MA 203 PROJECT

COVID-19 Epidemic Spread Modeling

Problem Statement

The COVID-19 pandemic, driven by the SARS-CoV-2 virus, has presented unprecedented challenges to global public health. Understanding the intricate dynamics of disease transmission is crucial for effective control measures. COVID-19 primarily spreads through respiratory droplets when an infected person talks, coughs, or sneezes, making close person-to-person contact a significant mode of transmission. Asymptomatic carriers, individuals who are infected but do not exhibit symptoms, contribute to the rapid and stealthy spread of the disease. Moreover, the virus has demonstrated the potential for pre-symptomatic transmission, where individuals can spread the virus before showing symptoms, emphasizing the significance of effective contact tracking and timely interventions.

The incubation period, which normally lasts between 2 and 14 days, adds a layer of complexity to disease modeling. During this period, individuals may be exposed and become infected yet remain asymptomatic or in the latent phase. In order to reduce transmission, quarantine measures, such as isolating infected individuals, are essential. Additionally, global vaccination efforts are altering the dynamics of COVID-19 spread by reducing susceptibility and the severity of the disease.

The SEQIR (Susceptible-Exposed-Quarantined-Infected-Removed) model, incorporating exposed and quarantined compartments, offers a more nuanced perspective on the disease's spread. This research delves into the development and analysis of a specific SEQIR mathematical model tailored to COVID-19 transmission dynamics. It encompasses understanding the latent period, quarantine measures, and recovery dynamics.

Utilizing the SEQIR framework accurately is pivotal for grasping COVID-19 transmission dynamics. This knowledge is critical for guiding public health policies, refining quarantine strategies, and evaluating vaccination efforts. By providing insights into the interaction between exposed, quarantined, and infectious populations, this research aims to facilitate the development of precise interventions to mitigate the pandemic's impact effectively.

While traditional SEIR models have been valuable, the SEQIR model's potential in accounting for quarantined individuals and latent periods, especially in the context of COVID-19, remains underexplored. Existing studies often oversimplify these complexities, hampering accurate predictions of disease spread. A more nuanced approach is necessary, considering real-world scenarios and the evolving nature of the virus.

This project aims to create a comprehensive SEQIR model specifically designed for COVID-19. The model will replicate a variety of intervention options by including accurate parameters and data. This study attempts to determine the best combinations of immunization campaigns and quarantine measures in order to evaluate the effects of these techniques on disease transmission. The goal is to provide policymakers and public health experts with practical advice for effectively managing and reducing the current pandemic.

1 Physical Model: Understanding Disease Dynamics

The SEQIR model, embodying the Susceptible-Exposed-Quarantined-Infectious-Recovered compartments, serves as a crucial physical representation of disease transmission within populations. Through this model, the intricate journey of an infectious disease unfolds, capturing individuals' states from vulnerability to recovery. This physical framework not only mirrors real-world infection pathways but also empowers researchers to predict disease spread accurately. By understanding the nuances of each compartment's transitions, we gain invaluable insights into the effectiveness of public health measures and the potential impact of interventions.

The accompanying schematic representation, tailored to the unique dynamics of the Indian context, offers a visual narrative of COVID-19's journey through communities.

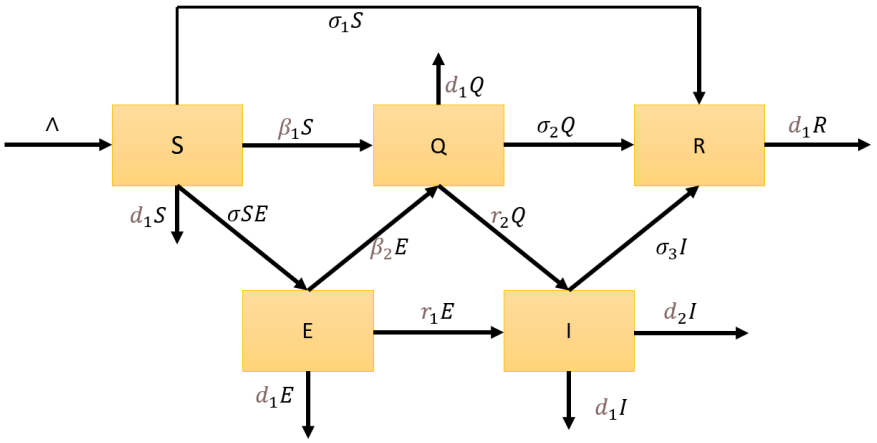


Figure-1: Schematic representation of SEQIR model

In this physical model, the population is divided into five distinct compartments: Susceptible (S), Exposed (E), Quarantined (Q), Infectious (I), and Recovered (R). The "Susceptible" compartment represents individuals who are vulnerable to the disease and can contract it upon exposure. Once exposed, individuals move to the "Exposed" compartment, signifying the latent period during which they are infected but not yet infectious. From the "Exposed" state, individuals can transition to the "Quarantined" compartment, representing those isolated due to potential exposure or symptoms. The "Infectious" compartment includes individuals capable of transmitting the disease to others. Finally, the "Recovered" compartment comprises individuals who have overcome the disease and gained immunity or, in some cases, have been vaccinated. The movement of individuals between these compartments is governed by differential equations that consider parameters like transmission rates, recovery rates, incubation periods, and the effectiveness of quarantine measures.

