American International University-Bangladesh (AIUB)

Network Based Modeling of Infectious Diseases Spread

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Abstract

This thesis explores the use of network-based modeling and graph theory to understand and predict the spread of infectious diseases. The research focuses on developing mathematical models and computational algorithms to analyze the dynamics of disease transmission within a population. The study employs various epidemic models, including the SIR (Susceptible-Infected-Recovered), SEIR (Susceptible-Exposed-Infected-Recovered), and SIRD (Susceptible-Infected-Recovered-Deceased) models, to capture different aspects of disease progression.

The research methodology involves data collection, estimation of infection and recovery rates, calculation of incubation periods, and the determination of initial numbers of exposed individuals. By simulating the spread of diseases using these models, valuable insights are obtained regarding the impact of various factors, such as disease parameters, network connectivity, and control measures, on the spread and containment of infectious diseases.

The study has ramifications for public health since its conclusions aid in the creation of practical plans for the prevention and management of illness. The research outcomes provide valuable information for policymakers and healthcare professionals, aiding in the formulation of targeted interventions and resource allocation.

The results and findings of the study are presented and analyzed, highlighting the effectiveness of the proposed network-based modeling approach in understanding disease spread dynamics. The discussions delve into the implications of the findings, potential future research directions, and the limitations of the current study.

In conclusion, this thesis demonstrates the significance of network-based modeling and graph theory in understanding and predicting the spread of infectious diseases. The research contributes to the existing body of knowledge in the field, offering valuable insights and practical implications for disease control and public health interventions.

Declaration by author

This thesis is composed of our original work, and contains no material previously published or written by another person except where due reference has been made in the text. We have clearly stated the contribution of others to our thesis as a whole, including statistical assistance, survey design, data analysis, significant technical procedures, professional editorial advice, financial support and any other original research work used or reported in our thesis. The content of our thesis is the result of work we have carried out since the commencement of Thesis.

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Approval

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Contributions by authors to the thesis

List the significant and substantial inputs made by different authors to this research, work and writing represented and/or reported in the thesis. These could include significant contributions to: the conception and design of the project; non-routine technical work; analysis and interpretation of research data; drafting significant parts of the work or critically revising it so as to contribute to the interpretation.

	Dihan, MD. Rafee-uzzaman	**Ayon, Israd Ahmed**	**Jim, Shanjida Sultana**	**Bari, K.M.Wasimul**	**Contribution (%)**
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Conceptualisation	30%	25%	25%	20%	100(%)
Data curation	50%	20%	20%	10%	100(%)
Formal analysis	35%	25%	25%	15%	100(%)
Investigation	35%	25%	25%	15%	100(%)
Methodology	50%	30%	10%	10%	100(%)
Validation	35%	25%	25%	15%	100(%)
Theoretical derivations	35%	20%	30%	15%	100(%)
Preparation of figures	35%	20%	30%	15%	100(%)
Writing – original draft	70%	5%	20%	5%	100(%)
Writing – review & editing	70%	5%	20%	5%	100(%)

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Keywords

network based modeling, infectious diseases spread, graph theory approach, epidemic models, sir modeling, seir modeling, sird modeling

Contents

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List of Abbreviations and Symbols

Abbreviations	
SIR	Susceptible - Infectious - Recovered
SI	Susceptible - Infectious
SEIR	Susceptible - Exposed - Infectious - Recovered
SIRD	Susceptible - Infectious - Recovered - Death
ODE	Ordinary Differential Equation
COVID	COronaVIrus Disease of 2019
SARS-CoV-2	Severe acute respiratory syndrome coronavirus 2
JAMA	The Journal of the American Medical Association
AI	Artificial Intelligence

Symbols	
α	alpha
β	beta
γ	gamma
μ	mu
σ	sigma

Chapter 1

Introduction

Infectious diseases represent serious hazards to worldwide public health, necessitating the development of efficient prevention, control, and management techniques. Modeling the spread of infectious diseases is crucial to understanding their transmission dynamics and predicting potential outbreaks. For this aim, traditional epidemiological models, such as compartmental models, have been widely used. However, as the complexity of human relationships has increased and vast data on social networks and contact patterns has been available, graph theory approaches have emerged as valuable tools for modeling infectious disease transmission. A mathematical framework for investigating the structure, characteristics, and interactions of complex networks is provided by graph theory. Graph theory enables us to capture complex patterns of conceitedness and pinpoint crucial network properties that affect the transmission of infectious diseases by resembling individuals or groups as nodes and their interactions as edges. Additionally, graph theory models can include dynamic components that simulate the temporal evolution of disease transmission via networks, making predictions more precise and realistic.

The purpose of this study is to investigate how graph theory modeling techniques can be used to simulate the spread of infectious diseases. This study aims to answer important research concerns about the network-based modeling of infectious disease transmission dynamics by utilizing the power of graph theory.

For a number of reasons, it is crucial to comprehend how infectious disease spreads through networks. First, network connectivity and structure can have a big influence on how quickly and how a disease spreads. A network's key nodes or strongly connected regions, for instance, can operate as super-spreaders and hasten the spread of illness. We can learn more about what influences disease onset, spread, and containment by incorporating network properties into disease models.

Second, graph theory models make it possible to examine different intervention tactics and how they affect the transmission of disease. We can investigate the effects of focused interventions like vaccination campaigns, quarantine measures, or contact tracing inside the network structure through

simulated experiments. Policymakers and public health authorities can use this research to help them make decisions about disease prevention and control that are supported by the available data.

Third, using graph theory methodologies offers the chance to examine their advantages and disadvantages with conventional epidemiological models. We can determine the applicability of graph theory models for various infectious diseases and situations by comparing their performance to currently used approaches.

By providing details on the use of graph theory methodologies for understanding disease propagation, this research study aims to make a contribution to the area of infectious disease modeling. We may deepen our comprehension of the intricate interactions between networks and infectious diseases by addressing the research concerns raised in this study. This will provide important knowledge to help decision-making and improve public health planning.

