An-Najah National University
Faculty of Graduate Studies

Closeness Centrality and Epidemic Spreading in Networks

By
Fares Masuod Abdelgani Rabaya'

Supervisors
Dr . Sobhi Rosyea'
Dr . Adwan Yasin

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This Thesis was defended successfully on 08/09/2008 and approved by

Committee Members	Signature
1. Dr. Sobhi Roseya' (Supervisor)	…………………
2 Dr. Adwan Yasin (Co-Supervisor)	…………………
3. Dr. Mohammad Najeeb (External Examiner)	…………………
4. Dr. Sayed Malak (Internal Examiner)	…………………

Dedication

To my mother Shamsah, to my wife and children Hedaya', Ieman, Aya and Abdelah , to my brother and sister

Acknowledgements

First of all I would like to thank my supervisors Dr Sobhi Roseya' and Dr Adwan Yasin for their valuable and useful guidance to fulfill this thesis. Second, I would like to thank Dr Sameer Mater and Dr Mohammad Najeeb for their special effort through the Masters course, and I would also like to thank Dr Khalid Rabaya' for his support and useful advices during my work in this thesis .

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الإقـــرار

أنا الموقع أدناه مقدم الرسالة التي تحمل العنوان:

Closeness Centrality and Epidemic Spreading in Networks

المركزية وانتشار الوباء في الشبكات

اقر بأن ما اشتملت عليه هذه الرسالة إنما هي نتاج جهدي الخاص، باستثناء مـــا تمـــت الإشارة إليه حيثما ورد، وان هذه الرسالة ككل، أو أي جزء منها لم يقدم من قبل لنيل أية درجة علمية أو بحث علمي أو بحثي لدى أية مؤسسة تعليمية أو بحثية أخرى.

Declaration

The work provided in this thesis, unless otherwise referenced, is the researcher's own work, and has not been submitted elsewhere for any other degree or qualification.

Student's name: **اسم الطالب:**

Signature: **التوقيع:**

Date: **التاريخ:**

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Closeness Centrality and Epidemic Spreading in Networks

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Dr . Sobhi Rosyea'
Dr . Adwan Yasin

Abstract

This thesis is about the relation between the closeness centrality of the first infected node in the network and each of the total infection time that needs to infect all nodes in that network ,the infection rate for spreading epidemics in that network ,which measures the fraction of nodes those infected per unit time and the infection spreading power of that node ,that measures the power for each node to spread the epidemic to other uninfected nodes in that network .

In this thesis, I deal with four types of networks ,unweighted small and large networks and weighted small and large networks and study that relation in these four types.

The importance of this work is when we find the closeness centrality and the infection spreading power of any node that help us understand which weakness or advantages this node has for maintenance or blocking dangers at the right time .

In this work, I made some development in the SI model for the epidemic network in which most of authors consider the infection rate in that model assumed and constant. In this work I found that this infection rate is not constant but it depends on the closeness centrality of the first infected node in the network ,hence I suggest to replace the infection rate in

the SI model by the closeness centrality of the first infected node in the network .

The results obtained from this work show that each of the total infection time, the infection rate and the infection spreading power when any node infected first in the network depend on the closeness centrality for that node .

Chapter 1
INTRODUCTION

The easy access and wide usage of the networks like the Internet, WWWnet makes it a primary target for malicious activities. In particular, the Internet has become a powerful mechanism for propagating malicious software programs. Worms and viruses, defined as autonomous programs that spread through computer networks by searching, attacking, and infecting romote computers automatically,have been developed since the first Morris worm in 1988. Today , our computing infrastructure is more vulnerable than ever before. The Code Red worm and Nimda worm incidents of 2001 have shown us how vulnerable our networks are and how fast a virulent worm can spread [1] . On July 19th , 2001, a self – propagating program , or worm, was released into the Internet. The worm, dudded "Code-Red v2" pobed random Internet host for a documented vulnerability in the popular Microsoft IIS web server. As susceptible host were infected with the worm,they too attempted to subvert other hosts-dramatically increasing the incidence of the infection . Over fourteen hours, the worm infected almost 360000 hosts, reaching an incidence of 2000 hosts per minute before peaking . The direct costs of recovering from this epidemic have been estimated in excess of $ 2.6 billion. While Code Red was neither the first nor the last widespread computer epidemic,it exemplifies the vulnerabilities present in today's Internet environment [10] . Therefore it is a good matter to study epidemics of the networks and how the infection spread through networks and what are the paramaters that affects that spreading . The term of epidemiology is used indeed for human disease for a long time and it deals with disease spreading within populations . As some viruses and worms popagated through the computer networks in a very high speed, that propagation can be described by epidemic models as those that have been used for biological epidemiology [11] . So computers in networks can be cosidered as a population, if some of them are infected it can infect other susceptible computers in that population by some infection rate 'β' or spreading rate 'λ' in some references.

Network worms and viruses represent a serious threat to confidentiality, integrity, and availability of computer resources on networks specially the Internet . The existing automated network security solutions (e.g. antivirus software, firewall,and intrusion detection systems) and human – dependent countermeasures (e.g. software patching, traffic blocking) are not sufficent for detection and control of worm and virus propagation because every day we have new worms and viruses those they are undescovered [17],[18] . Since the problem of network worms is worening every year despite increasing efforts and expenditure on Internet –security, devising techniques for controlling their propagation is of great practical importance. An important first step in developing control strategies is to understand the dynamics of worm and virus propagation and how worm and virus propagation are affected by the network structure [16] .

As a part of the network structure I will focus in my work on the effect of the centrality of the first infected node in the network , specially the closeness centrality of that node on worms and viruses popagation through that network [31].

The infection rate 'β' in most epidemic models is assumed and it is considered constant which gives those models large-scale for estimation and approximation . In this work and by analysis I will try to find that the relation between closeness centrality for the first infected node in network and the infection rate in that network, then I will try to suggest some devlopment in the SI model [22]using results obtained from my analysis .

The outline of this thesis will be as follows : in chapter 2 (graphs), I will review some general information about graphs and networks. In chapter 3 (centrality), I will discuss centrality of nodes and some methods that used to find it . In chapter 4 (related works), I will talk about previous work has been done by others and review some known epidemic models for worms and viruses propagation through networks . In chapter 5 (methodology), I will explain my methodology . In chapter 6 (analysis and results). I will analyze four different types of networks small and large ,weighted and unweighted to prove my hypothesis and I will apply my developed SI model on these network and compare my results with the previous works . Finally , in chapter 7 (discussion and conclusions) , I will have my discussion and conclusions .

1.1 The Problem and The Hypothesis

The problem

What is the relation between closeness centrality of the first infected node in the network and each of the total infection time ,the infection rate and the infection spreading power of that node in the unweighted and weighted networks ?

The Hypothesis

Closeness centrality of the first infected node in the network has a strong relation with each of the total infection time , the infection rate and the infection spreading power of that node in that network . In SI model which assumes that there is no recovery during the infection period :" a node with highest closeness centrality will infect all other nodes in the network in less time than any other nodes in that network and the infection rate at this case is the highest and its infection spreading power also the highest a mong all other nodes in that network" .

Chapter 2
Graphs

2.1 General

Graphs are a very flexible mathematical model for numerous and varied problems. Any system that can be described as a set of objects and relationships or interconnections between them can be naturally represented as a graph.

Graphs arising in real life are called "*Networks*". Networks pervade our daily life. Road railway and airline networks, connecting different sites, cities, or airports, allow us to travel from one place to another. Phone calls and emails are transmitted over a network of cables between telephones or computers. The World Wide Web (*WWW*) is a network of web pages connected by hyperlinks, and more and more becomes our primary source of information. We find ourselves being part of networks of people who are connected, for example, by friendship or professional relationships. There are also numerous networks within human body itself. They include the network of biochemical reactions between the molecules in a cell, and the brain which is a complex network of neurons and their synaptic connections. Human language, too, can be described as a network of words or concepts which are connected if one of us thinks of another.

The broad applicability of graphs has the major advantage that even very different problems can be approached using the same tools from *Graph Theory*. Furthermore, problems which can be modeled as graphs have a natural visual representation. This is a very useful aspect of graphs as visualization is often the key for understanding a set of data [27].

2.2 Terminology and Notation

A graph is made up of points, usually called *nodes*, and lines connecting them, usually called *edges*. The ***order*** of any graph is defined as the number of vertices of that graph, while the ***size*** of that graph is the number of edges in it. We denote the graph as $G(V, E)$, where V is the number of nodes in the graph, and E is the number of edges in that graph. Mathematically, a graph can be represented by a matrix called the *adjacency matrix, A,* which is an $n \times n$ symmetric matrix, where n, is the number of nodes in the graph. the adjacency matrix has the elements A_{ij}, where;

$$A_{ij} = \begin{cases} 1 \text{ , If there is an edge between node } i \text{ and } j. \\ 0 \text{ , Otherwise} \end{cases} \quad \text{----------------} \quad \textbf{(2.1)}$$

The matrix is symmetric since if there is an edge between i and j, it is obvious that there must be an edge between j and i. Thus, $A_{ij} = A_{ji}$ [28].

Example (2.1): Let $G(V,E)$ be a graph, where;

$V = \{1, 2, 3, 4, 5, 6\}$

$E = \{e_1, e_2, e_3, e_4, e_5, e_6, e_7\}$

See Figure (2.2.1).

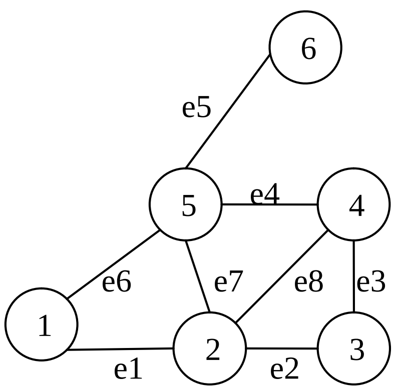


Figure (2.2.1): Undirected Graph with "6" nodes and "8" edges

The adjacency matrix that represents the graph is $A_{6\times6}$,

$$A_{6\times6} = \begin{bmatrix} 0 & 1 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 1 & 1 & 0 \\ 0 & 1 & 0 & 1 & 0 & 0 \\ 0 & 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 0 & 1 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 & 0 \end{bmatrix}$$

If the edges are given a direction, the graph is called a *directed graph*. In mathematical terms, the set of edges of a directed graph consistes of ordered pairs of nodes which can be referred to as *arcs*. The adjacency matrix of a directed graph is no longer needs to be symmetric. There may be an arc from node j to node i, but not from i to j.

Example (2.2): G (V, E) is a directed graph as shown in Figure (2.2.2).

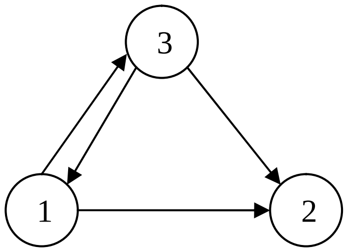


Figure (2.2.2) : Directed graph with "3" nodes .

The adjacency matrix for this directed graph is:

$$Aij = \begin{bmatrix} 011 \\ 000 \\ 110 \end{bmatrix}$$

where

$$a_{ij} = \begin{cases} 1\ , & \text{If there is an arc from node } i \text{ to node } j. \\ 0\ , & \text{Otherwise} \end{cases}$$

Both directed and undirected graphs may be weighted graph, that has a number associated with each edge which can be thought of as reflecting the strength of the connection. The weight of the edge between two nodes i and j is denoted by w_{ij}.

Example (2.3):

G is a weighted graph as shown in Figure (2.2.3).

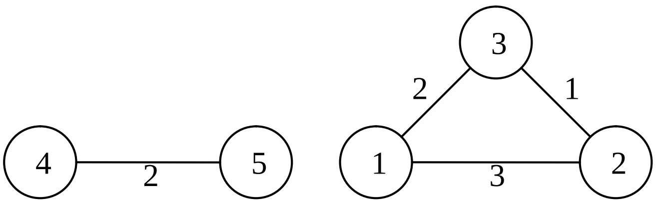


Figure (2.2.3) : Undirected weighted graph has "5" nodes .

The adjacency matrix of the weighted graph is shown below

$$A_{5\times 5} = \begin{bmatrix} 0 & 3 & 2 & 0 & 0 \\ 3 & 0 & 1 & 0 & 0 \\ 2 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 2 \\ 0 & 0 & 0 & 2 & 0 \end{bmatrix}$$

We note that the entries of the adjacency matrix of the weighted graph represent edges weights. [27]

The number of edges attached to the node is called the *degree* of that node. In mathematical terms, the degree (k_i) of a node (i) is:[28]

$$k_i = \sum_{j=1}^{n} A_{ij} \quad \text{------------------------} \quad \mathbf{(2.2)}$$

where n is the total number of nodes in the network .

Example (2.4):

In example (2.3), the degree of node (1) is 2, and the degree of node (4) is 1.

Directed graphs distinguish between a node’s *in-degree* and *out-degree*.

The in-degree is the number of edges arriving at a node. Similarly, a node's out-degree is given by the number of edges departing from it. Just as for undirected graphs, the degree of a node is the number of edges attached to it, which is equal to the sum of in-degree and out-degree.

Example (2.5):

In the directed graph in Example (2.2), node (1) has an in-degree 2 ,out-degree 1 and degree 3.

A graph is called *complete*, or *clique*, if there is an edge between any two of its nodes.

In the wieghted graph, the natural generalization of the degree "k_i" of a node "*i*" is the node strength (or node weight , or node weighted connectivity) "S_i", which is defined as

$$\mathbf{S}_{\boldsymbol{i}} = \sum_{\boldsymbol{j}} \mathbf{W}_{\boldsymbol{ij}} \quad \text{----------------} \quad \mathbf{(2.3)}$$

where W_{ij} is the weight of the edge between node "*i*" and node "*j*" [40],[41]

Example (2.6):

The complete graphs of orders one to five are shown in Figure (2.2.4).

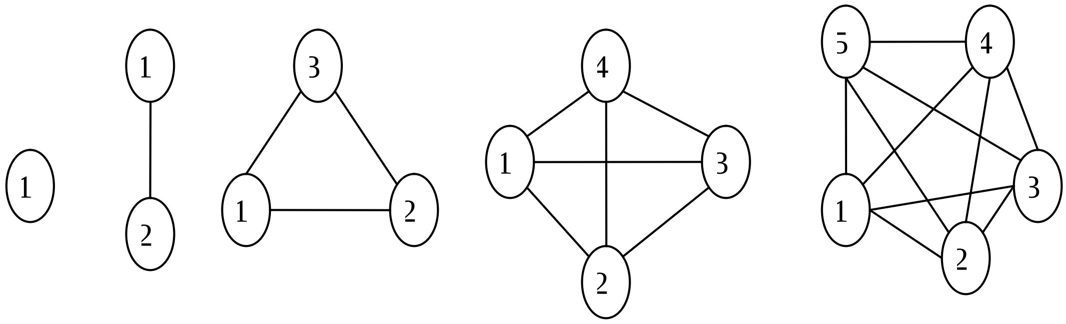


Figure (2.2.4) : The complete graphs of order from one to five .

In a complete graph of order *k*, each node is connected to all of the other *k*-1 nodes. In other words, each of the nodes has maximal degree *k*-1.

Two nodes are neighbors in a graph if they are connected by an edge. The neighborhood of a node (v) is the set of all its neighbors, and is denoted by $N(v)$.

Example (2.7):

In Example (2.6) the node (5) in the last graph in Figure (2.2.4) has neighbors $N(5) = \{1, 2, 3, 4\}$.

Two nodes are called adjacent if there is an edge between them, and two edges are called adjacent if they share a node, and a sequence of adjacent edges in the graph is called a *path*. The length of a path is the number of edges it is composed of.

Example (2.8):

A path of length 4 connecting nodes (1) and (6) in Example (2.1), Figure (2.2.1), is given by $\{e_1, e_8, e_4, e_5\}$

In the case of a weighted graph, we can speak of the weight of a path as the sum of the weights of the traversed edges.

Example (2.9):

In example (2.3), the weight of the path {1, 2, 3} equals 3 + 1 = 4.

A path connecting two nodes v and w is called a *shortest path* if it has the shortest length among all paths connecting v and w. if edges are weighted, the term shortest path is sometimes used to refer to the path of lowest weight rather than shortest length. The shortest path between nodes may not be unique.

Example (2.10):

In example (2.1) there are two shortest paths connecting nodes (3) and (5) which are $\{e_2, e_7\}$ and $\{e_5, e_4\}$.

The distance between two nodes in the graph is simply defined as the length of their shortest connecting path. In other words the distance between two nodes is the smallest number of steps that it takes to get from one to another.

A path is called a *cycle* if it ends at the same node it started from.

Example (2.11):

In example (2.1), the path {1, 2, 4, 5, 1} form a cycle of length 4.

A graph is connected if there is a path from any node to any other node. Otherwise, the graph is disconnected.

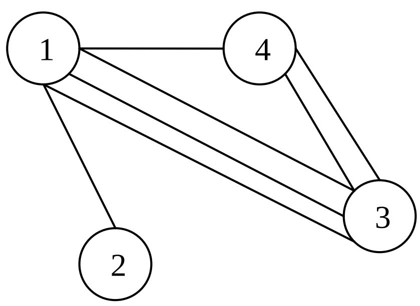
The connected pieces of a disconnected graph are called its *connected components*.

A connected graph without cycles is called *acyclic* graph (also called a *tree*).

If there is more than one edge between two nodes of the graph, or, in other words, the graph has multiple edges between node paires, then the graph is called *multigraph*. The adjacency matrix of the multigraph *A* has elements A_{ij} such that: [29]

$$A_{ij} = \begin{cases} \text{Number of edges between nodes } i \text{ and } j & \text{, If } i \text{ adjacent } j. \\ 0 & \text{, Otherwise} \end{cases} \qquad \text{-------}(2.4)$$

Figure (2.2.5) shows a multigraph.



Figuer (2.2.5) : Multigraph .

The adjacency matrix of the multigraph in Figure (2.2.5) is:

$$A_{4\times4} = \begin{bmatrix} 0 & 1 & 3 & 1 \\ 1 & 0 & 0 & 0 \\ 3 & 0 & 0 & 2 \\ 1 & 0 & 2 & 0 \end{bmatrix}$$

2.3 Computer Network

2.3.1 Computer Network Fundamentals

The basic ideas in all communications is that there must be three elements for the communication to be effective . First there must be two entities, called a sender and a receiver . These two must have something they need to share . Second there must be a medium through which the sharable item is channeled which is called the transmission medium . Third there must be an agreed on set of communication rules or protocals or policies. These three apply in every category or structure of communication . These are also the three components in the computer network .

What is a computer network ? A computer network is a distributed system consisting of loosely coupled computers and other devices . Each device is called " network element " or " transmitting elements " . Any two devices in the computer network can communicate with each other through a communication medium . In order for these connected devices to be considered a communicating network, there must be a set of communicating rules or protocols each device in the network must follow to communicate with another in the network .

The resulting combination consisting of hardware and software is a computer communication network, or computer network in short .

The hardware component is made of network elements consisting of a collection of nodes that include the end system commonly called " hosts " and intermediate switching elements that include hubs , bridges , routers and gateways . All of these are called network elements .

Network software consists of all application programs and network protocal that are used to synchronize, coordinate , and bring a bout the sharing and exchange of data a mong the network elements . Network software also makes the sharing of expensive resources in the network possible .

Network elements , network software , and users all work together in the computer network .

2.3.2 Computer Network Models

In computer network we have two main models , the first one is the centralized network model . In this model all correspondence must go through a central computer called the "master " , also all the sharable operations between all the network elements must be controlled by that master . The second one is the distributed network model . In this model computers and other network elements interconnected by a communication network consisting of connecting elements and communication channels . Also in this model communication and sharing of resources are not controlled by the central computer "master" but are arranged between any two communicating elements in the network .

2.3.3 Computer Network Types

Each network is a cluster of network elements and their resources . The size of the cluster determines the network type . There are in general three main network types :

1- Local Area Network (LAN)

It is a computer network with two or more computers or clusters of network and their resources connected by a communication medium sharing communication protocols,and cofined in a small geographical area such as a building floor, abuilding, or a few adjacent buildings . The advantage of this type is that the elements are close together so the communication links maintain a higher speed of data movement , and the disadvantage it is small and the information does not spread in wide area .

2- Wide Area Network (WAN)

It is the same thing like local area network but the elements of the clusters or the clusters themselves are scattered over a wide geographical area like in a region of a country , or a cross the whole country , several countries, or the entire globle like the Internet for example . The advantages of the wide area network include distributing sevices to a wider community and availability of a wide array of both hardware and software resources, that may not be available in the local area network . The disadvantages is, because of the large geographical areas are covered by the wide area network s, communication media are slow and often unreliable.

3- Metropolitan Area Network (MAN) :

It is a network between the local area network and the wide area network like the network that cover a city or a part of a city .

2.3.4 Network Topology

Networks have many topological shapes like mesh network, which allows multiple access links between network elements unlike other types of topologies , tree network which is very famous , bus network which is the cheapest topology and easy to implement and extend, star network which is easy to add new stations and can accommodate different wiring , ring network which is the growth of the system in it has minimal impact on performance and all stations in it have equal access , see figure (2.3.1) [30]

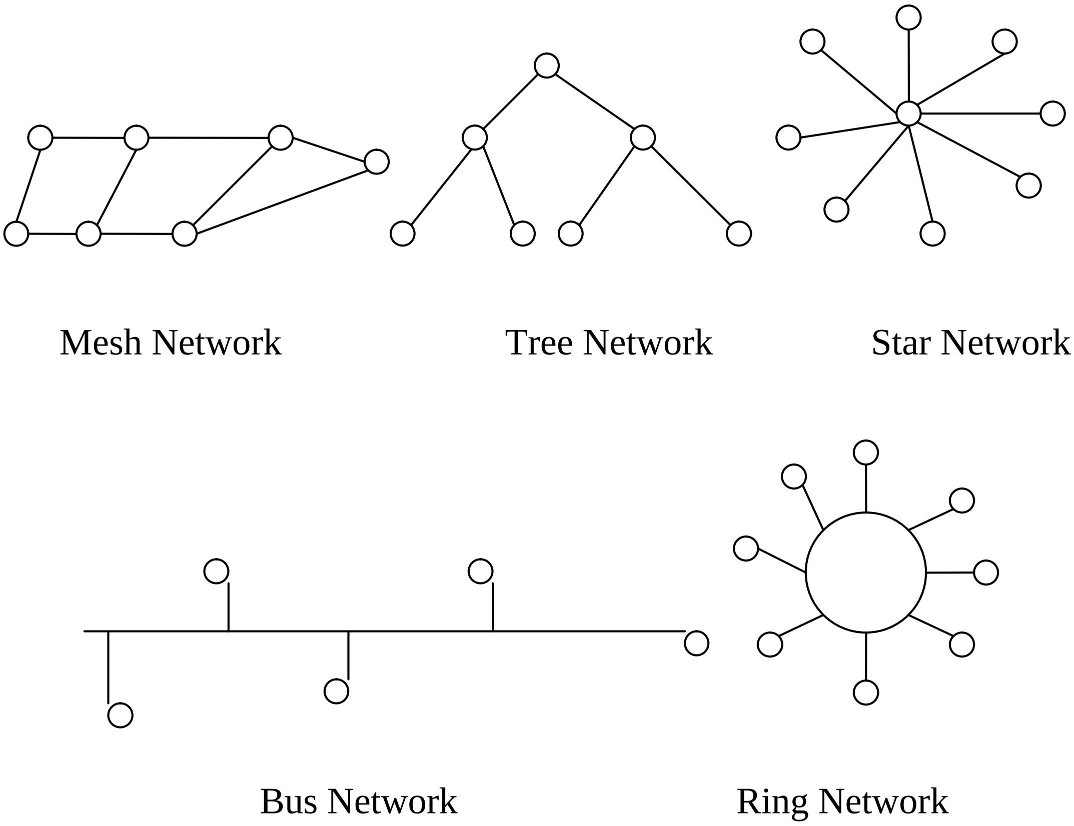


Figure (2 .3.1) : Some Network Topologies

Chapter 3
Centrality

3.1 Introduction

The idea of centrality was first applied to human communication by Bavelas (1948 and 1950), who was interested in the characterization of the communication in small groups of people and assumed a relation between *structural centrality* and influence in group process.

Since then, various measures of structural centrality have been proposed over the years to quantify the importance of an individual in a social network. Most of the centrality measures are based on one of two quite different conceptual ideas and can be divided into two large classes.

The measures in the first class are based on the idea that the centrality of an individual in a network is related to how he is near to the other persons. The simplest and most straightforward way to quantify the individual centrality is therefore the degree of the individual, i.e., the number of its first neighbors; the most elaboration of this concept is said by Neiman (1974). A degree-based measure of the individual centrality corresponds to the notation of how well connected the individual is within its local environment. The degree-based measure of centrality can be extended beyond first neighbors by considering the number of points that an individual can reach at distance two or three as Scott (2003) said. A global measure based on the concept of closeness was proposed by Freeman (1979) in terms of the distances among various points. One of the simplest notion of closeness is calculated from the sum of the geodesic distance from an individual to all the other points in the graph as said by Sabidusi (1966).

The second class of measure is based on the idea that central individual stand between others on the path of communication as said by Bavelas (1948); Anthonisse (1971) and Freeman (1977, 1979). The betweenness at a point measures to what extent the point can play the role of intermediary in the interaction between the others. The simplest and most used measure of betweenness was proposed by Freeman (1977, 1979), and is based on geodesic paths. In many real situations, however, communication does not travel through geodesic paths only. For such a reason, two other measures of betweenness, the first based on all possible paths between a couble of points as Freeman Borgatti and White said in 1991, and the second based on random paths as Newman said in 2003. [31]

3.2 Centrality for unweighted networks

There are many methods for measuring nodes centrality in the unweighted networks. We will discuss the most commonly methods in this section.

3.2.1 Degree Centrality

The simplest definition of node centrality is based on the idea that important nodes must be the most active, in the sense that they have the largest number of ties to the other points in the netwok. Thus, as centrality measure of a node "i" in the network is the degree of that node, i.e., the number of nodes adjacent to it.

To calculate the degree centrality for a node "*i*" in the network;

- ❑ N : Total number of nodes in the network (*Network Order*);
- ❑ K_i : degree of the node "*i*";
- ❑ $A_{N\times N}$: adjacency matrix for the graph, where;

$$a_{ij} = \begin{cases} 1 & \text{, If node } i \text{ is adjacent to node } j. \\ 0 & \text{, Otherwise} \end{cases}$$

Degree centrality of node "*i*" is denoted by C_i^D, and it is sometimes called the *normalized degree centrality*. Its value is calculated from the following equation:

$$C_i^D = \frac{K_i}{N-1} = \frac{\sum_{j=1}^{N} a_{ij}}{N-1} \quad \text{-------------------} \quad \textbf{(3.1)}$$

Here, N-1 = the maximum possible degree in network [32].

3.2.2 Closeness Centrality

The degree centrality is a measure of local centrality. A definition of node centrality on a global scale is based on how close that node to the other nodes. In this scale, the idea is that a node in a network is central if it can quickly interact with all other nodes, not only first neighbors. The simplest notation of closeness is based on the concept of minimum distance or *geodesic* or *shortest path* between two nodes in the network, i.e., the minimum number of edges traversed to get from the first node to the second one, [31].

Let d_{ij} be the shortest path between node "*i*" and node "*j*" and let N be the order of the network. Closeness centrality for node "*i*" denoted by C_i^c is:

$$C_i^c = (L_i)^{-1} = \left[\frac{\sum_{j=1}^{N} d_{ij}}{N-1}\right]^{-1} = \frac{N-1}{\sum_{j=1}^{N} d_{ij}} \quad \text{----------------------} \quad \mathbf{(3.2)}$$

Where L_i is the average distance from node i to all other nodes and the normalization, i.e., divided by "N-1" makes $0 \le C_i^c \le 1$. Such a measure is meaningful for connected graphs only, unless one assumed d_{ij} equal to a finite value, for instance, the maximum possible distance N-1, instead of $d_{ij} = +\infty$, when there is no path between two nodes i and j, [32].

3.2.3 Betweenness Centrality

Interaction between two non-adjacent nodes might depend on the other nodes in the network, especially on those on the paths between the two nodes. Therefore, nodes on the middle can have a strategic control and influence on the others. The important idea at the base of betweenness centrality measure is that the node in the network is central if it lies between many of the nodes. This concept can be simply quantified by assuming that the communication travels just along the geodesic, [31].

Let g_{ik} be the number of geodesic between node *"j"* and node *"k"*, and $g_{jk}(i)$ be the number of geodesics between node "*j*" and node "*k*" that contains node "*i*" . Let $C^B(i)$ be the betweenness centrality of node *"i"*,m where $C^B{}_i$ = the sum over all pairs (j, k) in the network of the ratio between $g_{jk}(i)$ and g_{jk}. Mathematically;

$$C_i^B = \sum_{\substack{j,k \\ j \neq k}} \left[\frac{g_{ik}(i)}{g_{ik}} \right] \qquad \text{---------------------} \quad \textbf{(3.3)}$$

To normalize betweenness centrality of node *i*, we divide by $\frac{1}{2}(N-1)(N-2)$, where

(N-1)(N-2) = the number of pairs of vertices not including the node "*i*" which we want to calculate its centrality.

So, the normalized betweenness centrality of node *"i"* is:

$$C_i^B = \frac{\sum_{\substack{j,k \\ j \neq k}} \left[\frac{g_{ik}(i)}{g_{ik}} \right]}{\frac{1}{2}(N-1)(N-2)} \qquad \text{-----------------} \quad \textbf{(3.4)}$$

Similarly to the other centrality measures, $C^B{}_i$ takes on values between 0 and 1, and it reaches its maximum when the node *i* falls on all geodesics, [31],[32].

