

# Mathematical Modeling of SIR Network Diseases Model

Project Seminar

Guided By:

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Mathematical Modeling, Simulation and Optimization

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# Declaration

We sincerely affirm that the project seminar report entitled "Mathematical Modeling of SIR Network Disease Model" is an original and distinctive outcome of our work. Under the careful supervision of Dr. Moritz Schäfer, this report has been prepared. This report presents concepts, ideas, and phrases that are the result of our intellectual work. When we have used ideas or concepts from external sources, we have made sure to properly credit and cite the source of the information. This report, which is turned in to meet our project seminar's academic criteria, is a true testimony of our comprehension, dedication, and diligence to the topic.

Date: 6 March 2024

# Acknowledgment

The accomplishment of this project seminar needed a great deal of direction and support from several sources. Having this all along after our project seminar is over makes us feel immensely fortunate. Our accomplishments are solely a result of their guidance and support, for which we will always be grateful. We are happy to distribute this study on the SIR model of Network Disease Model. Above all, we thank God Almighty for all the benefits we have experienced during our seminar work. We are very grateful to our esteemed mentor, Dr. Moritz Schäfer, for his essential guidance, outstanding mentoring, and unwavering inspiration during the project. Finally, we would like to thank everyone who helped and encouraged us during the project seminar, including our family and friends.

# Abstract

Transportation among regions is one of the main factors which affect the outbreak of diseases. In this study mathematical model is proposed to demonstrate the dynamics of the Network between three regions as Western Region, Central Region, and Eastern Region of Sri Lanka, particularly for infectious diseases, aiming to identify scenarios necessitating the Lockdown situation for effective disease control. The research modifies the classic SIR model by implementing the complete lockdown in individuals and explores the variability of peak levels of COVID-19. Key analyses include developing an equation of each region with considering a mobility rate[8] and simulation of the model with and without considering mobility. Moreover, Compare the results of infected cases with the given data. Results reveal that, In the beginning stage, the disease was mainly concentrated in the Western region, and with time, it spread to another region[11]. However, very less numbers of patients were identified in the Central and Eastern region, until March 2021. The peak of COVID-19 occurred in December and February 2021 in all provinces in Sri Lanka<sup>1</sup>.

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<sup>1</sup><https://www.reuters.com/graphics/world-coronavirus-tracker-and-maps/countries-and-territories/sri-lanka/>

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# Chapter 1

## Introduction

In this modern age, pandemics are not a rare phenomenon, presently management of infectious illnesses has been a serious concern. Infectious illnesses have resulted in enormous sickness, fatalities, and societal destruction, from dreadful pandemics to neighborhood outbreaks. Since the declaration of COVID-19 as a pandemic in March 2020, various measures aimed at containing the disease, such as enforcing physical distancing, have been implemented by governmental authorities worldwide. Here, we used data of infected cases during the Covid 19 from Srilanka including multiple cities of different regions such as Western, Central, and Eastern Region based on the data which is provided by Dr. Moritz Schäfer to determine the relationship of lock-downs relative to the first appearance of COVID-19 and the trajectory of COVID-19 spread in different region[6].

## Chapter 2

### SIR Network Model

The Kermack and McKendrick-developed SIR epidemiology model serves as the basis for the SIR model<sup>1</sup> employed in this investigation[2]. This model divides the population into three separate subgroups: Susceptible (S), Infected (I), and Recovered (R), while assuming constant birth and death rates. People who are susceptible (S) are at risk of infection but have not yet developed the illness. Recovered people (R) have already contracted the disease but have made a full recovery. Those who are infected (I) have the illness and run the risk of passing it on to other people. The diagram below illustrates the flow of the SIR model.

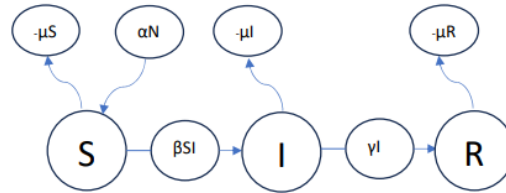


Figure 2.1: SIR Flow Diagram

The subsequent set of differential equations defines the fundamental SIR model.

$$\begin{aligned}\dot{S} &= \frac{dS}{dt} = \alpha N - \beta SI - \mu S \\ \dot{I} &= \frac{dI}{dt} = \beta SI - \mu I - \gamma I \\ \dot{R} &= \frac{dR}{dt} = \gamma I - \mu R\end{aligned}\tag{2.1}$$

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<sup>1</sup><https://maa.org/press/periodicals/loci/joma/the-sir-model-for-spread-of-disease-the-differential-equation-model>



Our goal is to examine the dynamics of an expanded SIR model that includes a mobility<sup>2</sup> network between multiple regions, such as the Western, Central, and Eastern regions of Sri Lanka. This model represents the spread of infectious diseases in different geographical regions that are connected by human movement of any kind, implying that individuals afflicted with a disease can spread it from one region to another through travel. This enhancement leads to the SIR Network model, built upon the original SIR framework. To overcome this situation government of Sri Lanka should initiate some defensive strategies for example by preventing individuals from leaving the borders of areas where there is a high danger of infection and from entering areas that are strictly regulated or have very low rates of infection. The model is assumed to have the conditions of constant population size( $N$ ). The following Figure Figure 2.2 shows a flow diagram of the SIR Network model.

