Leveraging SIR and Barabási-Albert Models for Epidemic Modelling

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***Abstract*—The Susceptible, Infected, and Recovered (SIR) model predicts the number of living beings in a population who are infected and recovering from a disease. This article addresses the critical challenge of modelling and simulating the spread of contagious diseases in a population. Drawing inspiration from global events like the COVID-19 pandemic, our proposed simulation aims to comprehensively understand the epidemic dynamics and thus enhances the public awareness for effective decision-making. The proposed simulation integrates the computational models and simulation techniques, including the logistic functions, agent-based models, SIR models, and network-based spread models.**

***Index Terms*—Epidemic Simulation, Computational Modeling, Intervention Strategies, Agent-Based Modeling, SIR Model, Visualization Tool, Public Awareness, epidemic modelling, COVID-19.**

I. Introduction

Studying the spread of diseases that investigates the determinants, occurrence and distribution of diseases in a population is Epidemiology. There has been significant progress in the theory and application using mathematical research. A lot of epidemic models are formulated as dynamical systems of ordinary differential equations [1]–[8]. On March 11, 2020, the World Health Organisation (WHO) declared COVID-19 a pandemic [9]. Some factors such as population density distribution in the local region and living conditions further spread the infection. Contact with other individuals, both in the private and public sphere, increases the risk of transmitting the infection, even over a distance of more than 1 m [10].

This paper introduces simulation programs that integrate SIR models and Barabási-Albert graphs to simulate the spread of diseases, providing a valuable tool for researchers and policymakers alike. COVID-19 has highlighted the necessity for robust epidemic modeling to guide decision-making processes. Accurate models help predict the trajectory of the disease, assess the effectiveness of interventions, and anticipate the healthcare demand. The complex nature of COVID-19 transmission, influenced by factors: asymptomatic carriers and varying transmission rates, necessitates effective modelling approaches to capture the intricacies of real-world scenarios.

The SIR model is usually applied to the entire population of a region. The population is divided into three components: susceptible (S), infected (I) and recovered (R) [8]. Still, considerable evidence shows that the rate at which diseases spread is different in urban and rural areas due to the difference in population density [10]. Epidemics do not occur in isolation; they spread through social interactions and networks. The Barabási-Albert graph is used to generate networks that mimic the structure of real-world networks and exhibit scale-free properties. It is based on the growth of preferential attachment. The model starts with m nodes connected by at least one link. At the beginning of each time step, one new node is added to n existing nodes where n is less than m. Preferential attachment determines how new nodes connect to existing nodes in the network. The probability of a new node connecting to a node i is proportional to how densely linked node i already is. This implies that well-connected nodes are more likely to receive new links. Integrating Barabási-Albert graphs into epidemic models allows researchers to account for the heterogeneity in contact patterns, capturing the dynamics of disease spread more accurately.

Interactive visualizations allow us to understand the simulated spread of diseases in real time. The visualization feature is precious for conveying complex epidemiological concepts to a diverse audience, including policymakers and the general public. The dynamic network structures, represented by Barabási-Albert graphs, provide a nuanced understanding of how diseases propagate through interconnected populations. Unlike dynamic models, they reflect changes in social interactions, travel patterns, and community dynamics. The models are parameterized to be tailored to specific real-world scenarios and fine-tuned to local conditions. This adaptability is crucial because disease characteristics vary in every region and environment. Parameterization allows researchers to incorporate data-driven inputs, enhancing the accuracy and applicability of the simulations. The simulations offer a more holistic view of disease spread by combining the time-tested principles of SIR models with the dynamic realism of Barabási-Albert graphs. This could help devise targeted interventions, optimise resource allocation, and prepare for potential future outbreaks. The usefulness of these simulation programs extends to multiple stakeholders. For researchers, integrating dynamic network structures opens avenues for exploring the role of social connectivity in disease transmission. Policymakers can benefit from more accurate predictions and scenario analyses, leading to informed interventions and resource allocation decisions. The public gains a clearer understanding of the factors influencing disease spread, fostering community engagement and adherence to public health measures.

II. Related Work

In [11], the Susceptible–Exposed–Infected–Recovered model is used to simulate the disease spread, considering parameters like transmission rate, recovery rate, and incubation period with a focus on intervention dependencies. Researchers in [12] utilized the SIR model to simulate and analyze the dynamics of COVID-19 on Erdős–Rényi networks in Punjab, Pakistan. The authors in [13] proposed a novel methodology named RL2G for analyzing complex network structures, showcasing its efficiency in revealing topologies and its adaptability in various scenarios. The model operates by dividing a large input network into smaller subgraphs, understanding the individual topology of each subgraph, and concatenating those to construct the topology of the original graph. In [11], COVID-19 data from Pakistan was used for simulations. In [12], the authors focused on the dynamics of COVID-19 in Punjab, Pakistan. In [14], deterministic epidemic models enhanced by stochastic elements like white noise were used to determine the conditions required for the extinction or persistence of diseases within populations. The research introduces a modified definition of the primary reproduction number and implements mathematical modelling, equilibrium analysis and theoretical constructs to analyze disease dynamics.