This physical model is instrumental in understanding and predicting the progression of infectious diseases within a population, aiding in the design and assessment of public health strategies and interventions. Recent refinements and adaptative advancements in the SEQIR model have sharpened its accuracy, making it an indispensable tool for guiding evidence-based policies, thereby playing a pivotal role in our collective efforts to combat infectious diseases and safeguard public health.

2 Assumptions

The SEQIR model, an advanced version of classical epidemiological SIR models, incorporates extra compartments and dynamics for a more accurate representation of infectious diseases. Here are the key assumptions guiding the SEQIR model:

1. Structured Compartments: The population is divided into distinct stages: Susceptible (S), Exposed (E), Quarantined (Q), Infectious (I), and Recovered (R). People move between these stages as the disease progresses.

2. Uniform Interaction: Individuals have equal chances of encountering and transmitting the infection to others within the population. This simplifies the model and is commonly used in compartmental models.

3. Stable Population Size: The total population size remains constant throughout the simulation, excluding factors like births, deaths, and migration. This ensures a consistent population size during the study.

4. Steady Parameters: The disease progression factors, such as transmission and recovery rates, remain constant throughout the outbreak. This simplification might not perfectly match real-world scenarios where these parameters can change.

3 Governing Equations

- **Modeling of S(t):**

  Increasing the susceptible population, individuals are recruited into India at a rate denoted by Λ. This population is reduced due to natural deaths (d_1) and interactions with undetected infected individuals. Additionally, susceptibles are further diminished by constant rates σ_1 and β_1, representing transitions to quarantined and recovered states. Notably, in certain districts like Purulia, Murshidabad, Birbhum (West Bengal), Gaya, and Bhagalpur (Bihar), individuals fearful of infection due to inadequate testing and treatment facilities are immediately transferred to secure zones. Consequently, the rate of change of the susceptible population is governed by the following differential equation:

$$\frac{dS}{dt} = \Lambda - \alpha SE - \sigma_1 S - \beta_1 S - d_1 S \quad (1)$$

- **Modeling of E(t):**

  The population of individuals infected but not detected by testing reflects those who have the virus but are not identified due to limited testing capabilities. This group increases at a rate α through interactions between susceptible and undetected infected individuals. Quarantine reduces this population at a rate of β_2, while natural deaths occur at a rate of d_1. Due to challenges in isolating these cases, they also directly decrease due to the infected population at a rate of r_1. Consequently, the rate of change of the undetected infected population is expressed by the following differential equation:

$$\frac{dE}{dt} = \alpha SE - r_1 E - \beta_2 E - d_1 E \quad (2)$$

- **Modeling of Q(t):**

  The incubation period for COVID-19 spans 2 to 14 days, a crucial phase for disease transmission. To curb the virus's spread, individuals must be isolated from both susceptible and undetected infected individuals for 14 days. This isolated group is termed the 'quarantined' population. Quarantined individuals increase due to β_1 from susceptibles and β_2 from undetected infected individuals. This population decreases due to r_2 (infected) and σ_2 (secured zone) while also experiencing natural deaths at rate d_1. Therefore, the rate of change of the quarantined population is represented by the following equation:

$$\frac{dQ}{dt} = \beta_1 S + \beta_2 E - r_2 Q - \sigma_2 Q - d_1 Q \quad (3)$$

- **Modeling of I(t):**

  The population of individuals confirmed positive for COVID-19 through testing increases due to two sources: firstly, from those previously undetected (at a rate denoted by r_1) - individuals who may have been infected but were not identified earlier. This group, having contracted the virus, subsequently tests positive and directly enters the infected population. Secondly, the infected population is augmented at a rate of r_2 from the quarantined group, as is the norm.

  The infected population diminishes due to two factors: firstly, at a rate σ_3, representing recoveries, and secondly, at a rate d1 due to natural deaths. To add realism, we introduce a parameter d_2 to account for deaths specifically caused by the infection. Therefore, the rate of change of the infected population is described by the following differential equation:

$$\frac{dI}{dt} = r_1 E + r_2 Q - \sigma_3 I - d_1 I - d_2 I \quad (4)$$

- **Modeling of R(t):**

  We assume that individuals in the susceptible, quarantine and infected states recover from the disease at rates σ_1, σ_2, and σ_3, respectively, and subsequently move to the secure zone population. This secure zone population, while being affected by natural deaths at a rate of d_1, remains unaffected by the presence of the COVID-19 virus. Consequently, the rate of change of the secure zone population is described by the following differential equation:

$$\frac{dR}{dt} = \sigma_1 S + \sigma_2 Q - \sigma_3 I - d_1 R \quad (5)$$

- Combining equations (1) to (5), our desired model structure can be expressed as follows:

