The fast growth of social networks and their privacy requirements in recent years, has lead to increasing difficulty in obtaining complete topology of these networks. However, diffusion information over these networks is available and many algorithms have been proposed to infer the underlying networks by using this information. The previously proposed algorithms only focus on inferring more links and do not pay attention to the important characteristics of the underlying social networks. In this paper, we propose a novel algorithm, called DANI, to infer the underlying network structure while preserving its properties by using the diffusion information. Moreover, the running time of the proposed method is considerably lower than the previous methods. We applied the proposed method to both real and synthetic networks. The experimental results showed that DANI has higher accuracy and lower run time compared to well-known network inference methods.

Categories and Subject Descriptors: G.2.2 [Graph Theory]: Graph algorithms; H.3.3 [Information Storage and Retrieval]: Information Filtering, Information Search and Retrieval

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Additional Key Words and Phrases: Social Networks, Network Inference, Diffusion Information, Community Structure, Random Process Model

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1. INTRODUCTION

Online Social Networks (OSNs) that play an important role in the exchange of information between people, have grown noticeably in the last few years. Diffusion is a fundamental process over these networks by which information, ideas and new behaviors, namely contagion, disseminate over the network [Gomez Rodriguez et al. 2010]. Propagation of a contagion over a network creates a trace that is called cascade (Fig. 1) [Gomez Rodriguez et al. 2010]. These cascades represent the diffusion behavior that convey valuable information about the underlying network.

Some previous studies indicate that diffusion behavior and network structure are tightly related [Easley and Kleinberg 2010; Eftekhar et al. 2013; Barbieri et al. 2013a; 2013b]. In other words, actions of users do not only emanate from their individual...
interests but also depend on the interaction pattern between them. Understanding
this relation can result in a more accurate analysis of social networks and the processes
taking place over them (e.g. diffusion).

One of the most important features of OSNs is their modular structure. Each module
in the network is a dense sub-graph called a community. In other words, a community
is a set of nodes which are densely connected to each other, and sparsely to the rest of
nodes. Nodes in a same community have common interests and similar actions [Chen
2011; Fortunato 2010]. For example, strongly connected communities of global web
networks often have pages with common topics [Fortunato 2010].

In many situations, the underlying network topology (nodes and the links between
them) may not be achievable for different reasons: 1) Rapid changes in the structure
of networks over time caused by the arrival and departure of members and alteration
in their friendships, and 2) Limited access to data due to the policy of OSNs and pri-
vacy of user profiles. Network topology inference is a solution to surmount the above
difficulties.

As mentioned before, the diffusion process is influenced by structure of the latent
underlying network which includes its community structure. Thus, observing the dif-
fusion behavior of nodes can help us to gain insight into the networks community
structure. In most cases, the only available observation is the time when a contagion
reaches a node, namely the infection time of a node [Gomez Rodriguez et al. 2010; My-
ers and Leskovec 2010; Eslami et al. 2011; Gomez-Rodriguez et al. 2011; Alpay et al.
2011; Gomez-Rodriguez and Schölkopf 2012]. Network inference includes a class of
studies, which aim to discover the latent network by utilizing these infection times in
different contagions. Several network inference algorithms have been proposed, but
most of them do not preserve the community structure during the inference process.
Despite their acceptable accuracy on detecting network links, the community structure
of the inferred network does not match with the original network.

Many community-based services are provided on OSNs. Since gathering information
about the entire network topology is often impossible, usually inferred networks from
the set of observations are being used. By considering community structures during
network inference, the community-based services such as optimizing search engines
[Zhong et al. 2008], visualizing large social networks [Heer and Boyd 2005], improving
recommendation systems [Sahebi and Cohen 2011], compressing network data [Boldi
and Santini 2010], and viral marketing [Leskovec et al. 2007] can be applied on the
inferred network, and lead to comparable results with the original underlying network.

In this paper, we propose a new Diffusion Aware Network Inference algorithm, called
DANI, which is intended to infer social networks from diffusion information while per-
severing the community structures. We consider the infection time of nodes in different
contagions as observations, and apply community detection algorithms on the inferred
network. Moreover, by comparing the detected communities of the actual network with
the inferred ones, we show that communities are detected successfully.

The main contributions of this paper are:

— Inferring networks while preserving their properties: Since it is not feasible to obtain
the real network structure, different structural based methods such as community
detection algorithms may use the inferred networks as an alternative. The previ-
ous network inferring works do not consider the density of edges and their degree
distributions in the underlying network. Consequently using community detection
methods on them deviates from community detection on the original network. How-
ever, other structural properties such as degree distribution and clustering coefficient
will be different from the ground truth. In this way, the ranking of nodes will be dis-
tributed based on their influence role. The proposed method overcomes this problem by preserving the community structure while inferring the networks.

— Inferring networks with more connected nodes: Network nodes in inference problems are the active nodes participating in at least one observed cascades. Hence, any active node must have at least one connected link providing the required infrastructure for cascades to spread through that link. Compared to the previous works, the proposed method can produce an inferred network with more connected links for each node as existed in the underlying network. In other words, our method produces less isolated nodes compared to the previous methods.

— More scalability: The proposed method offers lower run time compared to the state of the art methods while maintaining high precision. This property leads our work to have more scalability that is a main limitation of the pervious works.

— Good performance independent of the network structure: Many of the state of the art previous works such as [Gomez Rodriguez et al. 2010; Gomez-Rodriguez et al. 2011; Gomez-Rodriguez and Schölkopf 2012] have good performance on the tree-based networks [Alpay et al. 2011], while the performance of the proposed method is not limited to any type of structure.

The rest of this paper is organized as follows. In Section 2, we introduce the preliminaries on the concepts of community and diffusion and explain their interdependencies in order to ascertain our concerns about preserving community structures during the inference process. Related works are studied in Section 3. In Section 4, we define notations, formalize our problem and explain the proposed method. Experimental results on synthetic and real datasets are presented in Section 5. Finally, we conclude the paper and discuss future works in Section 6.

2. PRELIMINARIES ON COMMUNITIES AND DIFFUSION

A social network is usually represented by a graph \( G(V, E) \). Nodes \( V \) and links \( E \) of these graphs stand for people and their interactions, respectively. The role that different nodes and links play in the network processes such as diffusion, varies and can be described as [Chen et al. 2007; Xie et al. 2013; Fortunato 2010]:

— **Intra-community links** that connect nodes in the same community. Such nodes interact frequently; therefore, these links are known as strong ties. Nodes that only have links to other nodes in their own community are called core nodes. The core nodes mostly affect their cohorts in a community more than other members of the network.

— **Inter-community links** that connect nodes of different communities. Due to low interactions between such nodes, they are called weak ties. Nodes, which have at least one inter-community link, are called boundary nodes. Such nodes play an important role in information dissemination over different communities.

Analyzing the interactions between community members is an important issue in social networking [Chen 2011]. In fact, the probability that a person would reject or accept a contagion depends on the decision of his neighbors about that contagion. At the same time, this probability affects the future decisions of neighborhood nodes in the same community [Scripps et al. 2007]. By strong intra-community links, members in a community are exposed to a contagion during a small interval from several paths. In contrast, due to weak inter-community links between communities, propagation of a contagion among them takes place with lower probability and pace.

Another interesting finding is that in many cases the impact of weak ties on a network process (i.e. acceptance rate of a new product) is more powerful than strong ties [Bakshy et al. 2012; Goldenberg et al. 2001]. We try to explain the above facts through an example. A network with three communities is illustrated in Fig. 1. Suppose that
node $D$ gets infected by a contagion. Other nodes in the community of node $D$ will be exposed to this contagion and become infected with high probability due to similar interests and actions among them. Thus, the rate and extent of diffusion can be high within a community. But how does the contagion disseminate over the network? For this purpose, the contagion must spread out of the community by a boundary node such as $B$, and infect another boundary node like $K$ from a neighboring community, and this only happens if there exists at least one inter-community link such as $(B, I)$ or $(B, K)$. Therefore, weak ties have a critical role in the diffusion process over the network. Since interaction on weak ties happens with lower probability, the diffusion process may stop. In other words, diffusion and community may act against each other. Communities may prevent a cascade, and in most cases when a cascade stops, a community can be detected [Easley and Kleinberg 2010; Barbieri et al. 2013a].

Therefore, it is necessary to understand the relation between the community structure and diffusion behavior of nodes in a network in order to infer the network correctly.

