XIM UNIVERSITY

School of Computer Science and Engineering

ASSIGNMENT-02

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Course: Social Network & Analysis

1. Introduction

1.1 Epidemic Models

Epidemic model [11] is a good tool to understand the information (disease) spreading by relating the process of spreading to the individuals (hosts) properties. Anyway epidemic models are not easy to apply and to be sure of their results because of: 1. Their conclusions depend on assumptions which are rarely straightforward. 2. Some times they can fit the date virtually to their models easily because the epidemic threshold is very strong which is easy to be observed. 3. Depending on parameter values; such as number of population and units (rates) of the contact between them which are just assumptions.

SI model

SI model considers as one of the simplest epidemic model to describe the growth of an infection. The individuals (nodes) divided in to compartments or states: Susceptible (S) and Infectious (I) [3, 12]. In this model nearly each individual is susceptible. After spreading of information (disease) all individuals (susceptible) will be infected exponentially and will,remain infected. This model assumes [12, 4] that: first the infected individuals will remain infected for ever, that means there is no birth, latency, death, or recover among them, second the population size is large and fixed, and third the population is homogeneous.

$$\frac{dS}{dt} = -\beta IS$$

$$\frac{dI}{dt} = \beta IS$$

$$I(t) = \frac{NIe^{\beta tN}}{N + I(e^{\beta tn} - 1)}$$

Where: β is a rate of infection and it is an assumed constant

N is population number

I(t) infectives nodes (spreading the infection) at time t

SIS model

SIS model has ability to stop the information spreading before all individuals become infected. If some node recognizes that there are many infected among its last communication with neighbors, is not going to pass the disease because it became old. And in this model the removed individuals can get infection again. This model also is one of the simplest models of network epidemic models. This model consists of just two states, the susceptible (S) and the

infectious (I) states. Susceptible node can be infected by some infected neighbor. During the same time step the infectious nodes will be exposed to cure by some probability and become susceptible again. And due to that nodes will change their stated from susceptible to infectious and vice versa many times.

$$\frac{dS}{dt} = \Upsilon I - \beta IS$$

$$\frac{dI}{dt} = \beta IS - \Upsilon I$$

SIR model

SIR model has three states that depending on their status: 1. "Susceptible (S):" in this phase the individuals are free for any disease but they can be infected at any time. 2. "Infectious (I):" in this phase the individuals have the disease and they can infect others. 3. "Recovered (R):" in this phase the individuals have been cured and can not infect any others. Susceptible individuals will be infected with a constant probability per unit time by infectious individuals whom have contact to them. After they have been infected they will remain for some time before they can be recovered.

SIRS model

The individuals who have recovered will lose immunity after a certain period of time and will become susceptible again.

1.2 Epidemic networks and Centrality Measures

Centrality can be measured by betweenness, and betweenness can be considered as measurement of effect that a node has on the behavior of information propagation within the network [22] . Possibly there is another way to measure the centrality namely the degree of node which indicates the number of contact with other nodes in the network. And the degree represents in some way the popularity of a node. But the most powerful way to measure the centrality of some node is closeness which depends on the shortest possible path between this node and other nodes. Closeness measures the lasting of spreading information from one given node to all other nodes in the network.

1.3 Methodology

Our network has these properties:
   1. The population consist of N nodes.
   2. Just one node infected (I) and has ability to infect all other nodes by infection's rate
      (τ).
   3. (N − 1) nodes are susceptible (S) which they have no idea about the infection but
      they have ability to get it.
Initial Case-
   N(No. of nodes) = 1000
   B(Contact Probability) = highest value of the respective centrality measure.
   S(No of susceptible individuals) = N-1= 999
   I(No of Infected Individuals) = 1
   R(No of recovered Individuals) = 0

2. Procedures
2.1 Steps to be implemented

Step1: We would be using three centrality measures in order to calculate the β (Contact
 probability).
Step2: The node with the highest centrality will be chosen.
Step3: Find the susceptibility, infection, recovery for each time stamps.
Step4. Plot the values in a graph

3. Analysis
3.1 Graph Representation of the data
Graphic representation is very useful for data analysis and for describing data which is often
difficult to be analysis by just tables or other data forms. We will use scatter plot for analysis
purpose and to get overview on our data. We are using a small world network to implement
this models.