3.2.4 Eigenvector Centrality

Degree centrality gives a simple count of the number of connections a node has, but not all connections are equal.

For example, connections to people who are themselves influential will lend a person more influence than connections to less influential people.

Having a large number of connections is good for centrality, but a node with a smaller number of high-quality contacts may out rank another node with a larger number of low-quality contacts.

Eigenvector centrality acknowledges that both the number and the quality of the contacts of the node in the network is important when we compute the centrality of that node.

Let we denote the centrality of nod "*i*" by "x_i", then we can allow for this effect by making (x_i) proportional to the average of the centralities of "*i's*" network neigh bourse, [28].

Mathematically we can write that as:

$$x_i = \frac{1}{\lambda}\sum_{j=1}^{N} A_{ij} x_j \qquad \text{--------------------} \quad \mathbf{(3.5)}$$

Where;

- ❑ λ : an eigenvalue of the adjacency matrix (A);
- ❑ N : is the number of nodes in the network (*network order*);
- ❑ A_{ij} : an element in the adjacency matrix (A).

In the simplest case, (A) is an $n \times n$ symmetric matrix.

The adjacency matrix has elements A_{ij} (See Equation 2.1).

A is symmetric, since if there is an edge between (i) and (j), then clearly there is also an edge between (j)and (i).

Defining the vector of centralities: $X = (x_1, x_2, \ldots\ldots\ldots, x_n)$, where;

- x_1 : the centrality of node (1);
- x_2 : the centrality of node (2);
- x_n : the centrality of node (*n*).

We can rewrite Equation (3.6) in the matrix form as:

$$\lambda x = Ax \quad \text{----------------------} \quad \textbf{(3.6)}$$

Where;

- λ : an eigenvalue of the adjacency matrix;
- *X* : The corresponding eigenvector of that eigenvalue of the adjacency matrix.

If we wish the centralities to be non-negative, (λ) must be the largest eigenvalue of the adgacency matrix to ensure that all the corresponding eigenvectors is positive and (*X*) the corresponding eigenvector, [28].

Each node in the network has an entry in the corresponding eigenvector of the largest eigenvalue of the adjacency matrix of that network, this entry is the centrality of that node in that network.

Perron- Frobenius theorem ensures that for a strongly connected graph, there is a real positive maximum eigenvalue with a positive corresponding eigenvector, [33].

The numerical method for the computation of the largest eigenvalue (λ_{max}) and its corresponding eigenvector for the adjacency matrix of any network is the so-called "*Power Method*" [34] , [35] .

Power Method:

It is a method for computing the largest eigenvalue for the non-homogeneous system and its corresponding eigenvector. We have this procedure for the power method [34],[35]:

(1) Start with an initial guess for X, “the eigenvector in our case”;

(2) Calculate $w = A\,X$, where A is the adjacency matrix;

(3) Largest value (magnitude) in w is the estimate of the eigenvalue “λ”, which is the norm for the vector w;

(4) Get next eigenvector *“X”* by Equation (3.6);

(5) Continue until converged and at that point, λ is the largest eigenvalue and X is the corresponding eigenvector .

The corresponding eigenvector for the larget eigenvalue of the adjacency matrix for the network is the centrality vector for the nodes in that network.

There is another method for computing the largest eigenvalue for the adjacency matrix of the network and its corresponding eigenvector called the *Accelerated Power Method*. It uses the *Rayleigh Quotient* instead of the largest w_k value norm (w, *inf*), [35].

3.3 Centrality for weighted networks

In section (3.2) we discussed some common methods for computing the centrality for unweighted networks that all edges in those networks have the same weight which is equal one . But how can we calculate the centralities of nodes in networks when their edges have different weights , this is what we called the centrality of the weighted network .

In the real world networks like social networks, neural networks, the Internet and airline networks connections or links between the elements in these networks are not equals . For example the ties or relations between individuals in social networks may be strong or week or in between , also we have different capabilities of transmitting electric signals in neural networks , we have also unequal traffic on the Internet links or of the passengers in airline networks . These systems can be better described in terms of weighted networks rather than unweighted networks , i.e. networks in which each link carries a numerical value measuring the strength of the connection [40] .

Definition (3.1):

A weighted network is a network whose edges and nodes are weighted with different weights . We denote the weight of the edge between nodes "*i*" and "*j*" by " w_{ij}" .

Definition (3.2) : The adjacency matrix of a weighted network is called " A weighted adjacency matrix A_{NN}" where its entry A_{ij} is defined as:

$$A_{ij} = \begin{cases} \text{wij, if } i \neq j \text{ and the edge between i and j has weight equal" wij} \\ \\ 0 \qquad\qquad\qquad\qquad\qquad\qquad , \text{ Otherwise} \end{cases} \qquad \text{-----(3.8)}$$

where "N" is number of nodes in the network . [41]

3.3.1 Degree Centrality for weighted networks"Strength Centrality"

The degree centrality of a node in the unweighted network depends on the number of edges adjacent to that node , but if the network is weighted each edge in it has its own weight and those weights are not equal, so in the weighted networks we must look fore another criteria for the centrality which we will call the " Weight Centrality " or the "Strength Centrality" instead of the degree centrality in the unweighted networks .

In the unweighted networks the degree of a node is the number of edges attached to it , we could use the same definition for the weighted networks – simply count the number of edges attached to a node regardless of their weight – but this , ignores much potentially useful information contained in the weights . To the extent that degree is a measure of the importance of a node in a network, surely nodes with strong connections should be accorded more importance than nodes with only weak connections . [29]

Newman suggested a rule by which we can represent any weighted network by a multigraph network . The rule is :

"*We can map any weighted graph to unweighted multigraph . That is , every edge of weight " n " is replaced with " n " parallel edges of weight one each , connecting the same nodes* . " [29]

Example (3.1) :

We can map the weighted network in fig(3.3.1) to a multigraph network in fig (3.3.2) using the mapping rule

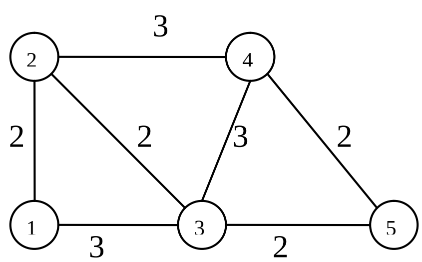


Figure (3.3.1) : A weighted Network

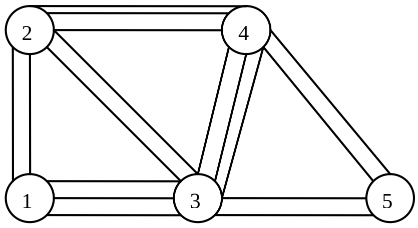


Figure (3.3.2) : A multigraph Network

In example (3.1) when we calculate the degree centralities for nodes in the multigraph network in fig (3.3.2) we found them as follow :

$$C_1^d = 5,\ C_2^d = 7,\ C_3^d = 10,\ C_4^d = 8,\ C_5^d = 4\ .$$

When we calculate the strength of nodes in the weighted network in fig (3.3.1) we found them as follow :

$$S_1 = 5\ ,\ S_2 = 7\ ,\ S_3 = 10\ ,\ S_4 = 8\ ,\ S_5 = 4$$

From those two results we note that the degree centrality for a node in the multigraph network equal the strenght of the same node in the weighted network before using the mapping rule . So by applying the mapping rule on the weighted network we note that the strenght of the node is a good meaure for the centrality of that node in that network .

Result : "*In the weighted network we can replace the degree centrality of the unweighted networks by a new measure called the" Strength Centrality which we will denoted as " C^{st} " .The strength centrality for a node "i" can obtained as*

$$C_i^{st} = S_i \text{ -------------} \quad (3.9)$$

The strength Centrality must be between "0" and "1" , i.e .

$$0 \le C_i^{st} \le 1$$

So we need to normalize the strength centrality of nodes in the weighted network to be between "0" and "1" .

Suppose we have a weighted network consists of " N " nodes . If we want a node "*i*" in that network to have the maximum strenght centrality which equals " 1 " that node must be adjacent to all nodes in that network , so its degree must equals " N – 1 " , which is the same condition as in the unweighted network " degree centrality " . But in the weighted networks the edges have weights and these weights are very important in the calculations of strength of nodes . In each network not all edges have the same weight , so we have an edge that has the maximum weight in the network , which we will denote as " W_{max} " .

If all the incident edges of the node that adjacent to all other nodes in the weighted network " N -1 nodes " have the maximum weight in that network " W_{max} " so its strength will be the maximum strength which we will denote as " S_{max} " , and it has also the maximum normalized strength centrality which is equals "1" .

So the maximum possible strength of the nodes in the weighted network " S_{max} " can given in the formula :

$$\begin{aligned} S_{max} &= (N-1)\, W_{max} \\ &= K_{max}\, W_{max} \quad \text{-----------------} \quad (3.10) \end{aligned}$$

To normalize the strength centralities of the nodes in the weighted network we must divided its strength by the maximum strength in that network " S_{max} " . Hence the normalized strength centrality of node "*i*" in the weighted network is

$$C_i^{st} = \frac{Si}{S\max} \text{ ------------- (3.11)}$$

which we can write as

$$C_i^{st} = \frac{Si}{(N-1)W\max} \text{ ------------ (3.12)}$$

If we return to example (3.1) and apply formula (3.10) to find the strength centralities of nodes in the weighted network in figure (3.3.1) we find that :

$$C_1^{st} = 5,\ C_2^{st} = 7,\ C_3^{st} = 10,\ C_4^{st} = 8,\ C_5^{st} = 4\ .$$

Which is the same result after mapping that network to the multigraph network in figure (3.3.2)

3.3.2 Eigenvector Centrality for weighted networks :

In section (3.2.4) we discussed the eigenvector centrality for the unweighted networks is defined to be proportional to the summation of the centralities of the node's neighbors , so that a node can acquire high centrality either by being connected to alot of others (as with simple degree centrality) or by being connected to others that themselves are highly central . we write .

$$X_i = \lambda^{-1} \sum_j AijXj \text{ -------------------- (3.13)}$$

In the matrix notation we can write equation (3.11) as

$$\lambda X = A X \text{ ---------------------- (3.14)}$$

where λ : is the eigenvalue of the adjacency matrix " A" of the network .

x : is the corresponding eigenvector of that eigenvalue .

By simple arguments one can show that one should take the eigenvector corrosponding to the leading eigenvalue or the largest eigenvalue of the adjacency matrix "A" [29] .

The question now is if the network is weighted can we find an equivalent eigenvector centrality for that weighted network ? What is the effect of the edge's weights on the centrality of the nodes when we use eigenvector method?

To answer these quastions let us go back to the mapping rule that was suggested by Newman which map any weighted network to a multigraph unweighted network . [29] .

We conclude from the mapping rule that the number of the adjacent times between any two nodes in the network have a weighted edge between them will icrease many times equal the weight of that edge when we map the weighted network to the multigraph network and that will affect the adjacency matrix of the network .

The adjacency matrix of the network in this case must be changed and equal the array multiplication between the adjacency matrix of the unweighted network and the weight matrix of the weighted network . The adjacency matrix in this case called the weighted adjacency matrix and denoted by " A_w" where

$$A_w = A.* W \text{ -------------------- } (3.15)$$

The method for computing the eigenvector centrality for the weighted network is the same as the unweighted network but we replace the adjacency matrix of the unweighted network by the weighted adjacency matrix of the weighted network . So the equation that compute the centrality of the weighted network using eigenvector method will become :

$$\lambda X = A_w X \text{ ------------------ } (3.16)$$

where λ : is the largest eigenvalue of the weighted adjacency matrix .

X : is the corrosponding eigenvector of that eigenvalue .

A_w : is the weighted adjacency matrix .

"X" here is the centrality vector of all the nodes in the network . So if we compute "X" we will compute the eigenvector centrality of all nodes in the weighted network.

To normalize the eigenvector centrality for the weighted network we must define the maximum eigenvector centrality of that weighted network which is the summation of the eigenvector centralities of all nodes in that weighted network

$$C^{eig}{}_{max} = \Sigma\, C_i{}^{eig} \text{ ------------------ } (3.17)$$

The normalized eigenvector centrality for node "*i*' in the weighted network is

$$C_i^{eign} = C_i^{eig} / C^{eig}{}_{max} \text{ ------------------}(3.18)$$

To compute λ_{max} and "X" from equation (3.14) we use the power method or the accelerated power method or Matlab functions again.

3.3.3 Closeness Centrality for weighted networks :

The method that use for computing closeness centralities for nodes in the weighted networks is the same as it for the unweighted network . The only different is that we must take the weights of the edges in mind when we compute the shortest paths between nodes in those networks . The formula that use for compute the closeness centrality for node "i" in the weighted network is

$$C_i^c = (L_i)^{-1} = \left[\frac{\sum_{j=1}^{N} d_{ij}}{N-1} \right]^{-1} = \frac{N-1}{\sum_{j=1}^{N} d_{ij}} \quad \textbf{----- (3.19)}$$

Where L_i is the average distance from node i to all other nodes and the normalization, i.e., divided by "N-1" makes $0 \le C_i^c \le 1$.

Chapter 4

RELATED WORKS

The first application of mathematical modeling to the spread of infectious disease was carried out by Daniel Bernoulli in 1760.He formulated and solved a differential equation describing the dynamics of the infection which is still of value in our day. Hamer formulated and analyzed a discrete time model in 1906 to understand the recurrence of measles epidemics. Ross developed differential equation models for malaria as ahost-vector disease in 1911. Mckendrick developed the first stochastic theory in 1926 and in 1930 Kermack and Mckendrick established the extremely important threshold theorem,showing that the density of susceptible individuals must exceed a certain critical value in order for an epidemic to occur [20],[39] . Mathematical epidemiology seems to have grown exponentially starting in the middle of the 20th century (the first edition in 1957 of Bailey's book is an important landmark), so that a tremendous variety of models have now been formulated, mathematically analyzed, and applied to infectious diseases [9]. Currently, there are several papers on mathematical epidemiology per month in many journals which publishes such work [20] . In 1994 Kephart and White presented the epidemiological model to understand and control the prevalence of viruses. This model is based on biological epidemiology and uses nonlinear differential equations to provide a qualitative understanding of virus spreading [19] . In the next section we will review some most known epidemiological models such as SI,SIS,and SIR models .

As I mentioned in chapter (2) we can represent any network as a graph consists of nodes which may be computers,routers,ect and edges contact between them which let the information which may be worms,viruses or any disease pass from one node to another.When any worm or virus is fired into any network,the Internet for example,it simultaneously scans many machines (computers or nodes) in an attempt to find a vulnerable machine to infect,when it finally finds its prey, it sends out a probe to infect the target . If successfull, a copy of this worm is transferred to this new host(computer) . This new host(computer) then begins running the worm and tries to infect other machines,and so on [19] .This infection process is a random process, and the propagation of worms and viruses through networks is also random .

4.1 Epidemic Models

The aim of epidemic modelling is to understand and if possible control the spread of disease through networks [14] .There are many epidemiological models that described the spreading of epidemics through networks such as SI,SIS,SIR,SIDR,and SIRS models.

Epidemiological models are based on two simplifications

1- At any given time t, each node can be in one of a finite number of states,e.g. susceptible, quarantined-susceptiblem, removed-susceptible, infectious, quarantined-infectious, removed-infectious and detected .

2- Translation of the worm or epidemic transmission mechanism into a probability that a node will infect another node. In a similar way, transitions between other states of the model are described by simple probabilities . Epidemiological models can be analyzed analytically or by means of simulation [16] , [12] .

The propagation takes place on a graph "G" with "n" nodes and "m" edges . let

S(t) : the number of susceptible nodes at time "t"

I(t) : the number of infectious nodes at time "t"

R(t) : the number of removed nodes at time "t"

$Qs(t)$: the number of quarantined – susceptible nodes at time "t"

$Rs(t)$: the number of removed – susceptible nodes at time "t"

Qi(t) : the number of quarantined – infectious nodes at time "t"

β : infection rate , which is the rate at which susceptible nodes are infected [23],[16],[10] .

Most models of propagation assume the infection rate 'β' is constant ,averaging out the differences in processor speed, network bandwidth, and location of infectious node . The existing models also assume that a node cannot be infected multiple times [16] .

4.1.1 Susceptible –Infectious Model : SI Model

It is a model at which a susceptible node becomes infectious,it does not change its state . This model can be used in the study of the worst – case propagation, when automated and human countermeasures are not available [22],[23],[16],[10],[25] ,[6] .

The model :

Let

N: the total number of nodes in the network" the population size"

d: be the average dgree of an infectious node

i(t) : the fraction of infectious nodes at time "t" where i(t) = I(t)/N

s(t) : the fraction of susceptible nodes at time "t" where s(t) = S(t)/N

As all nodes in the network either infectious or susceptible we have

$$s(t)+i(t) = 1 \rightarrow s(t) = 1- i(t) \quad \text{----------} \quad (4.1)$$

d s(t) : the expected number of susceptible neighbours that can be infected by a given infectious node .

Using equation 1 we have : d s(t) = d (1- i(t)

'β' d s(t) i(t) : the total rate of newly infected nodes .

Using equation 1 we have : β d s(t) i(t) = β d (1-i(t)) i(t)

The general susceptible – infectious SI model is described by the differential equation

$$\frac{di(t)}{dt} = \beta\, d\, (1-i(t))\, i(t) \quad \text{----------} \ (4.2)$$

$\frac{di(t)}{dt}$: is called the infection spreading velocity v(t).[2]

with boundary conditions :

1- $i(0) = I(0)/N > 0$

2- for all $t \geq 0$, $i(t) + s(t) = 1$

The solution of equation (2) for the fraction of infectious nodes is the logistic curve

$$i(t) = i(0)\, e^{\beta' t} / 1 - i(0) + i(0)\, e^{\beta' t} \text{ ---------- } (4.3)$$

where $\beta' = \beta\, d$.

The authors of [24],[26] describe the propagation of worms through networks with time by the differential equation

$$\frac{da}{dt} = K\, a\, (1 - a) \text{ ---------- } (4.4)$$

where $\frac{da}{dt}$ is called the infection velocity $v(t)$.[2]

with solution

$$a = e^{K(t-T)} / 1 + e^{K(t-T)} \text{ -----------} (4.5)$$

where T is a constant of integration and K is the infection rate or the initial compromise rate which is the number of vulnerable hosts which an infected host can find and compromise per unit time . K here is assumed and constant [24],[26]. Some authors proposed that the infection rate "K" should be considered as function of time ; K=K(t) , because of intervening network saturation and router collapse .[26] .

a : a proportion of the machines that have been compromised at time "t" .

t : the time .

When we plot equations (4.3) and (4.5) with some assumed and constant infection rate we have the S – Shaped curve that described the fraction of infectious nodes with time [23],[10],[25], see figure (4.1.1)

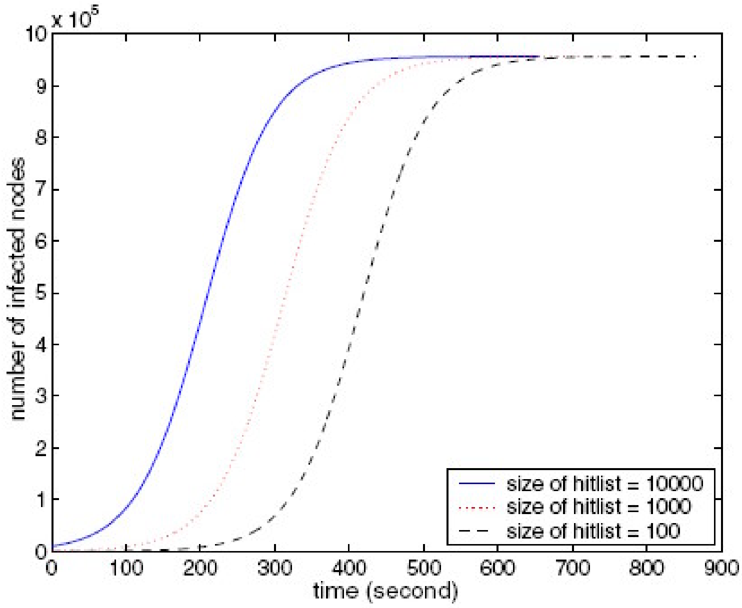


Figure (4.1.1) : Fraction of infectious nodes with time in SI model

We note from figure (4.1.1) that the S – Shaped Curve has three regions:

1- Slow start region , when only few nodes are infected at every time step .

2- Exponentially growth, when the number of newly infected nodes grows exponentially .

3- Equilibrium state , when the number of infectious nodes assumes some value around which it fluctuates steadily .

When we plot equations (4.2) and (4.4) with some assumed and constant infection rate we have the infection spreading velocity curve that describe the changing of the spreading velocity of infection with time .[2],[3] see figure (4.1.2)

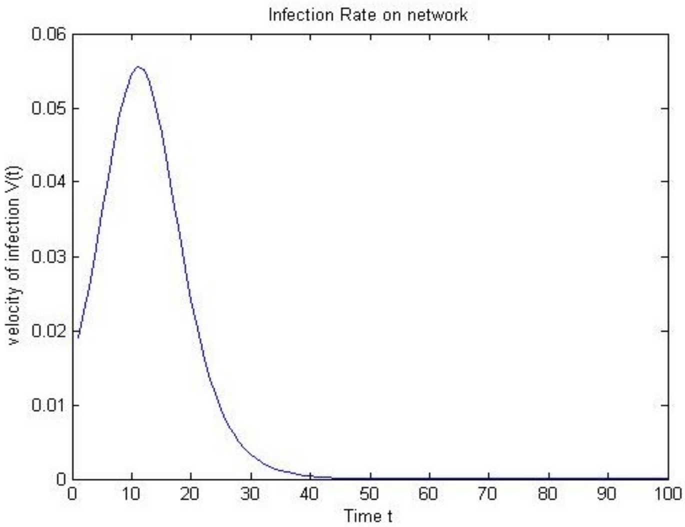


Figure .(4.1.2) : The infection Spreading velocity with time

4.1.2 Susceptible - Infectious - Susceptible Model : SIS Model

In this model an infectious node recovers at some rate, and thus it becomes susceptible again . This model can be used in the study of worm's or epidemic's propagation when some computers are temporarily turned off but are not patched [22],[23],[16] .

The Model

Let

N: the total number of nodes in the network (the population size)

d : the average degree of an infected node

γ : the rate at which an infectious node recovers .(recover rate)

The rate of newly infected nodes is proportional to :

1- the expected fraction of susceptible neighbours

2- the number of infected nodes

3- the infection rate or probability β .

The rate at which infectious nodes recover is proportional to :

1- the number of infected nodes .

2- the recover rate .

The general SIS model is described by the differential equation

$$\frac{di(t)}{dt} = \beta\, \underline{d}\, (1-i(t))\, i(t) - \gamma\, i(t) \quad \text{--------------} \ (4.6)$$

with boundary conditions

(1) $i(0) = I(0) / N > 0$.

(2) for all $t \geq 0$, $i(t) + s(t) = 1$.

The solution of equation (4.6) gives a functional form for the fraction of infectious nodes :

$$i(t) = (1 - \delta)\, i(0) / i(0) + (1 - \delta - i(0))\, e^{-(\beta' - \gamma)t} \quad \text{---------} \ (4.7)$$

where $\beta' = \beta\, \underline{d}$ and

$\delta = \gamma / \beta\, \underline{d}$: the epidemic threshold .

When we plot equation (4.7) with some constants β , $\underline{d}$, γ, and δ we have also the S-Shaped Curve . [23],[16] , see figure (4.1.3)

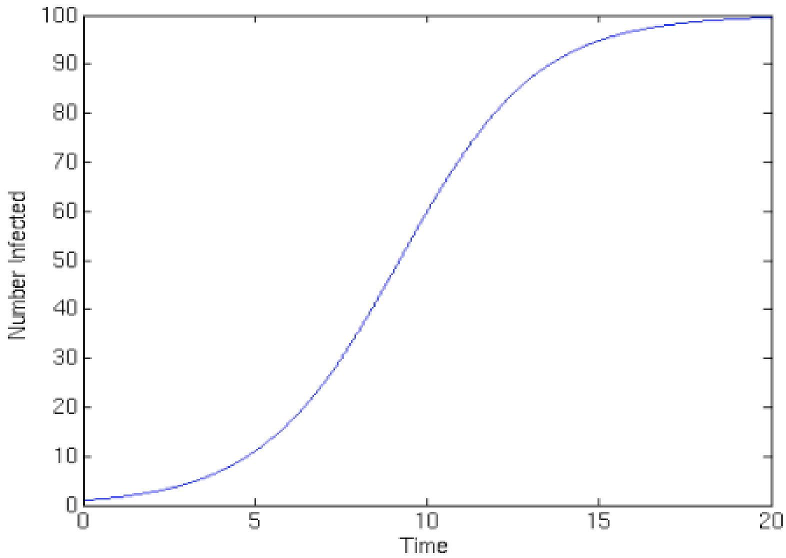


Figure (4.1.3) : Fraction of infectious nodes with time in SIS model

4.1.3 Susceptible - Infectious -Removed Model : SIR Model

In this model , an infectious node can be removed .(i.e. it can no longer spread the epidemic) . This model can be used to study the effects of software patching and traffic blocking . At any time "t" , a node can be susceptible, infectious, or removed .[23],[16], [25].

The Model

γ: the rate at which infectious nodes are removed . (removed rate) .

The general SIR model can be described by the differential equations

$$\frac{di(t)}{dt} = \beta\ \underline{d}\ (1- i(t)\ )\ i(t) - \gamma\ i(t) \quad \text{-----------} \ (4.8)$$

$$\frac{dr(t)}{dt} = \gamma\ i(t) \quad \text{----------} \ (4.9)$$

with boundary conditions :

(1) $i(0) = I(0)/N \geq 0$

(2) $r(0) = R(0)/N \geq 0$

(3) for all $t \geq 0$, $i(t) + s(t) + r(t) = 1$.

There are other epidemic models like Susceptible – Infectious – Removed – Susceptible (SIRS) model , Susceptible – Infectious – Detected – Removed (SIDR) model and others .[16]

Chapter 5
METHODOLOGY

To answer my research question and prove my hypothesis I will exhibit my method for that by the folowing steps

5.1 Research Subject

My subjects in this thesis are nodes (computers, routers, ect) which form one population or one network and there are links between them.Links may be unweighted or weighted . The weights of the links here represent time .All nodes in the networks here either infected or susceptible . All networks in this thesis have "N" nodes, just one node infected first "$I(0) = 1$" and has ability to infect all other nodes by an infection rate "β" which I will relate to the closeness centrality of the first infected node. We also have $(N – 1)$ nodes are susceptibles (S) which have the ability to be infected.

5.2 Research Tools

1- My program

It is a matlab program that I programed using matlab . It depends on Floyd's Algorithm for finding the shortest path between any two nodes in the network and putting all these shortest paths in a matrix that I called the shortest paths matrix . My program can also calculate the centralities for all nodes in the network using three methods , degree centrality, eigenvector centrality and the closeness centrality then ranking nodes according to their centralities in the same table . The input of my program is the total number of nodes in the network and the adjacency matrix of that network and the output of the program is the shortest path matrix of that network and the degree centralities, the eigenvector centralities and the closeness centralities for all nodes in the network ranking according to their values . See Appendix (A)

2 - Matlab

Matlab is a popular tool for dealing with matrices . I used matlab for running my program and having the results . I used it also for plotting all figures in my thesis .

3-POM – QM for windows program " V3"

It is a program that programed by Howard J . Weiss . It is the most user – friendly available in the fields of operations Management, which includes networks . The program deals with three problems in networks, minimum spanning tree, shortest path and maximal flow problem . The input in this program is number of edges, the start node,the end node,the weight for each edge . By using this program we can calculate the shortest path between any two nodes in the network and the minimum distance matrix. I used this program to check my matlab program by comparing my program result to POM-QM program result. I found that they were the same, which supported my program results .

To compare between the results of my program and the results of POM-QM program let us take example (5.1) .

Example (5.1) : Find the shortest path matrix for the network shown in fig (5.2.1) by POM – QM for windows program "V3" and by using my matlab program , then compare between the two results ?

