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Controlling COVID-19 Propagation with Quarantine of Influential Nodes

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Abstract.

We study importance of influential nodes in spreading of epidemic COVID-19 in a complex network. We will show that quarantine of important and influential nodes or consider of health protocols by efficient nodes is very helpful and effective in the controlling of spreading epidemic COVID-19 in a complex network. Therefore, identifying influential nodes in complex networks is the very significant part of dependability analysis, which has been a clue matter in analyzing the structural organization of a network. The important nodes can be considered as a person or as an organization. To find the influential nodes we use the technique for order preference by similarity to ideal solution (TOPSIS) method with new proposed formula to obtain the efficient weights. We use various centrality measures as the multi-attribute of complex network in the TOPSIS method. We define a formula for spreading probability of epidemic disease in a complex network to study the power of infection spreading with quarantine of important nodes. In the following, we use the Susceptible–Infected (SI) model to figure out the performance and efficiency of the proposed methods. The proposed method has been examined for efficiency and practicality using numerical examples.

Keywords: Infection, epidemic disease, COVID-19, complex network, TOPSIS method, influential nodes

1. Introduction

One of the Coronaviridae family in the Nidovirales order is so-called coronaviruses. Coronaviruses contain a single-stranded RNA as a nucleic material and they are atomic in size (65–125 nm in diameter). In particular COVID-19 is a family of RNA Beta virus in Nidoviral order. Coronaviruses are atomic in size (65–125 nm in diameter) and contain a single-stranded RNA as a nucleic material, size confining from 26 to 32kbs in length (Fig. (1)) [1].

The coronavirus disease 2019 (COVID-19) epidemic was a worldwide public health emergency unrivaled in the recent time. Infectious epidemic diseases are one of the serious factors in creating illness. Epidemic disease cause death hundreds and thousands of people all over the world. Corona prefix Comes from Latin word for Crown named for "crown-like" looks of virus. This virus first introduced in Wuhan Huanan seafood wholesale market that contain lentic products, and some savage animals [2, 3].

It is the seventh Corona virus discovered to causes illness in humans. Some researchers believed that the virus transmitted from either from bats or snakes to humans. For now, people are

suspecting bats are the source of COVID-19 [2]. Coronavirus infects viruses and mammals and bats host a large number of coronavirus genotypes. When viruses transfer from one's pieces to another species the epidemic occur. The cheeks that hostess the severe torrid respiratory syndrome corona virus 2 (SARS-CoV-2) is probably bat, containing 96% similar at the total-genome sequence level [2].

Human societies are faced to a great challenge like COVID-19. Because of this, it is necessary to study and analysis of the recent COVID-19 to provide more capable knowledge for a better conception of this virus. In this network, people play the role of nodes and connection between people are edges. Studying of a complex network to find influential nodes can be great helpful in controlling the epidemic disease such as COVID-19. We will show that quarantine the important and influential infected peoples or consider of health protocols by efficient infected peoples is very efficient in the controlling of spreading epidemic COVID-19 in a complex network. We will obtain the spreading probability of epidemic disease in a complex network to study the power of infection spreading with quarantine of important nodes.

Fig 1: Structure of respiratory syndrome causing human coronavirus [1].

2. Generating of random networks

To study of infection spreading rate by infected peoples in a society which include susceptible and infected peoples, we generated an undirected random network. To generate the random network, we used the following Matlab code,

```
N=52; %Total number of nodes
edges=randi([1 M], 2,M)';
names=compose('%d', 1:1:M);
x=edges(:,1);
y=edges(:,2);
hold on
G.Nodes = table(names);
G= graph(x, y); % create a graph from edges
figure (1);
h=plot(G, 'b','LineWidth',2, 'MarkerSize',6,'NodeColor','r');
```

In the generated network, isolated node plays non-important role in the spreading of epidemic disease in the main network society. Thus, to remove isolate or non-connected node from the main proposed graph we used a Matlab code as follows,

```
i=1;
for q=1:N
M =size(neighbors(G,q), 1);
if M<=1
K(i)=q;
i=i+1;
end
```

```

end
P1=size(K, 2);
N=N-P1;
names=compose('%d', 1:1:N);
G1=rmnode(G, K);
for s=1:N
    G2= rmedge(G1, 1:numnodes(G1), 1:numnodes(G1));
end
figure (2);
hold on
h=plot(G2, 'b','LineWidth',2, 'MarkerSize',6,'NodeColor','r' );

```

Figs. (2) and (3), indicate the generated random network and modified of presented network without unconnected and isolated nodes from main network.

