An Efficient homophilic Model and Algorithms for Community Detection using Nash Dynamics

Radhika Arava
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Abstract

The problem of community detection is important as it helps in understanding the spread of information in a social network. All real complex networks have an inbuilt structure which captures and characterizes the network dynamics between its nodes. Linkages are more likely to form between similar nodes, leading to the formation of some community structure which characterizes the network dynamic. The more friends they have in common, the more the influence that each person can exercise on the other. People use their attributes to assess the similarity of the other people with them, similarly, the attributes are also influenced with the people they interact and the network structure. Hence, we assume that communities capture homophily as people of the same community share a lot of similar features. The contributions of my thesis are as follows:

• We propose a disjoint community detection algorithm, NashDisjoint that detects disjoint communities in any given network.
• We evaluate the algorithm NashDisjoint against the best state of the art algorithms so far, and we find that our algorithm works at least as good as that of the state of the art algorithms on the standard LFR Benchmarks for the mixing factors less than 0.55 in all the cases.
• On Real Social Networks, we observe that the modularity values for the community structure detected by our algorithm NashDisjoint is in comparison to that of one of the best modularity optimization algorithms so far.
• We propose an overlapping community detection algorithm NashOverlap to detect the overlapping communities in any given network.
• We evaluate the algorithm NashOverlap against the best state of the art algorithms so far and we find that our algorithm works far better than the state of the art algorithms on the standard LFR benchmarks in around 140 different scenarios, generated by varying the number of nodes, mixing factor and overlapping membership.
• The algorithm NashDisjoint is modeled as a sequence of weighted potential games. As a part of the first game, the algorithm computes the closeness values for every edge. Worst case time for the first game to converge is $O(k_1 \cdot m)$ where $k_1$ is the number of iterations it takes for each of the $k$ subgames to converge. As a part of the second game, the algorithm picks the closeness values returned by the first game and computes the disjoint community structure. Its time complexity is $O(k_2 \cdot m)$ where $k_2$ is the number of iterations it takes for the second game to converge.
• Of all the community structures possible in the given network, our algorithm NashDisjoint detects the community structure which has a minimal value for the sum of the probability strengths of the cut edges of that community structure.
• Similarly, the overlapping community detection algorithm \textit{NashOverlap} can be formulated as a sequence of weighted potential games, where the value of the potential function for a given cover is constantly proportional to the sum of the probability strengths of the cut edges of that cover. For a given cover, duplicate the vertex for each community that it is a part of, and the cut edges are the edges between the vertices between two different communities. The time complexity is \(O(k \cdot k_1 \cdot m)\) for the first game and \(O(k_2 \cdot m)\) for the second game where \(k_1\) and \(k_2\) are respectively the number of iterations it takes for both first game and the second game to converge and \(k\) is the number of subgames.

• We run our algorithm \textit{NashOverlap} on DBLP dataset to detect the top collaboration groups. We have identified a giant component as a top collaboration group and the second largest collaboration group is much smaller than the giant component. This is due to the percolating regime characteristic of such networks, there exist very small connected clusters, each with very few edges in them, and of which most of them group to form a giant component with the increase in the number of edges in the network, leaving behind small clusters, which only group later into the giant component, with the further increase in connections. This leads to a reasoning which says that the scientific collaboration network is highly connected and there is a possibility of more interdisciplinary work in the future which is a good sign for the development of science. The diameter of the largest collaboration group for both the datasets is between 9 and 11 and has the average path length between 4 and 5, which strengthens the above argument. Also, the average number of intermediate researchers that connect any pair of researchers in the giant component is quite less.

• These results of our algorithm on DBLP collaboration network are compared with the results of the \textit{COPRA} algorithm and \textit{OSLOM}. We find that our algorithm has detected more collaboration groups of significant size each of which carries an identity, compared to that of \textit{COPRA} or \textit{OSLOM}. Also, the communities detected by our algorithm are much bigger in size with a least number of outlier nodes. The community structure is likely to have more mixing factor than that of detected by \textit{COPRA} and \textit{OSLOM}. It means, that the collaboration groups are big enough in size with several researchers in each, so that almost no researcher who concern this collaboration group is ignored.

1 Introduction

The insight of the topology of the network in terms of its community structure is important as it helps in understanding the spread of information, rumor, fashion, joke or any disease or any epidemic in a social network. For eg., social networks like Facebook can deploy viral marketing strategies and place online ads on user profiles in such a way that fetches them the maximum revenue. Future popularity of a meme can be predicted by quantifying its early spreading pattern in terms of its community concentration. For example, the more communities a meme permeates, the more viral it is. Thus, information about community structure gives predictive knowledge about what information will spread widely \cite{31}. Also, study of community structure in a power grid helps in estimating the robustness and stability of power transmission as in \cite{18,6}.

Community structure of metabolic or biological networks can help in identifying the cure for complex diseases as in \cite{16}. Using the data of the spread of epidemic over time in a certain region and the community structure of the network, one can identify the reasons behind the transmission of the disease and its eventual spread in the entire region and find out the ways that it can be controlled. In large protein-protein interaction data sets, protein-protein interactions enable proteins to act concerted to carry out their functions. Community structure on protein interaction networks show the potentially good candidates for the modules of proteins responsible for some function.
In real-world networks, each node is likely to be a part of more than one community. For example, in a social network like Facebook, MySpace, there can be overlap between a user’s high school friends’ circle and his university friends’ circle. Similarly, if the user made friends with people of common interests, and we associate each community to an interest, then it is very likely that the same person can be in more than one community. So, it is common to expect the overlap between the communities. In a citation network on research papers, a paper which proposes innovative methods with applications in varied fields is likely to be cited by research papers from different fields. Similarly, in a collaboration network, a researcher may have simultaneously worked in two different collaboration groups due to change in his geographical locations or research fields or having worked for a long timespan. In a biological network on genes, a gene can be responsible for more than one disease. So, it is common to observe overlap in the community structures in many networks.

However, there also exist real world networks such that we are interested in segregating the nodes into disjoint communities, even when there is a possibility of overlap between the communities. For example, in task scheduling on multiprocessors, and finding clusters in VLSI design circuits, overlapping is not allowed since we don’t want to run the same task on two processors simultaneously or similarly we do not allow the same transistor in two different clusters of the circuit.

Depending upon the problem in hand, we need an algorithm which detects the best community structure for the given network. We start by defining the notation needed for overlapping community structure in networks. Each node $i$ of a network can be characterized by an overlapping membership number $om_i$, which is the number of communities that the node belongs to. In turn, any two communities $C_1$ and $C_2$ can share $C_1 \cap C_2$ nodes, which we define as the overlap size between these communities. Naturally, any community structure constitutes a network with vertices as communities and edges exist between a pair of communities if there are any cut edges between the communities. The size of the community is its number of nodes. The weight of the edge between the vertices is the sum of the weights of the cut edges between the communities denoted by the vertices. A good community structure should have be very sparse or should be very lightweight in the weights of its edges.