$$\frac{dS}{dt} = \Lambda - \alpha SE - \sigma_1 S - \beta_1 S - d_1 S$$

$$\frac{dE}{dt} = \alpha SE - r_1 E - \beta_2 E - d_1 E$$

$$\frac{dQ}{dt} = \beta_1 S + \beta_2 E - r_2 Q - \sigma_2 Q - d_1 Q$$

$$\frac{dI}{dt} = r_1 E + r_2 Q - \sigma_3 I - d_1 I - d_2 I$$

$$\frac{dR}{dt} = \sigma_1 S + \sigma_2 Q - \sigma_3 I - d_1 R$$

with initial densities: S(0)>0, E(0)≥0, I(0)≥0, Q(0)≥0, R(0)>0

4 Influential factors in SEQIR

1. **Recruitment Rate (Λ)**: This represents the number of new susceptible individuals entering the population. A higher Λ means more new people, increasing the risk of virus spread.
2. **Interaction Rates (α, β_1, β_2, r_1, r_2, σ_1, σ_2, σ_3)**: These rates determine how quickly people move between different states like being exposed, quarantined, infected, and recovered. For example, α shows how fast people get exposed, and σ_3 indicates the recovery rate for infected individuals.
3. **Natural Death Rate (d_1)**: This represents the rate at which people naturally pass away. It impacts the population in all compartments, reducing their numbers over time.
4. **Secure Zone Transfers**: Individuals may move to safer areas, reducing the susceptible and quarantined populations in certain places.
5. **Infection-Related Death Rate (d_2)**: This parameter signifies the rate at which people die directly due to the infection, specifically impacting the infected compartment.
6. **Incubation Period ($\frac{1}{\alpha}$)**: It represents the average time it takes for exposed individuals to become infected, influencing the transition from the exposed to the infected state.
7. **Quarantine Effectiveness (β_2, r_2, σ_2)**: These rates determine how well quarantine measures work. For instance, β_2 shows how fast undetected infected people move to quarantine, r_2 indicates how quickly quarantined people return to being infected, and σ_2 demonstrates the rate at which people in quarantine recover.

5 Parameters

5.1 Values of the parameter of the model for the state Maharashtra

Parameters	**Values**
Λ	3300
α	2.1×10^{-9}
β_1	4×10^{-7}
β_2	5×10^{-3}

σ_1	5×10^{-4}
σ_2	0.1
σ_3	5×10^{-3}
r_1	0.04
r_2	2×10^{-3}
d_1	1.5×10^{-5}
d_2	3.2×10^{-3}

5.2 Initial Conditions

S(0) = 75×10^6

E(0) = 225

Q(0) = 800

I(0) = 58

R(0) = 3×10^7

6 Solution Methodology

In the context of our model, which involves solving a system of ordinary differential equations (ODEs) to simulate the dynamics of the compartments (S, E, Q, I, R), we employed the 4th order Runge-Kutta method because this is widely used numerical technique which is instrumental in approximating the solutions of ODEs accurately.

To initiate the process, we set the initial conditions for each compartment and selected a suitable step size h, to define the intervals between calculations. The ODEs, representing transitions between compartments, were broken down into smaller steps. At each step, we calculated four approximations k_1, k_2, k_3, and k_4, based on the current state of the compartments.

These approximations were then combined using specific weights, as per the Runge-Kutta formula:

$$y_{n+1} = y_n + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4)$$

Here, y_{n+1} represents the next approximation of the compartment populations, and y_n is the current state. This process was iteratively applied, updating the time t at each step until

reaching the desired simulation duration.

By employing the 4th-order Runge-Kutta method, we ensured that the solutions to the ODEs governing the model were calculated with high accuracy, allowing for a detailed and precise understanding of the disease dynamics within the population. This methodological approach was pivotal in generating reliable results for the compartments' behavior over time, contributing significantly to the insights gained from the model.

7 Analytical solution for epidemic spread

In our SEQIR model for COVID-19, deriving a closed-form analytical solution is highly challenging due to the intricate nature of the model. The complexity arises from the interactions between various compartments (S, E, Q, I, R) and the impact of interventions like quarantine and vaccination. Analytical solutions work well for simple models but struggle with the complexity of our SEQIR framework for COVID-19 due to intricate interactions between compartments and interventions.

Numerical methods like the Runge-Kutta method, Euler's method, and other advanced numerical techniques are commonly used to solve the SEQIR model and obtain more practical and accurate results. These methods discretize the differential equations governing the transitions between compartments, allowing us to obtain precise numerical approximations of the populations in each compartment over time. Utilizing numerical methods allows us to understand the complex interactions in our SEQIR model and gain precise insights into COVID-19's spread.

8 Numerical Solution

Here, we utilize a multi-step approach to estimate the changes in each compartment (S, E, Q, I, R) over a given time of step-size h.

Firstly, we calculate preliminary values ($k_1s, k_1e, k_1q, k_1i, k_1r$) based on the current state of the compartments. These values represent the rate of change in each compartment considering the initial conditions and the specified time step.

$$k_1 s = \frac{dS}{dt}(S, E, Q, I, R) * h$$

$$k_1 e = \frac{dE}{dt}(S, E, Q, I, R) * h$$

$$k_1 q = \frac{dQ}{dt}(S, E, Q, I, R) * h$$

$$k_1 i = \frac{dI}{dt}(S, E, Q, I, R) * h$$

$$k_1 r = \frac{dR}{dt}(S, E, Q, I, R) * h$$

Subsequently, using the updated compartments obtained from k_1 values, we compute intermediate values $(k_2s, k_2e, k_2q, k_2i, k_2r)$. These values provide a more refined estimation of how the compartments evolve over time.

