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Enabling Link Prediction Optimization on Social Networks

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Abstract

Virtual social networks are a modern age of spaces that play an important role in the world today. They are highly dynamic networks with a complex structure. This is why it is very difficult to predict communication in this field. The prediction has recently caught the attention of various researchers as one of the most important aspects of data mining. In addition to understanding the relationship between groups in social communities, the connection prediction in social networks also ensures that networks are popular. Link prediction is the prediction of the probability that two entities will interact based on some unique and common characteristics between them. Link prediction is intended to generate and propose a list of persons to whom the user communicates. This study introduces a prediction approach used to combine a genetic algorithm with an algorithm from Louvain. Data are first chosen from the default dataset as binary in this process. Then the best nodes are extracted and chosen based on merit using the genetic algorithm. Lastly, the modularity of the networks is obtained by using the Louvain algorithm. The findings indicated the optimal performance of this approach.

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1. Introduction

Social networks have long been recognized as the ties that bind humans in interactions that strengthen families, groups, communities, and societies. Explain that “networks are a way of thinking about social systems that focus our attention on the relationships among the entities that make up the sys-tem (Pierce et al., 2021). Social network analysis offers significant potential to elicit an advanced understanding of the network that must collaborate across complex organizational structures, and geographic distance. Social networks are popular with Facebook, Twitter, Google Plus, etc. (Pruinelli et al., 2020).

One of the key events of recent years is the rise of online social networks. Many social networks online, including Facebook, are increasingly popular. In recent years, many multimedia networks, including Flickr, were also very popular. In many of these networks' knowledge, content and communication can be used in research dramatically increased. A network of social networks is commonly characterized as a broad community of interactions or communications, in which actors are included in vertices and actors, communicate with each other (Fire et al., 2011).

It should be noted that with the rapid development of social networks, determining the future needs for analysis and forecasting in terms of reducing risks and increasing accuracy in decision-making, requires scalable modeling and selection of fast and accurate algorithms. To ensure understanding of network interactions, it is very difficult to select the appropriate algorithm to use network structural knowledge instead of behavioral knowledge.

Social network analysis is a research methodology that explores interaction dynamics between people, groups and organizations. Web metric scientists employed this method in web studies and examined online social networks. They agree that computer networks can be analyzed based on social media research because they can link individuals and organizations. Therefore, the rapid growth of social networks requires scalable modeling and selection of fast and precise algorithms to be considered and assess potential analytical and predict needs for risk mitigation and improved accuracy and precision. We decided to include an effective algorithm in this analysis to predict quickly in two consecutive decision times.

2. Literature Review

As previously described, the behavior and function of a network are to be analyzed in a prediction. This is why we should recognize the condition of a network for decision making in the future based on our ability to predict. Accurate prediction, precise prediction and speed are effective decision-making factors in the right prediction (Dhote et al.2013). The network structure and behavior dynamics question emphasize the need to predict decisions. The potential configuration of the network or its behavior may be investigated through projections in a network. For applications that do not need a learning process and applications that need knowledge of various communication backgrounds, "Foresight" is useful. Behavior prediction complexity and background problem are one of the drawbacks of big data work. Big data predictions are very expensive and sluggish.

Many biological networks, such as network protein foods and metabolism networks, predict whether the two nodes in the network have an advantage by conducting separate, typically very expensive experiments. Furthermore, there is typically minimal information on these networks. For instance, 80 percent of yeast cell molecular interactions (Yu et al., 2008) and 99 percent in humans are still unknown. New communications can be predicted based on established papers instead of testing all potential communications blindly (Stumpf, 2008).

Social networking friendships have the same general importance as two-person relations. A group friend hood identification system for proposing friendships recognizes secret links. The discovery of hidden connections allows these networks to predict future events or propose partnerships for participants. Friendship on social networks is defined as: If they are in touch with one another, two nodes are mates. In such situations, hidden communications include social nodes, which still do not have the above links. The production or loss in social media is generally called "link prediction" (Hopcroft, Lou & tang,2011) 'Link Prediction' also includes many non-social networking applications including e-commerce, genetically-motivated interactions, energy and output management as well as protein-protein communication. Many of these approaches use network graph structural properties. In some cases, the methods are non-structural. "Link prediction" refers, in the graphic structure of a social network, to the prediction of the relationship between two entities based on the properties of the entities and the other connections contained on the network graph (Ahmad et al, 2010). This means that if we have a snapshot of the link sequence at t time, then the objective is to predict links at t+1.

