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SOCIAL CONTACT NETWORK BASED EPIDEMIC CONTROL SCHEME IN WIRELESS BODY AREA NETWORK

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***Abstract*— Social contact information on social networks increased in recent days because of technology development. Controlling of epidemic disease is more complicated and difficult task for large population density areas. In addition it is a challenging to find a people who affected with this epidemic disease in large scale populated areas. The traditional offline based epidemic control schemes not effectively produce output since it insufficiently gathered such social contact and health information. However, our proposed wireless body area network can be sufficiently produced an output for large population and scalable when the population increases. In our proposed work we are going to split the population in number of clusters based on their location area and social contact information. For cluster the users location we use fuzzy c means clustering algorithm and we also provide support for inter cluster and intra cluster communication Our proposed work can able to with stand in both intra and inter cluster epidemic control critical node and cluster identification processes. In that we identify the critical node in intra cluster through Intra-cluster critical nodes identification algorithm. After that our proposed mechanism (Critical clusters identification algorithm) identifying the critical clusters. Finally those critical nodes and clusters are removed from the cluster and network to reduce disease spreading ratio. Our proposed N Threshold voting method is applied for finding the nodes whose information is missed from the cluster.**

***Keywords*— Clustering, Fuzzy C- means, Epidemic Control, Wireless Body Area Network.**

I.INTRODUCTION

A Body Area Network is formally defined by 802.15 as, a communication standard optimized for low power devices and operation on, in or around the human body (but not limited to humans) to serve a variety of applications including medical, consumer electronics / personal entertainment and other. BANs are highly localized wireless networks that can potentially support a variety of medical applications, from tracking vital signs to monitoring the functioning of implants and performing state-of-the-art endoscopic exams. Traditional patient monitoring consists of physiological sensors connected between a patient's body and a dedicated signal processing unit located nearby through unwieldy wires.

Those wires limit the patient's mobility and comfort, and some studies suggest they can be a source of in-hospital infections. Moreover, motion artifacts from the connected wires can negatively affect the measured results. A network of sensors is placed on or close to the surface of the patient's body or implanted statically into tissue to enable the collection of specific physiological data. Such an arrangement allows for the continuous monitoring of a patient's health regardless of the person's location. Sensed signals can be those for electroencephalography (EEG), electrocardiography (EKG), electromyography (EMG), skin temperature, skin conductance and electro oculography (EOG). Each of the sensors transmits collected information wirelessly to an external processing unit, located on the patient or at the patient's bedside.

The processing unit can then use traditional data networks, such as Ethernet, Wi-Fi or GSM, to transmit all information in real-time to a doctor's device or a specific server. The sensors used in a BAN generally require accuracy for their physiological parameter of interest and a certain level of low-power signal processing as well as wireless capability. The advantage is that the patient doesn't have to stay in bed, but can move freely across the room and even leave the hospital for a while. This improves the quality of life for the patient and reduces hospital costs. In addition, data collected over a longer period and in the natural environment of the patient, offers more useful information, allowing for a more accurate and sometimes even faster diagnosis.

II.RELATED WORKS

Cluster based epidemic control requires effective clustering approach. The clustering methods for network graph have been studied in the literature. proposed a criterion to combine internal density with external sparsity for social network clustering. DP-cluster algorithm based on the distance-preserving subgraphs, which finds the proper distance preserving subgraphs and partitions a graph into an arbitrary number of distance-preservingsubgraphs. However, these methods do not consider node's location and their attributes at the same time and thus are not applicable to the epidemic control applications.position cluster model (LPCM) for social network clustering method. LPCM clusters the social network based on nodes's locations and the probability of a social contact between two nodes, but it ignores the attributes of nodes such as gender, age, occupation and others that are related with epidemics. In this paper, we study a clustering approach that can consider both social relations and divergence (i.e., infection state) of nodes. On the other hand, the spread of epidemic disease has been investigated for many years. The modelings of epidemics are used to describe the mechanisms of disease spreading and predict the spread of the epidemic and evaluate the epidemic control strategies. An SIR model is widely used to characterize the epidemic spread for a fixed population. The compartments used in the SIR model are susceptible, infected and recovered models the epidemic and gives the threshold of the epidemics. However, it is designed based on the homogeneous population and does not consider the diversity of individuals. The spread of epidemic on social networks the spread of epidemic in social networks, but they ignore the fact that the epidemic spreads through physical contact rather than traditional social relationship represented by the social networks such as Facebook and Twitter. Therefore, these model-based approaches have too idea statistical assumption about the dynamics of social contact networks, and thus might not provide effective epidemic control. Graph partitioning is an NP hard problem for numerous applications. Some algorithms have been proposed to divide the graph into several small clusters. The scheme allows applications to find small edge separators.