$$k_2s = \frac{dS}{dt}(S + 0.5k_1s,\ E + 0.5k_1e,\ Q + 0.5k_1q,\ I + 0.5k_1i,\ R + 0.5k_1r) * h$$

$$k_2e = \frac{dE}{dt}(S + 0.5k_1s,\ E + 0.5k_1e,\ Q + 0.5k_1q,\ I + 0.5k_1i,\ R + 0.5k_1r) * h$$

$$k_2q = \frac{dQ}{dt}(S + 0.5k_1s,\ E + 0.5k_1e,\ Q + 0.5k_1q,\ I + 0.5k_1i,\ R + 0.5k_1r) * h$$

$$k_2i = \frac{dI}{dt}(S + 0.5k_1s,\ E + 0.5k_1e,\ Q + 0.5k_1q,\ I + 0.5k_1i,\ R + 0.5k_1r) * h$$

$$k_2r = \frac{dR}{dt}(S + 0.5k_1s,\ E + 0.5k_1e,\ Q + 0.5k_1q,\ I + 0.5k_1i,\ R + 0.5k_1r) * h$$

Similarly, we will calculate k_3 values for each compartment.

$$k_3s = \frac{dS}{dt}(S + 0.5k_2s,\ E + 0.5k_2e,\ Q + 0.5k_2q,\ I + 0.5k_2i,\ R + 0.5k_2r) * h$$

$$k_3e = \frac{dE}{dt}(S + 0.5k_2s,\ E + 0.5k_2e,\ Q + 0.5k_2q,\ I + 0.5k_2i,\ R + 0.5k_2r) * h$$

$$k_3q = \frac{dQ}{dt}(S + 0.5k_2s,\ E + 0.5k_2e,\ Q + 0.5k_2q,\ I + 0.5k_2i,\ R + 0.5k_2r) * h$$

$$k_3i = \frac{dI}{dt}(S + 0.5k_2s,\ E + 0.5k_2e,\ Q + 0.5k_2q,\ I + 0.5k_2i,\ R + 0.5k_2r) * h$$

$$k_3r = \frac{dR}{dt}(S + 0.5k_2s,\ E + 0.5k_2e,\ Q + 0.5k_2q,\ I + 0.5k_2i,\ R + 0.5k_2r) * h$$

Finally, we determine the final intermediate values i.e. k_4 values

$$k_4s = \frac{dS}{dt}(S + k_3s,\ E + k_3e,\ Q + k_3q,\ I + k_3i,\ R + k_3r) * h$$

$$k_4e = \frac{dE}{dt}(S + k_3s,\ E + k_3e,\ Q + k_3q,\ I + k_3i,\ R + k_3r) * h$$

$$k_4q = \frac{dQ}{dt}(S + k_3s,\ E + k_3e,\ Q + k_3q,\ I + k_3i,\ R + k_3r) * h$$

$$k_4i = \frac{dI}{dt}(S + k_3s,\ E + k_3e,\ Q + k_3q,\ I + k_3i,\ R + k_3r) * h$$

$$k_4r = \frac{dR}{dt}(S + k_3s,\ E + k_3e,\ Q + k_3q,\ I + k_3i,\ R + k_3r) * h$$

Using these intermediate values, we compute the changes in each compartment for the next

time step. By breaking down the process into these distinct steps, we can accurately approximate the progression of the disease within the population over multiple time intervals.

$$S_{i+1} = S_i + \frac{1}{6}(k_1 s + 2k_2 s + 2k_3 s + k_4 s)$$

$$E_{i+1} = E_i + \frac{1}{6}(k_1 e + 2k_2 e + 2k_3 e + k_4 e)$$

$$Q_{i+1} = Q_i + \frac{1}{6}(k_1 q + 2k_2 q + 2k_3 q + k_4 q)$$

$$I_{i+1} = I_i + \frac{1}{6}(k_1 i + 2k_2 i + 2k_3 i + k_4 i)$$

$$R_{i+1} = R_i + \frac{1}{6}(k_1 r + 2k_2 r + 2k_3 r + k_4 r)$$

9 Algorithm Used

The Runge-Kutta method is a popular numerical method used to solve ordinary differential equations (ODEs). It approximates the solution by breaking down the problem into smaller steps. The 4th-order Runge-Kutta method is one of the most widely used versions. Here's a general outline of the 4th-order Runge-Kutta algorithm:

Let's consider a first-order ordinary differential equation $y'(t) = f(t, y(t))$, where $y(t)$ is the unknown function.

1. Initialization:
    - Set the initial value y_0 at t_0, i.e., $y(t_0) = y_0$.
    - Choose a step size h (the size of the time step).
2. Iterative Process:
    - For each time step, calculate the four approximations:

      $k_1 = h \cdot f(t_n, y_n)$

      $k_2 = h \cdot f(t_n + \frac{h}{2}, y_n + \frac{k_1}{2})$

      $k_3 = h \cdot f(t_n + \frac{h}{2}, y_n + \frac{k_2}{2})$

      $k_4 = h \cdot f(t_n + h, y_n + k_3)$
3. Weighted Sum for the Next Value:
    - Compute the weighted sum to get the next approximation:

$$y_{n+1} = y_n + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4)$$

- Update the time:

$$t_{n+1} = t_n + h$$

4. Repeat:

   - Repeat steps 2 and 3 for the desired number of time steps or until you reach the desired end time.

The 4th-order Runge-Kutta method improves accuracy by considering four approximations for each step. It's widely used due to its balance between accuracy and computational efficiency.

For different or higher-order Runge-Kutta methods, the process is similar but involves additional approximations and calculations to achieve higher accuracy.