For a given community assignment to all the vertices of a network, mixing factor $\mu$ is the maximum fraction of degree of each vertex, outside its community. If the mixing factor is very low, then the community structure is very clear, with very minimal inter-community edges. If the mixing factor is very high, the community structure cannot be identified easily, as there will be several inter-community edges. Given a mixing factor, the network’s community structure can be either disjoint or overlapping. In the disjoint community structure, each node is a part of only one community. If the network has overlapping community structure, then there exists some nodes which are a part of more than one community. Having seen the significance of community detection in both overlapping and non-overlapping cases, there is a need for a single model which explains the reasons for why and how the communities form in the first place in a social network, which lead to the algorithms that can detect the communities in the network accurately. However, there is no standard definition as to what set of nodes describes a community accurately. So, there is a standard benchmark which generates the network with a community structure, given the mixing factor, and the distribution of degree, community size and the overlapping parameters which include overlapping membership and number of overlapping nodes. It is a common practice in the scientific community, that all the algorithms are tested for their quality against this benchmark.

An algorithm for community detection takes the network as input and outputs a community structure which is a set of groups of nodes, which we call communities/clusters. Each community is usually assumed to be a densely connected group of nodes with more links among themselves than between the group nodes and the rest of the network. A node can be a part of more than one community. Two community structures are evaluated for their similarity using the standard
measure, \textit{Normalized Mutual Information} [8].

The idea behind our model is as follows: all real complex networks have an inbuilt structure which captures and characterizes the network dynamics between its nodes. In a given geographical region, each person is more likely to interact with the other person, which can create a friendship link between them. People have a tendency to associate with people who are more similar to themselves in several socially significant ways. Any two people with several common interests, skills and cultural backgrounds are more likely to form a link. Also, people usually tend to become friends with the friends of their friends. Thus linkages are more likely to form between such similar nodes, leading to the formation of some community structure which characterizes the network dynamic. Also, the more friends they have in common, the more the influence that each person can exercise on the other. People use their attributes to assess the similarity of the other people with them, similarly, the attributes are also influenced with the people they interact and the network structure. We assume that communities capture homophily as people of the same community share a lot of similar features. In the literature, a large number of community detection algorithms have been proposed, however most of them are in the area of disjoint community detection.

The following are the methods used for both overlapping and nonoverlapping community detection, a) partitioning methods based on betweenness [12, 25], clique percolation methods [28], information-theoretic techniques [29, 30, 11], random walks [], modularity optimization methods [7, 26, 4], statistical inference through belief propagation [13], label propagation [15, 33, 32], game theoretic techniques [5, 24, 8, 22]. Of them, a very few algorithms are focussed at the problem of detecting overlapping community structures in a network.

Most of the existing community detection algorithms fall into the following categories: a) optimizing the network structural properties like modularity, betweenness, conductance b) inference based approach c) label propagation d) information theory e) game theory based algorithms. The first approach does not let us model the reason behind the formation of the communities probabilistically as it focusses on optimizing a graph structural property. The algorithms due to second approach so far are not very robust and scalable and that of third approach runs quadratic in time or make too simple assumptions. The information theory approach worked well for the disjoint community detection, but it is not efficient in case of the overlapping community detection. There are a very few game theory based algorithms and the best game theory based overlapping community detection algorithm so far, has running time which is quadratic in the number of edges and is not very efficient. We need an algorithm that outputs the network’s inbuilt community structure, even when the network has a fuzzy community structure.

2 Motivation

The algorithms for community detection should be simple to implement, scalable and should be natural in its construction, such that the model can reason the formation of the detected communities probabilistically. Also, in the literature, there are no simple and practically efficient game theory based algorithms which work for both disjoint community detection and overlapping community detection.

In a social network, it is natural that the friendship between a pair of nodes becomes more stronger with the increase in the number of their common friends. Each of them is more influenced by the other, and since they are under the influence of each other, they follow the same trend, or have similar behavior. Most certainly, each node behaves the same way as his closer friends who influence him the most does. We assume that given the topology of the network, and when enough number of the trends say $r$ are allowed to be adopted by the network, then the network adopts at
most $k$ number of trends, where $k$ is the number of communities that the network can naturally group into. This assumption makes sense because a pair of nodes is likely to make new connections to some other nodes, provided there exists some similarity in the pair and also between pair and the new connections that it makes. Also, the similarity increases with the number of connections that the pair makes. Hence in a closely connected groups of nodes, the clustering coefficient is higher and hence the number of triangles is higher, which means that for a pair of nodes to assume they influence each other, there are several common neighbors. This is the idea behind our model and algorithms for community detection which follow subsequently.

Our model is natural since its underlying principle is the formation of the network using network dynamics. It reasons the formation of the communities probabilistically in the following way. In a group of people, the more the attributes that each person characterizes, the more difficult it is to decide upon a good community structure that can be characterized by the entire group. This is because, the closeness of the link depends on the number of attributes that the two persons have in common. Also, the algorithms are very simple to implement and practically efficient.

3 Theory

In a social network $G = (V,E)$, $V$ is the set of vertices and $E$ is the set of undirected edges that represent relations between vertices in the network. Let $w(i,j)$ be the weight of the edge $(i,j) \in E$. If the graph is unweighted, we assume that each edge has unit weight. A community in a social network is a non-empty connected subset of vertices with denser connections within themselves than with the rest of the network. A network has a community structure if the vertices in the network can be grouped into communities such that the connections are dense within the community and are sparse between the communities. The community structure can be non-overlapping or overlapping.

Formally, let $C_i$ be a subset of vertices denoting a community.

**Definition 1.** A partition of the network $G$ is defined as $\Gamma = \{C_1, C_2, \ldots, C_m\}$, where $\bigcup_i C_i = V$ and $C_i \cap C_j = \emptyset$ for any $i \neq j$.

**Definition 2.** A cover of the network $G$ is defined as $\Gamma = \{C_1, C_2, \ldots, C_m\}$, where $\bigcup_i C_i = V$ and $C_i \cap C_j$ need not be $\emptyset$ for any $i \neq j$.

There is no standard notion as to how good the grouping of the subset of vertices should be, for it to be called as a community. A network can be naturally grouped into non-overlapping communities or overlapping communities. However, some scenarios require us to detect only disjoint community structure for its purposes, despite the existence of a few overlapping vertices. So, we proposed community detection algorithms one for each purpose: a) Disjoint Community Detection b) Overlapping Community Detection.

We pose each algorithm as a sequence of two weighted potential games. The first game is common for both the algorithms and at the end of the game, the closeness of vertices on each of its adjacent vertices is computed. The second game is slightly different for each of the algorithms, to accommodate its purpose. We first define the concept of weighted potential game and describe each algorithm as a sequence of weighted potential games.

A weighted potential game is first introduced by Monderer and Shapley in their landmark paper.

A game with a finite number of strategic players say $n$ is a weighted potential game if it admits a weighted potential function, which is as defined follows.

