# Inspecting COVID-19 Using SAIRS Model with Immunization

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**Abstract.** COVID-19, first appeared in December 2019, has created one of the greatest pandemics ever witnessed. Many investigations have been carried out during the past 2 years modeling the dynamics of this pandemic, among which is the popular SIR model and its variants. This paper presents the latest work of these models, and upon them, provides a new SAIRS model which includes immunization as a factor. We presented the mathematics behind this model, computed its equilibrium points and analyzed their stability. Computer simulation was further carried out to visualize and testify our claims. Results show that our model could simulate the pandemic well, and we argue that the factor of immunization could provide valuable insights into combating this worldwide pandemic.

**Keywords:** Mathematical Modeling · SAIRS model · COVID-19 · Immunization

## 1 Introduction

Throughout the human civilization, the outbreak of Coronavirus pandemic of coronavirus disease 2019 (COVID-19) has been one of the worst global pandemic that affects every aspect of people's life, including different business and health infrastructure around world. At the same time, various researches in different fields have been done in order to control and fight this challenging disease. We have seen different mathematical modeling papers in this direction in several stages. It could trace back to Kermack, W. and McKendrick, A.'s paper on the theory of epidemics as early as in 1991 [3], which proposed the use of the SIR model. Later generalization of the SIR model [1], and the SEIR models [4] have been improved and designed.

Specifically, in this paper, we are using a variant of the SIR model called the Susceptible-Asymptomatic-Infected-Recovered-Susceptible (SAIRS) model, which is very similar to Ottaviano, S., et al.'s SAIRS model [5]. The idea of our model also comes from Ansumali, S, et al.'s model [2]. We have chosen this model due to the fact that COVID-19 consists of many "silent spreaders", who are unidentified and asymptomatic, but still play important roles in the transmission of

the disease.

Thus, our main goal for this paper is to build the SAIRS model with the immunization factor for the COVID-19 pandemic. We will investigate our model's equilibrium points and their stability using both theoretical (mathematical) and numeric analysis. By doing so, we aim to find a equilibrium point that represent a desired outcome of the pandemic - possibly one where COVID-19 is controlled or eliminated. We will study what conditions could make that desired equilibrium point to be stable, and explore what feasible measures we could take in real life to achieve those conditions. Furthermore, simulations will be utilized to validate our model and confirm our mathematical analysis of the equilibrium points. We will also analyze and compare the experimental results using different plots, and tune the parameters to measure their respective impacts. We could then discuss the significance of each parameter in term of controlling the pandemic and aim to highlight the most critical ones that we should focus on.

## 2   Model Explanation

### 2.1   Definitions

Table 1 and table 2 show the definition of parameters and population groups in our model (we will use immunization and vaccination interchangeably in this report)

| Symbol | Definition |
|--------|------------|
| $S$ | The susceptible population. The susceptible people will become asymptomatic through contact with asymptomatic or infected population. They will also take vaccination. (This population go to A or R.) |
| $A$ | The asymptomatic population, directly recover or become infected population if showing symptoms. (This population go to R or I.) |
| $I$ | The identified infected population. People in this population will recover. (This population go to R.) |
| $R$ | The recovered and vaccinated population. People in this population could become susceptible again. (This population go to S.) |

Table 1: Definition of Population Groups

| Symbol | Definition |
|--------|------------|
| $\beta_A$ | the contact rate between susceptible (S) and asymptomatic (A). |
| $\beta_I$ | the contact rate between susceptible (S) and infected (I) |
| $\omega$ | the vaccination rate (vaccines turn susceptible (S) to recovered (R) |
| $\gamma_A$ | the recovery rate of asymptomatic population (A) |
| $\gamma_I$ | the recovery rate of infected population (I) |
| $\delta$ | the identification rate (which the asymptomatic (A) begin to show symptoms or get identified by tests and become identified as infected (I)) |
| $\theta$ | the re-susceptible rate: the rate which the recovered population (R) becomes as susceptible as if they weren't infected or vaccinated (go back to S again) |

Table 2: Definition of Parameters

## 2.2   Assumptions

Here are the assumptions we made in building the SAIRS model with immunization:

1. We assume that the total population is fixed, that means there's no vital dynamics included and the population is isolated. Here we fix S + A + I + R = 1, so the groups' numerical value represents their respective proportion with respect to the entire population.
2. Asymptomatic patients, while do not manifest any external symptoms, are capable of infecting susceptible persons. Since asymptomatic population are more likely to interact with others than population with symptoms, we assume that the contact rate between S and A, or $\beta_A$, is larger than the contact rate between S and I, or $\beta_I$.
3. Since asymptomatic population are likely to recover faster than those who already shows symptoms, we assume that the recovery rate of the asymptomatic group, or $\gamma_A$, is larger than that of the infected group, or $\gamma_I$.
4. Any person who is infected must first become asymptomatic before becoming infected (showing symptoms) since the virus has incubation period. This means persons from S who are in contact with persons in A or I move only to A and do not move directly to I.
5. The immunization rate, $\omega$, is a constant per unit of time, which turns individuals from S to R directly. We assume taking the immunization is as effective as if the individual is recovered.
6. We assume that only the susceptible population (S) will get vaccinated. People will not get vaccinated during A, I, or R stages.
7. We assume that some constant proportion of the recovered and vaccinated people (R) will become as susceptible as before (going back to S) within unit of time, possibly due to low antibody level or lack of awareness of continuous protection. This is represented by $\theta$ in our model. This rate can be reduced by improving the effectiveness of the vaccines or encouraging recovered people

to keep a high awareness of continuous protection – instead of believing that they will no longer be susceptible to infection or re-infection.
8. Finally, we assume that the relative amount of each groups in the population as well as the parameters in our model are non-negative. We assume them to be positive in most cases.

### 2.3  SAIRS Model with Immunization

Figure 1 shows the flowchart of our current model. Interactions between the susceptible population (S) and the two groups who could transmit the disease – the asymptomatic (A) and the infected (I) populations – causes people from S moving to A at the rates of $\beta_A$ and $\beta_I$, respectively. Note that people from S do not move directly to group I. People who are asymptomatic and infected will recover and move to the group R at the rate of $\gamma_A$ and $\gamma_I$, respectively. Asymptomatic patients (A) will show symptom and become infected (I) at a rate of $\delta$. Moreover, susceptible population (S) will get vaccinated at a rate of $\omega$, and thus get moved to group R. Finally, a portion of the person who are recovered or vaccinated will be as susceptible as before. This phenomenon makes the persons in R go back to S at the rate of $\theta$.
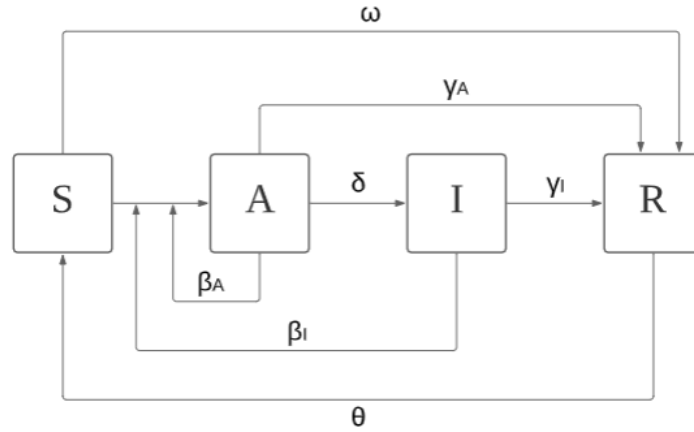


Fig. 1: SAIR Model flowchart

We believe this model can relatively accurately reflect the real situation of the COVID-19 in many aspects. Firstly, people that are infected are more likely to contact with susceptible population and infect others in the asymptomatic stage. So here we separate the asymptomatic population with the infected (showing symptoms) population. Secondly, with more and more people taking vaccination, the vaccination rate influences the spread of the virus significantly. In order to study how much impact the vaccination makes, we add vaccination rate that takes people from S to R directly. Lastly, recovery from an infection or taking a vaccination in real life does not necessarily guarantee the person is not susceptible again. These people could also take less protective measures like wearing a

mask less frequently or no longer following social distancing, or the immunization becomes no longer effective. In our model, we have the population in R goes back to S to simulate these phenomenons in real life.