Fig 2: Random network with 52 nodes.

Fig 3: Modified Random network.

3. Detecting influential spreaders effectively and efficiently

Identify the influential peoples or influential organizations effectively and efficiently can be helpful in controlling of spreading COVID-19. In this Section, we want to present a few methods to detect the influential nodes in the random networks. Identify influential spreaders in the complex networks is a big challenge up to now. We will present a large number of centrality indices such as degree centrality, closeness centrality, betweenness centrality, and eigenvector centrality to address this problem. In the following, we will have proposed the method for identifying influential nodes based on TOPSIS with new modified weights is proposed.

1.1. Node ranking using centrality measures

Centrality measures such as degree centrality (DC) [4], closeness centrality (CC) [5], betweenness centrality (BC) [6], and eigenvector centrality (EC) [7] have been proposed to identify the influential nodes within a graph and a complex network. Inverse sum of shortest distances from a focal node to all other nodes is define closeness centrality. Therefore, the high score of closeness centrality is for a node closer to the others. Betweenness measures the number of shortest paths through a node. As well as, eigenvector centrality is another way to identify influential nodes, which was introduced by Bonacich for first time [8]. In the eigenvector centrality method, importance of a node depends on not only the number of

neighbors but also the quality of the neighbors. Degree centrality (DC), closeness centrality (CC), betweenness centrality (BC), and eigenvector centrality (EC) are defined as follows,

a. Degree Centrality

The degree centrality (DC) of node i , denoted as $C_D(i)$ is defined as,

$$C_D(i) = \sum_{j=1}^N x_{ij} \quad (1)$$

where N is the total number of nodes, i is the focal node, j represents all other nodes, and x_{ij} represents the connection between node i and node j . If node i is connected to the node j , the value of x_{ij} is 1 and otherwise the value of x_{ij} is 0. By minimizing the number of intermediary nodes, the shortest path can be found in a binary network, and the minimum number of ties linking the two nodes either directly or indirectly define its length [4]. Binary shortest distance is defined as follows [9],

$$d(i, j) = \min_h (x_{ih} + \dots + x_{hj}) \quad (2)$$

where h is the number of intermediary nodes on paths between nodes i and j .

b. Closeness Centrality

The closeness centrality (CC) of node i , denoted as $C_C(i)$, is defined as follows,

$$C_C(i) = \left(\sum_{j=1}^N d_{ij} \right)^{-1}, \quad (3)$$

where d_{ij} denotes the distance between node i and node j .

c. Betweenness Centrality

The betweenness centrality (BC) of node i , denoted as $C_B(i)$, is defined as,

$$C_B(i) = \frac{N(N-1)}{2} \left(\sum_{k \neq i \neq l} \frac{p_{kl}(i)}{p_{kl}} \right)^{-1}, \quad (4)$$

where p_{kl} is the number of binary shortest paths between node k and node l , and $p_{kl}(i)$ is the number of those paths that go through node i . This formula $\frac{N(N-1)}{2}$ is used to normalize the betweenness centrality value.

d. Eigenvector Centrality

Let A be an $n \times n$ similarity matrix. The eigenvector centrality x_i of node i is defined as the i th entry in the normalized eigenvector belonging to the largest eigenvalue of similarity matrix A . Let n be the number of vertices and λ be the largest eigenvalue of matrix A then we have,

$$Ax = \lambda x, \quad x_i = \frac{1}{\lambda} \sum_{j=1}^n a_{ij} x_j, \quad i = 1, \dots, n \quad (5)$$

1.2. Node ranking using technique for order preference by similarity to ideal solution

Technique for order preference by similarity to ideal solution (TOPSIS) [10], developed in 1981 by Hwang and Yoon [11]. TOPSIS method is a ranking conception and application method in social network or complex network. The standard TOPSIS method choosing simultaneously that altogether have farthest distance from the negative ideal solution and shortest distance from the positive ideal solution. Maximizing the benefit criteria and minimizing the cost criteria is positive ideal solution, whereas minimizing the benefit criteria and maximizing the cost criteria is negative ideal solution.