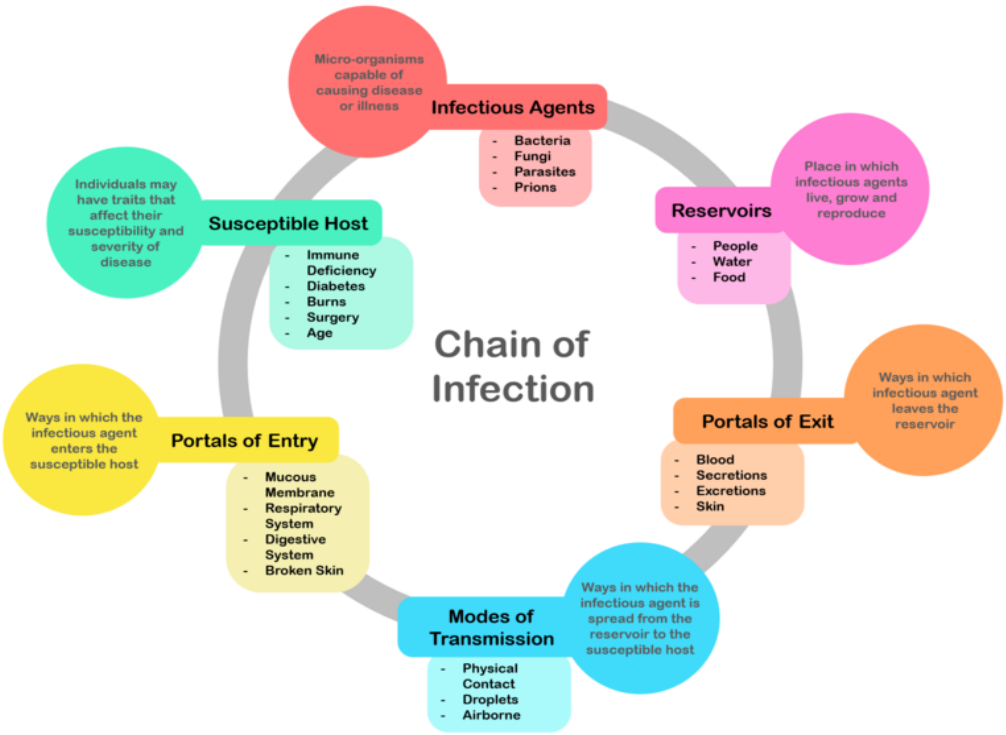

Figure 1.1: Chain of Infection

1.1 Problem Statement

Public health agencies around the world face considerable obstacles as a result of the infectious illnesses quick spread. It is essential to comprehend the patterns of disease transmission among communities in order to effectively reduce the impact of these diseases and devise focused intervention measures. Traditional epidemiological models frequently oversimplify the intricate relationships and connections between people, making it difficult to make accurate forecasts and implement efficient control measures. As a result, sophisticated modeling techniques that make use of graph theory are required to accurately represent the complex network structures that underlie the dynamics of disease transmission. In order to properly represent the transmission of infectious illnesses using a graph theory approach, the challenge that this research study seeks to address must be solved. The objectives of this project are to investigate the dynamics of disease transmission within populations, evaluate the influence of network structures on disease spread, and identify efficient disease management and prevention solutions.

1.2 Research Questions

1. How can models based on graph theory be modified and used to represent the connections and interactions important to the transmission of infectious diseases?

2. What are the main network metrics and features that affect the dynamics of disease transmission, and how do they change between various disease kinds and populations?

3. How may graph theory-based models, as opposed to conventional epidemiological models, improve the precision and prognostication of disease spread simulations?

4. How might the network-based insights be used to guide the design and assessment of focused intervention efforts, including vaccination campaigns, contact tracing, or focused quarantine measures?

5. What are the drawbacks and difficulties of utilizing a graph theory approach to describe the transmission of disease, and how may they be overcome or lessened?

   This work intends adds value to the creation of more thorough and precise models for comprehending as well as limiting the transmission of infectious illnesses by addressing these research concerns. The results will have an impact on public health policy and give decision-makers useful information for developing measures to control disease outbreaks and protect population health.

Chapter 2

Literature review

2.1 Introduction

Infectious diseases are an important threat to public health in the world. Analyzing their dynamics and implementing effective procedures for control need the use of broad methodologies, such as mathematical modeling. Because of its ability to capture complicated relationships and dynamics within populations. Network models can be used to study the spread of infectious diseases by modeling the interactions between individuals and the flow of the disease through the network. Graph theory, which provides an analytical framework for analyzing the structure and behavior of networks. Graph theory is used in various epidemic models to study the spread of infectious diseases.

2.2 Network-based Modeling

A modeling strategy known as ”network-based modeling” describes complicated systems as networks or graphs. A network in this sense consists of nodes, which represent individual items or components, and edges, which represent connections or relationships between nodes. This kind of modeling is especially beneficial for researching and comprehending the relationships and inter-dependencies between various system components. [1]

A method of analysis called network-based modeling visualizes complicated systems as networks or graphs. From the human brain to computer communications, transportation infrastructure to online social platforms, physiological reactions to financial markets, networks are the foundation of complex systems. Our comprehension of the physical, biological, economic, and social phenomena that shape our environment is improved by describing their structure. A variety of fields, including computer science, social sciences, biology, neuroscience, and transportation, use this modeling technique. Researchers can map the spread of diseases on the network and predict future states by using network-based models to study the structure and dynamics of systems, analyze their behaviors, simulate and predict disease dynamics, and evaluate the impact of different treatments. [2]

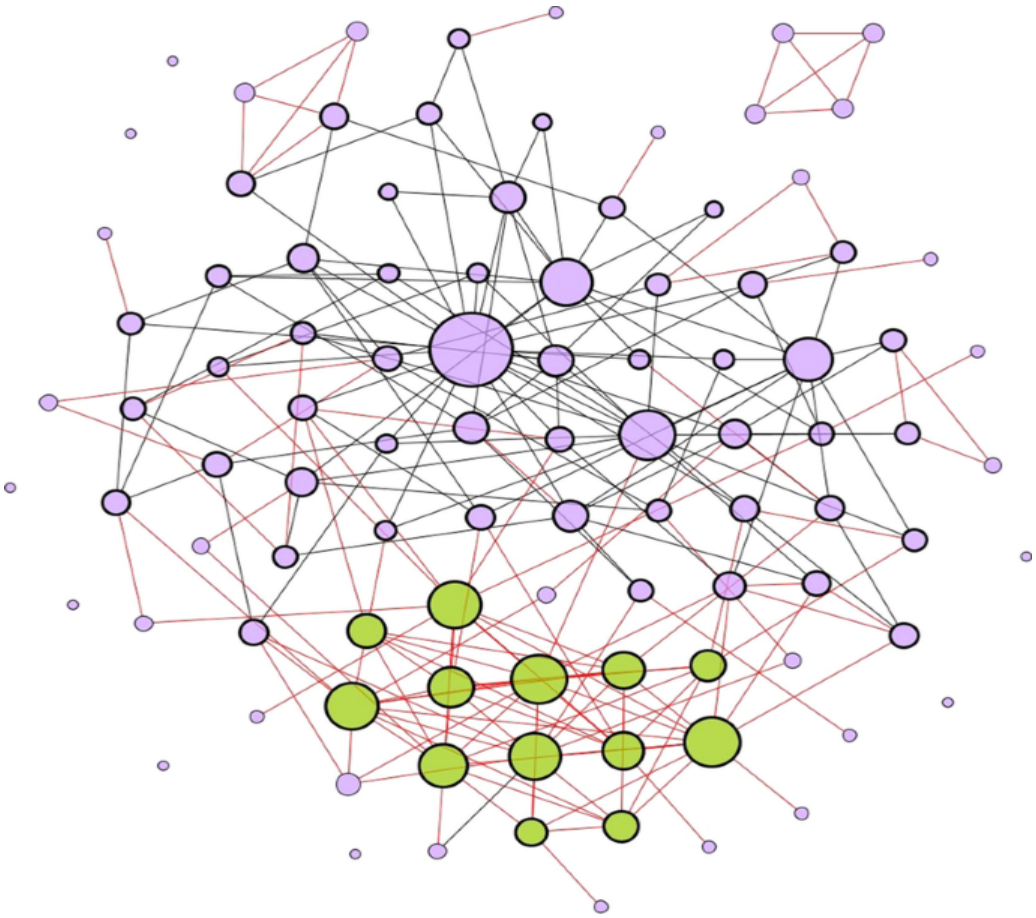

Figure 2.1: Network model and analysis of the spread of Covid-19

2.3 Epidemic Models

Mathematical and computational models known as epidemic models are used to predict and study the spread of infectious diseases within a population. These models seek to comprehend how infectious diseases, such as viruses or bacteria, travel from person to person, as well as how disease dynamics change over time. [3]

The link between social networks and the transmission of disease is one of the factors driving the scientific community's significant investment in the field. Diseases spread through networks of human connections. [4] Networks and the epidemiology of infectious diseases that are spread directly are inseparably linked. [5] Epidemic models often represent a population as a collection of compartments, each of which represents a distinct disease-related state. The most common kind of epidemic model is the compartmental model, which separates the population into different groups or compartments based on the disease status, is the most prevalent type of epidemic model. In order to evaluate the effectiveness of interventions and control measures, they enable researchers and public health professionals to investigate how diseases spread over time and under diverse settings. [6]

The SIR model, one of the most often used epidemic models, tracks the movement of people between several compartments depending on variables including transmission rates and recovery rates. Researchers can calculate the size of the susceptible population, the peak of the outbreak, and the final

number of recovered persons by examining these transitions. Other basic models are SI model and SEIR model. [4]