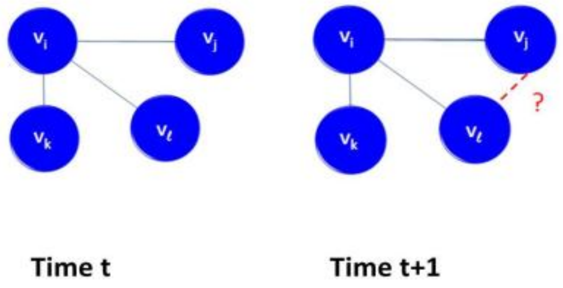


Fig. 1: Link prediction on social networks

Because of the presence or absence of a central observer, the different methods for "link prediction" can be divided into two general categories: "supervised" and "unsupervised" "Unsupervised" methods are methods that were built without looking at past "links" patterns and using structural functions on the network graph, which will answer possible "link predictions" Supervised approaches deal with possible "link predictions" after learning about one or more steps in building links in the past (Zhang, Kong & Philip, 2013).

"Unsupervised link prediction" as the number of common neighbors between two nodes, uses structural features. Often "Supervised link prediction algorithms" predict links by acquiring probabilistic model parameters or by analyzing the evolution of a specific network graph infrastructure. Any method showing the similarity of the two nodes in the red graph can be used to predict the relation. In several research projects on social media studies, user knowledge and social relations, including friendships, are manipulated. However, some studies use other data, including information on cluster and community, to improve link prediction performance. These findings led to the use of community data to enhance the efficiency of the predict (Li et al, 2013).

The similarity between the two nodes typically benefits from different algorithms of relation predictions. According to these algorithms, the more similar the two nodes would be, the greater the likelihood of a connection between them being formed in the future. Our purpose is to use this criterion of similarity. Although each old method uses a particular network structure-function, more information, including community and community information, can be used for that purpose, of which each node is a member. These methods of "link prediction" can be much more accurate than previous methods and better. They are however slower than the earlier form. But in large networks with millions of members, they can perform better (Cheng, & Zhang, 2019) Therefore, the method we are searching for is that we can measure this criterion in a short space of time for large data.

The first "link prediction" model specifically used in social networks, introduced by Novell et al. The prediction method relies on the similarities between the two nodes, which will likely be friends in the future. The nodes were ranked based on similarity. This method was later developed by Al-Hassan et al. (2011) in two other ways. They showed initially that the use of external data could improve the prediction of links. The "link prediction" problem was resolved through different criteria of similarity. In other words, the "link prediction" problem was suggested as a binary categories problem. Later, in connection data and the Internet, the "link prediction" was employed (Rezvanian et al, 2019). For "link prediction" Sherkat and al. (2014) employed the optimized ant colony algorithm. Wou and Wu (2022), proposed a triad link prediction algorithm (TLPA) to quantitatively evaluate the results of the evolution analysis of the SNEA (social network evolution analysis) method. The TLPA algorithm reduces the blindness of message forwarding and unnecessary waste of resources by predicting the probability of a connection between nodes in the network.

Singh and Kailasam (2021) studied the IM problem (Influence Maximization (IM) is the problem of finding a small set of highly influential users in the social networks) in a social network that evolves with time and proposes a new Link Prediction based Influential Node Tracking (LPINT) framework. In the proposed model, they applied the conditional temporal Restricted Boltzmann Machine (ctRBM) to predict the upcoming snapshot of the graph by predicting the links that may appear in the network by considering the evolutionary network’s temporal and structural pattern. And then, they applied an efficient IM technique for finding the seed nodes in the predicted snapshot of the network. Finally, they evaluated the spread of influence in the latest snapshot of the graph using predicted seed nodes.