3. RELATED WORK
As discussed in the previous sections, we would like to infer a network by utilizing diffusion information while taking into account its community structure. Consequently, the most related research areas to our work are:

— Diffusion aware network inference: The methods that infer networks by observing the diffusion network.
— Diffusion aware community detection: The methods that utilize the diffusion process during community detection.
In this section, we will survey and explain the state of the art methods in each research area.

3.1. Diffusion based Network Inference

This category of research tries to infer the edges of a network by using cascade information, which in most cases is the infection time of nodes in different cascades [Gomez Rodriguez et al. 2010; Myers and Leskovec 2010; Eslami et al. 2011; Gomez-Rodriguez et al. 2011; Alpay et al. 2011; Gomez-Rodriguez and Schölkopf 2012]. [Guille et al. 2013] introduces a comprehensive survey on previous works in this area. In the following, we describe some of the most important works in this category.

NETINF models each cascade as a tree on the network and uses an iterative algorithm to infer the network from these trees by optimizing a sub-modular function [Gomez Rodriguez et al. 2010]. Despite its high inference accuracy, it suffers from high runtime which is a serious problem in real datasets. In addition, the performance of NETINF decreases when the structure of the network being studied is not consistent with the tree model [Alpay et al. 2011].

NETRATE is an improvement over NETINF. It assumes that cascades occur at different rates and temporally infers heterogeneous interactions with different transmission rates, which is closer to reality [Gomez-Rodriguez et al. 2011].

CoNNIE improves NETINF by adding an optimal and robust approach which uses prior probabilistic knowledge about the relation between infection times [Myers and Leskovec 2010].

Similar to NETINF, MultiTree models cascades with the trees, but considers all the possible trees. By this approach, its accuracy is higher than NETINF, NETRATE and CoNNIE when low number of cascades is available. Although, its running time is several orders lower than other tree-based algorithms, but still it is not scalable [Gomez-Rodriguez and Schölkopf 2012].

DNE models diffusion as a Markov random walk and tries to define a weight for each link according to the difference between the infection times of connected nodes in different cascades [Eslami et al. 2011]. Its approach is independent of diffusion models. FastINF is another method which uses the same approach to define the weight of links [Alpay et al. 2011]. Both of these algorithms have a low runtime and work well on the networks that do not have meaningful community structures.

The overall goal in such studies is to obtain the maximal number of edges of the underlying network. The main drawbacks of this category of studies are as follows.

Algorithms like NETINF and others based on it, which use a spanning tree approach, maintain the structures, but are too slow. These methods have low performance on networks with non-tree structures.

Others like DNE and FastINF distinguish no preference between different types of the extracted edges. Despite their high accuracy, they do not consider the network community structure. Running community detection algorithms on the output of these methods leads to different communities from underlying network, because they do not recover some weak inter-community or strong intra-community links. Therefore, few large communities or many single members are seen in the networks inferred by them.

Our goal is to infer the network by utilizing cascade information such that the community structure of underlying network is preserved. In this regard, we desire to maintain network community structure through the inference process by finding more intra-community links to recognize relatively dense communities in the network.

3.2. Diffusion based Community Detection

Many community detection algorithms have been proposed in recent years. The main assumption of these algorithms is the availability of the underlying network topology
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(nodes and links between them). However, in many cases, the network topology (i.e. friends, followers or following of users) is latent which causes the accuracy of traditional community detection algorithms to reduce.

Different interpretations of diffusion are used in community detection algorithms. The most prevalent definitions are described in the following. 1) Artificial diffusion: It is mainly produced by well-known diffusion models [Kempe et al. 2003] such as Independent Cascade (IC) model [Saito et al. 2008] and Linear Threshold (LT) model [Chen et al. 2010]. Moreover, some studies have introduced new behaviors for diffusion [Shen et al. 2010]. 2) Real diffusion: It corresponds to a foreign traceable process on the network that appears as part of a dataset information. For example, in news cascade over Twitter (http://twitter.com), if user $u$ tweets a post, his follower node $v$ will see this action on his page. In general, we say node $v$ is exposed to a contagion, and can retweet. Another example is voting stories in Digg (http://digg.com) which allows users to post news that can propagate according to the rating of users.

We categorize community detection algorithms according to their diffusion type as follows:

**Detecting communities by artificial diffusion**: These studies create artificial diffusion over the network and offer a community detection algorithm that uses this diffusion as part of its procedure. In multi-agent approaches, information such as color, is exchanged between nodes via the edges according to different diffusion models. At the end, nodes with the same colors are detected as a community [Yang et al. 2009a]. Some works use label propagation in order to define communities. Nodes adopt the maximum label of their neighbors in an iterative process, and at last nodes with identical labels form communities [Raghavan et al. 2007; Costa 2004; Leung et al. 2009]. In another research, the number of common neighbors between nodes is used to define the weight of edges as a similarity measure [Chen 2011]. By considering this assumption, another work introduces a new comportment named diffusion, which combines weighted edges in a hierarchical method to detect communities [Shen et al. 2010].

**Detecting communities by real diffusion**: The only major work in this category proposes a stochastic generative model named CCN that uses both the complete network topology and diffusion information to extract communities [Barbieri et al. 2013a]. This model does not consider any special assumption about link formation, arrival probability of a contagion at each node, cascades models over the network, and rather tries to model them with a random process. Despite good features such as overlapping community detection, this method suffers from high running time complexity. In [Barbieri et al. 2013b], the authors expand CCN by considering that the underlying network is not available. This method adopts a mathematical model similar to CCN, and uses an independent cascade assumption to introduce a model called C-IC, and also uses NETRATE to introduce a model called C-Rate. The output of this method is the network communities without producing the links of network.

In general, low performance in the absence of network topology and being restricted to undirected networks are the main drawbacks of previous community detection algorithms. In contrast to prior algorithms, our method assumes the network topology to be latent, and aims to infer the network utilizing infection time of nodes, which is available in most realistic cases. In addition, our method performs well for both directed and undirected networks.

Network inference is the main goal of this article which is more related to works explained in the 3.1 category. Community detection algorithms that are based on diffusion concepts are not relevant to the proposed method in this paper, because they assume that the complete network topology is accessible. On the other hand, [Barbieri et al. 2013b] which is the only community detection work that does not consider the
4. PROPOSED METHOD

In this section, we first present the notations used in this paper, and then introduce the proposed algorithm.

4.1. Notations and Definitions

Let $G = (V, E)$ represent a network where $V$ contains the set of nodes, and $E$ contains the directed or undirected links between nodes. We assume $k = |E|$ (number of links) is known, while no more information about the links is available. We assume to have a set of different contagions as different cascades, $C = \{c_1, c_2, \ldots, c_M\}$. For each cascade $c_i$, we observe the infection time of nodes and have pairs of node ID and infection time, $c_i = \{(v_0, t_0), (v_1, t_1), \ldots, (v_n, t_n)\}$. During the spread of a contagion some nodes may not get infected. An infinity infection time is assigned to such nodes.

The propagation path of a contagion is hidden. In other words, we do not know by which node a node gets exposed to a contagion. It is assumed that a node can get infected with a certain contagion just by one other node.

In general, infection times form a continuous sample space which makes their interpretation somewhat difficult. In addition, the range of infection time may vary for each contagion. For example, the order of infection time maybe in seconds for cascade $C_a$, but in order of hours for another cascade $C_b$. Therefore, if we use the real value of the infection times, we will not infer the links that $C_b$ spreads over the network; since the time differences in $C_b$ are much larger than $C_a$, the information obtained from $C_b$ would be ignored. To overcome this problem, we define a function that maps these continuous values to a set of discrete values and refer to the corresponding random variable as infection label. Here, our goal is to discover the links of a static network structure from the observed cascades. We do not consider the speed of cascades and expect two different cascades to spread in the same manner for a same path on the graph. We also ignore the impact of cascades on each others. Therefore, instead of time of propagation, the sequence of propagation is important and we achieve this representation by mapping time values to infection sequence order per each cascade. The proposed infection time transformation can be described as follows.