The authors in [8] employed mathematical models to investigate optimal control strategies, specifically vaccination, for managing infectious diseases in populations. The study begins by analyzing a general epidemic model to identify an equilibrium state, then introduces vaccination as a control element in an optimal control problem. The methodology employs optimal control theory, Runge–Kutta [15] numerical methods, and real epidemic data to showcase the effectiveness of these strategies in minimizing infections and maximizing recoveries. The authors in [10] employed a mathematical model with two epidemiological models: population kinetics and regional kinetics models. The population kinetics model classifies individuals as susceptible, infected, recovered, or deceased (SIRD) and incorporates carriers who are unaware of their infection. The regional kinetics model extends the analysis to multiple geographical regions with individualized population movements. The methodology used in the work involves formulating differential equations for both models, incorporating carriers into the SIR model, and extending the model to regional dynamics. The time integration process utilizes the Crank and Nicholson [16] method with an iterative predictor-corrector scheme, improving accuracy and control through error-checking time-stepping algorithms. The models are initialized with known values, and they demonstrated the application of the methodology through numerical simulations.

The researchers in [17] developed the Susceptible-Exposed-Infected-Recovered (SEIR) epidemic disease model for investigating the infectious disease dynamics and control strategies. The model considers four population classes: Susceptible (S), Exposed (E), Infected/Infectious (I), and Recovered (R), and is governed by a set of differential equations. Parameters such as birth rate ($\wedge$), the natural death rate (μ), virus-induced fatality rate (α), and disease transmission probability (β) are defined. The paper introduces a numerical algorithm using a forward Euler finite-difference scheme [18] to solve the differential equations. The approach includes simulating disease dynamics, equilibrium points, and control measures like vaccination. Additionally, key epidemiological measures such as the basic Reproduction ratio (R0), Infection Fatality Rate (IFR), and Case Fatality Rate (CFR) are discussed to assess disease spread and severity. The methodology involves detailed mathematical analysis and numerical simulations to understand and control population infectious diseases.

The authors in [19] formulated the Susceptible-Exposed-Infected-Diagnosed–Recovered (SEIJR) epidemic model to analyze single outbreaks of SARS in Southern Ontario (Toronto), Singapore, and Hong Kong. The model incorporates important characteristics: varying susceptibility, the presence of asymptomatic individuals, mode of transmission, super-spreaders, etc. Two distinct susceptible classes, S1 and S2, are introduced in the work, representing varying degrees of susceptibility to SARS. The model includes classes for Exposed (E), Infected (I), Diagnosed (J), and Recovered (R) and considers disease-induced mortality. Diagnosed individuals are assumed to have a reduced impact on transmission (parameter l), trying to take into consideration effective isolation measures. A system of nonlinear differential equations describes the SEIJR model. Parameters p and q are arbitrarily fixed, while parameters l and a are optimized to fit data for Hong Kong, Singapore, and Toronto. The basic Reproductive ratio (R0) is calculated to evaluate the potential for spreading disease in each location. The values of l and a are adjusted to best match existing data, and the sensitivity of the model to variations in p and q is not explored due to its unknown nature. Parameters are optimized by least-squares criterion, providing epidemiological interpretations of the model's outcomes.

In [20], an SEIR model is used for modeling the spread of disease where vaccination and isolation are model parameters. The generation matrix method is used to analyze the model and to obtain the primary reproduction number and the global stability for COVID-19 spreading. Simulation of the model uses secondary data on the number of COVID-19 cases in Indonesia using MATLAB software [21] to provide preventive measures for spreading the disease.

The work [22] uses an SEIR epidemic model to study disease dynamics, dividing the population into Susceptible (S), Exposed (E), Infected/infectious (I), and Recovered (R) classes. Differential equations are built to determine the rates of change within each class. Defined parameters such as birth rate, natural death rate, virus-induced fatality rate, disease transmission probability, progression rate from exposed (E) to infectious (I), and recovery rate are also considered. The model accommodates the latent stages, crucial for diseases like COVID-19, and explores key parameters such as virus-induced fatality rate representing fatality rates. The study focuses on the transmission, incubation, and recovery processes, introducing a metric for the dead population and an alternative SEIDR

model. The basic reproduction ratio measures disease spread, as well as infection and case fatality rates (IFR and CFR). The paper presents a numerical algorithm using a forward Euler finite-difference scheme for solving differential equations, ensuring positive and bounded solutions that converge to an equilibrium state.