Daud et al (2020) provided a comprehensive review and discuss link prediction applications in different social network contexts and analyses, focusing on social networks. In this paper, they also presented conventional link prediction measures based on previous researches. Furthermore, they introduced various link prediction approaches and address how researchers combined link prediction as a base method to perform other applications in social networks such as recommender systems, community detection, anomaly detection and influence analysis.

Niknam et al. (2014) suggested an ideal voltage and power control response model in electrical systems. They tried to find the right solution by randomly configuring the parameter and changing the different parameters by combining the gravitational search algorithm. Mahmoodi and ghasemi (2018), proposed a method for predicting changes in the total stock index of Tehran stock exchanges. The purpose of this research was in the field of applied research. In terms of its implementation, the research was based on a causal research that is carried out using a data collection database. Wang and Li (2010) carried out an endless optimization analysis on boundary conditions. Hassanzadeh et al (2010) had a new approach for control and distribution, incorporating a uniform mutation operator and elitist strategy and a multi-objective search algorithm, of the global optimization problems. Amoozadkhalili et al (2011) reviewed the important theoretical work with highlighting the fundamental similarities and differences and the connection between the company, the knowledge basis of the company and innovation. they compared the principal findings of the research on innovation and knowledge creation. The main objective in this paper was that a company’s capabilities were primarily developed on the basis of social norms and values already existing in the social relations of the company.

Rashedi et al. (2010) have indicated how binary search space can be optimized. To model it, as they change from 0 to 1, they balance the speed with potential bits’ changes. Shaw et al (2012) addressed combined cost and electrical load delivery. This problem is extremely successful in solving the problems of large data networks or very large elements in social networks along with a multifactorial architecture.

Musial, & Budka discussed by achieving a threefold evolution pattern during consecutive, instantaneous network pictures. This is a structurally monitored system. When the graph is called directed, 64 different tertiary groups will be displayed in a graph since each pair of three nodes can be linked in four different forms, without connection, the connection between the first and the second, and connection between the second and first nodes. A triple shift matrix can be obtained by counting these sixty-four three nodes into two consecutive network graph snapshots. The analysis shows that for various datasets, the three-fold variance matrix varies. This distinction demonstrates the unique features of each dataset. In each of the sixty-four different seeds, we can estimate the likelihood of a relationship with this node pair by counting the number of contributions of a node pair that is not associated with each other.

Predicting lost links on social media or potential links in the future can be a challenge in itself. Although this issue has been extensively explored; however, the problem of how to optimally and effectively combine the information obtained from the network structure with the abundant descriptive data for nodes and edges remains large. This eliminates the need for the process of learning network changes at consecutive times and allows for quick prediction of two consecutive decision times for a large data set. This research has addressed this issue.

3. Material and methods

The different "link prediction" approaches can generally be divided into three groups. Methods based on standards of similarity are the first type. They are the simplest method of relation prediction, in which each pair of x nodes has a point dependent on the degree of similarity among the two nodes. The degree to which the two nodes are identical and the links with greater values is expected to be classified in all unseen links. This approach predicts network-based connections. As with distance-based approaches, "link prediction" between nodes would be more likely to occur in the future. The second group are approaches focused on statistics. The methods are based on mathematical models and distributions. Probability-based approaches are the third group. In these methods, it extracts properties and characteristics that make the relation more probable and examine the structure of the graph.

The purpose of the study is to obtain a circle of friends on social networks automatically. The social network offers an input list of users. We find a circle of possible friends for every user in the social network with the following algorithm. The "modularity" criterion in this study enables comparisons of network communities. Modularity first became an essential part of community deletion algorithms as a criterion for deciding the stop step. This criterion provides a method for the efficiency estimation of the division of nodes into separate communities. It has become the most commonly used quantitative norm in this area, thanks to its simplicity and performance.

3.1. Proposed algorithm

A relatively quick method of finding groups over large networks is the proposed algorithm. This approach optimizes and clusters the vertices of the map with the Louvain algorithm of "modularity" In this algorithm, the first nodes and nodes are selected with the genetic algorithm to find the sum of local optimization. Then they are placed and clustered in small groups. Clustering is then carried out to achieve an optimum large network by combining small groups. In this approach, we find communities and links in large networks using a combination of genetic algorithms and Louvain algorithms and trying to construct an optimal network.

