Link Prediction in Co-Authorship Network under Fuzziness and Application in Biomedical Analysis

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ABSTRACT

We aim to predict links in fuzzy social networks, where the existing methods based on common neighbors of two nodes are not effective. These methods are local measures that only work when the shortest distance between two nodes is less than or equal to two. Our method can handle cases where the shortest distance is between three and five. We define the concepts of link strength and path strength in a network and propose an algorithm for predicting links. We illustrate our method with a numerical example in a co-authorship network and discuss application areas in biomedical.

KEYWORDS

social network; path; link prediction

1 Introduction

S ocial networks (SNs) consist of social members and the links between them. SNs enable members to make new friends, share news, exchange business ideas, and so on. Some online social networks (OSNs) have become very popular. To extract useful information from SNs, we need to measure and analyze the nodes and links in the network. There are various centrality measures $[1, 2]$ that indicate the importance of nodes, such as degree centrality, closeness centrality, betweenness centrality, etc. However, the links in SNs are dynamic and change over time, as new members join and new links are created. Therefore, an important problem is to predict the future structure of the network based on the current state. This problem is called link prediction $(LP)^{[3,4]}$. LP has many applications in SNs, such as friend suggestions^[5], product recommendations[6], etc.

The most common LP method relies on common neighbours $[7,8]$, which are the nodes that are connected to both nodes of interest. There are many indices and methods that use common neighbours and other local information to predict links. For example, the Jaccard index[9] is the ratio of common neighbours to the union of neighbours of both nodes. The preferential attachment index^[10] is the product of the degrees of

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both nodes. Sorensen index $^{\text{\tiny{[1]}}}$ is twice the number of common neighbours divided by the sum of degrees of both nodes. Salton index^[12], Hub promoted index^[13], LHN index^[14], Hub depressed index^[15], Resource allocation^[15], and Adamic–Adar^[16] are other similar indices that use different combinations of common neighbours and degrees.

There are also some recent studies on LP that use more advanced methods. Yang and Zhang \vert^{17} proposed a model that considers both common neighbours and distance between nodes. Wang et al.[18] introduced a method that uses node popularity as a factor for link creation. Wu et al.^[19] formulated an influential nodebased LP method that incorporates both local and global information. Wen and Deng^[20] proposed a model that identifies influencers using local information and predicts links based on them. Ahmad et al.[21] proposed a score for LP that uses both common neighbours and closeness centrality.

However, in some cases, the objects and the relationships in SNs are not clearly defined and may have some fuzziness^[22]. Fuzzy graph theory was introduced by Kaufmann^[23] in 1973 to deal with such situations. Rosenfeld^[24] further developed fuzzy graph theory in 1975. Yeh and Bang^[25] introduced the concept of connectedness in fuzzy graphs in 1975. Bhutani and Rosenfeld^[26] studied strong arcs, strong paths, strength of connectedness, etc. in fuzzy graphs in 2003. Fuzzy graph theory has been evolving since then.

In this study, we focus on LP in fuzzy SNs, where the existing methods based on common neighbours are not suitable. These methods are local measures that only work when the shortest distance between two nodes is less than or equal to two. Our method can handle cases where the shortest distance is between three and five. We define the concepts of link strength and path strength in a fuzzy network and propose an algorithm for predicting links. We illustrate our method with a numerical example in a co-authorship network.

defined as follows: $M_i = \min\{\mu(u, w_i), \mu(v, w_i)\}\$, where $i = 1, 2, ..., n$. Then, the score of link prediction The study on link prediction in uncertain environment started by Bastani et al.[27] in 2013. There was another model by Tuan et al.^[28] in 2019. At the same time, Mahapatra et al.^[29] introduced Rupkumar–Sovan–Madhumangal (RSM) index for link prediction. The nature of every neighbour is is denoted by

$$
S_{uv}=\sum_{i=1}^n\frac{M_i}{n}.
$$

not found, i.e., $N_1(u) \bigcap N_1(v) = \emptyset$, then $|N_1(u) \bigcap N_1(v)| = 0$, But in real it may have some non-zero But in this index, the authors consider only the nature of the common neighbours that are direct neighbours and did not consider the indirect members that connected via path. If a common neighbour is value depending on indirect members. To remove this limitation of local predictions, we proposed a path based new model on link prediction, which counts all possible paths between the nodes through various members and predicts possibilities of link between two nodes having no common neighbours.

