Friend Recommendations in Social Networks using Genetic Algorithms and Network Topology

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Abstract—Social networking sites employ recommendation systems in contribution to providing better user experiences. The complexity in developing recommendation systems is largely due to the heterogeneous nature of social networks. This paper presents an approach to friend recommendation systems by using complex network theory, cognitive theory and a Pareto-optimal genetic algorithm in a two-step approach to provide quality, friend recommendations while simultaneously determining an individual's perception of friendship. Our research emphasizes that by combining network topology and genetic algorithms, better recommendations can be achieved compared to each individual counterpart. We test our approach on 1,200 Facebook users in which we observe the combined method to outperform purely social or purely network-based approaches. Our preliminary results represent strong potential for developing link recommendation systems using this combined approach of personal interests and the underlying network.

Index Terms—Centrality, Facebook, friend recommendations, Pareto optimization, social networks.

I. Introduction

The emergence of social networks from the Internet sparked a major reform in information spread. From data to search and from search to social interaction, users around the world are now more deeply involved with the Internet as user-generated content undergoes perpetual growth and expansion. Through adoption of social networks, user-generated content is far more accessible than before. A powerful aspect of social networks is the customization of user experiences.

Recommendation systems constitute a large role in providing quality customized user experiences. The main challenge in developing relevant friend recommendations is due to the dynamic nature of humans' perception of friendship, which constitutes a cause for heterogeneity in social networks [1], [2]. It is natural and frequent for humans to change their perception of friendship [3]. Further, this perception varies from person to person in which a social network can undergo frequent and abrupt change over time even without the introduction of new nodes [4].

In this paper, our goal is to study human interaction within social networks in order to gain insights into the preferences an individual considers when forming relationships so we can provide better quality, i.e., more relevant, friend recommendations.

Network-based approaches generally perform well in providing quality recommendations. Prior work in both industrial and academic sectors emphasize the use of the friends-of-friends method. The intuition is derived from the idea that it is more probable a person will know a friend of their friend rather than a random person [5]. This approach implies a person is more likely to pursue a relationship based a common association. However, this does not provide any insights into human cognitive components, which is a multi-dimensional belief system that may change over time [6].

The use of genetic algorithms has been used to supplement network-based approaches. Prior research has suggested genetic algorithms to be used to optimize a set of indices derived from complex network theory [7], [8]. This approach still relies purely on the underlying structural properties of social networks. Since participants within social networks are humans, it would be of significant interest to approach the recommendation problem by supplementing network theory with cognitive theory.

In this paper, we examine 1,200 Facebook users and generate individually customized quality sets of friend recommendations by applying a two-step filtering process using friends-of-friends, degree centrality and a Pareto-optimal genetic algorithm that optimizes relationship preferences. We aim to filter out likely irrelevant individuals using complex network theory before applying our Pareto-optimal genetic algorithm. In our genetic algorithm, we aim to identify a set of social features that defines an individual's perception of friendship, which in turn will filter out additional users. Finally, we rank a set of quality, relevant potential friends based on point valuations derived from the individual's set of preferred features.

The results of this paper demonstrate that our combinational approach outperforms purely social and purely network-based approaches and provides strong support for future exploration of this method in developing better recommendation systems and user experiences within social networks. We tested our results by randomly removing 10 friends from an individual's network in which a purely social, purely network-based, and the combined approach attempted to produce a recommendation list containing as many of the previously removed friends as possible.

The rate of return was used to compare the performances of each algorithm. The purely social approach yielded a 6.83% return rate, with 0 to 2 of the removed users being recommended; the network-based approach yielded a 22.38% return rate, with 1 to 4 users being recommended; and finally

the combined approach yielded a 31.78% return rate, with 1 to 6 users being recommended.

The remainder of this paper is organized as follows: In Section II, we describe prior approaches to developing recommendation systems. In Section III, we present complex network fundamentals used in the initial filtering step. Section IV presents our social genome representation and Section V describes the final filtering step and characterization of an individual's preferred social features. We present our results in Section VI along with a discussion and conclude with a summary and future work in Section VII.

II. RELATED WORK

Recommendation systems can be divided into two areas of focus: object recommendation and link recommendation. Companies such as Amazon and Netflix emphasize object recommendation where products are recommended to users based on past behavioral patterns. Social networking sites such as Facebook and LinkedIn focus on link recommendation where friend recommendations are presented to users. The work we present in this paper focuses on the latter, in which we develop friend recommendations within social networks.

