



## Age Structure SIR Model

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# Declaration

We hereby declare that we have written this seminar report, and the references we used during the learning are attached. This report's purpose is to fulfill academic requirements.

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# Acknowledgement

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# Abstract

This study investigates the application of an age-structured SIR model to analyze the control of infectious disease outbreaks. The SIR model, traditionally compartmentalizing the population into susceptible (S), infected (I), and recovered (R) classes, is augmented with an age structure to account for the differential susceptibility and infectiousness observed across age groups. We explore the effectiveness of interventions aimed at mitigating disease spread, focusing on the isolation of elderly individuals. By comparing the original disease dynamics with a modified model incorporating this intervention, we evaluate its impact on the transmission rates. The model leverages a Gaussian kernel function to represent the contact patterns between individuals within different age groups. Our findings demonstrate the potential of such interventions in controlling disease outbreaks.

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# Chapter 1

## Introduction

### 1.1 Mathematical Model

A mathematical model represents real-world phenomenons using variables and mathematical equations to understand the problem properly, and it helps to find new solutions to solve them. [1]

The purpose of mathematical modelling is to understand the situation of the real-world system, try to predict its future outputs, optimize its performance, or take some measures. During the process, assumptions are required to create an environment that is almost similar to real-world phenomena. However, assumptions are responsible for inaccuracies and limitations.

Variables also play an important role in the mathematical model. They are dependent or independent. In addition, equations represent the relationships between variables, including ordinary differential equations and partial differential equations.

### 1.2 SIR model

The SIR model in epidemiology has played a crucial role in forecasting the patterns of infectious diseases. It is also well known as Compartmental models[2]. In the early 20th century, pioneers Sir Ronald Ross [3] and Kermack-McKendrick [4] established the groundwork for modelling disease propagation in communities. The Susceptible-Infected-Recovered (SIR) model, a fundamental concept in epidemic modelling, was initially developed in the 1920s and has been modified throughout time to address different situations. These models provide a mathematical framework for understanding the complexities of disease transmission by including factors such as population

demographics, contact rates, and recovery dynamics.

The SIR model is a mathematical representation used to determine how the virus spreads within the system of a fixed number of individuals. The model is divided into three compartments. such as susceptible, infected, and recovered people [2].

Here,

- **Susceptible (S):** These individuals can become infected with the infectious disease over time when they come into contact with infected people.
- **Infected (I):** These individuals are responsible for spreading the disease to susceptible people when they come into contact with them.
- **Recovered (R):** After recovering from the infection, these individuals are considered recovered. These people are no longer able to be infected and will not spread the disease to others.

**Assumptions:**

1. There is no birth or death.
2. The total number of people (N) is 1.
3. The recovery time is 14 days.
4. The number of recovered people is not added to the number of susceptible people.

The total number of individuals,  $N = S(t) + I(t) + R(t)$

The following ODEs[2] represent the rates of susceptibility, infection, and recovery.

$$\frac{dS(t)}{dt} = -\frac{\beta S}{N}I, \quad S(t = 0, x) = S_0(x) \quad (1.1)$$

$$\frac{dI(t)}{dt} = \frac{\beta S}{N}I - \gamma I, \quad I(t = 0, x) = I_0(x) \quad (1.2)$$

$$\frac{dR(t)}{dt} = \gamma I, \quad R(t = 0, x) = R_0(x) \quad (1.3)$$

Here,

For time,  $t \in [0, T] \subset R$  and for space  $x \in [0, 1]^n \subset R^n$



Parameters:

$\beta$  = **Transmission rate** or **Contact rate**, It is the rate of spreading infection from infected people to susceptible people when they contact each other. It is greater than zero i.e  $\beta > 0$

$\gamma$  = **Recovery rate**, It is the rate by which the infected people will recover completely. it is greater than zero i.e  $\gamma > 0$