1.1 Problem definition

Suppose that there are 1000 items in an online shop. If a customer searches for an item, then the platform will show you the same searched item with some related items. So, which item should be displayed that is

calculated by the link prediction method? Figure 1 indicates a product network hidden in an online web platform. The numbers beside the items denote the number of times they sell a product, and the number between the products indicates the number of times both items sell. Now, if a customer searches for the soap of a company, then as per RSM index, shampoo and body oil will be displayed as the method considering only a common neighbour in the calculation.

 $N_1(u) \bigcap N_1(v) = \varnothing$ between two nodes in the network, then the method gives zero value. To overcome it method is applied when two distinct nodes have no common neighbour, and if $2 < \,$ distance between two nodes $\leqslant 6$. Also, this method is based on the strength of the path between two nodes and the degree of Thus, the previous method has a limitation since a common neighbour is not found, i.e., and to introduce a global method, we propose a new way of algorithm considering path and node membership values between two nodes in the network, which will display more related items. The proposed nodes.

1.2 Construction of the paper

In Section 1, the introduction is given. In Section 2, the preliminaries are discussed. Section 3 is the strength of edge and path and Section 4 is the link prediction method. The application in co-authorship network is presented in Section 5. And the conclusion is included in Section 6.

2 Preliminary

Let us consider a network $G = (V, E)$ having *n* nodes and *m* links, and it is represented by an adjacent $A = \{a_{ij}\} \in \mathbb{R}^{n \times n}$, where $a_{ij} = 1$, if node *i* is linked with node *j*; $a_{ij} = 0$, otherwise. In the social network, two nodes are related by a link. Their link identifies the relationship between two nodes.

Suppose that in Fig. 2, A, B, and C form a social network where AB and AC are two edges, but nodes *A* and *C* are not connected. In the immediate future, these nodes *A* and *C* may be connected. The probable value of future connection is the value of link prediction. Here $\,G\,$ is a network with $\,|E|\,$ edges and | n | nodes. We know that a complete network of $|n|$ *|n|*(*|n|*+1) nodes. We know that a complete network of |n| nodes contains $\frac{1+\frac{1}{2}+\cdots}{2}$ edges. Now, for any network of $|E|$ edges, the problem is to find out the link prediction of the remaining probable *|n|*(*|n|*+1) 2 *−|E|* edges.

Fig. 1 Network of products.

Fig. 2 Social network.

The neighbour of a node *i* in a network G is defined by $N_1(i) = \{j \in N : g_{ij} = 1\}$.

The common neighbour between two nodes u and v is defined by $N_1(u) \bigcap N_1(v)$.

which all nodes are distinct. Suppose $p_i : u - u_1 - u_2 - \cdots - u_{n-1} - v$ between u and v of length n. A succession of nodes where two nodes are connected by a link and a node or a link may occur more than once is called a walk. If all links are distinct in a walk, then it is called a trial. A path is called a trial in

Let $G = (V, E)$ be a graph with the pair of mappings $\sigma : V \to [0,1]$ and $\mu : E \to [0,1]$ such that the condition $\mu(x,y) \leqslant \sigma(x) \wedge \sigma(y)$ for all $(x,y) \in E \subseteq V \times V$, then $G = (V,E,\mu,\sigma)$ is called a fuzzy graph^[9].

Consider a sequence v_0, v_1, \ldots, v_n such that $(v_{i-1}, v_i) > 0, i = 1, 2, \ldots, n$, then it is a path of length n and the min{ $\mu(v_{i-1}, v_i)$, $i = 1, 2, ..., n$ } is called the strength^[1] of this path.

The strength of connectedness^[1] $S(u, v)$ between two vertices u and v is defined as the maximum of the strengths of all paths between the vertices u and v .

u is defined as $d(u) = \sum$ *v∈N*(*u*) Degree of a node *u* is defined as $d(u) = \sum \mu(u, v)$. *u* is defined as $d_T(u) = \sum$ *v∈N*(*u*) Total degree of a node u is defined as $d_T(u) = \sum_{\mu} \mu(u,v) + \sigma(u)$ and normalized total degree of a

u is defined as $d^*_T(u) =$ ∑ *v∈N*(*u*) $\mu(u, v) + \sigma(u)$ node *u* is defined as $d^*_T(u) = \frac{\sum_{u \in V} u}{\max_{u \in V} d_T(u)}$.