Definition 1.2. Suppose $D = (x_{mn})$ be a decision matrix, which consists of criteria and alternatives. The decision matrix $R = (r_{ij})$ can normalize as follows,

$$r_{ij} = x_{ij} \times \left(\sqrt{\sum_{k=1}^N (x_{ik})^2} \right)^{-1}, \quad i = 1, \dots, N; \quad j = 1, \dots, m. \quad (6)$$

weighted decision matrix $A = (v_{mn})$ can be obtained by multiply the associated weights by the columns of the normalized decision matrix as follows,

$$v_{ij} = w_j \times r_{ij}, \quad i = 1, \dots, N; \quad j = 1, \dots, m. \quad (7)$$

where w_j is the weight for j criterion. In this paper we propose, the new weights as follows,

$$w_j = \frac{\sum_{i=1}^N r_{ij}}{\sum_{i=1}^N \sum_{j=1}^m r_{ij}}, \quad i = 1, \dots, N; \quad j = 1, \dots, m. \quad (8)$$

we define the positive-ideal solution and the negative-ideal solution as follows:

$$A^+ = \{v_1^+, \dots, v_n^+\} = \left\{ \left[\max_i (v_{ij}) \mid j \in K_b \right] \times \left[\min_i (v_{ij}) \mid j \in K_c \right] \right\} \quad (9)$$

$$A^- = \{v_1^-, \dots, v_n^-\} = \left\{ \left[\min_i (v_{ij}) \mid j \in K_b \right] \times \left[\max_i (v_{ij}) \mid j \in K_c \right] \right\} \quad (10)$$

where K_b and K_c are the set of benefit criteria and the set of cost criteria, respectively. The separation measures from the positive ideal and negative ideal solutions based on Euclidean distance respectively, can define as follows,

$$S_i^+ = \sqrt{\sum_{j=1}^m (v_j^+ - v_{ij})^2}, \quad i = 1, \dots, N; \quad j = 1, \dots, m \quad (11)$$

$$S_i^- = \sqrt{\sum_{j=1}^m (v_j^- - v_{ij})^2}, \quad i = 1, \dots, N; \quad j = 1, \dots, m \quad (12)$$

using the positive ideal and negative ideal solutions S_i^+ and S_i^- the relative closeness can calculate as,

$$C_i = \frac{S_i^-}{S_i^- + S_i^+}, \quad i = 1, \dots, N. \quad (13)$$

All nodes ranking according to the relative closeness to the ideal solution. It is mean that, the influential and higher priority nodes have higher C_i .

1.3. Example explanation

In this part, a simple example is given to explain how works the centrality measures. To generate a random graph with N nodes and removing the isolate or non-connected nodes from the proposed graph we use the written Matlab codes as showed in the Section (1). Fig. (4) shows the proposed modified random graph with removed of isolate and unconnected nodes from the basic random graph with number of nodes $N = 12$. The adjacency matrix for this graph based on the connected and unconnected nodes is as,

Fig 4: Random network with different degree, closeness and betweenness value.

$$adj = \text{Adjacency Matrix} = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 \\ 1 & 1 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}_{12 \times 12}$$

A decision matrix $D = (x_{ij})$ for the random graph (1) can be found by using the written Matlab code as follows,

<pre>function dm=decisionmatrix(adj) d=zeros(n,3); b=degrees(adj); for i=1:n d(i,1)=b(1,i);</pre>	<pre>function [deg,indeg,outdeg]=degrees(adj) indeg = sum(adj); outdeg = sum(adj'); if isDirected(adj) deg = indeg + outdeg; % total degree</pre>	<pre>function C=closeness(adj) C=zeros(length(adj),1); for i=1:length(adj); C(i)=sum(simpleDijkstra(adj,i)); end</pre>
---	---	--

```

end
cc=closeness(adj);
for j=1:n
    d(j,2)=cc(j,1);
end
bc=betweenness_bin(adj);
bc=bc';
%ec=eigenCentrality(adj);
for k=1:n
    d(k,3)=bc(k,1);
end
else % undirected graph: indeg=outdeg
    deg = indeg + diag(adj); % add self-loops twice, if
    any
end