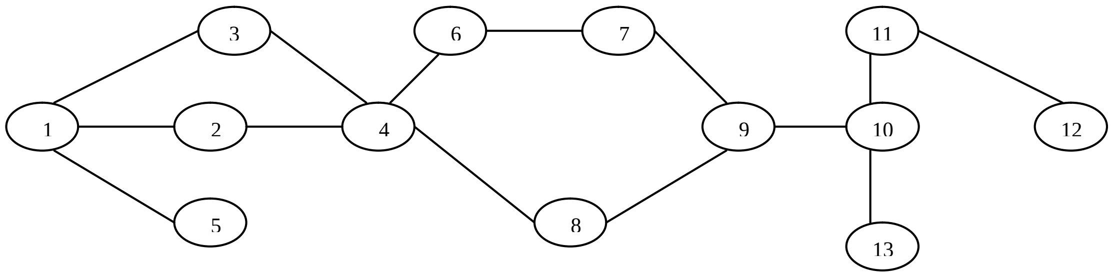


Fig (5.2.1) : Small unweighted network

Solution :

When I used POM – QM for windows program I found that the shortest path matrix is :

	1	2	3	4	5	6	7	8	9	10	11	12	13
1	0	1	1	2	1	3	4	3	4	5	6	7	6
2	1	0	2	1	2	2	3	2	3	4	5	6	5
3	1	2	0	1	2	2	3	2	3	4	5	6	5
4	2	1	1	0	3	1	2	1	2	3	4	5	4
5	1	2	2	3	0	4	5	4	5	6	7	8	7
6	3	2	2	1	4	0	1	2	2	3	4	5	4
7	4	3	3	2	5	1	0	2	1	2	3	4	3
8	3	2	2	1	4	2	2	0	1	2	3	4	3
9	4	3	3	2	5	2	1	1	0	1	2	3	2
10	5	4	4	3	6	3	2	2	1	0	1	2	1
11	6	5	5	4	7	4	3	3	2	1	0	1	2
12	7	6	6	5	8	5	4	4	3	2	1	0	3
13	6	5	5	4	7	4	3	3	2	1	2	3	0

The shortest path matrix for the small unweighted network in fig (5.2.1) using POM-QM program

When I used my matlab program for the same network in fig (5.2.1) I found that the shortest path matrix is :

	1	2	3	4	5	6	7	8	9	10	11	12	13
1	0	1	1	2	1	3	4	3	4	5	6	7	6
2	1	0	2	1	2	2	3	2	3	4	5	6	5
3	1	2	0	1	2	2	3	2	3	4	5	6	5
4	2	1	1	0	3	1	2	1	2	3	4	5	4
5	1	2	2	3	0	4	5	4	5	6	7	8	7
6	3	2	2	1	4	0	1	2	2	3	4	5	4
7	4	3	3	2	5	1	0	2	1	2	3	4	3
8	3	2	2	1	4	2	2	0	1	2	3	4	3
9	4	3	3	2	5	2	1	1	0	1	2	3	2
10	5	4	4	3	6	3	2	2	1	0	1	2	1
11	6	5	5	4	7	4	3	3	2	1	0	1	2
12	7	6	6	5	8	5	4	4	3	2	1	0	3
13	6	5	5	4	7	4	3	3	2	1	2	3	0

The shortest path matrix for the small unweighted network in fig (5.2.1) using my program

We note that they are the same which support my program's results

5.3 Procedures

1- I will generate four types of random networks , the first one is small unweighted network consists of "13" nodes linked together, large unweighted network consists of "80" nodes linked together also , small weighted network consists of "13" nodes linked by different weights edges and finally large weighted network consists of "80" nodes linked by different weights edges . The purpose of that is to support my result by different types of networks by comparing the result optained from each network to others .

2- I will calculate the closeness centrality for each node in each network , then ranking them according to their closeness centralities using my matlab program .

3- I will use the closeness centrality as assumption for the infection rate in networks instead of just assuming any constant number as almost all other models have been done . As we have seen in section (4.1) the authors of [22],[23], [10],[25] assumed a constant number for the infection rate . The authors of [16]and [6] used a constant number for the infection rate multiplied by the average of nodes degree "d" to get more sensible result . Also the authors of [24] and [26] assumed the initial compromise rate is constant . In my development of the SI model I will use the closeness centrality of nodes instead of the assumed and constant numbers as an infection rate, because I beleave that the closeness centrality depends on the summation of all shortest paths between the first infected node and all other nodes in the network . The node that have the smallest summation of all shortest paths between it and all other nodes has the smallest time to infect all other nodes in the network, so it has the smallest total infection time and it has the largest infection rate , also it can spread infection faster than any other nodes in the network ,so it has the largest infection spreading power . At the same time it has the largest closeness centrality

4- I will trace infections movements when different nodes with different closeness centralities infected first . I will analyze the infection process with time for three nodes in each of the four networks that I generate when they are infected first . The first node has the highest closeness centrality ,the second node has median closeness centrality and the third node has the smallest closeness centrality ,then calculate the total infection time and the infection rate in general for each case .

5- I will plot the total number of infected nodes with time for each of the three nodes , then compare the three cases by plotting the three curves of the three nodes in the same figure .

6 – I will plot the relation between the closeness centrality and the total infection time for the three nodes to declear the relation between them .

7 – I will plot the relation between the closeness centrality and the infection rate for the three nodes also to declear the relation between them .

8- I will test my hypothesis and apply it to the four networks that I generate and plot the number of infected nodes or their fractions with time and their infection spreading velocities with time , then compare my result with the prevuois results .

9 – Finally I will compare between my work and the work of the author of [12] who replaces the infection rate by the eigenvector principal of the first infected node in the network .

5.4 Proporation

To find the infection rate when any node infected first in the network we calculate it's closeness centrality as follow :

1- We find the shortest path between that node and all other nodes in the network either it is weighted or unweighted .

2- We find the summation of all these shortest paths .

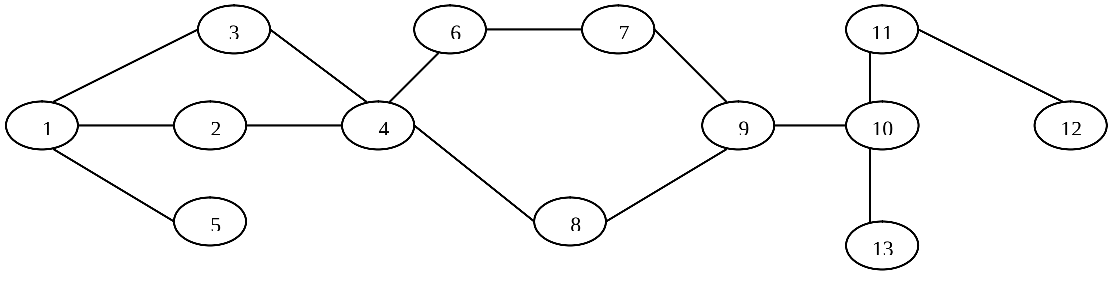
3- To find the closeness centrality of that node we divide one by that summation .

4- To normalize the closeness centrality we multiply (1/summation) by (N-1) where N is the nodes in the network , and we have the following formula :

$$C_i^c = \frac{(N-1)}{\sum_j dij} \text{ ---------- } (5.1)$$

Where dij : is the shortest path between node "*i*" and node "*j*" .

Example 5.2: Find the closeness centrality for all nodes in the network in figure (5.4.1) .



Figurer (5.4.1) : Small unweighted network for example (5.2)

Solution :

For node (1)

$d_{1,1}$ = 0,$d_{1,2}$ = 1, $d_{1,3}$ = 1, $d_{1,4}$ = 2, $d_{1,5}$ = 1, $d_{1,6}$ = 3, $d_{1,7}$ = 4, $d_{1,8}$ = 3, $d_{1,9}$ = 4, $d_{1,10}$ = 5, $d_{1,11}$ = 6, $d_{1,12}$ = 7, $d_{1,13}$ = 6

Sum of shortest paths = 43

$$C^c{}_1 = \frac{12}{43}$$

For node (2)

$d_{2,1}$=1, $d_{2,2}$=0, $d_{2,3}$=2, $d_{2,4}$=1, $d_{2,5}$=2, $d_{2,6}$=2, $d_{2,7}$=3, $d_{2,8}$=2, $d_{2,9}$=3, $d_{2,10}$=4, $d_{2,11}$=5, $d_{2,12}$=6, $d_{2,13}$=5

Sum of shortest paths = 36

$$C^c{}_2 = \frac{12}{36}$$

For node(3)

$d_{3,1}$=1, $d_{3,2}$=2, $d_{3,3}$=0, $d_{3,4}$=1, $d_{3,5}$=2, $d_{3,6}$=2, $d_{3,7}$=3, $d_{3,8}$=2, $d_{3,9}$=3, $d_{3,10}$=4, $d_{3,11}$=5, $d_{3,12}$=6, $d_{3,13}$=5

Sum of shortest paths = 36

$$C^c{}_3 = \frac{12}{36}$$

For node (4)

$d_{4,1}$= 2, $d_{4,2}$= 1, $d_{4,3}$= 1, $d_{4,4}$= 0, $d_{4,5}$= 3, $d_{4,6}$= 1, $d_{4,7}$= 2, $d_{4,8}$= 1, $d_{4,9}$= 2, $d_{4,10}$= 3, $d_{4,11}$= 4, $d_{4,12}$= 5, $d_{4,13}$= 4

Sum of shortest paths = 29

$$C^c{}_4 = \frac{12}{29}$$

For node (5)

$d_{5,1}$ = 1, $d_{5,2}$ = 2, $d_{5,3}$ = 2, $d_{5,4}$ = 3, $d_{5,5}$ = 0, $d_{5,6}$ = 4, $d_{5,7}$ = 5, $d_{5,8}$ = 4, $d_{5,9}$ = 5, $d_{5,10}$ = 6, $d_{5,11}$ = 7, $d_{5,12}$ = 8, $d_{5,13}$ = 7

Sum of shortest paths = 54

$C^c{}_5 = \frac{12}{54}$

For node (6)

$d_{6,1}$=3, $d_{6,2}$=3, $d_{6,3}$=3, $d_{6,4}$=3, $d_{6,5}$=3, $d_{6,6}$=3, $d_{6,7}$=3, $d_{6,8}$=3, $d_{6,9}$=3, $d_{6,10}$=3, $d_{6,11}$=3, $d_{6,12}$=3, $d_{6,13}$=3

Sum of shortest paths = 33

$C^c{}_6 = \frac{12}{33}$

For node (7)

$d_{7,1}$= 4 , $d_{7,2}$= 4 , $d_{7,3}$= 4 , $d_{7,4}$= 4 , $d_{7,5}$= 4 , $d_{7,6}$= 4 , $d_{7,7}$= 4 , $d_{7,8}$= 4 , $d_{7,9}$= 4 , $d_{7,10}$= 4 , $d_{7,11}$= 4 , $d_{7,12}$= 4 , $d_{7,13}$= 4

Sum of shortest paths = 33

$C^c{}_7 = \frac{12}{33}$

For node (8)

$d_{8,1}$=3, $d_{8,2}$=2, $d_{8,3}$=2, $d_{8,4}$=1, $d_{8,5}$=4, $d_{8,6}$=2, $d_{8,7}$=2, $d_{8,8}$=0, $d_{8,9}$=1, $d_{8,10}$=2, $d_{8,11}$=3, $d_{8,12}$=4, $d_{8,13}$=3

Sum of shortest paths = 29

$C^c{}_8 = \frac{12}{29}$

For node (9)

$d_{9,1}$=4, $d_{9,2}$=3, $d_{9,3}$=3, $d_{9,4}$=2, $d_{9,5}$=5, $d_{9,6}$=2, $d_{9,7}$=1, $d_{9,8}$=1, $d_{9,9}$=0, $d_{9,10}$=1, $d_{9,11}$=2, $d_{9,12}$=3, $d_{9,13}$=2

Sum of shortest paths = 29

$C^{c}_{9}= \frac{12}{29}$

For node (10)

$d_{10,1}$= 5, $d_{10,2}$= 5, $d_{10,3}$= 5, $d_{10,4}$= 5, $d_{10,5}$= 5, $d_{10,6}$= 5, $d_{10,7}$= 5, $d_{10,8}$= 5, $d_{10,9}$= 5,$d_{10,10}$= 5, $d_{10,11}$= 5, $d_{10,12}$= 5, $d_{10,13}$= 5

Sum of shortest paths = 34

$C^{c}_{10}= \frac{12}{34}$

For node (11)

$d_{11,1}$= 6, $d_{11,2}$= 6, $d_{11,3}$= 6, $d_{11,4}$= 6, $d_{11,5}$= 6, $d_{11,6}$= 6, $d_{11,7}$= 6, $d_{11,8}$= 6, $d_{11,9}$= 6, $d_{11,10}$= 6, $d_{11,11}$= 6, $d_{11,12}$= 6, $d_{11,13}$= 6

Sum of shortest paths = 43

$C^{c}_{11}= \frac{12}{43}$

For node (12)

$d_{12,1}$=7, $d_{12,2}$=6, $d_{12,3}$=6, $d_{12,4}$=5, $d_{12,5}$=8, $d_{12,6}$=5, $d_{12,7}$=4, $d_{12,8}$=4, $d_{12,9}$=3, $d_{12,10}$=2, $d_{12,11}$=1, $d_{12,12}$=0, $d_{12,13}$=3.

Sum of shortest paths = 54 .

$C^{c}_{12}= \frac{12}{54}$.

For node (13)

$d_{13,1}=6$, $d_{13,2}=5$, $d_{13,3}=5$, $d_{13,4}=4$, $d_{13,5}=7$, $d_{13,6}=4$, $d_{13,7}=3$, $d_{13,8}=3$, $d_{13,9}=2$, $d_{13,10}=1$, $d_{13,11}=2$, $d_{13,12}=3$, $d_{13,13}=0$.

Sum of shortest paths = 45.

$C^c_{13}=\frac{12}{45}$.

So the closeness centrality for all nodes of the network in figure (5.4.1) are tabulated in table (5.4.1) .

Table (5.4.1): Closeness Centralities for all nodes of network in figure (5.4.1)

Node	1	2	3	4	5	6	7	8	9	10	11	12	13
Closeness Cetrality	$\frac{12}{43}$	$\frac{12}{36}$	$\frac{12}{36}$	$\frac{12}{29}$	$\frac{12}{54}$	$\frac{12}{33}$	$\frac{12}{33}$	$\frac{12}{29}$	$\frac{12}{29}$	$\frac{12}{34}$	$\frac{12}{43}$	$\frac{12}{54}$	$\frac{12}{45}$

By ranking nodes according to their closeness centralities we have table (5.4.1)

Table (5.4.2) : Ranking nodes of network in figure (5.4.1) according to their closeness centralities

Rank	1	2	3	4	5	6	7	8	9	10	11	12	13
Node	4	8	9	6	7	10	2	3	1	11	13	5	12
Closeness Centrality	$\frac{12}{29}$	$\frac{12}{29}$	$\frac{12}{29}$	$\frac{12}{33}$	$\frac{12}{33}$	$\frac{12}{34}$	$\frac{12}{36}$	$\frac{12}{36}$	$\frac{12}{43}$	$\frac{12}{43}$	$\frac{12}{45}$	$\frac{12}{54}$	$\frac{12}{54}$

After finding the closeness centrality "C_i^c" of node in the network we assume that it represents the probability of infection rate when that node infected first .

5.5 My Method

My research subjects, as I exeplained in section(5.1) ,consist of "N" nodes and just one node is infected first "I(0) =1" and " N-1" nodes are susceptible " S(0) = N-1". I assumed that the closeness centrality "C_i^c" for node "*i*" represent the probability for rate of infection if node "*i*" is the first infected node. When any susceptible node infect if will still infected for ever ,that mean we have no recovery ,so after a period of time all susceptible nodes will become infected by the probability for rate of infection for that node "its closeness centrality" .

So I will develop the SI model of epidemic network by replacing the infection rate "β" by the closeness centrality of the first infected node as an assumption .

I assumed that each node in the network has different total infection time,different infection rate and different infection spreading power when they are infected first ,because they have different shortest paths to other nodes and different times to reach information to those nodes and they have different closeness centralities . The node that has the minimum time to reach all nodes it has the minimum summation of shortest paths and it has the largest closeness centrality, therefor it has the minimum total infection time, the maximum infection rate and the maximum infection spreading power .

The author of [12] assumed that we have just one infected node at the beginning of the infection process ,where the other authors of [16],[9],[24],[10],[22],[25],[26] do not determine how many nodes are infected at the beginning of that process . In my development of SI model I assume that I also have just one infected node at the beginning as author of [12]. The authors of [9],[24],[10],[22],[25],[26] depend on just assumed numerical number for the infection rate "β" and the author of [16] depends on " d" (average of degree) plus "β". The author of [12] used the principal egeinvector "PEV" for the first infected node "*i*" as rate of infection . In my development of SI model I will use the closeness centrality for the first infected node "*i*" ,"C_i^c" as rate of infection because it depends on the shortest paths between node "*i*" and other nodes in the network and shortest path means shortest time , as I considered the weights of edges in my networks as time . Nodes with high closeness centralities have the small time for propagate the epidemic to all nodes in the network and the large infection rate ,therefore , the propagation infection power for nodes depends on their closeness centralities ,so I think we can replace the infection rate in equation (4.2) and equation(4.3) by the closeness centrality of the first infected node "C_i^c" .

The differential equation that described SI model will become :

$$\frac{di(t)}{dt} = C_k^c\,(1-i(t))\,i(t) \text{ --------------(5.2)}$$

where "*k*" is the first infected node in the network.

with boundary conditions as I(0) = 1 and i(0) = I(0)/N , so

(1) i(0) = 1/N , i(t final) = 1 .

(2) for all $t \geq 0$, i(t) + s(t) = 1 .

The solution of equation (5.2) for the fraction of infectious nodes is the " logistic curve " :

$$i(t) = (1/N)\, e^{Ck\,t} / 1-(1/N) + (1/N)\, e^{Ck\,t} \text{ ---------------- (5.3)}$$

Equation (5.3) represents the logistic curve describing the rate of infection which I will use to measure the fraction of infected nodes as afunction of time "t" .

Chapter 6

ANALYSIS and RESULTS

In this chapter I will take four types of networks then I will analyze the infection process with time for some nodes in each of those networks and related that with their closeness centralities .Finally I will apply my hypothesis on these networks then compare my results with the previous results that obtained by other authors .

6.1 Result From Small Unweighted Network :

Let us take the same network that we took in example (1.5) which consist of " 13" nodes , see figure (6.1.1)

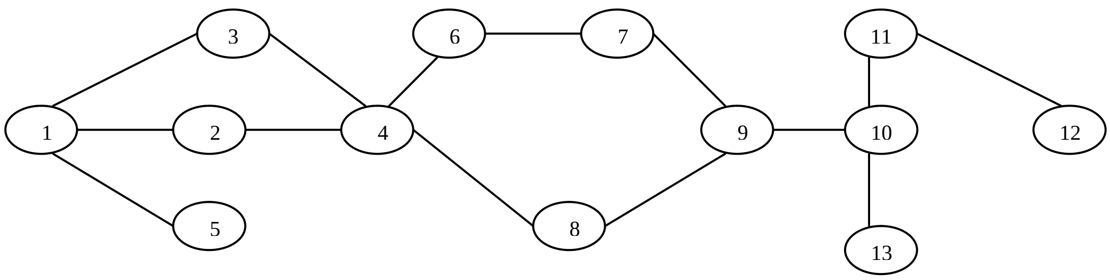


Figure (6.1.1) : Small Unweighted Network

By calculating the closeness centralities for all nodes in the network in figure (6.1.1) and ranking them according to their closeness centralities using my matlab program , I used the adjacency matrix of the network in fig (6.1.1) which is shown in Appendix (B) .We have first the shortest path matrix see figure (6.1.2)

	1	2	3	4	5	6	7	8	9	10	11	12	13
1	0	1	1	2	1	3	4	3	4	5	6	7	6
2	1	0	2	1	2	2	3	2	3	4	5	6	5
3	1	2	0	1	2	2	3	2	3	4	5	6	5
4	2	1	1	0	3	1	2	1	2	3	4	5	4
5	1	2	2	3	0	4	5	4	5	6	7	8	7
6	3	2	2	1	4	0	1	2	2	3	4	5	4
7	4	3	3	2	5	1	0	2	1	2	3	4	3
8	3	2	2	1	4	2	2	0	1	2	3	4	3
9	4	3	3	2	5	2	1	1	0	1	2	3	2
10	5	4	4	3	6	3	2	2	1	0	1	2	1
11	6	5	5	4	7	4	3	3	2	1	0	1	2
12	7	6	6	5	8	5	4	4	3	2	1	0	3
13	6	5	5	4	7	4	3	3	2	1	2	3	0

Figure (6.1.2): The shortest paths matrix for the small unweighted network in fig (6.1)

We have also table (6.1.1) in which we ranked nodes of the network in fig (6.1.1) according to their closeness centralities.

Table .(6.1. 1) : Ranks of nodes of network in fig (6.1.1) according to their closeness centralities .

Rank	Node	Closeness Centrality
1	4	0.4138
2	8	0.4138
3	9	0.4138
4	6	0.3636
5	7	0.3636
6	10	0.3529
7	2	0.3333
8	3	0.3333
9	1	0.2791
10	11	0.2791
11	13	0.2667
12	12	0.2222
13	5	0.2222

From table (6.1.1) we note that node (4) has the highest closeness centralities , so it is the most important node in the network , node (2) has median closeness centrality which means that it has median importance and node (12) has the smallest closeness centrality and it is the most unimportant node in the network .

6.1.1: Analysis of infection process for small unweighted network :

To clarify the relation between the closeness centrality of the first infected node and each of the total infection time, the infection rate and the infection spreading power let us take three nodes that have different closeness centralities and assume that they are infected first ,then analyze the infection process with time for each of them ,the compare between the three cases . The nodes are node (4) which has the largest closeness centrality , node (2) which has the median closeness centrality and node (12) which has the smallest closeness centrality .

When node (4) infected first the infection process with time shown in table (6.1.2)

Table (6.1.2) : Infection process with time when node (4) infected first in the network in figure (6.1.1)

Time	Infected nodes at that time	Number of infected nodes at that time
t0	4	1
t1	2,3,6,8	4
t2	1,7,9	3
t3	5,10	2
t4	11,13	2
t5	12	1

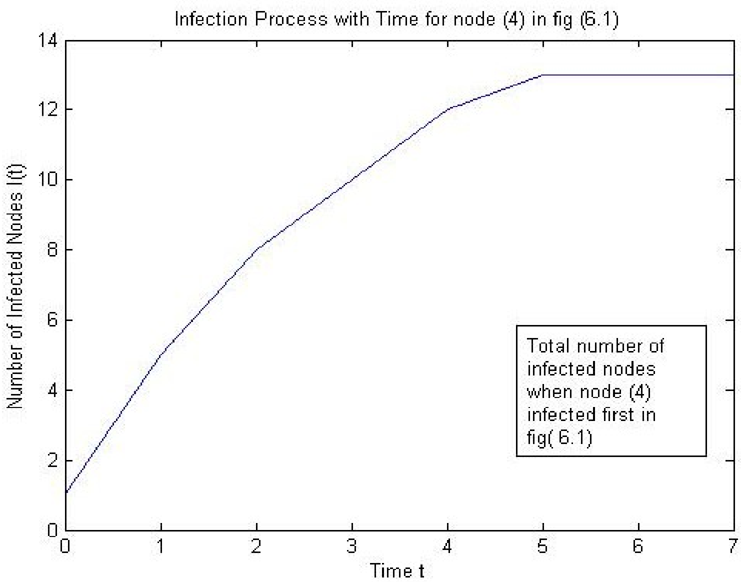
To explain the infection process when node (4) is the first infected node ,we start from node (4) which infects all nodes that adjacent to it which are nodes (2,3,6 and 8) at time "t1" , then each of these nodes infects nodes which adjacent to it . Node (2) infect node (1) , node (6) infect node (7) and node (8) infects node (9) at time "t2" . At time 't3" node (1) infects node (5) and node (9) infects node (10) . At time "t4" node (10) infects node (11) and node (13) . And finally at time "t5" node (11) infects node (12) which is the last infected node in the network . At the end of time "t5" all nodes in the network are infected .

To show the total number of the infected nodes at each unit of time when node (4) infected first in the network in figure (6.1) ,we have table (6.1.3)

Table .(6.1.3) : The total number of infected nodes with time when node (4) infected first in the network in figure (6.1.1) .

Time	Total Number of Infected Nodes
t0	1
t1	5
t2	8
t3	10
t4	12
t5	13

When we plot the total number of infected nodes with time when node (4) infected first in figure(6.1.1) ,we have figure (6.1.3)



Figure(6.1.3) : The total number of infected nodes with time when node (4) infected first in the network in fig (6.1.1)

We observe from table (6.1.3) and figure(6.1.3) that the total infection time when node (4) infected first in fig (6.1.1) that the total infection time , which is the time that we need to infect all nodes in the network , equal " 6t " unit of time , and the infection rate which is equal total number of infected nodes devided by the total infection time, so the infection rate at this case equals " 13/6t " node / unit of time , where "t" is unit of time .

When node (2) infected first the infection process with time shown in table (6.1.4).

Table. (6.1.4) : Infection process with time when node (2) infected first in the network in figure (6.1.1)

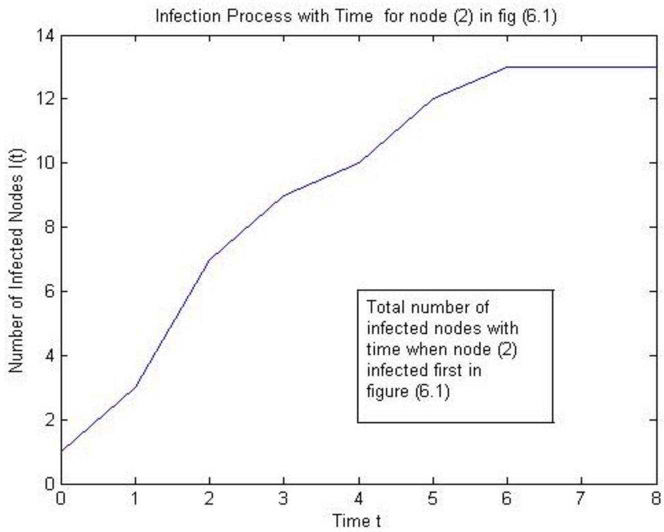
Time	Infected nodes at that time	Number of infected nodes at that time
t0	2	1
t1	1,4	2
t2	5,3,6,8	4
t3	7,9	2
t4	10	1
t5	11,13	2
t6	12	1

The total number of infected nodes with time when node (2) infected first is shown in table (6.1.5)

Table .(6.1.5) : The total number of infected nodes with time when node (2) infected first in the network in figure (6.1.1) .

Time	Total Number of Infected Nodes
t0	1
t1	3
t2	7
t3	9
t4	10
t5	12
t6	13

After plotting the total infected nodes with time from table (6.1.5) we have figure (6.1.4)



Figure(6.1.4) :The total number of infected nodes with when node (2) infected first in the network in fig (6.1.1)

From table (6.1.5) and figure (6.1.4) we found that the total infection time when node (2) infected first equal "7t" unit of time and the infectin rate in the case equal " 13/7t " node / unit of time .

When node (12) infected first the infection process with time shown in table (6.1.6)

Table (6.1.6) : Infection process with time when node (12) infected first in the network in figure (6.1.1)

Time	Infected nodes at that time	Number of infected nodes at that time
t0	12	1
t1	11	1
t2	10	1
t3	9,13	2
t4	8,7	2
t5	4,6	2
t6	2,3	2
t7	1	1
t8	5	1

Table (6.1.7) shows the total number of infected nodes with time when node (12) infected first in figure (6.1.1).

Table.(6.1.7) : The total number of infected nodes with time when node (12) infected first in the network in figure (6.1.1) .

Time	Total Number of Infected Nodes
t0	1
t1	2
t2	3
t3	5
t4	7
t5	9
t6	11
t7	12
t8	13

When we plot the total number of infected nodes with time we have figure (6.1.5)

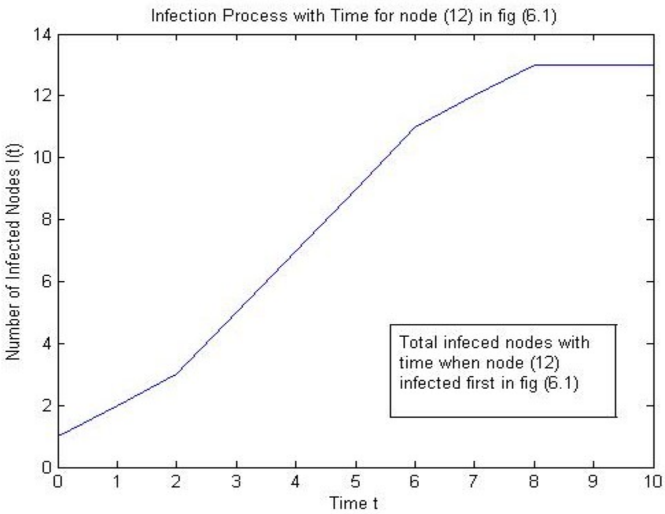


Figure (6.1.5) : The total number of infected nodes with time when node (12) infected first in the network in fig (6.1.1)

When node (12) infected first in fig (6.1.1) we note that the total infection time equal " 9t " unit of time and the infection rate equal " 13/9t " node / unit of time .

To compare between the three cases when nodes (4,2 and 12) infected first we put all their result in the same table , see table (6.1.8).

Table (6.1.8) : The total number of infected nodes with time when nodes (4,2 and12) infected first in the network in figure (6.1.1) .

Time	Total Number of Infected Nodes for node 4	Total Number of Infected Nodes for node 2	Total Number of Infected Nodes for node 12
t0	1	1	1
t1	5	3	2
t2	8	7	3
t3	10	9	5
t4	12	10	7
t5	13	12	9
t6		13	11
t7			12
t8			13

When we plot the total number of infected nodes with time when nodes (4,2 and 12) infected first, we have figure (6.1.6)

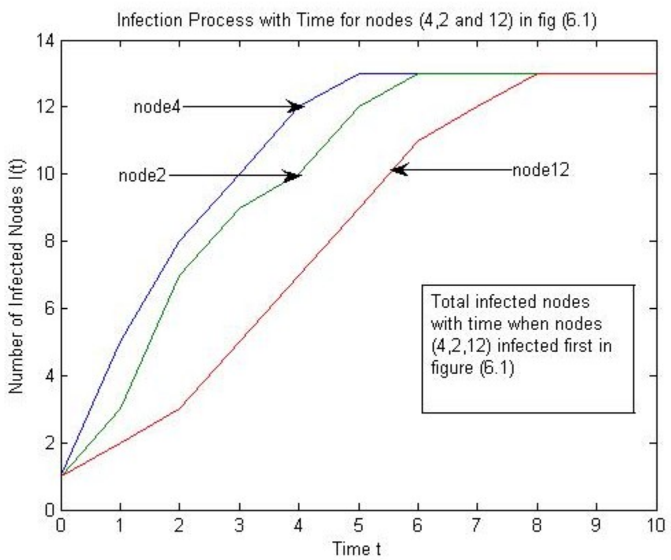


Figure (6.1.6) : The total number of infected nodes with time when nodes (4,2 and 12) infected first in the network in fig (6.1.1)

From table (6.1.8) and figure (6.1.6) we notice that :

1- The total infection time for node (4) which has the largest closeness centrality is the smallest , node (2) which has median closeness centrality has median total infection time and node (12) which has the smallest closeness centrality has the largest total infection time .