3.2 Tracing infections' movements
   Since one node can not be infected by another node if there is no contact between them,
   so we shall try to trace infections' movements from node to node and observing the
   number of nodes will be infected within each unit time. The number of infected nodes
   within one unit time depends on the number of susceptible neighbors for infected nodes.
   It means we will collect data spatiotemporally; in other words collecting data at a specific

location and at specific time. Note that by contact we mean for example if a machine is already infected by email virus; this virus shall spread to all who have e-mail address in your e-mail address list regardless to where they are and they become infected too.
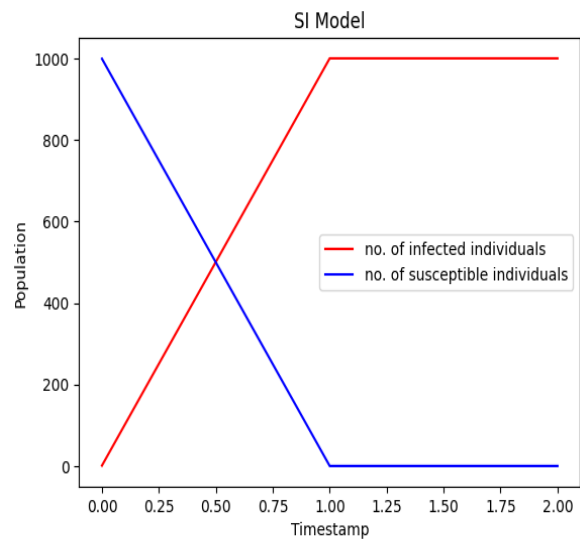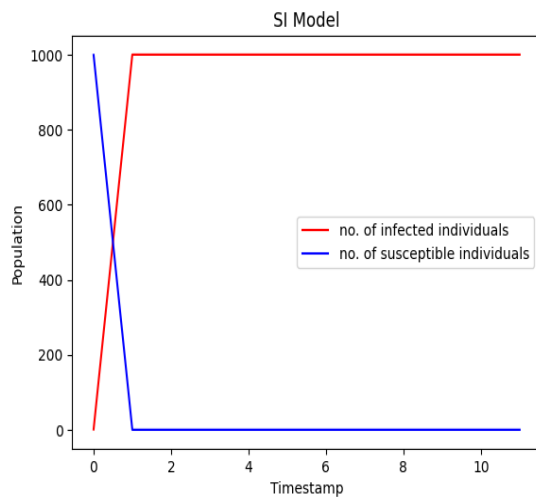
3.3 Result from the network