```

and

```

function BC=betweenness_bin(G)
n=length(G); %number of nodes
I=eye(n)~=0; %logical identity matrix
d=1; %path length
NPd=G; %number of paths of length |d|
NSPd=NPd; %number of shortest paths of length |d|
NSP=NSPd; NSP(I)=1; %number of shortest paths of any length
L=NSPd; L(I)=1; %length of shortest paths
while find(NSPd,1);
    d=d+1;
    NPd=NPd*G;
    NSPd=NPd.*(L==0);
    NSP=NSP+NSPd;
    L=L+d.*(NSPd~=0);
end
L(~L)=inf; L(I)=0; %L for disconnected vertices is inf
NSP(~NSP)=1; %NSP for disconnected vertices is 1
Gt=G.';
DP=zeros(n); %vertex on vertex dependency
diam=d-1; %graph diameter
for d=diam:-1:2
    DPd1=((L==d).*(1+DP)./NSP)*Gt.*(L==(d-1)).*NSP;
    DP=DP + DPd1; %DPd1: dependencies on vertices |d-1| from source
end
%BC=sum(DP,1)/(n*(n-1)/2); %compute betweenness
BC=sum(DP,1); %compute betweenness

```

therefore, the decision matrix $D = (x_{ij})$ can be obtained as follows,

Table 1: Decision matrix $D = (x_{ij})$.

Degrees Centrality	Betweenness Centrality	Eigenvector Centrality
3	23	35
3	22	30
2	27	0
2	25	0
3	26	29
1	33	0
2	27	12
1	36	0
1	36	0
3	26	20
5	19	63
2	30	9

To obtain the decision matrix we used three centrality measures degree centrality (DC), betweenness centrality (BC), and eigenvector centrality (EC) which values of these have been shown in Table (1). We normalize the decision matrix by equation (6), and then the normalized decision matrix $R = (r_{ij})$ is derived as follows,

$$r_{72} = \frac{x_{72}}{\sum_{k=1}^N (x_{7k})^2} = \frac{27}{\sqrt{23^2 + 22^2 + \dots + 19^2 + 30^2}} = 0.2786 \approx 0.28,$$

$$R = \begin{bmatrix} 0.34 & 0.34 & 0.22 & 0.22 & 0.34 & 0.11 & 0.22 & 0.11 & 0.11 & 0.33 & 0.56 & 0.22 \\ 0.24 & 0.23 & 0.28 & 0.26 & 0.27 & 0.34 & 0.28 & 0.37 & 0.37 & 0.27 & 0.20 & 0.31 \\ 0.40 & 0.35 & 0.00 & 0.00 & 0.33 & 0.00 & 0.14 & 0.00 & 0.00 & 0.23 & 0.31 & 0.10 \end{bmatrix}^T$$

here, T is transpose of matrix R . We used the equation (8) to obtain weighted decision matrix $A = (v_{mn})$ as,

$$\begin{aligned} w_1 &= \frac{\sum_{k=1}^{12} r_{k1}}{\sum_{j=1}^3 \sum_{k=1}^{12} r_{kj}} = \frac{r_{11} + \dots + r_{121}}{(r_{11} + r_{12} + r_{13}) + \dots + (r_{121} + r_{122} + r_{123})} \\ &= \frac{0.34 + 0.34 + \dots + 0.22}{(0.34 + 0.24 + 0.40) + \dots + (0.22 + 0.31 + 0.10)} = \frac{3.1305}{8.8132} = 0.3552, \end{aligned}$$

$$w = \{0.3552, 0.3868, 0.2584\}, \quad a_{27} = 0.3868 \times 0.2786 = 0.1077 \approx 0.108$$

$$A = \begin{bmatrix} 0.119 & 0.119 & 0.079 & 0.079 & 0.119 & 0.039 & 0.079 & 0.04 & 0.039 & 0.119 & 0.199 & 0.079 \\ 0.092 & 0.088 & 0.108 & 0.099 & 0.104 & 0.132 & 0.108 & 0.144 & 0.144 & 0.104 & 0.076 & 0.120 \\ 0.104 & 0.089 & 0.00 & 0.00 & 0.086 & 0.00 & 0.036 & 0.00 & 0.00 & 0.059 & 0.0187 & 0.027 \end{bmatrix}^T,$$

to obtain the weighted decision matrix we used the new weights as showed in the equation (8).