The methodology in [23] centers on an SEIR model to study epidemic dynamics. Differential equations with initial conditions define the changes in the four categories over time. The model ensures non-negativity and boundedness of solutions. Key to the analysis is the basic reproduction number, which indicates epidemic potential when more significant than one. Stability analysis involves identifying disease-free and epidemic equilibrium points, with their stability contingent on the R0 value. This approach allows for a detailed understanding of epidemic behaviour and containment possibilities.

Our paper proposes a novel approach for the simulation of infectious disease spread. The proposed approach integrates the SIR models with Barabási-Albert graphs, emphasizing the dual perspective of disease dynamics and underlying network structures. The proposed approach uses the COVID-19 Corona Virus India Data [24]. It contains real-time data of active, positive, cured and death cases of the previous and the current day for Indian states and union territories. The proposed model also uses day-to-day COVID-19 case numbers from Italy, Iran, China, Norway, Spain, Germany and New York [25]. Table I summarises the salient features of key related works.

III. Methodology

The proposed work outlined in this section introduces epidemic modelling methodologies. Aiming to improve the accuracy and applicability of simulations, integrating SIR models and Barabási-Albert graphs helps in capturing the complex dynamics of disease spread within interconnected populations.

A. Barabási-Albert Model for Simulation

The Barabási-Albert model is used to create networks that mimic the structure of real-world networks and exhibit scale-free properties. It creates a physical network with specified parameters: mean connectivity, degree distribution, and recovery rate. Based on the growth of preferential attachment, the model starts with m nodes, each connected by at least one link. One new node is added at each time-step such that it connects to n existing nodes where n is less than m. Preferential attachment determines how new nodes will connect to the existing nodes present in a network. The probability that a new node will connect to node i is proportional to the number of links i already has. This implies that densely connected nodes are more likely to receive new links.

The degree distribution of the graph is plotted. The graph is visualized so the nodes are coloured based on their infection status: blue if they are susceptible and orange if they are infected. A specified number of nodes are initialized as infected in the network, representing the initial number of infected people. The disease is then propagated in the graph with a probability influenced by the inception risk. The risk perception of each node in the graph is calculated based on its neighbours. The recovery of the infected nodes is modelled with a specified recovery probability k. The progression is visualised as the spread of the disease is simulated over the network. Physical and virtual networks create an information network with a given parameter. Finally, a Barabási-Albert physical network is generated, the degree distributions are visualized, and the disease spread is simulated, visualizing the physical network. Fig. 1 depicts the work flow of the proposed modelling approach.

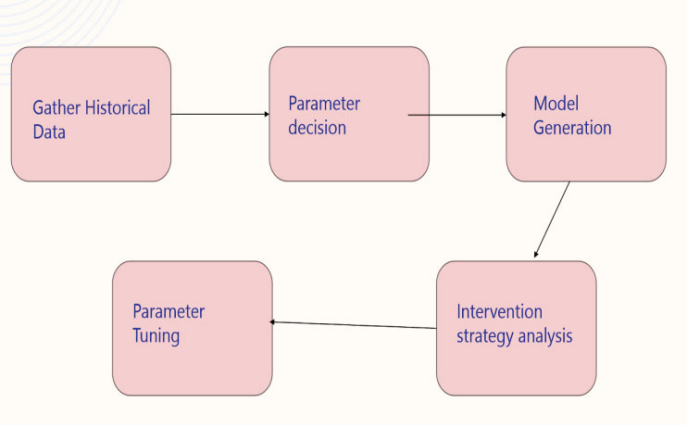


Fig. 1. The methodology of the proposed work

B. Spatio-temporal Dynamics of the SIR Model on a 2D Grid

Using the SIR model, the disease spread is simulated on a two-dimensional grid. This involves defining parameters such as initial_infected, infection_rate, and recovery_rate. A specified number of cells are randomly marked as infected, initiating the visualization of the epidemic's progression.

The computation of infected neighbours for each infectious cell is done by inspecting the adjacent cells, and the grid is updated based on the SIR model rules. Susceptible cells are infected with a probability proportional to that of the infected neighbours, and infectious cells recover with a specified probability k. The resulting grid is visually represented with a colour map denoting susceptible (blue), infectious (red), and recovered (green) states, including simulation step indications and spatial context labels in each frame. A visualization example is shown in Fig. 5.

