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Scientific Research and Essays

Full Length Research Paper

Theoretical framework for social network marketing based on genetic algorithm

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The social network played recently a major role as communication media in our daily life as it allows individuals to interact with one another and build relationships. When products or companies advertise on the social network, they expect that their product or advertisement reaches its target. Social networks is a hot research topic that has received great interest in the recent years due to its wide spreading and influence on organizations that advertise on the social network. In this research, the study proposed a theoretical framework that uses a genetic algorithm to enhance marketing and advertising by calculating the fitness function value for each member; the two factors used are the features provided by each member and the path between community's members, and then it displays a list of suggested suitable advertisement. The main advantage behind the presented framework is to enhance the marketing and advertising in social networks communities to provide the maximum profit for the advertiser and provide the users with the advertisements suitable for their interests.

Key words: Social network, marketing strategy, advertising, genetic algorithm, fitness functions.

INTRODUCTION

The advent of social media has made the world smaller. There are social reports that over 2 billion people worldwide use social media, meaning 28% of the global population is interconnected. For marketing organizations, this web of connections presents a massive opportunity to make an impact on an unprecedented number of people. Marketing via social media is a priority for more companies than ever before. According to Kevin (2015), social media accounts for 9.9% of digital marketing budgets in 2015 a figure that is projected to grow to 22.5% in the next five years (Kevin, 2015).

Social media networks and social networks for example, Facebook, Twitter, and Google plus provide interactive and cheaper ways for the user to share ideas and stay connected with people. Ease in using social media applications on mobile devices achieves rapid growth in social media network users and leads to generate a vast amount of user generated content (Amit and Pravin, 2015).

The study of social networks has received an enormous

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amount of attention from the scientific community in recent years (Amit and Pravin, 2015; Natarajan et al., 2013; Kwan and Amitava, 2012). Social media technology changes rapidly, offering consumers new ways to experience social media platforms, which must constantly innovate to keep up with consumer demands (Papadopoulos et al., 2012).

Marketing on social networking sites will increase awareness by increasing the online presence of products and brand. Social network structure can be used as a measure for the community divisions and interest in the network. Community in a network is a pattern with dense links internally and sparse links externally. These links can be characterized by the content similarity between users, friendship between them and also other similarities in their personal data such as their location, gender, age, etc. These close structures can then be used for various purposes such as targeted marketing schemes. An important practical problem in social networks is to discover communities of users based on their shared content and relationship with other users (Papadopoulos et al., 2012). According to Kevin (2015), using and distributing educational content is a very effective strategy to gain more exposure for the business and build a bigger and wider audience. Using targeted educational content that targeted customers find relevant and interesting, extend the reach and coverage of brand and business particularly if this is done on a regular basis.

Detecting the information structure of the social network allows one to mine information in a more efficient way, narrowing the exploration of a network as large as the World Wide Web to a limited portion of it (Palsetiay et al., 2012). Communities reveal the informal organization and the nature of information through the whole system. The analysis of community is very useful for companies and organizations to determine the target groups that are suitable for their advertisement and their marketing campaign and this will increase the profit and reduce the cost.

The ability to find suitable communities in large networks could be of considerable use. Communities in a web graph correspond to sets of websites dealing with related topics (Karsten and Nitesh, 2008), and in the social network represent the real groups with the same interests (Mini and Sonia, 2015). Revealing and finding the network structure is of great importance to understand the targeted marketing strategy and analyze the network properties, thus making it much more propitious to understand and develop the suitable advertising system for the social network.

The social commerce is a subset of e-commerce that involves the interaction and user contribution aspects of online social media to assist online buying and selling of products and services (Amir and Morad, 2011). While marketers typically employ a social media strategy alongside traditional channels, many marketers are increasingly incorporating social networks into their budgets. The demand to develop a new strategy to reach the targeted group through millions of users is the major concern of the advertisers. So it's very important to analyze the community information on the social network to reach the targeted customer (Natali and sune, 2008). This study proposes a theoretical framework that uses a genetic algorithm to enhance marketing through social media networks.