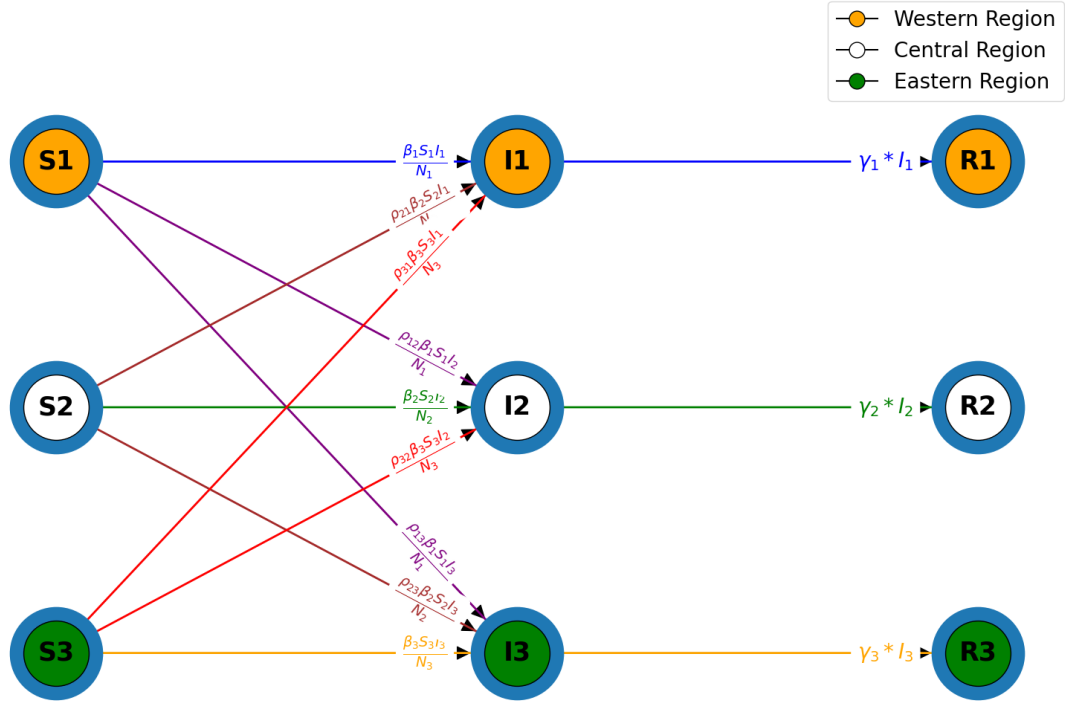


Figure 2.2: SIR Network Flow Diagram

The number of infected individuals in the population increases when individuals from the infected class come into contact with those from the susceptible class at rate  $\frac{\beta_i S_i I_i}{N_i}$ . Simultaneously, infected individuals recover from the infected class at a rate represented by  $\gamma_i I_i$ . The size of the infected class is influenced by individuals from the susceptible got infected when they come in contact with infected people while traveling from the other regions at a rate denoted by  $\frac{\rho_{ij} \beta_i S_i I_i}{N_i}$ . In our model, we only consider the movement of susceptible people while they traveling at a rate of  $\rho_{ij}$ . Reduction in population size in each region depends on the rate of mobility and transmission rate while traveling from one region to another region.

<sup>2</sup><https://link.springer.com/article/10.1007/s13278-021-00814-3>

## 2.1 Model Formulation

As per the given data, we made a region based on the nearby cities and geographic locations of Sri Lanka<sup>3</sup>. For example, Western region (Colombo, Gampaha, Kalutara, Matara, Ratnapura, Galle, Kegalle districts) where the population density is very high. With time, it spread to other districts. However, very low numbers of patients were identified in the Eastern Region (Mannar, Mullaitivu, Vavuniya, Kurunegala, Puttalam, Kilinochchi, Trincomalee, Anuradhapura, Jaffna) and Central region (Kandy, Polonnaruwa, Moneragala, Kalmunai, Ampara, Badulla, Batticaloa, Hambantota, Nuwara Eliya)[7]. This study shows in Sri Lanka with the increase in the transportation system among cities, the mass movement of a large number of people opens new gates for the spread and establishment of common or novel infectious diseases. Transportation between cities is found to be one of the main factors which affect the outbreak of diseases. COVID-19 spreads when people come in contact with others. A range of factors play a role including human mobility between the cities using public transport including buses, trains, air, etc. Thus, transportation among cities affects the disease dynamics and it motivates us to construct this mathematical model.

A mathematical model gives a true balance between complexities in the assumptions and simplicity within the formulation. The total population of each city  $N_i$  ( $i = 1,2,3$ ) is divided into three compartments: susceptible ( $S_i$ ), infected ( $I_i$ ), and recovered ( $R_i$ ). Therefore, the total population of each city will be  $N_i = S_i + I_i + R_i$  where ( $i = 1,2,3$ ). Some more assumptions are as follows:

1. The disease transmission rate from the susceptible class to infected class is ( $\beta_i$ ), and populations of city  $i$  leave city  $j$  at a rate ( $\rho_{ij}$ ).
2. Disease transmission rate is denoted by ( $\rho_{ij}\beta_i$ ), as the populations of the city  $i$  travel to the city  $j$ .
3. There is no birth and death during the travels of individuals.

Based on the assumptions made and according to the schematic diagram Figure 2.2, Below are the differential equations that define the SIR Network Model[10].

1. Western Region

$$\begin{aligned}\dot{S}_1 &= \frac{dS_1}{dt} = \alpha N_1 - \frac{\beta_1 S_1 I_1}{N_1} - \frac{\rho_{12}\beta_1 S_1 I_2}{N_1} - \frac{\rho_{13}\beta_1 S_1 I_3}{N_1} - \mu S_1 \\ \dot{I}_1 &= \frac{dI_1}{dt} = \frac{\beta_1 S_1 I_1}{N_1} - \mu I_1 - \gamma_1 I_1 + \frac{\rho_{21}\beta_2 S_2 I_1}{N_2} + \frac{\rho_{31}\beta_3 S_3 I_1}{N_3} \\ \dot{R}_1 &= \frac{dR_1}{dt} = \gamma_1 I_1 - \mu R_1\end{aligned}\tag{2.2}$$

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<sup>3</sup>[https://www.researchgate.net/figure/Figure-A3-District-Map-of-Sri-Lanka\\_fig4\\_283510114](https://www.researchgate.net/figure/Figure-A3-District-Map-of-Sri-Lanka_fig4_283510114)

## 2. Central Region

$$\begin{aligned}
\dot{S}_2 &= \frac{dS_2}{dt} = \alpha N_2 - \frac{\beta_2 S_2 I_2}{N_2} - \frac{\rho_{21} \beta_2 S_2 I_1}{N_2} - \frac{\rho_{23} \beta_2 S_2 I_3}{N_2} - \mu S_2 \\
\dot{I}_2 &= \frac{dI_2}{dt} = \frac{\beta_2 S_2 I_2}{N_2} - \mu I_2 - \gamma_2 I_2 + \frac{\rho_{12} \beta_1 S_1 I_2}{N_1} + \frac{\rho_{32} \beta_3 S_3 I_2}{N_3} \\
\dot{R}_2 &= \frac{dR_2}{dt} = \gamma_2 I_2 - \mu R_2
\end{aligned} \tag{2.3}$$

## 3. Eastern Region

$$\begin{aligned}
\dot{S}_3 &= \frac{dS_3}{dt} = \alpha N_3 - \frac{\beta_3 S_3 I_3}{N_3} - \frac{\rho_{31} \beta_3 S_3 I_1}{N_3} - \frac{\rho_{32} \beta_3 S_3 I_2}{N_3} - \mu S_3 \\
\dot{I}_3 &= \frac{dI_3}{dt} = \frac{\beta_3 S_3 I_3}{N_3} - \mu I_3 - \gamma_3 I_3 + \frac{\rho_{13} \beta_1 S_1 I_3}{N_1} + \frac{\rho_{23} \beta_2 S_2 I_3}{N_2} \\
\dot{R}_3 &= \frac{dR_3}{dt} = \gamma_3 I_3 - \mu R_3
\end{aligned} \tag{2.4}$$

Since we have assumed a constant population size it can be noticed that

$$N = \sum_{i=1}^3 N_i = S_i + I_i + R_i$$

. where (i = 1,2,3).