Raw data was analyzed and refined first by the assessment process in this study. A table of user objects is then generated to tabulate the objects. This process is achieved by using the Louvain system and the genetic algorithm. The data is subsequently pre-processed using the Louvain algorithm to work with this hypothetical graph. The graph is optimized, and the final method of working with the hypothesis graph is presented using a genetic algorithm. The sum of the data submitted to the user for display and suggestion is minimal because of the use of the genetic algorithm. The explanation is that the algorithm and fitting function were tested. The maximum filter applied to this data in the preceding steps. Thus, the data can be sent to the user more easily and equally.

3.2. Genetic algorithm

Genetic algorithms are part of the evolution-inspired computational model family. These possible solutions encode a problem into several basic chromosomes and apply these constructs to hybrid operators. They are often considered to be the genetic algorithm for optimizing functions. This algorithm selects from the randomly ordered information the most suitable strings. A new set of strings is generated in each generation using the best components of the previous dataset and a new random section to find the right answer. It is an algorithm, albeit random, but not a simple random algorithm. The genetic algorithm explores knowledge from the previous search space efficiently to find better solutions in a different search stage. The genetic algorithm does not conduct a simple randomization process during randomization. However, it uses the early data to pick a new quest to achieve the desired development. The genetic algorithm summary is shown in Fig. 2.

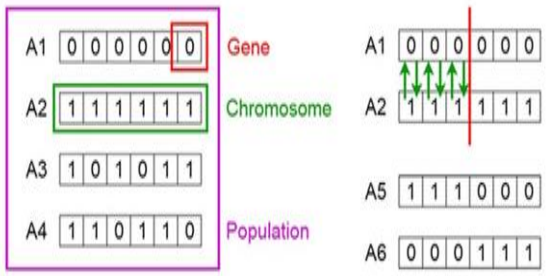


Fig. 2: Schematic definition of genetic algorithm

3.3. Louvain algorithm

"Modularity" was first regarded as a criterion for deciding the Newman algorithm stop-stage but soon became a major component of many community-detection algorithms. This criterion sets out the consistency determination formula for the division of various nodes and communities. It is the most frequently used quantitative calculation of the output of community detection algorithms because of its simplicity and performance. If there are no better intra-cluster edges than random graph mode, the "modularity" is 0. The full "modularity" is obtained by connecting all the vertices of each cluster and not connecting the cluster edges. Experience has shown that this is between 0.3 and 0.7 on graphs that belong to social networks. One of the fundamental features of "modularity" is its ability to equate various clusters with various clusters. As various algorithms create the same number of clusters, many of the current parameters do not equate. They cannot use them to examine the different clustering methods. The "modularity" property, on the other hand, allows for the measurement of cluster numbers. The trend of the "modularity" changes when clusters are split or merged. The clustering that one of the fundamental features of "modularity" is its ability to equate various clusters with various clusters. The "modularity" property, on the other hand, allows for the measurement of cluster numbers. The trend of the "modularity" changes when clusters are split or merged. The clustering that maximizes this amount can therefore be considered the best graph cluster. Thus, the hierarchical method is top-down or bottom-up. A simple and efficient algorithm for finding "communities" in large networks. The Louvain algorithm. This algorithm seeks to maximize the criterion of "modularity" in the graph. The input graphical size limit, not time, depends on our memory limit, unlike other clustering methods. That is why this algorithm can easily be applied to graphs distributed by hundreds of thousands and millions. This algorithm uses the greedy method "modularity" to optimize that method and clusters the vertices of the graph. Two steps are taken for this optimization:

A) Searches for small local optimized groups first.

B) Then, the grouping of small groups that can form larger groups continues.

