

生醫工程概論

Introduction to BME

HW1

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1 Biochemical Reaction Network

1.1 Differential Equation Model

$$\frac{d}{dt} a(t) = k_0 - k_1 a(t) b(t)$$

$$\frac{d}{dt} b(t) = k_2 d(t) - k_1 a(t) b(t)$$

$$\frac{d}{dt} c(t) = k_1 a(t) b(t) - k_3 c(t)$$

$$\frac{d}{dt} d(t) = k_1 a(t) b(t) - k_2 d(t)$$

$$\frac{d}{dt} e(t) = k_3 c(t) - k_4 e(t)$$

$$\frac{d}{dt} f(t) = k_4 e(t) - k_5 f(t)$$

1.2 State Variables and Parameters

state variables: (vary with time)
 $a(t), b(t), c(t), d(t), e(t), f(t)$

parameters: $k_0, k_1, k_2, k_3, k_4, k_5$

2 SARS-CoV-2

2.1 Molecules Detected by the Tests

Test	Molecules
PT-PCR Test	RNA genome
Antigen Test	Antigens
Antibody Test	Antibodies

2.2 How Each Type of vaccine Triggers an Immune Response

2.2.1 Inactive whole virus

The vaccine delivers the whole virus which has been weakened or inactivated, but the virus still contains antigens to trigger the immune response.

2.2.2 Antigen proteins

The vaccine delivers only the spike protein which is made the lab, and the antigen can trigger the immune response.

2.2.3 messenger RNA (genetic instructions)

The vaccine delivers inside an artificial membrane which is similar to the cell membrane. When the messenger RNA enters the cell, ribosomes translate the mRNA into spike protein antigen, which can trigger the immune response.

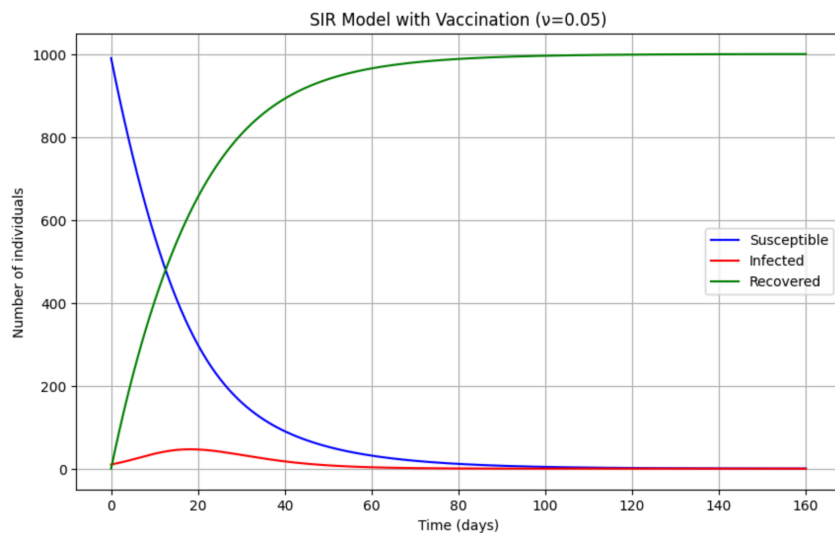
2.2.4 DNA (genetic instructions)

The vaccine delivers the spike protein DNA to trigger the immune response, using an inactivated adenovirus, which is a modified virus that can't multiply nor cause the disease.

3 SIR model extension

3.1 Solve Differential Equations

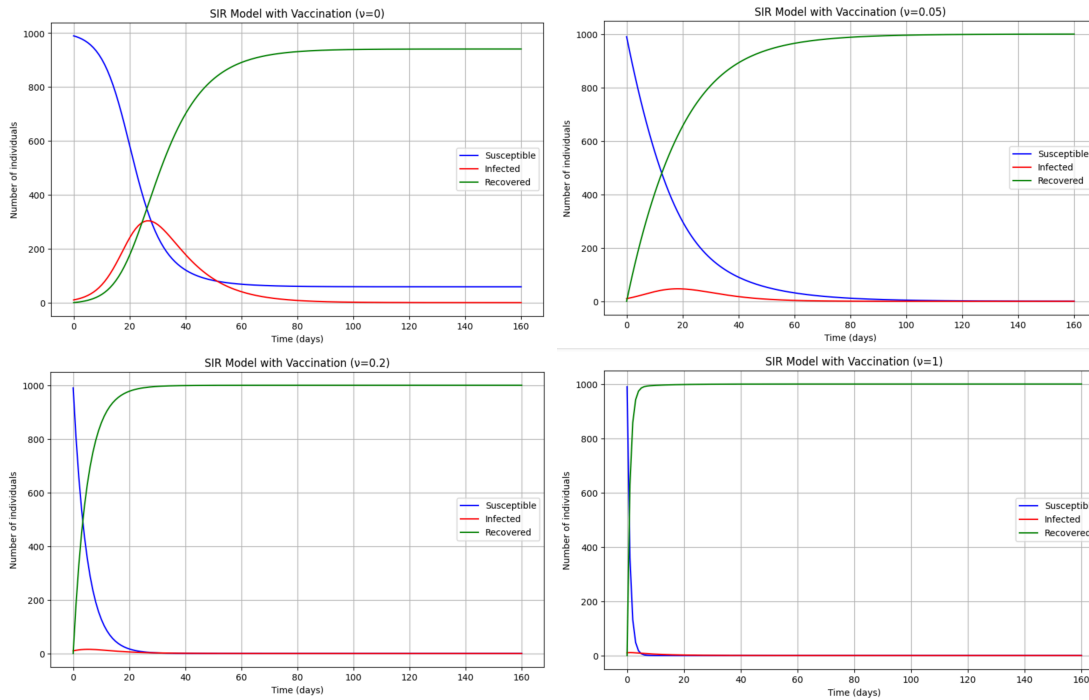
```
def sir_vaccine_model(y, t, beta, gamma, nu):  
    S, I, R = y  
    N = S + I + R  
    dS = -beta * S * I / N - nu * S  
    dI = beta * S * I / N - gamma * I  
    dR = gamma * I + nu * S  
    return [dS, dI, dR]  
  
S0 = 990 # Susceptible individuals  
I0 = 10 # Infected individuals  
R0 = 0 # Recovered individuals  
initial_conditions = [S0, I0, R0]  
beta = 0.3 # Infection rate  
gamma = 0.1 # Recovery rate  
nu = 0.05 # Vaccination rate  
  
t = np.linspace(0, 160, 160) # Time points  
  
solution = odeint(sir_vaccine_model, initial_conditions, t, args=(beta, gamma, nu))  
S, I, R = solution.T
```



3.2 Different Vaccination Rates

```
nu2 = [0, 0.05, 0.2, 0.5, 1]
```

```
for n in nu2:  
    solution = odeint(sir_vaccine_model, initial_conditions, t, args=(beta, gamma, n))  
    S, I, R = solution.T
```



According to the figures, it can be observed that the infected curve become lower as the vaccination rate increase, and the time period of being affected by the disease is also shortened.