SI Model

Degree Centrality-
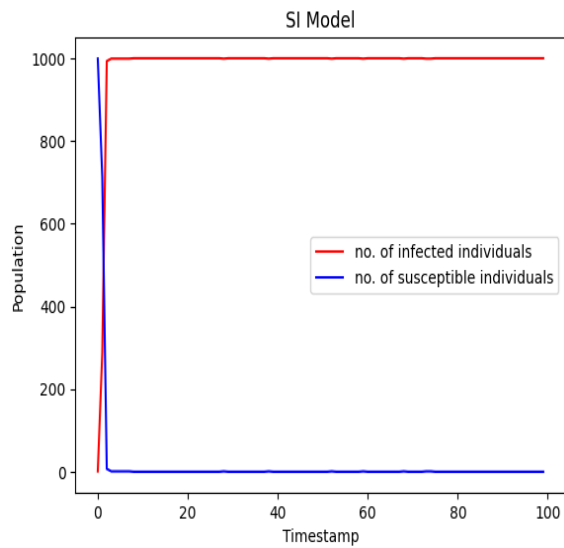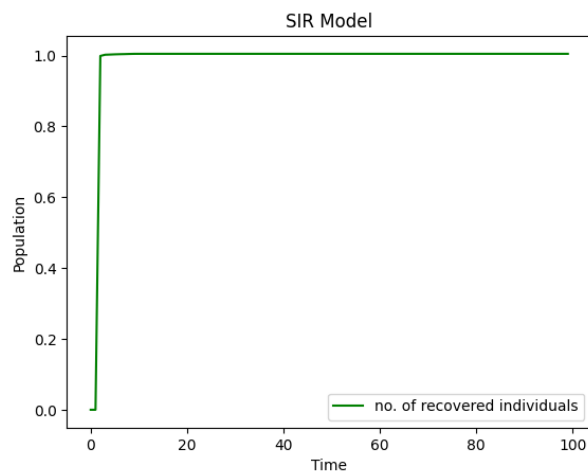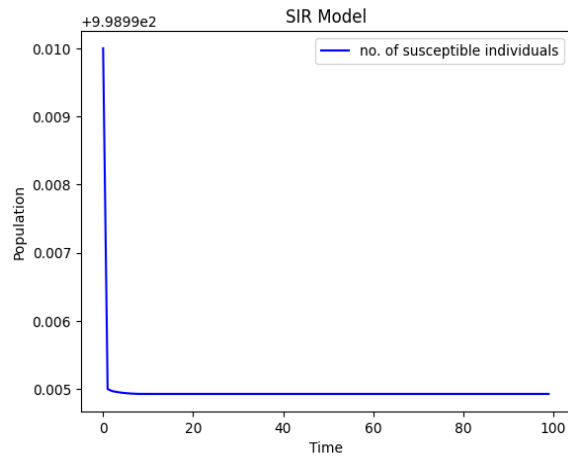
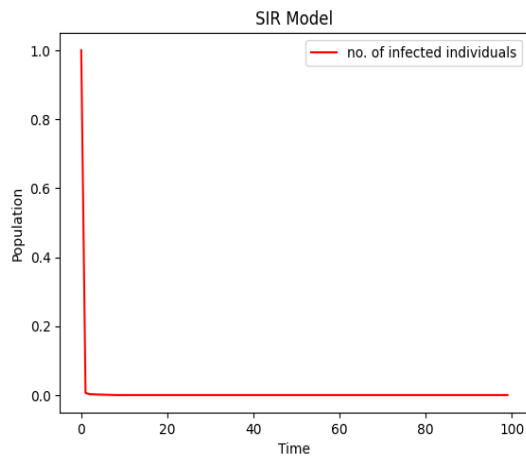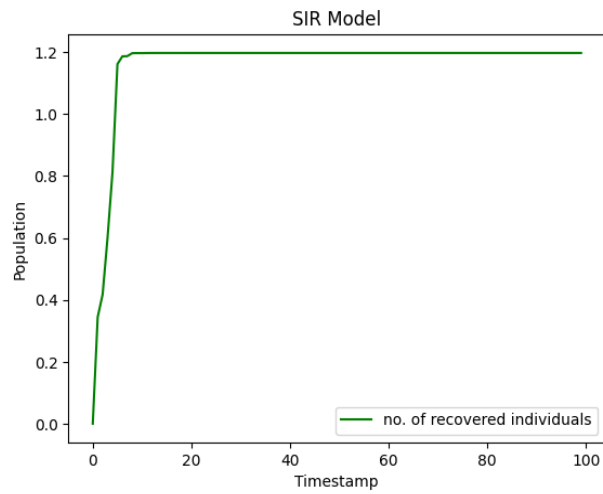### Betweenness Centrality-