To clear the relation between closeness centrality for the nodes and their total infection time when they are infected first we tabulate the closeness centralities for nodes (4,2 and 12) and their total infection time in table (6.1.9)

Table .(6.1.9) : The relation between closeness centralities for nodes (4,2 and 12) and their total infection time when they are infected first in fig(6.1.1)

Node	Closeness Centrality	Total Infected Time
4	0.4137	6 unit of time
2	0.3333	7 unit of time
12	0.2222	9 unit of time

When we plot data in table (6.1.9) we have figure (6.1.7)

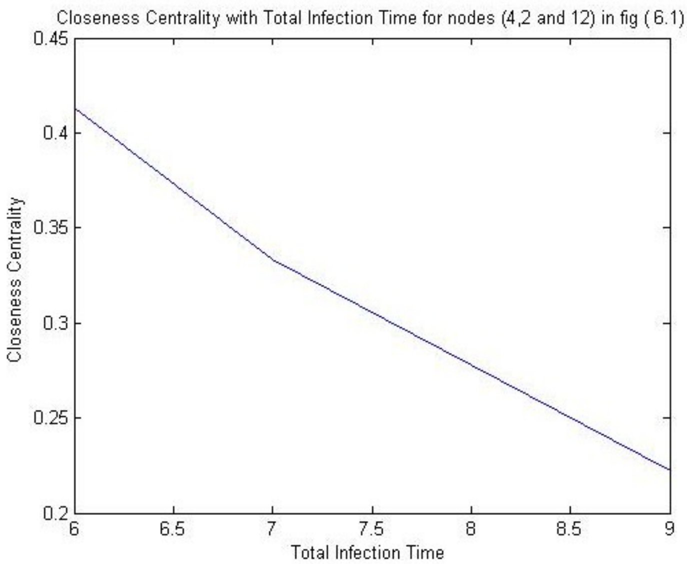


Figure (6.1.7) : A curve clears the relation between closeness centralities for nodes (4,2 and 12) and their total infection time when they are infected first in fig(6.1.1)

We conclude from table (6.1.9) ,figure (6.1.6) and figure(6.1.7) that the relation between the closeness centrality for the first infected node and their total infection time is inversly proportinal .

2- The infection rate for node (4) which has the largest closeness centrality when it is infected first is the largest , it is median when node (2) which has median closeness centrality infected first and it is the smallest when node (12) which has the smallest closeness centrality infected first . To clear the relation between the closeness centrality for the first infected nodes and the infection rate , let us tabulate the closeness centralities for nodes (4,2 and 12) and their infection rate in table (6.1.10)

Table .(6.1.10) : The relation between closeness centralities for nodes (4,2 and 12) and their infection rate when they are infected first in fig(6.1.1)

Node	Closeness Centrality	Infection Rate
4	0.4137	13/6t
2	0.3333	13/7t
12	0.2222	13/9t

By plotting data in table (6.1.10) we have figure (6.1.8)

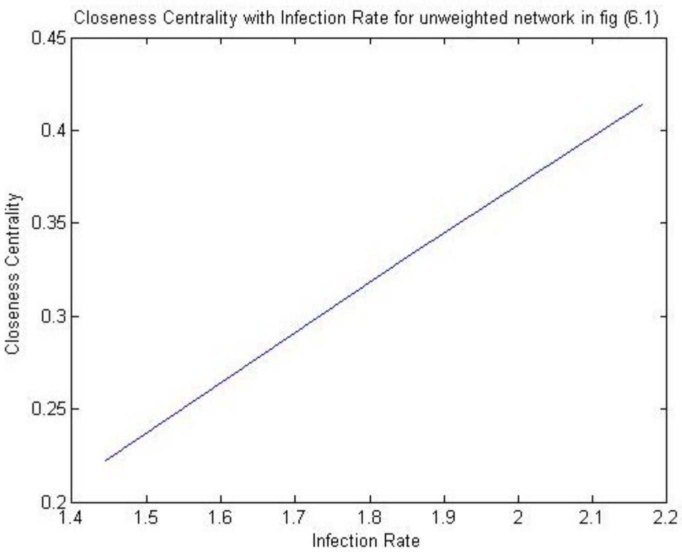


Figure (6.1.8) : A curve clears the relation between closeness centralities for nodes (4,2 and 12) and their infection rate when they are infected first in fig(6.1.1)

From table (6.1.10) and figure (6.1.8) we conclude that the relation between closeness centrality for the first infected node and the infection rate is directly proportinal .

3- As nodes, those have high closeness centralities, have small total infection time and high infection rate , so they have high infection spreading power , nodes, those have median closeness centralities, have median total infection time and median infection rate , so they have median infection spreading power and nodes, those have small closeness centralities, have large total infection time and small infection rate , so they have small infection spreading power .

From these results we can conclude that closeness centrality for the first infected node is directly proportinal to the infection spreading power of that node .

6.1.2 Application of my development SI model on small unweighted network

When we apply equation (5.2) that I developed according to my hypothesis by replacing the infection rate "β" in the SI model by the closeness centrality of the first infected node " C_k^c" on the small unweighted network in figure (6.1) . Equation (5.2) is

$$\frac{di(t)}{dt} = C_k^c(1-i(t))i(t) \text{ --------------(6.1)}$$

where di(t) / dt : is called the spreading velocity at time "t' and denoted some times by "V(t)" .

C_k^c: is the closeness centrality for node "k"

i(t) : the fraction of infected nodes at time "t" .

When we plot the infection spreading velocity with time which is shown in equation (6.1) after we assumed that each node in our network with different closeness centrality infected first ,we have figure (6.1.9)

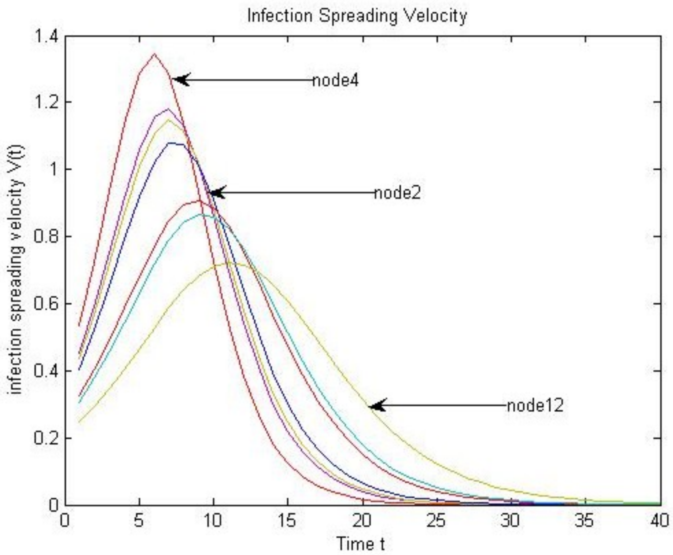


Figure (6.1.9) : Infection spreading velocity with time when each node in the small unweighted network in fig (6.1.1) with different closeness centrality infected first .

From figure (6.1.9) we note that :

1- It is the same shape curve optained by the authors of [2] and [3] . The infection spreading velocity goes up to a peak exponentially at the left side of the curve , then the curve follows the power – law behavior at the right side of it .

2- At the moment of infection outbreaks , the number of infected nodes is very small , as well as after a very long time from the outbreak, the number of susceptible nodes is very small . Thus when "t" is very small (close to zero) or very large , the spreading velocity is close to zero .

3- The spreading velocity goes up to a peak quickly , because at the left side of the curve we have few infected nodes but at the same time we have many susceptible nodes , so the infection process will increase very fast until it reachs the maximum spreading velocity at the top of the curve . At the right side of the curve the number of susceptible nodes will decrease very fast because we have many infected nodes that change a large number of susceptible nodes to infected nodes , so the spreading velocity will decrease very fast until it reachs zero after a large time of infection outbreaks

To compare between the infection spreading velocity when nodes (4),(2) and (12) are infected first in our network we plot the three curves of these nodes in one figure . see figure (6.1.10)

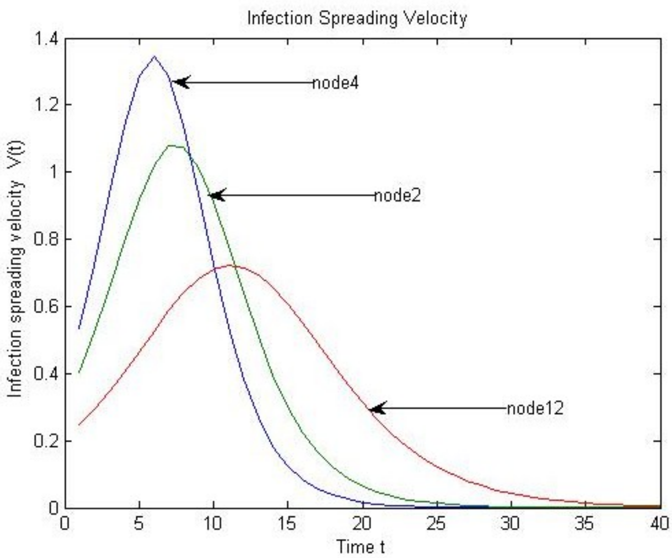


Figure (6.1.10) : Infection spreading velocity when nodes (4,2 and 12) infected first in the network in fig (6.1.1) .

We note from figure (6.1.10) that :

1- The maximum spreading velocity is the largest for node (4) which has the largest closeness centrality , it is median for node (2) which has median closeness centrality and it is the smallest for node (12) which has the smallest closeness centrality .

2- When node (4) infected first the curve in both sides is sharper than it when node(2) infected first and it is sharper when node (2) infected first than it when node (12) infected first . That means the time to reach the maximum spreading velocity is the smallest for node (4) which has the largest closeness centrality, then it is median for node (2) which has median closeness centrality and it is the largest for node (12) which has the smallest closeness centrality .

When we apply equation (5.3) on our small unweighted network in figure (6.1.1) which I developed also from the SI model , which is

$$i(t) = (1/N)\, e^{C_k t} / 1-(1/N) + (1/N)\, e^{C_k t} \text{----------------} (6.2)$$

This equation represents the fraction of infected nodes as a function of time "t" , where

"N= 13", " C_k " is the closeness centrality for node "k" when it is the first infected node and "t" is the time .

When we plot the fraction of the infected nodes with time that shown in equation (6.2) for the closeness centralities of all nodes in the network in figure (6.1.1) ,after we assumed that each node in our network with different closeness centrality infected first ,we have figure (6.1.11)

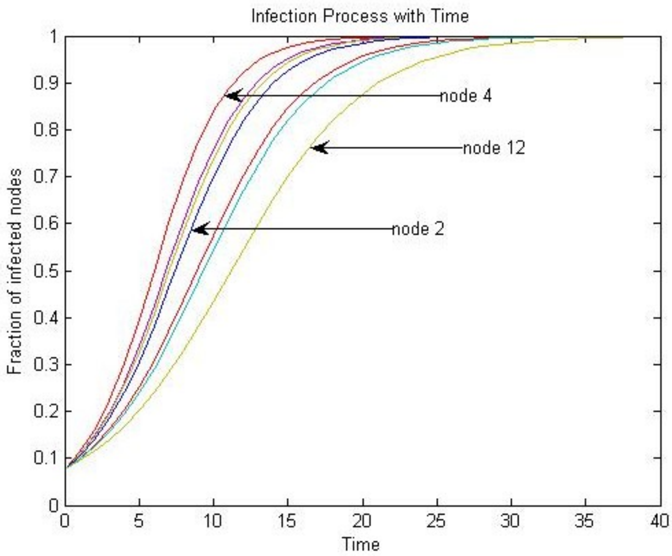


Figure (6.1.11): The fraction of infected nodes with time in the small unweighted network in figure (6.1.1)

From figure (6.1.11) we notice that :

1- The S- Shape is very clear which is the same shape that authors of [23],[10] and [25] obtained . The curve starts slowly at the first state then it groeth exponential at the second state and at the last stage the curve will take off until all nodes will be infected .

2- Node (4) which has the largest closenes centrality in the network spreading the infection faster than any other node in the network and that is clear from the smallest total infection time when it is infected first ,node (2) which has median closeness centrality spreading infection in median rate , and that is clear form the median total infection time and node (12) which has the smallest closeness centrality spreading the infection through the network slower than other nodes in that network and that is clear from the largest total infection time when it is infected first in that network .

To clear that, let us plot the curves just for nodes (4 , 2 and 12) to compare between the total infection time that we need to infect all nodes in the network when these nodes infected first in the network in fig (6.1.1) , see figure (6.1.12)

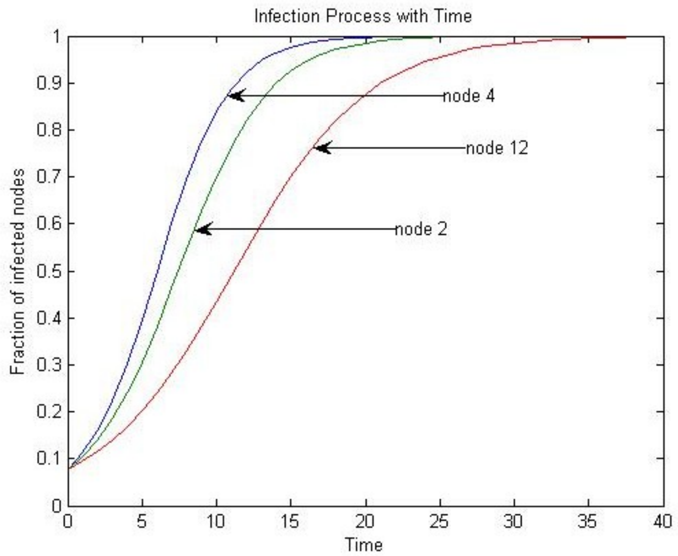


Figure (6.1.12): The fraction of infected nodes with time in the small unweighted network in figure (6.1.1) when nodes (4 ,2 and 12) infected first .

From figure (6.1.12) we notice that when node (4) which has the largest closness centrality, infected first in the network the total infection time that need to infect all nodes in the network is the smallest , it is median when node (2) which has median closeness centrality infected first and it is the largest when node (12) which has the smallest closeness centrality infected first .

6.2 Result from large unweighted network

To clarify the idea more let us take a large network that is shown in figure (6.2.1) , which consists of "80" nodes .

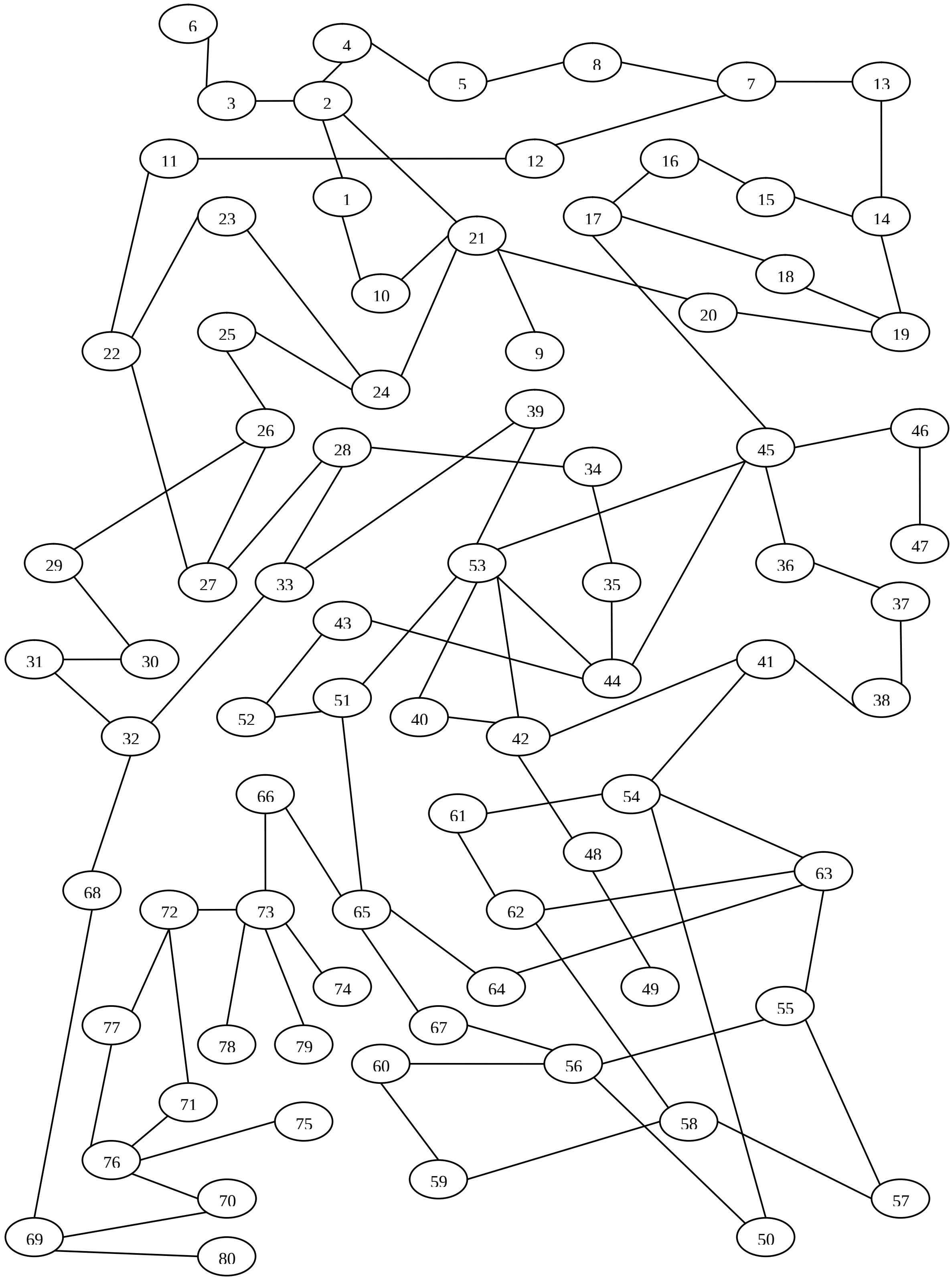


Figure (6.2.1) : Large Unweighted Network

To calculate the closeness centralities for all nodes of the large unweighted network in figure (6.2.1) I used my own matlab program again, and the adjacency matrix of the network in fig (6.2.1), see Appendix (C). Frist we have the shortest paths matrix for the large network in figure (6.2.1) which is shown in Appendix (D). From the shortest paths matrix we can calculate the summation of the shortest paths for each node in the network in figure(6.13) then we can calculate the closeness centralities for all those nodes.Table (6.2.1) shows the nodes of the network in figure (6.2.1), their shortest paths summation and their closeness centralities.

Table .(6.2.1) : Nodes ,the summation of their shortest paths and their closeness centralities for the network in figure (6.2.1) .

Node	Sum of Shortest Path	Closeness Centrality	Node	Sum of Shortest Path	Closeness Centrality
1	631	0.1252	41	424	0.1863
2	555	0.1423	42	371	0.2129
3	631	0.1252	43	391	0.2020
4	622	0.1270	44	337	0.2344
5	632	0.1250	45	351	0.2251
6	709	0.1114	46	427	0.1850
7	523	0.1511	47	505	0.1564
8	581	0.1360	48	436	0.1812
9	570	0.1386	49	484	0.1632
10	568	0.1391	50	515	0.1534
11	422	0.1872	51	354	0.2232
12	477	0.1656	52	406	0.1946
13	573	0.1379	53	322	0.2453
14	531	0.1488	54	457	0.1729
15	502	0.1574	55	548	0.1442
16	461	0.1714	56	493	0.1602
17	396	0.1995	57	620	0.1274
18	439	0.1800	58	622	0.1270
19	472	0.1674	59	629	0.1256
20	511	0.1546	60	565	0.1398
21	492	0.1606	61	527	0.1499
22	359	0.2201	62	555	0.1423
23	411	0.1922	63	485	0.1629
24	449	0.1759	64	441	0.1791
25	494	0.1599	65	383	0.2063
26	450	0.1756	66	437	0.1808
27	404	0.1955	67	445	0.1775
28	426	0.1854	68	507	0.1558
29	505	0.1564	69	561	0.1408
30	530	0.1491	70	596	0.1326
31	502	0.1574	71	596	0.1326
32	453	0.1744	72	546	0.1447
33	399	0.1980	73	491	0.1609
34	447	0.1820	74	569	0.1388
35	402	0.2015	75	700	0.1129
36	417	0.1894	76	622	0.1270
37	468	0.1688	77	596	0.1326
38	487	0.1622	78	569	0.1388
39	373	0.2118	79	569	0.1388
40	387	0.2041	80	639	0.1236

By ranking nodes in the network in figure (6.2.1) according to their closeness centralities we have table (6.2.2).

Table (6.2.2): Ranks of nodes in the network in figure(6.2.1) according to their closeness centralities .

Rank	Node	Closeness Centrality	Rank	Node	Closeness Centrality
1	53	0.2453	41	56	0.1602
2	44	0.2344	42	25	0.1599
3	45	0.2251	43	15	0.1574
4	51	0.2232	44	31	0.1574
5	22	0.2201	45	47	0.1564
6	42	0.2129	46	29	0.1564
7	39	0.2118	47	68	0.1558
8	65	0.2063	48	20	0.1546
9	40	0.2041	49	50	0.1534
10	43	0.2020	50	7	0.1511
11	35	0.2015	51	61	0.1499
12	17	0.1995	52	30	0.1491
13	33	0.1980	53	14	0.1488
14	27	0.1955	54	72	0.1447
15	52	0.1946	55	55	0.1442
16	23	0.1922	56	2	0.1423
17	36	0.1894	57	62	0.1423
18	11	0.1872	58	69	0.1408
19	41	0.1863	59	60	0.1398
20	28	0.1854	60	10	0.1391
21	46	0.1850	61	74	0.1388
22	34	0.1820	62	78	0.1388
23	48	0.1812	63	79	0.1388
24	66	0.1808	64	9	0.1386
25	18	0.1800	65	13	0.1379
26	64	0.1791	66	8	0.1360
27	67	0.1775	67	77	0.1326
28	24	0.1759	68	71	0.1326
29	26	0.1756	69	70	0.1326
30	32	0.1744	70	57	0.1274
31	54	0.1729	71	58	0.1270
32	16	0.1714	72	4	0.1270
33	37	0.1688	73	76	0.1270
34	19	0.1674	74	59	0.1256
35	12	0.1656	75	3	0.1252
36	49	0.1632	76	1	0.1252
37	63	0.1629	77	5	0.1250
38	38	0.1622	78	80	0.1236
39	73	0.1609	79	75	0.1129
40	21	0.1606	80	6	0.1114

From table (6.2.2) we note that node (53) has the highest closeness centrality which is equal "0.2453" , node (21) has median closeness centrality which is equal "0.1606" and node "6" has the smallest closeness centrality which equal " 0.1114" .

6.2.1 Analysis of Infection Process for Large Unweighted Network :

To explain the relation between the closeness centrality of the first infected node and each of the total infection time ,the infection rate and the infection spreading power of that node in large networks let us analyze the infection spreading process with time through the large network in figure (6.2.1).

We will take nodes (53),(21) and (6) as the first infected nodes , then analyze the infection spreading process for each case and compare between the three cases.

When node (53) which has the largest colseness centrality in network in figure(6.2.1) infected first , the infection process with time shown in table (6.2.1) .

Table(6.2.3) : Infection process with time when node (53) in the network in figure (6.2.1) infected first.

Time	Infected nodes at that time	Number of infected nodes at that time
T0	53	1
T1	39,44,51,42,40,45	6
T2	33,22,35,43,52,65,41,48,17,36,46	11
T3	28,32,11,23,27,34,64,67,66,54,38,49,16,18,37,47	16
T4	68,31,12,24,26,56,73,61,63,50,15,19	12
T5	69,30,7,21,25,60,55,74,79,78,72,62,14,20	14
T6	70,80,29,8,2,10,9,59,57,71,77,58,13	13
T7	76,5,1,3,4	5
T8	75,6	2

We note from table (6.2.3) that the infection process begin slowly then it grows very fast , then finally it returns slow at the end of that process when all nodes almost infected.

To show the relation between the total number of infected nodes and the time "t" , we tabulate that total number of infected nodes at each period of time and that time in table (6.2.4)

Table.(6.2.4) : The total number of infected nodes with time when node (53) infected first in figure (6.2.1).

Time	Total Number of Infected Nodes
T0	1
T1	7
T2	18
T3	34
T4	46
T5	60
T6	73
T7	78
T8	80

By plotting data in table (6.14) we have figure (6.2.2) :

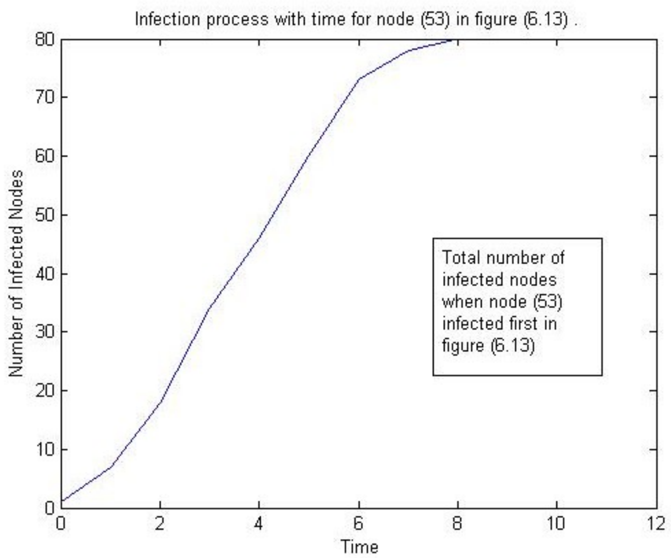


Figure (6.2.2) : Infection process curve with time when node (53) infected first in figure (6.2.1) .

We note from figure (6.14) that we have S – Shape curve , the total infection time is "9t" unit of time and the infection rate is " 80/9t" node / unit of time when node (53) which has the largest closeness centrality infected first , where "t" is the unit time .

When node (21) infected first in our network the infection spreading process with time "t" shown in table (6.2.5)

Table (6.2.5) : Infected nodes with time when node (21) in the network in figure (6.2.1) infected first.

Time	Infected nodes at that time	Number of infected nodes at that time
T0	21	1
T1	20,2,10,24,9	5
T2	19,1,4,3,25,23	6
T3	14,18,5,6,26,22	6
T4	13,15,17,8,27,29,11,44	8
T5	7,16,45,28,30,12,35,53,43	9
T6	36,46,33,31,34,42,40,39,51,52	10
T7	37,47,32,41,48,65	6
T8	68,54,38,49,64,67,66	7
T9	69,61,50,63,56,73	6
T10	80,70,62,60,55,72,78,79,74	9
T11	76,58,59,57,71,77	6
T12	75	1

When we tabulate that total number of infected nodes at each period of time we have table (6.2.6)

Table(6.2.6) : The total number of infected nodes with time when node (21) infected first in the network in figure(6.2.1) .

Time	Total Number of Infected Nodes
T0	1
T1	6
T2	12
T3	18
T4	26
T5	35
T6	45
T7	51
T8	58
T9	64
T10	73
T11	79
T12	80

By plotting data in table (6.2.6) we have figure (6.2.3)

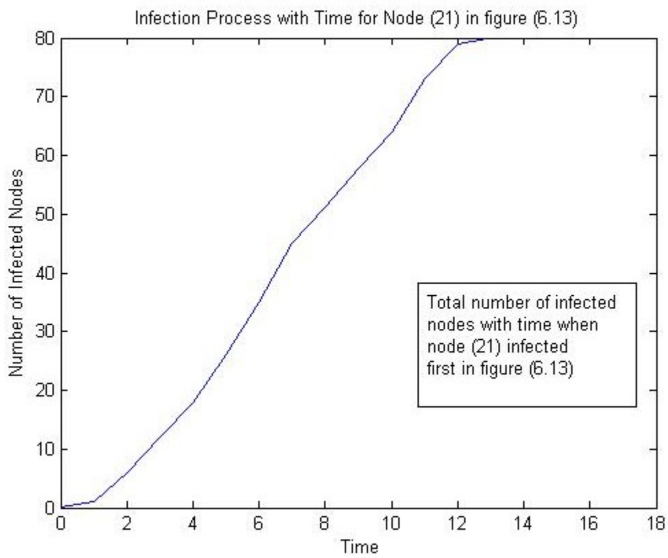


Figure (6.2.3) : Infection process curve with time when node (21) infected first in figure (6.2.1) .

We note from figure (6.2.3) that we also have S – Shape curve , the total infection time is "13t" unit of time and the infection rate is " 80/13t" node / unit of time when node (21) which has median closeness centrality infected first , where "t" is the unit time .

When node (6) infected first in our large unweighted network the infection spreading process with time shown in table (6.2.7)

Table (6.2.7) : Infected nodes with time when node (6) in the network in figure (6.2.1) infected first .