From the above ideas of the SAIRS model and the assumptions we made, we obtained the following system of differential equations for our SAIRS model with vaccination:

$$\frac{dS}{dt} = -\beta_A \cdot A \cdot S - \beta_I \cdot I \cdot S - \omega \cdot S + \theta \cdot R \tag{1}$$

$$\frac{dA}{dt} = \beta_A \cdot A \cdot S + \beta_I \cdot I \cdot S - \gamma_A \cdot A - \delta \cdot A \tag{2}$$

$$\frac{dI}{dt} = \delta \cdot A - \gamma_I \cdot I \tag{3}$$

$$\frac{dR}{dt} = \gamma_A \cdot A + \gamma_I \cdot I + \omega \cdot S - \theta \cdot R \tag{4}$$

Also, with our assumptions, the overall population as the sum of the groups is:

$$S + A + I + R = 1 \tag{5}$$

## 3    Theoretical Investigation

In this section, we mainly explore the equilibrium points of the differential equation system and their stability. We will also try to explain the the equilibrium points and their stability in real-life context to demonstrate the significance of our model. The equilibrium points of the system are found by setting each differential equation to zero and solve for S, A, I, and R.

### 3.1    Equilibrium Point 1

By setting equation (3) to 0, a simple relationship between A and I can be found: $A = \frac{\gamma_I}{\delta} I$. The relationship is then substituted into equation (2) to yield

$$I \cdot (\frac{\beta_A \gamma_I}{\delta} S + \beta_I S - \frac{\gamma_A \gamma_I}{\delta} - \gamma_I) = 0 \tag{6}$$

This yields one solution of I = 0, which correspondingly gives A = 0. Substituting these two values into the other equations and using the relationship in equation (5), we discover an equilibrium point:

$$\begin{cases} S = \dfrac{\theta}{\omega + \theta} \\ A = 0 \\ I = 0 \\ R = \dfrac{\omega}{\omega + \theta} \end{cases}$$

Notice that since both $\theta$ and $\omega$ are non-negative (assume WLOG that they are not both zero), S and R are in the interval of $[0, 1]$, which fits the real life context that they are proportion of the entire population. This supports the validity of this equilibrium point as well as our model.

**Stability Analysis with Symbolic Parameters**

In this part, we investigate the stability of this equilibrium point using symbolic parameters. To analyze the stability, the first order partial derivative matrix of the system of differential equations is utilized for linear approximations. Initially, a $4 * 4$ matrix is used. Nonetheless, the matrix has one eigenvalue of 0 and thus yields an inconclusive result.

However, due to the relationship in equation (5), the degree of freedom is in fact only 3 for this system of S, A, I, and R. Thus, by removing equation (4) from the system and substituting the R in equation (1) by $(1 - S - A - I)$, we get an equivalent system of 3 equations:

$$\frac{dS}{dt} = -\beta_A \cdot A \cdot S - \beta_I \cdot I \cdot S - \omega \cdot S + \theta \cdot (1 - S - A - I) \tag{7}$$

$$\frac{dA}{dt} = \beta_A \cdot A \cdot S + \beta_I \cdot I \cdot S - \gamma_A \cdot A - \delta \cdot A \tag{8}$$

$$\frac{dI}{dt} = \delta \cdot A - \gamma_I \cdot I \tag{9}$$

The first order partial derivative matrix of the new 3-equation system is:

$$\begin{bmatrix} -\beta_A A - \beta_I I - \omega - \theta & -\beta_A S - \theta & -\beta_I S - \theta \\ \beta_A A + \beta_I I & \beta_A S - \gamma_A - \delta & \beta_I S \\ 0 & \delta & -\gamma_I \end{bmatrix}$$

After substituting the equilibrium point into the matrix, we can get the characteristic polynomial of the resulting matrix:

$$(-\omega - \theta - \lambda)[\lambda^2 + (\gamma_A + \gamma_I + \delta - \beta_A \frac{\theta}{\theta + \omega})\lambda + (\gamma_A \gamma_I + \delta \gamma_I - \gamma_I \beta_A \frac{\theta}{\theta + \omega} - \delta \beta_I \frac{\theta}{\theta + \omega})]$$

So if we let

$$\begin{cases} b = \gamma_A + \gamma_I + \delta - \beta_A \dfrac{\theta}{\theta + \omega} \\ c = \gamma_A \gamma_I + \delta \gamma_I - \gamma_I \beta_A \dfrac{\theta}{\theta + \omega} - \delta \beta_I \dfrac{\theta}{\theta + \omega} \end{cases}$$

then, we can get the symbolic representation of the eigenvalues of the resulting matrix:

$$\begin{cases} \lambda_1 = -\omega - \theta \text{ (always negative)} \\ \lambda_2 = \dfrac{-b + \sqrt{b^2 - 4c}}{2} \\ \lambda_3 = \dfrac{-b - \sqrt{b^2 - 4c}}{2} \end{cases}$$