1. For each cascade $c_m$, sort the elements according to their infection time ($t_u$) in an ascending order. The resulting sorted set is named $S_m$. Elements with infinity infection time are omitted from $S_m$.
2. For each node $u$, assign a label equal to its position in $S_m$, and replace its infection time with that label.

$$L(t_u) = \begin{cases} \text{index}(S_m(t_u)) & \text{if } t_u \prec \infty \\ 0 & \text{else} \end{cases} \quad (1)$$

This way, each cascade $c_m$ is a vector containing pairs of nodes and infection labels that are sorted in an ascending order according to their infection labels, as depicted in Eq. (2). From now on, we call this vector the cascade vector, $CV_m$:

$$CV_m = \{(v_0, L(t_0)), (v_1, L(t_1)), \ldots, (v_n, L(t_n))\} \quad (2)$$

For simplicity we may use $L(t_i)$ and $L(v_i)$, interchangeably.

4.2. Problem Formulation

We assume, the underlying network $G = (V, E)$ is unknown, and the only observation is the set of cascades ($C$). If each node of network participates in at least one cascade,
the set of nodes $V$ can be extracted from the observation. By considering all the links between any pairs of these nodes $\{(u, v) | u, v \in V\}$, we have a complete graph $G$. Our goal is to obtain a weighted adjacency matrix $A = \{a_{uv} | u, v \in V, u \neq v\}$ for graph $G$ such that each element $a_{uv} \geq 0$ of $A$ is calculated considering the community structure preservation property. We utilize the same assumptions and maximum likelihood estimation as in [Gomez Rodriguez et al. 2010; Gomez-Rodriguez et al. 2011; Alpay et al. 2011; Gomez-Rodriguez and Schölkopf 2012]. These assumptions are used in the following to simplify the maximization process. We would like to assign weight for each edge of complete graph $G$ that maximizes the following likelihood function.

$$G' = \arg\max_{G} P(C|G)$$

(3)

Then, we extract a sub-graph $G^*$ of $G'$ that has the $k$ most weighted edges as probable edges of the latent network ($k$ is the number of underlying network links which is given as input).

For simplicity, we assume the spread probability of cascades to be independent and identically distributed (i.i.d) over the graph. Therefore, the probability of observing the cascade set over the networks is:

$$P(C|G) = \prod_{i=1}^{m} P(c_i|G)$$

(4)

Graph $G$ is composed of set of edges $(u, v)$, and we assume that all edges are mutually independent:

$$P(G) = \prod_{(u, v) \in G} P(u, v)$$

(5)

Therefore, the probability that cascade $c_i$ spreads over graph $G$ is given by Eq. (6), assuming that the joint probability of edges are conditionally independent:

$$P(c_i|G) = P(c_i|(u, v)) \prod_{(u, v) \in E} P(u, v)$$

(6)

Where $P(c_i)$ is the prior probability for cascade formation, and we assume it is constant for all cascades. Therefore, we can approximate the probability of cascade $c_i$ propagating over $G$ by Eq. (7):

$$P(c_i|G) \propto \prod_{(u, v) \in G} P(c_i|(u, v))$$

(7)
hence, by using Eq. (7), we can rewrite Eq. (4) as:

\[
P(C|G) \propto \prod_{i=1}^{m} \prod_{(u,v) \in G} P(c_i|(u,v))
\]

Applying log function on both sides of Eq. (8), yields:

\[
\log(P(C|G)) \propto \sum_{(u,v) \in G} \sum_{c_i \in C} \log(P(c_i|(u,v))
\]

where \( P(c_i|(u,v)) \) represents the probability that cascade \( c_i \) spreads through edge \((u,v)\). We try to define the probability \( P(c_i|(u,v)) \) in terms of observed information from the hidden network structure. We interpret \( \log(P(c_i|(u,v))) \) as the weight of edge \((u,v)\), and call it \( \alpha_{c_i} \). We try to estimate this weight for each presumable link in the network. In the rest of paper, we introduce the DANI algorithm in which \( \alpha_{c_i} \) is computed according to the relations between community structure and diffusion information.

4.3. The DANI Algorithm

As mentioned before, our goal is to define a weight \( P(u,v) \) for each edge \((u,v)\) that represents its existence probability in the underlying network. For this purpose, DANI first utilizes diffusion information and estimates the weight of all potential edges. At the second step, DANI considers the relation between community structures and diffusion behavior and assigns another weight according to the joint behavior of nodes. Finally, both of these weights are taken into account simultaneously, and the existence probability of each edge is computed. In summary, we follow three steps: using information diffusion network, maintaining the community structure, and the combination of these steps.

**Diffusion Information:** From each cascade vector \( CV_m \) we can construct a probable directed graph. Each node \( u \) in this graph can get infected by a node \( v \), if \( L(v) \prec L(u) \). The probability of existence of edge \((u,v)\) in this graph depends on the difference between the infection label of \( u \) and \( v \), such that more difference between the infection labels of these nodes in \( CV_m \), decreases the participation probability of link \((u,v)\) in the contagion [Gomez Rodriguez et al. 2010]:

\[
P(u,v) \propto \frac{1}{\Delta(L(u), L(v))}
\]

Fig. 2(a) illustrates a typical network and two of its distinct contagions. Their cascade vectors and corresponding probable graphs (simply referred to as graph) are shown in Fig. 2(b) and Fig. 2(c), respectively.

Each cascade vector \( CV_m \) can be modeled as a discrete time stochastic process where nodes stand for independent states and the sequence of nodes in the cascade vector \( CV_m \) represent the state of the process at discrete times. The transition probability between different states (nodes), or in other words, the contagion transmission probability from a node to another node is equivalent to the weighted link between them.

At the present time the contagion transmission probability of each node (state) depends on probability of being at its neighboring node in the immediate preceding period, and is independent of its previous time states or the traversed nodes. This property is called the Markov Property. Hence, it can be thought that the states of former
times are all accounted by incorporating the state of the last immediate time $t$. Assuming the First Order Markov Property to hold, we have:

$$Pr[X_{t+1} = x_{t+1} | X_t = x_t, X_{t-1} = x_{t-1}, \ldots, X_0 = x_0] = Pr[X_{t+1} = x_{t+1} | X_t = x_t]$$

(11)

This stochastic process that exhibits the Markov property is called a Markov Chain (MC). The number of states in our Markov chain is equal to the number of nodes, and each cascade vector $CV_m$ is a finite Markov chain [Levin et al. 2009].

In order to define the Markov chain, we must compute its transition matrix. Each element of this matrix represents the existence probability of an edge in the network. As shown in Fig. 2(c), our goal is to find the transition matrix for each chain by utilizing the corresponding cascade information.

At this point, we need to find the relation between the difference of the infection labels of two nodes, and the probability that an edge exists between them. As discussed before, this probability has an inverse relation with the difference of their infection labels. Two approximations are used in the previous works:

1. The probability of an edge only depends on the difference of the infection label of nodes connected by it. In other words, for all pairs of nodes with the same values of infection label difference, the existence probability is the same [Gomez Rodriguez et al. 2010].

2. Consider a cascade vector such that there exists a set of nodes ($D$), before $v$ in this vector. The probability that $u$ infected $v$ when $D = \{u\}$, is higher than the situation where $|D| > 2$, because a node $z \in D$ with $t_z < t_v$ may have infected $v$. This will reduce the probability that $v$ has been infected by $u$. Moreover, the authors in [Eslami et al. 2011] proved that in addition to the difference of infection times, the number of infected nodes before node $v$, namely $|D|$, also affects the edge weights.
Considering the above points, the existence probability of an edge between nodes \( u \) and \( v \) in the cascade vector \( (L(v) > L(u)) \), using the infection label is:

\[
d_{u,v} = \frac{1}{L(v) \times (L(v) - L(u))}
\]  
(12)

We use \( d_{u,v} \) to construct the transition matrix. The transition matrix \( P \), is a stochastic random matrix with the following features:

1. Each element in \( P \) satisfies the following condition:
   \[
   0 \leq P_{ij} \quad i, j = 1, 2, ..., n
   \]  
   (13)

2. The sum of each row is equal to one:
   \[
   \forall i : \sum_{j=1}^{n} P_{ij} = 1
   \]  
   (14)

To satisfy these conditions, the two-dimensional probability matrix should be normalized. Dividing each element of this matrix by the sum of its corresponding row, the Markov chain transition matrix \( (P_{c_i}) \), for cascade \( (c_i) \) is obtained:

\[
P_{c_i}(u,v) = \frac{d_{u,v}}{d_u} = \sum_{y \in V} d_{u,y}
\]  
(15)

**Community Structure Information:** As previously mentioned, community members have similar interests and behaviors, and diffusion is more likely to spread among them [Easley and Kleinberg 2010; Eftekhar et al. 2013; Barbieri et al. 2013a; 2013b]. Intuitively, they appear in same cascades more than nodes which are in different communities. Thus the number of cascades passed between node \( u \) and \( v \) can be a sign of coherence between these nodes. If \( u \) and \( v \) are community members, they become infected jointly in more cascades compared to the cascades that only one of them has been infected. We use the participations of pairs of nodes in different cascade as a mark for finding the similarity in their behaviours.