Parameter	Meaning
$\alpha, \mu$	Human death and birth rate (average life expectancy $\approx 70$ years)
$\gamma_i$	Human recovery rate ( $\approx 2$ weeks)
$\rho_{ij}$	Rate of mobility from region i to j
$\frac{\beta_i}{N_i}$	Transmission rate between infected human and uninfected human
$N_i$	Human population size (depends on investigated region)
$N$	Total Population

Table 2.1: Meaning of Parameters

## 2.2 Data Analysis

At the beginning of the study period, we have infected cases data of Sri Lanka commencing from 14 November 2020 to 30 March 2021, which shows that the disease was mainly concentrated in the Western region (Colombo, Gampaha<sup>4</sup>, Kalutara, Matara, Ratnapura, Galle, Kegalle districts) where the population density is very high. With some period of time, it spread to other districts. However, very low numbers of patients were identified in the Eastern

<sup>4</sup>[https://opendocs.ids.ac.uk/opendocs/bitstream/handle/20.500.12413/16901/E\\_Diary\\_Full\\_Report\\_Jan-2020\\_V8-1.pdf?sequence=1&isAllowed=y](https://opendocs.ids.ac.uk/opendocs/bitstream/handle/20.500.12413/16901/E_Diary_Full_Report_Jan-2020_V8-1.pdf?sequence=1&isAllowed=y)

Region (Mannar, Mullaitivu, Vavuniya, Kurunegala, Puttalam, Kilinochchi, Trincomalee, Anuradhapura, Jaffna) and Central region (Kandy, Polonnaruwa, Moneragala, Kalmunai, Ampara, Badulla, Batticaloa, Hambantota, Nuwara Eliya) until March 2021. The following figure shows a flow diagram of the Regional Values Over Time as per the given data, where the initial infected cases of Western, Central, and Eastern regions are given by 349, 7, 93, respectively. According to the dataset, the Western, Central, and Eastern regions have total populations  $N_1 = 10,236,000$ ,  $N_2 = 5,089,000$ , and  $N_3 = 6,594,000$ , respectively[1].

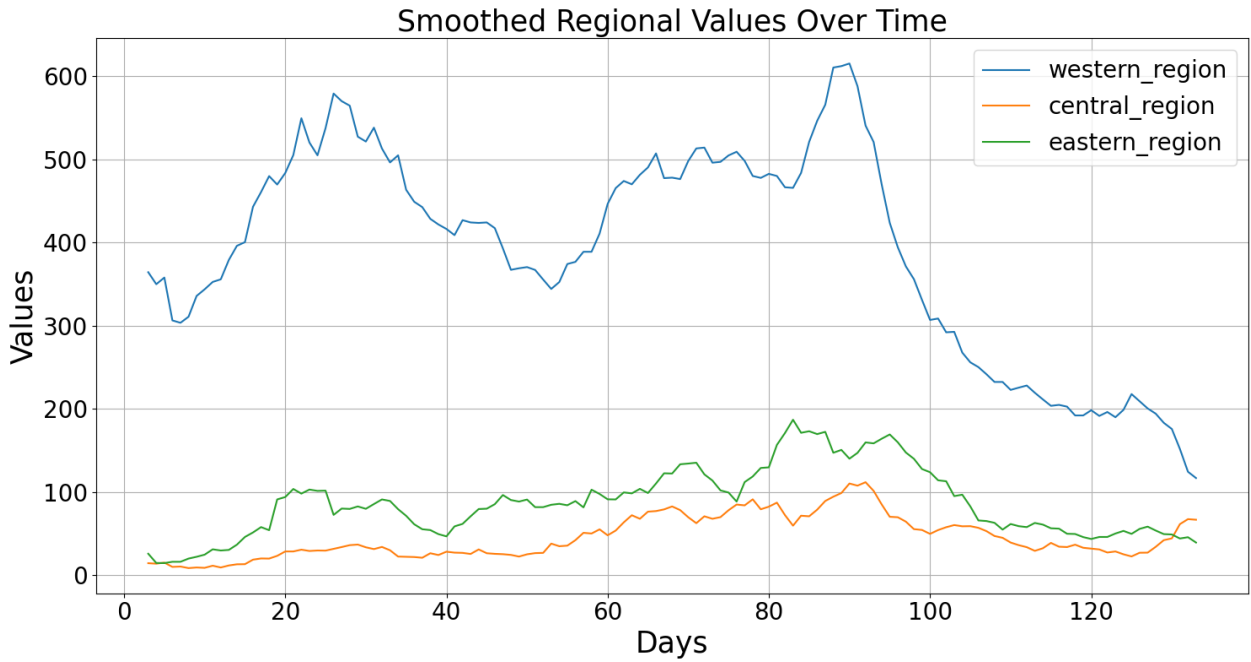


Figure 2.3: Regional Values Over Time as per the given data

As per the given database, the graph shows the distribution of the daily cases of COVID-19 in Sri Lanka between November 2020 to March 2021, which indicates two steady increases in COVID-19 cases in Western, Central, and Eastern regions during the period of December 2020 and January 2021.

Figure 2.4 shows that the number of Active Cases Distribution in individual cities as per the given data. The majority of the first infected patients were found in the Western region, which is home to a number of densely populated places like Kalutara, Gampaha, and Colombo. Though the disease's prevalence in the Eastern and Central areas was lower, it eventually spread to other districts[5]