Also, we have

$$\begin{cases} \lambda_2 + \lambda_3 = -b \\ \lambda_2 * \lambda_3 = c \end{cases}$$

So we must have b > 0 and c > 0 for all the eigenvalues to be negative. That is:

$$\frac{\theta}{\theta + \omega} < \frac{\gamma_A + \gamma_I + \delta}{\beta_A} \text{ and } \frac{\theta}{\theta + \omega} < \frac{\gamma_A \gamma_I + \delta \gamma_I}{\gamma_I \beta_A + \delta \beta_I}$$

If all the eigenvalues of the resulting matrix are negative, then the general solution of the form $c_1 e^{\lambda_1 t} v_1 + c_2 e^{\lambda_2 t} v_2 + c_3 e^{\lambda_2 t} v_3$ ($c_i$ are scalars and $v_i$ are $\lambda_i$'s corresponding eigenvector) will go to 0 as t goes to positive infinity, which means that the equilibrium point is stable.

If this equilibrium point is stable, then for certain initial conditions of the parameters, we could expect the asymptomatic population (A) and the infected population (I) to eventually approach 0 – which effectively means that COVID-19 is eliminated. This is of course the outcome we wish to see for the real life.

From the above inequalities, we could make several interesting observations. First, notice that since all the parameters are non-negative, if we set $\theta$ to 0 (assume WLOG that the other denominators and numerators are not 0), then the inequalities will always hold, making this a stable equilibrium point for our model without re-susceptible phenomena (i.e. SAIR instead of SAIRS).

Moreover, we can see that in general, increasing recovery rates ($\gamma$'s), the vaccination rate ($\omega$), and the identification rate ($\delta$) (in some situations), as well as decreasing contact rates ($\beta$'s) and the re-susceptible rate ($\theta$) will make the inequalities more likely to be satisfied. That is equivalent to make the eigenvalues of the resulting matrix more likely to be all negative, thus making the equilibrium point stable and leading to the outcome of eliminating COVID-19. We wish these changes can happen in real life, so here are a list of possible real life actions to achieve them:

1. Improving medical level or inventing specialized medicine will increase the recovery rates $\gamma$'s.
2. Promoting vaccination will increase the vaccination rate $\omega$.
3. Conducting COVID-19 tests more frequently to more quickly identify asymptomatic patients will increase the identification rate $\delta$.
4. Promoting protective measures such as wearing a mask and social distancing will decrease the contact rates $\beta$'s.
5. Encouraging people who are recovered or vaccinated to keep their awareness of continuous protection will decrease the re-susceptible rate $\theta$.

These suggestions are consistent with our real-life experience and expectations, and the fact that this equilibrium point could be stable provides us a theoretical support that COVID-19 could possibly be eliminated if we follow the above ideas.

**Stability Analysis with Numerical Parameters**

We used a set of parameters that is close to the empirical parameters from [2] to check the stability of this equilibrium point under a fairly realistic setting. Specifically, we choose $\beta_A = 0.28$, $\beta_I = 0.25$, $\gamma_A = 0.03$, $\gamma_I = 0.02$ and $\delta = 0.02$. For the parameters that are newly introduced by our model, $\theta$ and $\omega$, we choose them base on our understanding of the real-life scenario and set $\theta = 0.001$ and $\omega = 0.015$.

Substituting this set of parameters into the equilibrium point, we get $S = \frac{1}{16} = 0.0625$, $A = 0$, $I = 0$, $R = \frac{15}{16} = 0.9375$. Evaluating the first partials in the matrix at this equilibrium point, we can get that the eigenvalues of the resulting matrix are: -0.0160, -0.0450, and -0.0075, respectively. This means that under the empirical parameters and our assumption of the vaccination rate and re-susceptible rate, this equilibrium point is actually stable, and for some initial conditions, the model actually converge to this equilibrium point where A and I goes to 0. Thus, if we are able to achieve the assumed parameters in real life, we could expect COVID-19 to be eventually eliminated.