Closeness Centrality-

POINTS OBSERVED-

    In the SI model, we initially determined the beta value or contact probability based on the highest centrality measure. As different centrality measures yield varying contact probabilities, we aimed to identify the measure that best reflects the speed of disease spread akin to real-world networks. Our observation indicates that betweenness centrality offers results most closely resembling real-world scenarios, where the number of infected individuals increases while the number of susceptible individuals decreases. This trend aligns with a logistic growth pattern observed in the plotted data.
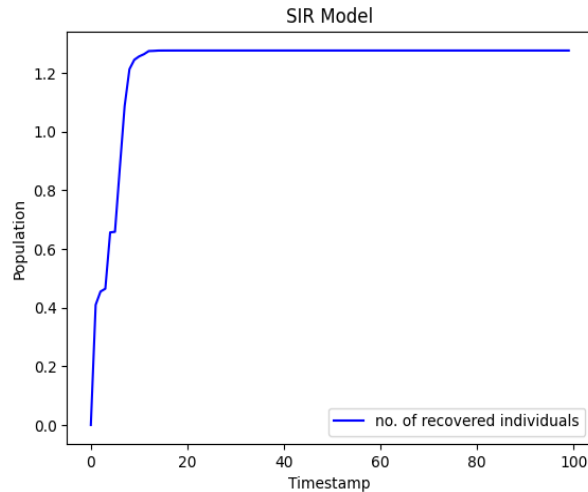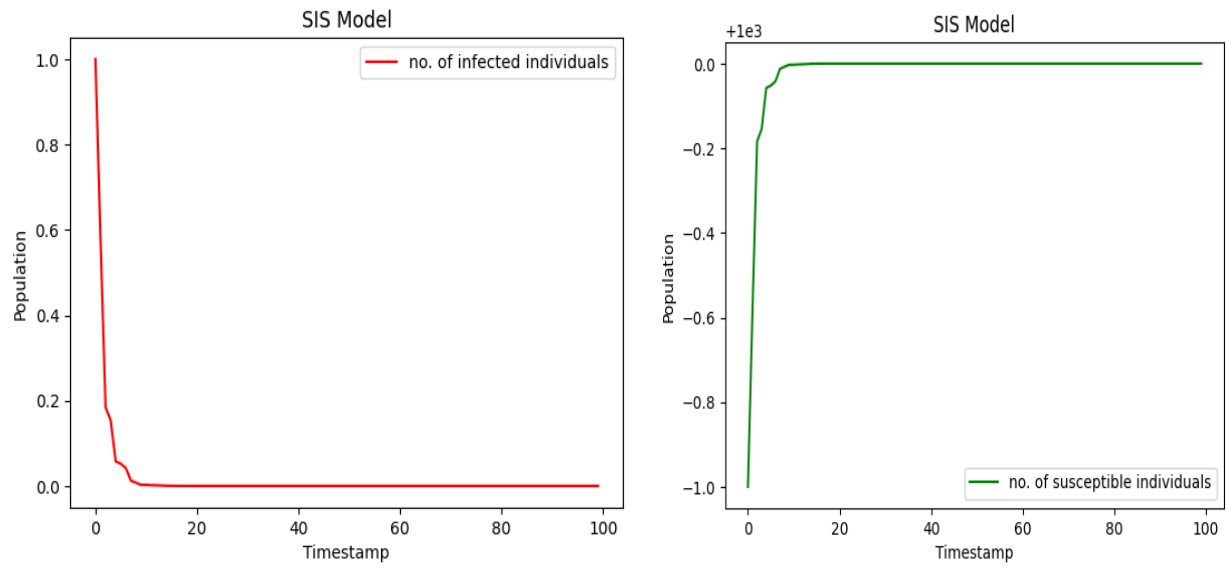
SIR Model
Degree Centrality-

Betweenness Centrality-
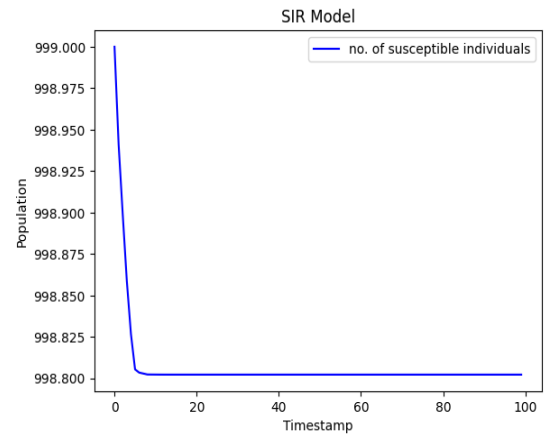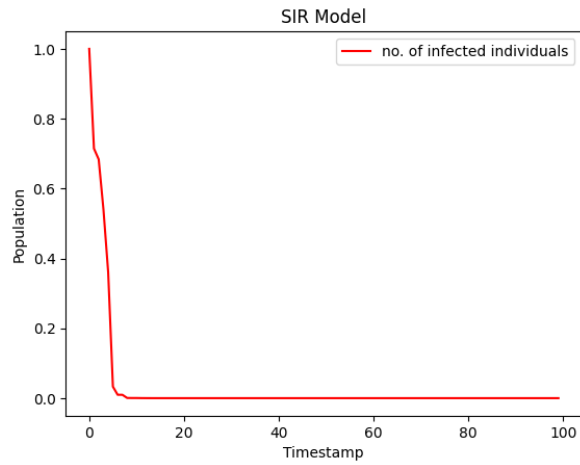
Closeness Centrality-
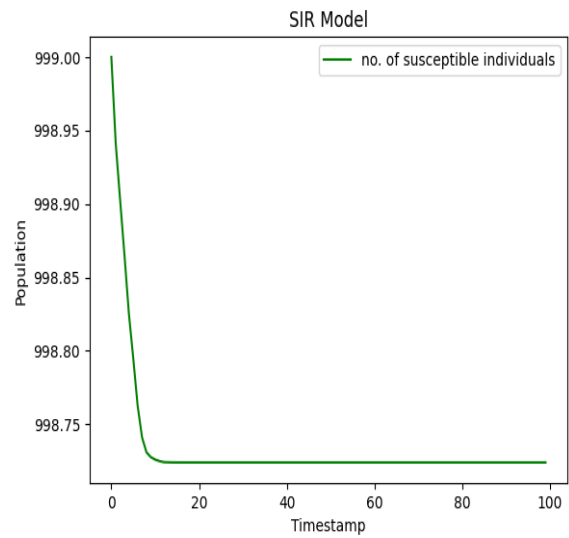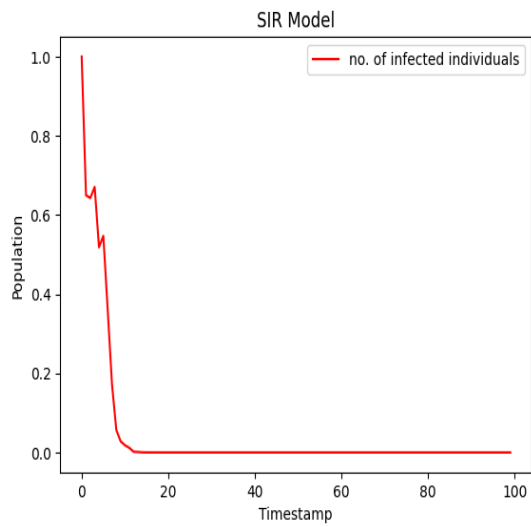
SIR Model