The authors in proposed a multilevel algorithm to partition graphs which are approximated by a sequence of increasingly smaller clusters. In the graphs, the number of links between clusters is minimized. A general framework of graph clustering is proposed , which balances the overlapped clusters and minimizes the sum of computational and communication time. A K-way partitioning algorithm is which reduces the size of the graph by collapsing vertices and edges. The above algorithms can divide a graph into smaller clusters by minimizing the links between clusters. These algorithms could be potentially used for solving the epidemic control problem. In this paper, the algorithm we proposed is to find the smallest separator node set to divide the graph into small clusters, which minimizes the correlations between clusters and thus is suitable for cluster-based epidemic control. It is widely accepted that the most efficient epidemic control strategies are based on high-degree targeted strategies By quarantining or immunizing the high-degree nodes, the network breaks down to smaller clusters, and then the epidemic spreading can be contained. To further improve the performance of epidemic control, a novel unequal graph partitioning algorithm called UGP is proposed in the paper. The details of the UGP methods are introduced in the following section.

III.SYSTEM REPRESENTATION

3.1 Framework

The framework of the proposed system includes two steps. At the first step, the critical network (i.e., population) is clustered to many small groups based on their locations and social contacts Vital signs and social interaction information collection. cluster based epidemic control will be implemented, which includes critical node identification, critical set identification and an unbalanced graph partitioning

method. The social sensing detection in this paper is to find physical social contact pattern. Our study is focused on the collections of physical social interactions (e.g., face-to-face interactions) which may cause epidemics spreading. The social information from traditional social networks could be helpful for detecting social ties among people. However, the information is different from the one obtained from the social sensing in the proposed scheme. In the proposed system, a social contact network graph called critical network in our previous work is employed to collect the vital signs and social

interaction information. The research in this paper is based on the data collection framework and the focus is on finding effective epidemic control strategies. The proposed algorithm runs on the critical networks which can quickly capture the critical epidemic information in different environments.

The detail of critical network definition can be refereed to our previous study Basically, the elements of a critical network are nodes, arcs, and a series of planes. A node represents a user of the data collection system. Each node can be white, gray, or black. White nodes denote people who have never been infected and are healthy Gray nodes denote people who were infected but now have already been recovered; black nodes denote people who are infected and have not been recovered yet. An arc between two nodes represents the infection relationship; the node pointed by the arc is infected by the one that originates the arc. We also define weights on each arc to indicate how much in terms of possibility the node at the tail of the arc is infected by the one at the head of arc. A

plane represents the above information during one time period unit. Planes are also called snapshots of a critical network. The proposed epidemic control strategy includes two major stages as discussed in the following:

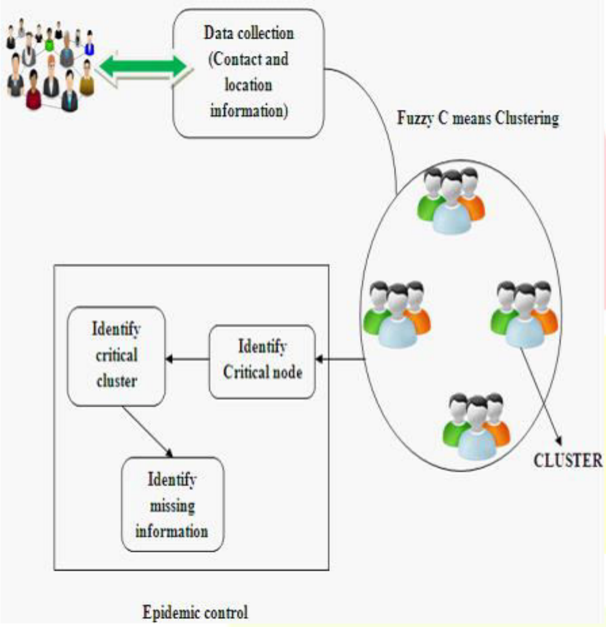

Fig. 1. Social interaction information collection

The first step: Clustering. The population represented in critical network is divided into clusters based on their location

and attribute similarities. The goal of this division is to partition the graph into k clusters with short mean distance and homogeneous attribute values. The problem is quite challenging because their location and attribute similarities

are two independent objectives we pursued. For the network

model accounts both observed attributes and euclidean distance between vertices vi and vj.