Time	Infected Nodes at that Time	Number of Infected Nodes at that Time
T0	6	1
T1	3	1
T2	2	1
T3	4,1,21	3
T4	5,24,20,10,9	5
T5	8,25,23,19	4
T6	7,26,22,14,18	5
T7	12,29,27,44,11,13,15,17	8
T8	30,28,53,43,35,45,16	7
T9	31,34,33,39,51,40,42,52,46,36	10
T10	32,65,48,41,47,37	6
T11	68,66,67,64,49,54,38	7
T12	69,73,56,63,50,61	6
T13	70,80,74,79,78,72,55,60,62	9
T14	76,71,77,57,59,58	6
T15	75	1

We can summarize the relation between the total number of infected nodes at each period of time in table (6.2.8)

Table. (6.2.8) : The total number of infected nodes with time when node (6) in figure (6.2.1) infected first .

Time	Total Number of Infected Nodes
t0	1
t1	2
t2	3
t3	6
t4	11
t5	15
t6	20
t7	28
t8	35
t9	45
t10	51
t11	58
t12	64
t13	73
t14	79
t15	80

When we plot data in table (6.2.8) we have figure (6.2.4)

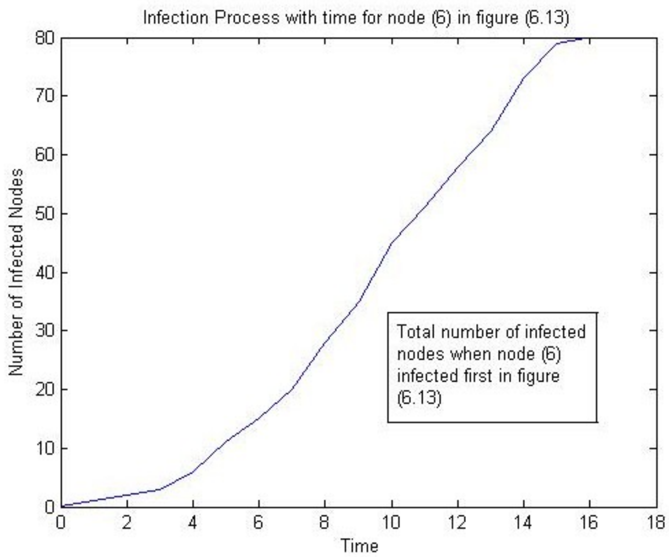


Figure (6.2.4) : Infection process curve with time when node (6) infected first in figure (6.2.1) .

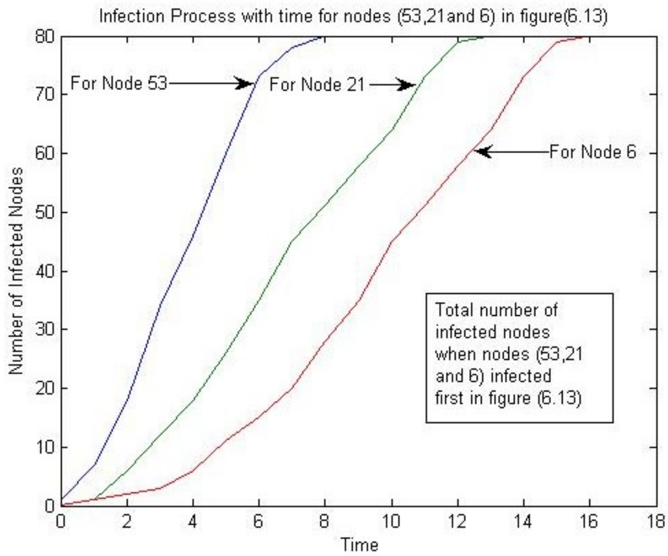
Also we note from figure (6.2.4) that we have S – Shape curve , the total infection time is "16t" unit of time and the infection rate is " 80/16t" node / unit of time when node (6) which has the smallest closeness centrality infected first , where "t" is the unit time .

To compare between cases when nodes (53,21 and 6) which have three different closeness centralities infected first , let us tabulate their data in table (6.2.9)

Table (6.2.9) : Total number of infected nodes when nodes (53), (21) and (6) infected first in figure (6.2.1) .

Time	Total Number of Infected Nodes for node 53	Total Number of Infected Nodes for node 21	Total Number of Infected Nodes for node 6
t0	1	1	1
t1	7	6	2
t2	18	12	3
t3	34	18	6
t4	46	26	11
t5	60	35	15
t6	73	45	20
t7	78	51	28
t8	80	58	35
t9		64	45
t10		73	51
t11		79	58
t12		80	64
t13			73
t14			79
t15			80

When we plot data in table (6.2.9) we have figure (6.2.5)



Figure(6.2.5):Infection process with time when nodes (53),(21) ,(6) infected first in fig (6.2.1)

From table (6.2.9) and figure (6.2.5) we notice that :

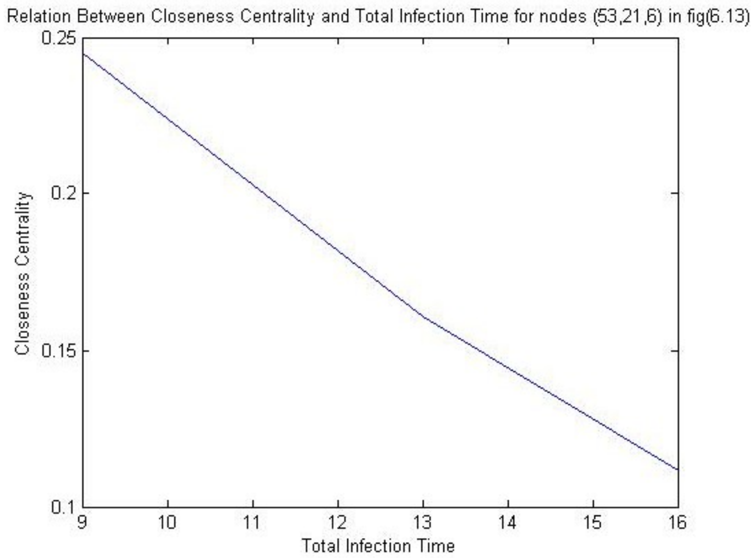
1- We have different S- Shape curves for the three nodes (53,21 and 6) ,which they have three different closeness centralities, when they are infected first .

2- The total infection time is the smallest for node (53) which has the largest closeness centrality , it is median for node (21) which has median closeness centrality and it is the largest for node (6) which has the smallest closeness centrality . When we tabulate the closeness centralities for nodes (53,21 and 6) and their total infection time when they are infected first in the network in figure(6.2.1) we have table (6.2.10)

Table .(6.2.10) : Closeness centralities for nodes (53,21 and 6) and their total infection time when they are infected first in fig(6.2.1)

Node	Closeness Centrality	Total Infection Time
53	0.2453	9t
21	0.1606	13t
6	0.1114	16t

By plotting data in table (6.2.10) , we have figure (6.2.6)



Figure(6.2.6) : The relation between closeness centralities and the total infection time for nodes (53,21,6) in fig (6.2.1) .

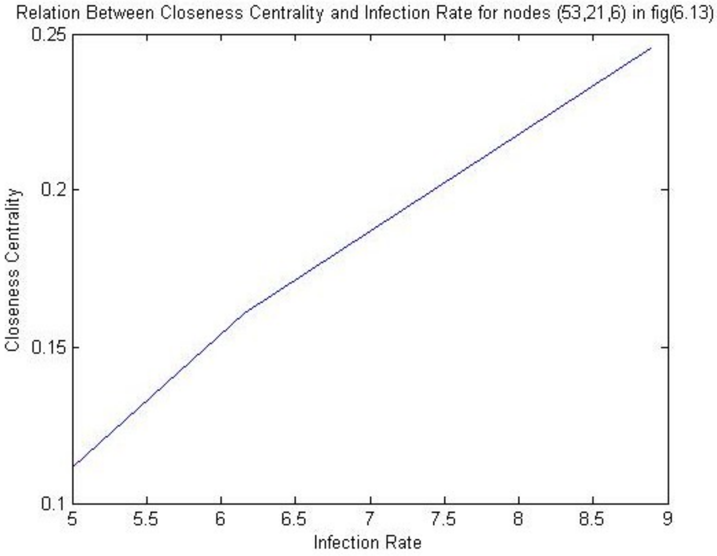
From tables (6.2.9) and (6.2.10) and figures (6.2.5) and (6.2.6) we can conclude that the relation between the closeness centrality of the first infected node and its total infection time is inversly proportinal .

3- The infection rate when node (53) which has the largest closeness centrality is the largest , it is median for node (21) which has median closeness centrality and it is the smallest for node (6) which has the smallest closeness centrality . By tabulate the closeness centralities for nodes (53,21,6) and their infection rate when they are infected first , we have table (6.2.11).

Table .(6. 2.11) : Closeness centralities for nodes (53,21 and 6) and their infection rate when they are infected first in fig(6.2.1) .

Node	Closeness Centrality	Infection Rate
53	0.2453	80/9t
21	0.1606	80/13t
6	0.1114	80/16t

When we plot data in table (6.2.11) , we have figure (6.2.7)



Figure(6.2.7) :The relation between closeness centralities and the infection rate for nodes (53,21,6) in fig (6.2.1)

From tables (6.2.9) and (6.2.11) and figures (6.2.5) and (6.2.7) we can conclude that the relation between the closeness centrality for the first infected node and its infection rate is directly proportinal **.**

4- As nodes those have high cloesness centralities , have small total infection time and large infection rate , so the have high infection spreading power , nodes those have median closeness centrality , have median total infection time and median infection rate , so they have median infection spreading power and nodes those have small closeness centralities have large total infection time , small infection rate , so they have small infection spreading power . Therefore we can conclude that the relation between the closeness centrality for the first infected node and its infection spreading power is directly proportinal .

6.2.2 Application of my development SI model on large unweighted network

When we apply equation (5.2) that I developed according to my hypothesis by replacing the infection rate "β" in the SI model by the closeness centrality of the first infected node " C_k^c " on the large unweighted network in figure (6.2.1) and plot the infection spreading velocity with time for closeness centralities of "25" different nodes in our large network in fig (6.2.1) ,we have figure(6.2.8)

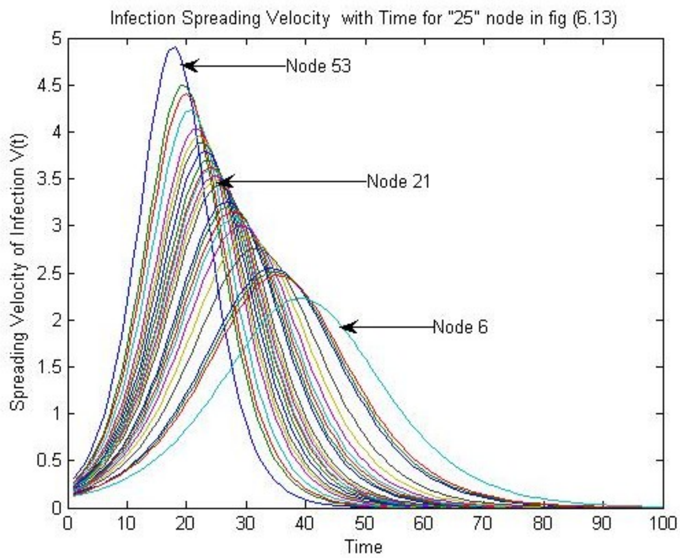


Figure (6.2.8) : Infection spreading velocity with time when "25' different nodes with different closeness centralities infected first in fig (6.2.1)

We note from fig (6.2.8) that the spreading velocity curve grows very fast exponentialy in the left side of the curve , reaching the peak of the curve , then it follows the power –law behavior as obtained by previous works [2],[3]

To clear that more, we plot just three curves for nodes (53),(21) and (6) for the infection spreading velocity with time in the same figure , see figure (6.2.9)

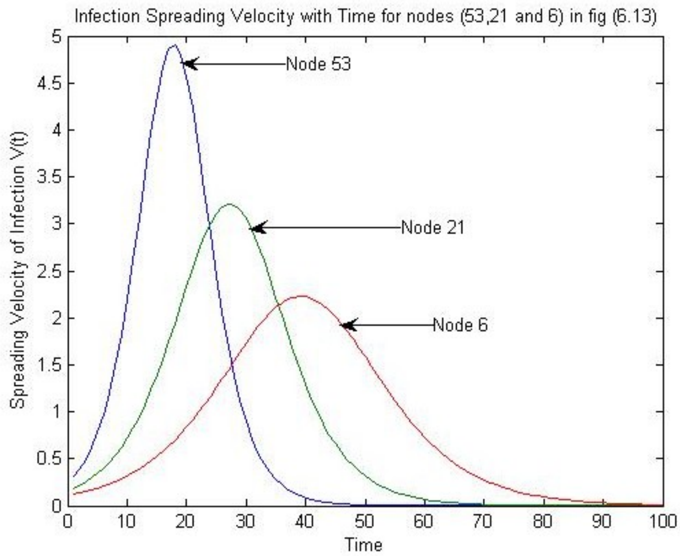


Figure (6.2.9) : Infection spreading velocity when nodes (53,21 an 6) infected first in fig (6.2.1)

From figure(6.2.9) we note that the maximum infection spreading velocity for node (53) which has the largest closeness centrality is larger than it for node (21) which has median closeness centrality and the maximum infection spreading velocity for node (21) is larger than it for node (6) which has the smallest closeness centrality . We note also that the curve from both sides is sharper when node (53) infected first than it when node (21) infected first and it is sharper when node (21) infected first than it when node (6) infected firs in figure (6.2.1) , and that means the infection spreading process when node (53) infected first is faster than it when node (21) infected first and it is faster when node(21) infected first than it when node (6) infected first .

When we apply equation (5.3) that I developed according to my hypothesis on the large network in figure (6.2.1) and plot the fraction of the infected nodes with time which is shown in that equation for closeness centralities of "25" different nodes in our large network in fig (6.2.1) ,we have figure(6.2.10)

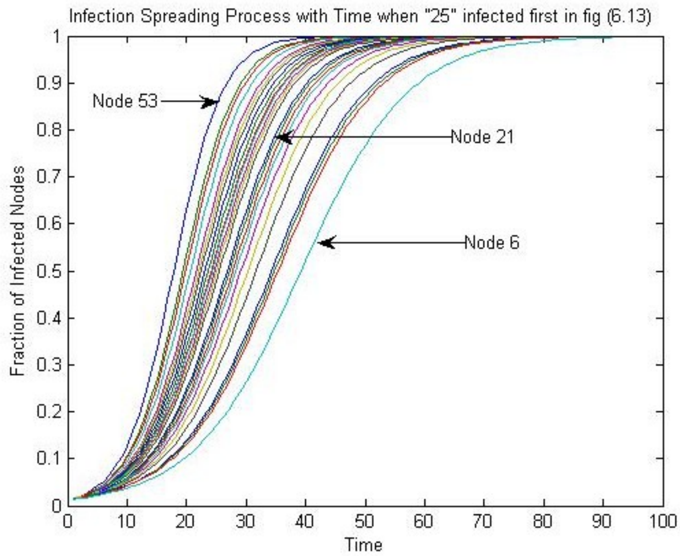


Figure (6.2.10) : Fraction of infected nodes with time in the large unweighted network in figure (6.2.1)

From figure (6.2.10) we notice again the clear S-Shape curve which starts slowly at the first state , then growth exponential at the second state and at the last state the curve will take off until all nodes will be infected .

To show the effects of nodes with different closeness centralities when they are infected first on the infection spreading process let us plot the curves for just three nodes (53.21 and 6) and compare betweenthem, see figure (6.2.11)

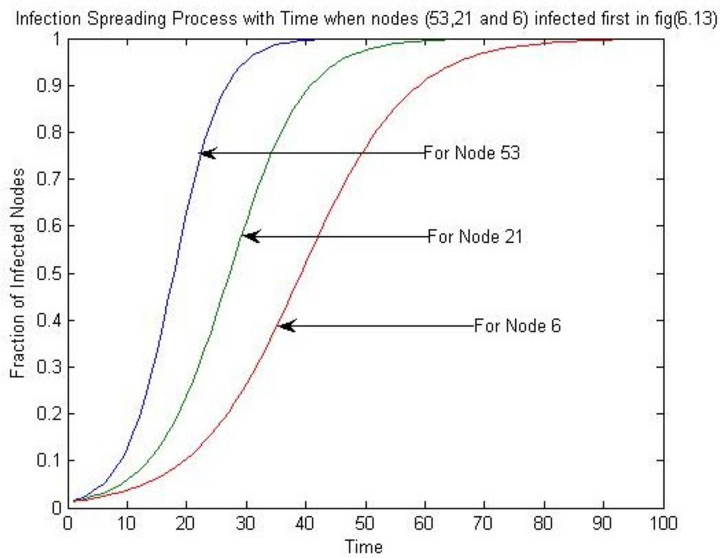


Figure (6.2.11) : The fraction of infected nodes with time in the large unweighted network in figure (6.2.1) when nodes (53 ,21 and 6) infected first .

From figure (6.2.11) we note that when node (53) which has the largest closeness centrality infected first ,the total infected time that we need to infect all nodes in our large network is the smallest , it is median when node (21) which has median closeness centrality infected first and it is the largest when node (6) which has the smallest closeness centrality .

6.3 Result From Small Weighted Network

Let us now take the same network in example (1) but its edges or links have weights . The weight in our network here means time , i.e. if we have an edge between node "*i*" and node "*j*" has weight "3" for example , that means the time to transmit any information from "*i*" to "*j*" equals "3" units of time . This weighted network is shown in fig (6.3.1) .

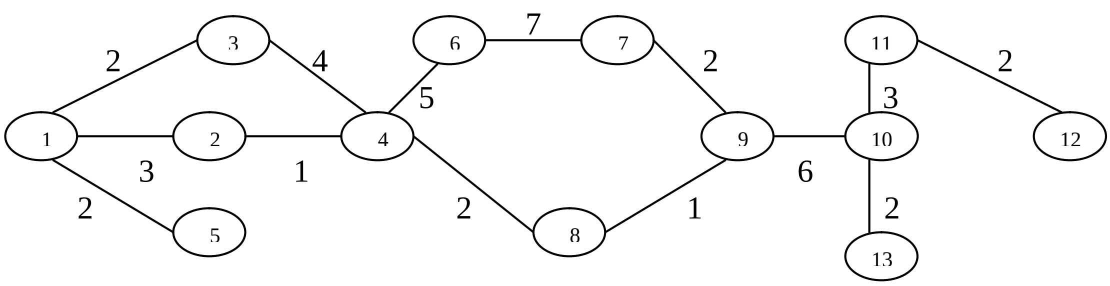


Figure (6.3.1) : Small weighted network

To calculate the closeness centralities for nodes in the weighted network in fig(6.3.1) I used also my matlab program , and the adjacency matrix of the network in fig (6.3.1), see Appendix (E). By using that program we have the shortest paths matrix shown in fig (6.3.2).

	1	2	3	4	5	6	7	8	9	10	11	12	13
1	0	3	2	4	2	9	9	6	7	13	16	18	15
2	3	0	5	1	5	6	6	3	4	10	13	15	12
3	2	5	0	4	4	9	9	6	7	13	16	18	15
4	4	1	4	0	6	5	5	2	3	9	12	14	11
5	2	5	4	6	0	11	11	8	9	15	18	20	17
6	9	6	9	5	11	0	7	7	8	14	17	19	16
7	9	6	9	5	11	7	0	3	2	8	11	13	10
8	6	3	6	2	8	7	3	0	1	7	10	12	9
9	7	4	7	3	9	8	2	1	0	6	9	11	8
10	13	10	13	9	15	14	8	7	6	0	3	5	2
11	16	13	16	12	18	17	11	10	9	3	0	2	5
12	18	15	18	14	20	19	13	12	11	5	2	0	7
13	15	12	15	11	17	16	10	9	8	2	5	7	0

Figure (6.3.2) : The shortest path matrix for the small weighted network in fig.(6.3.1) .

The summation of the shortest paths for each node and its closeness centrality is shown in table (6.3.1) .

Table . (6.3.1) : The summation of the shortest paths and the closeness centrality for each node in the network in fig (6.3.1)

Node	**Sum of the Shortest Paths**	**Closeness Centrality**
1	104	0.1154
2	83	0.1446
3	108	0.1111
4	76	0.1579
5	126	0.0952
6	128	0.0938
7	94	0.1277
8	74	0.1622
9	75	0.1600
10	105	0.1143
11	132	0.0909
12	154	0.0779
13	127	0.0945

After ranking nodes according to their closeness centralities we have table (6.3.2).

Table . (6.3.2) : Ranks of nodes according to their closeness centralities in the network in fig (6.3.1)

Rank	Node	Closeness Centrality
1	8	0.1622
2	9	0.1600
3	4	0.1579
4	2	0.1446
5	7	0.1277
6	1	0.1154
7	10	0.1143
8	3	0.1111
9	5	0.0952
10	13	0.0945
11	6	0.0938
12	11	0.0909
13	12	0.0779

We note from table (6.3.2) that node (8) has the largest closeness centrality , node (10) has median closeness centrality and node (12) has the smallest closeness centrality .

6.3.1 Analysis of Infection Process for Small Weighted Network :

To clarify the relation between closeness centrality of the first infected node and each of the total infection time , the infection rate and the infection spreading power in small weighted network let us analyze the infection process with time for the network in figure (6.3.1) when nodes (8,10,12) infected first , then compare between the results obtained from the three cases .

When node (8) infected first which has the largest closeness centrality , we have table (6.3.3).

Table . (6.3.3) : Infected nodes with time when node (8) infected first in the network in fig (6.3.1)

Time	**Infected Nodes at That Time**	**Total Number of Infected Nodes**
t0	8	1
t1	9	2
t2	4	3
t3	2,7	5
t4	----	5
t5	----	5
t6	1,3	7
t7	10,6	9
t8	5	10
t9	13	11
t10	11	12
t11	12	13

When I plot the relation between time and the total number of infected nodes we have figure (6.3.3) .

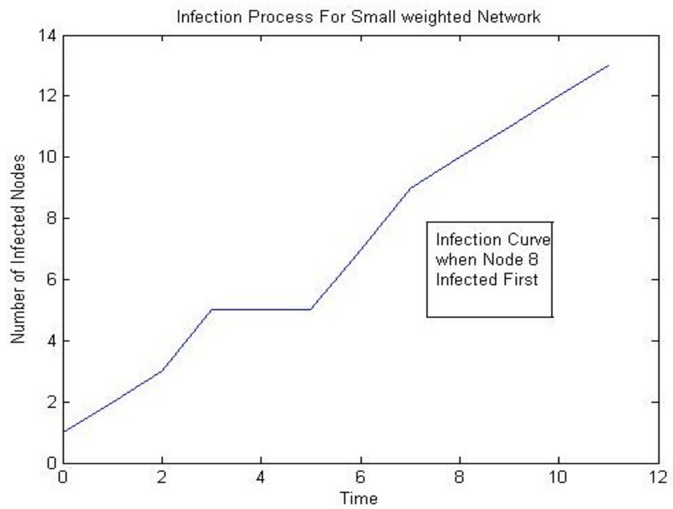


Figure (6.3.3) : The total number of infected nodes with time when node (8) infected first for network in figure (6.3.1) .

We note from figure (6.3.3) that the total infection time is "11" unit of time . If we supposed that each unit of time is "t" , so the total infection time in this case is "11t" and the infection rate equals "13/11t" node/unit of time "t" .

When node (10) infected first which has median closeness centrality we have table (6.3.4)

Table .(6.3.4) : Infected nodes with time when node (10) infected first in fig.(6.3.1)

Time	Infected Nodes at That Time	Total Number of Infected Nodes
t0	10	1
t1	------	1
t2	13	2
t3	11	3
t4	------	3
t5	12	4
t6	9	5
t7	8	6
t8	7	7
t9	4	8
t10	2	9
t11	-----	9
t12	-----	9
t13	1,3	11
t14	6	12
t15	5	13

By plotting the relation between time and the total number of infected nodes we have figure (6.3.4)

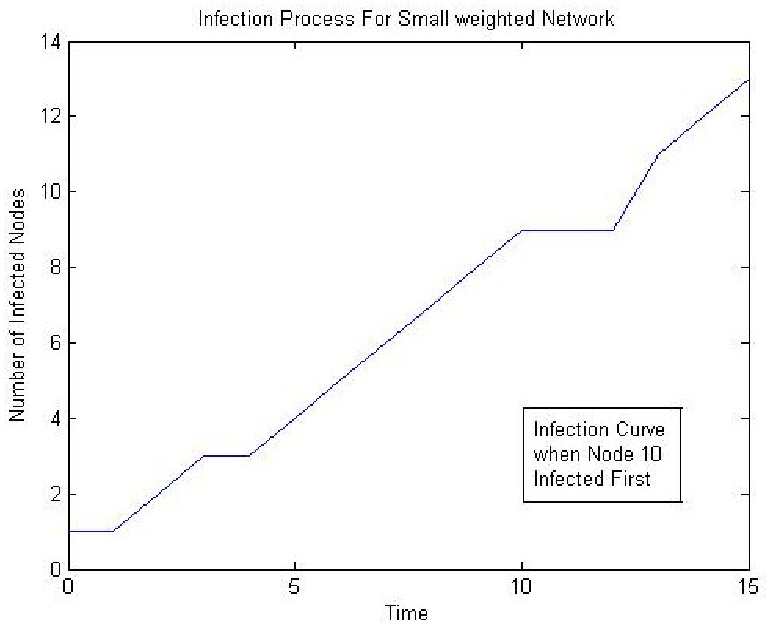


Figure (6.3.4): The total number of infected nodes with time when node (10) infected first in fig.(6.3.1) .

We note from figure(6.3.4) that the total infection time is "15t" where "t" is the unit time and the infection rate equal " 13/15t " node/unit of time .

When node (12) infected first which has the smallest closeness centrality we have table (6.3.5)

Table .(6. 3.5) : Infected nodes with time when node (12) infected first in fig.(6.3.1)

Time	Infected Nodes at That Time	Total Number of Infected Nodes
t0	12	1
t1	-----	1
t2	11	2
t3	-----	2
t4	-----	2
t5	10	3
t6	-----	3
t7	13	4
t8	-----	4
t9	-----	4
t10	-----	4
t11	9	5
t12	8	6
t13	7	7
t14	4	8
t15	2	9
t16	-----	9
t17	-----	9
t18	1,3	11
t19	6	12
t20	5	13

When we plot the relation between the total number of infected nodes with time we have figure (6.3.5)

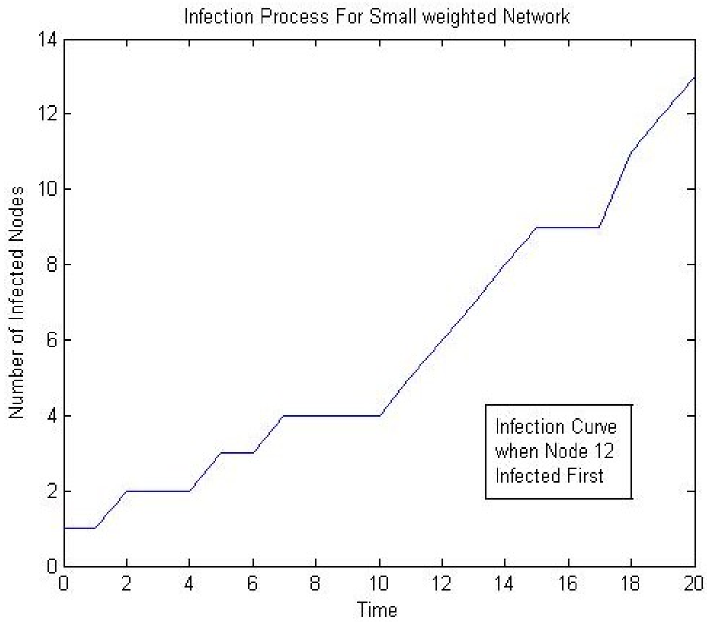


Figure (6.3.5) : The total number of infected nodes with time when node (12) infected first in fig.(6.3.1) .

From figure (6.3.5) we note that the total infection time is "20t" and the infection rate equals "13/20t" node/unit of time .

To compare between the three cases we put their results in one table . see table (6.3.6)

Table (6.3.6) : Infected nodes with time when nodes (8),(10), (12) infected first in fig.(6.3.1)

Time	Total Infected Nodes for Node 8	Total Infected Nodes for Node 10	Total Infected Nodes for Node 12
t0	1	1	1
t1	2	1	1
t2	3	2	2
t3	5	3	2
t4	5	3	2
t5	5	4	3
t6	7	5	3
t7	9	6	4
t8	10	7	4
t9	11	8	4
t10	12	9	4
t11	13	9	5
t12		9	6
t13		11	7
t14		12	8
t15		13	9
t16			9
t17			9
t18			11
t19			12
t20			13

When we plot the relation between the total number of infected nodes with time for the three cases in one figure we have figure (6.3.6)

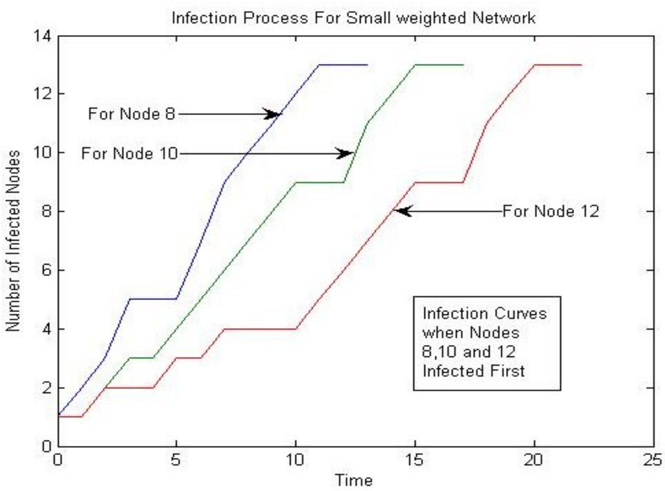


Figure (6.3.6) : The total number of infected nodes with time when nodes (8),(10) and (12) infected first in fig.(6.3.1) .