All the notations are summarized and displayed in Table 1.

3 Strength of Edge and Path

To define the strength of the edge and path, we take the membership of the edge and the membership of nodes into account so that higher nodes' importance implies a higher value of the strength of the edge and

higher information passes through this edge.

Definition 3.1 Define strength $\mu'(u, v)$ of an edge between two nodes u and v as

$$
\mu'(u,v) = \mu(u,v) f(u,v),
$$

where $f: V \times V \rightarrow [0,1]$ is a mapping that assigns a value depending on the membership values of nodes for an edge.

Example 3.1 Consider a network (Fig. 3) and take $f: V \times V \rightarrow [0,1]$ as $(u, v) = \max\{\sigma_u, \sigma_v\}$. Strength of each edge is evaluated in Table 2.

Definition 3.2 Define strength $S_p(u_0, u_n)$ of path $p: u_0 - u_1 - u_2 - \cdots - u_{n-1} - u_n$ between two nodes u_0 , u_n as

$$
S_p(u_0, u_n) = \min_{i=1,2,...,n} \mu'(u_{i-1}, u_i).
$$

Example 3.2 Consider the same network (Fig. 3), and the value is given in Table 3.

4 Link Prediction Method

In general, the link prediction value does not depend only on the nature of common neighbours in the fuzzy social network. Information in the network from one node to an indirect node passes through a path. Even two indirect friends may be friends if their path is strong. So, the path between the friends is very important to find link prediction in the immediate future. We neglect the path if the distance is greater than 6 as we consider that information may not pass through such a long path. Suppose that the nodes are highly influential (high degree centrality), so they may have links in future. So, how important are these nodes in the network have to be taken? In this case, we have taken the total degree of nodes when calculating link

Fig. 3 Small network.

prediction.

4.1 Link prediction

So, in this case, the link prediction value $LPV(u, v)$ between nodes u and v is

$$
LPV (u, v) = \alpha \cdot \max \{ S_i (u, v) : i = 1, 2, ..., m \} + \beta \cdot d_T^* (u) d_T^* (v),
$$

$$
S_i (u, v) = \min \{ \mu'_{ij} (u_{j-1}, u_j) : j = 1, 2, ..., n \}
$$
 (1)

provided

 $2 <$ distance between two nodes ≤ 6 ,

for each shortest path p_i : $u(=u_0) - u_1 - u_2 - \cdots - u_{n-1} - v(=u_n)$ between u and v, n is the number of edges and *m* is the number of shortest paths between *u* and *v*, $\mu'_{ij}(u_{j-1}, u_j)$ is the strength of the edge between u_{j-1} and u_j , $d_T^*(u)$ represents a normalized total degree of node u , and α and β are taken as a measure of coefficients such that $\alpha + \beta = 1$.

4.1.1 Computational cost of fuzzy link prediction

The computational cost of the fuzzy link prediction approach can be quite high, especially in the case of vast co-authorship networks. This is primarily due to the following factors:

(1) **Size of the network**: The number of nodes (authors) and edges (co-authorships) in the network can be enormous. Each potential link between two nodes needs to be evaluated, leading to a computational complexity of $O(n^2)$, where *n* is the number of nodes.

(2) **Fuzzification process**: The fuzzification process, which involves converting crisp input into a fuzzy set, can be computationally intensive. This is especially true when dealing with large datasets or complex membership functions.

(3) **Inference and defuzzification**: The fuzzy inference process, which involves applying fuzzy logic operators, and the defuzzification process, which converts the fuzzy output back into a crisp value, also add to the computational cost.

4.1.2 Optimization tactics

Despite these challenges, there are several optimization tactics that can be used in practice to reduce the computational cost:

(1) **Network pruning**: One common approach is to prune the network to remove nodes or edges that are less likely to be involved in future link formation. This can significantly reduce the size of the network and hence the computational cost.

(2) **Parallel computing**: The fuzzy link prediction process can be parallelized, with different parts of the network being processed simultaneously on different cores or machines. This can lead to a substantial reduction in computation time.