Epidemic models are essential for assisting in disease control efforts to protect the health of populations everywhere, facilitating preparedness for anticipated outbreaks, and directing public health decision-making. [7]

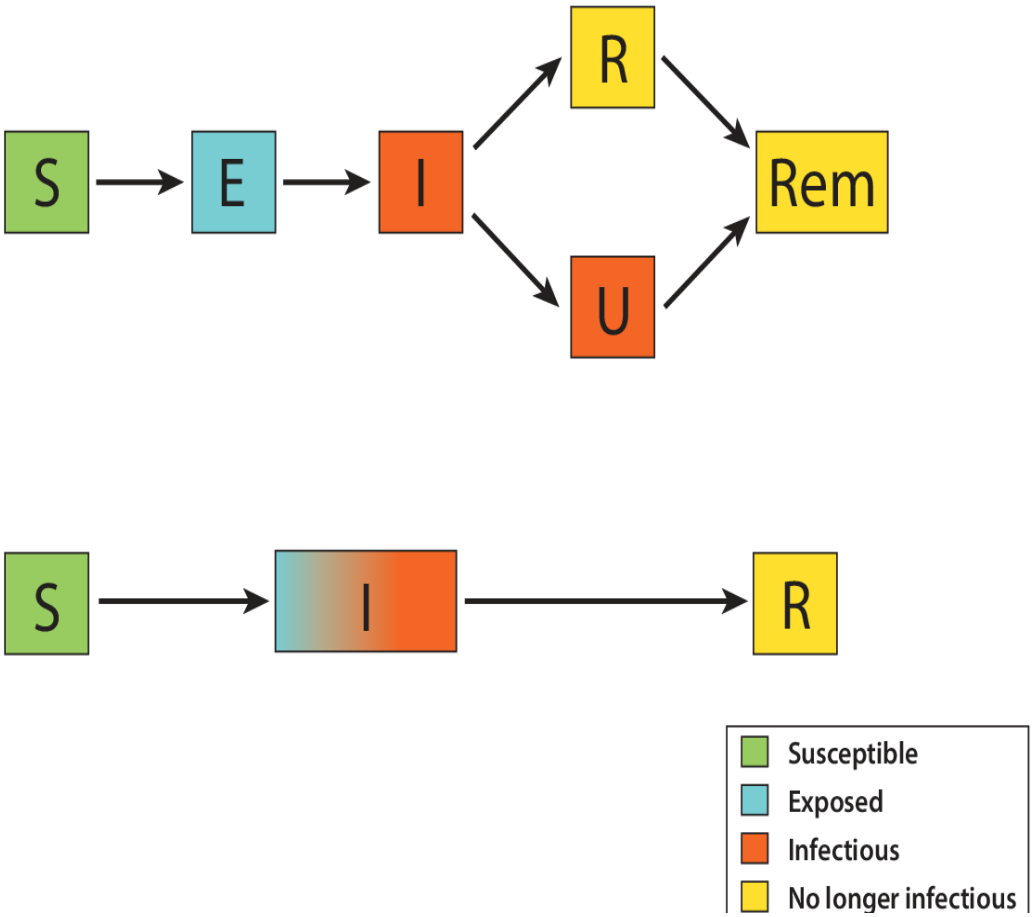

Figure 2.2: Epidemic Models

2.4 SIR Modeling

A sort of compartmental modeling called SIR modeling is used to research and assess how infectious illnesses propagate through a population. The code word ”SIR” stands for Susceptible (S), Infectious (I), and Recovered (R), the three basic compartments that make up the model. [8]

According to the SIR model, the population is split into the following three compartments: Susceptible (S), Infectious (I), and Recovered (R). The SIR model makes the assumption that people can switch between compartments in accordance with the dynamics of the illness. As opposed to infectious people who recover and move to the recovered compartment, susceptible people get sick and move to the infectious compartment. Importantly, because they have acquired immunity, those inside the restored compartment do not revert to the susceptible state. [9]

The SIR model's dynamics are controlled by a set of ordinary differential equations (ODEs) that define how the population transitions between the three compartments over time. The SIR model's important parameters are the transmission rate (β), which represents the rate at which susceptible individuals become infected, and the recovery rate (γ), which represents the pace at which infected individuals recover and migrate to the recovered compartment. [4]

Figure 2.3: SIR Epidemic Model

2.5 SEIR Modeling

SEIR modeling is a development of the classic SIR model, which is used to examine the transmission of infectious illnesses within a community. The SEIR model contains an additional compartment for persons who have been Exposed (E) to the infectious agent but are not yet infectious. This change allows the model to account for the disease's incubation period, which occurs when individuals have been exposed to the virus but are not yet capable of infecting others. [10]

The population is divided into four compartments in the SEIR model based on their disease status: Susceptible (S), Exposed (E), Infectious (I), and Recovered (R).

Transitions between these compartments are guided by a set of ordinary differential equations (ODEs) that define how the population travels between them over time. The SEIR model's key parameters are the transmission rate (β), which represents the rate at which susceptible individuals become infected, the incubation period ($1/\alpha$), which represents the time from exposure to becoming infectious, and the recovery rate (γ), which represents the rate at which infected individuals recover and move to the recovered compartment. [11]

The SEIR model is especially effective when examining diseases that have a notable incubation period, during which individuals are exposed to the pathogen but not infectious. By taking this delay in illness progression into account, the SEIR model gives a more realistic picture of disease dynamics and may be used to estimate disease peaks and evaluate the efficacy of control strategies. [12]

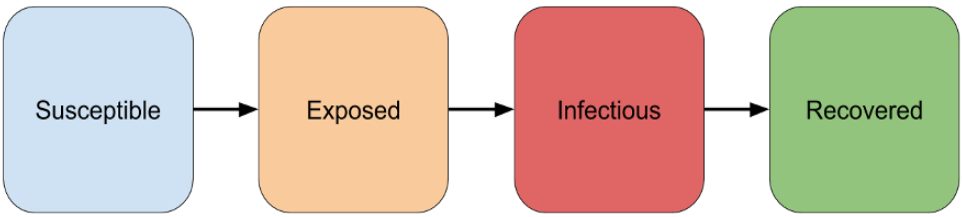

Figure 2.4: SEIR Epidemic Model

2.6 SIRD Modeling

In epidemiology, SIRD modeling is a mathematical framework used to understand and predict the spread of infectious diseases within a population. It categorizes individuals into four groups: Susceptible (S), Infected (I), Recovered (R), Deceased (D). In SIRD Model the disease transmission rate is (β), (γ) is the recovery rate, and (μ) is the mortality rate. The underlying hypotheses in this model are that recovered people are no longer susceptible to infection, and that deaths due to other causes (other than the disease under investigation) are ignored. Furthermore, when containment measures such as travel bans are applied, the territory under consideration is thought to be separated from other regions, which is a valid assumption. [13]

SIRD models use differential equations to explain how individuals transition between these states throughout time. It simplifies disease dynamics by assuming a fixed population size and homogeneous mixing. While SIRD models can not account for all real-world complications, they are useful for understanding how infectious illnesses spread in a population. [14]