On the other hand, consider two boundary nodes that connect adjacent communities. These nodes may appear in same cascades due to the bridge role of weak ties in the diffusion process. However, the frequency of such cases is negligible compared to the number of cascades that every single one of them has participated in.

According to the above justifications, and the goal of inferring the links for each pair of node \( (u, v) \), we define a function \( \psi(u, v) \) that assigns a weight to edge \( (u, v) \) by considering the nodes behaviours based on the cascades information. In other words, this weight is a node-node similarity based on the community structure that had impacted the diffusion information. The formula for \( \psi(u, v) \) is similar to the Jaccard index [Jaccard 1901]:

\[
\psi(u, v) = \frac{|In(u) \cap In(v)|}{|In(u) \cup In(v)|}
\]  
(16)

where \( In(u) \) is the set of cascades that \( u \) has participated in:

\[
In(u) = \begin{cases} 
M \cup \{i\} \text{ if } u \in CV_i \\
\emptyset \text{ else}
\end{cases}
\]  
(17)
For computing the numerator of Eq. (16), \(u\) should appear earlier than \(v\) when both participate in each \(CV_i\). The above node-node similarity can be used to detect the communities. The main idea of many structured-based community detection algorithms is grouping nodes based on the fact that when the similarity of two nodes is large, they have more chance to be in a community [Du et al. 2007; Weng et al. 2013]. We also provided a data driven study to show the relation between Eq. (16) and the aforementioned concept of community. To this end, we utilized an LFR network with 1000 nodes, 7692 links, 28 communities and 20000 cascades (which is described and analyzed in Section 5). We changed the name of nodes such that nodes of a community are consecutively listed. For each pair of nodes, the color map community matrix and similarity matrix in Fig. 3 show that nodes with more similarity are in the same community.

Since overlapping nodes are highly influential nodes [Bhat and Abulaish 2013], this formula also works for overlapping communities. Because by using this equation, the overlap nodes will take part in more common cascades and consequently gain large values.

**Total Information:** The probability of direct contagion propagation between two nodes would increase, if the difference of their infection times decreases. In other words, the existence probability of edge \((u,v)\) has a direct relationship with \(P_{c_i}(u,v)\). From other perspective, larger values of \(\psi(u,v)\) correspond to more probability that \(u\) and \(v\) are cohorts, and hence indicating edge \((u,v)\) to be an intra-community link. Therefore, direct impact of \(\psi(u,v)\) on the existence probability of edge \((u,v)\) will lead to infer the intra-community links that are the important links in the community detection step. We define the probability weight of an edge at each cascade \(c_i\) as:

\[
\alpha_{c_i}(u,v) = P_{c_i}(u,v) \times \psi(u,v)
\]  

where \(P_{c_i}(u,v)\) is the element \((u,v)\) in the Markov transition matrix of the cascade \(c_i\).

To mathematically justify the above equation (Eq. (18)), let us consider the following definition. According to [Malmgren et al. 2008], independent cascades over the network are Poisson point processes that follow the exponential distribution [Gomez Rodriguez et al. 2010]:

\[
P(c_i|(u,v)) \propto e^{-(t_v-t_u)/\theta_{u,v}}
\]  

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Then, the probability of cascade $c_i$ spreading over an edge $(u, v)$ has an inverse relation with the difference between infection times (infection labels) of node $u$ and node $v$, and the parameter $\theta_{u,v}$. According to discussion in the "Diffusion Information" section the authors in [Eslami et al. 2011] proved that a cascade spread over edge $(u, v)$ does not only rely on the infection label difference of nodes $u$ and $v$, but also the set of nodes $(D)$ that has been infected before activation of node $v$. Therefore, $P(c_i|(u, v))$ is given by:

$$P(c_i|(u, v)) \propto \exp\left(\frac{-1}{(L(v)L(v) - L(u))^{-1} \times \theta_{u,v}}\right)$$ \hfill (20)

By substituting Eq. (20) in Eq. (9) we obtain:

$$\log(P(C|G)) \propto \sum_{(u,v) \in G} \sum_{c_i \in C} \log(\exp\left(\frac{-1}{(L(v)L(v) - L(u))^{-1} \times \theta_{u,v}}\right))$$ \hfill (21)

Considering the logarithm of maximum likelihood function $\arg\max(P(C|G))$ for Eq. (21) we obtain:

$$G^* \propto \arg\max\left( \sum_{(u,v) \in G} \sum_{c_i \in C} \left(\frac{1}{(L(v)L(v) - L(u))^{-1} \times \theta_{u,v}}\right)\right)$$ \hfill (22)

In Eq. (22), the first term is identical to relation we extracted from diffusion information, and the second term corresponds to the information about link that can map to the relation extracted from community structure information:

$$G^* \propto \arg\max\left( \sum_{(u,v) \in G} \sum_{c_i \in C} \left(\frac{(L(v)L(v) - L(u))^{-1} \times \theta_{u,v}}{\psi(u,v)}\right)\right)$$ \hfill (23)

Then, according to our model the Maximum Likelihood Estimator (MLE) is given by:

$$G^* \propto \arg\max\left( \sum_{(u,v) \in G} \sum_{c_i \in C} [\frac{1}{P_{c_i(u,v)}} \times \psi(u,v)]\right)$$ \hfill (24)

where $P_C$ is the sum of the transition matrix of all cascades, preserving the Markov matrix properties, and it stands for the total transition matrix of the Markov chain.

The DANI pseudo-code is presented in Algorithm 1, where $P_{\text{temp}}$ is used to keep the sum of all transition matrices of cascade vectors. Then, $P_{\text{temp}}$ is normalized to obtain the stochastic transition matrix $P_C$, based on the diffusion information. In the next step, by considering the community structures, $\psi(u,v)$ is calculated and used along with $P_C$ to produce the inferred network adjacency matrix, $A$. The normalization in the process of computing $P_C$ keeps its stochastic transition property and its value within the limits of $\psi(u,v)$ values, and hence their multiplication stays in a fix range for all the possible edges. Finally, we choose $k$ edges of the inferred network with maximum weight to construct $G^*$.
**Algorithm 1: DANI Pseudo-Code**

**Input:** Set of cascades over network \( C = \{c_1, c_2, \ldots c_M\} \), Number of network links to be inferred \((K)\)

**Output:** Inferred network \((G^*)\)

for each \( c_m = \{(v_i, t_i)\} \in C \) do

\( S_m \leftarrow \text{sort } c_m \text{ by } t_i; \)

\( L(t_i) = \text{index } (S_m(t_i)); \)

\( CV_m = \{(v_i, L(t_i))\}; \)

for each \( u \in CV_{m}, v \in CV_m \) do

if \((L(t_u) < L(t_v))\) then

Compute \( d_{u,v} \) according to Eq. (12);

end

end

for each \((u,v) \in P_{C_i}\) do

\( P_{c_i}(u,v) \leftarrow \sum_{y \in V} d_{u,y} \);\n
\( P_{\text{temp}}(u,v) \leftarrow P_{\text{temp}}(u,v) + P_{c_i}(u,v); \)

end

for each \((u,v) \in P_{\text{temp}}\) do

\( P_{\text{temp}}(u,v) \leftarrow \sum_{y \in V} P_{\text{temp}}(u,y); \)

\( P_c(u,v) \leftarrow P_c(u,v) + P_{\text{temp}}(u,v); \)

end

for each \((u,v) \in P_C\) do

Compute \( \psi(u,v) \) according to Eq. (16);

\( A(u,v) = P_c(u,v) \times \psi(u,v); \)

end

\( G^* \leftarrow \text{sort } A \text{ values}; \)

for \( i = 1 \) to \( K \) do

\( G^* \leftarrow G^* \cup \{g_i \in G^*\}; \)

end

Return \( G^* \);