The recommendation algorithms employed by sites such as Facebook are proprietary. However, through observation, it is apparent that a friends-of-friends approach is being used. This approach is useful and efficient due to ease of implementation and the nature for humans to be drawn together through association [2], [6], [9], [10]. Similar network-based approaches such as graph-based induction [11] and link mining [12], [13] have been considered but fall in comparison to the effectiveness and efficiency of a friends-of-friends approach.

Kuan et al. proposes an algorithm to locate groups using a transitive extension-based approach [14]. This research proposed the use of a 1.5-clique extension method to derive sub-structures, or communities, within social networks. Results showed that this method was fairly effective in finding community of friends. However, this method does not provide insight into how these communities are formed. That is, it is significant to understand what common interests cause a formation in these communities.

Recent research has identified the potential effectiveness of combining complex network theory and genetic algorithms. Silva et al. treated the recommendation problem as a filtering problem where a genetic algorithm was used to optimize three indices derived from structural properties of social networks [7]. The results from this study was acknowledged as a baseline to initial work using a new methodology. A significant challenge in developing friend recommendation systems is the necessity to account for the heterogeneity in social networks. In dealing with heterogeneity, a successful approach using the combined methodology was demonstrated by Zhang et al. [15], in which recommendation was considered as a ranking problem. This approach focused on object recommendation where a random walk model was used to rank different objects while generating a pair-wise learning algorithm to learn the importance of each object for an individual. An agglomerative

genetic algorithm for clustering was presented by Lipczak and Milios [16]. This study employed a genetic algorithm to detect existing friendships within a social network by examining the *similarity* between each node. The similarity of each node was based on properties of social networks in which they formalized as a graph clustering optimization problem. Results showed this method to perform very well in detecting communities with exception to overlapping communities. However, the goals of this combined methodology is different as it is not concerned with recommending potential friendships, but rather, detection and confirmation of existing friendships. Further, no insight into an individual's perception of friendship is provided.

Research by Leskovec, et. al., emphasized the relevance and effectiveness of multi-objective functions in recommendation algorithms [17]. However, similarly to Lipczak and Milios, the focus of this research was on community detection. An analysis on brain networks using multi-objective functions was performed by Santana, et. al [18]. This study used Pareto-optimal evolutionary computation to optimize artificial networks with various topology features resembling brain networks. Recent results and progress in recommendation systems suggests the use of genetic algorithms with complex networks to be promising. In this paper, we treat the recommendation process as a filtering problem and present a method that uses structural properties of social networks along with cognitive theory to optimize a quality, relevant set of friend recommendations while identifying each individual's perception of friendship.

III. NETWORK THEORY

We initialize our filtering process by first removing likely irrelevant individuals using the friends-of-friends method. This method is widely accepted among existing social networking sites such as Facebook and LinkedIn as means of narrowing the search space for potential links. We utilize this method as people are generally drawn together through some common interest or association [9], [10]. This choice is essential in the filtering process, since it is more likely an individual will pursue a relationship given the common association of an existing friend. In this paper, we implemented results obtained from Facebook as described in Table I using Facebook's Graph API. A visualization of our network of users is shown in Figure 1. By filtering based on friends-of-friends, we significantly downsize the number of potential friends. Although it may be desirable to remove likely irrelevant users, the friends-of-friends approach may be too overwhelming in the filtering process. For this reason we employ the use of degree centrality after filtering by friends-of-friends.