10 Python programs for numerical computation

```
Λ = 3300
alpha = 0.0000000021
β1 = 4e-7
β2 = 0.005
sigma1 = 0.0005
sigma2 = 0.1
sigma3 = 0.005
r1 = 0.04
r2 = 0.002
d1 = 0.000015
d2 = 0.0032

# Initialize variables with initial conditions
S = 75000000
E = 225
Q = 800
I = 58
R = 30000000
t=0

delta_t = 0.1  # Time step (day)
T = 60    # Total duration of the simulation

def ds_dt(S, E, Q, I, R):
    return Λ - alpha * S * E - sigma1 * S - β1 * S - d1 * S

def de_dt(S, E, Q, I, R):
    return alpha * S * E - r1 * E - β2 * E - d1 * E

def dq_dt(S, E, Q, I, R):
    return β1 * S + β2 * E - r2 * Q - sigma2 * Q - d1 * Q

def di_dt(S, E, Q, I, R):
    return r1 * E + r2 * Q - sigma3 * I - d1 * I - d2 * I

def dr_dt(S, E, Q, I, R):
    return sigma1 * S + sigma2 * Q + sigma3 * I - d1 * R
```

```
def runge_kutta_step(S, E, Q, I, R, h):
    k1s = ds_dt(S, E, Q, I, R) * h
    k1e = de_dt(S, E, Q, I, R) * h
    k1q = dq_dt(S, E, Q, I, R) * h
    k1i = di_dt(S, E, Q, I, R) * h
    k1r = dr_dt(S, E, Q, I, R) * h

    k2s = ds_dt(S + 0.5 * k1s, E + 0.5 * k1e, Q + 0.5 * k1q, I + 0.5 * k1i, R + 0.5 * k1r) * h
    k2e = de_dt(S + 0.5 * k1s, E + 0.5 * k1e, Q + 0.5 * k1q, I + 0.5 * k1i, R + 0.5 * k1r) * h
    k2q = dq_dt(S + 0.5 * k1s, E + 0.5 * k1e, Q + 0.5 * k1q, I + 0.5 * k1i, R + 0.5 * k1r) * h
    k2i = di_dt(S + 0.5 * k1s, E + 0.5 * k1e, Q + 0.5 * k1q, I + 0.5 * k1i, R + 0.5 * k1r) * h
    k2r = dr_dt(S + 0.5 * k1s, E + 0.5 * k1e, Q + 0.5 * k1q, I + 0.5 * k1i, R + 0.5 * k1r) * h

    k3s = ds_dt(S + 0.5 * k2s, E + 0.5 * k2e, Q + 0.5 * k2q, I + 0.5 * k2i, R + 0.5 * k2r) * h
    k3e = de_dt(S + 0.5 * k2s, E + 0.5 * k2e, Q + 0.5 * k2q, I + 0.5 * k2i, R + 0.5 * k2r) * h
    k3q = dq_dt(S + 0.5 * k2s, E + 0.5 * k2e, Q + 0.5 * k2q, I + 0.5 * k2i, R + 0.5 * k2r) * h
    k3i = di_dt(S + 0.5 * k2s, E + 0.5 * k2e, Q + 0.5 * k2q, I + 0.5 * k2i, R + 0.5 * k2r) * h
    k3r = dr_dt(S + 0.5 * k2s, E + 0.5 * k2e, Q + 0.5 * k2q, I + 0.5 * k2i, R + 0.5 * k2r) * h

    k4s = ds_dt(S + k3s, E + k3e, Q + k3q, I + k3i, R + k3r) * h
    k4e = de_dt(S + k3s, E + k3e, Q + k3q, I + k3i, R + k3r) * h
    k4q = dq_dt(S + k3s, E + k3e, Q + k3q, I + k3i, R + k3r) * h
    k4i = di_dt(S + k3s, E + k3e, Q + k3q, I + k3i, R + k3r) * h
    k4r = dr_dt(S + k3s, E + k3e, Q + k3q, I + k3i, R + k3r) * h

    S += (k1s + 2 * k2s + 2 * k3s + k4s) / 6
    E += (k1e + 2 * k2e + 2 * k3e + k4e) / 6
    Q += (k1q + 2 * k2q + 2 * k3q + k4q) / 6
    I += (k1i + 2 * k2i + 2 * k3i + k4i) / 6
    R += (k1r + 2 * k2r + 2 * k3r + k4r) / 6

    return S, E, Q, I, R
```

```
import matplotlib.pyplot as plt

# Lists to store the values
time_steps = []
susceptible_values = []
exposed_values = []
quarantined_values = []
infected_values = []
recovered_values = []

# Main simulation loop
while t < T:
    time_steps.append(t)
    susceptible_values.append(S)
    exposed_values.append(E)
    quarantined_values.append(Q)
    infected_values.append(I)
    recovered_values.append(R)

    S, E, Q, I, R = runge_kutta_step(S, E, Q, I, R, delta_t)
    t += delta_t
```

```
# Plotting the graphs
plt.figure(figsize=(10, 6))
plt.plot(time_steps, susceptible_values, label='Susceptible', color='blue')
plt.xlabel('Time')
plt.ylabel('Population')
plt.title('Maharashtra')
plt.legend()
plt.show()
plt.plot(time_steps, exposed_values, label='Exposed', color='orange')
plt.xlabel('Time')
plt.ylabel('Population')
plt.title('Maharashtra')
plt.legend()
plt.show()
plt.plot(time_steps, quarantined_values, label='Quarantined', color='green')
plt.xlabel('Time')
plt.ylabel('Population')
plt.title('Maharashtra')
plt.legend()
plt.show()
plt.plot(time_steps, infected_values, label='Infected', color='red')
plt.xlabel('Time')
plt.ylabel('Population')
plt.title('Maharashtra')
plt.legend()
plt.show()
plt.plot(time_steps, recovered_values, label='Recovered', color='purple')
plt.xlabel('Time')
plt.ylabel('Population')
plt.title('Maharashtra')
plt.legend()
plt.show()
```

