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International Journal of Current Research
Vol. 8, Issue, 05, pp.30962-30964, May, 2016

INTERNATIONAL JOURNAL
OF CURRENT RESEARCH

ISSN: 0975-833X

RESEARCH ARTICLE

ANALYZING TECHNIQUES USED TO DETECT DISJOINT COMMUNITY IN EPIDEMICS

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ARTICLE INFO

Article History:
Received 04th February, 2016
Received in revised form
15th March, 2016
Accepted 01st April, 2016
Published online 10th May, 2016

Key words:
Infection, diseases,
Population, Infection agent,
Immune system, rate.

ABSTRACT

The infectious diseases are common now days. We catch these infections easily because of unbalanced diets that human being takes. Once person catches infectionthere are several ways by which that infection is spread to multiple persons. When infection is considered then there must be some infection agent and population. The infection agent will be responsible for passing the infection to the population. The infection separations will also depend upon the immune system of the human within the population. In the proposed paper we will study the rate at which the recovery of the human from the infection takes place and also the rate at which infection spread.If the rate of infection spreading is higher than whole of the population will be infected. So the proposed paper studies the rate at which recovery must happen so that population can recover from the infection. This paper present the comparison among various techniques used to detect the disjoint communities in epidemic networks.

Citation: Mini Singh Ahuja and Jobanpreet Singh, 2016. "Analyzing techniques used to detect disjoint community in epidemics", *International Journal of Current Research*, 8, (05), 30962-30964.

INTRODUCTION

The term epidemics refer to as increase in the spread infection beyond the certain level which is not expected. 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 in matter of few days. The figure below shows the spread of infection to the community from the infected agent (Chen *et al*., 2012). There exist legions of schemas which are used in order to disclose the disjoint communities in epidemics. The diseases are common and spreading fast in the community. Disclosure and prevention will be the target of the schemed mechanism. This paper suggests the various algorithmswhich are used to detect disjoint communities in epidemics networks (Reid *et al*., 2011).

Greedy Schema

This method is essentially a fast implementation of a previous technique proposed by Newman. Starting from a set of isolated nodes, the links of the original graph are iteratively added such as to produce the largest possible increase of the modularity of Newman and Girvan at each step. The fast version of Clauset, Newman and Moore, which uses more efficient data structures, has a complexity of O (N log2 N) on sparse graphs (Shang *et al*., 2015).

The GREEDY schema is a snap, efficient and easy-to-implement schema for diagnosing communities in massive networks. The schema has been worn with prosperity for networks of much divergent type and for sizes up to 100 million nodes and billions of links. The analysis of a symbolic network of 2 million nodes takes 2 minutes on a standard PC. The channel unveils hierarchies of communities and concedes zooming within communities to discover sub-communities, sub-sub-communities, etc (Reid and Hurley, 2011).

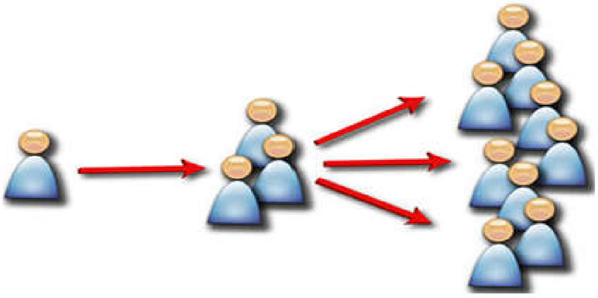

Fig. 1. Showing the spread of infection within the population from infection agent

It is today one of the utmost widely used schema for disclosing communities in large networks. The mechanism produces best result when huge network is used. The schema is a greedy gain schema that attempts to optimize the "modularity" of a partition of the network. The gain is performed in two steps. First, the

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schema looks for "small" communities by enhance modularity provincially. Second, it bulk nodes concerning to the clone community and constitution a new network whose nodes are the communities. These mechanisms are imitated iteratively until a maximal of modularity is acceding and a hierarchy of communities is produced. Although the exact computational complexity of the schema is not known, the schema seems to run in time O(N log2N) with utmost of the computational effort spent on the accretion at the first level. Exact modularity accretion is known to be NP-hard (Shang *et al.*, 2015). The stimulation for this schema of community disclosure is the accretion of Modularity as the algorithm progresses. Modularity is a hierarchy value which lies between -1 and 1. It measures the density of edges inside communities to edges in extraneous communities. Optimizing this value produce results in the best possible grouping of the nodes of a given network (Shang *et al.*, 2014). However going through all possible repetition of the nodes into assortment is impractical so heuristic algorithms are used. In the Louvain Schema of community disclosure, first small communities are found by optimizing modularity provincially on all nodes, then each small community is grouped into one node and the first step is imitated. The dendrogram indicates the results given by this algorithm (Shang *et al.*, 2014).

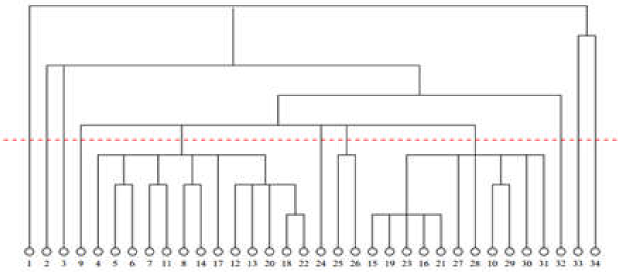

Fig. 2. Dendrogram predicting community

Label/Stamp Propogation

Within complex networks, real network tends to have community structure. Label propagation algorithm is used to finding communities. In comparison to others Label propagation algorithm has advantages in its running time, amount of prior information needed about network. But it has one disadvantage that it produces no unique solution (Singh and Ahuja, 2015).

