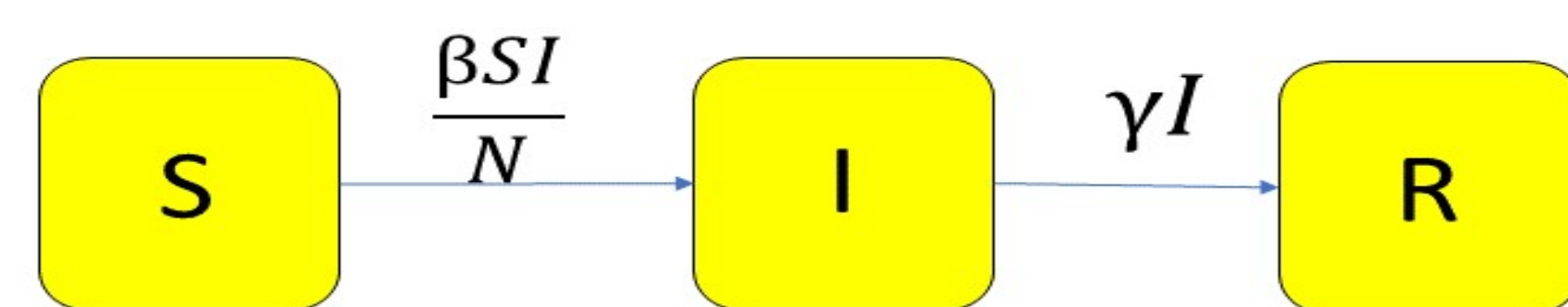


## Introduction

- Mathematical modeling of infectious diseases is fundamental in assessing, predicting, and controlling the spread of epidemic diseases. The SIR model, first published by Kermack and McKendrick in 1927, is a famous mathematical model for the study of infectious diseases dynamics.
- The SIR model with some additional compartments has been used extensively to study the transmission dynamics of COVID-19 since its first outbreak in December 2019.
- We study the basic SIR model and estimate the control parameters such as effective transmission rate, removal rate, and the basic reproduction number. We will derive mathematical formulas to calculate these parameters. We study the local stability of the disease-free equilibrium in terms of basic reproduction number.
- We add the vaccinated compartment in our model. We compute the reproduction number and study its stability under vaccination.

## SIR Model

Let  $N$  denote the total (closed) population size. Let  $S$ ,  $I$ , and  $R$  denote the number of susceptible, infectious, and removed (recovered + death) individuals at time  $t$ . The basic structure of SIR model is as follows:



$$\frac{dS}{dt} = -\frac{\beta SI}{N}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

where  $\beta$  represents the effective transmission rate and  $\gamma$  represents the removal rate.

## Estimation of Control Parameters

### Basic Reproduction Number ( $R_0$ ):

The disease free equilibrium is  $(N, 0, 0)$  and the basic reproduction number  $R_0$  is given by  $R_0 = \frac{\beta}{\gamma}$ . It is a key parameter determining whether or not the disease persists. If  $R_0 > 1$ , then the disease persists and if  $R_0 < 1$  the disease dies out.

$$\begin{aligned} \frac{dS}{dR} &= \frac{-\beta SI}{\gamma I} \Rightarrow dS = -\frac{R_0}{N} dR \\ \Rightarrow \int_t^{t+1} \frac{dS}{S} &= -\frac{R_0}{N} \int_t^{t+1} dR \\ \Rightarrow \ln(S(t+1) - S(t)) &= -\frac{R_0}{N}(R(t+1) - R(t)) \\ \Rightarrow R_0 &= -N \frac{\ln(S(t+1) - S(t))}{R(t+1) - R(t)} \\ \Rightarrow R_0 &= -\frac{2N}{R(t+1) - R(t)} \cdot \frac{S(t+1) - S(t)}{S(t+1) + S(t)} \end{aligned}$$

