

SIR model with COVID-19 Vaccination

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In 2021, the COVID-19 pandemic continued to shape global health, society, and research efforts. The SIRV (Susceptible-Infectious-Recovered-Vaccinated) model became a crucial tool for understanding and predicting the dynamics of the virus's spread. This year marked a significant phase in the pandemic response, characterized by widespread vaccination campaigns and evolving viral variants.

Introduction

Differential equations mathematically express how a function and its derivatives quantitatively relate to each other. They are crucial for modeling and analyzing the dynamic evolution of variables across continuous domains in various scientific disciplines.

The Susceptible-Infectious-Recovered-Vaccinated (SIRV) model is a compartmental model widely used in epidemiology to comprehensively capture the dynamics of infectious disease spread within a population.

A description of the main result

The independent variable is time t , measured in days, and we analyze two linked sets of dependent variables as the initial stage in the modeling procedure. To incorporate vaccinations into the SIR model,

- $S = S(t)$ is the number of susceptible individuals
- $I = I(t)$ is the number of infected individuals
- $R = R(t)$ is the number of recovered individuals
- $V = V(t)$ is the number of vaccinated individuals

A description of the main result

If N is the total population (approximately 7,900,000,000 globally in 2021), we define the following fractions:

$$s(t) = \frac{S(t)}{N}$$

$$i(t) = \frac{I(t)}{N}$$

$$r(t) = \frac{R(t)}{N}$$

$$v(t) = \frac{V(t)}{N}$$

A description of the main result

Parameter/Variable	Description
S	Number of susceptible population
V	Number of Vaccinated individuals
I	Number of Infected population
R	Number of Recovered population
β	transmission rate
γ	recovery rate
γ_ν	vaccination rate
N	total population

Table: 1. State variables and model parameters for the SIRV model.

Model Equations

By dividing each equation by N , we may introduce the fractions $s(t)$, $i(t)$, $r(t)$, and $v(t)$ and describe the following equations in terms of the percent of the entire population:

$$\frac{ds}{dt} = -\beta \cdot \frac{SI}{N} - \gamma_v \cdot S \cdot V$$

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

$$\frac{dr}{dt} = \gamma \cdot I$$

$$\frac{dv}{dt} = \gamma_v \cdot S \cdot V$$

Parameters:

- $\beta = 0.3$
- $\gamma = 0.1$
- $\gamma_v = 0.05$
- $N = 7,900,000,000$

Initial Conditions: (starting with 100 infected individuals)

- $s = 7,899,999,900$
- $i = 100$
- $r = 0$
- $v = 0$

Time Settings: T (total time in days) = 365

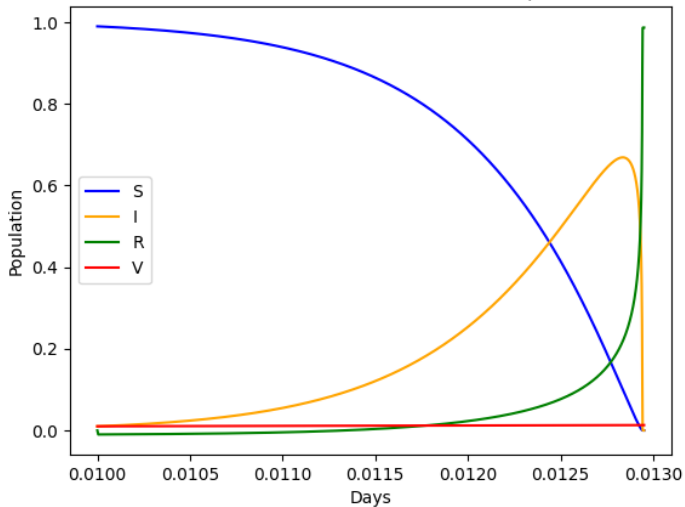
dt (time step in days) = 1

Differential Equation

code.py

```
1 import numpy as np
2 import matplotlib.pyplot as plt
3
4 def solve_SIR(S0, I0, beta=0.3, gamma=0.1, gamma_v=0.05, delta_t=0.01, T=365):
5     times = int(T / delta_t)
6     res = np.zeros((times, 4))
7     res[0, :] = [S0, I0, 1 - S0 - I0, delta_t]
8
9     def dS(S, I, V):
10         return -beta * I * S / N - gamma_v * S * V
11
12     def dI(S, I):
13         return beta * I * S / N - gamma * I
14
15     for i in range(1, times):
16         S, I, V = res[i - 1, 0], res[i - 1, 1], res[i - 1, 3]
17         res[i, 0] = res[i - 1, 0] + delta_t * dS(S, I, V)
18         res[i, 1] = res[i - 1, 1] + delta_t * dI(S, I)
19         res[i, 3] = res[i - 1, 3] + delta_t * gamma_v * S * V
20         res[i, 2] = 1 - res[i, 0] - res[i, 1] - res[i, 3]
21
22     return res
23
24 def plot_SIR(res, title=''):
25     cols = ['blue', 'orange', 'green', 'red']
26     time = res[:, 3]
27
28     plt.plot(time, res[:, 0], label='S', color=cols[0])
29     plt.plot(time, res[:, 1], label='I', color=cols[1])
30     plt.plot(time, res[:, 2], label='R', color=cols[2])
31     plt.plot(time, res[:, 3], label='V', color=cols[3])
32
33     plt.xlabel('Days')
34     plt.ylabel('Population')
35     plt.title(title)
36     plt.legend()
37     plt.show()
38
39 # Example usage:
40 S0_example = 0.99
41 I0_example = 0.01
42 N = 7_900_000_000
43 result = solve_SIR(S0_example, I0_example, N, T=365)
44 plot_SIR(result, 'SIR Model with Vaccinations Example')
45
```