Let $t = (t_i)_{i \in V}$ be a vector of positive real numbers called weights. Let $Y_i$ be the set of strategies of vertex $i$ and the utility function of player $i$ is $u_i : Y \mapsto \mathbb{R}$ where $Y = Y_1 \times Y_2 \times \ldots \times Y_n$. A
function $\Phi : Y \mapsto \mathbb{R}$ is a weighted potential function if for every $i \in V$, and for every $y_{-i} \in Y_{-i}$, and for every $y_i, y'_i \in Y_i$,

$$\Phi(y'_i, y_{-i}) - \Phi(y_i, y_{-i}) = t_i(u_i(y'_i, y_{-i}) - u_i(y_i, y_{-i}))$$  \(1\)

**Definition 3.** A strategy profile is called a (pure) Nash Equilibrium if no individual $i$ can improve his utility by unilaterally changing his own strategy (i.e., adopting another strategy).

Every weighted potential game has a pure nash equilibrium \[23\].

First, the model and the assumptions underlying the algorithms are described. Each algorithm is described as a sequence of weighted potential games and show the existence of the pure nash equilibrium in all the cases by proving conditions of convergence wherever they are required.

### 3.1 Model

For a given social network $G$, consider the following game: Each vertex $i \in V$ represents a player. There are two types of strategies $a$ and $b$, and each player $i$ determines which strategy to adopt. To begin with, each vertex $i$ picks a strategy $s_i \in \{a, b\}$ at random. Approximately, half the vertices pick strategy $a$ and the other half pick the strategy $b$. In any given round, an arbitrary vertex $i$ changes its strategy if it can increase its utility, greater than that of its current utility. At any moment, the cut is defined as the subset of vertices which adopt a single strategy while its complement adopts another strategy and the cut edge is the edge between two vertices playing different strategies. This model is inspired from the paper by Bei et al. \[3\].

Let $s_i \in \{a, b\}$ denote the strategy that player $i$ chooses; then $(s_i)_{i \in V}$ defines a strategy profile of the game. For any given strategy profile, the normalized utility of player $i$ is defined as follows:

$$u_i = \frac{\sum_{\forall j: (i,j) \in E \land s_i = s_j} t(i,j)}{\sum_{j: (i,j) \in E} t(i,j)}$$  \(2\)

where

$$t(i,j) = w(i,j) + \sum_{\forall k: (i,k) \in E \land (k,j) \in E} \{w(i,k) + w(j,k)\}$$

Observe that $t(i,j)$ is the sum of the weights due to all common friends $k$ of $i$ and $j$ plus the edge weight $w(i,j)$. The numerator in the above formula is the total tie-strength of the neighbors of $i$ that choose the same strategy as him, and the denominator is the total tie-strength of all edges incident to $i$, which is a fixed number. The utility of an individual thus completely depends on his and his friends’ strategies.

Let the potential function $\Phi$ be the function from the cut to the sum of the tie-strengths of the edges which are not cut edges. Let $t_i$ be the sum of the tie-strengths of the adjacent edges of player $i$. Let $u_i(s_i, s_{-i})$, be the utility of the player $i$ when his strategy is $s_i$, while the strategy vector of the other players is $s_{-i}$. According to the definition, the utility function $u_i(s_i, s_{-i})$ is the fraction

\[3\]The function $t(i,j)$ gives the tie strength between $i$ and $j$. The concept of tie strength was first introduced by Granovetter in his landmark paper \[14\]; a basic hypothesis is that the stronger the tie strength between two individuals, the larger the proportion of individuals in the rest to whom they both are tied.
of the sum of the weights of the adjacent edges with condition $s_i = s_j$.

$$u_i(s_i, s_{-i}) = \frac{\sum_{\forall j: (i,j) \in E \land s_i = s_j} t(i,j)}{t_i} \tag{3}$$

We now prove that in each round, when an arbitrary vertex $k$ changes its strategy, along with the increase in the utility of the vertex $k$, the potential function also increases in its value and the difference in the change of the potential function is constant times proportional to the increase in the utility of the vertex $k$. The constant is $t_i$, which is given by the sum of the tie-strengths of adjacent edges of the vertex $k$.

**Proof.** When an arbitrary vertex $k$ changes its strategy from $s_k$ to $s'_k$ to increase its utility, the set of cut edges changes from $E_c$ to $E'_c$. The potential function increases in value and the increase in the value of the potential function $\Phi$ is as follows

$$\sum_{\forall (i,j) \in E \setminus E'_c} t(i,j) - \sum_{\forall (i,j) \in E \setminus E_c} t(i,j) \tag{4}$$

Since, in this round, only vertex $k$ changes its strategy, the cut edges due to $k$ become internal edges and internal edges before the change in the strategy become cut edges, and the rest of the cut edges do not change their state. So, the above expression is same as

$$\sum_{\forall (k,l) \in E \setminus E'_c} t(k,l) - \sum_{\forall (k,l) \in E \setminus E_c} t(k,l) \tag{5}$$

For each edge $(k,l)$ in $E \setminus E'_c$, since $s_k$ is same as $s_i$, the above expression is written as

$$t_k \cdot [u_k(s'_k, s_{-k}) - u_k(s_k, s_{-k})] \tag{6}$$

However, since the vertex $k$ changes its strategy only when his utility is greater than that of its current strategy, the expression 6 is always positive. Also, the difference in the potential function is same as the difference in the utility function of the player who changed its strategy. So, we formulated the dynamic as a weighted potential game and hence the dynamic always converges. $\square$

Thus, a pure Nash equilibrium always exists, and can be achieved by the best response dynamics, where players sequentially choose strategies that yield the highest utilities. This simulation or the sub-game is repeated 1000 times on the network, with different random initializations. The number of times the sub-game is repeated depends on the size of the network and increases with its size to improve the accuracy of the algorithm. For every pair of vertices $i$ and $j$ that are connected by an edge, we compute the frequency that $i$ and $j$ end up with using the same strategy among all 1000 simulations and normalize it and call the normalized value as $p(i,j)$, defined as the edge closeness.

The simulation is run enough number of times to get an accurate value for the edge closeness $p(i,j)$, for all the edges. In each game, we can use more than two strategies to compute the cut and still the game converges. However, we choose 2 strategies to simulate each sub-game in order to decrease the convergence time to reach Nash equilibrium.

The output of the first game is given as input to the second game which now differs for both the algorithms $NashDisjoint$ and $NashOverlap$.

Closeness of a vertex $v$ to a community $C$ is defined as follows:
Definition 4. Given a vertex $i$ and a community $C \in \Gamma$, define the closeness $p(i, C)$ to be the sum of probability of closeness of all edges between $i$ and $C$. That is,

$$p(i, C) = \sum_{\forall (i, j) \in E, j \in C} p(i, j).$$

Our algorithm for disjoint community detection computes the community structure of the network such that each vertex chooses to be a part of that community to which its closeness is higher than the rest of the communities that it can be a part of. Our algorithm for overlapping community detection computes the community structure of the network such that each vertex chooses to be a part of those communities to which its closeness is at least $\alpha$ times its maximum closeness to any of its adjacent communities. Thus in both the cases, we chose to pick a community structure which happens to be at equilibrium for all the vertices, such that no vertex would like to change its community(ies) at equilibrium.