**Time complexity analysis:** Consider a cascade \( c_m \) with \( n_{c_m} \) infected nodes. According to Algorithm 1, any sorting has the time complexity of \( O(n_{c_m} \log(n_{c_m})) \). There are \( \binom{n_{c_m}}{2} \) pair of nodes \((u,v)\) for calculating \( d_{u,v} \) and other normalizations with the time complexity of \( O(n_{c_m}^2) \). Therefore, if we have \( M \) different cascades with average number of nodes \( \bar{n}_c \) as the input, the DANI algorithm has a complexity of \( O(M \times \bar{n}_c^2) \). It is worth to mention that the baselines works for the competing methods in our experimental analysis did not provide time complexity analysis for their algorithms, because their methods are heavily dependent to the network structure. Instead they just relied on experimental results for running times, which we also compare in the next section. MultiTree and Netinf use greedy hill climbing to maximize the corresponding sub-modular function through an iterative approach where an edge is inferred at each step if by adding the edge a marginal improvement is achieved. After finding \( K \) edges, their algorithms are terminated. In contrast, DANI is free of any iteration and thus outperforms MultiTree and Netinf in running time.
5. EXPERIMENTAL EVALUATION

In this section, first we introduce the evaluation criteria for two concepts of network inference and community structures detection. In order to evaluate the proposed method, we apply DANI to synthetic and real datasets and compare our results with other static works under the same conditions. Since the main goal of this paper is network inference while preserving the community structure, the community detection methods should work better when used with the proposed method. Therefore, we have selected the state of the art inferring works for our comparison study instead of using different community detection methods which is not necessary and feasible in the context of this paper. The three selected methods for comparison include NETINF (as the first proposed method in this area), DNE (as the fastest method), and MultiTree (as the newest approach with superior performance over the previous tree-based methods based on accuracy and running time).

5.1. Evaluation metrics

As mentioned before, previous methods focus on inferring network links with high accuracy and overlook network properties such as community structure. Moreover, most of these methods suffer from high running time. Considering the best practices, we utilize two types of analysis as follows.

5.1.1. Network inference. The main goal of this area is to obtain the highest similarity between inferred and underlying networks. The most common and important issues in this regard are the number of discovered links, and inference process duration. To this end, the main criteria are as follows:

**F-measure.** Precision and recall are two frequently used metrics, and are defined as:

\[
\text{Precision} = \frac{|E_G \cap E_{G^*}|}{|E_{G^*}|} \\
\text{Recall} = \frac{|E_G \cap E_{G^*}|}{|E_G|}
\]  

(25)

where \(E_G\) and \(E_{G^*}\) represent the set of links in the original and inferred network, and \(|E_G|\) is the cardinality of \(E_G\). There is an inverse relation between recall and precision. To consider both, their geometric mean, named F-measure (or F-score) is used [Makhoul et al. 1999].

\[
F\text{-measure} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}
\]  

(26)

**Running time.** Most of the previous methods require more time to gain high accuracy. Therefore, running time is an important parameter to be considered in evaluation of these methods.

**Number of nodes.** The previous works only focus on the number of correct inferred links. Despite their high accuracy, no connected links maybe detected for some nodes. Hence, these nodes are omitted in the inferred network and consequently would not be assigned to any community. As a result, only a fraction of original nodes, that are presented in the inferred network, is used in evaluations.

**Other network properties.** Preserving the clustering coefficient and degree distribution of nodes is another important concern. For each node, we calculate the relative error between the exact value of each measure in the ground truth and inferred network.
5.1.2. Preserving community structure: As mentioned before, our goal is to propose a method to infer networks by preserving community structure of underlying network. In order to compare the methods in this regard, we extract communities of underlying and inferred networks by a well-known community detection algorithm and compare the communities of these two networks in two ways:

— Comparing members of communities (NMI, PWF). These metrics evaluate the similarity of each pairs of communities in real and inferred networks.

— Comparing properties of communities (density, conductance and number of communities). The average of these criteria over all communities of a network is utilized to evaluate the differences of community structure for real and inferred networks. Hence, for each criterion \( Y \), we compute \( |\triangle(\text{Avg}(Y_r), \text{Avg}(Y_i))| \), in which \( \text{Avg}(Y_r) \) and \( \text{Avg}(Y_i) \) are average of criterion \( Y \) for all communities in real and inferred networks, respectively.

Normalized Mutual Information (NMI): NMI is a probabilistic information theoretic metric that compares the similarity of two sets of communities [Manning et al. 2008], and is defined as:

\[
NMI(A, B) = \frac{-2 \sum_{i=1}^{C_A} \sum_{j=1}^{C_B} N_{ij} \log \left( \frac{N_{ij} N_i N_j}{N N_i N_j} \right)}{\sum_{i=1}^{C_A} N_i \log \left( \frac{N_i}{N} \right) + \sum_{j=1}^{C_B} N_j \log \left( \frac{N_j}{N} \right)}
\]  

(27)

where \( N \) is a \( C_A \times C_B \) matrix, and \( C_A \) and \( C_B \) are number of communities for original and inferred networks, respectively. Each element of \( N \) corresponds to the number of common memberships for each pair for communities. \( N_i \) (column \( j \)) summation, and \( N \) is the total number of nodes or the sum of all matrix elements [Duch and Arenas 2005]. The range of NMI values is between 0 and 1. Actually, NMI for the same communities reaches 1, and 0 represents the overall difference. However, for the overlapping communities this metric has been modified [McDaid et al. 2011; Lancichinetti et al. 2009].

Pairwise F-measure (PWF): Let \( H_G \) and \( H_G^* \) represent the sets of node pairs in the same community in the underlying network and the inferred network, respectively. PWF measures how many pairs of nodes in a community at original network are cohort in the communities of the inferred network [Yang et al. 2009b; Qi et al. 2012].

\[
\text{Precision} = \frac{|H_G \cap H_G^*|}{|H_G^*|}, \text{Recall} = \frac{|H_G \cap H_G^*|}{|H_G|} \\
\text{PWF} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}
\]

(28)

We considered PWF, because it is not enough to rely solely on NMI [Xie et al. 2013]. Moreover, recent studies have discovered modularity [Newman 2006a] is not a reliable measurement [Duch and Arenas 2005]. In addition, because of sparsity in real networks, the obtained modularity values are often incorrect.

Density: Density indicates the ratio of actual intra-community links to all possible links in a community [Vasudevan and Deo 2010]:

\[
\delta(S) = \frac{|E_S|}{\left( \frac{|V_S|(|V_S|-1)}{2} \right)}
\]

(29)
Table I. LFR-benchmark characteristics. \((N: \#\text{nodes}, k: \text{Avg degree}, \text{maxK: max degree}, t1: \text{minus exponent for the degree sequence}, t2: \text{minus exponent for the community size distribution}, \text{minC: Min community sizes, maxC: Max community sizes})\).

| N  | k  | maxK | t1 | t2 | minC | maxC |
|----|----|------|----|----|------|------|
| 1000 | 15 | 50   | 2  | 1  | 20   | 50   |

where \(V_s\) and \(E_s\) represent the set of nodes and links for the community \(S\), respectively.

**Conductance.** This criterion presents the ratio between number of inter-community links \((c_S)\), and intra-community links \((m_S)\) as follows: [Leskovec et al. 2008b].

\[
\emptyset = \frac{c_S}{2m_S + c_S} \tag{30}
\]

Density and conductance are complementary measures and are often considered together. For instance, the density of a k-clique subgraph with many links to the rest of the graph is high, while its conductance low. Therefore, these two criteria are often used together to evaluate the candidate methods. In this paper, we desire to have more similarities in density and conductance among original and inferred networks.

**Number of communities.** A measure called “Accuracy in the number of communities” was introduced in [Yang and Leskovec 2012] to determine whether the inferred network has the same number of communities as the original network:

\[
NC = \frac{|CO_G| - |CO_{G^*}|}{|CO_G|} \tag{31}
\]

where \(|CO_G|\) and \(|CO_{G^*}|\) are the cardinality of the set of communities for original and inferred networks, respectively. The lower values of this metric indicate more similarity.

