finite time. Fatalities become important in realistic settings since this will set a sort of limit to the number of acceptable infections a society can tolerate. However, the plausibility of death in an outbreak does not necessarily make it harder to overcome. Higher death rates in a pandemic can result in an earlier end as fewer individuals can spread the virus. CT has shown to be effective in societies without fatalities, but in our model CT happens within the same time step and doesn't account for time delays in the tracing or testing process.

With inclusion of the before-mentioned variables the determination of the effective reproductive number  $R(t)$  becomes an important time-dependent reference for pandemic regulation, yet in our case we have replaced this with a simplified metric  $R_{\text{inf}}$  since the effective reproductive number would converge towards 0 once more agents have recovered.

Overall our model has worked to develop a more realistic spectrum of an epidemic outbreak and has simulated different containment strategies. In the agent-based model the three strategies were compared based on different parameters and the number of infected agents and recoveries. The values assigned to some of the model parameters though are rough estimations. It must be emphasized that a variety of aspects of Covid-19 are still unknown; hence building a comprehensive model of the virus' behavior is an impossible task. Some parameters, including lockdown effectiveness, expected movement of individuals, mainly depend on the target society (cultural, economic, etc.) and cannot be generalized. In realistic settings, a plethora of factors additionally come into play that could not be included in this model. In these cases a combination or tradeoff of the containment strategies may be most effective in combating the spread.

## 6 Contributions

All the members of the group elaborated on the design of the model. The implementation of the computer model was done by Arash Hatefi, guided by Alba Téllez, while all the members cooperated in the computational part and generating results. The article was written mainly by Jonah Book and Dinesh Krishnan, and Jonah Book and Alba Téllez prepared the video presentation.

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