3.1.1 Disjoint Community Detection

The first game outputs the closeness for each edge, which measures the number of sub-games in which each vertex shared the same strategy as its adjacent vertex. Compute the connected components $\Gamma$ in the network, considering only the network edges $(i, j)$ with edge closeness $p(i, j) > \beta$. We pick $\beta = 0.95$ for all our cases. As we decrease the value of beta, the number of connected components detected after the first game decrease and we are likely to detect the community structure of greater mixing factor, i.e., fuzzy community structure. So, we are at disadvantage when we pick a lower value of $\beta$ when the network has a good community structure.

Let the initial community structure computed using the results of the first game be $\Gamma$. Consider the second game in which in each round, each player chooses to join the community to which his closeness is higher and dissociates himself from his previous community. In each round, an arbitrary player $k$ is picked and he computes his closeness $p(k, C)$ to all communities. Note that the closeness to all communities other than his adjacent communities is zero (since $p(k, l) = 0, \forall (k, l) \notin E$). The player, since he is strategic and rational, chooses to associate with the community to which his closeness $p(k, C)$ is higher and if it is different from his previous community, he dissociates from his previous community. The utility of the player $i$ towards his new community is his closeness to community $C$. The game is played until, no player finds it in his best interest to change his community. We show that the game halts in finite number of rounds, by showing it as a weighted potential game.

Here, the potential function is a mapping of community assignment due to the partition to the sum of the edge-closeness values of the edges which are not cut-edges of that partition. A cut edge is an edge which has its vertices in two different communities. Formally, let $\Phi$ be a potential function of a partition as follows : $\Phi : \{C_1, C_2, \ldots, C_n\} \rightarrow \mathbb{R}$, where $C_k$ is the community of player $k$.

We now show that when a player $k$ leaves community $C_k$ and moves into community $C'_k$, the value of the potential function increases and the increase in the potential function $\Phi$ is same as the change in the utility of the player $k$.

Proof. When player $k$ changes its community from $C_k$ to $C'_k$, let $E_c$ be the cut-edges at the beginning of the round and $E'_c$ be the set of cut edges at the end of the round. So, the change in the potential function is as follows:

$$\sum_{\forall (i, j) \in E \setminus E'_c} p(i, j) - \sum_{\forall (i, j) \in E \setminus E_c} p(i, j)$$

(7)
The internal edges of $k$ at the beginning of the round become cut edges at the end of the round. Some of the cut edges at the beginning of the round become the internal edges of $k$ at the end of the round. Edges which are not adjacent to $k$ do not change their state. So, the above expression can be written as

$$\sum_{\forall (k,l) \in E \setminus E'} p(k,l) - \sum_{\forall (k,l) \in E \setminus E'} p(k,l) \quad (8)$$

Since, the adjacent edges to $k$ to all its adjacent communities other than $C_k$ and $C'_k$ do not change their state before and after the round, the above expression can be written as

$$\sum_{\forall (k,l) \in E \setminus E'} p(k,l) - \sum_{\forall (k,l) \in E \setminus E'} p(k,l) \quad (9)$$

which is same as

$$p(k, C'_k) - p(k, C_k) \quad (10)$$

The player leaves the community $C_k$ and moves into the community $C'_k$, because the sum of its closeness to $C'_k$ is more than that of to $C_k$. So, the difference $10$ is always positive. So, each time the player changes his community, he maximizes the potential function and the difference of the potential function in each round is same as the change in the utility function of the player which changes its community. So, this game converges to a nash equilibrium. □

At equilibrium, we get a set of subsets of network, which are pairwise disjoint, such that each player do not wish to change his strategy any more. However, these subsets need not be connected. So, we compute the set of connected components of each of the subsets computed by this game and return it as the disjoint community structure detected by our algorithm.

3.2 Overlapping Community Detection

The output of overlapping community detection algorithm is a community structure in which a vertex can be a part of more than one community, which we call as a cover. Our algorithm $NashOverlap$ computes the community structure of the network such that each vertex chooses to be a part of those communities to which its closeness is at least $\alpha$ (where $0 \leq \alpha \leq 1$) times its maximum closeness to any of its adjacent communities.

The first game outputs the closeness for each edge, which measures the number of sub-games in which each vertex shared the same strategy as its adjacent vertex. Compute the connected components $\Gamma$ in the network, considering only the network edges $(i, j)$ with edge closeness $p(i, j) > \beta$. We choose $\beta$ to be either 0.95 or 1 for the considered networks. This partition on the induced network along with the edge closeness values from the first game constitutes the input for the subsequent game.

Consider the following game: in each round, an arbitrary vertex $k$ computes the closeness values to all the communities and associates itself only with the communities which are enough close to it i.e., $p(k, C) \geq \alpha \cdot \max$, where $\max$ is the maximum closeness of $k$ to any community $C$. If it is previously associated with any community to which its closeness $p(k, C')$ is less than $\alpha \cdot \max$ in the current round, then it dissociates itself from that community. The game is played until, there exists no vertex $k$ such that it needs to change its set of communities. We show that the game ends in finite number of rounds, by showing it as a weighted potential game.

For a given cover, we shall duplicate every vertex in each of its overlapping communities. Let $C_k$ be the set of communities of player $k$ in a given cover. So, in each of its communities $C \in C_k.$
a copy of vertex $k$ is put. Define, the utility of the player $k$ as the sum of the probabilities of the edges of $k$ to the communities $C \in C_k$. Define $\Phi$, the potential function as the function from a cover to the sum of the edge-closeness values of the edges which are not cut-edges.

Formally, let $\Phi$ be a potential function of a cover as follows: $\Phi : \{C_1, C_2, \ldots, C_n\} \mapsto \mathbb{R}$, and is given by

$$\frac{1}{2} \cdot \sum_{\forall i \in V} \sum_{\forall C \in \zeta} p(i, C)$$

(11)

We now show that the difference in the potential function is same as the utility of the player $k$ who changes his communities in that round.

Proof. When player $k$ changes his communities from $C_k$ to $C'_k$, let us say that the cover changes from $\zeta$ to $\zeta'$. Then the difference in the potential function is as follows:

$$\frac{1}{2} \cdot \left\{ \sum_{\forall i \in V} \sum_{\forall C \in \zeta'} p(i, C) - \sum_{\forall i \in V} \sum_{\forall C \in \zeta} p(i, C) \right\}$$

(12)

Note that $p(i, C) = 0$ for all $C$, which are not adjacent communities of player $i$. This is same as

$$\sum_{\forall C : C \subseteq \zeta'} \sum_{\forall (i,j) \in E} p(i,j) - \sum_{\forall C : C \subseteq \zeta} \sum_{\forall (i,j) \in E} p(i,j)$$

(13)

where $C_i$ denotes the set of communities of player $i$. When player $k$ changes in its communities, then only the $k$'s adjacent edges $(k,l)$ need to be taken into account.

$$\sum_{\forall (k,l) \in E} p(k,l) - \sum_{\forall C : C \subseteq C'_k \cap C_l} \sum_{\forall (k,l) \in E} p(k,l)$$

(14)

which is same as the

$$\sum_{\forall C : C \subseteq \zeta'_k} p(k,C) - \sum_{\forall C : C \subseteq \zeta_k} p(k,C)$$

(15)

So, the above equation gives the difference in the utility of the player $k$ when it changed its set of communities from $C_k$ to $C'_k$. So, this defines a weighted potential game and hence the game converges.