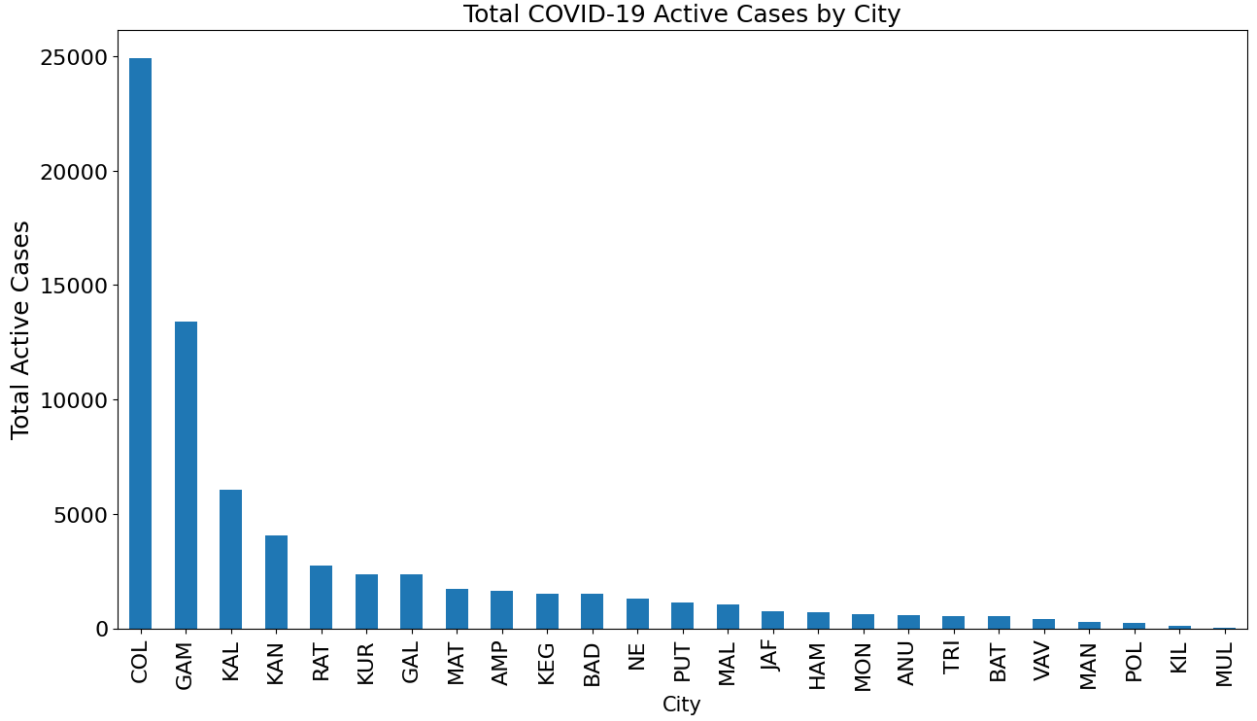


Figure 2.4: Total COVID-19 Active Cases by City

## 2.3 Mobility

Mobility for multi-region involves the movement of people across diverse geographical areas using various transport modes like road, air, and rail. It's influenced by globalization, technological advancements, natural disasters, political and economic factors [9], and pandemics, which affect the efficiency and accessibility of transportation networks, trade, and travel between regions. The Mobility matrix(M)<sup>5</sup> is defined as follows:

$$M = \begin{bmatrix} 0 & \rho_{12} & \rho_{13} \\ \rho_{21} & 0 & \rho_{23} \\ \rho_{31} & \rho_{32} & 0 \end{bmatrix}$$

Where:

$$\rho_{12} = 0.0004$$

Travelling rate From Western to Central Region

$$\rho_{13} = 0.0006$$

Travelling rate from Western to Eastern Region

$$\rho_{21} = 0.0015$$

Travelling rate from Central to Western Region

$$\rho_{23} = 0.0007$$

Travelling rate from Central to Eastern Region

$$\rho_{31} = 0.0011$$

Travelling rate from Eastern to Western Region

$$\rho_{32} = 0.0006$$

Travelling rate from Eastern to Central Region

<sup>5</sup><https://journals.sagepub.com/doi/10.1177/02601079231176390?icid=int.sj-full-text.citing-articles.4>

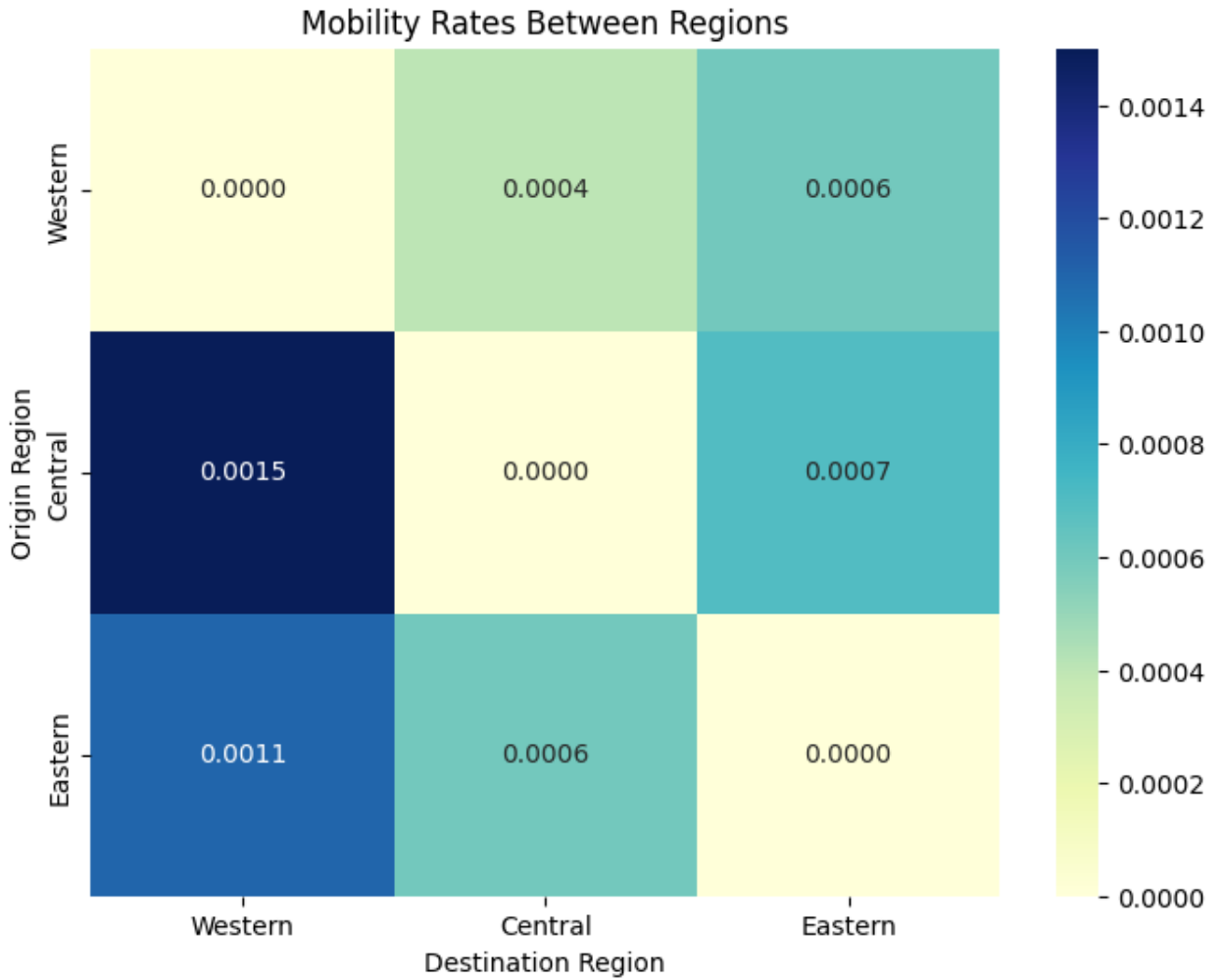


Figure 2.5: Mobility Rates Between Region

Here's how you can construct a 3x3 mobility matrix for a three-region SIR network model:

- In this model we have three regions such as Western Region, Central Region, and Eastern Region
- Assign rates of mobility (denoted by  $(\rho_{ij})$ ) for individuals moving from one region to another. These rates could be based on factors such as transportation infrastructure, population density, and geographic proximity. For simplicity, let's assume these rates are constant over time.
- In Figure 2.5 there has been a mobility rate which shows that the number of people who belong to the western region is less likely to leave their region because that region contains the main capital of the country which fulfilled basic requirements of people.