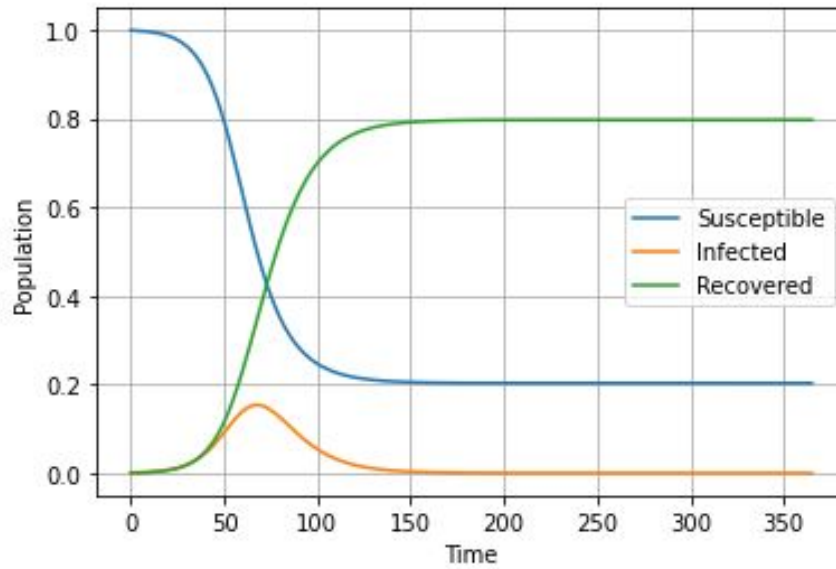


Figure 1.2.1: SIR model

The model shows the flow of the people, from susceptible to infected and infected to recovered. The number of susceptible people will decline, and they will become infected. The number of infected people will increase first; after a peak, they will start to decline, and the number of infected people will recover. (According to the assumption, the number of recovered people will not get infected again.). Overall, this model helps make suitable public health policies to decrease the spread of the virus[5].

# Chapter 2

## Age Structure Model

### 2.1 What is Age Structure Model

The age structure model is a mathematical framework that is useful to simulate the spreading pattern of the virus from one group to another and its impact on every group within the population. [6]

In the SIR model, the entire population is a homogeneous group. In addition, there are only three compartments, for example, for susceptible people, infected people, and recovered people. However, in the age structure model, the population of each compartment will be divided into different groups according to their ages. For example, 0–10 years, 11–20 years, 21–30 years,... 91–100 years. Once we have the number of groups, then we have to notice how often individuals from each group get in contact with other individuals from different groups and with the individuals within the group as well.

With the help of contact rates in the form of a contact matrix and equations, we can find the spreading pattern of the virus from one group to another. In addition, we can decide which group will be affected more. Accordingly, we can take interventions to control the spread of the disease. The age structure model is used in various fields, i.e., epidemiology, physics, and biology.

## 2.2 Why is the Age Structure Model required?

The age structure model is helpful for the following reasons:

- It helps to know the spreading pattern of the virus among different age groups.
- According to the spreading pattern, we can decide which group is at risk.
- To know the time to implement the lockdown, vaccination, and other interventions.
- It is used in the field of epidemiology (the study of how viruses spread and affect populations.).

## 2.3 The equations for Age structure model

Here, the total population (N) is given by,

$$N = S(t) + I(t) + R(t)$$

$$\Rightarrow s + z + r = 1. \text{ Where, } s := \frac{S(t)}{N}, z := \frac{I(t)}{N}, r := \frac{R(t)}{N}$$

$$\Rightarrow s = 1 - z - r$$

Now, replace the value of  $s = (1 - z - r)$  in the equations (1.1), (1.2), and (1.3)

$$\frac{ds(t, x)}{dt} = -\beta(1 - z - r)z, \quad s(t = 0, x) = s_0(x) \quad (2.1)$$

$$\frac{dz(t, x)}{dt} = \beta(1 - z - r)z - \gamma z, \quad z(t = 0, x) = z_0(x) \quad (2.2)$$

$$\frac{dr(t, x)}{dt} = \gamma z, \quad r(t = 0, x) = r_0(x) \quad (2.3)$$

Here, for time  $t \in [0, T] \subset R$  and space  $x \in [0, 1]^n \subset R^n$ .