At equilibrium, we get a set of subsets of network, which are pairwise need not be disjoint, such that each player do not wish to change his strategy any more. However, these subsets need not be connected. So, we compute the set of connected components of each of the subsets computed by this game and return it as the overlapping community structure detected by our algorithm.
4 Algorithm *NashDisjoint*

**Algorithm 1 NashDisjoint**

\textbf{Algorithm 1} \textit{NashDisjoint}

\textbf{G}(V, E): is the input network

\textbf{for} \textbf{v} \in V \textbf{do}

\hspace{1em} Pick one of the strategies \textbf{s}_v \text{ in } \{a, b\} \text{ uniformly at random}

\textbf{end for}

\textbf{for} iter \in 1000 \textbf{do}

\hspace{1em} \textbf{for} \textbf{v} \in V \textbf{ do}

\hspace{2em} choose \textbf{s}_v \text{ such that } u_v(s_v, s_{-v}) \text{ is maximum}

\hspace{1em} \textbf{end for}

\hspace{1em} update the closeness probabilities \(p(i, j)\) for all edges

\textbf{end for}

Compute the connected components of the graph induced on the network with edges of closeness probability \(p(i, j) > \beta\)

\textbf{repeat}

\hspace{1em} \textbf{for} \textbf{v} \in V \textbf{ do}

\hspace{2em} \text{T} \text{ is the set of } \textbf{v}'s \text{ adjacent communities}

\hspace{2em} \textbf{for} \textbf{C} \in \text{T} \textbf{ do}

\hspace{3em} Compute the closeness function \(p_v(C)\)

\hspace{2em} \textbf{end for}

\hspace{2em} Let \(C' = \arg_{C \in T} \max p_v(C)\)

\hspace{2em} Add \textbf{v} to community \(C'\) and remove \textbf{v} from its old community.

\hspace{1em} \textbf{end for}

\textbf{until} partition computed is the same in two consecutive iterations

\textbf{return}  List out the connected components in the final partition as the output
5 Algorithm $NashOverlap$

**Algorithm 2 $NashOverlap$**

$G(V,E)$ is the input network

for $v \in V$ do
  Pick one of the strategies $s_v$ in $\{a,b\}$ uniformly at random
end for

for $iter \in 1000$ do
  for $v \in V$ do
    choose $s_v$ such that $u_v(s_v, s_{-v})$ is maximum
  end for
  update the closeness probabilities $p(i,j)$ for all edges
end for

Compute the connected components of the graph induced on the network with edges with closeness probability $p(i,j) > \beta$

$\alpha$ is a parameter to be tuned.

repeat
  for $v \in V$ do
    Let $T$ be set of $v$’s adjacent communities
    for $C \in T$ do
      Compute the closeness function $p_v(C)$.
    end for
    Compute $\max_C \{p_v(C)\}$
    Let $R = \{C| p_v(C) > \alpha \max_C(p_v(C))\}$
    Assign $R$ as $v$’s communities
  end for
until Cover computed is the same in two consecutive iterations

return List out the connected components in the final cover as the output

5.1 Time Complexity

The value of the potential function at convergence increases with increase in the value of $\alpha$. The number of iterations that the algorithm takes increases with decrease in $\alpha$. If $\alpha$ is one, then the algorithm $NashOverlap$ is same as NashDisjoint.

6 Performance of $NashDisjoint$ on Synthetic Networks

In this section, we compare the performance of our algorithm $NashDisjoint$ with the best known state of the art algorithms: CFinder [28], Louvain [4], MarkovCluster [9], Infomap [30], Infomod [29] on the standard LFR benchmarks.
Figure 1: Performance of \textit{NashDisjoint} on 1000 node network and large communities

![Performance on 1000 node LFR benchmark networks with large communities]

Figure 2: Performance of \textit{NashDisjoint} on 1000 node network and small communities

![Performance on 1000 node small community]
6.1 Tests on LFR Benchmarks

We used the following parameters to generate LFR benchmark graphs \cite{20}: The exponent of the degree distribution and community size distribution are 2 and 1 respectively. The average degree and the maximum degree are set to 20 and 50, respectively. The other graph parameters are varied as follows:
The experiments to compare the performance of community detection algorithms are conducted on these benchmark graphs for several reasons. First, these benchmarks come along with a ground truth community structures. Secondly, as these benchmark graphs resemble real social networks, they provide a good challenge to all the algorithms which claim to detect the communities in real networks. We used the authors’ source code for all the algorithms.

6.2 Experimental Setup

Louvain algorithm [4] generates a hierarchy of partitions and we picked the partition that gives the maximum NMI against the ground truth community structure. CFinder algorithm [28] is run for each of the values \(k = 3, 4, 5, 6, 7, 8, 9, 10\) and the partition that returns the maximum NMI is picked. The algorithms, Infomap [30] and Infomod [29] are run with parameters set to default values. For Markov Cluster algorithm [10], we set the exponent \(k\) value to \(1, 1.4, 1.6, 1.8, 2.0, 2.2, 2.4, 2.6, 3.0\) and run the algorithm once on each graph for each exponent value. We picked the partition that gives the best NMI. Each algorithm is run on all the 10 graphs with these settings and the best NMI for each graph and the average NMI over all the 10 graphs is recorded.

6.3 Performance Analysis of NashDisjoint

NashDisjoint performs the same as the algorithm Infomap till the mixing factor 0.65 or 0.7 for 5k size networks and Infomap continues to perform till the mixing factor 0.7 or 0.75. For 1k networks, the performance of NashDisjoint is the same as Infomap until the mixing factor reaches 0.6 and falls down abruptly after 0.6. Infomap continues to perform well till the mixing factor reaches 0.65. Even for the graphs with larger mixing factors around 0.6, our algorithm NashDisjoint detects a good community structure almost as better as the best algorithm Infomap. However, our algorithm is the first game theory based disjoint community detection algorithm which comes close to this efficiency and which is simple to implement, natural, scalable and is efficient.

7 Performance of NashOverlap on synthetic networks

To study the performance of NashOverlap, we conducted extensive experiments on LFR benchmark synthetic networks [19] whose ground truth community structure is already known. We generated networks of size 1000, and 5000 and compared the performance of our algorithm with that of the other four well-performing algorithms: CFinder [28], oslom [21], copra [15], slpa [17]. The recent algorithms svinet [13], linkcluster [2], Infomap [11] performed comparably bad on all the synthetic networks considered. All the results are averaged over 10 different LFR benchmark graphs for each case.

In our simulations, we pick the following parameters in generating the LFR benchmark graphs for overlapping communities: The exponent of the degree distribution is 2 and the exponent of the community size distribution is 1. The other parameters are as follows:

- network size \((n)\) 1000 and community size in \([20, 50]\).
• network size \(n\) 1000 and community size in \([20, 100]\).

• network size \(n\) 5000 and community size in \([20, 50]\).

• network size \(n\) 5000 and community size in \([20, 100]\).