From figure (6.3.6) we note that :

1- Node (8) which has the largest closeness centrality has the minimum total infection time when it is infected first . Also node (10) which has median closeness centrality has median total infection time when it is infected first and node (12) which has the smallest closeness centrality has the maximum total infection time when it is infected first .When we tabulate the closeness centralities and the total infection time for the three nodes we have table (6.3.7)

Table .(6.3.7) : Closeness centrality and total infection time for nodes (8),(10)and (12) in fig (6.3.1)

Node	8	10	12
Closeness Centrality	0.1622	0.1143	0.0779
Total Infection Time	11t	15t	20t

When we plot the relation between the closeness cetrality and the total infection time for nodes (8),(10) and (12) we have figure (6.3.7) .

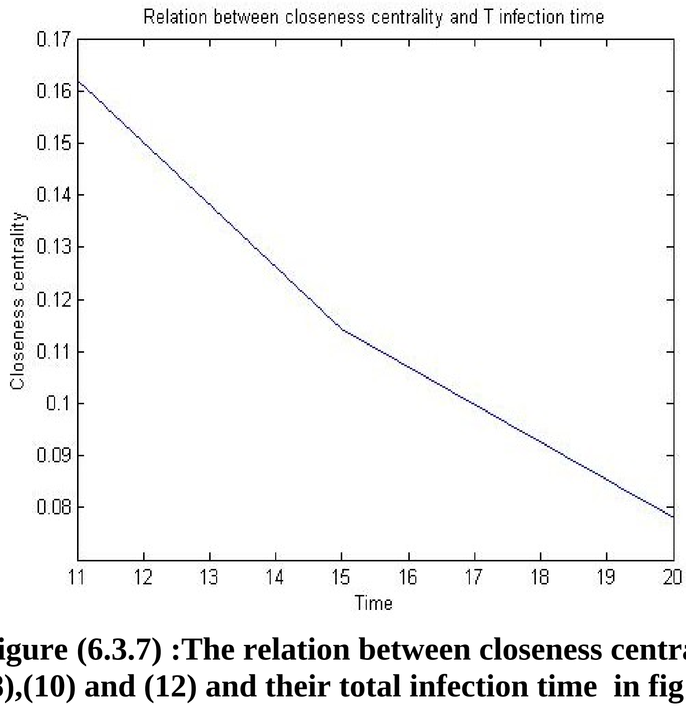


Figure (6.3.7) :The relation between closeness centrality for the first infected nodes (8),(10) and (12) and their total infection time in fig (6.3.1) .

From figure (6.3.7) we conclude that the relation between the closeness centrality for the first infected node and the total infection time is inversly proportinal .

2- The infection rate when node (8) infected first is the largest which is equal "13/11t" node/unit of time ,it is median when node (10) infected first which equal "13/15t" node/unit time and it is the smallest when node (12) infected first which equals "13/20t " node/unit time . When we tabulate the closeness centralities and the infection rate for nodes (8),(10) and (12) in fig (6.3.1) we have table (6.3.8)

Table (6. 3.8): Closeness centrality and infection rate for nodes (8),(10)and (12) in fig (6.3.1).

Node	8	10	12
Closeness Centrality	0.1622	0.1143	0.0779
Infection Rate	13/11t	13/15t	13/20t

When we plot the relation between the closeness centralities and the infection rate for nodes (8),(10)and (12) in figure (6.3.1) we have figure (6.3.8)

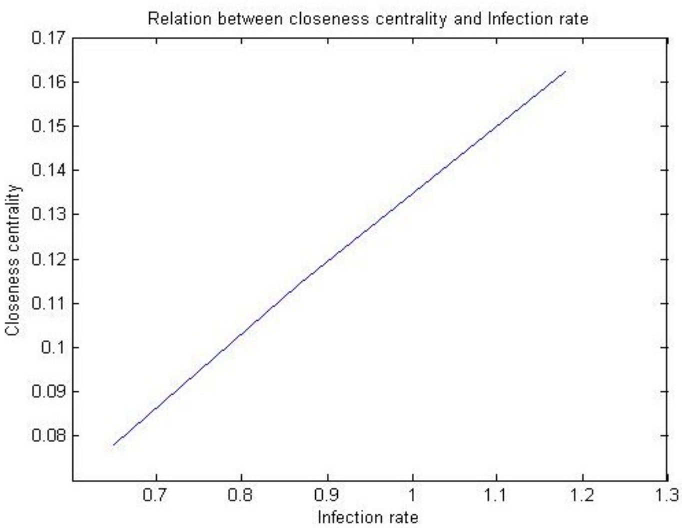


Figure (6.3.8) : The relation between closeness centrality for the first infected nodes (8),(10) and (12) and their infection rate in fig (6.3.1)

From figure (6.3.8) we conclude that the relation between the closeness centrality for the first infected node and its infection rate is directly proportinal .

3- As node (8) which has the highest closeness centrality has the smallest total infection time and the largest infection rate we conclude that it has the largest infection spreading power ,node (10) which has median colseness centrality has median total infection time and median infection rate we conclude that it has median infection spreading power and node (12) which has the smallest closeness centrality has the largest total infection time, the smallest infection rate ,we conclude that it has the smallest infection spreading power . From these three cases we note that nodes those have high closeness centralities have high infection spreading power and nodes those have small closeness centralities have small infection spreading power when they are infected first . So we conclude that the relation between closeness centrality for the first infected nodes and their infection spreading power is directly proportinal .

6.3.2 Application of my development SI model on Small weighted network

When we apply equation (5.2) that I developed according to my hypothesis on the small weighted network in figure (6.3.1) and plot the infection spreading velocity with time for the closeness centralities of all nodes in that network,we have figure(6.3.9)

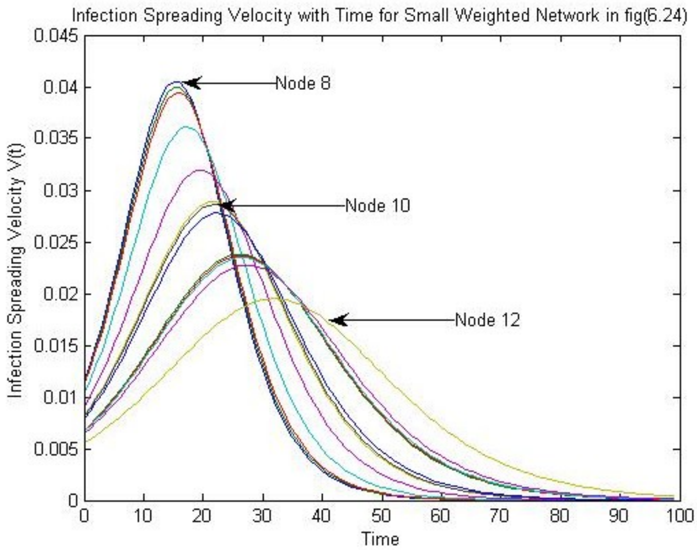


Figure (6.3.9) : Infection Spreading Velocity with Time for small weighted network in fig (6.3.1)

We note from fig (6.3.9) that the spreading velocity curve grows very fast exponentialy in the left side of the curve , reaching the peak of the curve , then it follows the power –law behavior in the right side as optained by previous works [2],[3]

To clear that more we plot the curves of the infection spreading velocity with time when nodes (8),(10) and (12) infected first in the same figure , see figure (6.3.10)

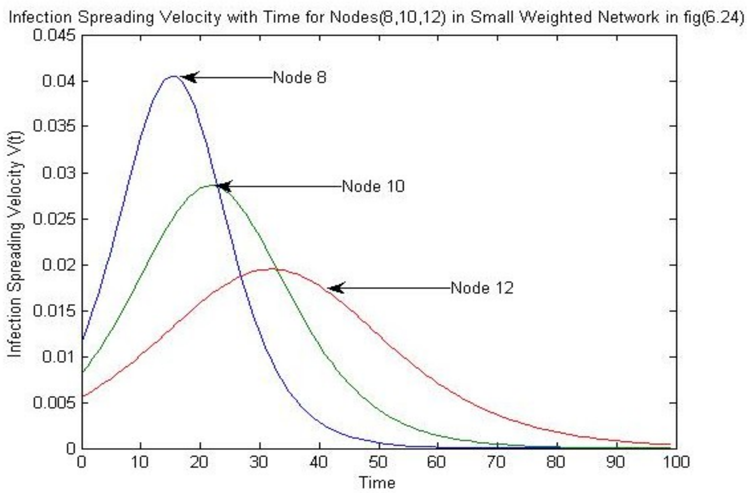


Figure (6.3.10) : Infection spreading velocity when nodes (8,10 and 12) infected first in fig (6.3.1)

From figure(6.3.10) we note that the maximum infection spreading velocity for node (8) which has the largest closeness centrality is larger than it for node (10) which has median closeness centrality and the maximum spreading velocity for node (10) is larger than it for node (12) which has the smallest closeness centrality . We note also that the curve from both sides is sharper when node (8) infected first than it when node (10) infected first and it is sharper when node (10) infected first than it when node (12) infected first in figure (6.3.1) , and that means the infection spreading process when node (8) infected first is faster than it when node (10) infected first and it is faster when node(10) infected first than it when node (12) infected first .

When we apply equation (5.3) that I developed according to my hypothesis on the small weighted network in figure (6.3.1) and plot the fraction of the infected nodes with time that shown in that equation for all closeness centralitiy of all nodes in our small weighted network in fig (6.3.1) ,we have figure(6.3.11)

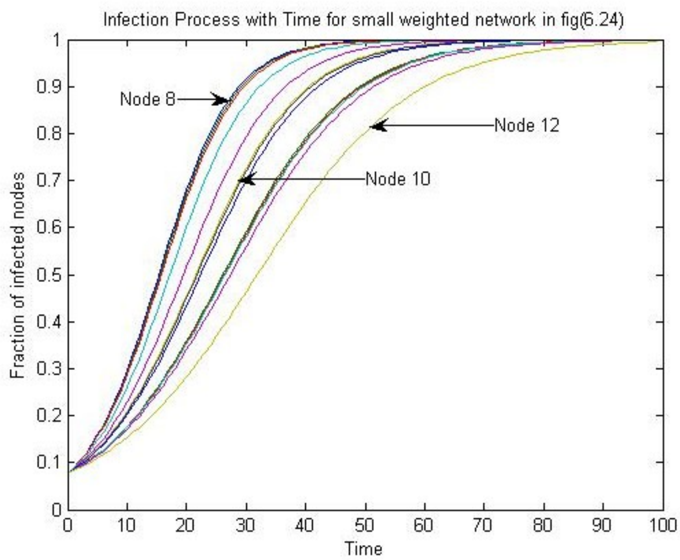


Figure (6.3.11) : Fraction of infected nodes with time in the small weighted network in figure (6.3.1)

From figure (6.3.11) we notice again the clear S-Shape curve which starts slow at the first state , then growth exponential at the second state and at the last state the curve will take off until all nodes will be infected .

To show the effects of nodes with different closeness centralities when they are infected first on the infection spreading process let us plot the fraction of the infected with time which shown in equation (5.3) for just three nodes (8,10 and 12) and compare between their curves , see figure (6.3.12)

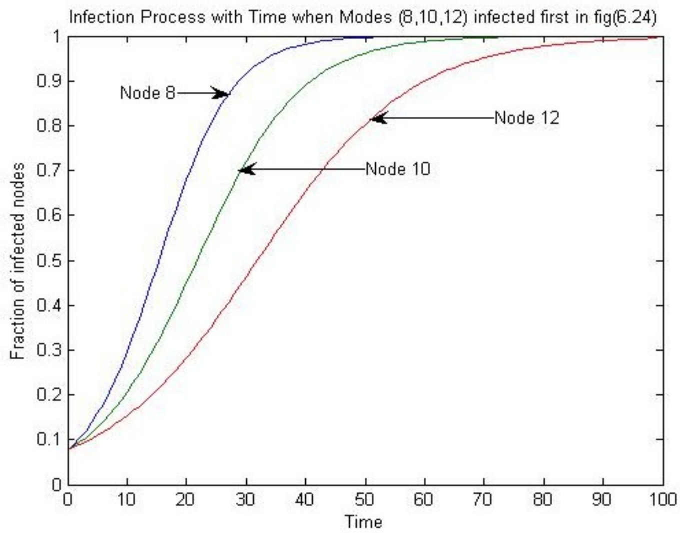


Figure (6.3.12) : The fraction of infected nodes with time in the small weighted network in figure (6.3.1) when nodes (8 ,10 and 12) infected first .

From figure (6.3.12) we note that when node (8) which has the largest closeness centrality infected first ,the total infected time that we need to infect all nodes in our small weighted network is the smallest , it is median when node (10) which has median closeness centrality infected first and it is the largest when node (12) which has the smallest closeness centrality .

6.4 Results from Large Weighted Network :

Let us now take the same large network in figure (6.10) , but it is weighted . See figure (6.4.1) .

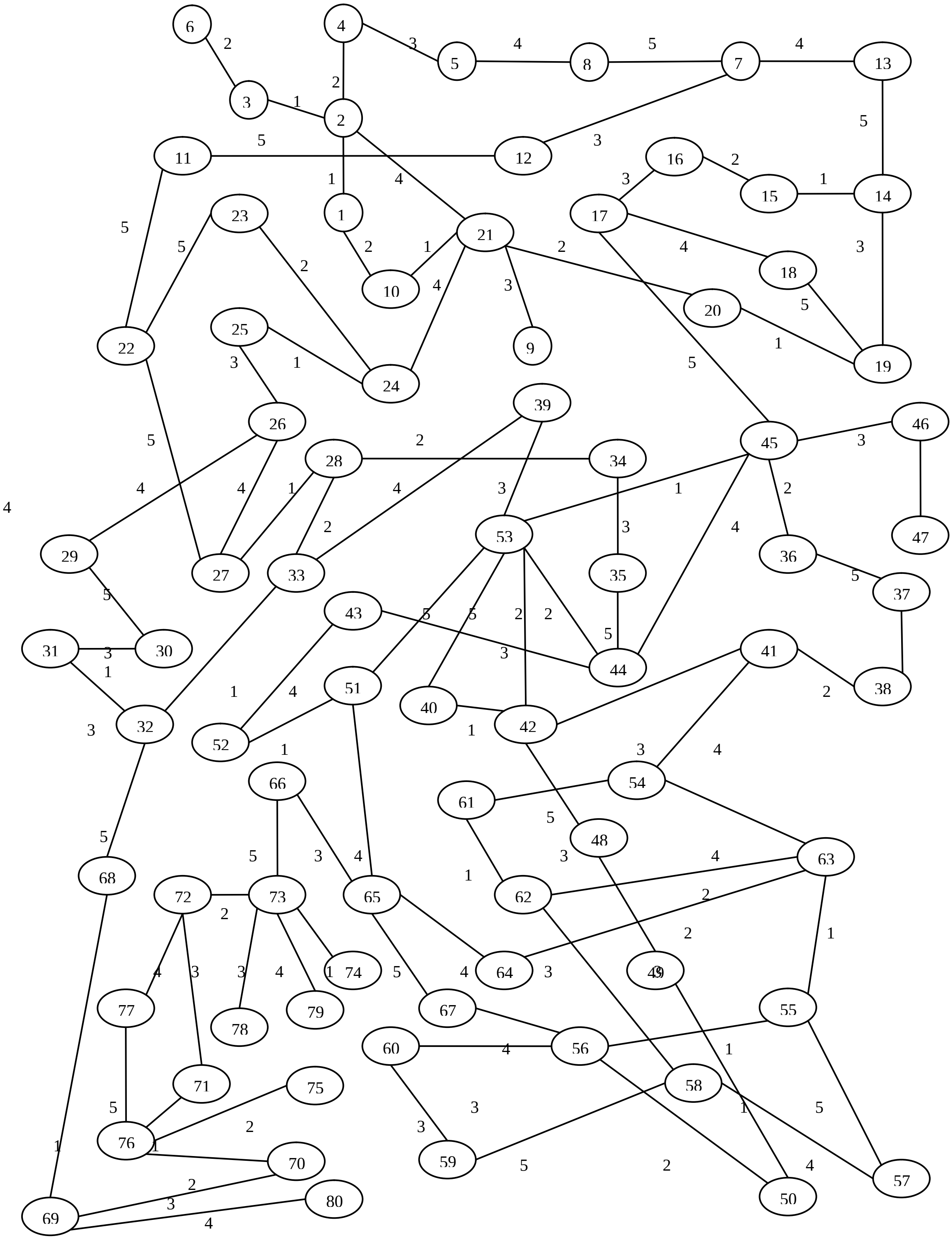


Figure (6.4.1) : Large Weighted Network

To calculate the closeness centralities for nodes in the network in figure (6.4.1) I used my matlab program and the adjacency matrix of the network in fig (6.4.1), see Appendix (F) . Frist we have the shortest paths matrix for our large weighted network which is shown in Appendix (G) .

By calculating the summation of the shortest paths for each node in our large weighted network and their closeness centralities using my matlab program , we have table (6.4.1)

Table .(6. 4.1): Summation of shortest paths and closeness centralities for nodes of the large weighted network in fig.(6.4.1)

Node	Sum of Shortest Paths	Closeness Centrality	Node	Sum of Shortest Paths	Closeness Centrality
1	1601	0.0493	41	1215	0.0650
2	1665	0.0474	42	1045	0.0756
3	1741	0.0454	43	1170	0.0675
4	1802	0.0438	44	1014	0.0779
5	2006	0.0394	45	1016	0.0778
6	1897	0.0416	46	1244	0.0635
7	1736	0.0455	47	1556	0.0508
8	2006	0.0394	48	1203	0.0657
9	1645	0.0480	49	1305	0.0605
10	1475	0.0536	50	1337	0.0591
11	1358	0.0582	51	1161	0.0680
12	1612	0.0490	52	1212	0.0652
13	1790	0.0441	53	962	0.0821
14	1457	0.0542	54	1351	0.0585
15	1430	0.0552	55	1416	0.0558
16	1359	0.0581	56	1387	0.0570
17	1249	0.0633	57	1795	0.0440
18	1430	0.0552	58	1809	0.0437
19	1516	0.0521	59	1760	0.0449
20	1521	0.0519	60	1612	0.0490
21	1411	0.0560	61	1570	0.0503
22	1022	0.0773	62	1590	0.0497
23	1233	0.0641	63	1444	0.0547
24	1246	0.0634	64	1444	0.0547
25	1287	0.0614	65	1265	0.0625
26	1312	0.0602	66	1421	0.0556
27	1163	0.0679	67	1540	0.0513
28	1201	0.0658	68	1457	0.0542
29	1580	0.0500	69	1499	0.0527
30	1509	0.0524	70	1603	0.0493
31	1423	0.0555	71	1686	0.0469
32	1201	0.0658	72	1693	0.0467
33	1155	0.0684	73	1636	0.0483
34	1318	0.0599	74	1714	0.0461
35	1285	0.0615	75	1812	0.0436
36	1164	0.0679	76	1656	0.0477
37	1417	0.0558	77	1908	0.0414
38	1363	0.0580	78	1870	0.0422
39	1100	0.0718	79	1948	0.0406
40	1123	0.0703	80	1811	0.0436

After ranking nodes according to their closeness centralities using my matlab program we have table (6.4.2)

Table . (6.4.2): Ranking nodes of the large weighted network in fig (6.4.1) according to their closeness centralities .

Rank	Node	Closeness Centrality	Rank	Node	Closeness Centrality
1	53	0.0821	41	63	0.0547
2	44	0.0779	42	64	0.0547
3	45	0.0778	43	14	0.0542
4	22	0.0773	44	68	0.0542
5	42	0.0756	45	10	0.0536
6	39	0.0718	46	69	0.0527
7	40	0.0703	47	30	0.0524
8	33	0.0684	48	19	0.0521
9	51	0.0680	49	20	0.0519
10	27	0.0679	50	67	0.0513
11	36	0.0679	51	47	0.0508
12	43	0.0675	52	61	0.0503
13	28	0.0658	53	29	0.0500
14	32	0.0658	54	62	0.0497
15	48	0.0657	55	1	0.0493
16	52	0.0652	56	70	0.0493
17	41	0.0650	57	12	0.0490
18	23	0.0641	58	60	0.0490
19	46	0.0635	59	73	0.0483
20	24	0.0634	60	9	0.0480
21	17	0.0633	61	76	0.0477
22	65	0.0625	62	2	0.0474
23	35	0.0615	63	71	0.0469
24	25	0.0614	64	72	0.0467
25	49	0.0605	65	74	0.0461
26	26	0.0602	66	7	0.0455
27	34	0.0599	67	3	0.0454
28	50	0.0591	68	59	0.0449
29	54	0.0585	69	13	0.0441
30	11	0.0582	70	57	0.0440
31	16	0.0581	71	4	0.0438
32	38	0.0580	72	58	0.0437
33	56	0.0570	73	80	0.0436
34	21	0.0560	74	75	0.0436
35	55	0.0558	75	78	0.0422
36	37	0.0558	76	6	0.0416
37	66	0.0556	77	77	0.0414
38	31	0.0555	78	79	0.0406
39	18	0.0552	79	5	0.0394
40	15	0.0552	80	8	0.0394

6.4.1 Analysis of Infection Process for Large Weighted Network

From table (6.4.2) we note that node (53) has the largest closeness centrality which equal " 0.0821", node (15) has median closeness centrality which equal " 0.0552" and node (8) has the smallest closeness centrality which equal " 0.0394" .

To compare between the infection process when each of these three nodes infected first let us analyze the infection process for each of them with time "t" .

When node (53) infected first we have table (6.4.3)

Table .(6. 4.3): Infected nodes with time when node (53) infected first in network in fig.(6.4.1)

Time	Infected Nodes at That Time	Total Number of Infected Nodes at That Time
t0	53	1
t1	45	2
t2	42,44	4
t3	40,39,22,36	8
t4	46	9
t5	51,48,41,43	13
t6	52,17	15
t7	35,33,38	18
t8	32,47,37,49	22
t9	54,65,27,23,11,28,16,50	30
t10	34,24,18	33
t11	31,25,15,56	37
t12	66,26,14,55	41
t13	12,68,30,63,64	46
t14	69,67,60,61,21	51
t15	19,62,10	54
t16	7,20,59	47
t17	57,73,70,9,1,13	63
t18	29,2,80,74,58	68
t19	3,76,72	71
t20	4,71,78	74
t21	6,8,75,79	78
t22	-------	78
t23	5,77	80

By plotting the total number of infected nodes with time "t" when node (53) infected first we have figure (6.4.2)

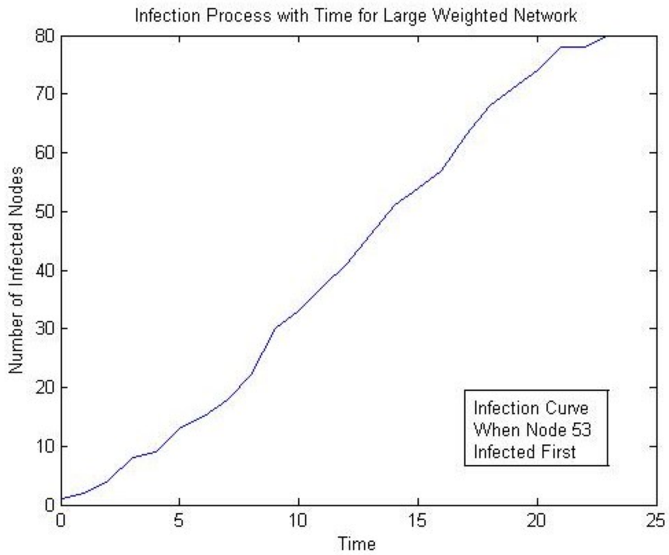


Figure (6.4.2) : The total number of infected nodes with time when node (53) infected first in fig.(6.4.1) .

We note from figure (6.4.2) that the total infection time is "23t" when node (53) which has the largest closeness centrality infected first and the infection rate in this case equals " 80/23t" node / unit time where "t" is the unit time .

When node (15) infected first we have table (6.4.4)

Table (6. 4.4) : Infected nodes with time when node (15) infected first in network in fig.(6.4.1)

Time	Infected Nodes at That Time	Total Number of Infected Nodes at That Time	Time	Infected Nodes at That Time	Total Number of Infected Nodes at That Time
t0	15	1	t18	35,33,38	44
t1	14	2	t19	27,32,29,49	48
t2	16	3	t20	28,54,50,65	52
t3	-----	3	t21	34	53
t4	19	4	t22	31,56	55
t5	20,17	6	t23	55,66	57
t6	13	7	t24	30,68,63,64	61
t7	21	8	t25	69,67,61,60	65
t8	10	9	t26	62	66
t9	18	10	t27	59	67
t10	45,7,1,9	14	t28	70,73,57	70
t11	2,53,24	17	t29	80,74,58	73
t12	3,25,36	20	t30	72,76	75
t13	4,23,12,44,46,42	26	t31	78,71	77
t14	6,22,39,40	30	t32	79,75	79
t15	8,26	32	t33	------	79
t16	5,41,48,43,51	37	t34	77	80
t17	11,47,37,52	41			

When we plot the total number of infected nodes with time " t" when node (15) infected first we have figure (6.4.3)

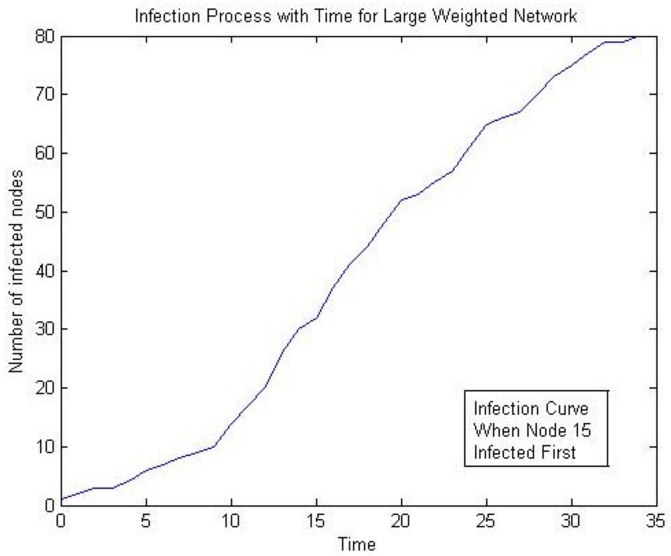


Figure (6.4.3) : The total number of infected nodes with time when node (15) infected first in fig.(6.4.1) .

From figure (6.4.3) we note that the total infection time is " 34t" and the infection rate equals "80/34t "node/unit time , where "t" is the unit of time when node (15) infected first which has median closeness centrality .

When node (8) which has the smallest closeness centrality infected first we have table (6.4.5)

Table .(6. 4.5) : Infected nodes with time when node (8) infected first in network in fig.(6.4.1)

Time	Infected Nodes at That Time	Total Number of Infected Nodes at That Time	Time	Infected Nodes at That Time	Total Number of Infected Nodes at That Time
t0	8	1	t22	45,43	30
t1	-----	1	t23	27,42	32
t2	-----	1	t24	35,39,28,36,40	37
t3	-----	1	t25	29,46	39
t4	5	2	t26	34,33,41,51,52,48	45
t5	7	3	t27	32	46
t6	-----	3	t28	38	47
t7	4	4	t29	47,37,49	50
t8	12	5	t30	30,31,54,65,50	55
t9	13,2	7	t31	------	55
t10	3,1	9	t32	68,56	57
t11	------	9	t33	55,66,69	60
t12	6,10	11	t34	63,64	62
t13	21,11	13	t35	61,67,60	65
t14	14	14	t36	62,70	67
t15	15,20	16	t37	59,80	69
t16	9,19	18	t38	57,73,76	72
t17	16,24	20	t39	58,74,71	75
t18	22,25	22	t40	72,75	77
t19	23,44	24	t41	78	78
t20	17	25	t42	79	79
t21	18,26,53	28	t43	77	80

By plotting the total number of infected nodes with time "t" when node (8) infected first we have figure (6.4.4)

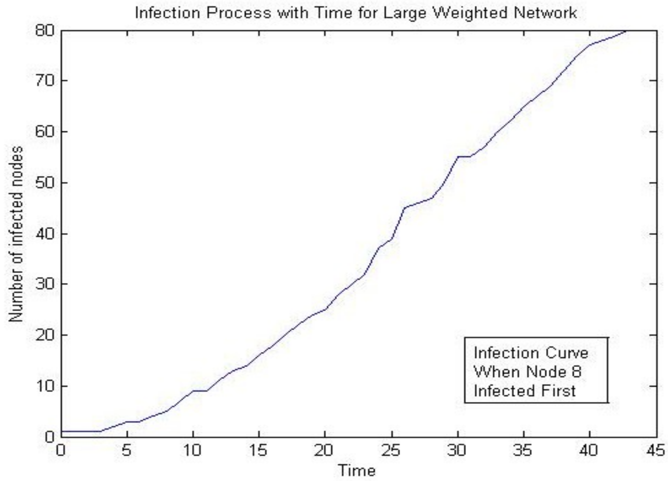


Figure (6.4.4) : The total number of infected nodes with time when node (8) infected first in fig.(6.4.1) .

We note from figure(6.4.4) that the total infection time is " 43t " and the infection rate equal "80/43t" node /unit time where "t" is the unit time when node (8) infected first .