The positive ideal and the negative ideal solutions are derived by using equations (9) and (10),

$$\begin{aligned} &\{\max_i(v_{ij}) \mid j \in K_b\} \\ &= \max\{0.1191, 0.1191, 0.0794, 0.0794, 0.1191, 0.0397, 0.0794, 0.0397, 0.0397, 0.1191, 0.1986, 0.0794\} \\ &= 0.1986. \\ &\{\min_i(v_{ij}) \mid j \in K_c\} \\ &= \min\{0.0917, 0.0877, 0.1077, 0.0997, 0.1037, 0.1316, 0.1077, 0.1436, 0.1436, 0.1037, 0.0758, 0.1196\} \\ &= 0.0397. \\ &A^+ = \{0.1986, 0.1436, 0.1872\}; \quad A^- = \{0.0397, 0.0758, 0.0\} \end{aligned}$$

from the positive ideal alternative and the negative ideal alternative based on the Euclidean distance the separation measures S_i^+ and S_i^- are calculated using equations (11) and (12), respectively as follows,

$$\begin{aligned} S_7^+ &= \sqrt{\sum_{j=1}^3 (v_j^+ - v_{7j})^2} \\ &= \sqrt{(0.1986 - 0.0794)^2 + (0.1436 - 0.1077)^2 + (0.1872 - 0.0357)^2} \\ &= \sqrt{0.0142 + 0.0013 + 0.0229} = \sqrt{0.0384} = 0.1961, \end{aligned} \tag{11}$$

$$\begin{aligned}
S_7^- &= \sqrt{\sum_{j=1}^3 (v_j^- - v_{7j})^2} \\
&= \sqrt{(0.0397 - 0.0794)^2 + (0.0758 - 0.1077)^2 + (0 - 0.0357)^2} \\
&= \sqrt{0.0016 + 0.0010 + 0.0013} = \sqrt{0.0039} = \mathbf{0.0622}, \\
C_7 &= \frac{S_7^-}{S_7^- + S_7^+} = \frac{0.0622}{0.0622 + 0.1960} = \frac{0.0622}{0.2582} = \mathbf{0.2408},
\end{aligned} \tag{12}$$

Table 2: Relative closeness to the ideal solution can result the nodes ranking.

Nodes	S_i^+	S_i^-	C_i	Ranking
1	0.1262	0.1318	0.5110	2
2	0.1380	0.1200	0.4651	4
3	0.2248	0.0509	0.1847	11
4	0.2262	0.0464	0.1701	12
5	0.1346	0.1205	0.4724	3
6	0.2458	0.0558	0.1851	10
7	0.1961	0.0622	0.2408	7
8	0.2455	0.0678	0.2164	9
9	0.2455	0.0678	0.2164	8
10	0.1557	0.1031	0.3983	5
11	0.0678	0.2455	0.7836	1
12	0.2013	0.0649	0.2439	6

4. Disease spreading probability in a network

In this Section, we study the disease spreading probability in a social network or complex network with quarantine of the infected important and influential nodes. With suppose, G as proposed graph, N as number of total nodes and E as number of influential nodes with top ranking, the spreading probability $P(G_j)$ for graph G_j can defined as follows,

$$\begin{aligned}
P(G_j) &= \frac{N - j + 1}{N} \times \frac{\sum_{k=1}^N \{Degree(G_j)\}}{\sum_{k=1}^N \{Degree(G_0)\}}, \quad j = 1, \dots, E; \quad G_0 = G, \\
P(G_1) &= \frac{12 - 2 + 1}{12} \times \frac{\sum_{k=1}^{12} \{2, 1, 1, 3, 0, 1, 1, 1, 2, 2\}}{\sum_{k=1}^{12} \{3, 3, 2, 2, 3, 1, 2, 1, 1, 3, 5, 2\}} = \frac{11}{12} \times \frac{14}{28} = \mathbf{0.4583}
\end{aligned} \tag{14}$$