For each of the above four scenarios, we varied the mixing factor parameter \(\mu\) from 0.1 to 0.5 and we varied the overlapping membership parameter \(om\) from 2 to 8, thus considering a total of 140 different scenarios. In each scenario, the number of overlapping nodes \(om\) is fixed at 10\% of the total number of nodes. The average degree and the maximum degree are fixed at 20 and 50, respectively, for all of the above scenarios. For the execution of NashOverlap, we change the parameter \(\alpha\) from 0.30 to 0.60, in steps of 0.02 and the cover which returns the maximum NMI is picked as the final output.

Figure 5: Performance comparison of algorithms for network size 5000 with large communities.
Figure 6: Performance comparison of algorithms for network size 5000 with small communities.

7.1 Experimental Setup

CFinder algorithm [28] is run for each of the values $k = 3, 4, 5, 6, 7, 8, 9, 10$ and the partition that returns the maximum NMI is picked. svinet [13], Infomap [11] algorithms are run with parameters set to default values. We ran SLPA algorithm [17] on each value of $r = 0.05, 0.10, 0.15, 0.20, 0.25, 0.30, 0.35, 0.40, 0.45$ for 10 times, which is a parameter which decides the number of times the algorithm can be repeated to improve its accuracy. We ran the algorithm COPRA, for each $v \in \{1, \ldots, 10\}$, enabling the $mo$ for 10 times, as suggested by its manual. OSLOM is run with the parameter $r$ set to 10 and the rest of the parameters are set to default values. In all the above 140 scenarios that we have chosen, when we have performed the experiments as stated, NashOverlap
works very well over the other algorithms. A few observations from the plots are as follows:

- The best performance of NashOverlap is found to be almost same as its performance at $\alpha = 0.5$. These plots are not shown.

- For the case of 1000 node and large communities, NashOverlap (Figure 7) performs well over all the other algorithms, with COPRA, OSLOM, SLPA, CFinder happening to be the next best performing algorithms in order. As the mixing factor increases, the performance of all the other algorithms appear to be almost the same except CFinder, which happens to be the worst performing algorithm and NashOverlap is the best performing algorithm.

- For the case of 1000 node small communities, (Figure 8): NashOverlap happens to be best performing algorithm for all the mixing factors from 0.1 to 0.5. CFinder, OSLOM, COPRA, SLPA are the best performing algorithm in order after NashOverlap. With increase in the mixing factor, the algorithms OSLOM, COPRA, SLPA performance appears almost same, while the performance of CFinder becomes worse.

- For the case of 5000 node small communities, (Figure 6): NashOverlap happens to be the best performing community detection algorithm of all with SLPA performing the worst of all the algorithms.

- For the case of 5000 node large communities, (Figure 5): NashOverlap happens to be the best performing community detection algorithm of all with CFinder performing the worst of all the algorithms, which even worsens with increase in mixing factor.

- For both the network sizes 1000 and 5000, the performance in the case of small communities is much better than that in the large communities.

- The performance of all the algorithms deteriorates with increase in the mixing factor. The performance of CFinder algorithm deteriorates with increase in the network size for both the variations in the community sizes. The performance of NashOverlap increases with increase in the network size for a given community size.

- The performance of all the algorithms falls down with increase in overlapping membership.

- This algorithm works as a disjoint community detection algorithm for the networks with clear community structure and can always detect communities which have weak links with the rest of the network.
Figure 7: Performance comparison of algorithms for network size 1000 with large communities.
8 DBLP collaboration Network

DBLP is the Computer Science Bibliography. In this section, we identify and study the collaboration groups (communities) in DBLP collaboration network using our algorithm NashOverlap. We also study the distributions of both the sizes of collaboration groups and the overlapping membership in the detected community structure. We compared the results with that of the best algorithm, COPRA which is found to work reasonably good on synthetic datasets and on large datasets and since it is able to identify good enough collaboration groups in DBLP, compared to the other community detection algorithms considered in this paper.

We considered the dblp dataset [1] of only the papers published in tier one rank conferences in almost all the fields in computer science from the year 1966 to 2014. We considered 69 conferences on
the whole from the following fields: algorithmic game theory, general algorithms and data structures, quantum computing, cryptography, computational complexity, computational geometry, databases, computer architecture, artificial intelligence, principles of programming languages, automata theory, computer networks, multimedia, computer vision, pattern recognition, Internet Fault tolerance, Data mining, machine learning. We constructed the DBLP network as a weighted graph with vertices as authors. An edge is put between a pair of authors if they have at least one paper that they have coauthored together. We constructed two datasets based on this DBLP data as follows:

- The first dataset consists of the authors who have published papers from 1966 to 2014 in only top ranked computer science conferences. We have considered 69 conferences altogether. The authors from the dataset form the vertices of the network. We put an edge between a pair of authors if they have coauthored a paper together. The weight of the edge is the number of papers that they have coauthored together. There is no edge between the authors, only if they have never coauthored any paper. The dataset has 122684 authors and 384320 edges. Excluding self-loops, the average degree of this network is 6 and the maximum degree is 284.

- The second dataset considers only the papers of top ranked conferences whose authors have published at least 10 papers from 1966 in only top ranked computer science conferences. So, the set of authors considered in this dataset is a subset of the set of authors of the above dataset. The authors in this dataset are the authors who have published papers only with the authors who also have published at least 10 papers from 1966 in only tier one computer science conferences. The weight of the edge is the number of the papers that both the authors have coauthored. There is no edge between the authors, if they have never coauthored any paper. Note that even if a pair of authors have not coauthored 10 papers together, then there may be an edge between them. The dataset has 7349 number of authors and 24161 number of edges. Excluding self-loops, the average degree of this network is 5.6 and the maximum degree is 86.

On the first dataset, it took 9000 seconds to run 1000 subgames of the first game and compute the closeness probabilities for all the edges. For the second game, the algorithm took 50 seconds to compute the final community structure. In the first game, observe that each subgame is independent of each other and takes around 2.5 million rounds to reach a Nash equilibrium. The network is very fuzzy and the the average degree differs from the maximum degree by a large amount and the distribution of community sizes and the distribution of node degrees are found to follow a very steep power law distribution.

On the second dataset, the first game took 558 seconds to run all the 1000 subgames of Nash dynamics (actually, 100 subgames is enough for the network size of 7000 if a clearer and well defined community structure is present). The second game, takes around 20 seconds to detect the communities. Each iteration in phase one is independent of each other, and it takes on average 123,000 rounds to converge to a Nash equilibrium. At the end of the first game, the number of Nash components detected is 4366. That is, the number of disjoint communities found at the end of the first game are 4366 and 99.99% of the sizes of all the disjoint communities which are output at the end of the first game, are all less than 15. In the second game, we choose to analyze the network with $\alpha = 0.5$ for both the datasets where the identified collaboration groups are much clearer.