These equations show that the spreading pattern at a certain point would completely depend on the initial relations among  $r_0$ ,  $z_0$ ,  $\gamma$ , and  $\beta$ . To consider the contact between the specific locations, we have to change the term  $\beta(1 - z - r)z$  with the integral kernel function  $k(t, x-y)$  [7]. Where  $t$  is time and  $|x - y|$  is the difference between the locations  $x$  and  $y$ .

$$\frac{ds(t, x)}{dt} = -\beta(1 - z - r) \int_0^1 z(t, y)k(t, x - y) dy, \quad s(t = 0, x) = s_0(x) \quad (2.4)$$

$$\frac{dz(t, x)}{dt} = \beta(1 - z - r) \int_0^1 z(t, y)k(t, x - y) dy - \gamma z, \quad z(t = 0, x) = z_0(x) \quad (2.5)$$

$$\frac{dr(t, x)}{dt} = \gamma z, \quad r(t = 0, x) = r_0(x) \quad (2.6)$$

Here,  $z(t, y)$  is the proportional function. It represents a percentage of the population (Infected people) at age  $y$  and at time  $t$ .

## 2.4 The Gaussian Kernel Function

The kernel function plays an important role in simulating the spread of the virus among different age groups. It represents the interaction between different age groups and how the infection will spread because of these interactions.[8]

Here, we selected the Gaussian Kernel Function:

$$k(t, x - y) = e^{-\frac{(x-y)^2}{2\sigma^2}} \quad (2.7)$$

Here,  $k(t, x-y)$  depends on time, and the distance between  $x$  and  $y$ .  $\sigma$  is the standard deviation.

The following are the reasons for the selection of Gaussian Kernel Function:

- **Smoothness[9]:** Whenever there is a transition from one value to another, The Gaussian kernel function provides a smooth transition with gradual change. A smooth transition is desirable in the mathematical model instead of fluctuation. In addition, it has a bell-shaped curve.

- **Flexibility:** By adjusting the value of  $\sigma$ , we can control the spread of the virus. Such a type of control may not be possible with other simple functions.
- **Desirable mathematical properties:** This function gives the positive definite numbers[8], which represent the contact rate in the contact matrix. (Values in the contact matrix should always be positive-definite.) In addition, the radially symmetric and continuous derivatives of this function are also responsible for maintaining smoothness in the model.

## 2.5 Contact Matrix

The contact matrix is a matrix that represents the **frequency** or **Intensity** of contact between individuals of different groups within the population.

Each cell of the contact matrix represents the rate of interaction or contact between two age groups. For example, the following contact matrix displays the interactions of three groups only. (Here, we write each cell's values randomly.)

Age groups	0-10 years	11-20 years	21-30 years
0-10 years	0.25	0.35	0.28
11-20 years	0.33	0.34	0.39
21-30 years	0.42	0.38	0.41

Table 2.1: Sample example of the contact matrix

# Chapter 3

## Numerical Solution

The numerical implementation simulates the spread of infectious diseases using the SIR model with a kernel function. The SIR model and contact patterns represented by the kernel function result in a system of ODEs that are complicated to solve analytically. Moreover, infectious disease dynamics involve continuous changes in the number of susceptible, infectious, and recovered individuals. So, we preferred the numerical method (Python) that provides a practical way to approximate solutions for such complex systems and simulate the dynamic process according to the model equations. Not only that, but we can also generate predictions about future epidemic trends and assess the impact of potential interventions.

### 3.1 Model with kernel discretization

#### 3.1.1 Original dynamics

Firstly, we will define the necessary parameters.

Transmission rate,  $\beta = 0.11$

Recovery rate,  $\gamma = 1/14$  .

The total number of people,  $N = 1$

The initial number of infected individuals,  $I_0 = 0.01$

The initial number of recovered individuals,  $R_0 = 0$

As mentioned above the Gaussian kernel function, Which is defined as,

$$k(t, x - y) = e^{-\frac{(x-y)^2}{2\sigma^2}} \quad (3.1)$$

Here, 'x', and 'y' are age groups. we considered 10 age groups. Such as,

$$x = [5, 15, 25, 35, 45, 55, 65, 75, 85, 95]$$

$$y = [5, 15, 25, 35, 45, 55, 65, 75, 85, 95]$$

' $\sigma$ ' = The standard deviation.