These steps are repeatedly used to achieve the maximum "modularity." The algorithm is a quick way to find a hierarchy of clusters in a large graph, as mentioned earlier. Two alternating phases consist of this algorithm. Suppose we have a "weighted network with n vertices" The Louvain algorithm steps are shown in Fig. 3. Two phases comprise this iteration: local "modularity" optimization by shifting the vertices in the clusters, and building the clusters obtained during the last stage and generating a new network. Both phases are repeated alternately until the "modularity" has increased. For spacious graphs, the algorithm is linear. The reason for its high speed is the simplicity to calculate the "modularity" difference and to reduce the graph size after a little repeat, as most time spent on the algorithm is usually used for the first iteration.

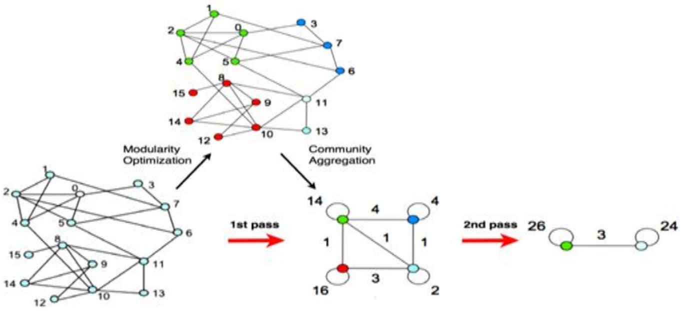


Fig. 3: General process of Louvain algorithm steps

4. Implementing the Proposed algorithm

The general method for the proposed method is shown in Fig. 4. Generally, the method is divided into four steps:

- Data entry stage: The data is placed in this phase as a binary matrix or matrix consisting of the "communication". The above matrix is square and expresses network connections. The presence or absence of the connection of two nodes in this matrix is shown by a number larger than "1" and the absence of connection by 0.
- The formation step of "Adjacency matrix": from the first step on we create an array called the "adjacency matrix" if we have a number series or file. Connections between nodes are standardized and uniformly expressed in the matrix.
- The GA is used to optimize and communicate: we examine data with

GA and apply GA to data in this step. This means that the first assessment code is applied to the data of intersections, hops, etc., and the best combination is displayed on the outcome. This list will almost be an optimal list for investigating and extracting all possible connections between nodes.

- To achieve "modularity" use the Louvain method:
- "Link prediction" means that this method is responsible for the presence or absence of communication in the network between two entities and two nodes. All communication in the previous step obtained by GA. Communications will then be calculated using this method for their "modularity" and "modularity." The higher the "modularity," more powerful the communication prediction.

GA takes all of the above steps to obtain the best combination and the highest possible probability of path between nodes. The GA examines all possible paths between nodes and takes paths like transitive relationships into account. The GA's output is a matrix that has as many paths as possible between its vertices. This matrix is eventually input to the Louvain algorithm. The GA pseudocode is displayed in Table 1 and the Louvain algorithm in Table 2.

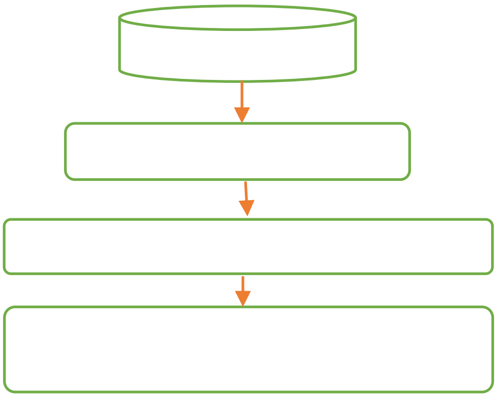


Fig. 4: proposed method

Table 1. Pseudocode of the proposed GA for calculating the adjacency matrix

1.Generate The Initial Population Using Dataset
2.Evaluate The Population With Fitness An Operator Of GA
3.Create Adjacy Matrix From First Generation
4.Create Matrix M From Adjacy Matrix
5.Using Louvain Algorithm To Calculate Madularity