We visualize the collaboration groups using the Gephi tool. Gephi is a tool to visualize and manipulate the networks. We used Fruchterman-Reingold, a forced layout algorithm to visualize the network. In the figures that visualize each community, the size of vertices is proportional to their degree, and the thickness of the edges is proportional to their tie-strengths $t(i,j)$ computed in the algorithm. All the overlapping nodes are shown red in color. When we say, we load at least one community into gephi, we are actually loading the induced subgraph of the network on the vertices.
of all those communities into gephi. Fruchterman Reingold is a force directed layout. It simulates a physical system, in which nodes repulse each other, while edges attract the nodes they connect. These forces create a movement that converges to a balanced state. The final configuration of each of the layout algorithms is expected to explore and understand the network structure. We thus use the tool gephi, in each case to justify the quality of our community detection algorithm.

We justify the strength of our community detection algorithm in the following ways. We compare our community structure with that of the community structure identified by COPRA, for both the datasets. For each dataset, we manually, look into the top collaboration groups (ordered in terms of size) and find that our algorithm has identified more meaningful community structure than COPRA. We find that our algorithm has detected more collaboration groups of significant size each of which carries an identity, compared to that of COPRA. Also, the communities detected by our algorithm are much bigger in size with a least number of outlier nodes. The community structure is likely to have more mixing factor than that of detected by COPRA. It means, that the collaboration groups are big enough in size with several researchers in each, so that almost no researcher who concern this collaboration group is ignored. We visualise the community structures detected for both the datasets for both the algorithms and the significant collaboration groups detected in the community structures detected by both the algorithms. For visualization convenience, we have only shown the high degree researchers in each of the identified collaboration groups, by loading the gephi with the induced network of the collaboration group with the higher degree nodes.

8.1 Results

Our algorithm detected a large collaboration group of size 38% of the network size for the large dataset and 22% of the network size for the small dataset. The large collaboration group detected for each dataset has the researchers, mostly based in United States, from almost all the fields, and the second largest collaboration group is far smaller in size than the first. This finding is in congruence with the statement from the paper [27] which says that in all the collaboration networks studied, they identified a giant component which is a considerable fraction of the network size and the second group happened to be far smaller than the first. The existence of a giant component and the subsequent smaller components is due to the percolating regime characteristic of collaboration networks. When the network has a fewer edges, there exist a large number of small connected clusters. With the increase in the number of edges, most of these small clusters group to form a giant component, leaving behind smaller clusters which join the giant component in the future with the increase in the number of connections. This leads to a reasoning that the scientific collaboration network is highly connected and there is a possibility of more interdisciplinary work in the future which is a good sign for the development of science. The diameter of the largest collaboration group for both the datasets is between 9 and 11 and has the average path length between 4 and 5, which strengthens the above argument. Note that, this is because the average number of intermediate researchers that connect any pair of researchers in the giant component is quite less.

Figure 11 and Figure 9 show the community structures of small and large dataset respectively, identified by the algorithm NashOverlap at $\alpha = 0.5$ and $\beta = 1$. In the figures, the vertices represent communities, and the weight of the edge between two vertices is the sum of the weights of the cutedges between the two communities. The size of the vertex is proportional to the size of the community. The weight of the edge shows how close the researchers of both the communities are collaborating with each other. So, the larger the weight of the edge between two communities, the larger the overlap between two communities or the larger the collaboration between the two communities. In the figures, the numbers on the vertices show the size of the community represented by the vertex.
Figure 9: Depiction of Community Structure of DBLP collaboration network (large dataset) as detected by NashOverlap with vertices as communities and weight of edge between vertices show the sum of the weights of the cutedges between the communities represented by the vertices.
Figure 10: WordCloud for the conferences of giant component detected by NashOverlap in DBLP collaboration network (large dataset). Observe that almost 90% of the conferences show up and even some of the conferences based on industry oriented fields also show up in the same font and size as that of the theory based conferences.

From both figure 11 and figure 9, the following are observed. Some of the communities have a large overlap with the giant component. Some larger collaboration groups with the weaker links to the giant component are based in Asia. For the large dataset, the large collaboration group has size 46385, and the second collaboration group has size 426. Almost all the collaboration groups are connected to the giant component, which strengthens the percolating characteristic of the collaboration groups in this network. For the large dataset, there are 20 collaboration groups of size at least 100 and all of them belong to the following fields: computer vision, cadence, software engineering, multimedia, artificial intelligence, machine learning, data mining, data management, data engineering, computational geometry. There can be multiple collaboration groups detected for a given field. However, these detected collaboration groups of the same field are in most of the cases pair-wise disjoint. For the small dataset, the major collaboration groups on fields cryptography, algorithms are found to be merged into the giant component and some of the small collaboration groups which have weaker links with the giant component of the same fields are detected. For the large dataset, a major group at least one for each of the fields cryptography, algorithms, computer networks, complexity are detected.
Figure 11: Depiction of Community Structure of DBLP collaboration network (small dataset) as detected by NashOverlap with vertices as communities and weight of edge between vertices show the sum of the weights of the cutedges between the communities represented by the vertices (only major communities are shown).
The distribution of the fields of the researchers in the giant component and the distribution of the fields identified uniquely by each of the subsequent larger collaboration groups detected for both the datasets differ. This owes to the fact that the fields like computer vision, multimedia, machine learning, software engineering, embedded systems are more industry oriented and any two collaborating researchers of those fields are less likely to stay in academics for a long time and publish. Hence, the possibility of each such researcher having at least 10 publications in top tier conferences is less likely. So, we termed it as the reason for finding several large collaboration groups of those fields in the community structure detected for the large dataset, where as in the case of small dataset, those groups are almost non-existent, not even of lesser size. Also, this is the reason for the giant component in the large dataset to contain the researchers from all the fields equally in proportion, whereas the researchers from industry oriented fields are very less in number in the giant component in the small dataset. This is observed as in the figures 10 and 12. The average tie-strength of the links between the researchers in most of the collaboration groups of the industry oriented fields is also found to be less compared to the theory fields of computer science. We identified the fields corresponding to each collaboration group by looking at the frequency of the conferences in which those researchers have published, the keywords in their papers and the research interests, affiliations of the researcher.
We studied only the collaboration groups of size more than 20 for the case of small dataset. We identified that the collaboration groups in the following fields: computational geometry, formal methods and automata theory, programming languages, Artificial Intelligence, Machine Learning, Database theory group have a large overlap with the giant component. Figure 13 depicts the high degree researchers of second largest collaboration group detected for the small dataset. The researchers in this group are found to be working in various areas: Big Data, Database theory, query optimization, database consistency and efficiency, data streaming, Machine Learning, Artificial Intelligence and Pattern Recognition. The underneath wordcloud corresponds to all the conferences in which the researchers of that group publish and as you can see, all of them are conferences related to Databases, Big Data, machine learning and Artificial Intelligence. This collaboration group has a large overlap with the giant component, which depicts the currently happening percolating regime of these fields in a huge way. It can be seen in a much clearer way in the case of collaboration groups.
identified for the large dataset. The largest collaboration group has researchers from almost all the fields and shows all the conferences in equally sizes in the conferences wordcloud as is seen in the figure [10].