The system of ODEs that control the dynamics of the model are:

$$\frac{dS}{dt} = -\frac{\beta * S * \text{integralterm}}{N} \quad (3.2)$$

$$\frac{dI}{dt} = \frac{\beta * S * \text{integralterm}}{N} - \gamma * I \quad (3.3)$$

$$\frac{dR}{dt} = \gamma * I \quad (3.4)$$

Here, integral term = (contact matrix \* I)

We set the time step  $dt = 0.01$ , then solved the ODEs using the **Runge-Kutta method** to obtain the solution trajectory over time. We retrieved the scaled results as mentioned above in Figure 3.1.1

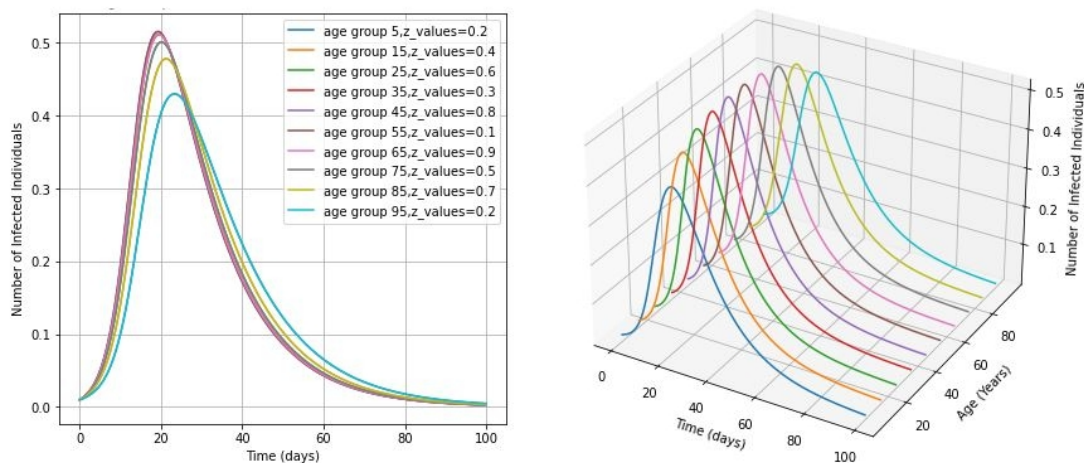


Figure 3.1.1: Original Dynamics of infected individuals over time and age (**Model**).

These are the Peak infection values for each age group with kernel discretization and without any kind of interventions.

Age Group	Peak Infections
5	0.43
15	0.478
25	0.501
35	0.512
45	0.516
55	0.516
65	0.512
75	0.501
85	0.478
95	0.43

Table 3.1: Peak infections for each age group without interventions

### 3.1.2 Modified dynamics

In this part of the analysis, we generated a modified dynamics of disease by considering a condition based on our problem.

The problem states that **what happens if we want to prevent infections from one group to the other by 'isolation' of old people.**

To solve this problem, we isolated the old people, whose ages are **greater than 70 years**. We reduce the interaction by multiplying the kernel function value by a reduction factor of 0.1 (which means the interaction is reduced by 90%). Here, we got the contact matrix with the help of the Gaussian Kernel function.

