



Learning Network Graph of SIR Epidemic Cascades Using Minimal Hitting Set based Approach

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Outline

- Introduction
- Related Work
- System Model
- Main Design
- Performance Evaluation
- Conclusion



Networks are everywhere



Intrition Syste CAL S2 culoskeletal ADRB1 Pathologi Diseas Conditio Cardiovascula C051 MAP Chemic and RAZA ALOXI D27 HMOXI Diseas ADRA2C [C17] CONE Nervous Reproductive Urogenital System ysten [C10]

Facebook Social Network



The Internet

Human Disease Network



Introduction

Learning the underlying network structure is very important.

 In this paper, we consider learning the network structure, based on some observations of the network in the context of epidemic spreading.



Epidemic Spreading Model

- Various phenomena can be modeled as epidemic spreading model (epidemic cascade).
 - Biological
 - Diseases via contagion
 - Technological
 - Cascading failures
 - Spread of information
 - Social
 - Rumors, news, new technology
 - Viral marketing
 - Wireless
 - Information dissemination
 - Internet
 - Propagation of worms



Infection Spread Model

- Models of Infection [Easley 10b]:
 - SIS: Susceptible-Infective-Susceptible (e.g., flu)
 - SIR: Susceptible-Infective-Recovered (e.g., chickenpox)



Susceptible, Infected and Recovered

- Susceptible
 - the nodes that can catch disease from a network neighbor
- Infected
 - the nodes that have caught the disease and can pass it on
- Recovered
 - the nodes that have recovered and cannot be infected again



Susceptible, Infected and Recovered

- How is the epidemic spread in SIR model?
- Process
 - Initially, each node independent of other nodes gets infected with probability p_{init} . These infected nodes are seeds.
 - Each node in the *infected* state remains infectious for one time step.
 - Each node i in the *infected* state can infect each of its susceptible neighbors j, with a probability of p_{ij} .
 - After one time step, each infected node is no longer infectious or susceptible and enters the *recovered* state.
- This SIR model is suitable for modeling a disease that each individual can only catch once during his/her life time.



Example SIR Epidemic in One Cascade







t = 2

R



R

t = 3







Observation Model

- We model the network as a Graph, G = (V, E).
- We denote $V_i = \{j: j \text{ is the parent of node } i\}$.
- Consider a number of cascades.
- In each cascade *u*, seeds start to spread the infection.
- We observe the time that each node $i \in V$ gets infected, denoted by t_i^u .
- We set $t_i^u = 0$ for the seeds, and $t_i^u = \infty$ for the nodes that never get infected.



Goal

What is the smallest number of cascades (i.e., sample complexity) to recover a correct network structure with high probability?



Related Work

- Maximum Likelihood (ML) [SIGMETRICS'12]
 - ML guarantees to detect a subset of the parents of a node rather than its exact parental set
 - ML requires a relatively high sample complexity for reliable graph recovery when the graph is dense (i.e., nodes have high degrees)
 - To achieve high performance, ML requires an appropriately predefined threshold parameter



Our proposal

We propose to use a minimal hitting set approach to recover network graph G.



Minimal Hitting Set

- Hitting set of a collection of sets
 - a set that intersects all of the sets in the collection
- Minimal hitting set of a collection of sets
 - if and only if no proper subset of it is a hitting set for this collection
 - Consider a collection of sets

 {{1,2}, {1,3}, {1,2,4}, {1,3,5}}. {2,3} is a minimal hitting set of the collection



Minimal Hitting Set Algorithm

- Process
 - We have *m* epidemic cascades.
 - Recovering the network structure is equivalent to recovering the parental nodes of every node j, $\forall j \in V$.
 - In each cascade u, we denote t_j^u as the infection time of the node j.
 - We denote S_j^u as the set of nodes *i* that have infection time = $t_j^u - 1$ in observation *u*, i.e., $S_j^u = \{i: t_i^u = t_j^u - 1\}$
 - Therefore, for *m* cascades, we have a collection of S_i^u sets.
 - The parent set of node j is the minimal hitting set of the collection of S_i^u sets from all the cascades.



Minimal Hitting Set Algorithm

- Theorem: as the sample complexity m → ∞, the parent nodes of node j is the minimal hitting set of the collection of S_j^u sets.
- For details of the proof, please refer to the paper.
- Simple rationale: the parent nodes of node *j* is definitely a minimal hitting set of the collection of S^u_j sets. A minimal hitting set must include all the parents of node *j*. Otherwise, as *m* → ∞, there must exist one cascade that node *j* is infected by the parent that are not in the minimal hitting set.



Minimal Hitting Set Algorithm

- Lower bounds (sufficient condition)
 - Recover the network structure with high probability
 - find the sample complexity $m, \forall \delta > 0$
 - guarantee that the network structure is recovered with probability at least 1δ , $\delta > 0$
 - Sample complexity

•
$$m \ge \frac{\log \delta - 2\log n}{\log(1 - p_{init} * p_{min})} = O(\log n)$$

• p_{min} is the minimum probability for the edge propagation



Evaluation

- Trace-driven simulation
- Comparing method
 - maximum likelihood (ML)
- p_{init} =0.3, p_{ij} = 0.8
- The predefined parameter (infection probability threshold) of ML
 - set to x=0.1, 0.2, 0.5, 0.8, denote as MLx
- Recover only a subset of the parents for ML
 - denoted as MLxSub





• Grid Graph. We see the superior performance of our proposed minimal hitting set algorithm.





- A sub-graph of the Google+ network with 500 users.
- We see the superior performance of our proposed minimal hitting set algorithm.



Conclusion

- We consider learning the underlying graph structure of an epidemic cascade based on infection times of nodes.
- We propose a minimal hitting set algorithm to recover the network structure.
- We demonstrate the effectiveness of minimal hitting set algorithm by trace-driven simulation.



Thank you! Questions & Comments?

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