5.2. Network data

5.2.1. Synthetic datasets. We utilize two types of synthetic networks:

**LFR-benchmark.** As mentioned before, one of the most important features of real social networks is their community structure. To study the impact of this property on the performance of algorithms, we used the LFR-benchmark [Lancichinetti and Fortunato 2009; Lancichinetti et al. 2008] which provides real networking characteristics, and its properties can be controlled to provide networks with built-in communities. The generated networks have 1000 nodes with the characteristics shown in Table I. An important attribute of these networks is a mixing parameter called \(\mu\), which represents the network community structure. For each node, \(\mu\) is a numeric value which is equal to the ratio of inter-community to entire links of that node. The value of \(\mu\) can change between 0 and 1, and its alterations would change the community structure of the network. Larger values of \(\mu\) corresponds to less community structure in the network, while decreasing this parameter would improve the community structure of the network. According to the experimental results, values over 0.5 for \(\mu\) are not suitable for highlighting the community structures. Therefore, we evaluated the competing methods against various types of LFR-benchmark by using different values of \(\mu\) in the range of \([0.1, 0.2, 0.3, 0.4, 0.5]\).

**Real structures.** We used the real co-authorship network of scientists dataset that inherently contains many community structures.
Table II. Real networks and diffusion information over them. The specifications are for different months. Each network had been changed during the months in a year [Gomez-Rodriguez et al. 2013].

### a) LinkedIn

| Month | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 |
|-------|---|---|---|---|---|---|---|---|---|----|----|
| #Node | 203 | 306 | 509 | 552 | 536 | 490 | 586 | 560 | 541 | 464 | 497 |
| #Edge | 426 | 831 | 2043 | 2858 | 2248 | 2071 | 3395 | 3011 | 2770 | 1550 | 1760 |
| #Cascade | 671409 | 694917 | 721301 | 748705 | 716312 | 707227 | 758696 | 743881 | 729078 | 717272 | 740978 |
| Avg Cascade Length | 1.68 | 2.11 | 2.37 | 2.44 | 2.50 | 2.58 | 2.43 | 2.45 | 2.47 | 2.26 | 2.26 |
| #Community | 10 | 13 | 16 | 14 | 23 | 25 | 24 | 30 | 26 | 30 | 23 |
| Avg Community size | 16.70 | 20.23 | 30.06 | 37.57 | 22.39 | 19.84 | 24.75 | 18.60 | 20.42 | 14.10 | 20.17 |
| Avg Density | 0.5074 | 0.5031 | 0.4079 | 0.4428 | 0.4461 | 0.5386 | 0.4250 | 0.4810 | 0.4204 | 0.5430 | 0.5055 |
| Avg Conductance | 0.0114 | 0.0449 | 0.1462 | 0.1519 | 0.1611 | 0.1744 | 0.2191 | 0.2202 | 0.1658 | 0.1414 | 0.0889 |

### b) News of the World

| Month | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 |
|-------|---|---|---|---|---|---|---|---|---|----|----|
| #Node | 161 | 318 | 392 | 410 | 1188 | 1033 | 843 | 675 | 517 | 559 | 594 |
| #Edge | 559 | 1581 | 1786 | 1502 | 14637 | 7393 | 6453 | 7499 | 8040 | 7480 | 7688 |
| #Cascade | 490207 | 610465 | 704268 | 742863 | 1358394 | 1207854 | 1025146 | 908798 | 836215 | 952824 |
| Avg Cascade Length | 1.87 | 2.40 | 2.51 | 2.38 | 2.40 | 2.43 | 2.42 | 2.55 | 2.62 | 2.60 | 2.58 |
| #Community | 9 | 18 | 21 | 19 | 43 | 39 | 30 | 32 | 26 | 25 | 28 |
| Avg Community size | 15.89 | 17.50 | 18.76 | 19.63 | 29.14 | 27.26 | 22.05 | 20.38 | 23.94 | 21.82 | 15.89 |
| Avg Density | 0.4916 | 0.5067 | 0.4963 | 0.5254 | 0.4692 | 0.4488 | 0.3934 | 0.5708 | 0.5540 | 0.5247 | 0.5859 |
| Avg Conductance | 0.0587 | 0.1272 | 0.0938 | 0.0811 | 0.2537 | 0.2034 | 0.1746 | 0.2045 | 0.1305 | 0.1789 | 0.1789 |

For each of these networks, we generated various artificial cascades by using the SNAP library [Leskovec 2014] with different models, and utilized the average behaviors against different cascade models in our analysis to show independence of the proposed method from cascade models.

5.2.2 Real datasets. In this paper, we refer to a dataset as real, when its topology and corresponding diffusion are accessible. We utilized two real networks over different months for LinkedIn and News of the World sites; with community structures, nodes and links that change overtime. All the specifications are listed in Table II.

These datasets have been gathered by using the MemeTracker from March 2011 to February 2012 [Leskovec et al. 2008a]. We split all the months into eleven intervals and discuss the performance of algorithms in these intervals. The network visualizations available at [Gomez-Rodriguez et al. 2013; Leskovec 2013] maybe used to demonstrate the changes in structures and illustrate the communities for different months.

5.3 Results

We analyzed the results of three types of qualified networks based on the evaluation metrics described above. The interpretation of the results are provided in the following subsections.

5.3.1 Network inference:

**F-measure**: As Fig. 4 illustrates, the proposed algorithm (DANI) has a better performance in inferring underlying networks compared to the competing methods. As shown, DANI has a higher F-measure for LFR-benchmark networks with different community structures (different values of $\mu$). In this figure, X-axis represents the number of cascades in the network. For various community structures (mixing parameters) and number of cascades, DANI outperformed DNE and MultiTree. When $\mu$ changes from 0.1 to 0.3, DANI achieves higher F-measures in lower running time than NETINF. As the community structure fades away ($\mu > 0.3$), F-measure for DANI is four times better than DNE, and two times better than MultiTree. When
the number of cascades over the network becomes more than the number of links (> 7692), F-measure for NETINF is 0.1 more than the F-measure for DANI, while the time complexity of NETINF was much more than DANI. For the same case, MultiTree achieved the same F-measure as NETINF, while its running time was better than NETINF, but higher than DANI.

For the NetScience dataset (Fig. 5), F-measure of DANI was consistently more than DNE. For small number of cascades, DANI had higher F-measure than NETINF and MultiTree. Therefore, when the number of cascades are higher than the number of the links (> 2742), NETINF and MultiTree infer the links accurately, but they require considerably higher running time compared to DNE and DANI.

For the real datasets, we display the results for 11 different months (Figs. 6 and 7). It can be seen that DANI with higher F-measure retrieves more network links.
Fig. 5. (Color online) Test of the algorithms on a real network with the NetScience [Newman 2006b] artificial cascade; 1590 nodes, 2742 edges, and 191 communities. The communities are detected by the OSLOM algorithm [Lancichinetti et al. 2011]. Results are shown for the inferring scope: a) F-measure, and b) Running Time, and the community detection scope: c) Pairwise F-measure, and d) Normalized Mutual Information. Figures show averages over 10 runs.

Fig. 6. (Color online) Tests of the algorithms on LinkedIn dataset in 11 consecutive interval months.

Investigations show that most of the cascades over real networks are short, and the number of long diffusion processes are small [Leskovec et al. 2006]. A major contagion over networks usually does not have one seed user, and broadcasts in several different locations on the network. Each cascade motion from different users is being seen as a separated cascade. Furthermore, the wide spread of a contagion may situate on a network, but inevitably does not occur during a long cascade.
By checking the number and the length of cascades in these datasets, we concluded that the lengths of cascades are short in every month (Table II). Based on our experiments on a real network with artificial set of cascades (Fig. 8), NETINF and MultiTree accuracy are low in short cascade lengths, and their dependency on the length of cascades is greater than DANI. However, MultiTree serves better than NETINF in short cascades, and therefore performs better in real networks.

On average, in LinkedIn network, DANI has 35.1% improvement in F-measure versus NETINF, 34.3% versus MultiTree, and 10.0% versus DNE. Moreover, in News of the World network, this improvement is 77.91% against NETINF, 74.40% against MultiTree, and 42.26% against DNE.

**Number of nodes**: Table III displays the behavior of these algorithms for the number of detected nodes of the inferred networks. DNE can just retrieve a few set of nodes, and most of the links of the networks are not inferred. Although, NETINF and MultiTree are better than DNE in this regard, but their loss error is more than 20%. DANI infers the nodes with an accuracy close to 90%. In other words, DANI infers maximum number of nodes compare to the other methods. The results show that DANI is more capable in detecting nodes in the inference process, which has not been considered in prior works.