### Removal Rate ( $\gamma$ ):

$$\begin{aligned} \frac{dI}{dt} &= \frac{\beta SI}{N} - \gamma I \\ \Rightarrow \frac{dI}{I} &= \left( \frac{\beta S}{N} - \gamma \right) dt \\ \Rightarrow I(t) &= I(t_0) e^{\gamma \left( \frac{S(t_0)}{N} - 1 \right) (t - t_0)} \\ \Rightarrow I(t) &= I(0) e^{\gamma (R_0 - 1)t} \quad (t_0 = 0, S(0) \approx N) \\ \frac{dR}{dt} &= \gamma I \quad \& \quad I(t) = I(t_0) e^{\gamma \left( \frac{S(t_0)}{N} - 1 \right) (t - t_0)} \\ \Rightarrow \int_{t_0}^{t_0+1} dR &= \gamma \int_{t_0}^{t_0+1} I(t_0) e^{\gamma \left( \frac{S(t_0)}{N} - 1 \right) (t - t_0)} dt \\ \Rightarrow R(t_0 + 1) - R(t_0) &= \frac{I(t_0)}{R_0 \frac{S(t_0)}{N} - 1} \left( e^{\gamma \left( \frac{S(t_0)}{N} - 1 \right)} - 1 \right) \\ \Rightarrow \gamma &= \frac{\ln \left[ 1 + \frac{(R(t_0 + 1) - R(t_0)) \left( R_0 \frac{S(t_0)}{N} - 1 \right)}{I(t_0)} \right]}{R_0 \frac{S(t_0)}{N} - 1} \end{aligned}$$