Fig. (5) shows, the proposed random graph with $N = 12$ nodes and five first ranking nodes highlighted with green color. Fig. (6) indicates, probability of disease spreading in the presented network with removing infected five first ranking nodes step by step. We suppose disease spreading probability is 1 for the proposed graph network without removing any nodes. It represents the effective power of influential nodes in a social networks or complex networks. As seen from the disease spreading probability results, two first ranking nodes have much more effectiveness in the spreading of infection in the network compared with the next influential nodes.

Fig 5: Five top ranking nodes highlighted with green color in the proposed random network.

Fig 6: Probability of disease spreading in the network with removing infected first ranking nodes

5. Performance evaluation of ranking nodes with SI model

The Susceptible–Infected (SI) model [12] has been used to evaluation of ranking nodes performance [13]. By using SI model, can examine the spreading influence of top-ranked nodes. Fig. (7) show an SI model for epidemic disease transmission in a population of individuals who are at high-risk.

Fig 7: A schematic of SI model.

Mathematically the dynamic system for SI model can be shown as follows,

$$\begin{cases} \frac{dS}{dt} = -\lambda S \\ \frac{dI}{dt} = \lambda S \end{cases} \quad (1)$$

where, the infection rate, λ , depends on the transmission probability per partner ($\beta > 0$), the number of partners per individual per unit time ($r > 0$) and the proportion of infected individuals to sexually active individuals $\frac{I}{I+S}$ as follows,

$$\lambda = r\beta \frac{I}{I+S}.$$

In this system, the susceptible population in class S going to be infected with the infection rate λ . With using the initial conditions $S(0) = S_0$ and $I(0) = I_0$ analytical solutions of systems (1) are as follows,

$$\begin{cases} S(t) = S_0 e^{-\lambda t} \\ I(t) = S_0 + I_0 - S_0 e^{-\lambda t} \end{cases} \quad (2)$$

In the SI model, $S(t)$ represents the number of susceptible individuals and $I(t)$ denotes the number of infected individuals that are able to spread the disease to susceptible individuals. One randomly susceptible neighbor gets infected by each infected node with probability λ at each step. In this paper for uniformity we supposed infection rate $\lambda = 0.3$. Infection rate can determine the range which a node can exert influence in the epidemic spreading on networks. Here is a good example to explicate the multi-scale concept which an infected node can spread the disease to its higher order neighbors through the intermediaries not only to its immediate neighbors. Therefore, detection the influential nodes play an important role in spreading of an epidemic disease on networks. Figs. (8) and (9) show the population size vs time and vs infection rate, respectively during the infection spreading. In these figures, we supposed the initial susceptible and infected peoples as $S_0 = 32$ and $I_0 = 1$.

Fig 8: Population size vs time when $\lambda = 0.3$.

Fig 9: Population size vs infection rate λ .

6. Numerical analysis and validation

To illustrate the efficiency and practicality of the proposed method in controlling the spreading of epidemic disease in a social network we generate networks with large nodes number to evaluate the performance. Two network we used to evaluate the proposed method, (i): generated random network with 71 nodes, (ii): real e-mail network interchanges between members of the University Rovira i Virgili (Tarragona) [14]. Email network and random network have been used to compare the proposed method with basic method and DC, CC, EC methods. In Email network, the information flows by means of walks. In this paper, a large number of centrality measures and their applications have been proposed for detecting important nodes. All those methods have some restrictions and drawbacks and all of them focused on only one centrality measure. The information flows are essential in order to identify the influential nodes in a network. In the different networks with the different information need to use the different types of centrality measures as pointed by several authors [4-7]. Fig. (10) show the flow chart of the proposed method. The generate random network using Matlab code is shown in the Fig. (11), and top-10 ranked nodes highlighted as green color. The lists