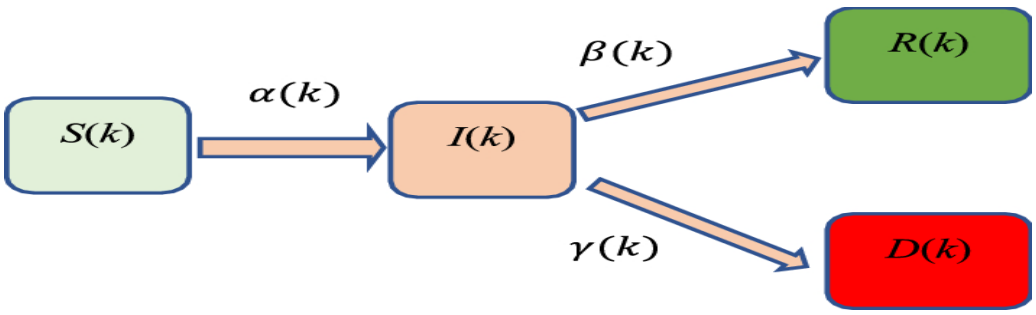

Figure 2.5: SIRD Epidemic Model

2.7 Implications for Public Health

Epidemic models, such as the SIR, SEIR and SIRD models, are useful in public health and real-world scenarios. [15] They are critical in understanding the dynamics of infectious illnesses and directing public health treatments. [16] Here are some ways these models are applied: Predicting Disease Spread, Assessing Intervention Strategies, Optimizing Resource Allocation, Designing Vaccination Strategies, Real-Time Monitoring and Early Warning Systems, Understanding Disease Severity and Impact, COVID-19 Pandemic Response, Influenza Vaccination Campaigns, Predicting Disease Spread in Urban Areas. [17]

During infectious disease outbreaks and pandemics, epidemic models provide critical tools for public health authorities to make data-driven choices, implement effective disease control methods, and protect the health and well-being of populations.

The article "Networks and epidemic models," authored by Matt J. Keeling and Ken T. D. Eames, explores the close relationship between networks and epidemiology in the early models that relied on population-wide random-mixing. Comprehending network topology facilitates the computation of epidemic dynamics in models at the population level. Comprehending mixing networks and their distinctions from the random-mixing norm can prove beneficial in the anticipation and management of epidemics. [5]

Weiss, Howard (Howie) proposed an article titled "The SIR model and the Foundations of Public Health." Present and examine a fundamental infectious disease transmission model, providing a theoretical framework for public health interventions and emphasizing key elements. [18]

The COVID-19 pandemic has spread quickly throughout the world, with 55 studies examining epidemic prediction models. This is discussed in a paper titled "COVID-19 epidemic prediction and the impact of public health interventions: A review of COVID-19 epidemic models," which was proposed by Yue Xiang, Yonghong Jia, Linlin Chen, Lei Guo, Bizhen Shu, and Enshen Long. [19]

2.8 Literature Analysis

Implementing epidemic models like the SIR and SEIR models involves several key steps to make them applicable and effective in real-world scenarios. Like Data Collection and Preprocessing, Model Selection and Calibration, Numerical Simulation, Validation and Sensitivity Analysis, Model Refinement, Real-Time Data Integration, Scenario Planning and Policy Evaluation, Visualizations and Communication, Model Updating and Iteration, Collaboration and Feedback.

Collect relevant information, preprocess it, select the best model, calibrate the parameters, and employ numerical techniques to create an effective epidemic model. To determine the accuracy of forecasts, compare them to historical data and run a sensitivity analysis. Refine the model if it doesn't fit actual observations. Integrate the model with surveillance data to make predictions in real time and evaluate the effectiveness of control measures. To evaluate intervention techniques, guide decision-making, and effectively convey findings, simulate numerous scenarios using the model. As new information

becomes available or conditions change, the model should be updated and its parameters recalculated. To guarantee a thorough strategy, work with epidemiologists, data scientists, policymakers, and healthcare professionals. Also, take stakeholder feedback into account to increase applicability and usefulness.

Chapter 3

Method

We have proposed a framework or a methodology flowchart according to which we have proceeded with the research work. The first step was collecting the data. After collecting data, we calculated the initial Susceptible, deaths and recoveries then we calculated the value of estimated Infection rate and Recovery rate then we have created the SIR model using this data and values.

After that we have created the SEIR Model. To create SEIR Model firstly, we need the initial number of Exposed individuals then we need the incubation period and the rate of progression from exposed to infection.

Lastly, to create the SIRD model we have calculated the Morality rate then we created the SIRD Model

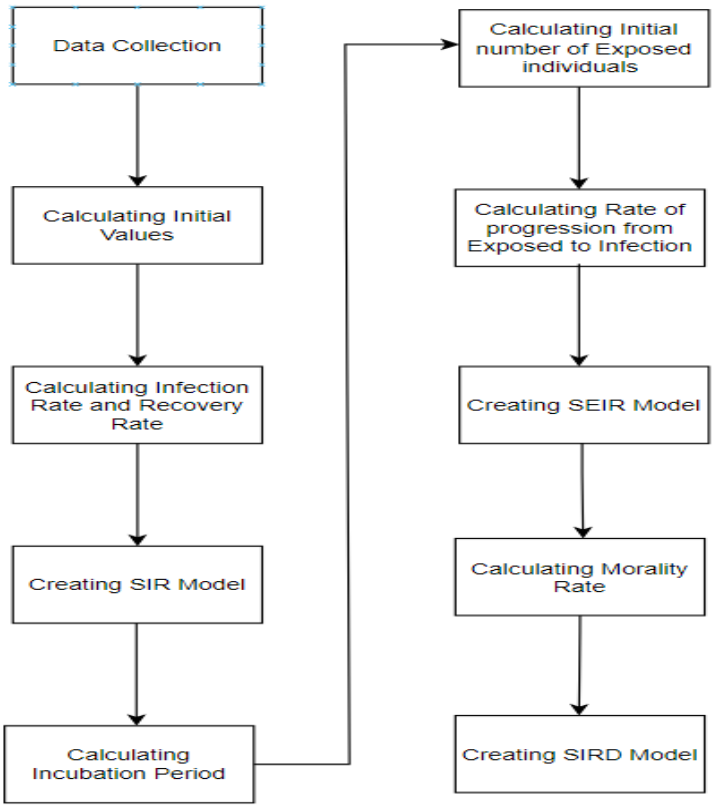

Figure 3.1: Proposed Framework

3.1 Data Collection

The purpose of this research is to make mathematical model to understand and predict the spread of Infectious Diseases. To make an SIR model we need some data, we need the day-by-day data. We have collected the data of COVID-19 in Bangladesh from Kaggle [20]. The Data-set we are using has 4 attributes: Date, Infected, Recovered and Deaths. The data type of Date is string and the data type of Infected, Recovered and Deaths is integer. We have also made another data set with the help of this data-set. On the another data-set we have 5 attributes: Date, Infected, Recovered, Deaths and Exposed. The data type of Date is string, the data type of Infected, Recovered and Deaths is integer and the data type of Exposed is float. With this data-set we will be able to calculate the initial values.

3.2 Calculating the initial Susceptible, Deaths and Recoveries

Firstly, we need to calculate some initial values to make the SIR model. Total population will be constant while making an SIR model. The total population of Bangladesh is 167,420,951 [21] as of 2020. To calculate the initial susceptible, we have to subtract the initial infected, deaths and recoveries from the total population by assuming that the recovered people will not be infected again.
From the data we found that, the initial infected is 3 individuals and recovered and deaths are 0.
The initial susceptible is 167420948.

3.3 Estimating the Infection rate and Recovery rate

We need an estimated value of Infection rate and Recovery rate to create the SIR model. The infection rate can vary depending on the characteristics of the virus. Highly transmissible viruses, such as the Delta variant of SARS-CoV-2, have shown higher infection rates compared to earlier variants [22]. Factors like population density, social interactions, and adherence to preventive measures (e.g., mask-wearing, social distancing) can influence the transmission rate [23]. The recovery rate depends on factors such as the severity of the disease, available healthcare resources, and treatment interventions. Age, pre-existing health conditions, and the effectiveness of medical interventions (e.g., therapeutics, vaccines) can influence the recovery rate. As we don't have enough information about the actual value of infection rate and recovery rate of COVID-19 in Bangladesh, we have taken an assumption value of Infection rate(β). And we have also taken the Recovery rate(γ) as an assumption. Which is 1/14. This is based on the recovery time of COVID-19, which is 14 days.
The estimated value of Infection rate: 0.25
The estimated value of Recovery rate: 0.07

3.4 Creating SIR model

First, we define the initial conditions, which include the total population of Bangladesh in 2020, the initial number of infected, recovered, and death individuals. The initial number of susceptible individuals is calculated based on the total population and the other initial conditions. Next, the we define the model parameters, including the transmission rate (beta), the recovery rate (gamma), and the maximum time to simulate. Then, we define the SIR model as a set of differential equations that describe the rate of change of susceptible, infected, and recovered individuals over time.