### Effective Transmission Rate ( $\beta$ ):

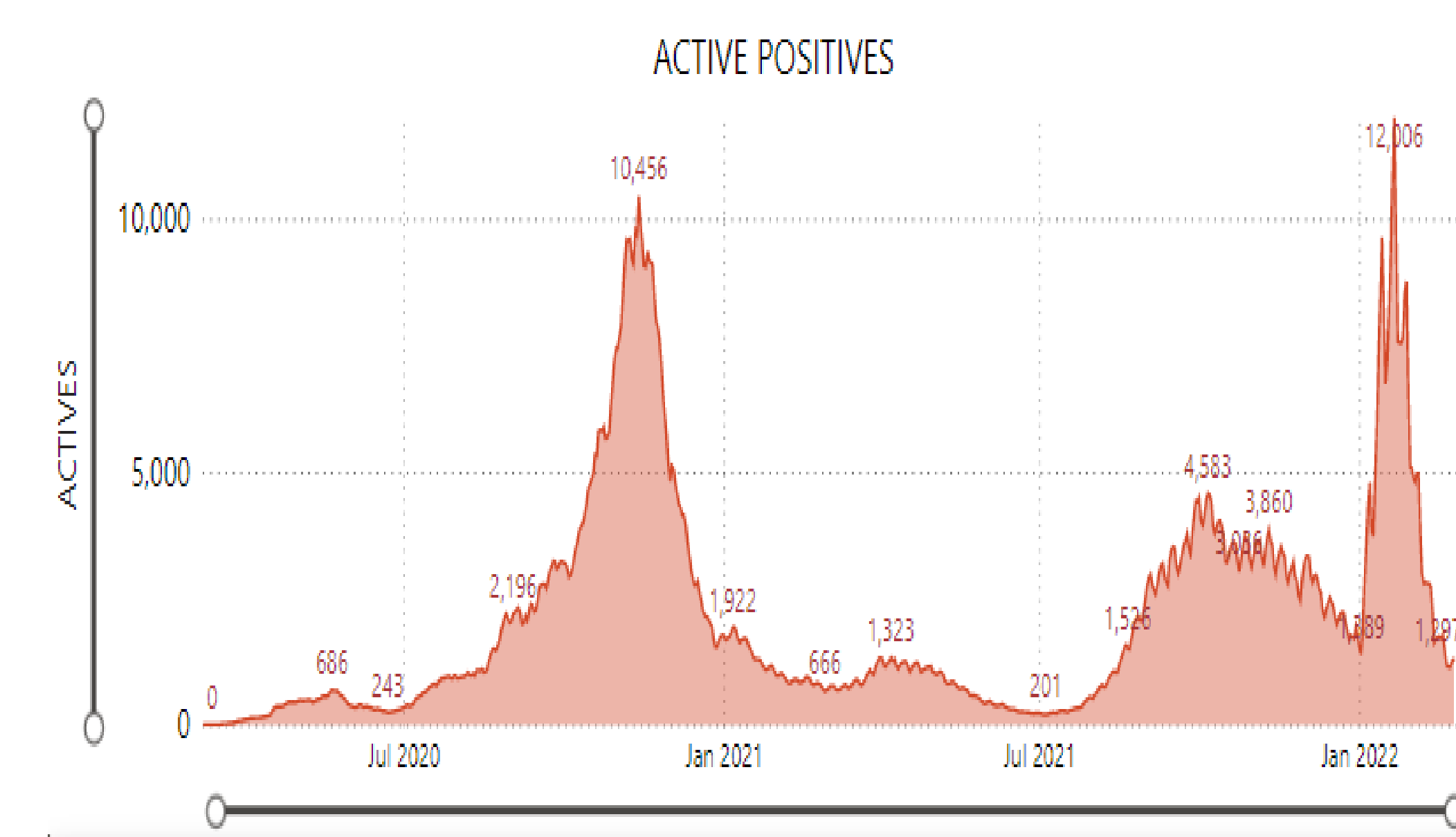