These are the snippets of the code in Python programming language that facilitated the computation of the complex ordinary differential equations of the SEQIR model.

11 Results and Discussion

1.

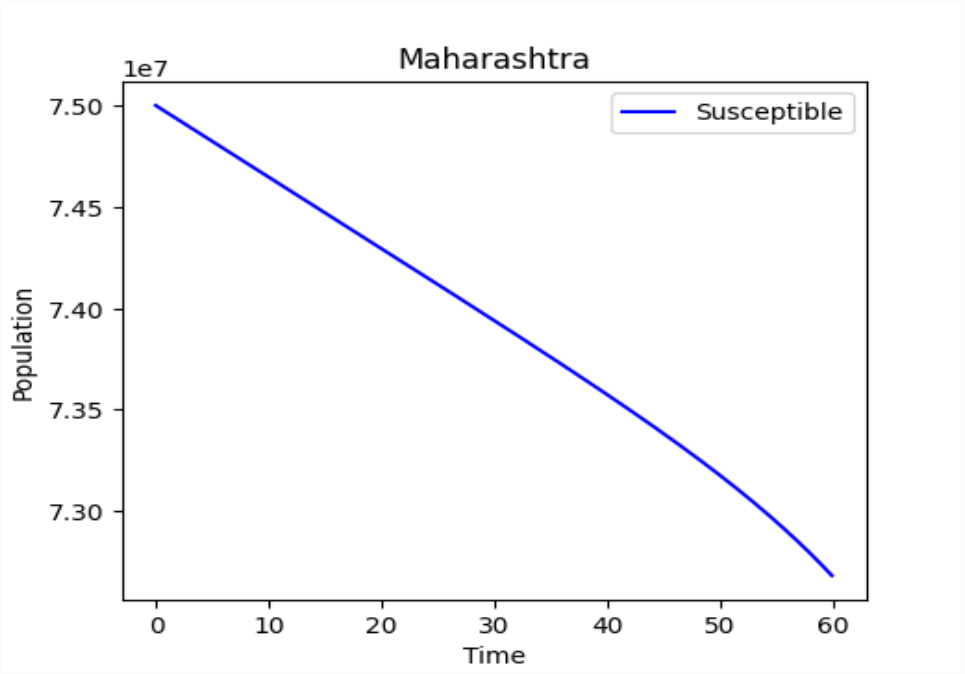


Figure 2: Susceptible population with time

As we can see in the graph, the susceptibility ($S(t)$) typically decreases as people get exposed to the disease. As the epidemic progresses, $S(t)$ approaches a minimum value but does not stabilize or increase.

2.

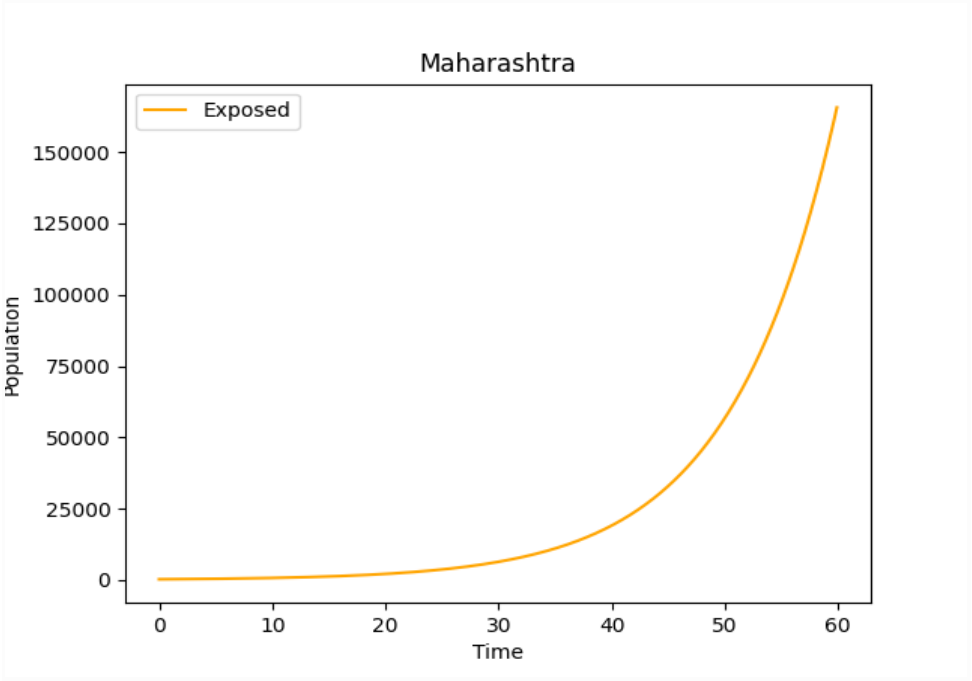


Figure-3: Exposed population with time

In Figure (2), The exposure ($E(t)$) represents the number of individuals who have been exposed to the disease but are not yet infectious. It is expected to increase as people come into contact with infectious individuals.