RELATED WORK

Many methods have been proposed so far to reveal the underlying community structure in networks (Steve et al., 2014; Xie and Szymansk, 2013; Gregory, 2010; Raghavan et al., 2007). Genetic-based approaches for community structure identification can be found in the study of Shi et al. (2009), Dongxiao et al. (2009), Pizzuti (2009), Rohan (2011). In the following the study reviews some of the most important work in social network and genetic algorithms:

Minimum-cut method (Vishakha and Kamal, 2015) applying this method involves, dividing the network into a predetermined number of parts. The method works well for many of the applications, but it is less than ideal for finding community structure, in general networks.

Newman and Girvan method (Vishakha and Kamal, 2015) have discussed the traditional community detecting algorithms and also discussed the new ‖ledge between ness‖ algorithm for detecting the community structure on computer-generated graphs and real-world networks. The method is a divisive hierarchical clustering method based on an iterative removal of edges from the network. The edge removal splits the network into communities.

Hopcroft et al. (2004) present an agglomerative hierarchical method for clustering large linked networks to identify stable or natural cluster. A cluster is deemed natural if it appears in the clustering process when a given percentage of links are removed.

Radicchi et al. (2004) propose two quantitative definitions of community and an algorithm to identify communities. The quantitative definitions of community are based on the degree of a node. A sub graph is a community in strong sense if each node has more connections within the community than the rest of the graph. A sub graph is a community in a weak sense if the sum of all in-degrees is greater than the sum of the out-degrees. The algorithm is a divisive hierarchical method based on the concept of the edge-clustering coefficient, defined in analogy with the node clustering coefficient [21], as the number of triangles an edge participates, divided by the number of triangles it might belong to, given the degree of the adjacent nodes. Their algorithm works like that of Newmann and Girvan, the difference

being that instead of choosing to remove the edge with the highest edge in between, the removed edges are those having the smallest value of the edge-clustering coefficient.

Blondel et al. (2008) propose one of the most popular algorithms in the field of community detection (Louvain method (LM)). LM is perhaps one of the best algorithms regarding of accuracy. This popularity derives by the fact that LM provides excellent performance even if the networks to the process are very large. LM consists of two stages that are iteratively repeated. The input of the algorithm is a weighted network G = (V, E, W) where W represents the weights associated with each edge.

Raghavan et al. (2007) proposed an algorithm relies on a label propagation strategy Community Overlap Propagation Algorithm (COPRA). COPRA works in three stages: (1) Initially, each vertex v is labeled with a set of pairs (c, b), where c is a community identifier and b (belonging coefficient) a coefficient indicating the strength of the membership of v to the community c; belonging coefficients are also normalized so that the sum of all the belonging coefficients associated with v is equal to 1. Initially, the communities associated with a vertex coincide with the vertex itself and the belonging coefficient is 1. (2) Then, repeatedly, v updates its label so that the set of community identifiers associated with v is put equal to the union of the community identifiers associated with the neighbors of v. At each, iteration all the pairs in the label of v having a belonging coefficient less than a threshold are filtered out; in such a case the membership of v to one of the deleted communities is considered not strong enough. It is possible that all the pairs in a vertex label have a belonging coefficient less than the threshold. In such a case, COPRA retains only the pair that has the greatest belonging coefficient and deletes all the others. Finally, if more than one pair has the same maximum belonging coefficient, below the threshold, COPRA selects at random one of them, and this makes the algorithm non-deterministic. After deleting pairs from the vertex label, the belonging coefficients of each remaining pair are re-normalized so that they sum to 1. A stopping criterion ensures COPRA ends after a finite number of steps. In such a case, the set of community identifiers associated with v identify the communities to which v belongs to.

Pizzuti (2009) proposes a genetic algorithm to discover the community structure hidden within social networks. The algorithm called GA-Net, uses the locus-based adjacency representation proposed in Park and Song (1989). GA-Net uses the community score as the fitness function. This community structure measure can identify densely connected groups of nodes with sparse connections among them. Also, the genetic algorithm employs specialized variation operators that take into consideration only the actual correlations among the nodes. Pizzuti (2009) presents the results obtained by running GA-Net on a social network with known community structure. Results obtained by running GA-Net with two different fitness functions are presented and compared to each other. Both the network modularity proposed by Newman and Girvan (2002) and the community score proposed by Pizzuti (2009) are employed as fitness functions.