TABLE I
NETWORK DETAILS

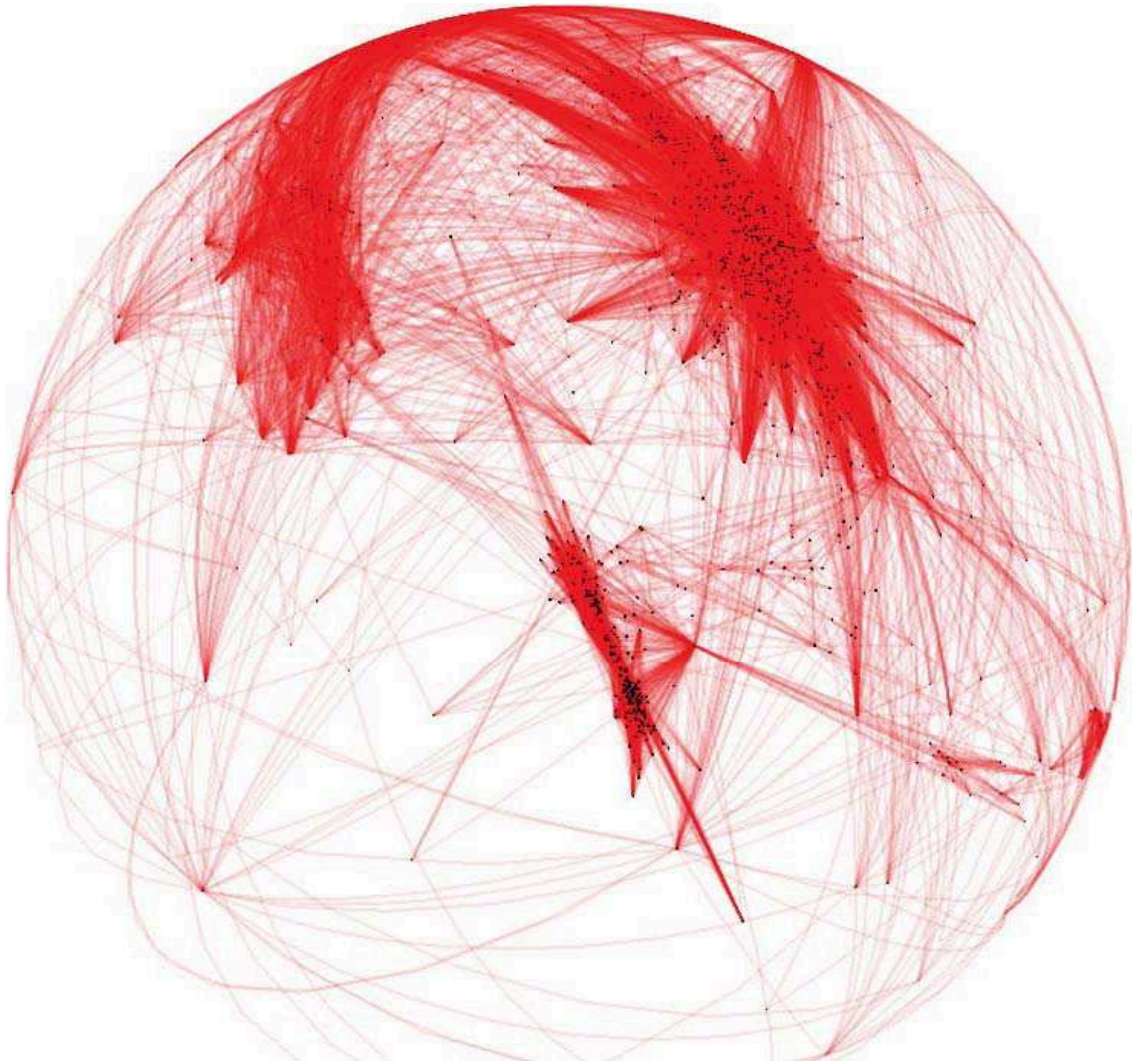|	
Nodes	1200
Edges	23377
Average Degree	39.53

Fig. 1.   Network of 1200 Facebook users.

The use of degree centrality aims to balance out the overwhelming filtering effects of friends-of-friends. Degree centrality effectively expands our filtered set by looking at users whom have many outbound links. That is, we append our filtered set with users whom exhibit a large number of friendships. Individuals with many friends can be considered as extroverted or popular. It is important to include these types of users into our set due to their trend in acquiring friendships. However, it is equally important to note that this type of link may not be genuine. That is, an extroverted or popular individual may simply form relationships for the sake of forming relationships [2], [19], [20]. Nonetheless, our research is concerned only with the formation of links.

IV. SOCIAL GENOME

Until now, the filtering process has only accounted for structural properties of the social network. In this paper, we improve upon the filtering process by added an additional step aimed at personalizing friend recommendations. In our algorithm, we present a 10-dimensional binary genome whose genes are based on social features obtained using the Facebook Graph API. The social features are preferences users may apply in the decision to pursue a friendship. A logarithmic point distribution is applied to the features based on the commonality between two users. The intuition behind using a logarithmic distribution is based on the law of diminishing returns.