3.

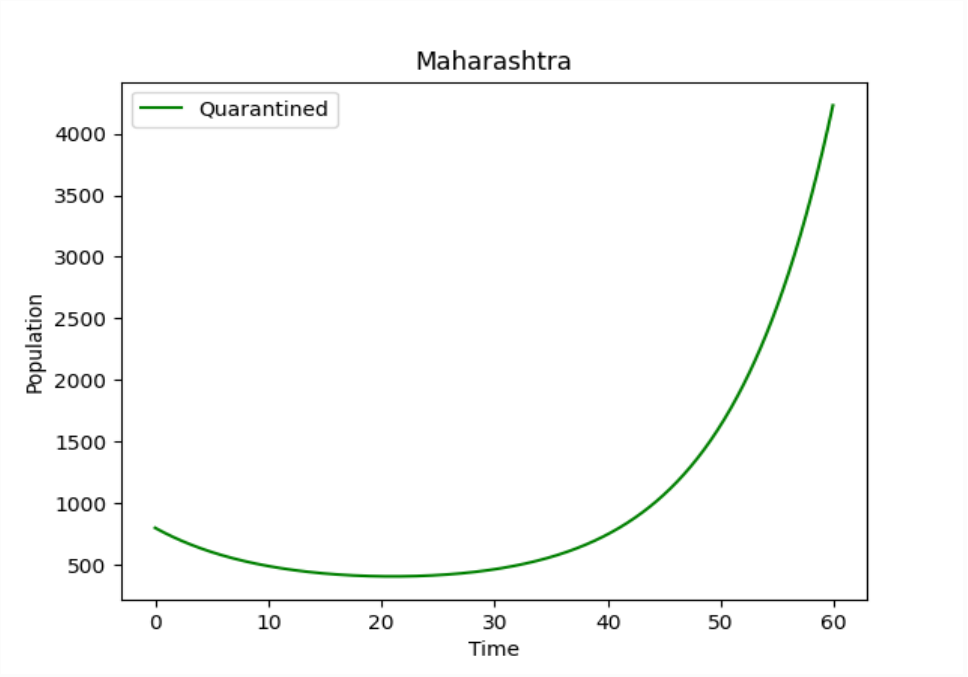


Figure-4: Quarantined population with time

In Figure (3), the initial slight decrease in the population under quarantine might indicate a relaxation of measures or a decline in compliance. The subsequent increase could signify a rapid escalation due to a resurgence of cases or a reactive response to a new wave of infections.

4.

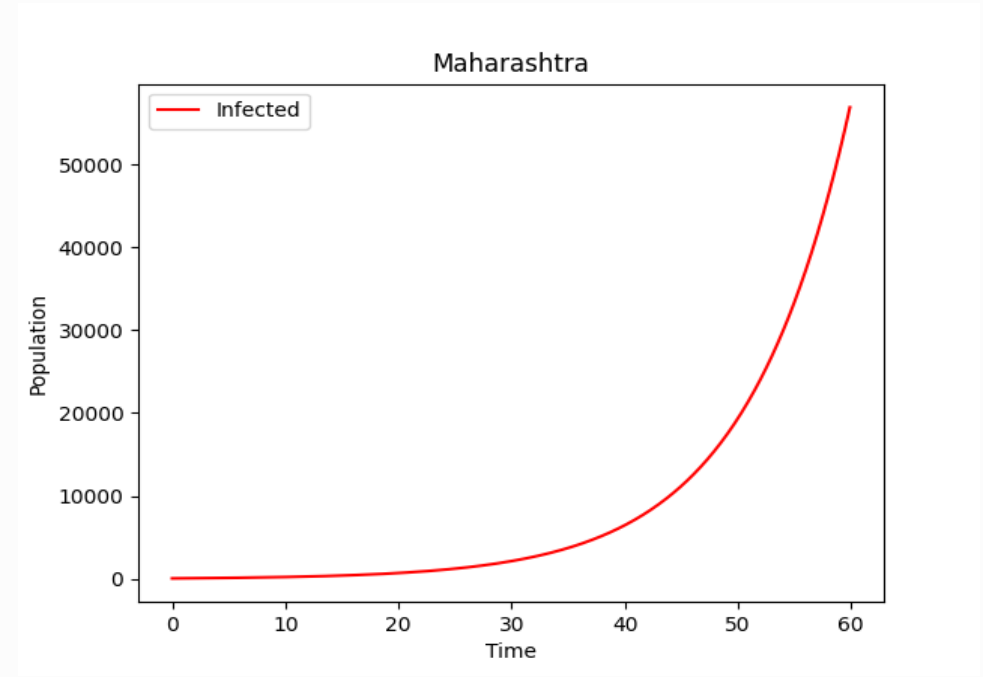


Figure-5: Infected population with time

In Figure (4), Infections initially remain constant and then increase could result from effective early control measures and stringent healthcare protocols. epidemics generally exhibit an initial rise in infections before public health responses can stabilize or mitigate the spread.

5.