POINTS OBERVED-

In the SIR model, various centrality measures yield similar outcomes where the number of susceptible and infected individuals decreases while the number of recovered individuals increases. The contact probabilities calculated through different centrality measures are as follows: degree centrality = 0.05, betweenness centrality = 0.16, and closeness centrality = 0.05. Notably, the beta value obtained from degree centrality and closeness centrality is the same. However, the overall contact probability is quite low, which results in a limited increase in the number of infected individuals and a subdued spread of the disease. This contrasts with real-world scenarios where the number of infected individuals typically experiences an initial increase followed by a decrease.
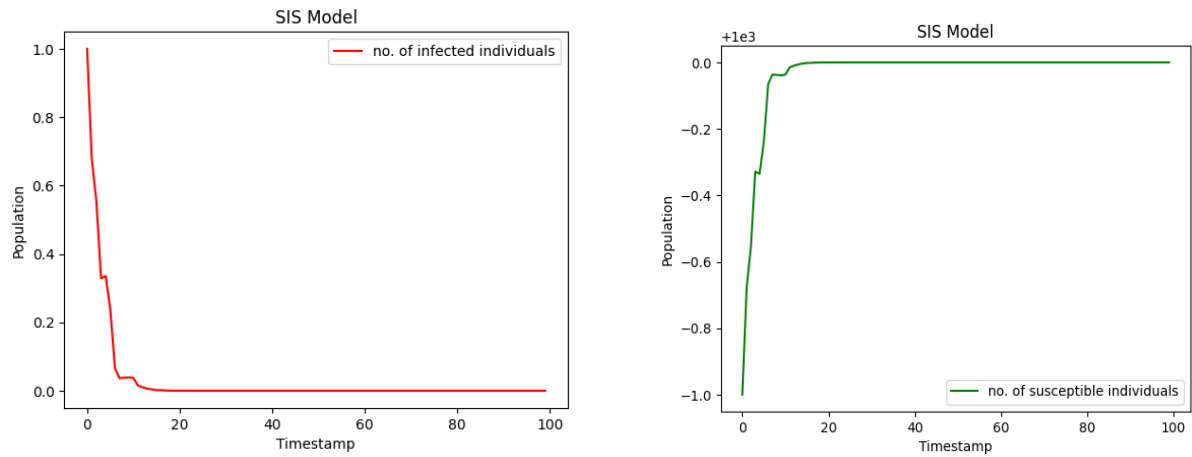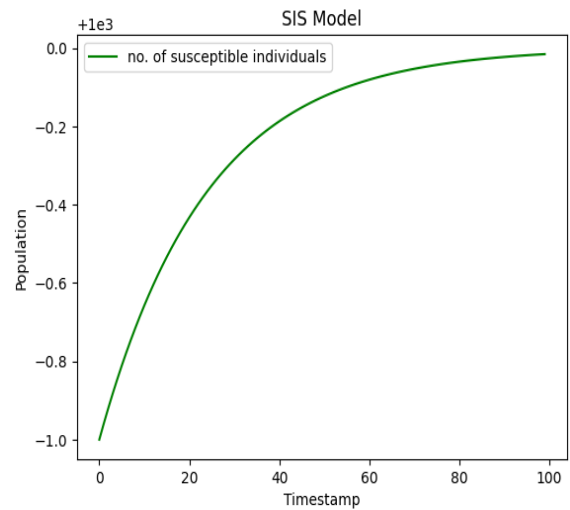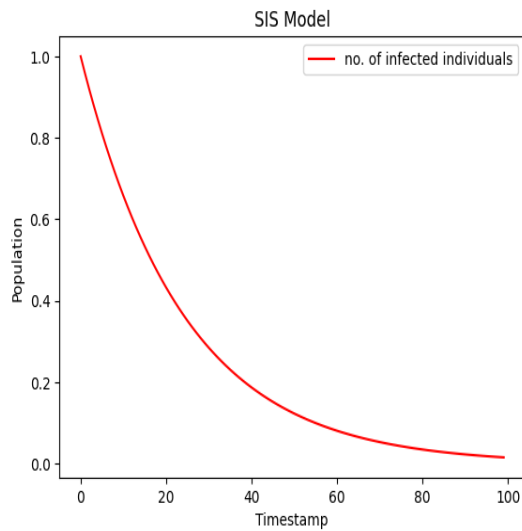
SIS Model
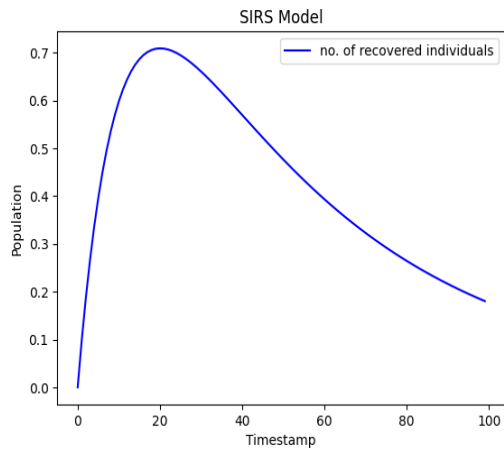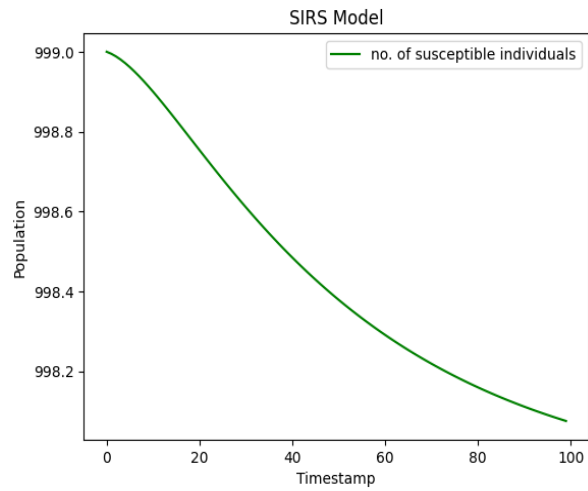
Degree Centrality
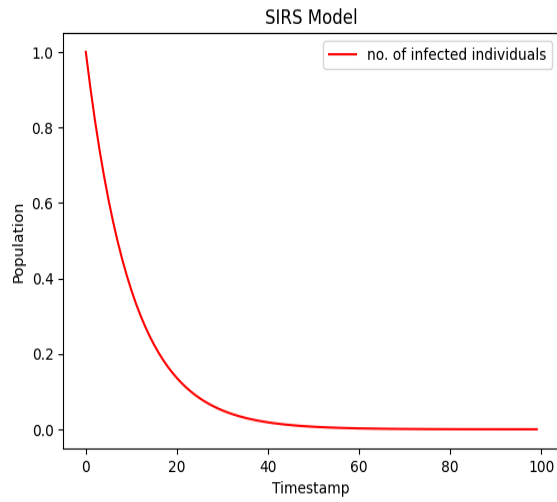