A. Shared Friends

Relationships generally form through shared common interests [9]. Through these common interests, two different individuals may share the same set of friends [20]. A potential friend will rank higher if there exists a large amount of common friends.

B. Location

Location plays an important factor in pursuing and retaining friendships. It is far more convenient and probable for individ-

TABLE II
AGE RANGE

Age Range	Difference
15-20	± 3
21-25	± 5
26-30	± 7
31+	± 10

uals to maintain relationships if their geographical distances are relatively short [2], [6]. We address this by considering three pieces of information gathered from the Facebook API: locale, timezone, and current location, with each being more influential than the last with respect to point distribution.

C. Age Range

Individuals are placed into different groups of age ranges. The main idea is that a difference in years has less of an effect on an older individual than a younger one. For example, a difference of five years means less to a 40 year-old adult than a 10 year-old child. For simplicity, we consider only individuals above the age of 15 where groups are defined by Table II, in which we compare individuals in each age group based on the difference of years as shown in the second column of Table II. Users satisfying the age range preference will rank higher among those that do not. That is, our algorithm still associates points to users whom do not satisfy the age range, simply because existing outside an age range does not necessarily mean two users may never become friends.

D. General Interests (Likes and Music)

The Facebook Graph API groups shared *likes* and shared *music* together. We combine these two and consider them as shared *general interests*. Potential friends will rank higher as the number of shared general interests increase.

E. Photo Tags

The intuition behind consideration of photo tags is derived from the idea that ongoing interaction with a person may result in possible friendship. For example, although an individual may not know a particular person, if they are in the same photo, that implies they were in company of each other. Chances of them creating a link between each other would increase as chances for them to interact and discover common interests would increase.

F. Events

The notion of *events* is similar to that of *photo tags*. Users that share many attendance to the same events imply an increased likelihood of interaction. If two users somehow never interact despite an arbitrary amount of shared attendance to events, there still exists the common interest of having attended these events. In our implementation, we consider three choices a user can make according to the Facebook Graph API: attended, unsure, or not going. Users with statuses of *attending* or *attended* will rank higher among those with *unsure* statuses. That is similar said with *unsure* statuses compared to *not going* statuses. A user will still receive points if they both share uncertainty of attending an event or if one user is attending and the other is unsure, since we cannot determine whether the users have attended that event or not.

G. Groups

Groups allow users to gather among each other in support for some common interest. Within the Facebook platform, users within the same groups have the ability to interact with each other by wall posts and group chat. Our system emphasizes simplicity in that potential friends are ranked higher depending on the amount of shared groups.

H. Movies

The Facebook Graph API separates *movies* from *general interests*. For this feature, we utilize the same concept as implemented for *general interests*.

I. Education

In our research, we were able to gather different levels of detail pertaining to education: high school, undergraduate, and graduate and professional education. Firstly, users will rank higher if they have attended the same schools. Second, more points will be given to those that share the same degree programs and same level of education. Lastly, we consider class standing with a two-year difference. We believe this range is a great enough differential to determine the likelihood of interaction among individuals. For example, a senior in an undergraduate degree typically will not be enrolled in classes a freshman is taking. The likelihood of interaction between these individuals would be less compared to the contrary of them being in the same year and enrolled in the same classes.

J. Religion/Politics

Individuals sharing similar points of views with respect to religion and politics will receive more points than those that do not. However, the difference in beliefs does not necessarily mean two individuals may never become friends. For this reason we would still attribute a small amount of points for these potential friends.

In this paper, we use a Pareto-optimal genetic algorithm to optimize a set of preferences unique to each individual that determines their perception of friendship. Since we are using a binary genome representation, that means our algorithm only allows for users to use a particular feature or not. We acknowledge this deficiency as grounds for future work by associating weights to each feature using floating point numbers. Additionally, we acknowledge addition future work in expanding our search space to include hundreds of social features. That is, our social genome consists only of 10 features which yields a search space of 2^{10}, or 1024, solutions. It is apparent that an exhaustive search can be performed to discover an optimized solution. However, the perception of

friendship extends far greater than our initial 10 features. [6], [10]. Our research represents a preliminary contribution to the human social genome in which we choose to employ a genetic algorithm in foresight of an expanded social genome consisting of many more features. This increase in social features will exponentially affect the search space, thus making an exhaustive search infeasible.