C. Visualizing the Dynamics using Pygame

The simulation involves creating and moving entities (”Dots”) representing individuals on a two-dimensional grid. Each Dot can exist in one of three states: Susceptible (Blue), Infectious (Green), or Recovered (Purple). The simulation ensures continuity by incorporating periodic boundary conditions for the grid. Characteristics of a dot in the simulation include position, velocity, and state. Features such as periodic boundary conditions and velocity normalization are incorporated, including the option to initialize random velocities. A

TABLE I. SUMMARY OF KEY RELATED WORKS

Reference	Model Used	Focus	Methodology	Special Notes
[10]	SIR extended	Population and regional kinetics	Differential equations, Crank-Nicholson method	Carriers, regional dynamics
[12]	SIR on networks	COVID-19 dynamics on Erdős–Rényi networks	Numerical simulation	Dynamics in Punjab, Pakistan
[13]	RL2G	Analyzing network structures	Novel methodology	Topology revelation and adaptability
[14]	Stochastic models	Extinction/persistence of diseases	Mathematical modelling with stochastic elements	Modified reproduction number, equilibrium analysis
[8]	Epidemic model	Optimal control strategies (vaccination)	Optimal control theory, numerical methods	Utilizes real epidemic data
[11]	SEIR	Disease spread simulation with intervention dependencies	Simulation with transmission, recovery rates	Focus on COVID-19 in Pakistan
[17]	SEIR	Infectious disease dynamics and control strategies	Numerical algorithm, forward Euler scheme	Discusses R0, IFR, CFR
[23]	SEIR	Epidemic dynamics analysis	Differential equations, stability analysis	Basic reproduction number, equilibrium points
[20]	SEIR	Spread of disease with vaccination and isolation	Generation matrix method, MATLAB simulations	Focus on COVID-19 in Indonesia
[22]	SEIR (SEIDR)	Disease dynamics, including latent stages	Forward Euler finite-difference scheme	Transmission, incubation, recovery, fatality rates
[19]	SEIJR	SARS outbreaks analysis in closed populations	Nonlinear differential equations	Incorporates symptomatic/asymptomatic individuals, superspreaders

killswitch mechanism is implemented to simulate mortality or recovery after a specified number of cycles. Simulation parameters include grid size, the number of susceptible, infected, and quarantined individuals, and the simulation duration.

Pygame is used to create and update the graphical representation of the simulation. Populations of susceptible and infected individuals on the grid are initialized. Statistics like the number of infections, recoveries, and deaths are displayed over time. We simulate how susceptible and infected individuals interact, and the rates at which new infections or recoveries change can be observed. Randomness in initial velocity and mortality rates are introduced. Parameters can be customized, such as the number of susceptible, infected, and quarantined individuals, mortality rates, and simulation duration. These randomization options add stochastic elements to the simulation. Fig. 4 shows an example of the disease spread visualization using Pygame.

D. Analyze and model the growth of cases

A logistic growth model and an exponential growth model are used to analyze the growth of cases. Given a set of input values, the observed data is fit into a function and the best-fitting curve is found. Optimal parameters for the chosen function are found and the R-squared score is calculated. In a regression model, the R-squared score indicates how well the independent variables predict or explain the variation in the dependent variable. Its value ranges from 0 to 1, where 0 means that the model does not explain any of the variation in the dependent variable around its mean, and 1 means it perfectly explains the variation.

The original data and the fitted curve are plotted as green dots and orange curves for visual inspection. The time it takes for the growth to slow down is calculated, given a certain threshold difference (*diff*) between consecutive data points. It takes the fitted parameters, the data, and the chosen growth function as its inputs. COVID-19 data for New York from a JSON file is loaded. Daily confirmed cases are extracted, and corresponding time points are created. The logistic growth model is fitted to the data where the time until growth is less than a specified threshold (*diff*). The number of cases at each point is calculated, and the time beyond which the growth becomes slower than the specified threshold is found. The result includes the number of days until growth is less than the threshold and the estimated number of cases.

E. Overview of Working of the Proposed Model

The proposed work uses the Barabási-Albert model to simulate real-world network structures with scale-free properties. It generates networks with specified parameters, such as mean connectivity and degree distribution. It introduces the concept of preferential attachment, where new nodes prefer to attach to already well-connected nodes. This model facilitates the simulation of disease spread within a network, considering factors like infection status, recovery probability, and risk perception among nodes.

The SIR (Susceptible, Infected, Recovered) model is applied on a two-dimensional grid to simulate how an epidemic progresses. It describes how the simulation accounts for the infection and recovery processes, visualizing these states with different colours (blue for susceptible, red for infectious, and green for recovered) and incorporating spatial context into the simulation frames.