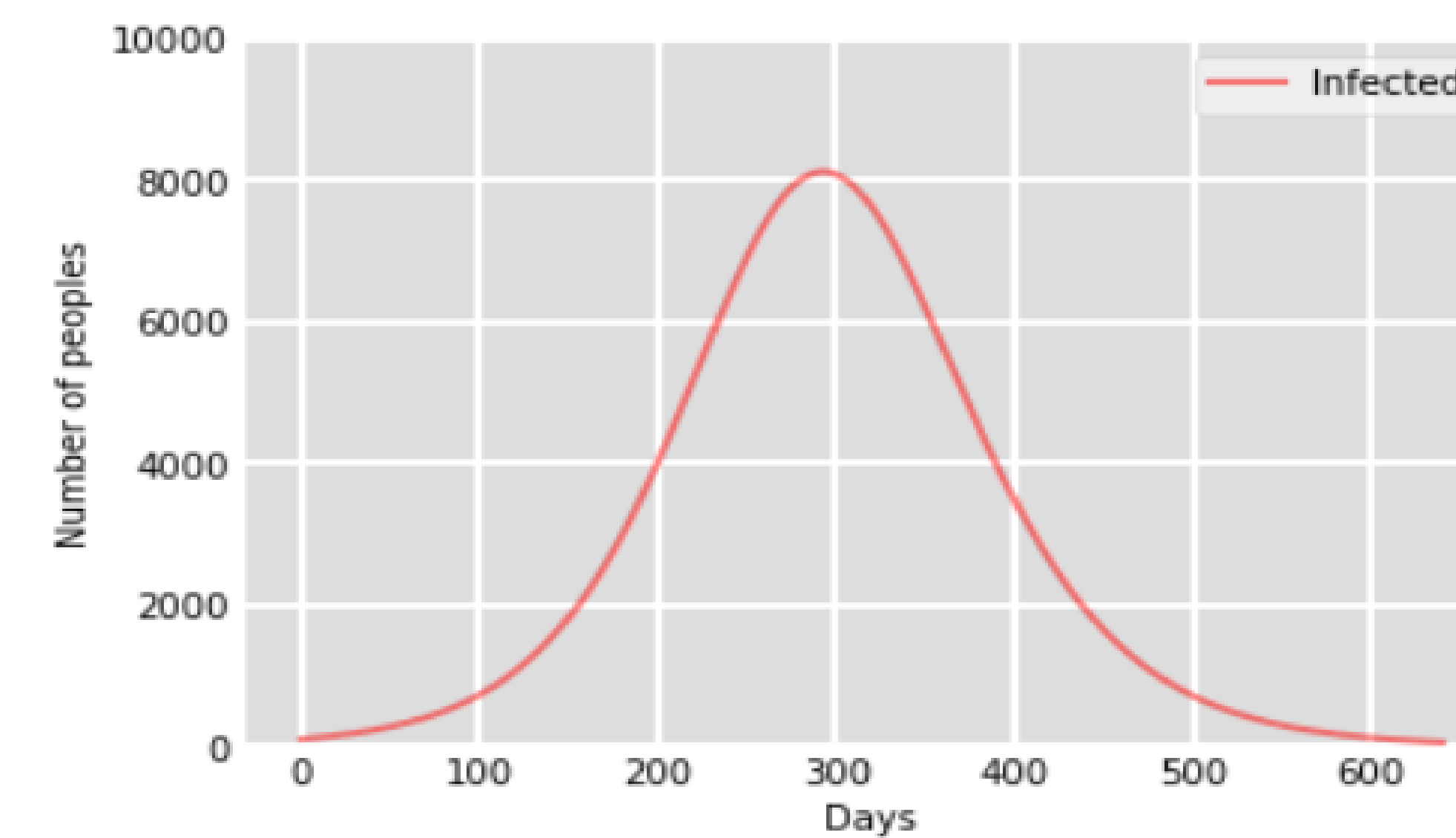
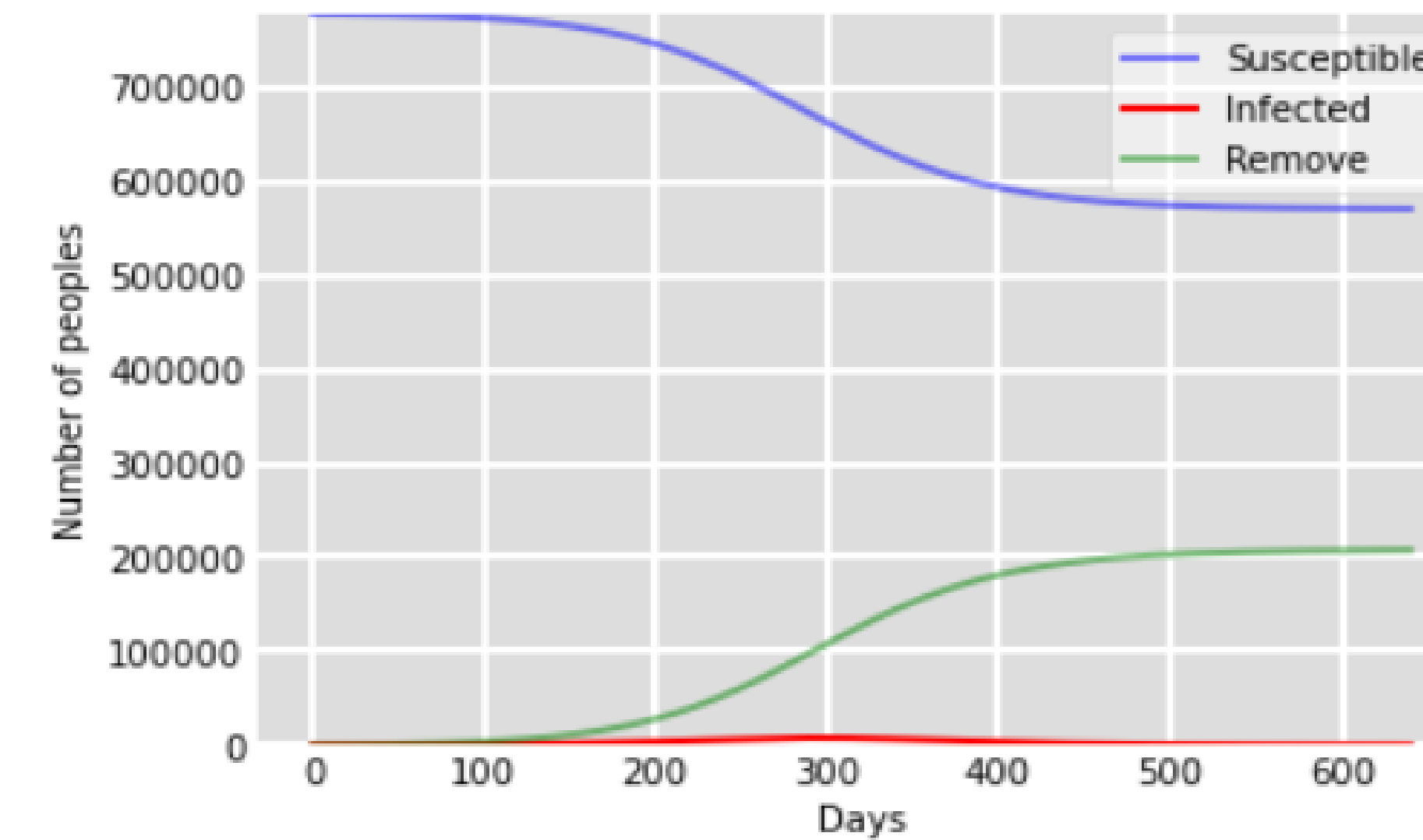
$$\beta = R_0 \cdot \gamma$$