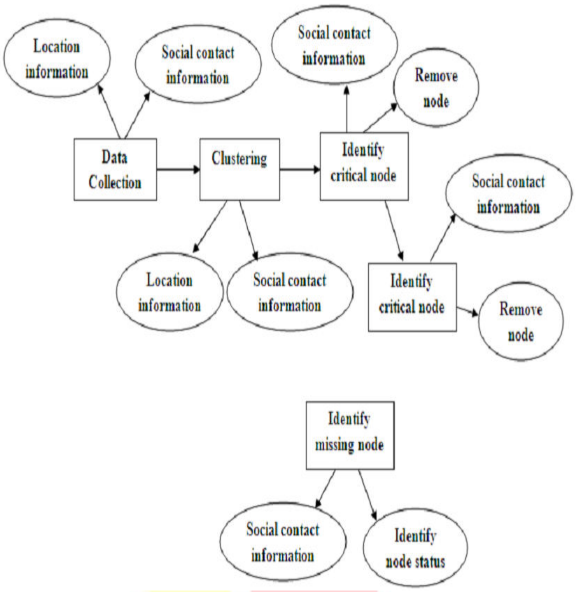

Fig. 2. System framework.

3.2 Node Formation:

First we have to forms the node to transmit and also receive the packets in the WBAN. Here, we can set more number of nodes for clustering and sending and receiving the packets from sender to receiver. Here we form 50 nodes for processing. The node formation is the first step of our process. In which nodes are added in to the network. The nodes are in mobile nature. The nodes are free to move.

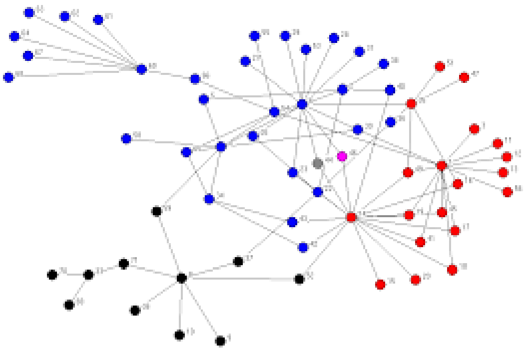

Fig.3. Node Formation

3.3 Clustering:

Next, process is to clustering the nodes. In clustering process the nodes presented in the network can be grouped. Here, we are grouping the moving nodes. The moving nodes are grouped and again it can be moved to some other locations. According to the movement of the nodes and it social contact information it can be grouped with every node in the network. The newly created grouping details are updated in the network. The infected nodes are grouped with the help of fuzzy c means clustering algorithm which balances the overlapped clusters and minimizes the sum of computational and communication time.

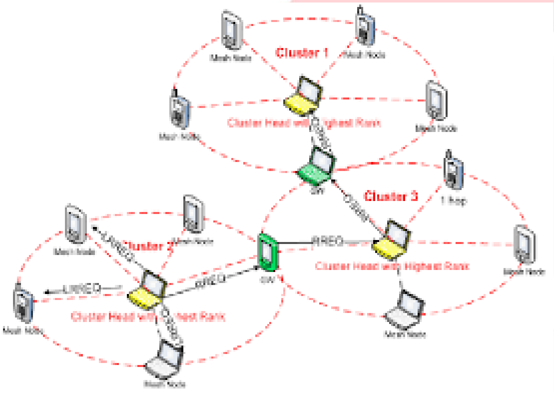

Fig.4. Clustering

3.4 Critical node identification:

Critical node identification process takes place within the cluster that means it happens in intra cluster. In this process the most affected node within the cluster is removed from that particular cluster. It is possible to reduce who will be more or less likely to be infected in some future time can be detected. First the number of infected nodes and recovered nodes in the network can be detected. Add that infected nodes in the critical node set. After that we can remove all the possible critical nodes from the cluster. For removing those nodes we are using Intra-cluster critical nodes identification algorithm.