## 3.2   Equilibrium Point 2

Instead of taking I = 0 for equation (6), we can set the other factor to 0 to get another equilibrium point where $S = \frac{\gamma_A \gamma_I + \delta \gamma_I}{\beta_A \gamma_I + \delta \beta_I}$. Substituting this S into the other equations, we get the symbolic representation of another equilibrium point:

$$
\begin{cases}
S = \dfrac{\gamma_A \gamma_I + \delta \gamma_I}{\beta_A \gamma_I + \delta \beta_I} \\[4mm]
A = \dfrac{-\gamma_I (\delta \gamma_I \omega - \beta_I \delta \theta - \beta_A \gamma_I \theta + \gamma_A \gamma_I \omega + \delta \gamma_I \theta + \gamma_A \gamma_I \theta)}{\beta_A \delta \gamma_I^2 + \beta_I \delta^2 \gamma_I + \beta_A \gamma_A \gamma_I^2 + \beta_I \delta^2 \theta + \beta_A \gamma_I^2 \theta + \beta_A \delta \gamma_I \theta + \beta_I \delta \gamma_I \theta + \beta_I \delta \gamma_A \gamma_I} \\[4mm]
I = \dfrac{-\delta (\delta \gamma_I \omega - \beta_I \delta \theta - \beta_A \gamma_I \theta + \gamma_A \gamma_I \omega + \delta \gamma_I \theta + \gamma_A \gamma_I \theta)}{\beta_A \delta \gamma_I^2 + \beta_I \delta^2 \gamma_I + \beta_A \gamma_A \gamma_I^2 + \beta_I \delta^2 \theta + \beta_A \gamma_I^2 \theta + \beta_A \delta \gamma_I \theta + \beta_I \delta \gamma_I \theta + \beta_I \delta \gamma_A \gamma_I} \\[4mm]
R = \dfrac{\begin{array}{l}(\beta_A \delta \gamma_I^2 - \gamma_A^2 \gamma_I^2 - \delta^2 \gamma_I^2 + \beta_I \delta^2 \gamma_I + \beta_A \gamma_A \gamma_I^2 - 2\delta \gamma_A \gamma_I^2 \\ \quad + \delta \gamma_I^2 \omega + \delta^2 \gamma_I \omega + \gamma_A \gamma_I^2 \omega + \delta \gamma_A \gamma_I \omega + \beta_I \delta \gamma_A \gamma_I)\end{array}}{\beta_A \delta \gamma_I^2 + \beta_I \delta^2 \gamma_I + \beta_A \gamma_A \gamma_I^2 + \beta_I \delta^2 \theta + \beta_A \gamma_I^2 \theta + \beta_A \delta \gamma_I \theta + \beta_I \delta \gamma_I \theta + \beta_I \delta \gamma_A \gamma_I}
\end{cases}
$$

This equilibrium point with symbols is overly complicated for stability analysis, so we only analyze the stability of it with the same set of realistic numerical parameters: $\beta_A = 0.28$, $\beta_I = 0.25$, $\gamma_A = 0.03$, $\gamma_I = 0.02$, $\delta = 0.02$, $\theta = 0.001$, and $\omega = 0.015$. Here is the resulting second equilibrium point: $S = 0.094340$, $A = -0.009797$, $I = -0.009797$, $R = 0.925254$. This equilibrium point is unrealistic, since the relative amount of different groups of population

cannot be negative in our model.

Note that the eigenvalues for Jacobian Matrix corresponding to the second equilibrium point are $\lambda_1 = -0.0442, \lambda_2 = -0.0173$, and $\lambda_3 = 0.0071$. we find that this equilibrium point is actually unstable since one of the eigenvalues is positive, and the constant corresponding to this eigenvalue in the linear approximation is negative, which means the population to go to negative infinity as time goes to infinity.

In fact, we also used MATLAB to confirm that the system of differential equations of our model has two equilibrium points. Using linear approximations at the neighborhood of the equilibrium points, we find that one equilibrium point is stable and explainable while the other is neither stable nor realistic with the empirical parameters. Therefore, we hypothesize that the relative amount of different groups of population in our model will converge to the stable, explainable equilibrium point within a range of initial conditions with the empirical set of parameters. In fact, we explore different initial conditions in the simulation and the results are consistent with our hypothesis.

