

DETECTING RATE OF RECOVERY IN EPIDEMICS THROUGH MODIFIED LV METHOD THROUGH SINK NODES

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ABSTRACT

The infectious diseases are common now days. These infections are generally happens because of diets that human being takes now days. Once the infection happens to a person then there could be several ways by which that infection is spread to multiple persons. The community algorithm can be used in order to analyze the behavior of the disease expansion within the community. The wwcommunity overlapping mechanism can be enforced to suggest the rate at which cure must be spread so that epidemics can be rectified. The immune system will become feeble and hence the

persons will be infected quickly. The persons in the simulation will be represented in the form of nodes. The overall representation will be represented in the form of graph. The algorithm to detect unaffected person is LV algorithm with sink node consideration. The proposed algorithm performs better as compared to simple LV algorithm.

Keywords

Infection, Diseases, Population, Infection Person, Immune System, Rate. LV, Sink Node.

1. INTRODUCTION

The epidemics describe way by which disease spread between the communities. It is possible that disease spread from one community to another. The reason for extension is slow recovery rate. It is also a possibility by which recovered person again is infected from the disease. All of these possibilities will be tackled in the proposed paper. The prime reason for the spread of disease is rate at which recovery is suggested. The proposed algorithm modifies the existing LV algorithm. The sink nodes which are unaffected will be detected through the proposed technique.

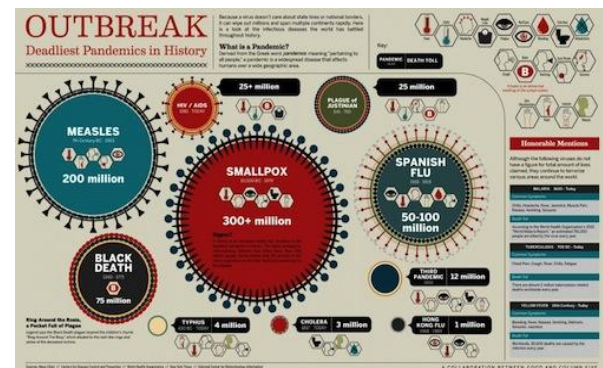


Fig 1: Showing the Epidemics in terms of various diseases
The outbreak of these diseases is primarily due to lack of awareness between the community and the lack of cure mechanism implemented. The proposed system suggests the rate at which the cure should be given to avoid circumstances of epidemics. The infection will spread within the population which will not allow the persons to recover from the infection since the rate of spread is very high. It will spread from few to many for the matter

of few days. The figure below shows the spread of infection to the community from the infected agent.

1.1 RELATED WORK

The work has been done toward the analysis of the infection and diseases which spread very quickly among the population. (1) Many real networks are characterized by overlapping community structures in which vertices may belong to more than one community. In this paper, we propose a network model with non-overlapping community structure. The analytical and numerical results show that the connectivity distribution of this network follows a power law. We employ this network to investigate the impact of non-overlapping community structure on susceptible-infected-susceptible (SIS) epidemic spreading process. The simulation results indicate that significant non-overlapping community structure results in a major infection prevalence and leads to a peak of the spread velocity in the early stages of the emerging infection. (2) In this work we study diffusion in networks with community structure. We first replicate and extend work on networks with non-overlapping community structure. We then study diffusion on network models that have overlapping community structure. We study contagions in the standard SIR model, and complex contagions thought to be better models of some social diffusion processes. Finally, we investigate diffusion on empirical networks with known overlapping community structure, by analyzing the structure of such networks, and by simulating contagion on them. We find that simple and complex contagions can spread fast in networks with non-overlapping community structure. We also find that short paths exist through non-overlapping community structure on empirical networks. (2) Many real-world networks exhibit community structure where vertices belong to one or more communities. Recent studies show that community structure plays an important role in epidemic spreading. In this paper, we investigate how

the extent of overlap among communities affects epidemics. In order to experiment on the characteristic of overlapping communities, we propose a rewiring algorithm that can change the community structure from overlapping to non-overlapping while maintaining the degree distribution of the network. We simulate the Susceptible-Infected-Susceptible (SIS) epidemic process on synthetic scale-free networks and real-world networks by applying our rewiring algorithm. Experiments show that epidemics spread faster on networks with higher level of overlapping communities. Furthermore, overlapping communities' effect interacts with the average degree's effect. Our work further illustrates the important role of non-overlapping communities in the process of epidemic spreading. (4) This paper studies the overlapping community effect in the spread of the infectious disease in the population. The overlapping of community may cause the spread of the infection from one community to another. (5) This paper presents the comparison of the various techniques like SIS, SISR etc which are used for the detection of the epidemic. The fast growth of the infection will be detected using this model. (6) Community detection in inhomogeneous structured network is an attractive research problem that searches for methods to discover groups in which individuals are more densely interconnected with each other with higher probability of internal information propagation. While most of the previous approaches attempt to divide networks into communities according to the algorithm results of network or edge measurement, Label Propagation Algorithm (LPA) adopts semi-supervised machine learning and implements community detection in an intelligent way with the automatic convergent process of network entity label iteration. In this work, (2,3,7-16) we study the early community detection approaches, explore the low efficacy and stagnant converging rate of LPA in its response to network with overlapped

communities, and propose a new approach for community detection using epidemic spreading virus to discover groups with super positioned members. Extensive experiments in synthetic signed network and real-life large networks derived from Internet social media are conducted to explore the optimal mechanism of the most suitable community-detecting virus infection.