V. LINK RECOMMENDATION

The main idea of our link recommendation algorithm is to treat friend recommendations as a filtering problem where we optimize a set of quality, relevant friends customized for each individual while simultaneously discovering their perception of friendship. We begin by examining an individual in a social network which we consider to be the central node, C. With respect to C, we then examine candidates for potential friendship, i.e., all users, P_u, whom are not friends with C. First, we filter P_u using a friends-of-friends approach and degree centrality to obtain a smaller set of potential friends. Next, we evolve a social genome with respect to C and C's friends, C_f, using a Pareto-optimal genetic algorithm. Our social genome is represented as a binary string of 10 social features. The fitness of our social genome is determined as follows:

for each individual **in** C_f **do**
    associate point valuation with respect to active genes in
    the social genome, such as the example in Figure 2
end for
Sort C_f according to descending point valuation
$PF = pf = \texttt{length}(C_f)$
while $C_f > 0$ **do**
    I += $C_f[0]$ (i.e., $\texttt{pop}(C_f)$)
    for each individual **in** C_f **do**
        I += $\texttt{pop}(C_F)$ **if** individual **in** I
    end for
    fitness += $\texttt{length}(I) \times \frac{pf}{PF}$
    pf -= 1
end while

In this computation, each consequent Pareto frontier attributes less and less to the fitness of the social genome. The intuition behind this is that friends with low point valuation share less of a commonality with C and would therefore contribute less to C's perception of friendship. Once we compute the optimal social genome, we proceed by examining all potential friends, P_u. The algorithm for this filtering step is as follows:

0	1	2	3	4	5	6	7	8	9
0	1	1	0	1	0	0	0	1	0

Fig. 2. Genome representation of social features. Active genes in this genome include *shared friends*, *location*, *general interests*, and *movies*. This string represents a candidate for an individual's perception of friendship.

for each individual **in** P_u **do**
    for each active gene **in** social genome **do**
        associate point valuation
    end for
end for
for each p **in** P_u **do**
    $F = f = \texttt{length}(C_f)$
    for each c **in** C_f **do**
        if $\texttt{value}(p) \geq \texttt{value}(c)$ **then**
            p.score += $1 \times \frac{f}{F}$
            f -= 1
        end if
    end for
end for
sort P_u according to descending point valuation
for $i = 1$ **to** 10 **do**
    recommended friends += $\texttt{pop}(P_u)$
end for

The recommendation process ends by recommending the top 10 individuals determined by point valuations based on the previously computed optimal social genome. Further, the social genome implies the perception of friendship for that individual. This process is repeated for each individual in the social network with respect to each genome in a population of social genomes.

In evolving our social genome, we exploit the search space of our genome by employing strong selection through tournament selection and use an elitist replacement strategy. Our strategy is to have less fit social genomes be removed from the population though the evolutionary process. However, it is equally important to account for exploration of the search space. For this, we used single-point crossover and bit-flip mutation at high rates. Replacement of less-fit individuals in the population was done using generational replacement.

A. Pareto Domination

In calculating Pareto domination, each active gene is examined. A gene is considered active if, for a particular genome, its value is set to 1. Figure 2 shows a genome with active positions 1, 2, 4, and 8, which means our algorithm will examine *shared friends*, *location*, *general interests*, and *movies* for this particular genome. Firstly for each individual friend in C_f, our algorithm will generate values for each active gene in the genome. In the example above, all friends would examine the string [0, 1, 1, 0, 1, 0, 0, 0, 1, 0] and produce values only for those positions. Finally, we compare all friends against each other in which the fitness is determined by which Pareto frontiers they reside on.

An individual's genome will outperform another if and only if all of its genes have greater values than genes of the another person. For example, consider two friends, A and B, represented according to the social genome as described in Figure 2. Let A have a makeup of [0, 12, 43, 0, 25, 0, 0, 0, 62, 0] and B have a makeup of [0, 13, 44, 0, 26, 0, 0, 0, 99, 0]. B is considered to dominate A,

or $B \succ A$, since all genes in B are strictly greater than those of A. In our genetic algorithm, all individuals residing on a particular Pareto frontier are removed after contributing to a social genome's overall fitness in order to obtain the next Pareto frontier and employ diminishing returns. A social genome's fitness will be determined by the summation of friends multiplied by a scalar represented by the Pareto frontier they reside on. The ideal fitness would be the equal to the total number of friends pertaining to an individual. This case would imply that all friends of the individual exhibit extremely similar traits. That is, there would exist an extreme lack of diversity among the individual's friends.