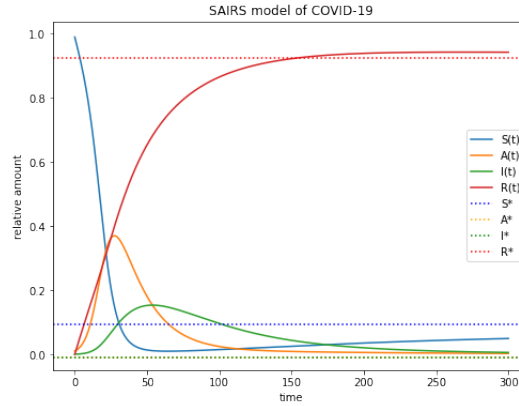## 4   Simulation

### 4.1   Equilibrium Points



Fig. 2: SAIR Model with Equilibrium points

Simulation of the SAIRS model is carried out with Python. The basic setup is to establish the model as a function that accepts the amount of individuals of each group at a specific time step, and returns such information for the next time step. By setting up the initial conditions and calling the function iteratively, we could get the dynamics of COVID-19 with respect to time. We further used the matplotlib module to visualize the results. Figures below shows the results we gained from the above experiment.

It is worth noting that we used the same set of empirical parameters from [2] and our assumed $\omega$ and $\theta$ again to run the simulation. That is, $\beta_A = 0.28$, $\beta_I = 0.25$, $\gamma_A = 0.03$, $\gamma_I = 0.02$, $\delta = 0.02$, $\theta = 0.001$, and $\omega = 0.015$. In section 4.2, we will tune these parameters to see their impact on the model.

Figure 2 shows the relations between the relative amount of different groups of the population as a function of time. Susceptible individuals drop vastly at the beginning, then slowing increases afterward, whereby the recovered individuals vastly increases at first, then slowly decreases. The number of asymptomatic and infected, on the other hand, both show a peak at the beginning, then drops to zero later on.

The dotted lines represent the first equilibrium point of each group of individuals calculated in section 3.1. It can be seen clearly that each group converges to their respective equilibrium points as time elapses, thereby supporting our claim that this equilibrium point is stable.

Our claim of the stability is further supported by phase plane simulation, in which we interpolate the number of individuals of each group, and plot the change of curve of each combination. Specifically, 19 values of $S$ are chosen equally-spaced from $[0,1)$, with $A = 1 - S$ and $I = R = 0$ as the sequence of initial conditions. Figure 3 shows the result of our simulation. The phase plane is consistent with our result of math analysis, where the relative amount of different groups converges to the first equilibrium point in 3.1.
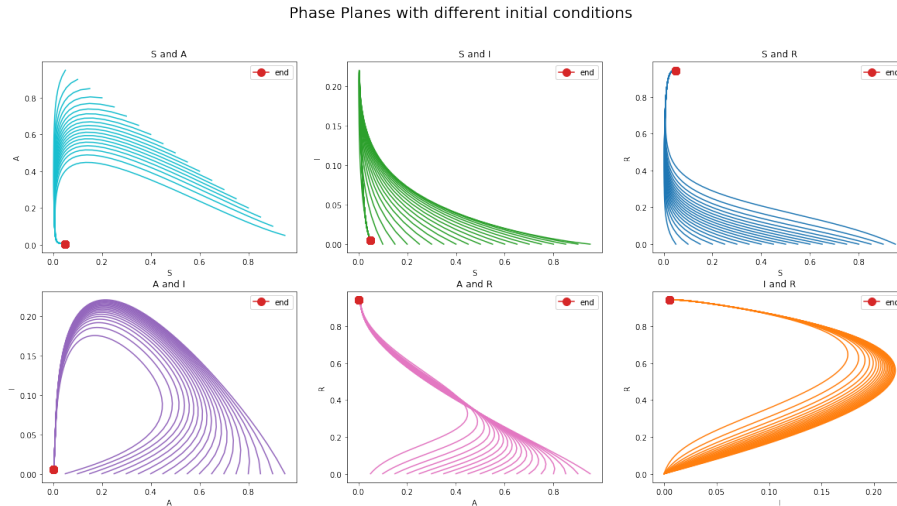