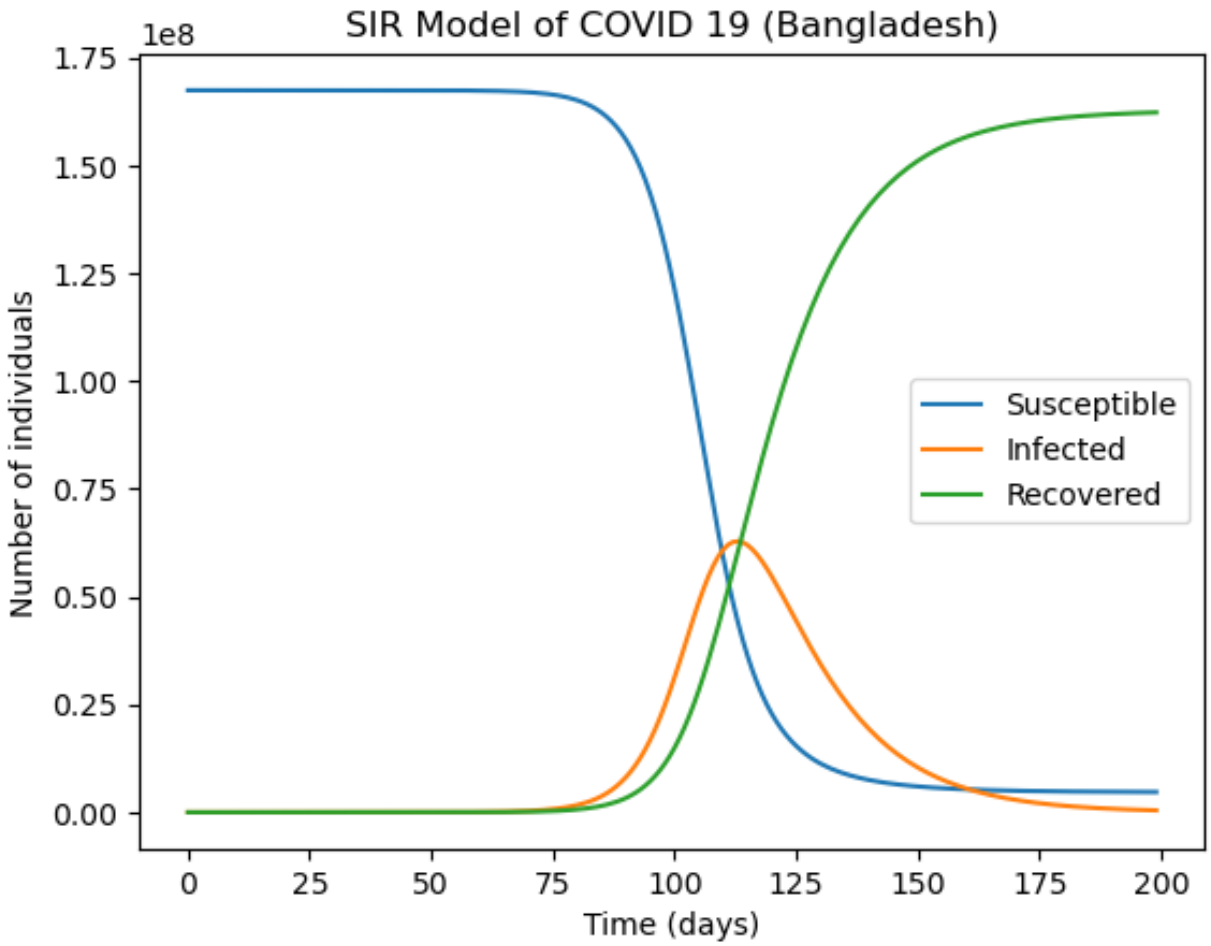

Figure 3.2: SIR Model

3.5 Calculating Incubation Period

The incubation period of COVID-19, which is the time it takes for symptoms to appear after a person has been infected with the virus, typically ranges from 2 to 14 days. [24] There have been rare cases where the incubation period exceeded 14 days, but they are not common. However, on February 22, the local government of Hubei Province reported a case that required a 27-day incubation period. [25] Additionally, a JAMA study of five cases that was published on February 21 included a case that had an incubation period of 19 days. [26] A study published on February 9th had seen the first observation of an outlier during the 24-day incubation period. [27]

The mean incubation period was estimated to be 6.4 days. The incubation period ranges from 2.1 to 11.1 days. The upper limit of 11.1 days could be considered conservative. [28]

A mean of 6.4 days was estimated for the incubation period. The duration of incubation spans from 2.1 to 11.1 days. One could argue that the 11.1-day upper limit is conservative. Our incubation period is set at 6.4 days. The time frame for incubation spans from 2.1 to 11.1 days. Let's say nine days. Using the following formula, we have determined the proportion of people in the exposed compartment at any given time,

Percentage of individuals in the exposed compartment = (Incubation period / Total infectious period) * 100

Therefore, with an incubation period of 6.4 days and an infectious period of 9 days, approximately 71.11 percentage of the infected individuals would be in the exposed compartment at any given time.

3.6 Calculating Initial number of Exposed individuals

We have found that, approximately 71.11 percentage of the infected individuals would be in the exposed compartment at any given time. In March 3, 2020 the initial number of infected individuals were 3 persons. So, the initial number of exposed individuals will be 2.1333.

3.7 Calculating the rate of progression from Exposed to Infection

In the SEIR model, the parameter sigma represents the rate at which exposed individuals become infectious. It is defined as the inverse of the average duration of the latent period.

To estimate the value of sigma for a specific disease and population, we need data on the progression of the disease in that population, such as the incubation period of the disease and the time between infection and the onset of symptoms. One common approach is to fit the SEIR model to the observed data using a statistical modeling technique such as maximum likelihood estimation or Bayesian inference. This involves estimating the values of all the model parameters, including sigma, that best fit the observed data.

To calculate the value of Sigma, we need to take the reciprocal of the average duration of the latent

period (incubation period). The average duration of the latent period can be calculated as the average of the lower and upper bounds of the incubation period range. Using the given incubation period range of 2.1 to 11.1 days, the calculation would be as follows:
Average duration of the latent period = (2.1 + 11.1) / 2 = 6.6 days
The value of Sigma would then be the reciprocal of the average duration of the latent period.
Therefore, in the SEIR model with an incubation period ranging from 2.1 to 11.1 days and a latent period of 6.6 days, the value of Sigma is approximate 0.1515

3.8 Creating SEIR Model

First, we define the total population (N), initial numbers of infected, exposed, and recovered individuals, as well as the infection rate, recovery rate, and rate of progression from exposed to infectious (sigma). Then we represent the differential equations of the SEIR model. It takes the current state (y), time (t), and model parameters (beta, gamma, and sigma) as input and returns the rates of change for each compartment (dSdt, dEdt, dIdt, dRdt).