(3) **Efficient algorithms**: Using more efficient algorithms for the fuzzification, inference, and defuzzification processes can also help reduce the computational cost. For instance, using fast Fourier transforms for the defuzzification process can be more efficient than numerical integration.

(4) **Hardware acceleration**: Using hardware accelerators such as GPUs can also help speed up the

computation, especially for tasks like fuzzification and defuzzification that involve a lot of matrix operations.

In conclusion, while the fuzzy link prediction approach can be computationally intensive, especially for large co-authorship networks, there are several optimization tactics that can be used to make it more feasible in practice. These include network pruning, parallel computing, efficient algorithms, and hardware acceleration.

4.2 Method of link prediction algorithm

The method of link prediction is given in Algorithm 1.

4.3 Example

Consider a small WhatsApp network where nodes are the persons having WhatsApp, and a link exists between nodes if two persons have a common WhatsApp group.

To find LPV(*A,E*) between nodes *A* and *E*,

$$
N_1(A) = \{B, C\}, N_1(E) = \{D, F\}, \text{ and } N_1(A) \cap N_1(B) = \emptyset,
$$

$$
\mu'(A, B) = 0.42, \mu'(B, D) = 0.3, \mu'(D, E) = 0.12,
$$

$$
\mu'(A, C) = 0.25, \mu'(C, D) = 0.2, \mu'(C, F) = 0.2, \mu'(F, E) = 0.16,
$$

$$
S_1(A, E) = \min\{0.42, 0.3, 0.12\} = 0.12,
$$

$$
S_2(A, E) = \min\{0.25, 0.2, 0.12\} = 0.12,
$$

$$
S_3(A, E) = \min\{0.25, 0.2, 0.16\} = 0.16,
$$

LPV (A, E) = 0.7 × max {0.12, 0.12, 0.16} + 0.3 × 1 × 0.58 = 0.29.

Explanation: Fuzzification is a process of transforming crisp inputs, which have a binary truth value, into fuzzy sets with a range of truth values between 0 and 1. This process is crucial in fuzzy logic systems, including those used for link prediction in networks.

In the context of link prediction in a network of authors, the relationships between authors can be

fuzzified to better capture the nuances of their interactions. For example, instead of representing an author's relationship with another author as simply "connected" or "not connected", a fuzzy set could represent the strength of their connection on a scale from 0 to 1.

The membership function is a key component of a fuzzy set. It defines how each element in the input space is mapped to a membership value (or degree of membership) between 0 and 11. The choice of membership function depends on the specific problem and the nature of the input data. For example, in a network of authors, the membership function could be defined based on the number of papers co-authored by two authors, the number of citations they have in common, or other relevant metrics.

The use of fuzzy sets and membership functions in link prediction allows for a more nuanced representation of relationships in the network. This can lead to more accurate predictions, especially in cases where the relationships are complex and cannot be adequately captured by binary values.

For example, consider a network of authors where the nodes represent authors and the edges represent co-authorship relationships. A fuzzy set could be used to represent the strength of the co-authorship relationship between each pair of authors. The membership function for this fuzzy set could be defined such that it assigns a higher membership value to pairs of authors who have co-authored many papers together, and a lower membership value to pairs of authors who have co-authored fewer papers together.

This fuzzification strategy allows the system to capture the varying degrees of collaboration between authors, which can be crucial for accurately predicting future collaborations. By using fuzzy sets and membership functions, the system can handle the inherent uncertainty and complexity in the data, leading to more robust and accurate link predictions.

Fuzzy inference is a method of decision making that is used to obtain a definite output from fuzzy input based on fuzzy logic. The fuzzy inference process typically involves the following steps:

(1) Fuzzification of the input variables: This involves transforming crisp inputs into fuzzy sets using membership functions.

(2) Application of the fuzzy operator (AND or OR) in the antecedent: This step involves applying fuzzy logic operators to the fuzzy sets obtained from the fuzzification process.

(3) Implication from the antecedent to the consequent: This step involves mapping the fuzzy input sets to fuzzy output sets based on the fuzzy rules defined in the system.

(4) Aggregation of the consequents across the rules: This step involves combining the fuzzy output sets obtained from each rule into a single fuzzy set.

(5) Defuzzification: This involves transforming the aggregated fuzzy set into a crisp output.