## 2.4 Model Analysis

Assume a person is infected. He or she may infect people when traveling or coming into touch with infected people in a certain region, colleagues at work, friends at gatherings, and people in the market, as well as his or her neighbors in the area. These interactions vary in dynamics, such as the number of connections, the risk of transmission, and how they are produced. Our model shows the network of regions which includes the different cities as per the location of SriLanka which is shown in Figure 2.2

### 2.4.1 SIR Model for Western Region

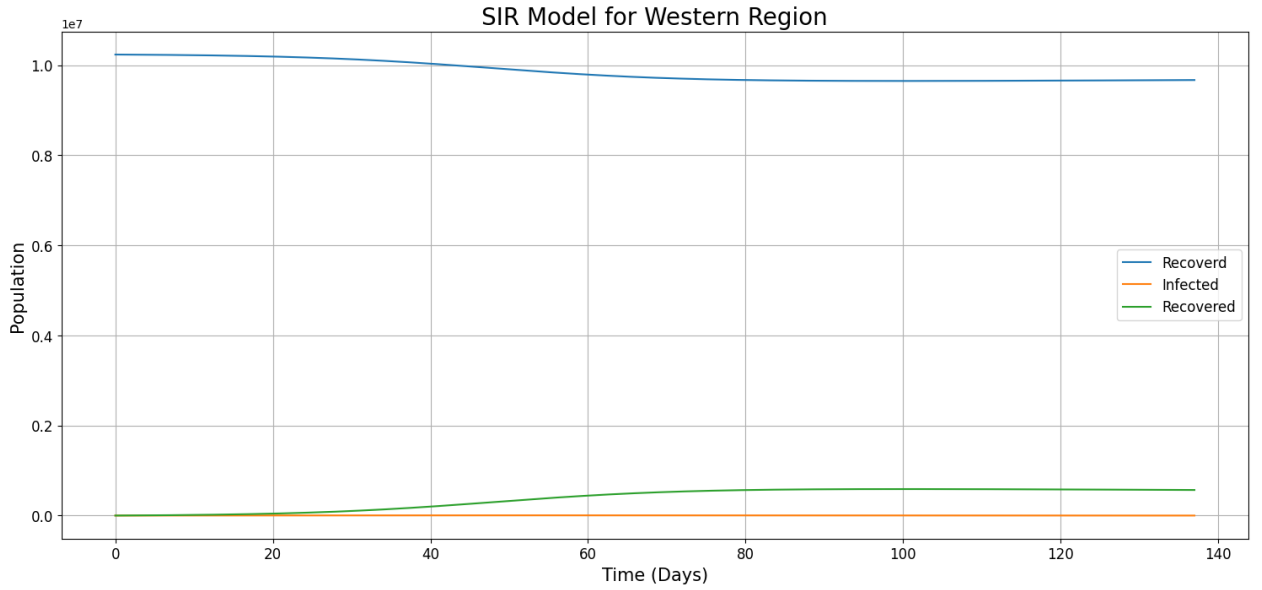


Figure 2.6: SIR Model for Western Region

In this Region, the Population is very high because of capital city of Sri Lanka is located in this part of the country. simulations are generated for a better understanding of the SIR Network Disease Model. We choose initial conditions in which Susceptible is 10,235,651, Infected is 349, and Recovered is zero as well as we use other parameters like  $\alpha = 0.00004$ ,  $\beta = 0.0735$ ,  $\gamma = (1/14)$ ,  $\mu = 0.00004$ , and  $d = 137$ . (X-axis is represent time(d) in days and Y-axis is represent population(N))

## 2.4.2 SIR Model for Central Region

In the Central Region, the number of susceptible people which is indicated by blue line in Figure 2.7 decreases as soon as the number of infected people increases. In addition, it seems like a flat line for infected people because of the large population, which is in yellow line in the figure, however, it shows significant correction in between 80 to 100 days. For the Central region, we choose initial conditions in which Susceptible is 5,088,993, Infected is 7 and Recovered is zero as well as we use other parameters like  $\alpha = 0.00004$ ,  $\beta = 0.0735$ ,  $\gamma = (1/14)$ ,  $\mu = 0.00004$ , and  $d = 137$ . (X-axis is represent time(d) in days and Y-axis is represent population(N))

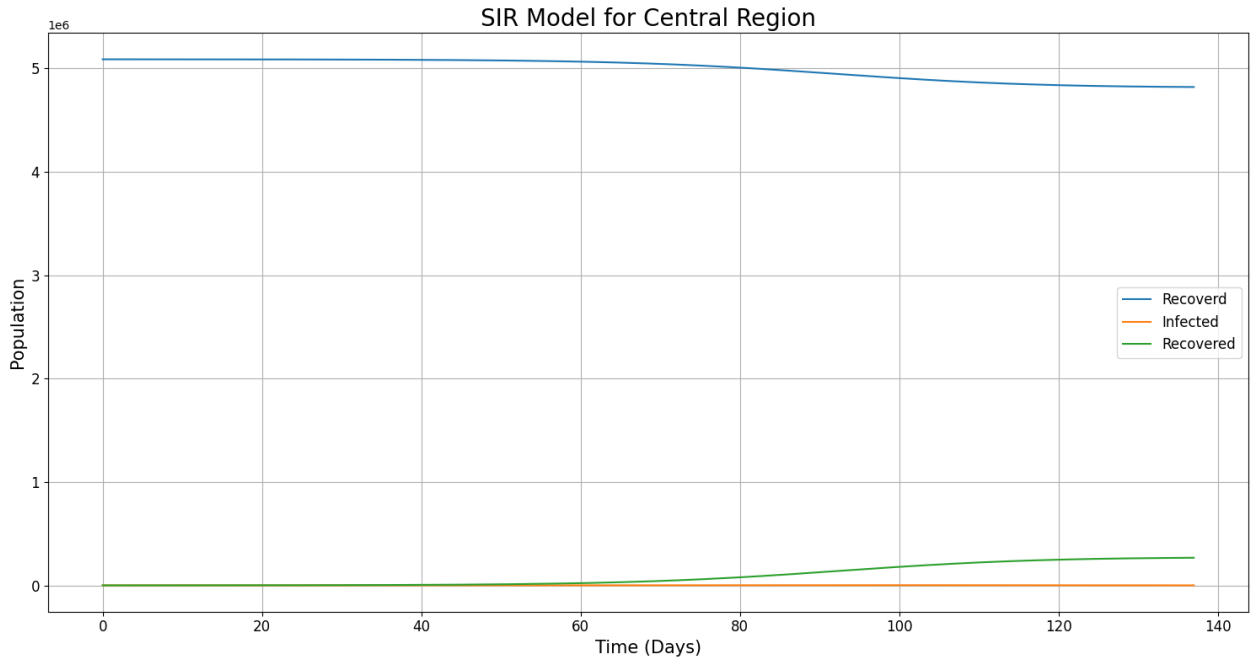


Figure 2.7: SIR Model for Central Region



### 2.4.3 SIR Model for Eastern Region

Seeing simulations with graph visualizations helps us to understand how the model behaves and how near it is to real-world data. Playing with the infectious rate, numbers of healthy and infected individuals at the start, recovery time, and infectious radius may teach a lot about how our Models work. As for the Eastern region, We choose initial conditions in which Susceptible is 6,593,907, Infected is 93, and Recovered are zero as well as we use other parameters like  $\alpha = 0.00004$ ,  $\beta = 0.0735$ ,  $\gamma = (1/14)$ ,  $\mu = 0.00004$ , and  $d = 137$ . (X-axis is represent time(d) in days and Y-axis is represent population(N))