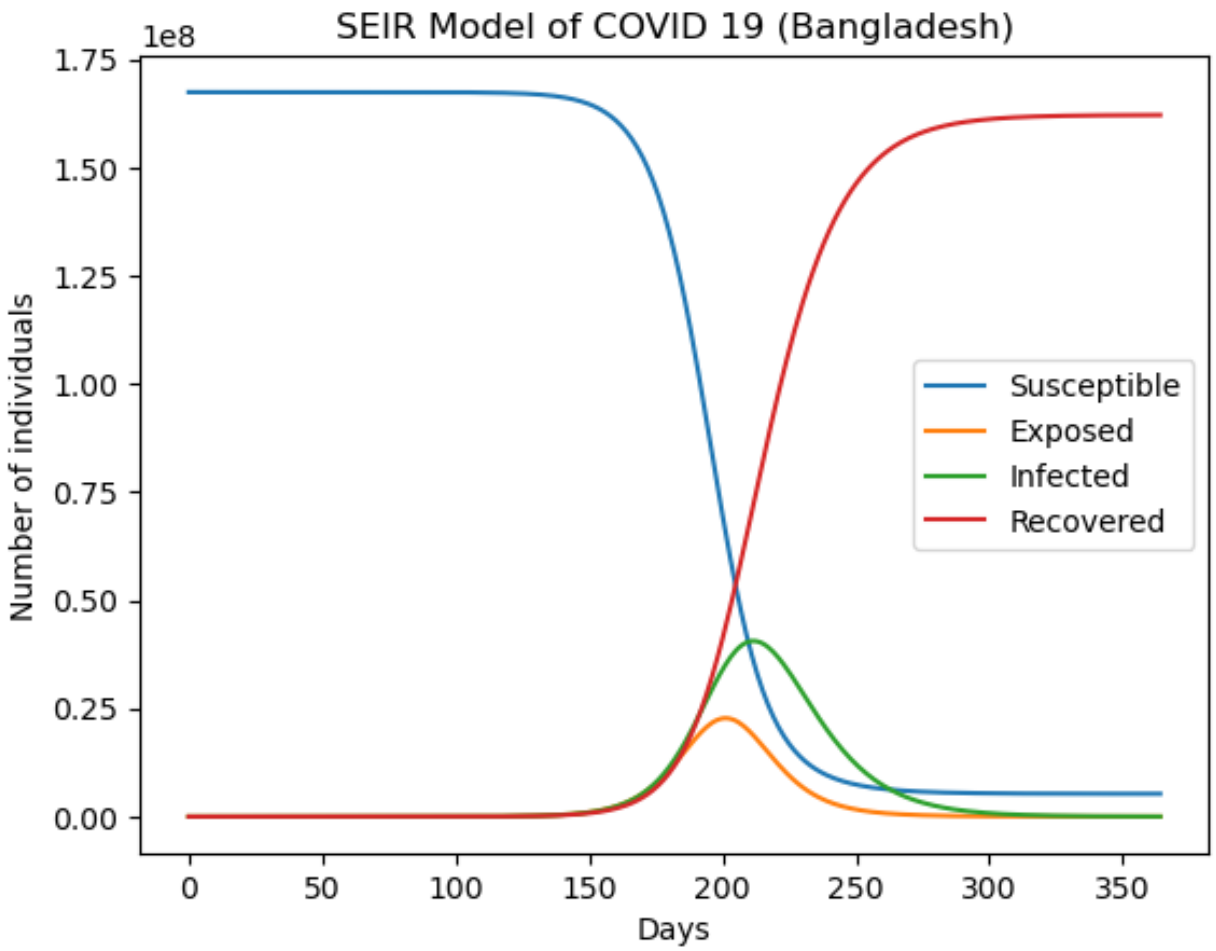

Figure 3.3: SEIR Model

3.9 Calculating the Mortality rate

The mortality rate (mu) can be approximated by dividing the number of deaths (D) by the number of infected individuals (I). This calculation assumes that all deaths are reported accurately and that the number of reported infections is a reasonable estimate of the true number of infections.

mu = D / I

Total Deaths = 183

Total Infected = 10,929

Death Rate = $\left(\frac{183}{10{,}929}\right) \times 100 \approx 1.67\%$

Therefore, the death rate based on the provided data is approximately 1.67%

3.10 Creating SIRD Model

First, we define the total population (N), initial numbers of infected, recovered, and death individuals, as well as the infection rate, recovery rate, and morality rate. Then we represent the differential equations of the SIRD model. It takes the current state (y), time (t), and model parameters (beta, gamma, and mu) as input and returns the rates of change for each compartment (dSdt, dEdt, dIdt, dRdt).

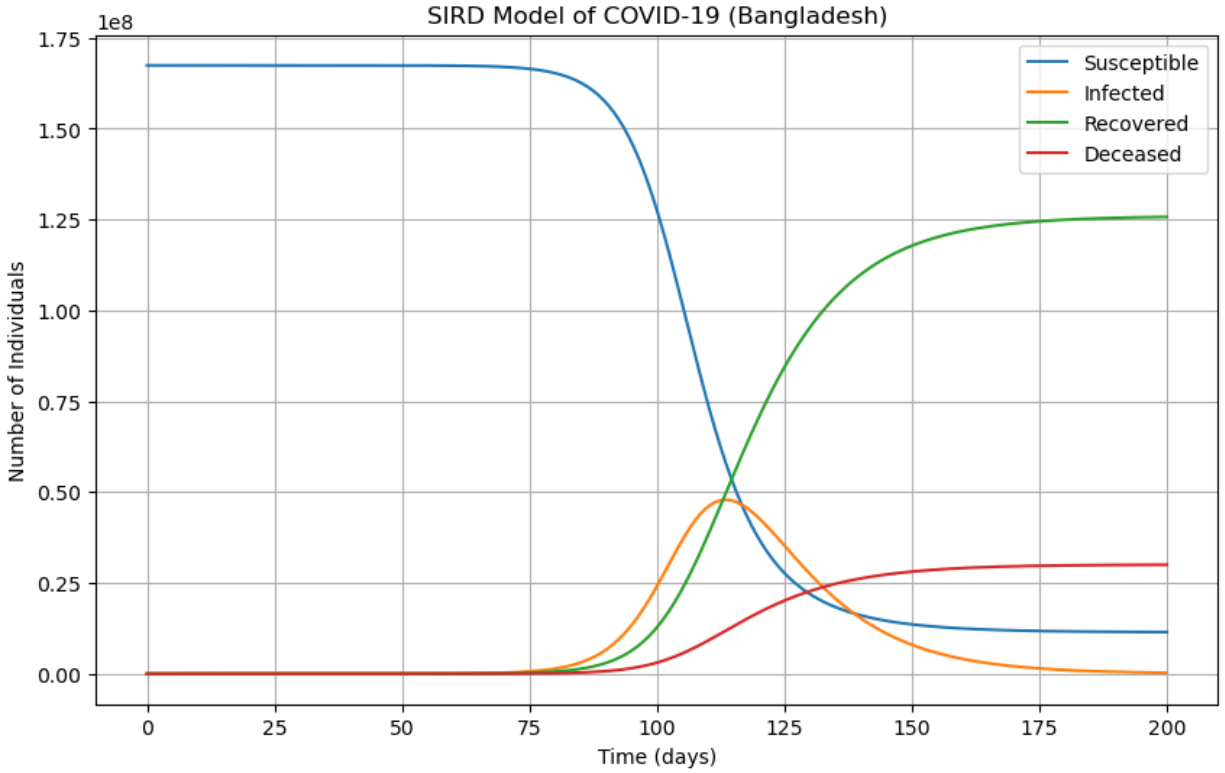

Figure 3.4: SIRD Model

Chapter 4

Results

4.1 Introduction

Considering infectious diseases pose serious risks to public health, modeling and analysis of these diseases are essential for efficient disease control and prevention. This study models the spread of infectious diseases within communities using a graph theory approach, providing useful knowledge into the dynamics of disease. The outcomes and conclusions of this study give us a complete understanding of how network-based modeling might improve our capacity to predict, control, and manage infectious disease epidemics.