Mursel et al. (2007) present a genetic algorithm that uses as fitness function the network modularity, proposed by Newman and Girvan (2002). A candidate solution is represented as a chromosome with N genes, where N is the number of nodes in the network. Thus, each gene corresponds to a node. The value stored in each gene represents the identifier of the community to which the corresponding node belongs. Mursel et al. (2007) employ a one-way crossover operator. Given two individuals, a community identifier is randomly chosen from one of them and then transferred to the same gene in the other individual.

The study propose a theoretical framework to optimize marketing and advertising in social networks using a genetic algorithm, the algorithm uses the genetic algorithm proposed by Handle and Knowles (2007) for community detection. However, an alternative approach to enhance marketing in the social network has been adopted. Also, the study modified the fitness function to calculate the lowest value taking into consideration the path for that member in the social network. The study analyzed the composed chromosome for both the user profile and the advertiser information and calculated the fitness functions, both from the point of view of efficiency and adaptability. The study then propose a combined fitness that achieves better results in the social network.

Genetic algorithm

A genetic algorithm is an optimization method applied to artificial intelligence problems that mimics the process of natural evolution. According to Vishakha and Kamal (2015) genetic algorithm is practical method when the solution space of a problem is very large, and an exhaustive search for the exact solution is impractical. Each member of the solution set, which is called a chromosome, represents a possible solution to the problem, and the algorithm tries to find the best fitting solution member. In order to improve the quality of the solution members, the algorithm uses genetic operations on possible solution members for a predefined number of iterations (Vishakha and Kamal, 2015). The algorithm randomly initializes the chromosomes at the beginning. Then for a number of iterations, it uses a fitness function to assign a fitness value to each solution member, which shows how good a solution member is to solve the problem (Gregory, 2010) As shown in the Figure 1,

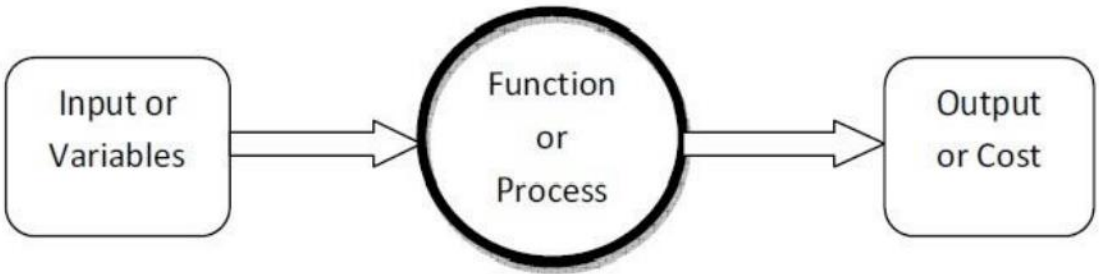

Figure 1. Optimization process (Source: Vishakha and Kamal, 2015).

optimization is the mechanism by which one finds the maximum or minimum value of a function or process. Optimization consists in trying variations on an initial concept and using the information gained to improve on the idea. A computer is a perfect tool for optimization as long as the idea or variable influencing the idea can be input in electronic format. Feed the computer some data and output solution (Xie and Szymanski, 2013).

RESULTS AND DISCUSSIONS

A social network structure can be represented as a graph G = (V, E) where V is a group of objects, called nodes or vertices, and E is a set of edges between nodes represent links that connect two groups of V. User profile in a network is a group of vertices having a high density of edges that represent the interest of the user in concern with its surrounding community. The proposed genetic algorithm fitness function calculates the minimum value for each individual that is suitable for best marketing strategy based on two factors: the features provided by each member of the social network and the path for that individual; the shortest path considered to be optimal.

In social network graph, each node represents an individual (a member of the social network), and each member has a lot of features that construct his node details that will be used to construct the chromosome. The problem of determining the best advertisement to be displayed to the best user in the social network can be formulated as finding a partitioning of the nodes in the network subsets that are highly connected. To treat graphs, the study used the adjacency matrix, since the network contains N nodes, the graph is represented with the N × N adjacency matrix A, where the entry at position (i, j) is 1 if there is an edge from node i to node j, and 0 otherwise. The problem can then be focused on finding a partitioning of A in the social network with sub-matrices that maximize the sum of densities of the sub-matrices.