The Pygame simulator is used for graphical simulation, representing individuals as dots moving on a grid, each dot's state influencing its interactions and the overall dynamics of the disease spread. This part of the simulation considers various changeable parameters, including mortality rates and the number of individuals in different states, to provide a stochastic element to the disease modelling. Parameterized models provide adaptability to diverse situations, enabling researchers to input real-world data and customize the models for specific pathogens or community characteristics.

Finally, exponential and logistic growth models are used to model the growth of cases. Observed data is fitted to these models to find the best-fitting curves, and the R-squared score is calculated to assess the model's accuracy. The logistic growth model estimates the days until growth decreases below a specified threshold.

Combining theoretical foundations, interactive features, and adaptability, the proposed work synergizes the strengths of established epidemiological models with dynamic network representations, enhancing our capacity to model and respond to infectious diseases more effectively.

IV. Simulation Models and Equations

The theoretical underpinning of the proposed epidemic modelling framework lies in the integration of the SIR model governed by a system of differential equations and the Barabási-Albert graph, which incorporates preferential attachment principles.

A. The SIR Model Theory

The SIR model helps understand the way infectious diseases spread within a population. It divides the population into three compartments, namely: Susceptible (S), Infected (I), and Recovered (R).

It is important to know the number of infected and recovered people as recovered people have immunity to the disease. The dead are also included in the recovered group as they are no longer susceptible. If we do not consider the movement of people in and out of the borders surrounding the population, then the remainder of the population is still susceptible to the disease. Thus, at any time, the fixed total population may be divided into three distinct groups:

- people who have contracted the disease,
- people who have recovered, and
- those who are susceptible.

The epidemic dynamics are captured through a set of differential equations representing the rates of change in each compartment over time. The SIR model parameters are given in Table II.

TABLE II. SIR Model Parameters

Parameter	Symbol
Individuals who are Susceptible	S
Individuals who have been Infected	I
Individuals who have Recovered	R
Susceptible fraction	s
Infected fraction	i
Recovered fraction	r
Number of new Infections everyday	b
Recovery rate	k
Total time elapsed	t
Total Population	N

B. Parameters and Assumptions

Initially, the independent and dependent variables are identified. Time t, measured in days, is the independent variable. The dependent variables are divided into two sets. The first one is as follows:

- $S = S(t)$: Individuals who are Susceptible
- $I = I(t)$: Individuals who have been Infected
- $R = R(t)$: Individuals who have Recovered

If N denotes the total population, the fractions of population in the three categories are defined as follows:

- $s(t) = S/N$: Susceptible population fraction
- $i(t) = I/N$: Infected population fraction
- $r(t) = R/N$: Recovered population fraction

Fractions are used instead of population counts due to the resulting simplicity in calculations. Both dependent variables are proportionally related, providing equivalent information about the epidemic's progression. Under the established assumptions, considerations are made regarding the variation of $s(t)$, $r(t)$, and $i(t)$ with time. A visual representation of the anticipated graphs for the said functions is suggested through sketches as shown in Fig. 2.

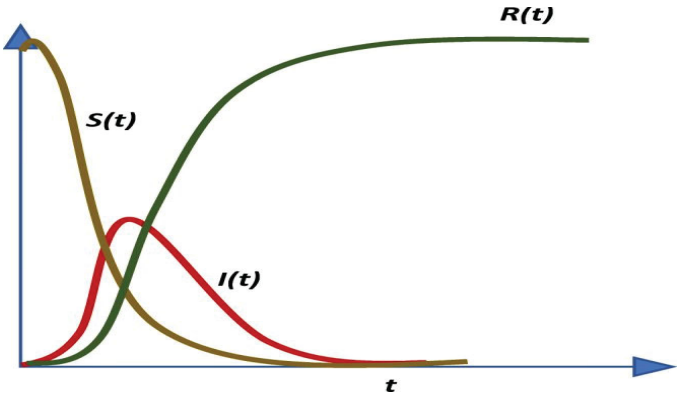


Fig. 2. A visual representation of graphs for the functions

The expression $s(t)+i(t)+r(t) = 1$ implies that the susceptible, infected, and recovered fractions collectively account for the entire population at any given time, ensuring a consistent representation. Following are a few assumptions made related to change in dependent variables:

- Births and immigration do not affect the Susceptible population. Susceptible individuals transition to the infected group, assuming homogeneous population mixing.
- The rate of change of $S(t)$ (susceptible population) depends on the susceptible and infected population, and contact intensity between the two groups. Infected individuals generate new infections per day, considering a fixed number b of contacts and a fraction $s(t)$ of these contacts being with susceptible individuals.
- k is the fraction of Infected population that recovers every day.

These assumptions lead to differential equations governing the dynamics of the epidemic.