After applying this condition to the model, we observed that people in age groups over 70 years, such as 75, 85, and 95 years old, got a lower infection rate. As a result, **the overall infection is decreased.**

The result obtained is shown in Figure 3.1.2



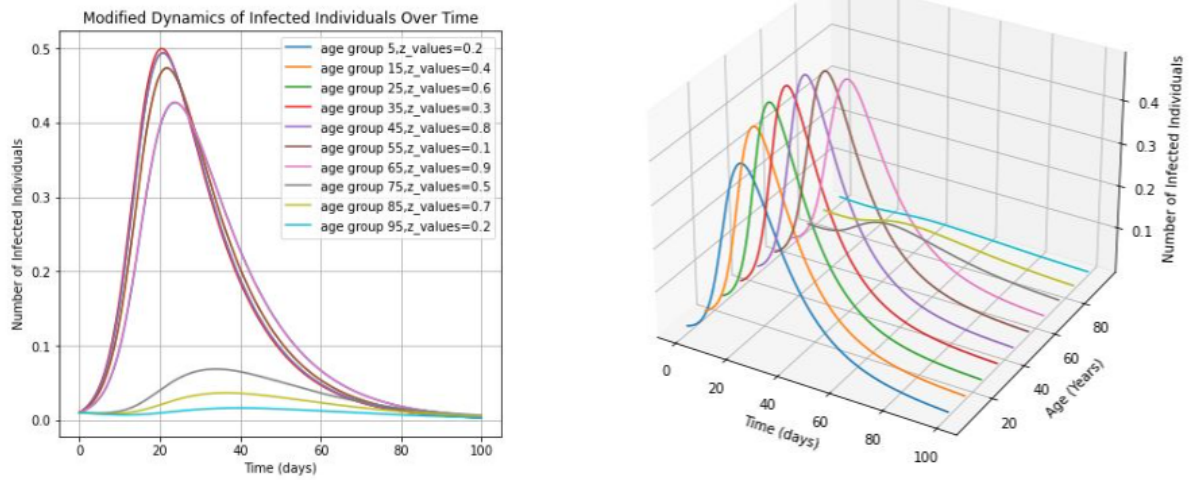


Figure 3.1.2: Modified dynamics of infected individuals over time and age (**Model**).

Age Group	Peak Infections
5	0.427
15	0.473
25	0.494
35	0.5
45	0.494
55	0.474
65	0.428
75	<b>0.068</b>
85	<b>0.036</b>
95	<b>0.016</b>

Table 3.2: Peak infections for each age group with interventions

## 3.2 Model with dataset:

We took the dataset from the following source for implementing it in our model.[10].

Age of Contacts	70+	0.21	0.59	0.46	0.41	1.08	0.81	0.83	1.34
	[60,70)	0.57	0.54	0.89	1.33	1.26	1.24	1.17	0.99
	[50,60)	0.56	0.81	1.38	1.49	1.52	1.86	0.96	0.75
	[40,50)	0.88	1.70	1.58	1.98	2.90	1.32	0.85	0.87
	[30,40)	1.77	1.32	1.57	2.76	1.93	1.26	0.87	0.32
	[20,30)	1.14	1.32	3.60	1.82	1.79	1.35	0.68	0.41
	[10,20)	1.18	8.06	1.30	1.50	1.88	0.78	0.41	0.52
	[0,10)	5.15	1.31	1.24	2.24	1.09	0.60	0.48	0.21
		[0,10)	[10,20)	[20,30)	[30,40)	[40,50)	[50,60)	[60,70)	70+
		Respondent's Age							

Figure 3.2.1: Age-contact matrix

We used the data shown in Figure 3.2.1 and we normalized it using the 'Vector Normalization method'.

### 3.2.1 Vector Normalization

The normalization process refers to making something into a standard form or bringing all values into a comparable range.

Normalizing each row or column of the matrix independently is called Vector normalization. We can perform normalization for the matrix in two ways. 1. Row-wise

normalization 2. Column-wise normalization. Here we normalized the matrix using **column-wise normalization**. [11]

1. Take the first column of the matrix.
2. Compute the Euclidean norm of the vector obtained from the first column as.

$$\|a_1\| = \sqrt{(a_{11}^2 + a_{21}^2 + \dots + a_{n1}^2)} \quad (3.5)$$

3. Then we have to normalize the first-column vector by dividing each element by the norm.

$$Normalized\ a_1 = [\frac{a_{11}}{\|a_1\|}, \frac{a_{21}}{\|a_1\|}, \dots, \frac{a_{n1}}{\|a_1\|}] \quad (3.6)$$