To compare between these three cases , i.e. when nodes (53,15 and 8) infected first we tabulate their total number of infected nodes in the same table , see table (6.4.6)

Table .(6. 4.6) : Infected nodes with time when nodes (53,15 and 8) infected first in network in fig.(6.4.1)

Time	Total Infected Nodes for Node 53	Total Infected Nodes for Node 15	Total Infected Nodes for Node 8	Time	Total Infected Nodes for Node 53	Total Infected Nodes for Node 15	Total Infected Nodes for Node 8
t0	1	1	1	t22	78	55	30
t1	2	2	1	t23	80	57	32
t2	4	3	1	t24		61	37
t3	8	3	1	t25		65	39
t4	9	4	2	t26		66	45
t5	13	6	3	t27		67	46
t6	15	7	3	t28		70	47
t7	18	8	4	t29		73	50
t8	22	9	5	t30		75	55
t9	30	10	7	t31		77	55
t10	33	14	9	t32		79	57
t11	37	17	9	t33		79	60
t12	41	20	11	t34		80	62
t13	46	26	13	t35			65
t14	51	30	14	t36			67
t15	54	32	16	t37			69
t16	57	37	18	t38			72
t17	63	41	20	t39			75
t18	68	44	22	t40			77
t19	71	48	24	t41			78
t20	74	52	25	t42			79
t21	78	53	28	t43			80

When we plot the total number of infected nodes with time for three nodes in the same figure we have figure (6.4.5)

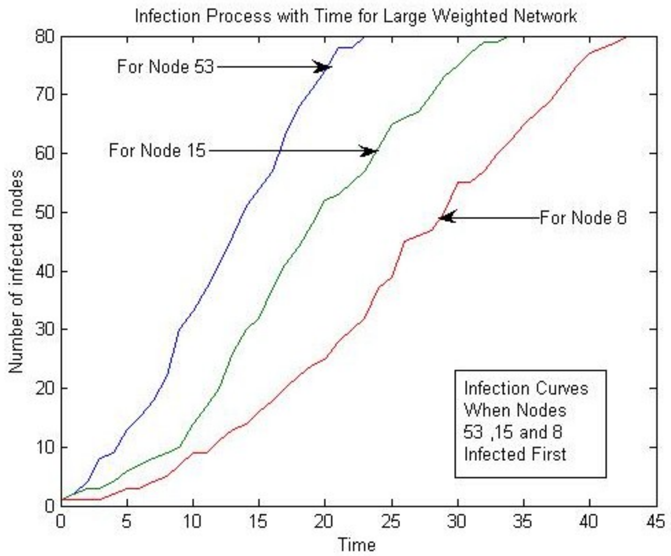


Figure (6.4.5) : The total number of infected nodes with time when nodes (53,15 and 8) infected first in fig.(6.4.1) .

From figure (6.4.5) we note that :

1- Total infection time when node (53) infected first which has the largest closeness centrality is the smallest ,it is medain when node (15) infected first which has median closeness centrality and it is the largest when node (8) infected first which has the smallest closeness centrality . When we tabulate the closeness centralities for nodes (53,15 and 8) in figure (6.4.1) and their total infection time we have table (6.4.7)

Table (6.4.7): Closeness centrality and total infection time for nodes (53),(15)and (8) in fig (6.4.1)

Node	53	15	8
Total Infected Time	23t	34t	43t
Closeness Centrality	0.0821	0.0552	0.0394

When we plot the closeness centralities for nodes (53,15 and 8) in figure (6.4.1) with their total infection time we have figure (6.4.6)

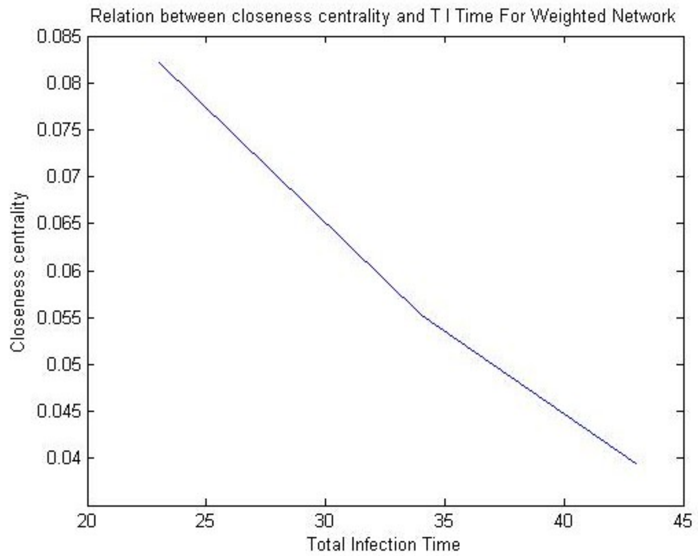


Figure (6.4.6) : The relation between closeness centrality for the first infected nodes (53), (15) and (8) and their total infection time in fig (6.4.1).

From all these results we conclude again that closeness centrality for the first infected node in the weighted network is inversly proportinal with the total infection time that needs to infect all nodes in that network .

2- Infection rate when node (53) infected first which has the largest closeness centrality is the largest ,it is median when node (15) infected first which has median closeness centrality and it is the smallest when node (8) infected first which has the smallest closeness centrality .When we tabulate the closeness centralities for nodes (53,15 and 8) in figure (6.4.1) and their infection rate we have table (6.4.8)

Table (6.4.8) : Closeness centrality and infection rate for nodes (53),(15)and (8) in fig (6.36)

Node	53	15	8
Infection Rate	80/23t	80/34t	80/43t
Closeness Centrality	0.0821	0.0552	0.0394

When we plot the closeness centralities for nodes (53,15 and 8) in figure (6.4.1) with their infection rate we have figure (6.4.7)

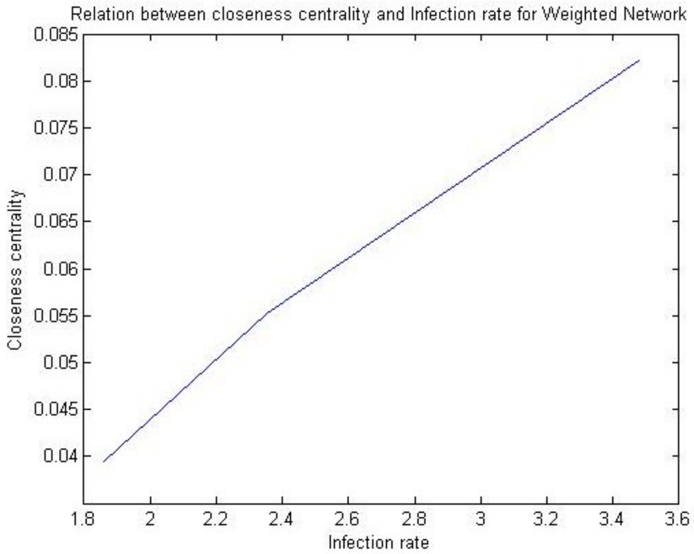


Figure (6.4.7) : The relation between closeness centrality for the first infected nodes (53),(15) and (8) and their infection rate in fig (6.4.1) .

Here we also conclude that the closeness centrality for the first infected node in the weighted network is directly proportional to the infection rate in that network .

3- As nodes that have high closeness centralities have small total infection time and large infection rate ,so they have high infection spreading power . Nodes which have small closeness centralities have large total infection time and small infection rate , so they have small infection spreading power . Thus we can conclude that closeness centrality for the first infected node in weighted networks is directly proportional with the infection spreading power of that node .

6.4.2 Application of my development SI model on large weighted network

When we apply equation (5.2) that I developed according to my hypothesis on the large weighted network in figure (6.4.1) and plot the infection spreading velocity with time which is shown in equation (5.2) using the closeness centralities of "25" different nodes in our large weighted network in fig (6.4.1) , that we assumed they are infected first in that network ,we have figure(6.4.8)

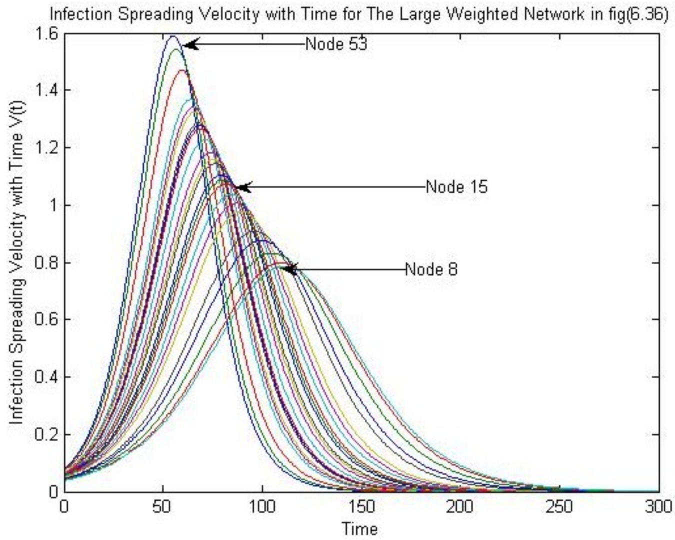


Figure (6.4.8) : Infection spreading velocity when "25' different nodes with different closeness centralities infected first in fig (6.4.1)

We note from fig (6.4.8) that the spreading velocity curve grows very fast exponentialy in the left side of the curve , reaching the peak of the curve, then it follows the power –law behavior in the left side of the curve as optained by previous works [2],[3]

To clear that more we plot just three curves for nodes (53),(15) and (8) for the infection spreading velocity with time in the same figure , see figure (6.4.9)

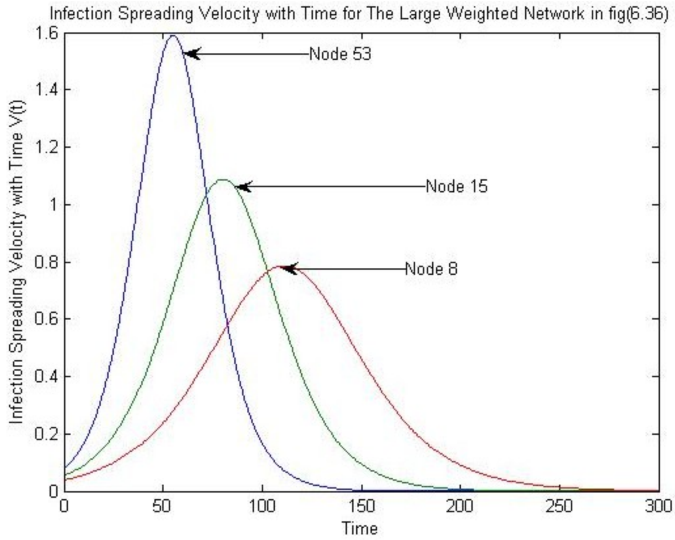


Figure (6.4.9) : Infection spreading velocity when nodes (53,15 an 8) infected first in fig (6.4.1)

From figure(6.4.9) we note that the maximum infection spreading velocity for node (53) which has the largest closeness centrality is larger than it for node (15) which has median closeness centrality and the maximum spreading velocity for node (15) is larger than it for node (8) which has the smallest closeness centrality . We note also that the curve from both sides is sharper when node (53) infected first than it when node (15) infected first and it is sharper when node (15) infected first than it when node (8) infected firs in figure (6.4.1) , and that means the infection spreading process when node (53) infected first is faster than it when node (15) infected first and it is faster when node(15) infected first than it when node (8) infected first.

When we apply equation (5.3) that I developed according to my hypothesis on the large weighted network in figure (6.4.1) and plot the fraction of the infection nodes with time that shown in that equation using the closeness centralities of "25" different nodes in our large weighted network in fig (6.4.1) that we assumed they are infected first in that network ,we have figure(6.4.10).

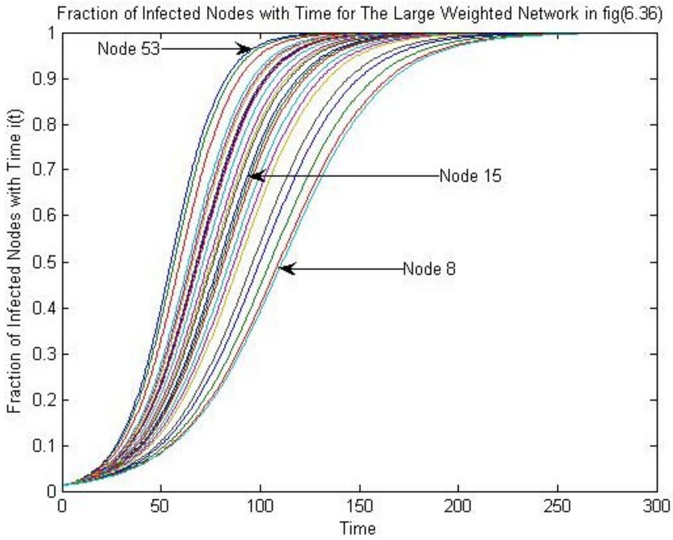


Figure (6.4.10) : Fraction of infected nodes with time in the large weighted network in figure (6.4.1)

From figure (6.4.10) we notice again the clear S-Shape curve which starts slow at the first state , then growth exponential at the second state and at the last state the curve will take off until all nodes will be infected .

To show the effects of nodes with different closeness centralities when they are infected first on the infection spreading process let us plot the curves for just three nodes (53,15 and 8) and compare between them , see figure (6.4.11).

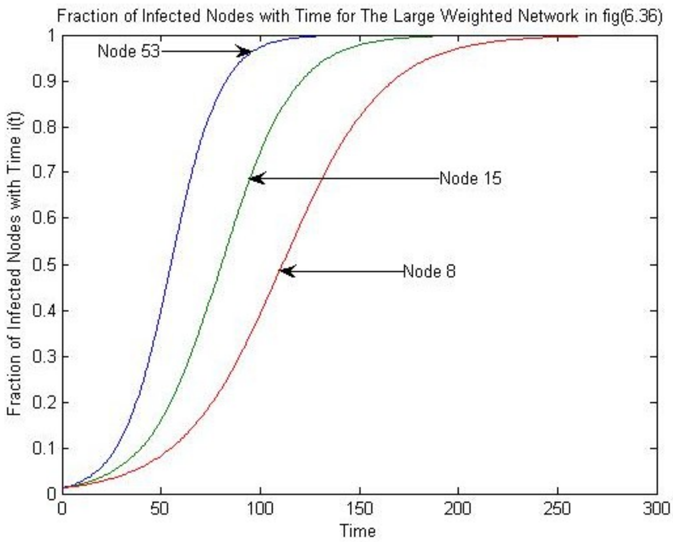


Figure (6.4.11) : The fraction of infected nodes with time in the large weighted network in figure (6.4.1) when nodes (53 ,15 and 8) infected first .

From figure (6.4.11) we note that when node (53) which has the largest closeness centrality infected first ,the total infected time that we need to infect all nodes in our large weighted network is the smallest , it is median when node (15) which has median closeness centrality infected first and it is the largest when node (8) which has the smallest closeness centrality .

6.5 Comparison Between the Effect of Eigenvector Principle and Closeness Centrality of Nodes on Infection Rate .

The author of [12] suggested a relation between the infection rate "β" or "λ" and the eigenvector principle"EVP" of the first infected node and in my thesis I suggested a relation between the infection rate and the closeness centrality" C_k^c " of the first infected node . To compare between the two hypothesis let us take two examples , the first one is small network and the second is large network and find the eigenvector principles and the closeness centralities for all nodes in them using my matlab program then compare between the two results and their effect on the infection rate .

6.5.1 Comparesion in The Small Network:

Let us take the same small unweighted network in figure (6.1.1) . By using my matlab program I found the eigenvector principles and the closeness centralities for all nodes in that network and ranked them according to their eigenvector principles and closeness centralities and we have table (6.5.1)

Table(6.5.1): The Eigenvector Principles and the Closeness Centralities for all nodes in the network in fig (6.1.1).

Rank	Eigenvector Principle		Closeness Centrality	
	Node	EVP	Node	C_k^c
1	4	0.1628	4	0.4138
2	2	0.1048	8	0.4138
3	3	0.1048	9	0.4138
4	8	0.1028	6	0.3636
5	1	0.0996	7	0.3636
6	6	0.0953	10	0.3529
7	9	0.0945	2	0.3333
8	7	0.0758	3	0.3333
9	10	0.0580	1	0.2791
10	5	0.0398	11	0.2791
11	11	0.0276	13	0.2667
12	13	0.0232	12	0.2222
13	12	0.0110	5	0.2222

From table (6.5.1) we note that the EVP for node (3) is larger than it for node (9) which means that the infection rate when node (3) infected first is larger than it when node (9) infected first . Also we note from the table that C^c for node (9) is larger than it for node (3) which means that the infection rate when node (9) infected first is larger than it when node (3) infected first . So we have contradiction between result from EVP and result form C^c hypothesis . To solve this contradiction let us analyze the infection process with time when the two nodes (3),(9) infected first .

When node (3) infected first the infection process with time shown in table (6.5.2)

Table (6.5.2) : Infection Process with time when node (3) in fig (6.1.1) infected first and the total number of infected nodes with time .

Time	Infected Nodes at That Time	Total Number of Infected Nodes
t0	3	1
t1	1,4	3
t2	2,5,6,8	7
t3	7,9	9
t4	10	10
t5	11,13	12
t6	12	13

When we plot the total number of infected nodes with time when node (3) infected first we have figure (6.5.1)

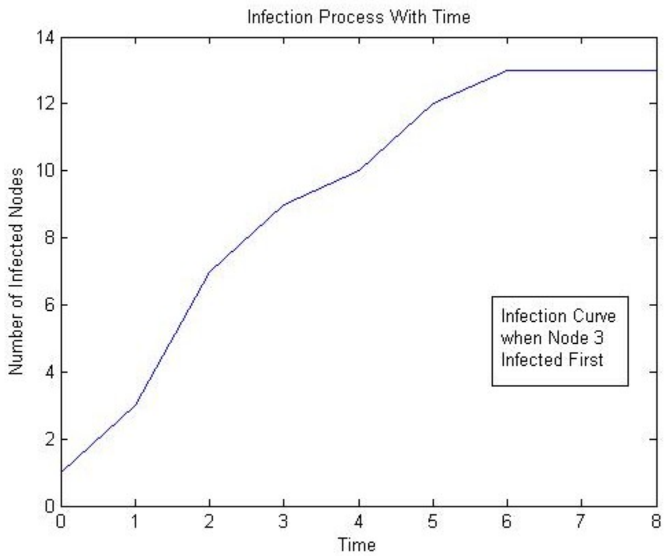


Figure (6.5.1) : Total Number of Infection Nodes with time when node (3) in fig(6.1.1) infected first

From table (6.5.2) and figure (6.5.1) we note that the total infection time when node (3) infected first equals "7t" and the infection rate in this case equals "13/7t" node / unit time where "t" is time for each period .

When node (9) infected first the infection process with time shown in table (6.5.3)

Table(6.5.3) : Infection Process with time when node (9) in fig (6.1.1) infected first and the total number of infected nodes with time .

Time	Infected nodes at that time	Total Number of Infected Nodes
t0	9	1
t1	7,8,10	4
t2	6,4,13,11	8
t3	3,2,12	11
t4	1	12
t5	5	13

By plotting the total number of infected nodes with time when node (9) infected first we have figure (6.5.2)

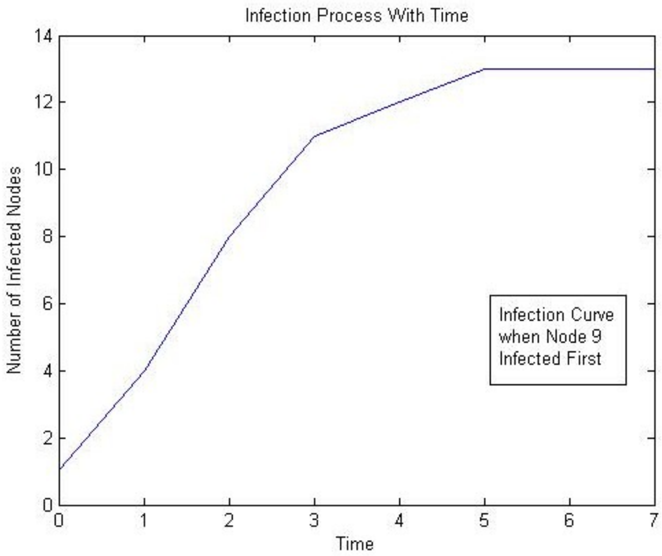


Figure (6.5.2) : Total Number of Infection Nodes with time when node (9) in fig(6.1.1) infected first

From table (6.5.3) and figure (6.5.2) we note that the total infection time when node (9) infected first equals "6t" and the infection rate equals " 13/6t " node/unit of time .

From these two cases we note that the infection rate when node (9) infected first is larger than it when node (3) infected first , which agreed with the result obtained from" C_k^c" hypothesis which says that nodes with high closeness centralities have high infection rates when they are infected first , and it contradicts with the EVP hypothesis as EVP for node (3) is larger than EVP for node (9)

We conclude from this example that the relation between closeness centrality for the first infected node and the infection rate is stronger than it with the eigenvector principle for that node .

6.5.2 Comparesion in The Large Network :

Let us take the same large unweighted network in figure (6.2.1) . By using my matlab program I found the eigenvector principles and the closeness centralities for all nodes in that network and ranked them according to their eigenvector principles and closeness centralities and we have table (6.5.4)

Table .(6. 5.4) : The Eigenvector Principles and the Closeness Centralities for all nodes in the network in fig (6.2.1) .

Rank	Eigenvector Principle		Closeness Centrality	
	Node	EVP	Node	C_k^c
1	53	0.101447	53	0.2453416
2	44	0.082694	44	0.2344213
3	45	0.078828	45	0.22507122
4	42	0.0562683	51	0.2231638
5	40	0.0467953	22	0.2200557
6	51	0.0421593	42	0.21293800
7	22	0.0373649	39	0.2117962
8	39	0.0351625	65	0.2062663
9	43	0.0309745	40	0.20413436
10	35	0.0300918	43	0.20204603
11	17	0.0292802	35	0.20153061
12	36	0.0266098	17	0.19949494
13	46	0.0256470	33	0.19799498
14	41	0.02276205	27	0.19554455
15	52	0.02169939	52	0.19458128
16	65	0.01894417	23	0.19221411
17	34	0.01872456	36	0.1894484
18	48	0.01863779	11	0.18720379
19	27	0.01798350	41	0.18632075
20	33	0.01706195	28	0.18544600
21	28	0.0159539	46	0.18501170
22	23	0.01291647	34	0.18202764
23	11	0.01233716	48	0.18119266
24	37	0.01085483	66	0.18077803
25	54	0.01047267	18	0.17995444
26	18	0.01004865	64	0.17913832
27	38	0.00997438	67	0.17752808
28	16	0.00980621	24	0.17594654
29	63	0.00812470	26	0.1755555
30	64	0.00803154	32	0.17439293
31	47	0.00760966	54	0.17286652
32	26	0.00729127	16	0.17136659

33	67	0.00710604	37	0.16880341
34	66	0.00655096	19	0.16737288
35	49	0.00654700	12	0.16561844
36	32	0.00638772	49	0.16322314
37	24	0.00616773	63	0.162886597
38	56	0.005005469	38	0.162217659
39	19	0.004586937	73	0.16089613
40	55	0.00448982	21	0.160569105
41	61	0.00440952	56	0.16024340
42	62	0.00438881	25	0.159919028
43	12	0.00421528	15	0.157370517
44	25	0.00399339	31	0.15737051
45	21	0.00387736	47	0.15643564
46	15	0.00376984	29	0.15643564
47	50	0.0034277	68	0.15581854
48	73	0.003134668	20	0.15459882
49	14	0.00289936	50	0.15339805
50	29	0.00259703	7	0.15105162
51	20	0.00251142	61	0.14990512
52	31	0.00232894	30	0.149056603
53	58	0.00225749	14	0.14877589
54	68	0.00213776	72	0.1446886
55	57	0.00200198	55	0.144160583
56	7	0.001869700	2	0.14234234
57	60	0.00184645	62	0.14234234
58	2	0.00180282	69	0.14081996
59	30	0.00146157	60	0.13982300
60	10	0.00143553	10	0.13908450
61	13	0.00141501	74	0.13884007
62	72	0.00122363	78	0.13884007
63	59	0.00121767	79	0.13884007
64	9	0.00115044	9	0.13859649
65	1	0.00096084	13	0.13787085
66	79	0.00093008	8	0.13597246
67	78	0.00093008	77	0.13255033
68	74	0.00093008	71	0.13255033
69	69	0.000817236	70	0.13255033
70	8	0.000671183	57	0.12741935
71	4	0.00065134	58	0.12700964
72	3	0.000586549	4	0.12700964
73	77	0.00049468	76	0.1270096
74	71	0.00049468	59	0.12559618
75	76	0.000443602	3	0.12519809
76	5	0.000392403	1	0.12519809
77	70	0.00037410	5	0.1250000
78	80	0.000242480	80	0.12363067
79	6	0.000174033	75	0.11285714
80	75	0.000131620	6	0.11142454

We see from table (6.5.4) that the EVP for node (58) is larger than it for node (69) which means that the infection rate when node (58) infected first is larger than it when node (69) infected first . Also we see from the table that " C_k^c "for node (69) is larger than it for node (58) which means that the infection rate when node (69) infected first is larger than it when node (58) infected first . So we have again contradiction between result from EVP and result form " C_k^c" hypothesis . To solve this contradiction let us analyze the infection process with time when the two nodes (58),(69) infected first in the network in figure (6.2.1) .

When node (58) infected first the infection process with time shown in table (6.5.5)

Table(6.5.5) : Infection Process with time when node (58) in fig (6.2.1) infected first and the total number of infected nodes with time

Time	Infected nodes at that time	Total number of infected nodes
t0	58	1
t1	62,57,59	4
t2	63,61,55,60	8
t3	64,54,56	11
t4	65,41,67,50	15
t5	51,66,38,42,49	20
t6	52,73,37,53,40,48	26
t7	43,72,78,79,74,36,45,39,44	35
t8	71,77,17,46,33,22,35	42
t9	76,16,18,47,32,28,11,23,27,34	52
t10	75,70,15,19,68,31,12,24,26	61
t11	14,20,69,30,7,21,25,29	69
t12	80,13,8,2,10,9	75
t13	5,4,3,1	79
t14	6	80

When we plot the total infection nodes with time when node (58) infected first we have figure (6.5.3)

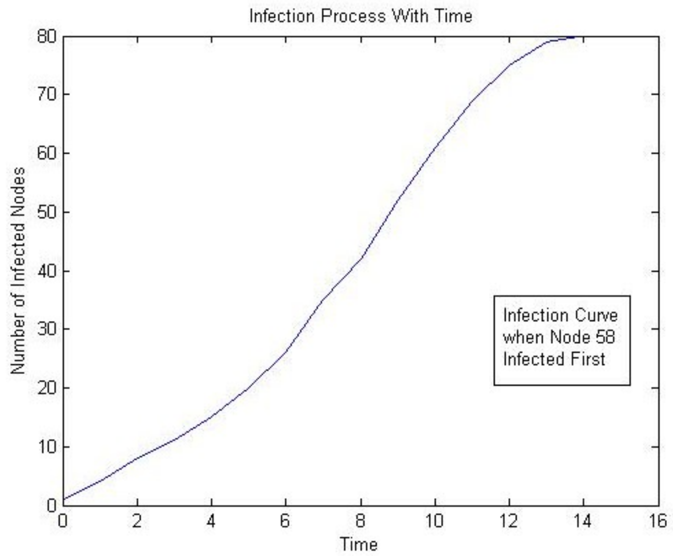


Figure (6.5.3) : Total Number of Infection Nodes with time when node (58) in fig(6.2.1) infected first.

From table (6.5.5) and figure (6.5.3) we found that the total infection time when node (58) infected first equals "15t" and the infection rate equals "80/15t" node/unit time .

When node (69) infected first the infection process with time shown in table (6.5.6)

Table . (6.5.6) : Infection Process with time when node (69) in fig (6.2.1) infected first and the total number of infected nodes with time

Time	Infected nodes at that time	Total number of infected nodes
t0	69	1
t1	68,80,70	4
t2	32,76	6
t3	33,31,71,77,75	11
t4	28,39,30,72	15
t5	27,34,53,29,73	20
t6	22,35,45,40,42,51,44,26,66,74,79,78	32
t7	11,23,17,36,46,41,48,52,43,25,65	43
t8	12,18,16,37,47,54,38,49,24,64,67	54
t9	7,19,15,61,50,21,63,53	62
t10	8,13,14,2,20,10,9,62,55,60	72
t11	5,3,4,1,58,57,59	79
t12	6	80

By plotting the total number of infected nodes with time when node (69) infected first ,we have figure (6.5.4)

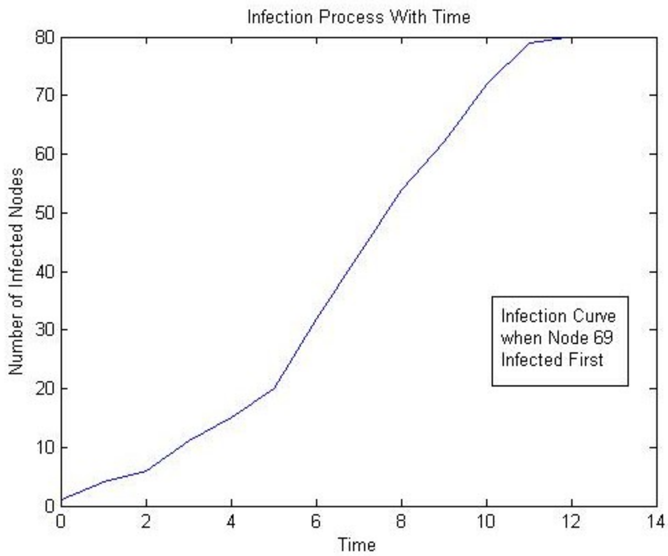


Figure (6.5.4) : Total Number of Infection Nodes with time when node (69) in fig (6.2.1) infected first.