4.2 Result Analysis

We have organized clearly every stage of our study process, from data collecting to final result analysis, in the Methodology portion of Chapter 3. Our research aims to provide a comprehensive framework for analyzing disease dynamics, directing intervention options, and eventually improving our ability to prevent and control infectious disease outbreaks, so protecting public health. Using graph theory to represent infectious diseases allows for the identification of key nodes (individuals, locations, or communities) that play critical roles in disease transmission. These nodes frequently serve as network hubs, and targeting them for intervention strategies can have a major influence on disease control. The degree of connection within a population network is an important component in disease communication. Rapid transmission is facilitated by well connected networks, whereas fractured networks can slow the spread. Understanding these network structures is critical for putting effective control strategies in place. Models based on graph theory can locate developing disease hot-spots, areas with a high risk of disease introduction, or local outbreaks. These results help to prioritize resource allocation and surveillance operations. In order to better understand risks and potential for enhancing healthcare systems and response capacities, it is helpful to analyze the durability and adaptability of networks in the event of disease outbreaks. The goal of this study is to create mathematical model that may be used to understand and forecast the spread of infectious diseases. We work with mathematical

models-SIR, SEIR and SIRD. We approached this network models with connecting nodes and graph. The description of patterns of interaction using a network of nodes and links is a critical component of applying the network approach to simulating an epidemic. Individuals or families are represented by nodes, and the links describe the interactions that may spread disease.

In Chapter 3 we can see the results of the SIR, SEIR and SIRD model. During making this model, our infection rate was 0.25 and our recovery rate was 0.07. Now, the results can be different if we change the infection rate and recovery rate. Reducing the infection rate of COVID-19 requires a comprehensive and multi-faceted approach involving both individual actions and collective efforts. Here are some effective measures to help reduce the transmission of COVID-19:

1. Vaccination: Encouraging widespread vaccination is one of the most effective ways to reduce the infection rate. Vaccines help protect individuals from severe illness and reduce the risk of transmission. Promote vaccination campaigns and ensure equitable access to vaccines.

2. Wearing masks: Encourage the use of masks, especially in crowded indoor settings or when physical distancing is challenging. 3. Practicing good hand hygiene: Promote frequent hand-washing with soap and water for at least 20 seconds or use hand sanitizers.

4.Maintaining physical distance: Encourage people to maintain a safe distance of at least 1 meter (3 feet) from others, particularly in public spaces

5. Travel Restrictions and Border Controls: Implement travel restrictions, quarantine measures, and screening protocols to limit the importation and spread of the virus across borders.

While the recovery rate of COVID-19 is primarily dependent on an individual's immune response and overall health, there are several measures that can support and improve recovery outcomes. Here are some key approaches:

1. Early Detection and Diagnosis: Prompt detection and diagnosis of COVID-19 cases allow for early intervention and appropriate medical care. Widely available testing, contact tracing, and surveillance systems help identify cases early and prevent delays in treatment.

2. Vaccination: Encouraging vaccination against COVID-19 is crucial in reducing severe illness and increasing recovery rates. Vaccines have been shown to be highly effective in preventing hospitalizations and improving outcomes for those who do contract the virus.

3. Treatment Options: Stay updated with the latest treatment guidelines and recommendations from reputable health organizations and regulatory bodies. Explore and implement evidence-based treatments, such as antiviral medications, anti-inflammatory drugs, and oxygen therapy, as appropriate and under medical supervision.

4. Research and Collaboration: Support ongoing research efforts to better understand COVID-19 and its long-term implications. Collaborate with the scientific community to identify innovative approaches and treatments that can enhance recovery outcomes.

By following the upper steps, we can reduce the infection rate and increase the recovery rate. By this, our results can be different.

Chapter 5

Discussion

5.1 Discussion

Network-Based Modeling of Infectious Disease Spread Using a Graph Theory Approach provides a comprehensive toolkit for understanding and managing infectious disease transmission dynamics within populations. This method offers a number of important benefits and implications for public health and epidemiology. For example, it provides a comprehensive view of disease propagation by portraying interactions between individuals or things as a network. This model accounts for the intricate web of interactions and relationships that underpins disease transmission. This method pinpoints essential intervention locations by identifying significant nodes and hubs in the network. Targeting these influential nodes can have a disproportionate impact on disease control efforts, resulting in more efficient resource allocation.

Another key feature of the technique is its capacity to consider time and space dynamics. It recognizes that geography and seasonality influence disease propagation, allowing for location-specific and time-sensitive interventions. This versatility is especially useful when dealing with infectious diseases that have varied patterns in different places and seasons.

Furthermore, incorporating network models into real-time disease surveillance systems improves early warning capabilities. Authorities can swiftly identify and respond to epidemics by continuously monitoring the network's evolution and spotting deviations from normal patterns, thereby averting their progression. The discussion also emphasizes the significance of data-driven decision-making in infectious disease control. Accurate data collection and analysis are essential for building trustworthy network models. This highlights the need of having a solid data infrastructure and monitoring technologies in place to support efficient network-based modeling.

5.2 Future Work

Future study could benefit greatly from network-based modeling of infectious disease spread utilizing a graph theory approach. Integrating big data, machine learning and AI, dynamic network models, multi-scale modeling, behavioral and social factors, network-based vaccination strategies, model validation and calibration, global collaboration, ethical considerations, interdisciplinary research, and validation through real-world events are just a few of the key areas. These developments will aid in improving the accuracy and granularity of disease transmission models, allowing for more precise forecasts and interventions. Incorporating behavioral and social elements into network models can also assist researchers understand how human behavior promotes disease spread. Additionally, tailoring vaccination techniques based on network topology and characteristics can improve coverage and decrease disease transmission. Real-world occurrences can provide vital input and increase model correctness when validated continuously. Our modeling techniques must adapt to the changing nature of infectious illnesses in order to effectively counter new dangers and safeguard public health worldwide.

Chapter 6

Conclusion

The findings and uses of network-based modeling are not limited to a particular illness but are adaptable to a wide range of infectious agents, making it a valuable tool for both endemic and emerging diseases. As infectious diseases continue to pose threats to global health security, the knowledge generated via this method informs evidence-based decision-making, optimizes resource allocation, and strengthens our ability to protect public health. As we progress, it is critical that we continue to improve our understanding of network-based modeling, refine our methodology, and increase our data sources. Collaboration between researchers, clinicians, and policymakers will strengthen the applicability of this technique in real-world circumstances

In an ever-changing environment, Network-Based Modeling of Infectious Diseases Spread via Graph Theory is a critical pillar in our collective response to pandemics and endemic health challenges.