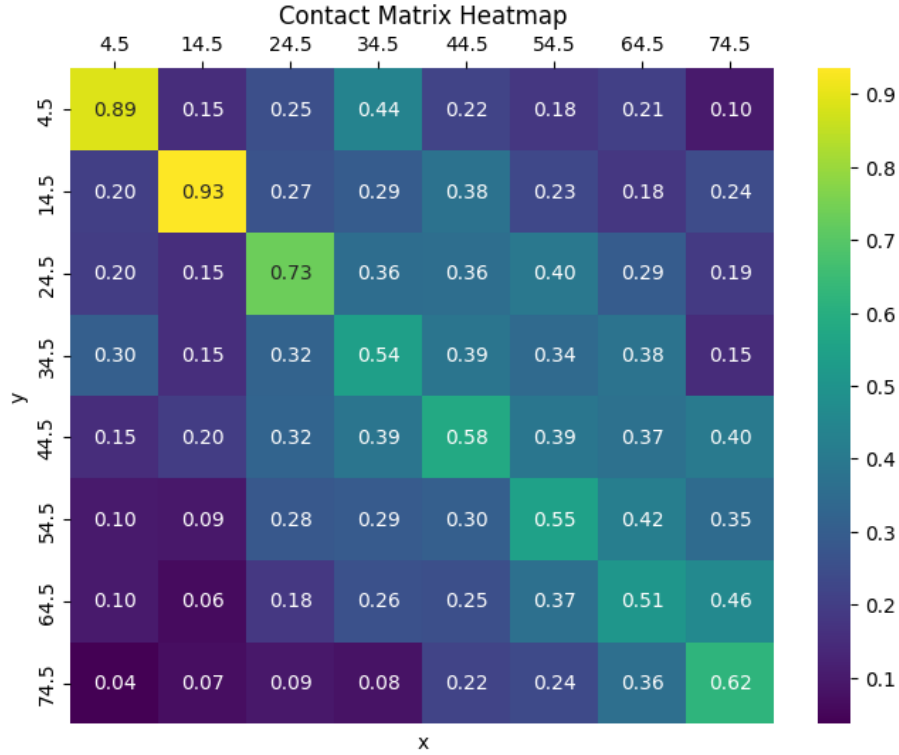


Figure 3.2.2: Normalized Matrix

Here in Figure 3.2.2, you can observe the result of normalized matrix.

### 3.2.2 Original dynamics with dataset

As we described earlier, the process of numerical implementation. We did the same process here, but without using the kernel function.

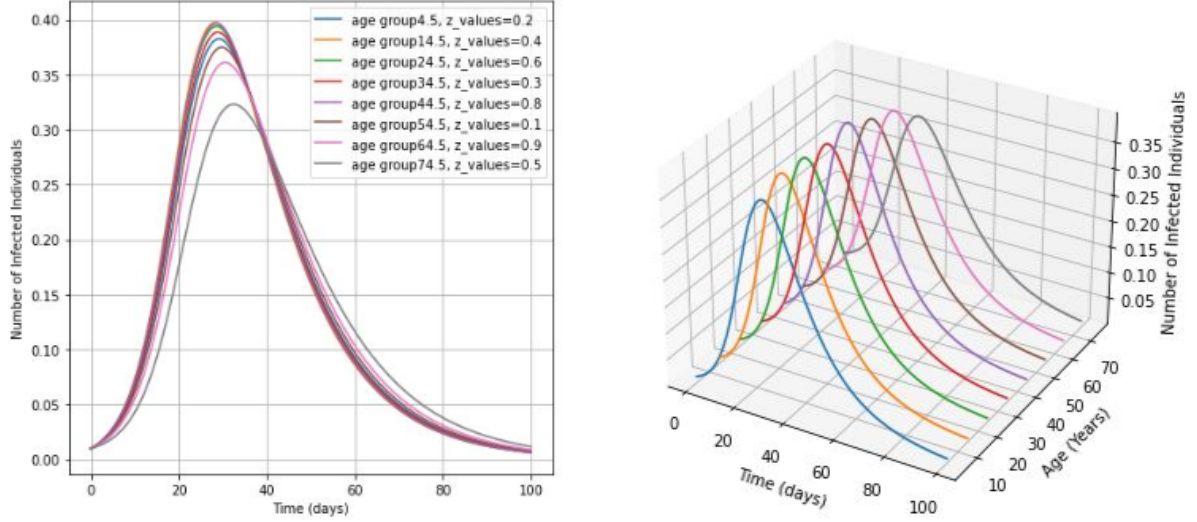


Figure 3.2.3: Original dynamics of infected individuals over time and age (**Dataset**).