Once the optimal social genome is computed, we undergo one final Pareto domination tournament. In this tournament, we compare an individual's friends against the set of previously filtered potential friends. The computation is similar to the domination tournaments during the evolution of our social genome. Similarly, the same principles of diminishing returns and implications of a lack of diversification among the individual's friends are relevant.

VI. Experimental Results

To validate our approach to the link prediction problem we processed our algorithm using Facebook users obtained by creating a Facebook application and using the Facebook Graph API. Our data consisted of 1200 nodes and 23377 edges as shown in Table I. The goal of our experimentation was to show that by combining social-based and network-based methodologies, we can achieve better friend recommendations as opposed to using each method individually.

A. Experimental Setup

We tested our friend recommendation algorithm against two other approaches: a purely social and purely network-based approach. The social-based approach uses our Pareto-optimal genetic algorithm as described earlier in the paper without the initial filtering step by social network structural properties. A recommendation list is produced after the final round of Pareto domination tournaments in which friends are recommended based on their genome's fitness. The network-based approach employs filtering using friends-of-friends method. Once the network-based approach produces a final filtered set, the top 10 recommended friends are selected based on the number of shared friends between each candidate and the individual the algorithm is looking at.

For each scenario, we chose 100 Facebook users and randomly removed 10 friends from each individual. The reason for choosing 100 Facebook users as opposed to using all 1200 is due to the limitations of social-based approaches. Since social-based approaches rely on behavioral information, we had to manually select users whose data is more *complete*. Completeness of data correlates to the amount of information a Facebook user reveals online. In the case of our algorithm, if our tested set consisted of users whom all reveal no information, then all users would receive the same rating. Since all users have nothing in common, all users would
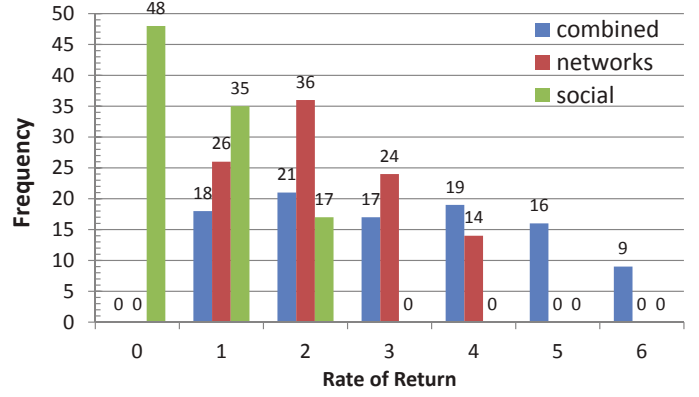

Fig. 3. Histogram showing the frequency of randomly removed users being selected for recommendation for each of the tested algorithms.

have the same minimal score that implies a small chance of friendship, regardless of the lack of commonality. The choice in randomly removing 10 friends is due to the number of recommended friends we limited as output. All algorithms can only select a maximum of 10 friends for recommendation. Therefore, ideally an algorithm will have a return rate of 100% if all removed users return as members of the recommendation list. Thus, an algorithm is considered to outperform another if a higher number of previously removed friends was selected for recommendation.

B. Results

We tested and compared each algorithm's performance by examining the rate of return for the randomly removed friends as describe above. In particular, we observe the frequency and average return rate produced by each algorithm.

In the social-based approach, we found the algorithm to perform poorly such that, out of 10 randomly removed individuals, 0 to 2 users were consistently returned. Further, the rate of return was 0 users 48% of the time as described in Figure 3. This algorithm averaged a return rate of 6.83% as described in Table III. The reason for this algorithm's poor performance is the large set of potential friends due to the lack of filtering beforehand. This implies the existence of people with more commonality with the individual than some of the individual's removed friends. We hypothesized this method to perform much better than it did since people generally pursue relationships based on common interests. This leads us to the primary area of concern for this algorithm's poor performance. As mentioned earlier, social-based approaches