Table 2. Louvain algorithm for calculating the "modularity" of each graph

```
Function Louvian Algorithm (Graph G)
G'=G
C the index of community of each nodes of G'
Initialize each node with its own community
q=-∞
while q>Q (G', C) do
    q=Q (G', C)
    C=Move Nodes(G')
    G'=Aggregate (G', C)
    C=put each node of (G') In its own community
end while
return G'
End function
Function Move Nodes (Graph G)
    C the index of communities for each nodes of G
    while one or more nodes are moved do
        for random v∈V(G) do
            best_q=-∞
            best_c= community of v
            for all neighboring nodes n of v do
                gain_q=ΔQ between v and n
                if best_q<gain_q then
```

```
                best_q= gain_q
                best_c= community   of   n
            end if
        end for
        C=Place v in the best_q
    end for
  end while
return C
end function
Function Aggregate (Graph G,Partition C)
    G'= Aggregate nodes which are in same community based on C
return G'
end function
```

4.1. Research data

This article downloaded and used the dataset based on information gathered from the standard Konect website. This site provides binary and non-binary information on various topics, including a number of nodes and edges. Dolphins, Facebook-friendships, Zachary Karate Club databases were used in this research. This dataset contains information on various objects, including the 'vertices' of the 'undirected graph' and their 'communications' edges, such as users, animals, etc. This dataset is particularly in the form of a text analyzed and taken as input data in two phases. The dataset of vertices is initially introduced, followed by specifying their relationships.

5. Result

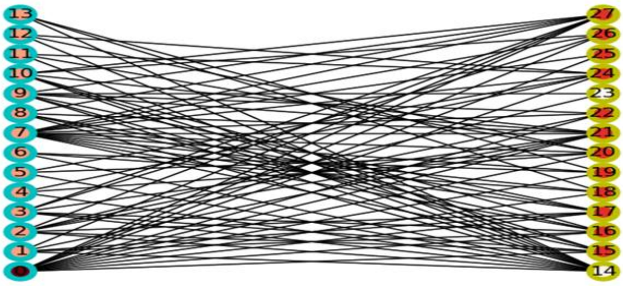
Table 3 presents the specifications of the datasets utilized in the present study.

Table 3. Experimental dataset specifications

N.	Dataset name	No. of vertices	No. of edges
1	Dolphins	62	159
2	Facebook friendships	63731	817035
3	Florida ecosystem dry	128	2137
4	Zachary karate club	34	78

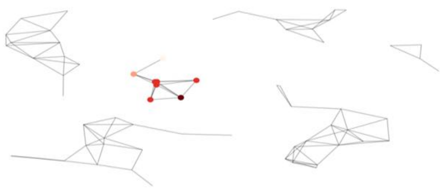
The architectural models proposed in the Python platform for the desired algorithm have been evaluated and tested using the dataset in Table 1. The trial system has the i5 dual-core CPU and 8G RAM with Windows 10. Details of the dataset and descriptions are provided below. Each data package provides a particular application used in the fields of animal social networking, for example. Because "link prediction" methods depend on the network type and structure, a link prediction model for all networks cannot be provided. The correct selection of various datasets can therefore help remove this defect. For the first time, the algorithms have been tested using various types of datasets with different structural features. Different assessment methods are then presented for comparing the algorithms of "link prediction." The following is a dataset used.

The following results are achieved by applying the Louvain algorithm to the 34 nodes database of the Zachary karate club without GA application. Fig. 5 shows the corresponding graphical representation. In 1977 Wayne W. Zachary compiled this database of information from members of the College Karate Club. Each node is a



club member, and each edge is a connection among the two club members. The network is "undirected." One problem often discussed with this dataset is that two groups of people are split into a karate club after a dispute between two teachers.

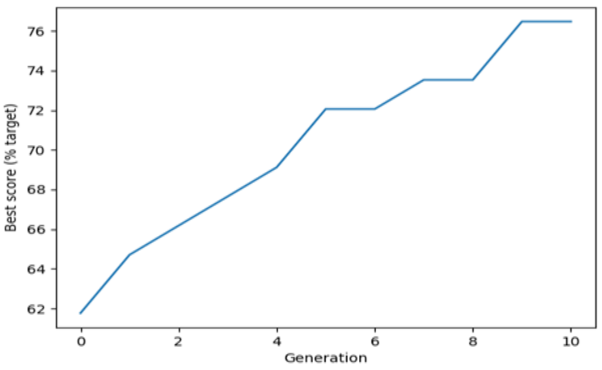
Fig. 5: Vertices and the connections between by the Louvain method



The red links show the strong connections with which the vertices are linked by edges in the graphic representation of every form. The nodes and their links are shown in Fig. 6. The colored nodes here indicate that they are strong and dynamic.