Age Group	Peak Infections
4.5	0.382
14.5	0.397
24.5	0.394
34.5	0.389
44.5	0.397
54.5	0.375
64.5	0.361
74.5	0.323

Table 3.3: Peak infections for each age group without interventions for **Dataset**.

After the normalization(Column-wise normalization) of the data, we observed the virus spreading among all age groups nearly the same. That we can check according to the peak values of the infections.

### 3.2.3 Modified dynamics with dataset

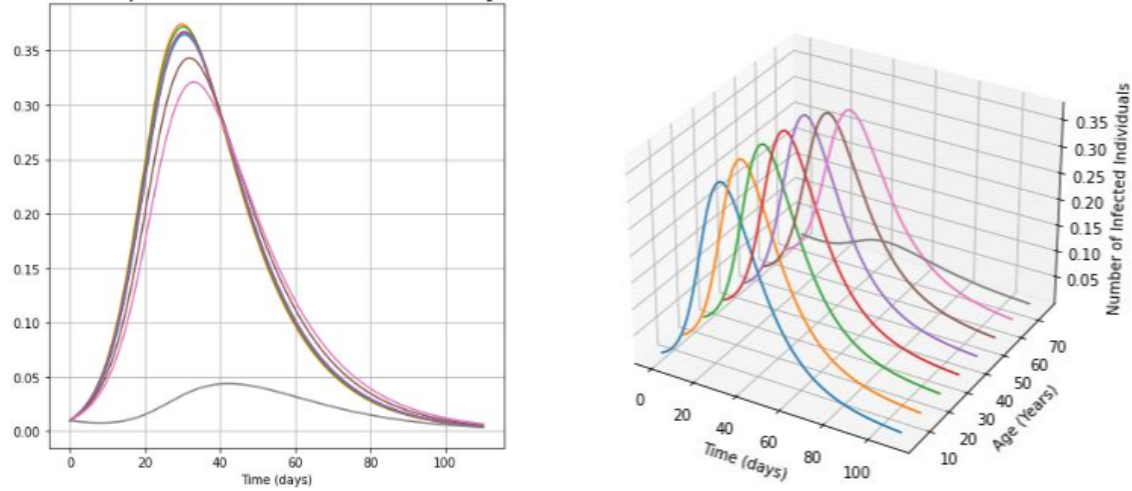


Figure 3.2.4: Modified dynamics of infected individuals over time and age (**Dataset**).

Age Group	Peak Infections
4.5	0.365
14.5	0.374
24.5	0.372
34.5	0.367
44.5	0.366
54.5	0.343
64.5	0.321
74.5	<b>0.044</b>

Table 3.4: Peak infections for each age group with interventions for **Dataset**.

Here, the peak infection for age group 74.5 is 0.044. It was 0.323 before their isolation. It shows that the isolation of old people helps to decrease overall infection.

We observed a decrease in the infection rate in both cases after implementing interventions (isolation). From that, we can conclude that carrying out such types of interventions can be responsible for a decrease in the dynamics of disease.

# Chapter 4

## Conclusion

In conclusion, the age-structured SIR model successfully captured the dynamics of infectious disease spread across different age groups. Notably, the model demonstrated that reducing contact rates among older age groups significantly decreased infections across all ages. This finding suggests the model's potential application to a broader range of age-dependent infectious diseases and informs public health strategies by simulating the impact of targeted interventions.

By continuously adapting and refining the model, we can gain deeper insights into disease control and optimize public health interventions during future outbreaks.

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