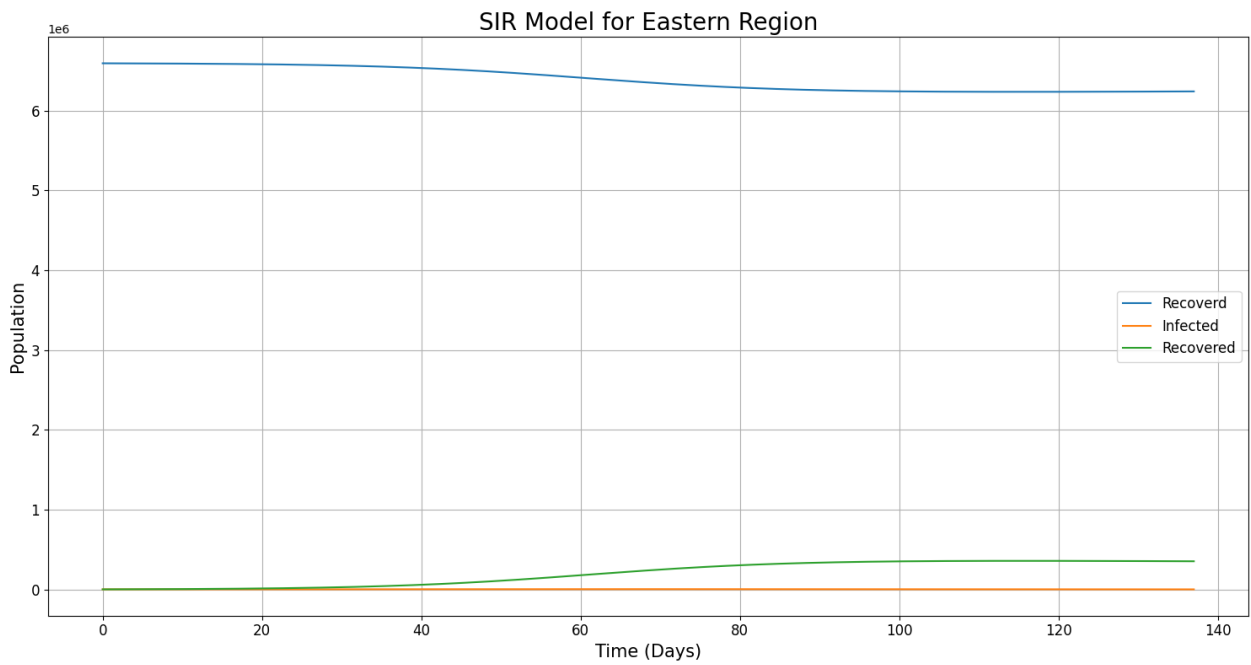


Figure 2.8: SIR Model for Eastern Region

# Chapter 3

## Simulation

Simulations are powerful tools that allow us to explore the potential outcomes of various scenarios in a controlled environment. we will utilize simulations to explore the spread of infectious disease using our model, and the impact of lockdown on controlling a pandemic[3]. By simulating different situations and analyzing the results, we aim to gain a deeper understanding of the underlying processes and predict potential outcomes.

### 3.1 Infected Cases in Different Regions with and without Lockdown

Now we consider three scenarios where we implement the Lockdown<sup>1</sup> in individual regions.

Case 1. Lockdown in Western Region.

Case 2. Lockdown in Central Region.

Case 3. Lockdown in Eastern Region.

Case 4. Infected Cases in Different Regions with and without Lockdown.

#### 3.1.1 Case 1. Lockdown in Western Region

We implemented a lockdown in the western region, which resulted in a dramatic reduction in peak infected cases from 5149 on day 48 to 3289 on day 54. Peak cases in the central region occurred on day 95 of 2015, with 117 cases declining. Furthermore, following the lockdown in the western region, the eastern region experienced a decline of nearly 236 cases at its high, which occurred on day 63, with a peak of 2688 cases. Overall, Figure 3.1 shows that this method looks to be effective.

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<sup>1</sup>[https://en.wikipedia.org/wiki/COVID-19\\_lockdown](https://en.wikipedia.org/wiki/COVID-19_lockdown)