C. Differential Equations

The three differential equations are as follows:

- The Susceptible Equation relates $S(t)$ with $I(t)$, where b and $s(t)$ play crucial roles.

$$\frac{dS}{dt} = -s(t) \cdot b \cdot I(t) \tag{1}$$

- The Recovered Equation: Represents the recovery dynamics of $r(t)$ based on the recovery fraction k.

$$i(t) \cdot k = \int_t k \cdot \frac{d}{dt} r \cdot i(t) \tag{2}$$

- The Infected Equation: Incorporates the flow rate from the infected to the recovered population, influenced by $i(t)$, k, and b.

$$\frac{ds}{dt} + \frac{di}{dt} + \frac{dr}{dt} = 0 \tag{3}$$

$$\frac{dr}{dt} + \frac{ds}{dt} = \frac{-di}{dt} \tag{4}$$

$$\frac{di}{dt} = -k \cdot i(t) + b \cdot s(t) \cdot I(t) \tag{5}$$

The model is completed by specifying initial conditions for each differential equation.

D. Barabási-Albert Graph

Barabási-Albert graphs contribute uniquely to epidemic modelling by introducing a dynamic network structure. Unlike static models assuming a uniform distribution of connections, these dynamic graphs evolve, reflecting preferential attachment observed in various social systems. Two mechanisms govern this model:

- Growth: The model initially has m nodes connected by at least one link. A new node is added at each time step such that it connects to n existing nodes where n is less than m.
- Preferential attachment: Determines how new nodes connect to existing nodes in the network. The probability that a new node will connect to node i is proportional to how well connected node i already is. This means that high-degree nodes (hubs) are more likely to receive new connections.

The scale-free nature of Barabási-Albert graphs implies that many nodes have a significantly higher degree than others. This mirrors real-world scenarios where a few individuals, often called super-spreaders, play a disproportionate role in disease transmission. Incorporating such network structures into epidemic models allows for a more realistic representation of how outbreaks initiate and propagate within populations. They are also crucial for capturing the heterogeneity in contact patterns.

In the model, each time a new node enters the network, an existing node's degree is increased. This new node will link to m of the $N(t)$ nodes already present in the system. The probability that one of these links connects to node i is given by equation 6:

$$p_i = \frac{k_i}{\sum_j k_j} \tag{6}$$

Here, k_i is the degree of node i, and the denominator is the sum of the degrees of all nodes in the network.

The rate at which an existing node i acquires links as a result of new nodes connecting to it is given in equation 7.

$$\frac{dk_i}{dt} = m \cdot p_i \quad \text{where} \quad p_i = \frac{k_i}{\sum_{j=1}^{N-1} k_j} \tag{7}$$

Each new node arrives with m links. This implies that node i has m chances of being chosen.

$$\sum_{j=1}^{N-1} k_j = 2 \cdot m \cdot t - m \tag{8}$$

Therefore equation 7 becomes the equation 9.

$$\frac{dk_i}{dt} = \frac{k_i}{2 \cdot t - 1} \tag{9}$$

For large t,

$$\frac{dk_i}{k_i} = \frac{1}{2} \cdot \frac{dt}{t} \tag{10}$$

We know that node i joins the network at time t_i with m links. Using this, we integrate equation 10 to obtain equation 11.

$$k_i(t) = m \left(\frac{t}{t_i} \right)^{\beta} \tag{11}$$

E. Logistic Growth Model

The logistic growth model describes population growth that starts slowly, accelerates, and slows down as it approaches a maximum limit or carrying capacity. It is characterized by an initial phase of exponential growth, followed by a gradual decrease in the growth rate. The mathematical formula for logistic growth is given as

$$P(t) = \frac{K}{1 + e^{-r(t - t_0)}} \tag{12}$$

where:

- $P(t)$ is the population at time t,
- K is the carrying capacity or the maximum population,
- r is the rate of growth,
- t_0 is when the population starts its rapid growth.

F. Exponential Growth Model

The exponential growth model describes a scenario where a quantity increases at a constant proportional rate over time. It is characterized by continuous and unrestricted growth. The exponential growth is often denoted by equation 13:

$$P(t) = P(0) \cdot e^{r \cdot t} \tag{13}$$

where:

- $P(t)$ is the population at time t,
- r is the growth rate,
- t_0 is the time at which the population starts its rapid growth,
- P_0 is the initial population.

V. Experimental Results and Analysis

Integrating SIR models, Barabási-Albert graphs, and dynamic network structures allows for a comprehensive understanding of epidemic outcomes. Parameters like transmission rate (b), recovery rate (k), and initial infected ($I(0)$) count are defined, gives a foundation for comprehending the dynamics of simulated epidemics. The initialized parameters are:

- $b = 0.3$
- $k = 0.05$
- $I_0 = 3$
- $t = 100$

The parameters used in the simulation and their corresponding notations are given in Table I. The experiments involve visualizations that expose the inner workings of Barabási-Albert graphs. These visualizations are dynamic illustrations of the graph's evolution over time. Nodes connect preferentially.