## Solution of SIR Model

Using the data set of North Dakota from April 1, 2020 to December 31, 2021, we estimated that  $\beta = 0.14$

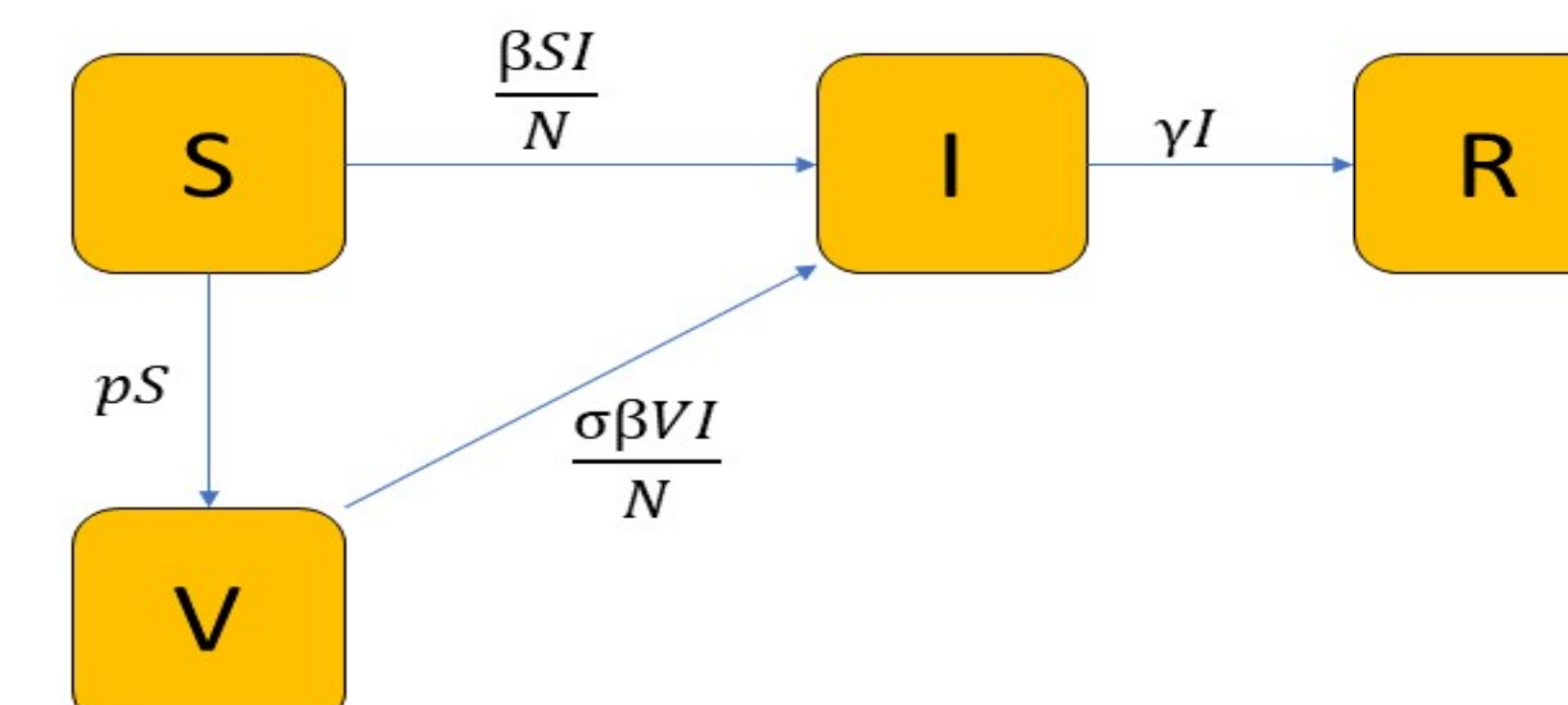
## Solution of SIR Model

and  $\gamma = 0.12$  and solved the system of differential equations using Python. The data set can be found in the following link: <https://github.com/longnguyen1112/SIR-Model-of-COVID-19-ND>



## SIRV Model

The description of SIR model after adding a vaccinated compartment is as follows:



## SIRV Model

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta SI}{N} - pS \\ \frac{dI}{dt} &= \frac{\beta SI}{N} + \frac{\sigma \beta VI}{N} - \gamma I \\ \frac{dR}{dt} &= \gamma I \\ \frac{dV}{dt} &= -\frac{\sigma \beta VI}{N} + pS, \end{aligned}$$

where  $V$  denotes the number of vaccinated individuals at time  $t$ ,  $p$  denotes the proportion of population vaccinated per unit time, and  $\sigma \in [0, 1]$  so that  $(1 - \sigma)$  represents vaccine efficacy. The disease free equilibrium is  $((1 - p)N, 0, 0, pN)$  and the reproduction number is given by  $R_0^v = R_0(1 - (1 - \sigma)p)$ .

## Conclusion

- Derivation of mathematical formulas to estimate  $\beta$  and  $\gamma$ .
- Model is a good approximation about the peak of the epidemic.
- $R_0^v$  can be used to predict the epidemic in the case of vaccinations.

## Future Direction

We will extend the SIR model to fit the number of hospitalized people, ICU people, and fatalities and conduct a more comprehensive study of the COVID-19 disease outbreak in North Dakota.

## References

- Kermack, W. and McKendrick, A., 1927. *A contribution to the mathematical theory of epidemics*. Proc. R. Soc. London A 115, 700-721.
- Mohamed A, Nouredine K. *Modeling the dynamic of COVID-19 with different types of transmissions*. Chaos, Solitons Fractals, Volume 150, 2021.

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