From table (6.5.6) and figure (6.5.4) we see that the total infection time when node (69) infected first equals " 13t " and the infection rate equals " 80/13t " node/unit of time .

Again we see that form these two cases that the infection rate for node (69) is larger than it for node (58) which agreed again with "C_k^c" hypothesis which is " high closeness centralities nodes have high infection rates when they are infected first , and contradict with the EVP hypothesis as EVP for node (69) is less than it for node (58) .

From this result we conclude that the relation between the closeness centrality for the first infected node and the infection rate is stronger than it for the eigenvector principal for the same node .

Chapter 7

DISCUSSION and CONCLUSIONS

In this thesis I studied the effect of closeness centralities of nodes on the infection process in unweighted and weighted networks when those nodes are infected first in those networks.

My research question in section (1.2) was : " what is the relation between closeness centrality of the first infected node in the network and each of the total infection time, the infection rate and the infection spreading power of that node in unweighted and weighted networks ? ."

To answer my research question I used two methods:

First I used the analysis method for the infection process with time for four types of network , unweighted small and large networks and weighted small and large networks, see sections (6.1.2), (6.2.2), (6.3.1), (6.4.1). The result from those sections supported my research hypothises as we saw from figure (6.1.6) that node (4) which has the largest closeness centrality in the small unweighted network has the smallest total infection time, the largest infection rate and the largest infection spreading power . Node (2) which has median closeness centrality has median total infection time, median infection rate and also median infection spreading power. Node (12) which has the smallest closeness centrality has the largest total infection time, the smallest infection rate and the smallest infection spreading power. From fig (6.2.5) I noticed that node (53) which has the largest closeness centrality in the large unweighted network has the smallest total infection time, the largest infection rate and the largest infection spreading power. Node (21) which has median closeness centrality has median total infection time , median infection rate and median infection spreading power . Node (6) which has the smallest closeness centrality has the largest total infection time, the smallest infection rate and the smallest infection spreading power . From fig (6.3.6) I noticed that node (8) which has the largest closeness centrality in the small weighted network has the smallest total infection time , the largest infection rate and the largest infection spreading power . Node (10) which has median closeness centrality has median total infection time , median infection rate and median infection spreading power . Node (12) which has the smallest closeness centrality has the largest total infection time , the smallest infection rate and the smallest infection spreading power . From fig (6.4.5) I observed that node (53) which has the largest closeness centrality in the large weighted network has the smallest total infection time , the largest infection rate and the larest infection spreading power . Node (15) which has median closeness centrality has median total infection time,median infection rate and median infection spreading power . Node (8) which has the smallest closeness centrality has the largest total infection time, the smallest infection rate and the smallest infection spreading power.

When I ploted the relation between the closeness centrality for nodes (4,2,12) in the small unweighted network with their total infection time , see fig (6.1.7) I noted that the relation between them was inversly proportional and when I ploted the closeness centrality for those nodes with their infection rate I noted that the relation between them was directly proportional , see fig (6.1.8). From fig (6.2.6) which represents the relation between the closeness centrality for nodes (53,21,6) in the large unweighted network and their total infection time , I noted that this relation was also inversly proportional and from fig (6.2.7) which represent the relation between the closeness centrality of those nodes and their infection rate , I found that this relation was also directly proportional . Fig (6.3.7) which represents the relation between the closeness centrality of nodes (8,10,12) in the small weighted network and thier total infection time , I noted from that figure that this relation was also inversly proportional and from fig (6.3.8) which represents the relation between the closeness centrality of those nodes and their infection rate , I noted that this relation was also directly proportional . I noted from fig (6.4.6) which represents the relation between the closeness centrality of nodes (53,15,8) in the large weighted network and their total infection time , that this relation was also inversly proportional and I noted from fig(6.4.7) which represents the relation between the closeness centrality of those nodes and their infection rate , that this relation was directly proportional . From all these figures and results we can conclude that " *closeness centrality for the first infected node in the unweighted and weighted networks is inversly proportional to the total infection time , directly proportional to poth of the infection rate "β" or "λ" and the infection spreading power of that node*."

Second I used my developed SI model and replaced the assumed and constant infection rate "β" by the closeness centrality of the first infected node . see sections (6.1.2) , (6.2.2),(6.3.2) and (6.4.2). The exponantial growth at the left side of the curve, the beak and the power – law behavior at the right side of the curve is so clear when we plot equation (6.1) which described the infection spreading velocity with time which is the same result that optained from previous works, see [2],[3] and the S – Shape curve is very clear when we plot equation (6.2) that described the fraction of infected nodes with time which is the same result that optained from previous works , see [23],[10],[25].The result optained from those four sections support my research hypothises .I noticed that nodes those have high closeness centralities have small total infection time,large infection rate and high infection spreading power and velocity and nodes those have small closeness centralities have large total infection time, small infection rate and small infection spreading power and velocity, seefigure (6.1.9), (6.1.10), (6.1.11), (6.1.12), (6.2.8), (6.2.9), (6.2.10), (6.2.11), (6.3.9), (6.3.10), (6.3.11), (6.3.12), (6.4.8), (6.4.9), (6.4.10) and (6.4.11). We conclude from these results that closeness centrality for the first infected nodes is inversly proportinal to the total infection time,it is also directly proportinal to the infection rate and it is directly proportinal to the infection spreading power of those nodes .

From all these results I suggest that we can replace the infection rate "β" in the SI network epidemic model by the closeness centrality of the first infected node and that model will be :

$$\frac{di(t)}{dt} = C_k^c\ (1 - i(t))\ i(t) \text{ --------------}(7.1)$$

with boundary conditions as I(0) = 1 and i(0) = I(0)/N , so

(1)i(0) = 1/N , i(t final) = 1 .

(2) for all $t \geq 0$, i(t) + s(t) = 1 .

which is the differential equation that described the infection spreading velocity with time for that model .

The solution of equation (7.1) for the fraction of infectious nodes is the " logistic curve " :

$$i(t) = (1/N)\, e^{Ckc\, t} / 1-(1/N) + (1/N)\, e^{Ckc\, t} \text{ ---------------- } (7.2)$$

By equation (7.2) we can measure the fraction of infected nodes as a function of time "t".

In section (6.5) I made some comparisons between my work which suggested replacing the infection rate by the closeness centrality of the first infected node in the network and the work of the author of [12] which suggested replacing the infection rate by the eigenvector principal of the first infected node . To do this comparison I took the same two unweighted network small and large in my thesis, fig(6.1.1) and fig (6.2.1).

For the small unweighted network fig (6.1.1) I calculated the eigenvector principals and the closeness centralities for all nodes in that network using my matlab program . I took two nodes from that network node (3) and node (9) and compared between them when they were infected first in that network , I found that the closeness centrality for node (9) was larger than it for node (3) which means according to my hypothises that the infection rate when node (9) infected first was larger than it when node (3) infected first . I found also that the eigenvector principal for node (3) was larger than it for node (9) which means according to the author of [12] hypothises that infection rate when node (3) infected first was larger than it when node (9) infected first see table (6.5.1) . when I analyzed the infection process with time I found that the infection rate when node (9) infected first was larger than it when node (3) infected first , see tables (6.5.2),(6.5.3) and figures (6.5.1),(6.5.2).

For the large unweighted network , fig(6.2.1) , I also calculated the eigenvector principals and the closeness centralities for all nodes in that network using my matlab program . I took nodes nodes (69) and (58) to compare between them . I found that the closeness centrality for node (69) was larger than it for node (58) which means according to my hypothises that the infection rate when node (69) infected first was larger than it when node (58) infected first . I found also that the eigenvector principal for node (58) was larger than it for node (69) which means according to the author of [12] hypothises that the infection rate when node (58) infected first was larger than it when node (69) infected first , see table (6.5.4) . When I analyzed the infection process with time for that large unweighted network with time I found that the infection rate when node (69) infected first was larger than it when node (58) infected first , see tables (6.5.5), (6.5.6) and figures (6.5.3) , (6.5.4).

From these two cases I think that closeness centrality for the first infected node is better than the eigenvector principal for it to replace the infection rate by it.

Last Note:

From my search and studying I noticed that almost all previous works for finding the infection rate depend on assumption and we have no exact answer for how to find the infection rate in the real world networks . In my thesis I found that there is a strong relation between the closeness centrality of the first infected node and the infection rate , so I suggested to replaced the infection rate by the closeness centrality of the first infected node in the network .

8. Future Work:

In this thesis I dealed with just one model of the epidemic models which is the SI model and related that model by the closeness centrality of the first infected node in networks ,but we have many others models that described the epidemic spreading through networks , like SIS ,SIR models and others . In the future I will try to study if there is some relation between these models and the closeness centralities of nodes in networks . Also I will try to deal with another types of graphs to represent the real networks , like directed networks , weighted directed networks ,trees and others types .

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Appendices

Appendix (A)

My matlab program :

```
clc;
clear;
n= input (' Number of nodes in the network = ');
for i=1:n
 for j=1:n
 d(i,j)=input (' Entry of the adjacency matrix of the network = ');
 end
 end
 y=[1:n];
 y=y';
 r=[1:n];
r = r';
% Degree Centrality
for i= 1:n
x(i)=(sum(d(i,:)))/(n-1);
 end
 x=x';
 for i=1:n
 for j=1:n
  if x(i)> x(j)
  x([j i],:)=x([i j],:);
   y([j i],:)=y([i j],:);
   ran1=[y x];
   end
   end
  end
 y=[1:n];
 y=y';
```

```
%Eigenvector Principle
[V2,D2]=eigs(d,1);
for i=1:n
 V2(i)=abs(V2(i));
end
s=sum(sum(V2));
pf=1/s;
pev=pf*V2;
for i=1:n
for j=1:n
 if pev(i)> pev(j)
 pev([j i],:)=pev([i j],:);
  y([j i],:)=y([i j],:);
  ran2=[y pev];
   end
   end
   end
%Closeness Centrality
y=[1:n];
y=y';
for i=1:n
for j=1:n
 if i~=j & d(i,j)==0
 d(i,j)=inf;
    end
    end
       end
d;
k=1;
while k<=n
for i=1:n
```

```
  for j=1:n
  if d(i,k)+d(k,j)<d(i,j)&i~=j&i~=k&j~=k
 d(i,j)=d(i,k)+d(k,j);
  end
    end
end
if k= =n
break
end
k=k+1;
end
for i=1:n
 s(i)=sum(d(i,:));
 c(i)=(n-1)/s(i);
end
c=c';
for i=1:n
 for j=1:n
 if c(i)> c(j)
 c([j i],:)=c([i j],:);
  y([j i],:)=y([i j],:);
   ran3=[y c];
    end
    end
    end
dd=[r d]
p=[r s']
q=[r ran1 ran2 ran3]
ppp=[r ran3]
```

Appendix (B)

Adjacency Matrix for Small Unweighted Network in Fig(6.1.1)

[0 1 1 0 1 0 0 0 0 0 0 0 0
1 0 0 1 0 0 0 0 0 0 0 0 0
1 0 0 1 0 0 0 0 0 0 0 0 0
0 1 1 0 0 1 0 1 0 0 0 0 0
1 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 1 0 0 1 0 0 0 0 0 0
0 0 0 0 0 1 0 0 1 0 0 0 0
0 0 0 1 0 0 0 0 1 0 0 0 0
0 0 0 0 0 0 1 1 0 1 0 0 0
0 0 0 0 0 0 0 0 1 0 1 0 1
0 0 0 0 0 0 0 0 0 1 0 1 0
0 0 0 0 0 0 0 0 0 0 1 0 0
0 0 0 0 0 0 0 0 0 1 0 0 0]

Appendix (C)

Adjacency matrix for large unweighted network in fig (6.2.1)

[0 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0
1 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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Appendix (D)

The Shortest Path Matrix for the unweighted large network in figure(6.2.1)

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	0	1	0	2	3	3	5	4	3	1	6	6	6	5	6	7	6	5	4	3
2	1	0	1	1	2	2	4	3	2	2	5	5	5	4	5	6	5	4	3	2
3	2	1	0	2	3	1	5	4	3	3	6	6	6	5	6	7	6	5	4	3
4	2	1	2	0	1	3	3	2	3	3	5	4	4	5	6	7	6	5	4	3
5	3	2	3	1	0	4	2	1	4	4	4	3	3	4	5	6	7	6	5	4
6	3	2	1	3	4	0	6	5	4	4	7	7	7	6	7	8	7	6	5	4
7	5	4	5	3	2	6	0	1	6	6	2	1	1	2	3	4	5	4	3	4
8	4	3	4	2	1	5	1	0	5	5	3	2	2	3	4	5	6	5	4	5
9	3	2	3	3	4	4	6	5	0	2	5	6	5	4	5	6	5	4	3	2
10	1	2	3	3	4	4	6	5	2	0	5	6	5	4	5	6	5	4	3	2
11	6	5	6	5	4	7	2	3	5	5	0	1	3	4	5	5	4	5	5	5
12	6	5	6	4	3	7	1	2	6	6	1	0	2	3	4	5	5	5	4	5
13	6	5	6	4	3	7	1	2	5	5	3	2	0	1	2	3	4	3	2	3
14	5	4	5	5	4	6	2	3	4	4	4	3	1	0	1	2	3	2	1	2
15	6	5	6	6	5	7	3	4	5	5	5	4	2	1	0	1	2	3	2	3
16	7	6	7	7	6	8	4	5	6	6	5	5	3	2	1	0	1	2	3	4
17	6	5	6	6	7	7	5	6	5	5	4	5	4	3	2	1	0	1	2	3
18	5	4	5	5	6	6	4	5	4	4	5	5	3	2	3	2	1	0	1	2
19	4	3	4	4	5	5	3	4	3	3	5	4	2	1	2	3	2	1	0	1
20	3	2	3	3	4	4	4	5	2	2	5	5	3	2	3	4	3	2	1	0
21	2	1	2	2	3	3	5	4	1	1	4	5	4	3	4	5	4	3	2	1
22	5	4	5	5	5	6	3	4	4	4	1	2	4	5	5	4	3	4	5	4
23	4	3	4	4	5	5	4	5	3	3	2	3	5	5	6	5	4	5	4	3
24	3	2	3	3	4	4	5	5	2	2	3	4	5	4	5	6	5	4	3	2
25	4	3	4	4	5	5	6	6	3	3	4	5	6	5	6	7	6	5	4	3
26	5	4	5	5	6	6	5	6	4	4	3	4	6	6	7	6	5	6	5	4
27	6	5	6	6	6	7	4	5	5	5	2	3	5	6	6	5	4	5	6	5
28	7	6	7	7	7	8	5	6	6	6	3	4	6	7	7	6	5	6	7	6
29	6	5	6	6	7	7	6	7	5	5	4	5	7	7	8	7	6	7	6	5
30	7	6	7	7	8	8	7	8	6	6	5	6	8	8	9	8	7	8	7	6
31	8	7	8	8	9	9	8	9	7	7	6	7	9	9	8	7	6	7	8	7
32	9	8	9	9	9	10	7	8	8	8	5	6	8	8	7	6	5	6	7	8
33	8	7	8	8	8	9	6	7	7	7	4	5	7	7	6	5	4	5	6	7
34	8	7	8	8	8	9	6	7	7	7	4	5	7	7	6	5	4	5	6	7
35	7	6	7	7	7	8	5	6	6	6	3	4	6	6	5	4	3	4	5	6
36	8	7	8	8	8	9	6	7	7	7	4	5	6	5	4	3	2	3	4	5
37	9	8	9	9	9	10	7	8	8	8	5	6	7	6	5	4	3	4	5	6
38	10	9	10	10	10	11	8	9	9	9	6	7	8	7	6	5	4	5	6	7
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7	6	6	6	6	7	8	7	7	6	4	5	5	6	6	5	7	7	7	6
10	9	9	9	9	10	11	10	10	9	7	8	8	9	9	8	10	10	10	9
9	8	8	8	8	9	10	9	9	8	6	7	7	8	8	7	9	9	9	8
8	7	7	7	7	8	9	8	8	7	5	6	6	7	7	6	8	8	8	7
7	6	6	6	6	7	8	7	7	6	4	5	5	6	6	5	7	7	7	6
7	6	6	6	6	7	8	7	7	6	4	5	5	6	6	5	7	7	7	6
8	7	8	7	7	8	9	8	9	10	7	8	6	9	11	10	12	12	12	11

61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
11	12	11	10	9	10	10	10	11	12	13	12	11	12	14	13	13	12	12	12
10	11	10	9	8	9	9	9	10	11	12	11	10	11	13	12	12	11	11	11
11	12	11	10	9	10	10	10	11	12	13	12	11	12	14	13	13	12	12	12
11	12	11	10	9	10	10	10	11	12	13	12	11	12	14	13	13	12	12	12
11	12	11	10	9	10	10	10	11	12	13	12	11	12	14	13	13	12	12	12
12	13	12	11	10	11	11	11	12	13	14	13	12	13	15	14	14	13	13	13
9	10	9	8	7	8	8	8	9	10	11	10	9	10	12	11	11	10	10	10
10	11	10	9	8	9	9	9	10	11	12	11	10	11	13	12	12	11	11	11
10	11	10	9	8	9	9	9	10	11	12	11	10	11	13	12	12	11	11	11
10	11	10	9	8	9	9	9	10	11	12	11	10	11	13	12	12	11	11	11
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10	11	10	9	8	9	9	9	10	11	12	11	10	11	13	12	12	11	11	11
9	10	9	8	7	8	8	9	10	11	11	10	9	10	13	12	11	10	10	11
8	9	8	7	6	7	7	8	9	10	10	9	8	9	12	11	10	9	9	10
7	8	7	6	5	6	6	7	8	9	9	8	7	8	11	10	9	8	8	9
6	7	6	5	4	5	5	6	7	8	8	7	6	7	10	9	8	7	7	8
7	8	7	6	5	6	6	7	8	9	9	8	7	8	11	10	9	8	8	9
8	9	8	7	6	7	7	8	9	10	10	9	8	9	12	11	10	9	9	10
9	10	9	8	7	8	8	9	10	11	11	10	9	10	13	12	11	10	10	11
9	10	9	8	7	8	8	8	9	10	11	10	9	10	12	11	11	10	10	10
6	7	6	5	4	5	5	5	6	7	8	7	6	7	9	8	8	7	7	7
7	8	7	6	5	6	6	6	7	8	9	8	7	8	10	9	9	8	8	8
8	9	8	7	6	7	7	7	8	9	10	9	8	9	11	10	10	9	9	9
9	10	9	8	7	8	8	6	7	8	10	10	9	10	10	9	10	10	10	8
8	9	8	7	6	7	7	5	6	7	9	9	8	9	9	8	9	9	9	7
7	8	7	6	5	6	6	4	5	6	8	8	7	8	8	7	8	8	8	6
7	8	7	6	5	6	6	3	4	5	7	8	7	8	7	6	7	8	8	5
9	10	9	8	7	8	8	4	5	6	8	9	9	10	8	7	8	10	10	6
9	10	9	8	7	8	8	3	4	5	7	8	9	10	7	6	7	10	10	5
8	9	8	7	6	7	7	2	3	4	6	7	8	9	6	5	6	9	9	4
7	8	7	6	5	6	6	1	2	3	5	6	7	8	5	4	5	8	8	3
6	7	6	5	4	5	5	2	3	4	6	7	6	7	6	5	6	7	7	4
7	8	7	6	5	6	6	4	5	6	8	8	7	8	8	7	8	8	8	6
6	7	6	5	4	5	5	5	6	7	8	7	6	7	9	8	8	7	7	7
5	6	5	5	4	5	5	6	7	8	8	7	6	7	10	9	8	7	7	8
4	5	4	5	5	6	6	7	8	9	9	8	7	8	11	10	9	8	8	9
3	4	3	4	5	6	6	7	8	9	9	8	7	8	11	10	9	8	8	9
5	6	5	4	3	4	4	3	4	5	7	6	5	6	7	6	7	6	6	5
4	5	4	4	3	4	4	5	6	7	7	6	5	6	9	8	7	6	6	7
2	3	2	3	4	5	5	6	7	8	8	7	6	7	10	9	8	7	7	8
3	4	3	4	3	4	4	5	6	7	7	6	5	6	9	8	7	6	6	7
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5	6	5	4	3	4	4	5	6	7	7	6	5	6	9	8	7	6	6	7
5	6	5	4	3	4	4	5	6	7	7	6	5	6	9	8	7	6	6	7
6	7	6	5	4	5	5	6	7	8	8	7	6	7	10	9	8	7	7	8
7	8	7	6	5	6	6	7	8	9	9	8	7	8	11	10	9	8	8	9
4	5	4	5	4	5	4	6	7	8	8	7	6	7	10	9	8	7	7	8
5	5	4	5	4	5	3	7	8	9	8	7	6	7	10	9	8	7	7	9
5	4	3	4	3	4	2	8	9	9	7	6	5	6	9	8	7	6	6	10
5	4	3	2	1	2	2	5	6	7	5	4	3	4	7	6	5	4	4	7
6	5	4	3	2	3	3	6	7	8	6	5	4	5	8	7	6	5	5	8
4	5	4	3	2	3	3	4	5	6	6	5	4	5	8	7	6	5	5	6
1	2	1	2	3	4	4	7	8	9	7	6	5	6	9	8	7	6	6	9
3	2	1	2	3	4	2	9	10	9	7	6	5	6	9	8	7	6	6	11
4	3	2	3	2	3	1	8	9	8	6	5	4	5	8	7	6	5	5	10
3	2	2	3	4	5	3	10	11	10	8	7	6	7	10	9	8	7	7	12
2	1	2	3	4	5	4	10	11	10	8	7	6	7	10	9	8	7	7	12
3	2	3	4	4	5	3	10	11	10	8	7	6	7	10	9	8	7	7	12
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0	1	2	3	4	5	5	8	9	10	8	7	6	7	10	9	8	7	7	10
1	0	1	2	3	4	4	9	10	9	7	6	5	6	9	8	7	6	6	11
2	1	0	1	2	3	3	8	9	8	6	5	4	5	8	7	6	5	5	10
3	2	1	0	1	2	2	7	8	7	5	4	3	4	7	6	5	4	4	9
4	3	2	1	0	1	1	6	7	6	4	3	2	3	6	5	4	3	3	8

5	4	3	2	1	0	2	7	6	5	3	2	1	2	5	4	3	2	2	7
5	4	3	2	1	2	0	7	8	7	5	4	3	4	7	6	5	4	4	9
8	9	8	7	6	7	7	0	1	2	4	5	6	7	4	3	4	7	7	2
9	10	9	8	7	6	8	1	0	1	3	4	5	6	3	2	3	6	6	1
10	9	8	7	6	5	7	2	1	0	2	3	4	5	2	1	2	5	5	2
8	7	6	5	4	3	5	4	3	2	0	1	2	3	2	1	2	3	3	4
7	6	5	4	3	2	4	5	4	3	1	0	1	2	3	2	1	2	2	5
6	5	4	3	2	1	3	6	5	4	2	1	0	1	4	3	2	1	1	6
7	6	5	4	3	2	4	7	6	5	3	2	1	0	5	4	3	2	2	7
10	9	8	7	6	5	7	4	3	2	2	3	4	5	0	1	2	5	5	4
9	8	7	6	5	4	6	3	2	1	1	2	3	4	1	0	1	4	4	3
8	7	6	5	4	3	5	4	3	2	2	1	2	3	2	1	0	3	3	4
7	6	5	4	3	2	4	7	6	5	3	2	1	2	5	4	3	0	2	7
7	6	5	4	3	2	4	7	6	5	3	2	1	2	5	4	3	2	0	7
10	11	10	9	8	7	9	2	1	2	4	5	6	7	4	3	4	7	7	0

Appendix (E)

Adjacency Matrix for The Small Weighted Network in figure (6.3.1):

[0 3 2 0 2 0 0 0 0 0 0 0 0
3 0 0 1 0 0 0 0 0 0 0 0 0
2 0 0 4 0 0 0 0 0 0 0 0 0
0 1 4 0 0 5 0 2 0 0 0 0 0
2 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 5 0 0 7 0 0 0 0 0 0
0 0 0 0 0 7 0 0 2 0 0 0 0
0 0 0 2 0 0 0 0 1 0 0 0 0
0 0 0 0 0 0 2 1 0 6 0 0 0
0 0 0 0 0 0 0 0 6 0 3 0 2
0 0 0 0 0 0 0 0 0 3 0 2 0
0 0 0 0 0 0 0 0 0 0 2 0 0
0 0 0 0 0 0 0 0 0 2 0 0 0]

Appendix (F)

Adjacency Matrix for Large Weighted Nework in Fig (6.4.1)

```
[0 1 0 0 0 0 0 0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0
1 0 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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0 0 0 0 0 0 0 5 0 0 0 3 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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0 0 0 0 0 0 4 0 0 0 0 0 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 5 0 1 0 0 0 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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0 0 0 0 0 0 0 0 0 0 0 0 0 3 0 0 0 5 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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Appendix (G)

The Shortest Path Matrix for The Large Weighted Network in figure (6.4.1)

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	0	1	2	3	6	4	15	10	6	2	19	18	14	9	10	12	15	11	6	5
2	1	0	1	2	5	3	14	9	7	3	20	17	15	10	11	13	16	12	7	6
3	2	1	0	3	6	2	15	10	8	4	21	18	16	11	12	14	17	13	8	7
4	3	2	3	0	3	5	12	7	9	5	20	15	16	12	13	15	18	14	9	8
5	6	5	6	3	0	8	9	4	12	8	17	12	13	15	16	18	21	17	12	11
6	4	3	2	5	8	0	17	12	10	6	23	20	18	13	14	16	19	15	10	9
7	15	14	15	12	9	17	0	5	18	16	8	3	4	9	10	12	15	17	12	13
8	10	9	10	7	4	12	5	0	16	12	13	8	9	14	15	17	20	21	16	15
9	6	7	8	9	12	10	18	16	0	4	19	21	14	9	10	12	15	11	6	5
10	2	3	4	5	8	6	16	12	4	0	17	19	12	7	8	10	13	9	4	3
11	19	20	21	20	17	23	8	13	19	17	0	5	12	17	18	17	14	18	19	18
12	18	17	18	15	12	20	3	8	21	19	5	0	7	12	13	15	18	20	15	16
13	14	15	16	16	13	18	4	9	14	12	12	7	0	5	6	8	11	13	8	9
14	9	10	11	12	15	13	9	14	9	7	17	12	5	0	1	3	6	8	3	4
15	10	11	12	13	16	14	10	15	10	8	18	13	6	1	0	2	5	9	4	5
16	12	13	14	15	18	16	12	17	12	10	17	15	8	3	2	0	3	7	6	7
17	15	16	17	18	21	19	15	20	15	13	14	18	11	6	5	3	0	4	9	10
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19	6	7	8	9	12	10	12	16	6	4	19	15	8	3	4	6	9	5	0	1
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22	14	15	16	17	20	18	13	18	14	12	5	10	17	15	14	12	9	13	14	13
23	9	10	11	12	15	13	18	19	9	7	10	15	17	12	13	15	14	14	9	8
24	7	8	9	10	13	11	19	17	7	5	12	17	15	10	11	13	16	12	7	6
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جامعة النجاح الوطنية
كلية الدراسات العليا

المركزية وإنتشاء الوباء في الشبكات

إعداد
فارس مسعود عبد الغني ربايعة

إشراف
د. صبحي رزية
د. عدوان ياسين

قدمت هذه الأطروحة استكمالاً لمتطلبات الحصول على درجة الماجستير في الرياضيات المحوسبة بكلية الدراسات العليا في جامعة النجاح الوطنية في نابلس، فلسطين.

2008م

المركزية وإنتشاء الوباء في الشبكات

إعداد

فارس مسعود عبد الغني ربايعة

إشراف

د. صبحي رزية

د. عدوان ياسين

الملخص

هذه الرسالة تناقش العلاقة بين المركزية لأول نقطة تصاب بالعدوى في الشبكة وكل من الزمن الكلي الذي تصاب به الشبكة كلها بتلك العدوى وكذلك معدل انتشار العدوى في الشبكة والذي يقيس نسبة النقاط التي تصاب في الشبكة في وحدة الزمن وكذلك علاقتها بقدرة النقطة المصابة في الشبكة على نشر الوباء فيها.

في هذه الرسالة تعاملنا مع أربع أنواع من هذه الشبكات وهي شبكات صغيرة ليس فيها اوزان وكبيرة ليس فيها اوزان وصغيرة فيها اوزان وكبيرة فيها اوزان، ودرسنا تلك العلاقة في هذه الانواع جميعاً.

وتكمن اهمية هذا العمل في انه إذا وجدنا مركزية النقطة وقدرتها على نشر الوباء فإن ذلك يساعدنا على فهم ضعف ومحاسن تلك النقطة من اجل تفادي خطر إنتشار الوباء الذي يصيبها في الوقت المحدد.

في هذه الدراسة حاولنا تطوير نموذج (SI) في وصف انتشار الوباء في الشبكات وذلك باستبدال معدل الإنتشار مع الزمن في الشبكة (B) بمركزية النقطة التي تصاب أولاً في الشبكة. وقد وجدنا في هذه الدراسة أن معدل الوباء مع الزمن الذي كان يعتبر ثابتاً وكان يفرض افتراضاً في النماذج السابقة، أنه غير ثابت وأنه يعتمد على طبيعة النقطة التي تصاب اولاً في الشبكةن وان هناك علاقة قوية بين معدل إنتشار الوباء في الشبكة ومركزية النقطة التي تصاب أولاً.

من النتائج المستنبطة من هذه الدراسة وجدنا أن كل من الزمن اللازم لإصـــابة الشـــبكة كلها ومعدل إنتشار الوباء فيها وقدرة النقطة على نشر الوباء تعتمد على مركزية النقطـــة التـــي تصاب اولاً.