Counting the number of interactions does not give any information about the interconnections between the nodes. A density measure based on volume and row/column means - allowing detecting maximal and dense sub-matrices and applied to find Co-clusters in sparse binary matrices (Angiulli et al., 2006). Co-clustering (Angiulli et al., 2006), also known as bi-clustering, differently from clustering, tries to simultaneously group both the dimensions (objects and features) of a data set. In the proposed approach, the objects are user communities and the features are the information and interest provided by each user that can be used to calculate the fitness function in the genetic algorithm.

A quality measure of the profile information provided by the social network member S that maximizes the in-degree of the nodes belonging to S and that implicitly minimizes their out-degree has been introduced by Pizzuti (2009). The study will use this information as a strategy for marketing and advertising in the social network, and then show how it can be exploited to find the best fitness function after applying the genetic crossover and mutation to the represented data.

Applied algorithm

Input: graph S = (i, j), represent community graph in the social network
Output: Best path according to best fitness value calculated

For all *i* = *j* do
Select randomly the initial populations,
Determine a set of all paths linking to (*i, j*)
For all *i* =j do
Evaluate the fitness for individuals from the population
Perform the operation of reproduction,
Perform the mutation operation,
Store in the array the path that has best fitness value
Delete *(i,j)* that has the worst fitness value
End

For gene representation and initial population, the study uses an array to store community identifier of nodes. The

Table 1. A graphical representation for the genetic chromosome constructed from the provided user information.

1	0	2	1	0	0	5	1	7	1

array sustains n elements called chromosomes. The chromosomes hold different social member profile information and interests. The gene representation of a chromosome for the algorithm is shown in Table 1.

The value of the fitness function is computed by using respective chromosome as input data. The value returned used to evaluate that chromosome, which encodes a possible marketing strategy. Then for each *n* member features in the social network form a chromosome $\{Ri = \{r \dashv\} \downarrow i \uparrow k \ , k = 1 \ldots . ki\}$ available for this member. Each chromosome has Ri features that are represented by a list of natural numbers from the range 1 *to n* where *n* is the number of possible paths from the corresponding set of paths. Fitness function *S* of all individuals in population is calculated as follows:

$$Sfit = \sum_{k=1}^{m} Ok$$

Where: *m* - is the community Size, that is, the number of individuals (chromosomes), and individual features in the population.

Ok - the fitness of the *k*-th individual,

The probabilities Pr for the new population were *calculated by the following equation:*

$$Pr = Sfit/ \sum_{j=1}^{m} Sfit_{(j)}$$

Where *m* is the community size, due to the independence of probabilities of each path

The study added favorite value paths that utilize shortest path to the fitness function according to the following equation:

$$Pr = \sum_{l \in p} \frac{\mathbf{c1 - b1}}{\mathbf{c1}}$$

Where the component *cl* is the assumed weight of the path *l*, and *bl* is the actual weight of the whole path.

The binary strings of these individuals (chromosomes) that have highest fitness values (high profit) will be the basis for building a new generation (population). The strings with lower fitness values, give the study the basis for constructing the marketing strategy. The proposed strategy crossover point for each chromosome is selected, after that, all the elements of the chromosomes are exchanged between the two chromosomes.

The proposed strategy select two chromosomes, one of which is called as the source chromosome; the other is called the destination chromosome. Then it randomly selects multi-point from source chromosome replaced with the destination chromosome corresponding value, the mutation operator randomly changes the value of the gene according to the node information provided by the social network user. Thus, the possible values are restricted to the neighbors of the selected gene. It guarantees the generation of a mutated child in which each is linked only with the advertisement that has the best fitness value.

The quality of a chromosome is represented by the amount of data which results from the genetic operations. It is noticed that using the genetic algorithm produced more varied generations which leads to more diversified suggestions of the marketing and advertisement strategy decisions that will guide the best advertisement that will be displayed to the user.

Conclusions

The study presented a theoretical framework for social network advertising and marketing using a genetic algorithm. The proposed framework calculated the fitness values for each member based on the features provided by each member and the path between communities' members and then it displays a suitable advertisement for each member in an intelligent way. The main advantage behind the presented framework is to enhance the marketing and advertising in social networks communities to provide the maximum profit for the advertiser and provide the user with the advertisement that is suitable for their interests, since the genetic algorithm and its operations is able to produce several acceptable solutions, using the given data and a set of criteria. As for future, a further research direction includes the creation of a friendship recommender system that suggests new possible connections to the users of a very large-scale online social network, based on the communities they belong to.

Conflict of interests

The authors have not declared any conflict of interests.

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