Figure 14: WordCloud for the conferences of second largest component detected by NashOverlap in DBLP collaboration network (small dataset). Observe that all the conferences are based in Machine Learning, Databases and Artificial Intelligence.
Figure 15: Two major collaboration groups of sizes 408 and 239 on Database theory and systems are detected on the small dataset. Overlap size is 92 and the number of overlap edges is 187. Only high degree nodes are shown for visualization convenience. Each of the groups have an overlap of 61 and 39 with the giant component respectively. Overlapping nodes are colored red.
Figure 16: Two major collaboration groups of sizes 222, 219 on Multimedia, Computer Vision are detected on the small dataset. Both are based in Asia, and have very weaker links with the giant component. Most of the high degree researchers are based in Microsoft research Asia. Overlap size is 117 and overlap edges are 291. Overlapping nodes are colored red. Each of the groups has an overlap of 6 and 7 with the giant component respectively.
Figure 17: Asian collaboration group in Data mining, Machine Learning, Knowledge Representation of size 152 detected for the small dataset. It has overlap of 16 with the giant component. Only high degree nodes are shown for visualization convenience.
Some of the collaboration groups identified in the case of small dataset have very weak links with the giant component and they are mostly the groups based in east asia. These groups are in the fields of data engineering, multimedia, computer vision and have most of its people from Microsoft research Asia and is dominated by Asians. Two collaboration groups on Media Computing, Data and Web Mining, Pattern Recognition, Vision, Human Computer Interaction are detected as can be seen at figure [16]. 99% of both the groups are dominated mostly by asian community, and the top degree people in this community are all affiliated to MS Research Asia. Both the groups are highly clustered and have some overlapping nodes colored red and are shown in the figure [16]. Both the collaboration groups differ in their research interests and their methods.

Some large collaboration groups of other fields like databases, BigData have researchers from Microsoft and IBM in at least their top 10% set of researchers as can be seen in the figure [15]. Our algorithm has identified a collaboration group for every possible area of the computer science. Our algorithm gives all the possible collaboration groups, and there is no restriction on the size of overlap.
detected between pairs of groups. However, the clustering returned by the algorithm depends on the $\alpha$ chosen. The algorithm detects more collaboration groups of large size, however with a lot of overlap when the $\alpha$ is lesser. To detect more fuzzy collaboration groups, we can tune the parameter used in the first game to 0.95 or 0.9.

In most of the cases, each collaboration group happens to represent a field of computer science, as can be seen in figure 18 and figure 17. However, the collaboration group need not contain all the researchers in the world working in that field. This is intuitive because all the researchers in the world who are working on a common area of interest need not have strong collaborations with each other. The collaboration groups are formed because of the common institution or the common race or the common nationality or the common geographical area or the common culture or the common university or the common research labs or the common time span in which the researchers in that group are active or any combination of the above.

Figure 19: Cumulative distribution of Overlapping membership of community structure detected by NashOverlap for small dataset at $\alpha = 0.5$. Overlap membership of 2,3,4 is found to more common.
Figure 20: Cumulative distribution of Community Size of community structure detected by NashOverlap for small dataset at $\alpha = 0.5$. Observe that most of the significant communities are between sizes 50 and 100.

Figure 19 and Figure 20 shows the cumulative distribution of overlap membership and the cumulative distribution of the community size of the community structure detected for the small dataset.

The figures 22, 23, 21 shows the community structure detected by the algorithms COPRA, OSLOM and NashOverlap respectively. In the layout, the communities detected by COPRA algorithm appear denser as that of NashOverlap. There is not much overlap that is detected by COPRA algorithm and the communities apart from the giant community are not of significant size. Also, the running time of COPRA is $O(m^2)$. The community structure detected by OSLOM algorithm is not in tune with the layout as in figure 23. In the layout, the detected communities are not very dense and it is difficult to identify all the communities with a field name or affiliation name.
Figure 21: Community Structure of the DBLP Collaboration network (small dataset) detected by NashOverlap algorithm at parameter $\alpha = 0.5$ and $\beta = 1$ using Fruchterman-Reingold layout algorithm in gephi. Each community is given a separate color and the overlapping nodes are red in color. The community structure given by the Fruchterman-Reingold layout and the algorithm NashOverlap are in tune with each other. However, the communities are bigger in size and most of the possible communities are identified.
Figure 22: Community Structure of the DBLP Collaboration network (small dataset) detected by COPRA algorithm at parameter $v = 5$ using Fruchterman-Reingold layout algorithm in gephi. Each community is given a separate color and the overlapping nodes are red in color. The community structure given by the Fruchterman-Reingold layout and the algorithm COPRA are in tune with each other. However, the communities are not bigger in size and all the possible communities are not identified. Also, it did not detect much of the overlap between the pair of collaboration groups.
We find that our algorithm has detected more collaboration groups of significant size each of which carries an identity, compared to that of COPRA or OSLOM. Also, the communities detected by our algorithm are much bigger in size with a least number of outlier nodes. The community structure is likely to have more mixing factor than that of detected by COPRA and OSLOM. It means, that the collaboration groups are big enough in size with several researchers in each, so that
almost no researcher who concern this collaboration group is ignored. These results are much more pronounced and clearly seen as in the large dataset of the DBLP collaboration network. This shows that our algorithm finds better collaboration groups than the other algorithms for the case of DBLP collaboration network.

9 Conclusion

We have examined the problem of community detection in interaction networks using game theory. Our model is under the assumption that the similarity of any pair of nodes increases with the number of connections that the pair makes. Also, the more the similar the pair of nodes are, the more the number of common friends that the pair makes eventually.

We proposed two simple and scalable algorithms that inputs the interaction network and outputs its community structure, and the overlapping nodes present in the network. We proposed the algorithms for each of the cases of detecting the disjoint communities and the overlapping communities in a given network.

In this thesis, we proposed a disjoint community detection algorithm, NashDisjoint which works as good as the state of the art algorithms on both GN Benchmarks and LFR Benchmarks for the mixing factors less than 0.55. We have observed that the modularity values for the community structure detected by our algorithm on real social networks is in comparison to that of the Louwain algorithm, one of the best modularity optimization algorithms so far. We proposed an overlapping community detection algorithm NashOverlap which works better than the state of the art algorithms on LFR benchmarks by a large margin, for the mixing factors from 0.1 to 0.5 and overlapping membership varying from 2 to 8 and when the percentage of overlapping nodes is 10%. This algorithm also works well on the networks with disjoint community structure and can detect the existence of disjoint communities.

Our algorithms can be very much parallelized, as in the first game, all the subgames are independent of each other. We performed experiments on DBLP co-authorship network and identified the top collaboration groups of the network, ordered in terms of their size. We observed that the largest collaboration group has people from almost all the computer science fields and the largest degree researchers are from the theoretical computer science, Machine Learning and Data mining. The largest collaboration group has size around 40% of the actual network size. Using these results, we want to show that our algorithm can detect meaningful information from collaboration networks.

One important thing to note in the context of community detection algorithms is that there is no community detection algorithm so far that can be considered best for all kinds of networks. This field lacks a theoretical framework which gives the definition of a community and the definition of the best measure that the entire research community agrees upon. Until there is such a framework, there is no other way to compare the performance of any two community detection algorithms other than to evaluate their performance on the networks whose groundtruth is already known. Also, there are no scalable game theoretic algorithms that can detect communities in dynamic networks.

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