**Other network properties**: The relative error of network properties between the inferred and underlying network is illustrated in Table III. In most cases, DANI has much less error than baseline methods in term of nodes degree. In addition, the clustering coefficient metric is better maintained by DANI.

**Running time**: In order to have a fair comparison, we used the available C++ implementations in SNAP library [Leskovec 2014] for all prior algorithms, and implemented DANI in the same framework. We compared runtimes in the LFR-benchmark (Fig. 4) that showed DANI was several order of magnitude faster. In the NetScience dataset for different number of cascades, the run time is shown in Fig. 5. For running time in real data sets, similar to the approach used in [Alpay et al. 2011], we measured time versus number of cascades and links as shown in Figs. 6 and 7. On average,
DANI is 85.35% faster than NETINF, and 84.11% faster than Multitree. In general, the running time of algorithms is ordered as $t_{NETINF} \succ t_{MultiTree} \succ t_{DANI} \succ t_{DNE}$.

In all cases, our method has lower run time than tree-based algorithms, and its speed is close to DNE. The running time performance must be analyzed against inference accuracy and preserving community structures.

As illustrated, DANI achieves acceptable results with low running times, while other algorithms require higher running times to infer the networks with high accuracy.

**Evaluating the scalability:** As we already mentioned the time complexity of DANI depends on the number of users involved in cascades (nodes of network) which could be extremely large. Here, we demonstrate the scalability of DANI against the competing methods by showing the results on a real large scale network. In addition, parallel methods such as MapReduce can be used for making DANI even more scalable, but to observe fairness, we did not utilize any of them here. We studied a large Twitter network that sampled public tweets from the Twitter streaming API in the range of 24 March to 25 April at 2012 [Weng et al. 2013]. By utilizing the follower network and hashtag retweeting, we did some preprocessing by: 1) Considering any unique pair of hashtag and source ID as a separate cascade, 2) Keeping links that were being involved in at least one cascade, 3) Choosing users taking part in more than 2 cascades, and 4) Removing nodes of cascade that were not a member of network nodes. The result was a network of 124023 nodes, 182783 links, and 213875 cascades with an average length of 2.29. While DANI correctly inferred 79.64% of the links in terms of F-measure during 1 hour and 4 minutes, the other three competing methods did not yield any reasonable results during this time period.

5.3.2. Preserving community structure: One of the important properties of social networks is their community structure and our goal in this paper is to preserve this property during the network inference process. To achieve this goal, the inferred network must have the same community structure as the underlying network. Therefore, the properties such as density, conductance, community size and number of communities are some important characteristics, which we considered in our evaluations.

To detect communities in real and inferred networks, we reviewed different community detection algorithms to find an algorithm which can work with a variety of networks such as directed and undirected, support overlapping communities, detect communities with high accuracy, not require prior knowledge about the number of output communities, and require low memory and time for a sparse graph. Finally, the OSLOM algorithm was chosen which meets the above requirements. OSLOM is
the first algorithm that uses statistical features to identify the communities. To assess the accuracy, OSLOM uses local modularity measurement to avoid global errors [Lancichinetti et al. 2011].

**NMI.** Fig. 9 illustrates the values of NMI on each inferred LFR-benchmark network with varying values for $\mu$, and different number of cascades. As it can be observed, specially for fewer number of cascades, DANI performs perfectly. For higher number of cascades, the NMI values for DANI is closer to NMI of NETINF and MultiTree, while DNE has lower NMI values in all cases. Figs. 6 and 7 show the NMI values of all algorithms for real datasets. As illustrated in Fig. 5, for Netscience with artificial cascades, the running time of DANI is much lower, while its NMI is equal or more than NETINF.

For the LinkedIn dataset, as a real network, on average DANI performs 24.09%, 89.98% and 23.89% better than NETINF, MultiTree and DNE, respectively. Our improvements in News of the World dataset against NETINF, MultiTree, and DNE was...
Table III. Difference of metrics between communities at inferred and original networks for real datasets. Values are averaged over different number of cascades for the NetScience dataset, and over different months for LinkedIn and News of the World. Variances are shown in parentheses.

| Dataset         | Total Metrics | DNE | NETINF | DANI | MultiTree |
|-----------------|---------------|-----|--------|------|-----------|
|                 | #Node         | 453.77 (210502.3) | 445.41 (217805) | 445.41 (217805) | 445.41 (217805) |
|                 | Degree        | 0.583 (0.0498) | 0.575 (0.0645) | 0.529 (0.0714) | 0.569 (0.064) |
|                 | Clustering coefficient | 0.457 (0.0395) | 0.487 (0.0418) | 0.359 (0.0733) | 0.478 (0.0418) |
|                 | Density       | 0.0403 (0.0004) | 0.0401 (0.0003) | 0.0232 (0.0002) | 0.0433 (0.0006) |
|                 | #Community    | 0.477 (0.060) | 0.460 (0.076) | 0.404 (0.093) | 0.474 (0.069) |
|                 | Conductance   | 0.00515 (0.00002) | 0.00703 (0.00004) | 0.00786 (0.00006) | 0.00511 (0.00003) |
| LinkedIn        | #Node         | 109.73 (399.42) | 53.64 (79.25) | 8.91 (19.70) | 54.18 (95.36) |
|                 | Degree        | 0.747 (0.003) | 0.807 (0.001) | 0.712 (0.002) | 0.805 (0.001) |
|                 | Clustering coefficient | 0.0416 (0.0006) | 0.0757 (0.0018) | 0.0643 (0.0004) | 0.0772 (0.0018) |
|                 | Density       | 0.24 (0.01) | 0.10 (0.006) | 0.05 (0.002) | 0.09 (0.003) |
|                 | #Community    | 0.21 (0.02) | 0.45 (0.30) | 0.30 (0.08) | 0.35 (0.03) |
|                 | Conductance   | 0.04 (0.0007) | 0.08 (0.003) | 0.02 (0.0004) | 0.02 (0.0003) |
| News of the World | #Node         | 67.73 (20242.22) | 26.04 (902.25) | 3.91 (111.49) | 26.001 (402) |
|                 | Degree        | 0.888 (0.024) | 0.925 (0.016) | 0.888 (0.007) | 0.918 (0.015) |
|                 | Clustering coefficient | 0.12 (0.004) | 0.09 (0.004) | 0.09 (0.001) | 0.09 (0.004) |
|                 | Density       | 0.315 (0.0193) | 0.124 (0.005) | 0.107 (0.003) | 0.134 (0.007) |
|                 | #Community    | 0.17 (0.01) | 0.29 (0.02) | 0.16 (0.01) | 0.30 (0.03) |
|                 | Conductance   | 0.035 (0.0006) | 0.029 (0.0001) | 0.029 (0.0006) | 0.035 (0.0012) |

14.48%, 94.83%, and 15.84%, respectively. The differences between inferred and original networks, based on the criteria of Subsection 5.1 is listed in Table III. As the results show, DANI has the closest values to the original network which indicates its capability in preserving the community structures.

**PWF**: For the NetScience dataset, DANI achieves higher PWF compared to the other methods at all number of cascades smaller than 5000. For the LinkedIn network, on average DANI achieves 67.72%, 73.30% and 29.08% improvement in PWF against NETINF, MultiTree and DNE, respectively. Moreover, for News of the World, on average DANI achieves 31.29%, 35.57% and 19.94% improvement against NETINF, MultiTree and DNE, respectively.

**Density**: The inferred network by DNE has a high density which is very different from the underlying network. However, NETINF, MultiTree and DANI achieve a density similar to the underlying network, while DANI performs better than the competing algorithms.

**Conductance**: The conductance of all competing algorithms are similar. Considering the average and variance of all intervals in one year, DANI performs marginally better than other methods for all datasets.

**Number of communities**: For this metric, DANI achieved the best performance in detecting the number of communities for the inferred network compared to the original network.

6. CONCLUSION
Many works have been done to infer networks by using information diffusion, but they often neglect preserving the features of underlying networks. Community structure is one of the most important features in social networks and community detection algorithms need the network topology to extract their communities. Therefore, these algorithms cannot be applied on networks derived by the previous proposed network inference methods.