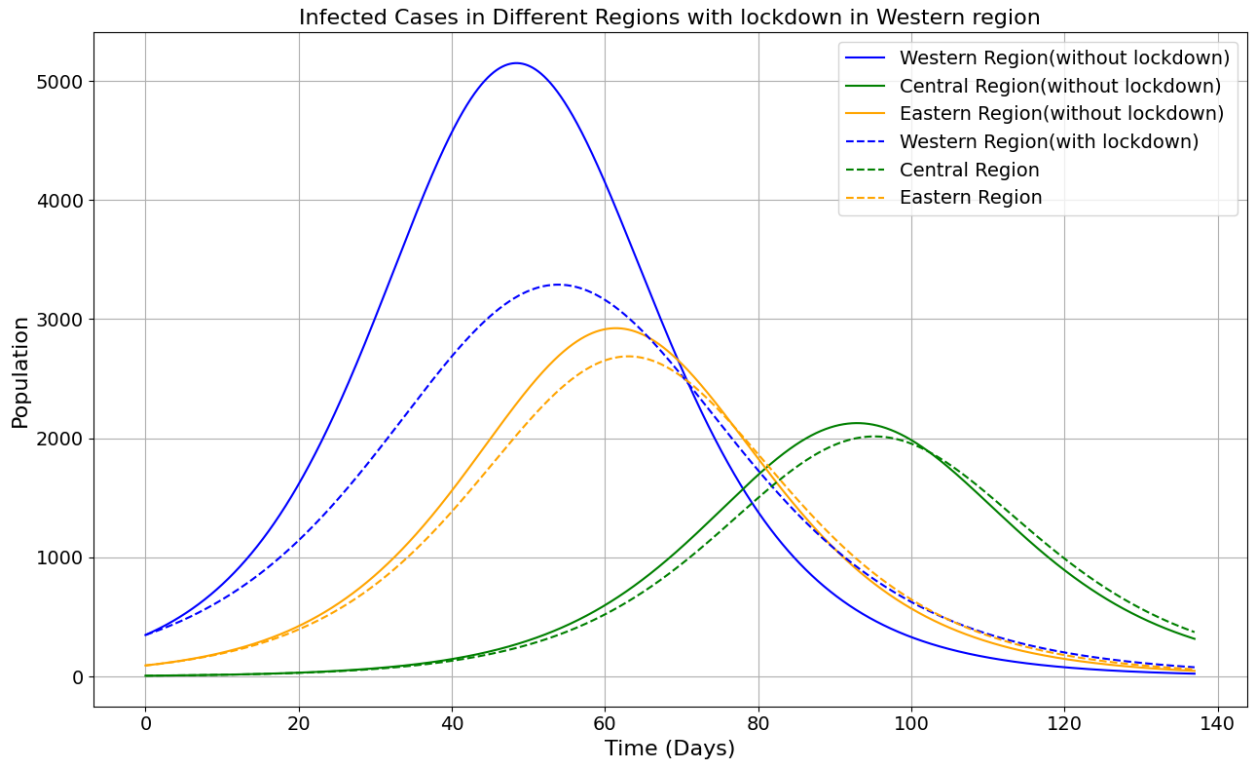


Figure 3.1: Lockdown in Western Region

### 3.1.2 Case 2. Lockdown in Central region

Lockdown in the Central region has benefited the Western region, where more people tend to transfer. Observing Figure 3.2, the lockdown reduced the number of active cases in the Western region by 786, with a peak of 4363 cases on day 50. In the Central area, cases decreased from 2127 on day 93 to 1482 on day 107. While, the number of infected people remained as same as during the lockdown in western region, with a peak of 2688 infected people on day 63 in the eastern region.

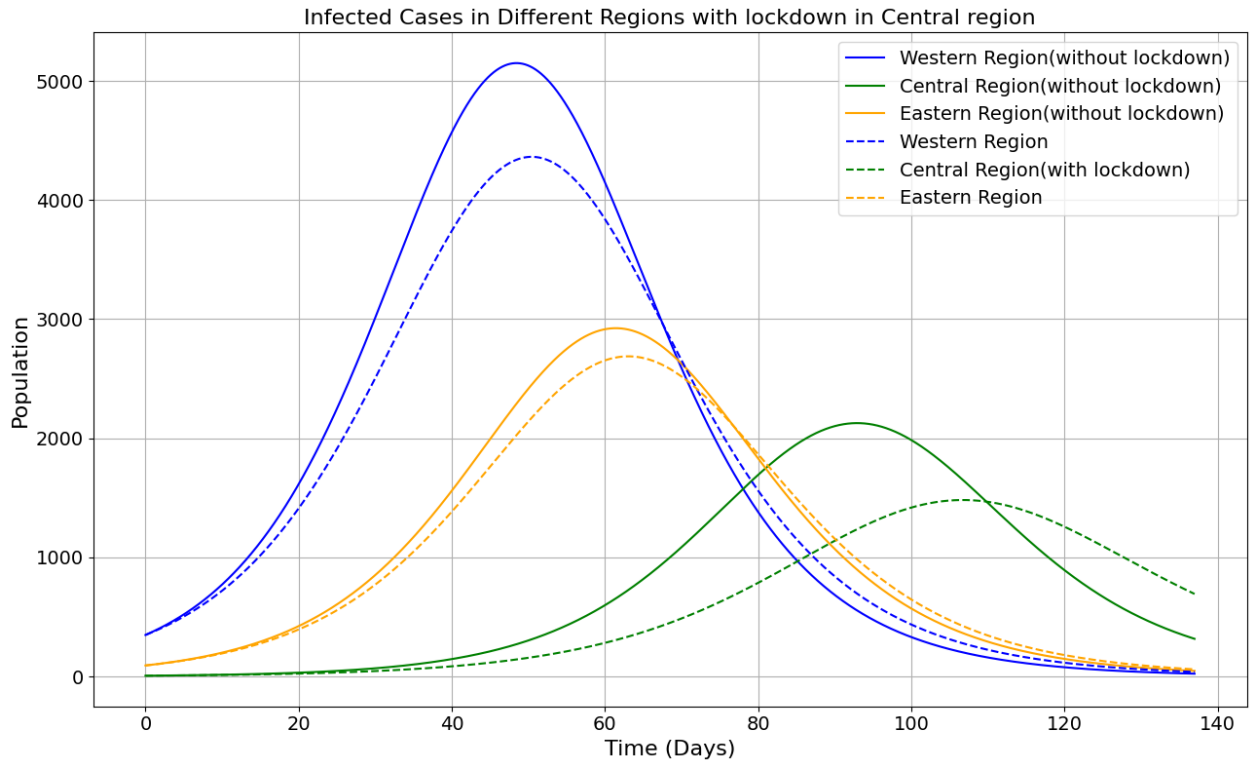


Figure 3.2: Lockdown in Central region

### 3.1.3 Case 3. Lockdown in Eastern Region

observing Figure 3.3, the Eastern region's lockdown seems effective, with infections dropping by 928 cases, peaking at 1996 cases on day 69 instead of 2924 cases on day 61 before the lockdown. Similarly, the Western region saw a comparable reduction in cases to when the Central region was locked down, peaking at 4363 cases on day 50. Likewise, the Central region experienced a similar decrease to when the Western region was locked down, with cases peaking in 2015 on day 95.