Fig. 3: 2D Phase Plane of SAIRS Model

### 4.2    Parameters Tuning

As there are a total of 5 parameters in our model ($\beta$'s and $\gamma$'s are grouped to 2 parameters here), we would like to find out how these parameters affects our model's behavior with time. For each of the parameters, we set up a group of three values, each differs by 10 times, while keeping the other parameters unchanged. To observe the significance of the general contact and recovery rates, we kept a constant ratio between $\beta_A$ and $\beta_I$ (also between $\gamma_A$ and $\gamma_I$) while tuning the parameters. That means we only change $\beta_A$ and $\gamma_A$, while $\beta_I$ and $\gamma_I$ change accordingly. Figure 4 to Figure 8 shows the results of the experiment. From the plots, we could reach the following results:
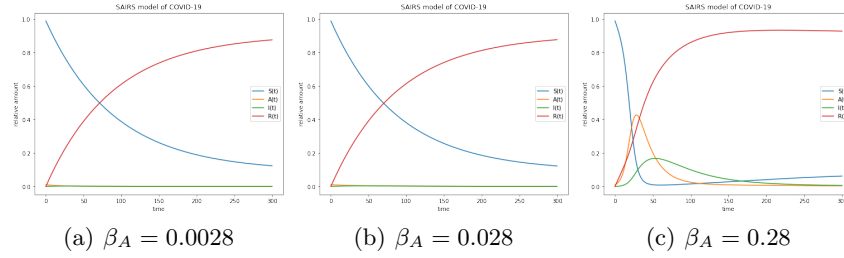


(a) $\beta_A = 0.0028$          (b) $\beta_A = 0.028$          (c) $\beta_A = 0.28$

Fig. 4: parameter change of $\beta$

1. The higher the $\beta$, the higher the peak infected rate. This is fairly straightforward. Higher $\beta$ represents higher contact rate, which in turn would led to increase in infected people.
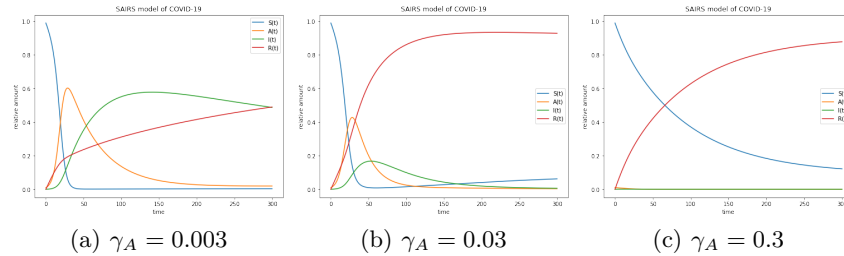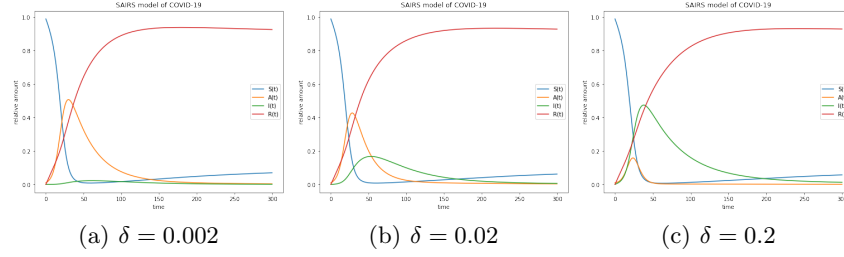


(a) $\gamma_A = 0.003$          (b) $\gamma_A = 0.03$          (c) $\gamma_A = 0.3$
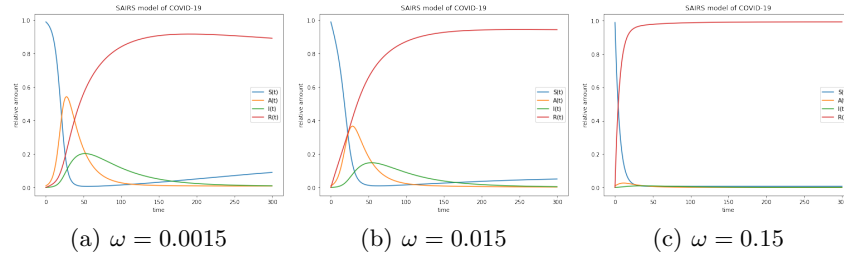
Fig. 5: parameter change of $\gamma$

2. Higher $\gamma$ leads to lower $A$ and $I$. Indeed, higher $\gamma$ means faster recovery from the disease, thus brings the numbers of infected and asymptomatic people down.

(a) $\delta = 0.002$      (b) $\delta = 0.02$      (c) $\delta = 0.2$

Fig. 6: parameter change of $\delta$

3. Higher $\delta$ leads to decrease in $A$ but increase in $I$. This is again straightforward. Having higher identification rate will accelerate the shift from asymptomatic to infected.