3.5 Critical cluster identification:

The major idea of epidemic control is to identify the critical clusters and to remove the links among clusters. In this method each cluster is viewed as a node. The infected cluster is removed by using critical clusters identification algorithm. In that the probability that a social contact information between two clusters are identified .

First According to their social contact information that clusters is removed from the network. Here the edge and distance between the two clusters are identified for removing cluster.we use algorithm as given below. Logically, if the infection possibility for each individual is available, it is highly possible to deduce whom will be more (or less) likely to be infected in some future time. First, the number of infected nodes at the next time moment can be predicted by using the epidemic spread model. As long as the social contact information and vital signs (i.e., infectedstatus) are available, the potential infected nodes at the next time moment are predictable.Epidemic spreading. Let s(t), I(t),R(t), respectively denote the number of susceptible nodes, infective nodes and recovered nodes at the time t, and suppose that at time t = 0 these numbers are given by S(0) = n –m, I(0)= m and R(0)= 0.

We use the a typical q-influence model to describe the epidemic spreading. It has been often used to simulate the spread of computer virus in computer network and spread of epidemic diseases in social network q-influence model, a susceptible node could be infected by one of its neighbors with a fixed probability of q. In the model, the influences from its neighbors are independent. Suppose that a susceptible node vi has n neighbors and m of them are infective nodes, the probability that the node will be infected by its infective neighbors .

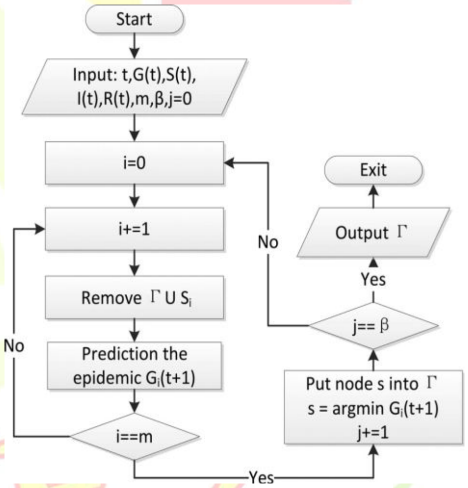

Fig. 5.Critical clusters identification algorithm.

3.6 Missing node identification:

This is the final module of our proposed system in that the node not give their privacy information is identified. Since, privacy issue is critical for data collection, the infected person may not want to share their vital sign health information with others due to their privacy concerns. Our proposed system can accurately estimate the status of the unknown nodes. In our concept the unknown nodes information can be collected by the neighboring nodes to check their health status. The N threshold voting algorithm is working well for identifying the infected nodes information from their neighbors.

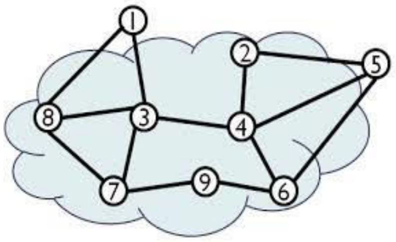

Fig.6. missing Node Identification

The major idea for inter-cluster control is to identify the critical clusters and to remove the links among clusters. Under the limited medical resources, we want to identify the most significant clusters to be isolated so that the

spread of epidemics can be effectively contained. The inter-cluster method is similar to the intra-cluster epidemic control method. In this method, each cluster is viewed as a node. Comparing to the critical nodes identification number of nodes in mth cluster. If node vi is in mth cluster and node vj is in nth cluster, the probability that a social contact exist between vertices vi and vj . Suppose that the mth cluster Cm and the nth cluster consist of Nm and Nn nodes, respectively, then the probability that a social contact exists between clusters Cm and Cn is defined to be the mean value of all edge probabilities between the two clusters. The inter-cluster critical node identification algorithm is described .where Em;n and Dm;n are the edge and distance between the m and the nth clusters, respectively.and t in the network presented in Object u is co cited by s and t. This co-citation is represented by two edges (s,u) and (t,u). However, unable to send a flow from s to t along the two edges, unless reverse the direction of the edge (t,u) to (u.t). Therefore, construct a doubled network by adding to every original edge in G a reversed edge whose direction is opposite to the original one.