TABLE III
Results

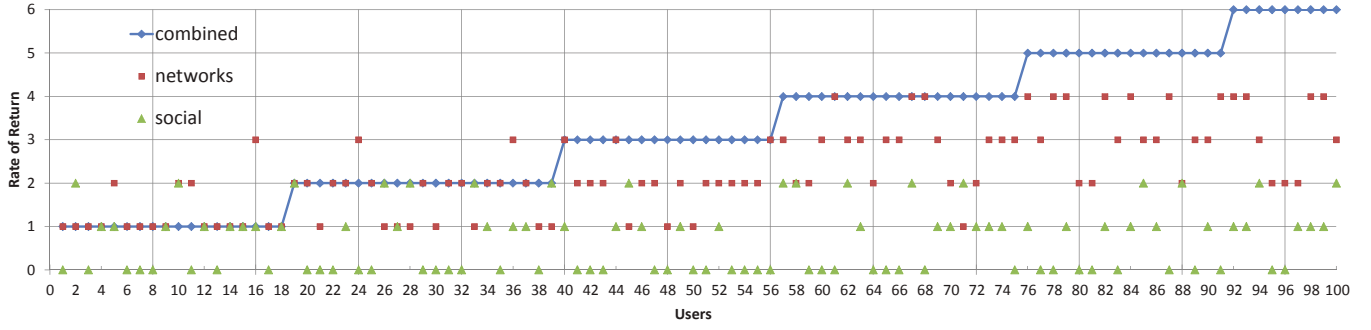|	Social	Networks	Combined
Average Rate of Return	6.83%	22.38%	31.78%
Standard Deviation	0.74%	1.02%	1.62%

Fig. 4. Rate of return for all users sorted in ascending order with respect to the combined approach along with corresponding rate of returns for the social and network-based approaches.

to friend recommendation systems rely heavily on the quality, or *completeness*, of data. In Facebook, users have the option of excluding information from their profiles. Further, users may post false information which may alter the outcome of the final recommendation list.

We observed the network-based approach to consistently perform better than the social-based approach. We believe this to verify the phenomenon of the likelihood of a person pursing a friendship of someone they know than someone they do not know [5]. Results show the network-based approach with an average return rate of 22.38% as shown in Table III. By applying the friends-of-friends method as the network-based approach, 1 to 4 users were selected for recommendation. We notice removed friends to be more successful in qualifying for the recommendation list if the central individual belongs to fewer cliques. The ideal situation would be for an individual to only have friends within one clique where all friends are friends with each other. Individuals whom are more popular, or belong to many cliques, show more difficulty in re-acquiring their randomly removed friends by the recommendation list. This is due to friends across different cliques not sharing a sufficient amount of friends with respect to the central individual.

In our combined approach, we utilized our two-step filtering process by applying the friends-of-friends method and degree centrality with our Pareto-optimal genetic algorithm based on 10 social features. This approach outperformed both approaches described earlier. A range of 1 to 6 as described in Figure 3 was produced. Results showed a 31.78% average rate of return. Further, since this method produces a genome which represents an individual's perception of friendship in the form of a binary string of social features, we gain addition insight as to why each particular friendship may have formed. Lastly, this combined approach is subject to the same limitations of the social and network-based approach.

All methods were performed on each user as shown in Figure 4. This graph is sorted in ascending order according to the rate of return produced for each user by our combined methodology. Corresponding rate of returns were also plotted for the social and network-based methodologies for each user. We observe from these results that network-based approaches

generally outperform social-based approaches. Moreover, a combined approach outperforms both social and network-based approaches.

VII. Conclusion and Future Work

We presented a method for friend recommendation systems in social networks to address the problem of determining how and why links are formed within social networks.

By addressing this problem with support from complex network theory, cognitive theory and genetic algorithms, our claim is that the combination of social-based and network-based approaches is more effective in recommendation compared to its individual counterparts. In this paper, we developed a friend recommendation system that produced quality, relevant friend recommendations in addition to providing insights into each individual's perception of friendship. This method has shown that a combined approach has thus far outperformed purely social and purely network-based approaches but still has much room for improvement. The primary issue attributing to lower performance in social-based approaches is due largely to the completeness of data. In order for social-based approaches to thrive, it is important to work with users whom expose more information on these social networks. Additionally, social-based approaches will perform better if user information is truthful. Our methodology and results in this paper presents initial findings to a potentially strong method of providing friend recommendations in social networks while additionally gaining insights into how friendships are established.

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