Fig. 6: Graphical representation of karate network and links between users

The modularity of 0.57 is obtained in this kind of implementation by examining and displaying the "modularity" by the Louvain algorithm without using GA.



The graph is achieved in Fig. 7 by applying the Louvain algorithm to the 34 nodes Zachary Karate club database and applying GA to the proposed method. Fig. 8 illustrates the corresponding graphical representation.

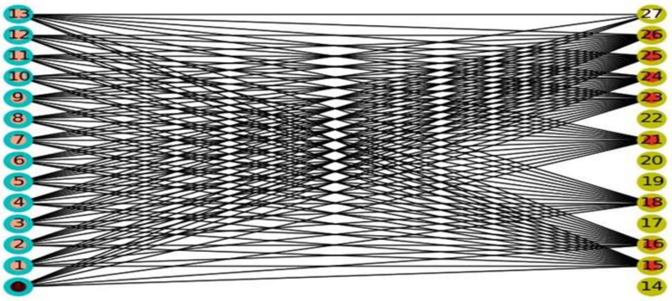


Fig. 7: GA output on the proposed data and production of the first generation

Fig. 8: Vertices and connections between in the karate network by the proposed method

As Fig. 8 shows, almost all "connections between vertices" are taken into account and plotted using the proposed method. Our method takes almost all equivalence cases into account and specifies how they can be connected. After the proposed method is applied, Fig. 9 shows the graphic representation of the karate network and user links.

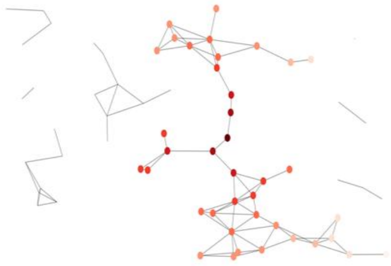


Fig. 9: Graphical representation of the karate network and links between users after applying the proposed method

The network shown in Fig. 6 is nearly more dynamic, and links are better than the previous case when using its proposed method, combining the Louvain algorithm and GA. In this case, the algorithm output has a "modularity" of 0.77.

Similar results are obtained by applying the proposed method to other datasets, whose output is shown in Table 4.

Table 4. Experimental results and comparing the proposed method and the Louvain algorithm

N.	Dataset name	No. of edges	No. of vertices	Modularity without Louvain method	Modularity with the proposed method
1	Dolphins	159	62	0.7	0.81
2	Facebook friendships	81703	63731	0.71	0.91
3	Florida ecosystem dry	2137	128	0.75	0.82
4	Zachary karate club	78	34	0.57	0.77

6. Conclusion

In this research, a combination of GA and Louvain algorithm was used as a "link prediction" In the first place, the characteristic matrix, the same links between "vertices" and graph nodes, are binary loaded with the same method in the simulator software. Then important features were selected with the GA and the closest neighbor fitness function. The data were categorized after choosing and fitting the best features. Then the best "modularity" between the vertices was achieved using the Louvain function. The results have shown that the method proposed has good network accuracy and performance, especially in networks with a high number of nodes.

In this study, GA and a modular function, Louvain, were used to detect "communities." Our method has been tested using various datasets, and the results are acceptable. The advantage of these methods over other methods is a broader investigation into and the higher speed and accuracy of all network partitions than other GA-based techniques. Because the genes are separate from one another in this algorithm, link overhead learning is not present in this method. The proposed method was evaluated for various data with different vertex and edge numbers. The experiments showed the ability of the algorithm to detect "communities."

In this method, considering that almost all possible cases were investigated, in the data set that had more vertices, the modularity is better and higher, which means that using genetic algorithm and using the function of fitting, organ transplantation and the best a link is found. This method can also be used in networks that have overlapping associations. The use of scoring in forums as objective functions and the idea of non-evolutionary methods to improve the answer obtained from the process of evolution are examples of these ideas.

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