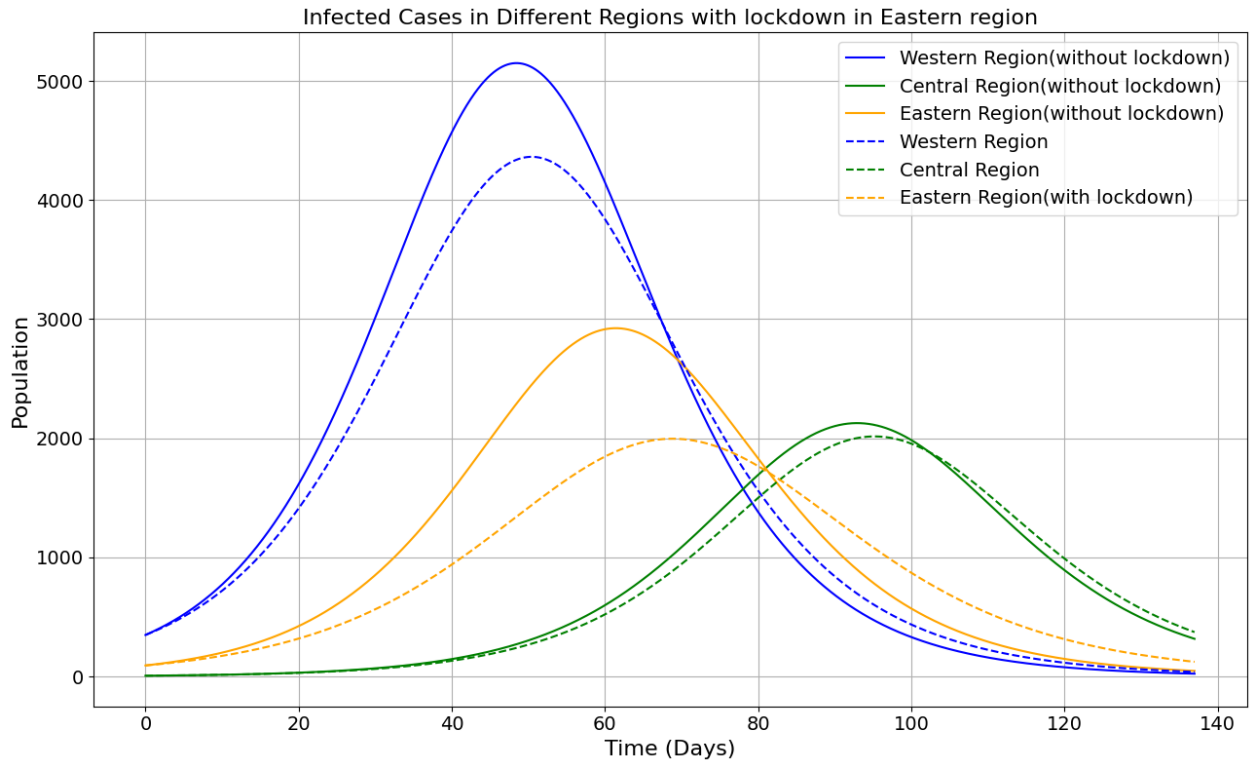


Figure 3.3: Lockdown in Eastern Region

### 3.1.4 Case 4. Infected Cases in Different Regions with and without Lockdown

Now, consider a total lockdown scenario in all locations to simulate the behavior of an infectious disease. In figure 3.4, the number of infected people in the western region is notably massive, as indicated by the blue line, because the western region includes the majority of the population, which totals 10,236,000 people. In addition, the central and eastern regions have produced infected persons relative to their populations. After simulation, in the western region number of infected cases began at 349 and peaked at 5149 cases on the 48th day. While the central region's initial infected cases were 7, they peaked at 2127 cases on day 93. Moreover, 93 initial cases were considered for the eastern region, but it touched a peak of 2924 cases on day 61.

However, the prohibition between each region for the community depicts a decreasing number of infected cases with a delay in the peak of infected cases[4]. As soon as the complete lockdown situation is imposed, it might reduce the infection rate so we have made some slight changes in the infection rate( $\beta$ ). In Figure 3.4, dashed lines represent the lockdown scenario for each region. Following the total lockdown, the Western region peaked at 3289 cases on the 54th day, indicating a considerable improvement over before the lockdown. Similarly, the Central and Eastern regions peaked at 1482 cases on day 107 and 1996 cases on day 69, respectively. This illustrates that the lockdown strategy effectively lowers the number of infected cases over time.

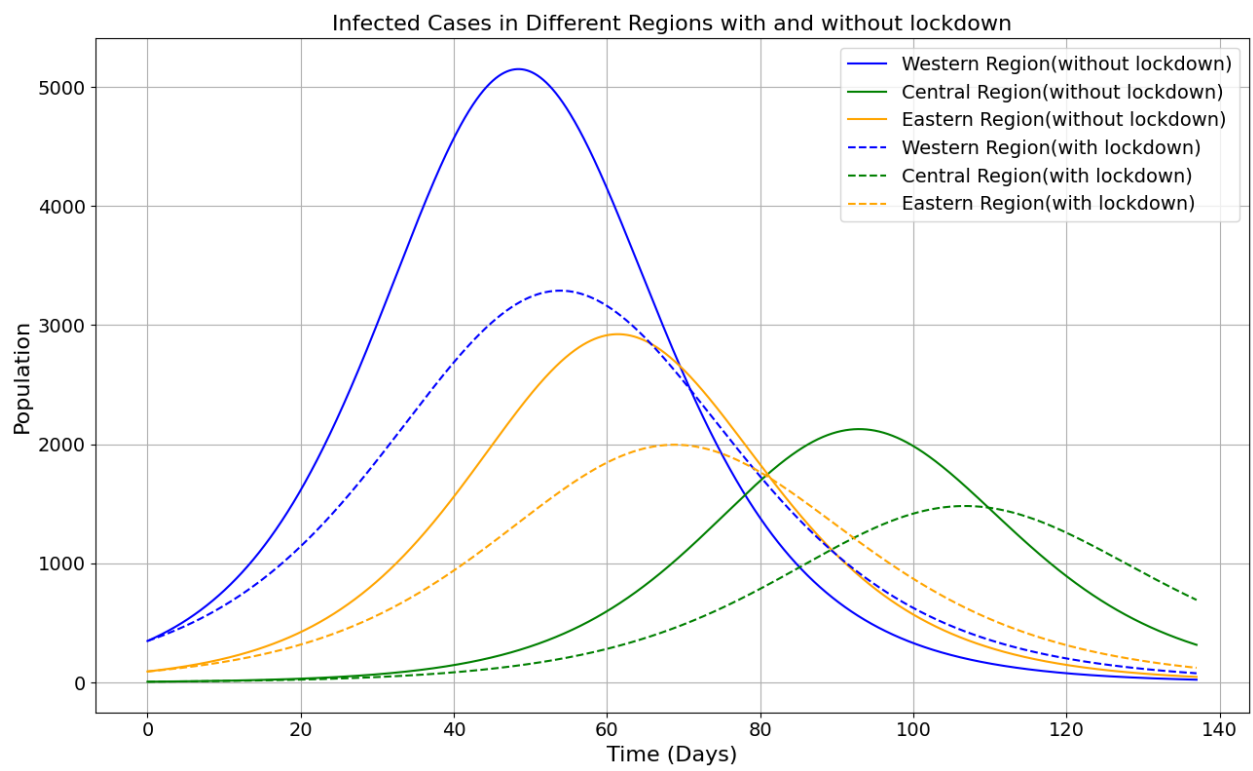


Figure 3.4: Infected Cases in Different Regions with and without Lockdown

# Chapter 4

## Conclusion

Analyzing all the comparison graphs, we can conclude that restricting the mobility between each region shows that reducing the number of infected cases in each region and delays the peak of infected compartment. We obtain that lockdown is an effective solution in fighting a pandemic crisis. we also simulated the real-world scenario by considering the COVID-19 cases in Western, Central, and Eastern regions in Sri Lanka. Simulation reveals that the mobility-based SIR model can be helpful in forecasting the expected number of cases after the lockdown is introduced in society.

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