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Appendix A

Codes

A.1 Source Code

SIR, SEIR, SIRD Model code

A.2 Screenshots of code

```python
import numpy as np
import matplotlib.pyplot as plt

# Define the initial conditions
total_population = 167420951 # Total population of Bangladesh in 2020
initial_infected = 3          # Initial number of infected individuals
initial_recovered = 0         # Initial number of recovered individuals
initial_deaths = 0          # Initial number of deaths individuals
initial_susceptible = total_population - initial_infected - initial_recovered - initial_deaths

# Define the model parameters
beta = 0.25 # Transmission rate
gamma = 0.07 # Recovery rate
t_max = 200 # Maximum time to simulate (days)

# Define the time grid
t = np.arange(t_max)

# Define the SIR model
def sir_model(S, I, R, beta, gamma, N):
    dSdt = -beta * S * I / N
    dIdt = beta * S * I / N - gamma * I
    dRdt = gamma * I
    return dSdt, dIdt, dRdt

# Simulate the model
S = np.zeros(t_max)
I = np.zeros(t_max)
R = np.zeros(t_max)
S[0] = initial_susceptible
I[0] = initial_infected
R[0] = initial_recovered

for i in range(1, t_max):
    dSdt, dIdt, dRdt = sir_model(S[i-1], I[i-1], R[i-1], beta, gamma, total_population)
    S[i] = S[i-1] + dSdt
    I[i] = I[i-1] + dIdt
    R[i] = R[i-1] + dRdt

# Plot the results
plt.plot(t, S, label='Susceptible')
plt.plot(t, I, label='Infected')
plt.plot(t, R, label='Recovered')
plt.xlabel('Time (days)')
plt.ylabel('Number of individuals')
plt.title('SIR Model of COVID 19 (Bangladesh)')
plt.legend()
plt.show()
```

Figure A.1: SIR Model code

```python
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt


# set model parameters
N = 167420951          # total population
I0 = 3                 # initial number of infected individuals
E0 = 2.1333            # initial number of Exposed individuals
R0 = 0                 # initial number of recovered individuals
S0 = N-I0-E0-R0        # initial number of susceptible individuals
beta = 0.25           # infection rate
gamma = 0.07          # recovery rate
sigma = 0.1515         # rate of progression from exposed to infectious

# define SEIR function
def SEIR_model(y, t, beta, gamma, sigma):
    S, E, I, R = y
    dSdt = -beta * S * I / N
    dEdt = beta * S * I / N - sigma * E
    dIdt = sigma * E - gamma * I
    dRdt = gamma * I
    return dSdt, dEdt, dIdt, dRdt

# set initial conditions
y0 = S0, 0, I0, R0

# set time points
t = np.arange(365)

# solve SEIR model
from scipy.integrate import odeint
sol = odeint(SEIR_model, y0, t, args=(beta, gamma, sigma))

# plot the results
plt.plot(t, sol[:, 0], label='Susceptible')
plt.plot(t, sol[:, 1], label='Exposed')
plt.plot(t, sol[:, 2], label='Infected')
plt.plot(t, sol[:, 3], label='Recovered')
plt.xlabel('Days')
plt.ylabel('Number of individuals')
plt.title('SEIR Model of COVID 19 (Bangladesh)')
plt.legend()
plt.show()
```

Figure A.2: SEIR Model code

```python
import numpy as np
from scipy.integrate import odeint
import matplotlib.pyplot as plt

# Set the initial conditions
N = 167420951  # Population of Bangladesh
I0 = 3  # Initial number of infected individuals
R0 = 0  # Initial number of recovered individuals
D0 = 0  # Initial number of deceased individuals
S0 = N - I0 - R0 - D0  # Initial number of susceptible individuals

# Set the model parameters
beta = 0.25  # Transmission rate
gamma = 0.07  # Recovery rate
mu = 0.0167  # Mortality rate

# Set the time points to simulate
t = np.linspace(0, 200, 200)  # Simulate for 365 days

# Define the SIRD model equations
def sird_model(y, t, N, beta, gamma, mu):
    S, I, R, D = y
    dSdt = -beta * S * I / N
    dIdt = beta * S * I / N - gamma * I - mu * I
    dRdt = gamma * I
    dDdt = mu * I
    return dSdt, dIdt, dRdt, dDdt

# Solve the SIRD model equations
y0 = S0, I0, R0, D0
sol = odeint(sird_model, y0, t, args=(N, beta, gamma, mu))
S, I, R, D = sol[:, 0], sol[:, 1], sol[:, 2], sol[:, 3]

# Plot the results
plt.figure(figsize=(10, 6))
plt.plot(t, S, label='Susceptible')
plt.plot(t, I, label='Infected')
plt.plot(t, R, label='Recovered')
plt.plot(t, D, label='Deceased')
plt.xlabel('Time (days)')
plt.ylabel('Number of Individuals')
plt.title('SIRD Model of COVID-19 (Bangladesh)')
plt.legend()
plt.grid(True)
plt.show()
```

Figure A.3: SIRD Model code

Appendix B

Data-set

B.1 COVID-19 Data-set for SIR Model

	A	B	C	D
1	Date	Infected	Recovered	Deaths
2	3/8/2020	3	0	0
3	3/9/2020	3	0	0
4	3/10/2020	3	0	0
5	3/11/2020	3	2	0
6	3/12/2020	3	2	0
7	3/13/2020	3	2	0
8	3/14/2020	3	2	0
9	3/15/2020	5	2	0
10	3/16/2020	8	3	0
11	3/17/2020	10	3	0
12	3/18/2020	14	3	1
13	3/19/2020	17	3	1
14	3/20/2020	20	3	1
15	3/21/2020	24	3	2
16	3/22/2020	27	5	2
17	3/23/2020	33	5	3
18	3/24/2020	39	5	4
19	3/25/2020	39	5	5
20	3/26/2020	44	11	5

Figure B.1: Data-set 1

B.2 COVID-19 Data-set for SEIR Model

Date	Infected	Recovered	Deaths	Exposed
3/8/2020	3	0	0	2.1333
3/9/2020	3	0	0	2.1333
3/10/2020	3	0	0	2.1333
3/11/2020	3	2	0	2.1333
3/12/2020	3	2	0	2.1333
3/13/2020	3	2	0	2.1333
3/14/2020	3	2	0	2.1333
3/15/2020	5	2	0	3.5555
3/16/2020	8	3	0	5.6888
3/17/2020	10	3	0	7.111
3/18/2020	14	3	1	9.9554
3/19/2020	17	3	1	12.0887
3/20/2020	20	3	1	14.222
3/21/2020	24	3	2	17.0664
3/22/2020	27	5	2	19.1997
3/23/2020	33	5	3	23.4663
3/24/2020	39	5	4	27.7329
3/25/2020	39	5	5	27.7329
3/26/2020	44	11	5	31.2884

Figure B.2: Data-set 2

Appendix C

Equations

C.1 SIR Model

SIR model Equation:

$$\begin{aligned} \frac{dS}{dt} &= -\beta \cdot S \cdot I \\ \frac{dI}{dt} &= \beta \cdot S \cdot I - \gamma \cdot I \quad [4] \\ \frac{dR}{dt} &= \gamma \cdot I \end{aligned}$$

where,

S = number of susceptible individuals

I = number of infected individuals

R = number of recovered individuals

t = time

dS/dt, dI/dt, dR/dt = rates of change of S, I, R with respect to time

C.2 SEIR Model

SEIR model Equation:

$$\begin{aligned}
\frac{dS}{dt} &= -\beta \cdot \frac{S \cdot I}{N} \\
\frac{dE}{dt} &= \beta \cdot \frac{S \cdot I}{N} - \sigma \cdot E \qquad [11] \\
\frac{dI}{dt} &= \sigma \cdot E - \gamma \cdot I \\
\frac{dR}{dt} &= \gamma \cdot I
\end{aligned}$$

where:

S = number of susceptible individuals

E = number of exposed individuals

I = number of infected individuals

R = number of recovered individuals

N = total population size (N = S + E + I + R)

t = time

β = average rate of transmission (infection rate)

σ = average rate of transition from exposed to infectious

γ = average rate of recovery

C.3 SIRD Model

SIRD model Equation:

$$\begin{aligned}
\frac{dS}{dt} &= -\beta SI \\
\frac{dI}{dt} &= \beta SI - \gamma I - \mu I \quad [13] \\
\frac{dR}{dt} &= \gamma I \\
\frac{dD}{dt} &= \mu
\end{aligned}$$

In these equations:
S represents the number of susceptible individuals.
I represents the number of infected individuals.
R represents the number of recovered individuals.
D represents the number of deceased individuals.
(β) is the transmission rate, representing the probability of disease transmission from an infected individual to a susceptible individual per unit of time.
(γ) is the recovery rate, representing the rate at which infected individuals recover and move into the recovered compartment.
(μ) is the mortality rate, representing the rate at which infected individuals die.