SIR Model with Vaccinations Example



Euler's Method

Solving the given system of differential equations for the SIRV model involves integrating the equations to obtain the functions $s(t)$, $i(t)$, $r(t)$, and $v(t)$ over time.

One commonly used numerical method is Euler's method. Here's a simplified Python code snippet using Euler's method to approximate the solutions: To create a graph for the given system of differential equations, we need initial conditions and specific parameter values.

$$s_{n+1} = s_n + \left(-\beta \cdot \frac{si}{N} - \gamma_v \cdot s \cdot v \right) \cdot \Delta t$$

$$i_{n+1} = i_n + \left(\beta \cdot \frac{si}{N} - \gamma \cdot i \right) \cdot \Delta t$$

$$r_{n+1} = r_n + (\gamma \cdot i) \cdot \Delta t$$

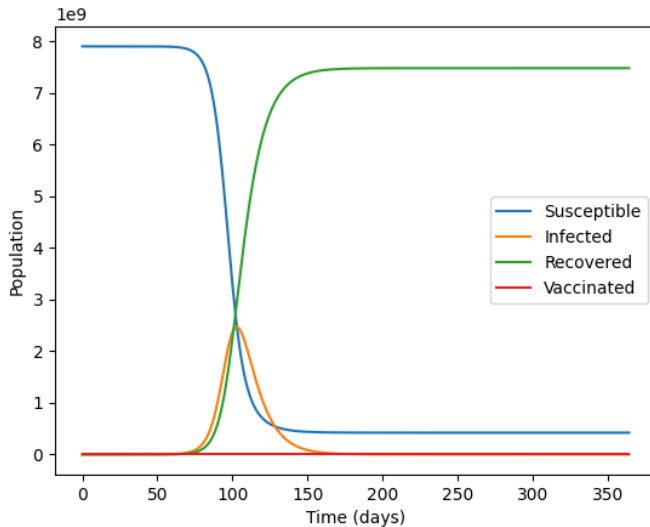
$$v_{n+1} = v_n + (\gamma_v \cdot s \cdot v) \cdot \Delta t$$

graph.py

```

1  import matplotlib.pyplot as plt
2
3  # Define parameters
4  beta = 0.3
5  gamma = 0.1
6  gamma_v = 0.05
7  N = 7_900_000_000 # Total population
8
9  # Initial conditions
10 s, i, r, v = 7_899_999_900, 100, 0, 0 # Starting with 100 infected individuals
11
12 # Time settings
13 T = 365 # Total time in days
14 dt = 1 # Time step in days
15
16 # Lists to store results
17 s_values, i_values, r_values, v_values, time_values = [], [], [], [], []
18
19 # Euler's method
20 for t in range(int(T/dt)):
21     s_values.append(s)
22     i_values.append(i)
23     r_values.append(r)
24     v_values.append(v)
25     time_values.append(t*dt)
26
27     ds = (-beta * s * i / N - gamma_v * s * v) * dt
28     di = (beta * s * i / N - gamma * i) * dt
29     dr = (gamma * i) * dt
30     dv = (gamma_v * s * v) * dt
31
32     s += ds
33     i += di
34     r += dr
35     v += dv
36
37 # Plot the results
38 plt.plot(time_values, s_values, label='Susceptible')
39 plt.plot(time_values, i_values, label='Infected')
40 plt.plot(time_values, r_values, label='Recovered')
41 plt.plot(time_values, v_values, label='Vaccinated')
42 plt.xlabel('Time (days)')
43 plt.ylabel('Population')
44 plt.legend()
45 plt.show()
46

```



Conclusion and Future Work

- The model allows us to understand how the introduction of a vaccination program affects the dynamics of the disease.
- The SIRV model helps in assessing the effectiveness of vaccination as a control measure against the spread of COVID-19.
- The SIRV model can be employed to project the long-term trends of the epidemic, considering the interplay between natural immunity, waning immunity, and the ongoing vaccination efforts.

References



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The compartmental SIRVI model

An extended epidemic model with vaccination: Weak-immune SIRVI .



Smith, David and Moore, Lang (2004)

The Differential Equation Model

The SIR Model for Spread of Disease



(2023)

Population Reference Bureau

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The End