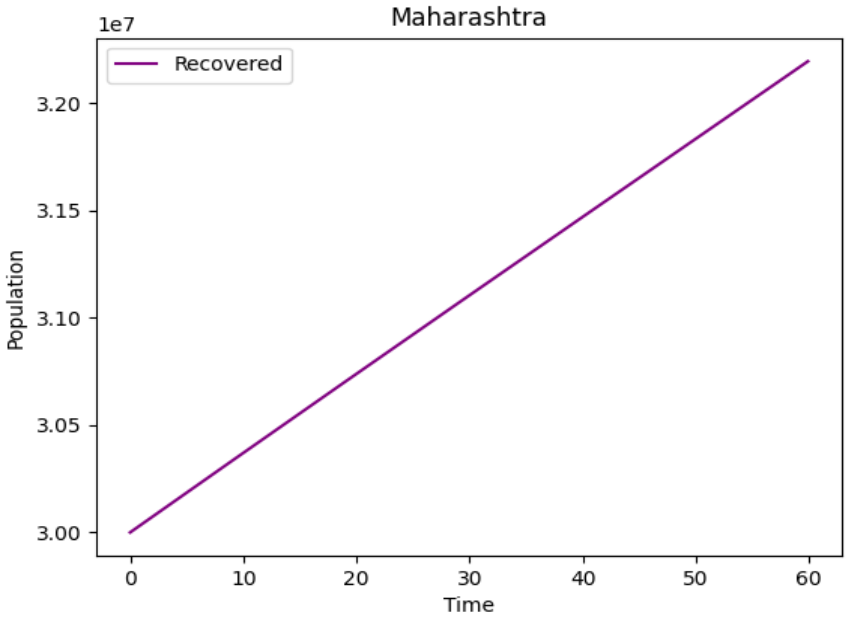
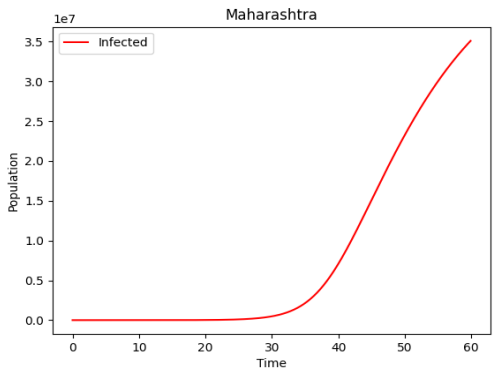


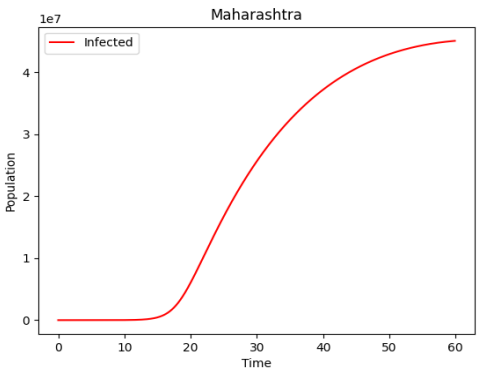
Figure-6: Recovered population with time

In Figure (5), Recovery increases linearly due to effective healthcare and treatments. As the healthcare system improves or treatments become more efficient, a subsequent increase in recoveries occurs, reflecting enhanced recovery rates and better patient outcomes. This pattern signifies a progression from early stabilization to later optimization of recovery efforts.

6.



$\alpha=5 \times 10^{-9}$

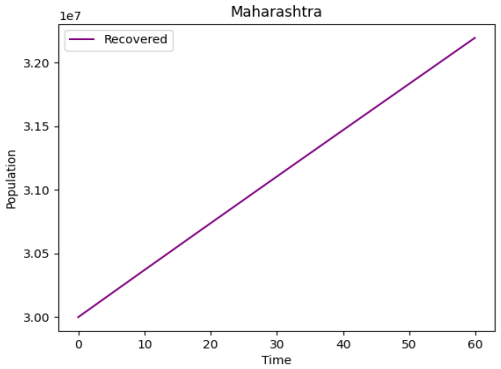


$\alpha=1 \times 10^{-8}$

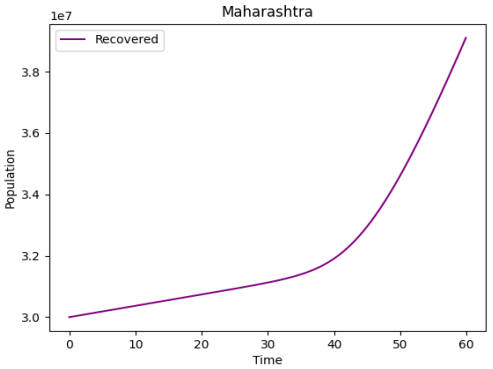
α is the transmission rate from the susceptible population to the infected but not detected by the testing population.

We have analyzed the influence of the α parameter on the infected population by keeping the other parameters constant. We observed that by increasing the α, the population infected by the disease also increases.

7.



σ_3=0.005



σ_3=0.01

σ_3 is the transmission rate from the quarantine population to the secured zone population.

When we scrutinize the graphs of recovered population with time, we can infer that as the σ_3 is increasing while the other parameters are constant, the number of recovered population increases. It can also be seen that there is a sudden steep rise in recovery after the population recovered exceeds 3.2×10^7.

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