Betweenness Centrality-
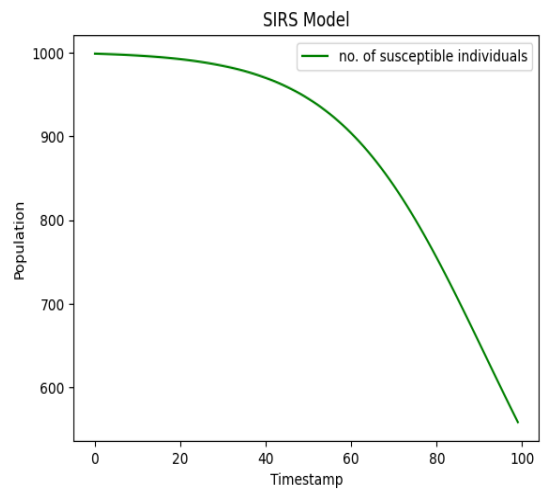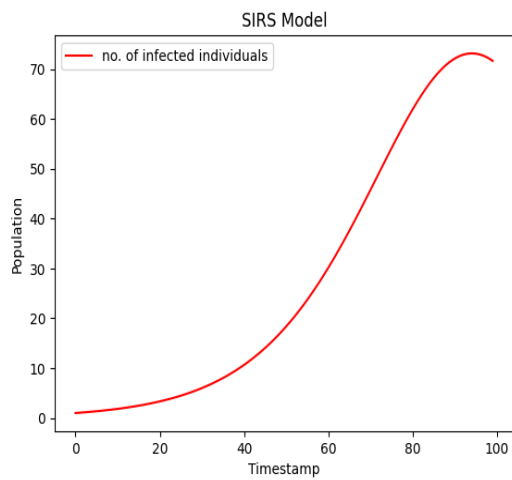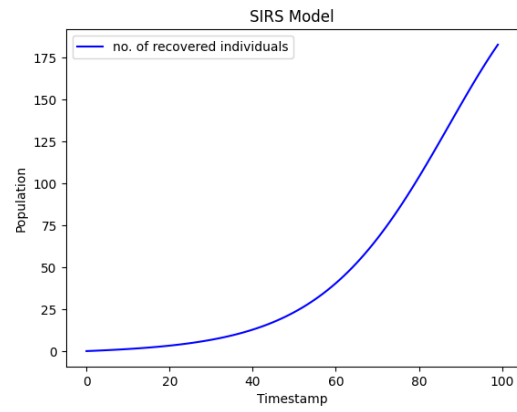
Closeness Centrality-