of top-10 influential nodes for random network and Email network are given in Table (1) and Table (2), respectively. In random network, comparing with the proposed method and basic method or BC, there are ten same members with different ranking in the top-10 lists. For proposed method, *Node 61* > *Node 10* but for basic TOPSIS method *Node 10* > *Node 61*. Performance evaluation of ranking nodes with SI model shows that *Node 61* > *Node 10* and the proposed method has been act worthy compared with basic TOPSIS method and BC method (see Fig. (12)). According to Figs. (13) and (14), *Node 60* > *Node 61* > *Node 32*, therefore the proposed method works capable compared with CC and DC methods. As seen from Figs. (15), (16), (17) and (18), *Node 42* > *Node 76*, *Node 41* > *Node 578*, *Node 76* > *Node 233* and *Node 42* > *Node 578*, the proposed method works proper compared with the basic TOPSIS method. Results of Fig. (19) and Fig. (20) show that *355* > *Node 21* and *42* > *Node 355*, and this mean that the proposed method operates competent compared with the DC and BC methods.

Table 1. The top-10 ranked nodes by the proposed method and basic TOPSIS method, degree centrality (DC), closeness centrality (CC), betweenness centrality (BC) in random networks with 71 nodes.

Rank	DC	CC	BC	Basic TOPSIS Method	Proposed Method
1	61	32	60	60	60
2	60	44	26	26	26
3	39	24	10	10	61
4	26	19	61	61	10
5	22	48	8	8	8
6	10	5	39	39	39
7	8	52	63	67	67
8	71	6	67	22	22
9	70	36	38	38	38
10	67	42	22	63	63

Table 2. The top-10 ranked nodes by the proposed method and basic TOPSIS method, degree centrality (DC), betweenness centrality (BC) in the network of e-mail interchanges between members of the University Rovira i Virgili.

Rank	DC	BC	Basic TOPSIS Method	Proposed Method
1	105	333	105	105
2	333	105	333	333
3	42	23	23	23
4	23	578	76	42
5	16	76	578	41
6	41	233	233	76
7	196	135	41	233
8	233	41	42	578
9	76	355	135	135
10	21	42	355	355

Fig 10: The flow chart of the proposed method.

Fig 11: Random network with top-10 ranked nodes

Fig 12: Comparison of infected nodes between Node 61 and Node 10.

Fig 13: Comparison of infected nodes between Node 60 and Node 32.

Fig 14: Comparison of infected nodes between Node 60 and Node 61.

Fig 15: Comparison of infected nodes between Node 76 and Node 42.

Fig 16: Comparison of infected nodes between Node 578 and Node 41.

Fig 17: Comparison of infected nodes between Node 233 and Node 76.

Fig 18: Comparison of infected nodes between Node 578 and Node 42.

Fig 19: Comparison of infected nodes between Node 355 and Node 21.

Fig 20: Comparison of infected nodes between Node 355 and Node 42.

7. Conclusion

In this paper, we showed that the important and influential nodes are very efficient in controlling spreading of COVID-19. In the follows, we showed that quarantine of important and influential nodes or consider of health protocols by efficient nodes is very helpful and effective in the controlling of epidemic COVID-19 in a complex network. Also, the obtained spreading probabilities of epidemic disease using new proposed formula showed the importance of quarantine of important nodes in a society network. Therefore, identifying influential nodes in a social network or complex networks is the very significant part. To find the influential nodes we used a modified TOPSIS method with a new formula to obtain the efficient weights. Different centrality measures as the multi-attribute of complex network in the TOPSIS method has been used. The SI model was applied to figure out the performance and efficiency of the proposed methods.

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Figures

Figure 1

Structure of respiratory syndrome causing human coronavirus [1].

Figure 2

Random network with 52 nodes.

Figure 3

Modified Random network.

Figure 4

Random network with different degree, closeness and betweenness value.

Figure 5

Five top ranking nodes highlighted with green color in the proposed random network.

Figure 6

Probability of disease spreading in the network with removing infected first ranking nodes

Figure 7

A schematic of SI model.

Figure 8

Population size vs time when $\lambda = 0.3$.

Figure 9

Population size vs infection rate λ .

Figure 10

The flow chart of the proposed method.

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