IV CLUSTER-BASED EPIDEMIC CONTROL THROUGH WBAN

cluster-based epidemic control includes two tier control: intra-cluster and inter-cluster control.

4.1 INTER – CLUSTER CONTROL:

The major idea for inter-cluster control is to identify the critical clusters and to remove the links among clusters. Under the limited medical resources, we want to identify the most significant clusters to be isolated so that the spread of epidemics can be effectively contained. The inter-cluster method is similar to the intra-cluster epidemic control method. In this method, each cluster is viewed as a node. Comparing to the critical nodes identification. A case for epidemic spreading. algorithm above, the critical clusters identification algorithmcontains a set of big “nodes”. In addition, the information of some nodes may not available due to several reasons, such as privacy concerns, failure of the device, and even people who are infected turn off the WBANs to escape from quarantining. Thus, it is important to accurately estimate the status of the unknown nodes. We proposed to use the social contact information of a node’s neighbor to estimate its health status .The information of two nodes, A and B, are lost. We need to estimate the status of the two nodes to fully understand the spread of endemic disease. It is easy to use an N-threshold voting method to classify the center node. By the N-threshold, a node is infected when last least N of its neighbors are infected. Suppose we set the threshold N ¼ 3, then node A is estimated not infected and B is infected, because A only has two infected neighbors but B has four infected neighbors. Although the N-threshold voting method works well, it is sensitive to the number of neighbors. In the proposed social contact network, we use a local majority estimation method, by which an unknown node is infected if over h fraction of its neighbors are infected. Compared with the above Nthreshold voting method, the threshold number of nodes in majority varies automatically according to the number of neighbors the unknown nodes have.

4.2 INTRA- CLUSTER CONTROL:

The goal of intra-cluster control is to remove minimal number of nodes in a cluster so that the epidemic spread within the cluster can be effectively contained. Intra-cluster critical nodes identification algorithm is designed based on the q-influence model. It will be easy to extend our model to other typical epidemic models. The focus of the algorithm is to find a set of critical nodes to be removed to minimize the overall number of infected nodes within a specified time period T. Logically, if the infection possibility for each individual is available, it is highly possible to deduce whom will be more (or less) likely to be infected in some future time. First, the number of infected nodes at the next time moment can be predicted by using the epidemic spread model. As long as the social contact information and vital signs (i.e., infected status) are available, the potential infected nodes at the next time moment are predictable. The proposed intra-cluster critical nodes identification algorithm works as follows.

(i) The inputs of the algorithm are current time t, network graph Gt, susceptible nodes S(t), infective nodes I(t), recovered nodes R(t), and the isolation (i.e., immunization or treatment) capability b. n is the number of individuals in the network and k is the number of infected individuals. Then, we initialize the variables to

(ii) Remove one infected node from the network and predict the epidemic spread at the next time and then remove the infective nodes one by one to get a set of predicted infective nodes at the next time In the process, a critical nodes is the one that leads to minimized number of infective nodes after it is removed.

(iii) Put the critical nodes into the critical nodes set G and increase the count of critical nodes by Check whether the algorithm has found all critical nodes. If j < b, set and the algorithm goes to. Otherwise, the algorithm outputs the critical nodes set G and exits.

VI.CONCLUSION AND FUTURE WORKS

6.1 Conclusion

This paper discussed with the fuzzy based clustering algorithm which is used for epidemic control. This epidemic control mechanism is applied with the help of social contact information between infected persons and their physical location. In our proposed system we group the infected nodes into a number of clusters. From the cluster we identify the critical node and critical cluster by using different algorithms. Our proposed system is also applicable for identifying and collects the missing node's current status information. Since, there is a possibility to disease spreading from the lost node. Some potential statistical estimation algorithms such as missing data estimation algorithms could be applied to mitigate the impact of the unavailability of the information. Finally our simulation result proves that our proposed system reduces computational complexity and reduces data collecting time which also reduces time delay.

6.2 Future Enhancement

The missing data estimation algorithms impact of the unavailability of the information which would be the part of our future studies. In future we improve our research for missing node identification process. It should accurately identify missing nodes current status and their physical location information. Finally our simulation result proves that our proposed system reduces computational complexity and reduces data collecting time which also reduces time delay.

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