POINTS OBSERVED-

In the SIS model, all three centrality measures yield similar outcomes where the number of infected individuals decreases and the number of susceptible individuals increases. This pattern is in stark contrast to real-world graphs, where the number of infected individuals typically increases while the number of susceptible individuals decreases. The contact probabilities calculated from these centrality measures are exceptionally small, leading to minimal spread of the infection. This discrepancy highlights the need for more accurate or realistic contact probability estimates to better simulate real-world epidemic dynamics in the SIS model.
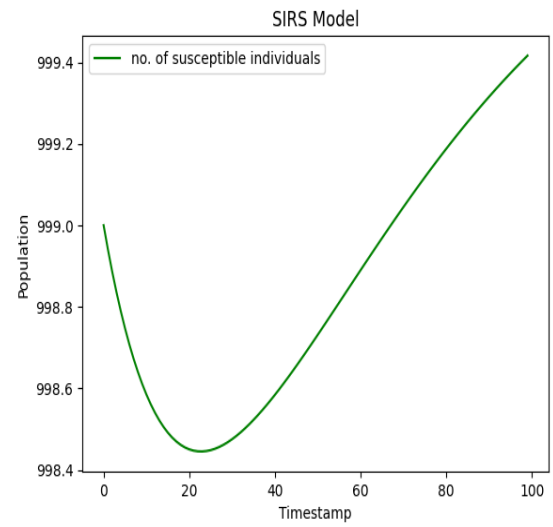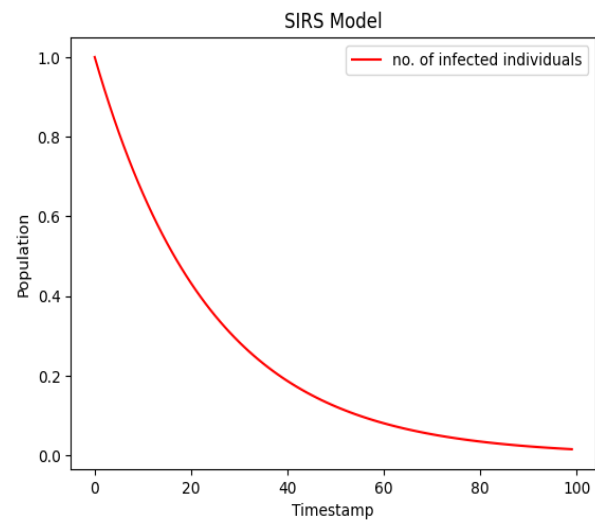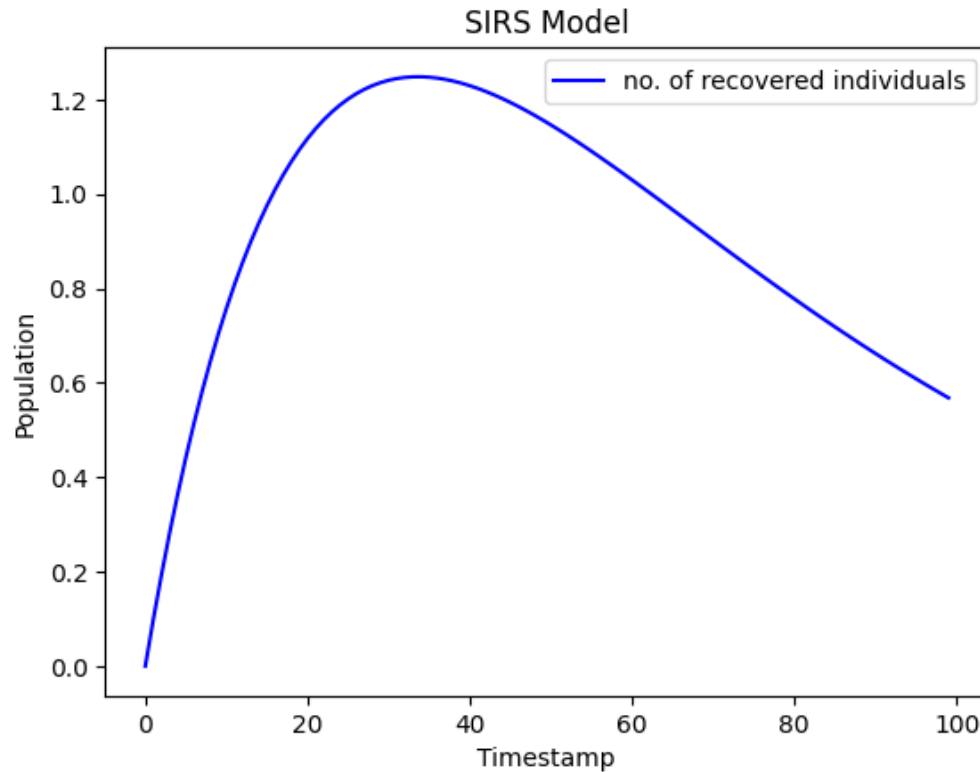
SIRS Model-
Degree Centrality-

Betweenness Centrality-

Closeness Centrality-

SIRS Model

POINTS OBSERVED

In degree centrality and closeness centrality there is a sharp decrease in the plot which tells that there is very less spread of the infection the reason is due to the extremely less contact probability obtained that is close to 0.05. But in the case of betweenness centrality we see that there is increase in the number of infected individuals similar to real world graph. The contact probability calculated in betweenness centrality is 1.5 which is higher compared to that of degree closeness centrality. In case of recovery we see that in degree centrality case, the recovery rate increases and then again starts to dip while in betweenness centrality we see that there is slow increase in recovery rate.

4. CONCLUSION

In the SI model, the betweenness centrality measure provided results most similar to real-world networks, where the number of infected individuals increases and the number of susceptible individuals decreases. This indicates that betweenness centrality can offer valuable insights into the speed of disease spread in complex networks.

In the SIR model, various centrality measures such as degree centrality, betweenness centrality, and closeness centrality resulted in similar outcomes, with a decrease in the number of susceptible and infected individuals and an increase in the number of recovered individuals. However, the overall contact probability was found to be very low, leading to limited spread of the infection, which differs from real-world scenarios where infections often follow an initial increase and then decrease pattern.

In the SIS model, all three centrality measures yielded similar results with a decrease in the number of infected individuals and an increase in the number of susceptible individuals, contrary to real-world trends. The contact probabilities calculated from these measures were also significantly small, contributing to less spread of the infection.
In SIRS model also we can see that the centrality measures does not give us the appropriate results and the results vary. Due to the very less contact probability, there is very less infected individuals.

Overall, while centrality measures can provide insights into the dynamics of disease spread in network models, the accuracy and realism of contact probabilities play a crucial role in replicating real-world epidemic patterns. Further refinement and validation of these models are necessary to better simulate and understand complex epidemic dynamics.