A. Simulation of Disease Spread on Barabási-Albert Network

The Barabási-Albert model creates a physical network with specified parameters, including mean connectivity, degree distribution, and recovery rate. The graph's degree distribution is plotted, nodes are colour-coded based on infection status, and several nodes are initially infected. Node risk perception is calculated from neighbours, influencing disease propagation with a probability tied to the perceived risk. Recovery is modelled with a specified probability (k). The disease spread is simulated over the network as shown in Fig. 3, visually depicting its progression. An information network is formed by combining physical and virtual networks. Degree distributions are visualized, and disease spread is simulated over time with updates. Finally, a Barabási-Albert physical network is generated for disease spread simulation and visualisation, as shown in Fig. 3. In the developed network, the nodes are coloured blue if susceptible and orange if infected.

B. Spatiotemporal Dynamics of the SIR Model on a 2D Grid

A spatial domain is represented by creating a 2D grid with dimensions of 200 $\times$ 200, where each cell can exist in one of three states: Susceptible (0), Infectious (1), or Recovered (2). The SIR model parameters, including initial_infected denoting the initial count of infected cells, infection_rate determining

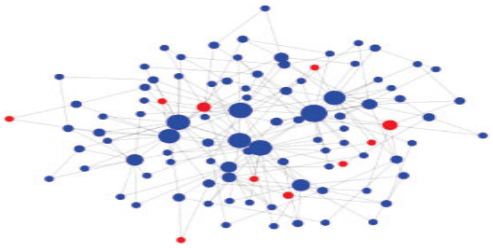


Fig. 3. Barabasi-Albert Physical network

the probability of infection, and recovery_rate representing the probability of recovery, are defined. An initial selection of a specified number of cells, randomly marked as infected on the grid, is observed. Fig 5 facilitates visualising the epidemic's progression over time. The number of infected neighbours for each infectious cell is computed by inspecting adjacent cells. The grid undergoes updates according to the SIR model rules:

- Susceptible cells undergo infection with a probability proportional to the number of infected neighbours.
- Infectious cells recover with a specified probability.

The resulting grid is visually represented using a colour map reflecting susceptible (blue), infectious (red), and recovered (green) states. Simulation step indications and spatial context labels are incorporated into each frame's title and axes. Fig 5 shows the disease spread using the SIR model on a 2D grid.

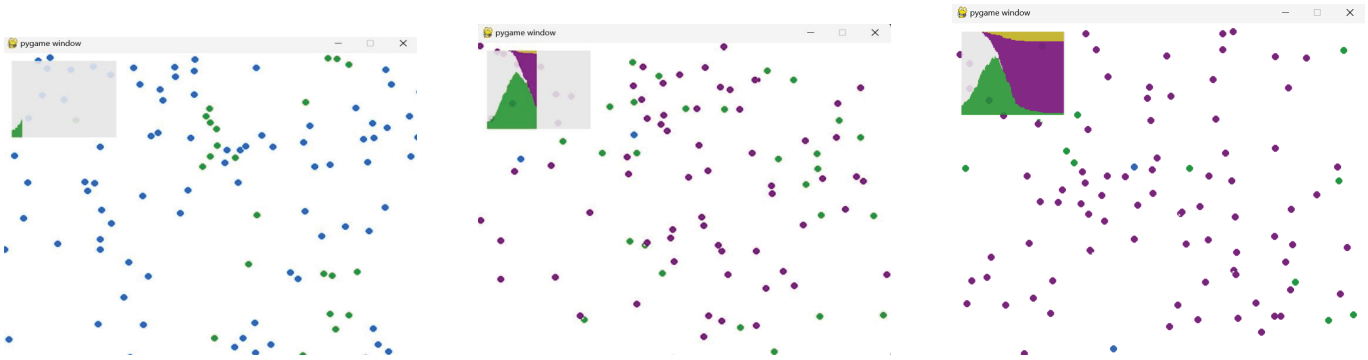
C. Visualizing the Dynamics using Pygame

The simulation employs entities ("Dots") representing individuals on a two-dimensional grid with states: Susceptible (Blue), Infectious (Green), or Recovered (Purple). Periodic boundary conditions ensure grid continuity. Dot characteristics include position, velocity, and state, with features like periodic boundaries and velocity normalization. A killswitch simulates mortality or recovery after a specified cycle count. Parameters include grid size, individuals' numbers, and simulation duration.