1.2 RESEARCH GAP

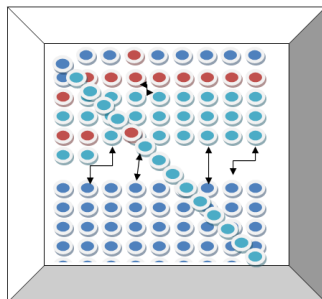
From the study of the above papers we conclude that the epidemics have been studied without the concentration on rate at which recovery must take place to make the infection growth slow. So in the proposed model we will study the rate at which recovery must takes place so that epidemic can be slow down or terminated.




2.1 PROPOSED SYSTEM

The proposed system utilizes the modified LV algorithm in which only sink nodes are considered. These nodes are unaffected nodes. The rate at which the disease spread within the community will be estimated by looking at the unaffected node. The rate of disease spread if given by α and rate of cure if given by β then $\alpha < \beta$ in order for recovery to take place within the community. The modified LV algorithm will use equation 1 of rate suggestion

$$rate = abs(n * \alpha - n * \beta) \quad Eq-1$$

The proposed model is described as



The  describes infected Nodes  shows the suspicious nodes  shows infection free nodes
Arrow heads indicates that the nodes are infected by the infected nodes and the nodes are shifting from safe to infected categories.

The algorithm will suggest the rate and also discover the agents which are yet uninfected. The proposed algorithm will be as follows

2.2 LV with Sink node detection

- a) Obtain Adjacency(A)=Adj(G)
- b) Set i=1
- c) Repeat while i<=n
- d) Check Adj_i
- e) If(Adj_i==0)
- f) Accept the node(AC_i)=N_i
- g) Else
- h) Reject the node
- i) End of if
- j) Move to the next node
- k) I=i+1
- l) End of loop
- m) Calculate Modularity(Q) from eq 1

The proposed algorithm will use the modularity equation of neuman indicating the community separation in multiple communities.

$$Q = \frac{1}{4m} \sum_{ij} (A_{ij} - \frac{k_i k_j}{2m})(s_i s_j + 1) \quad Eq-1$$

3. SIMULATION AND RESULTS

The simulation is conducted in MATLAB and results are obtained through the simulation. Results are generated and represented in terms of tabular structure and plotted through the graphs.

Parameters	Simple LV Method	LV with Sink node	K-clique
Execution Speed(us)	1.768	1.987	0.383
Recovery Rate (us)	N.A	5.432	2.432
Sim 1	N.A	6.342	3.322
Sim 2	N.A	5.325	3.423
Sim 3	N.A	4.345	3.544
Sim 4	N.A		
Sink Nodes	0	20	10

Detected(100 nodes graph)			
Modularity(Q)	2.345	5.523	3.553

Table 1: Showing the parameter values obtained from the simulation

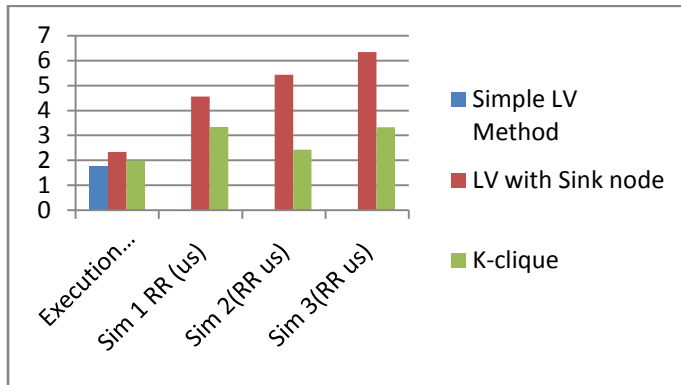


Fig 3: Showing the result of simulation

The simulation describes that LV with sink node is better as compared to previous LV method.

4. Conclusion

The study of the Modified LV algorithm suggests that the result will improve by eliminating the sink nodes from the graph. The adjacency matrix where value greater than 1 is placed is considered. The comparison table also indicates that the LV method with sink node will give least results as the sink nodes are considered. Detection mechanisms are many. We highlighted the methods and also described which method is useful in detecting the cliques. The Modified LV with sink node is one of the simplest methods for the detection of the overlapping community detection. This method is modified in the proposed work by considering sink nodes.

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