Algorithm: Each node is initialized with unique label later on label diffuse through network based on the label that neighboring nodes possess. Consequently, densely connected group reach a common label quickly. When many such dense group are connected throughout network, they continue to expand outward until, it is possible to do so (Singh and Ahuja, 2015)

This process is in 5 steps:

1. Initialize labels at all nodes in network for given node X, C_x (0) =X.
2. Set t=1.
3. Arrange nodes in network in random order and set it to X.
4. For each x belongs to X chosen in specific order, Let $C_x(t)= f(C_{xi1}(t), C_{xim}(t), C_{xi(m+1)}(t-1), C_{xk}(t-1))$. F here returns label occurring with highest frequency among neighbors.
5. If every node has a label that max number of their neighbors have, then stop algorithm else set t=t+1 and go to step 3.

LV schema for community non-overlapping discloseion

Communities are group of nodes within a network that are more densely connected to one another than to other nodes. Modularity is metric that quantify quality of assignment of nodes to communities by evaluating how much more densely connected nodes within community are compared to how connected they would be on average, in suitable defined random network (Wen *et al.*, 2014). The LV method of community detection algorithm for detecting communities in network that relies upon a heuristic for maximizing modularity. This method consists of repeated applications of two steps (Wen *et al.*, 2014).

- First step is greedy assignment of nodes to community, favoring local optimization of modularity.
- Second step is definition of new coarse grained network in terms of community found in first step.

These two steps are repeated until no future modularity increasing reassignment of communities are possible. LV method achieves modularity comparable to preexisting algorithms, typically in less time. So it enables study of much larger network (Andrea Lancichinetti and Santo Fortunato, 2014). It also generally reveals a hierarchy of communities at different scales and this hierarchical perspective can be useful for understanding global functioning of network. Meanwhile, there are certain pitfalls to interpreting community structure uncovered by LV method. These difficulties are actually shared by all modularity optimization algorithms (Andrea Lancichinetti and Santo Fortunato, 2014).

Related Work

In Feb. 2012 (Chen, 2012) J. Chen, H. Zhang, Z.-H. Guan, and T. Li study the analysis of the infection and diseases which spread very quickly among the population. Many real networks are characterized by non-overlapping community structures in which vertices may belong to more than one community.

Table 1. Comparison of various techniques used to find the overlapping community

Parameter	Greedy Method	LV Method	Label Propagation
No of Nodes	2 millions	2 millions	1.3 millions
Speed	1.2 Detections/S	1.4 Detections/S	2.1 Detections/S
Cliques	203	204	320
Quality	Low	Medium	High
Modularity	1.3135	1.62222	1.8324
Scalability	Yes	Yes	Yes
Time for Community Detection	2 minutes	1.54 minutes	6 sec
Optimal	No	No	Yes

In 2011, (Reid and Hurley, 2011) F. Reid and N. Hurley, study diffusion in networks with community structure. Experiments show that epidemics spread faster on networks with higher level of non-overlapping communities. Furthermore, non-overlapping communities' effect interacts with the average degree's effect.

In 2014, (Shang *et al*., 2015) J. Shang, L. Liu, X. Li, F. Xie, and C. Wu, study how the epidemic disease spreads on both Overlapping and non Overlapping communities. In this paper they find the community detection structure for both communities.

In 2014, (Shang *et al*., 2015) J. Shang, L. Liu, F. Xie, and C. Wu, study about How Overlapping Community Structure Affects Epidemic Spreading in Complex Networks. In this paper they find overlapping community structure that affects spreading of epidemic disease in networks.

This paper present the comparison of the algorithms among Greedy, LV, and Label Propagation, which are used for the detection of community structures in epidemic. The fast growth of the infection will be detected using this model.

Comparison of various techniques

The algorithms which are described above have number of parameters which are distinct. The parameters differ both in range as well as quality. The comparison table is shown as follows

Conclusion and Future Work

The Non-overlapping community detection used in epidemics will detect the diseases which are spreading within the communities. We discussed three non-overlapping algorithms here. Greedy LV and Label Propagation. Out of the discussed techniques label propagation is considered to be the best. In the future we will discovered the rate at which disease must be healed so that spreading of the disease within the community can be controlled.

REFERENCES

Andrea Lancichinetti and Santo Fortunato, "Community detection algorithms: a comparative analysis" in 2014.

Chen, J., Zhang, H., Guan, Z.H., and Li, T. 2012. "Epidemic spreading on networks with overlapping community structure," *Phys. A Stat. Mech. its Appl.*, vol. 391, no. 4, pp. 1848–1854, Feb. 2012.

Reid, F. and Hurley, N. 2011. "Diffusion in networks with overlapping community structure," *Proc. - IEEE Int. Conf. Data Mining, ICDM*, pp. 969–978.

Shang, J., Liu, L., Li, X., Xie, F. and Wu, C. 2015. "Epidemic spreading on complex networks with overlapping and non-overlapping community structure," *Phys. A Stat. Mech. its Appl.*, vol. 419, pp. 171–182, Feb.

Shang, J., Liu, L., Xie, F. and Wu, C. 2014. "How Overlapping Community Structure Affects Epidemic Spreading in Complex Networks," in *2014 IEEE 38th International Computer Software and Applications Conference Workshops*, pp. 240–245.

Singh, J. and Ahuja, M. S. 2015. "COMPARISON OF THE VARIOUS EPIDEMICS MODELS IN COMPLEX NETWOKS," no. 6, pp. 93–97.

Wen, Y., Chen, Y. and X. Deng, 2014. "Epdemic spreading model based overlapping community detection," in *2014 IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining (ASONAM 2014)*, 2014, pp. 954–959.

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