Pygame updates the graphical representation, displaying statistics like infections, recoveries, and deaths. Interactions simulate disease spread, introducing randomness in velocity and mortality rates. Parameters, including the number of individuals and simulation duration, are customizable, adding stochastic elements to the simulation. Fig. 4 shows the modeling of the disease spread with changing parameters and time.

D. Analyzing and Modeling Growth of Cases

Logistic and exponential growth models are applied to the observed data, finding the best-fitting curve with optimal parameters. COVID-19 cases in New York are used for plotting. The R-squared score assesses the model performance and accuracy. Original data and the fitted curve are visually represented using the model shown in Fig 6. The time taken for growth slowdown is calculated using a specified threshold difference. Modeling results provide the number of days until



(a) (b) (c)

Fig. 4. Visualization of the spread of the disease (as t continuously increases). Susceptible individuals are represented by blue dots, Infected individuals by green, and Recovered individuals by purple.

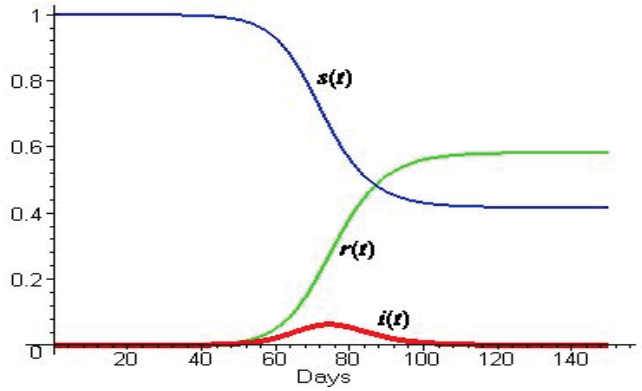


Fig. 5. The spread of disease using SIR model on a 2D grid

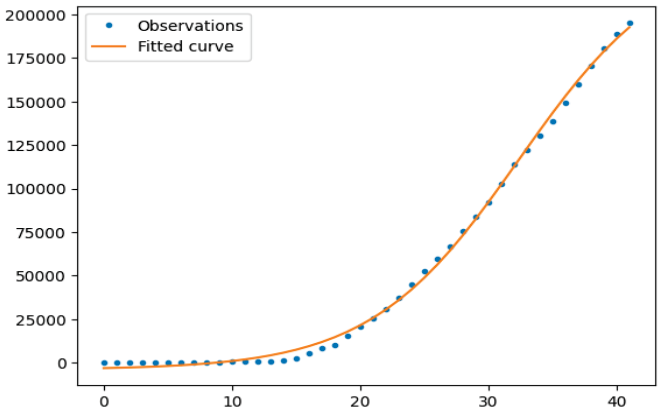


Fig. 6. Logistic fitted curve for growth cases

the growth is below the threshold and the count of the number of cases at that point.

The R-squared score indicates how well the independent variables predict or explain the variation in the dependent variable. Its value ranges from 0 to 1, where 0 means that the model does not explain any of the variation in the dependent variable around its mean, and 1 means it perfectly explains the variation.

For the simulation experiments carried out in the work, the R-squared score is 0.9984, and there were 18 days until growth was less than 500. The model estimates the number of cases to be 234700.

VI. Conclusion and Future Scope

The methodology presented in the paper covers a range of strategies, including simulating disease spread on a Barabasi-Albert network, exploring spatiotemporal dynamics on a 2D grid, and visualizing these dynamics using Pygame. Including logistic and exponential growth models enhances the research, providing a holistic understanding of epidemic growth patterns. A distinctive feature of the proposed work is the combination of established epidemiological models with dynamic network representations, incorporating interactive visualizations and parameterized models. This synergy enhances the accuracy and applicability of simulations. One of this research's primary contributions lies in enhancing realism within epidemic simulations. By embracing weakly-supervised methods, the simulation programs move closer to mimicking real-world conditions.

The analysis of experimental results opens avenues for future research. Researchers may consider exploring variations in SIR model parameters, different network topologies, or alternative graph evolution mechanisms. The dynamic simulations provide a foundation for further investigations into the complex interplay between individual-level interactions and population-wide disease dynamics. The proposed simulation programs are a robust and versatile framework for studying epidemics. Future work could delve into integrating spatial dynamics and considering heterogeneous populations. Benchmarking against existing models and datasets would contribute to a more comprehensive understanding of the proposed simulation programs' strengths and limitations. Exploring the integration of human behaviour models and intervention strategies represents an exciting trajectory for future research. Understanding how individual behaviors impact disease spread and evaluating the effectiveness of various intervention measures can provide invaluable insights for public health planning

and policy-making. As we look ahead, the trajectory involves refining the existing models, embracing additional complexities, and ensuring these simulations' continued relevance and applicability in addressing evolving global health challenges.

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