In this paper, we introduced a new algorithm to infer networks which maintains the community structure. To verify this claim, we applied the proposed (DANI), NET-
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INF, DNE, and MultiTree methods to real and artificial networks, and compared the community structure of original and inferred networks with each other. Moreover, we utilized some of the main community structure metrics to evaluate the inferred networks by different methods. The results showed that our algorithm accurately infers networks while preserving the community structures. In addition, DANI consumed less time to achieve the same or higher accuracy than the competing methods. Another advantage of the proposed method is the fact that its performance is independent of the length of cascades.

As a future work, we are trying to detect communities just based on diffusion information without the need for inferring networks. In other words, we try to find the community of each node only based on the diffusion process.

REFERENCES

Altan Alpay, Deniz Demir, and Jie Yang. 2011. FASTINF: A Fast Algorithm to Infer Social Networks from Cascades. (2011). http://snap.stanford.edu/class/cs224w-2011/proj/jieyang_Finalwriteup_v3.pdf

Eytan Bakshy, Itamar Rosenn, Cameron Marlow, and Lada Adamic. 2012. The Role of Social Networks in Information Diffusion. In Proceedings of the 21st International Conference on World Wide Web (WWW ’12). ACM, New York, NY, USA, 519–528.

Nicola Barbieri, Francesco Bonchi, and Giuseppe Manco. 2013a. Cascade-based community detection. In WSDM, Stefano Leonardi, Alessandro Panconesi, Paolo Ferragina, and Aristides Gionis (Eds.). ACM, 33–42.

Nicola Barbieri, Francesco Bonchi, and Giuseppe Manco. 2013b. Influence-Based Network-Oblivious Community Detection. In ICDM. 955–960.

S.Y. Bhat and M. Abulaish. 2013. Overlapping Social Network Communities and Viral Marketing. In Computational and Business Intelligence (ISCBII), 2013 International Symposium on. 243–246.

Paolo Boldi and Massimo Santini. 2010. Compressing Social Networks by Community Detection. Technical Report RI-DSI 330-10. Dipartimento di Scienze dell’Informazione.

Weidong Chen. 2011. Discovering communities by information diffusion. In Fuzzy Systems and Knowledge Discovery (FSKD), 2011 Eighth International Conference on, Vol. 2. 1123–1132.

Wei Chen, Yifei Yuan, and Li Zhang. 2010. Scalable influence maximization in social networks under the linear threshold model. In Data Mining (ICDM), 2010 IEEE 10th International Conference on. IEEE, 88–97.

Xiaojie Chen, Feng Fu, and Long Wang. 2007. Prisoner’s Dilemma on community networks. Physica A: Statistical Mechanics and its Applications 378, 2 (May 2007), 512–518.

L. F. Costa. 2004. Hub-Based Community Finding. (2004). (unpublished).

Nan Du, Bin Wu, Xin Pei, Bai Wang, and Lizong Xu. 2007. Community Detection in Large-scale Social Networks. In Proceedings of the 9th WebKDD and 1st SNA-KDD 2007 Workshop on Web Mining and Social Network Analysis (WebKDD / SNA-KDD ‘07). ACM, New York, NY, USA, 16–25.

J. Duch and A. Arenas. 2005. Community detection in complex networks using Extremal Optimization. Physical Review E 72 (2005), 027104.

D. Easley and J. Kleinberg. 2010. Networks, Crowds, and Markets: Reasoning About a Highly Connected World. Cambridge University Press.

Milad Eftekhari, Yashar Ganjali, and Nick Koudas. 2013. Information Cascade at Group Scale. In Proceedings of the 19th ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD ’13). ACM, New York, NY, USA, 401–409.

Motahhare Esfami, Hamid R. Rabiee, and Mostafa Salehi. 2011. DNE: A Method for Extracting Cascaded Diffusion Networks from Social Networks. In SocialCom / PASSAT. IEEE, 41–48.

Santo Fortunato. 2010. Community detection in graphs. Physics Reports 486 (2010), 75–174.

M. Girvan and M. E. J. Newman. 2002. Community structure in social and biological networks. Proceedings of the National Academy of Sciences 99, 12 (2002), 7821–7826.

Jacob Goldenberg, Barak Libai, and Eitan Muller. 2001. Talk of the network: A complex systems look at the underlying process of word-of-mouth. Marketing letters 12 (2001), 211–223.

Manuel Gomez-Rodriguez, David Balduzzi, and Bernhard Scholkopf. 2011. Uncovering the Temporal Dynamics of Diffusion Networks. In Twenty-eighth International Conference on Machine Learning. Bellevue, Washington, Lise Getoor and Tobias Scheffer (Eds.). Omnipress, 561–568.

ACM Transactions on Intelligent Systems and Technology, Vol. V, No. N, Article A, Publication date: January YYYY.
DANI: A Fast Community-Preserving, Diffusion Aware Network Inference Algorithm

M. E. Newman. 2006a. Modularity and community structure in networks. *Proc Natl Acad Sci USA* 103, 23 (Jun 2006), 8577–8582.

M. E. J. Newman. 2006b. Finding community structure in networks using the eigenvectors of matrices. *Physical Review E* 74, 3 (2006), 036104.

Guo-Jun Qi, Charu C. Aggarwal, and Thomas S. Huang. 2012. Community Detection with Edge Content in Social Media Networks. In ICDE, Anastasios Kementsietsidis and Marcos Antonio Vaz Salles (Eds.). IEEE Computer Society, 534–545.

Usha Nandini RAGHAVAN, Réka ALBERT, and Soundar KUMARA. 2007. Near linear time algorithm to detect community structures in large-scale networks. *Physical Review E, Statistical, nonlinear, and soft matter physics* 76, 3 (2007).

Shaghayegh Sahebi and William Cohen. 2011. Community-based recommendations: a solution to the cold start problem. In *Workshop on Recommender Systems and the Social Web, RSWeb*.

Kazumi Saito, Ryohei Nakano, and Masahiro Kimura. 2008. Prediction of Information Diffusion Probabilities for Independent Cascade Model. In *KES* (3), Ignac Lovrek, Robert J. Howlett, and Lakhmi C. Jain (Eds.). Vol. 5179. Springer, 67–75.

Jerry Scripps, Pang-Ning Tan, and Abdol-Hossein Esfahanian. 2007. Node roles and community structure in networks. In *Proceedings of the 9th WebKDD and 1st SNA-KDD 2007 workshop on Web mining and social network analysis (WebKDD / SNA-KDD ’07)*. ACM, New York, NY, USA, 26–35.

Keyi Shen, Li Song, Xiaokang Yang, and Wenjun Zhang. 2010. A Hierarchical Diffusion Algorithm for Community Detection in Social Networks. *2013 International Conference on Cyber-Enabled Distributed Computing and Knowledge Discovery* 0 (2010), 276–283.

Mahadevan Vasudevan and Narasingh Deo. 2010. Community Identification Algorithm using Relative edge density measure. *Congressus Numerantium* 204 (2010), 147–160.

Lilian Weng, Filippo Menczer, and Yong-Yeol Ahn. 2013. Virality prediction and community structure in social networks. *Scientific reports* 3 (2013).

Jierui Xie, Stephen Kelley, and Boleslaw K. Szymanski. 2013. Overlapping Community Detection in Networks: the State of the Art and Comparative Study. *ACM Computing Surveys (CSUR)* 45, 4 (2013), 43:1–43:35.

Bo Yang, Jing Huang, Dayou Liu, and Jiming Liu. 2009a. A Multi-Agent Based Decentralized Algorithm for Social Network Community Mining. *2012 IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining* 0 (2009), 78–82.

Jaewon Yang and Jure Leskovec. 2012. Community-Affiliation Graph Model for Overlapping Network Community Detection. In *ICDM*, Mohammed Javeed Zaki, Arno Siebes, Jeffrey Xu Yu, Bart Goethals, Geoffrey I. Webb, and Xiaodong Wu (Eds.). IEEE Computer Society, 1170–1175.

Tianbao Yang, Rong Jin, Yun Chi, and Shenghuo Zhu. 2009b. A Bayesian Framework for Community Detection Integrating Content and Link. In *Proceedings of the Twenty-Fifth Conference on Uncertainty in Artificial Intelligence*. 615–622.

Ming Zhong, Cao Zhong, and others. 2008. TopSeer: A Novel Scholar Search Engine based on Community Detection in Citation Network. In *11th Joint International Conference on Information Sciences*. Atlantis Press.

ACM Transactions on Intelligent Systems and Technology, Vol. V, No. N, Article A, Publication date: January YYYYY.