(a) $\theta = 0.001$      (b) $\theta = 0.01$      (c) $\theta = 0.1$
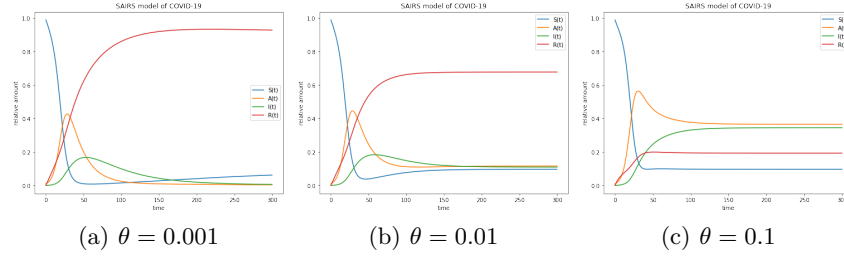
Fig. 7: parameter change of $\theta$

4. Note that $\theta$, which is the re-susceptible rate, affects the general trend through time. Specifically, as $\theta$ grows, higher proportion will eventually stay in the A and I groups.



(a) $\omega = 0.0015$      (b) $\omega = 0.015$      (c) $\omega = 0.15$

Fig. 8: parameter change of $\omega$

5. Higher $\omega$, or higher immunization rate, leads to lower peak of $A$ and $I$, and also faster convergence of S and R to more extreme values (i.e. more close to 0 and 1, respectively).

It can be seen that the observation of the experiment is quite consistent with our real world intuition. Note that low contact rate is important to keep the pandemic under control in our model. As shown in Figure 4, the peak of infected cases significantly decreases as contact rate becomes smaller. This is consistent with the real-world scenario, where social distancing and masks are required to

reduce the contact rate and therefore "flatten the curve".

Additionally, high re-susceptible rate is dangerous. From Figure 7, we see that $\theta$ controls the behavior the general trends. Higher $\theta$ leads to higher stable points of A and I, which means the pandemic may never end. In the current COVID-19 pandemic, the re-susceptible rate is negatively correlated with the effectiveness of protection provided by vaccination or from recovery. Our model implies that if the protection rate is constantly low, then the number of infection cases would stay stable at a significant level. In fact, this implication agrees with the fact that mutants of the virus that can lead to breakthrough infection would escalate the pandemic. Hence, the result of model reminds people to be aware of the risks of being susceptible even after they have already vaccinated or recovered.

As expected, high immunization rate is crucial for controlling the pandemic. As illustrated above, high immunization rate successfully decreases the number of infection cases. Similar to the reality, our model predicts that high vaccination rate helps to control the cases of asymptomatic and symptomatic infection, and even has the effect of eliminate the spread of the virus via the "herd effect".

## 5    Summary

In this project, we use SAIRS model with immunization rate to study the COVID-19 pandemic. We use theoretical methods to investigate the equilibrium points of the differential equation system of our model, aiming to find an equilibrium point that proposes an end to the pandemic and explore what measures we could take to approach that equilibrium point. Through our exploration, one equilibrium point is found that makes both the asymptomatic population and the identified infected population approach 0. This equilibrium point represents a possible outcome where COVID-19 is eventually eliminated. Through mathematical analysis, we further conclude that this equilibrium point is stable under certain conditions that are achievable in real life. If we can meet the condition that make the equilibrium point stable, we could expect COVID-19 to eventually come to an end. We also discussed several real-life measures that we could employ to reach these conditions.

Computer simulation is carried out for visualization and validation. We argue that the results provide strong support for both the validity of our model and the results of our mathematical analysis. Furthermore, we showed by tuning parameters that their impact on the model align closely with their real world meanings. We found that the two new parameters, re-susceptible rate ($\theta$) and immunization rate ($\omega$) are crucial for controlling the pandemic. Especially, we need to control $\theta$ to prevent the possible outcome that a portion of the population staying in an infected stage. Overall, we argue that our model could realistically simulate the dynamics of the pandemic, and provide novel insights

of the effects of immunization and re-susceptible rates on the pandemic.

Further studies could be carried out for several aspects. First, the factor of immunization could be more thoroughly investigated. Specifically, vaccinated people could be regarded as a separate group of the population to study its effects. Second, vital dynamics could be added to our model. Third, the influence of the parameters for the asymptomatic population and the identified infected population - such as their respective contact rates and recover rates - could be explored separately and more thoroughly to fully utilize the feature of our model. Moreover, as discussed in literature review, more factors could be added to our SAIRS model, like the nonlinear relationship between susceptible and infected group discussed in Wang's paper [6]. These modifications would surely add complexity to the model, but could provide more comprehensive and valuable insights to the dynamics of the pandemic.

# References

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