In the context of forecasting the possibility of connecting writers, the fuzzy inference rules could be defined based on various factors such as the number of co-authored papers, the number of common citations, etc. For example, consider the following fuzzy inference rule:

IF "Author A and Author B have co-authored a high number of papers" **AND** "Author A and Author B have a high number of common citations" **THEN** "The possibility of Author A and Author B collaborating in the future is high".

Here, "high number of papers" and "high number of common citations" are fuzzy sets defined on the

universes of discourse "number of co-authored papers" and "number of common citations", respectively. The membership functions for these fuzzy sets could be defined such that they assign a higher membership value to a larger number of co-authored papers or common citations.

The fuzzy inference rule is then used to map the fuzzy input sets (i.e., the degrees of membership of the number of co-authored papers and common citations in the fuzzy sets "high number of papers" and "high number of common citations") to a fuzzy output set (i.e., the degree of membership of the possibility of future collaboration in the fuzzy set "high possibility").

Finally, the defuzzification process is used to transform the fuzzy output set into a crisp output, which represents the forecasted possibility of Author A and Author B collaborating in the future.

5 Application in Co-Authorship Network

Prediction of links in the immediate future of a social network is an important task in social network analysis. In this study, to analyze the prediction of future co-authorship between two authors, we collect data from the Scopus database. There are fifteen authors, and they work in various fields. We collected two types of data: the number of articles published individually and the number of articles co-authored.

5.1 Network construction

We consider the co-authorship network (Fig. 4) from the collecting data of fifteen authors where the authors are taken as nodes, and there exists a link if two authors work in a single article. Now, the number of articles published by an individual is taken as node membership value after normalized it, and the number of co-authored articles is taken as link membership value after normalized it. Membership values of nodes in the considered network are shown in Table 4, and that of links are shown in Table 5.

5.2 Result and analysis

We calculate all possible link predicted values between nodes where no common neighbour exists and the distance between two nodes is less than six. Taking the strength of edges and degree of nodes, we find all the values depicted in Tables 6–8. The predicted values are shown in the chart area (Fig. 5), and the highest predicted value occurs for the edge between Node 11 and Node 15.

Fig. 4 Co-authorship network.

Node	Number of published articles	Node membership value (normalized value)	Degree	Total degree	Normalized total degree
$\mathbf{1}$	251	1.00	0.79	1.79	1.00
$\overline{2}$	44	0.18	0.21	0.39	0.22
3	74	0.29	0.31	0.600	0.34
$\overline{4}$	53	0.21	0.14	0.35	0.20
5	30	0.12	0.13	0.25	0.14
6	29	0.12	0.09	0.21	0.12
7	17	0.07	0.09	0.16	0.09
8	53	0.21	0.09	0.3	0.17
9	142	0.57	0.10	0.67	0.37
10	20	0.08	0.06	0.14	0.08
11	227	0.90	0.13	1.03	0.58
12	231	0.92	0.20	1.12	0.63
13	10	0.04	0.04	0.08	0.04
14	9	0.04	0.06	0.10	0.06
15	40	0.16	0.14	0.30	0.17

Table 4 Calculation of node membership values.

To analyze the performance of the proposed link prediction method, we use the area under the curve (AUC) method. Taking the edges having link (value 1) with scores calculated by the proposed method and without link (value 0) with scores calculated by the proposed method, we found the AUC score as 0.96 (Table 9 and Fig. 6), which is acceptable.

The AUC is a common metric used to evaluate the performance of binary classification models, particularly for receiver operating characteristic (ROC) curves. After getting the prediction score, we sort them in descending order and then compute the true positive rate (TPR) and false positive rate (FPR) at various threshold levels. The ROC curve is created by plotting the TPR against the FPR at different

Node	Normalized membership value														
	Node 1	Node 2	Node 3	Node 4 Node 5		Node 6				Node 7 Node 8 Node 9 Node 10	Node 11	Node 12	Node 13	Node 14 Node 15	
1	Ω	0.16	0.16	0.08	0.07	0.07	0.06	0.06	0.04	$\mathbf{0}$	0.05	0.02	$\overline{0}$	0.02	Ω
\overline{c}	0.16	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\boldsymbol{0}$	$\mathbf{0}$	0.03	0.02	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	Ω
3	0.16	$\bf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\boldsymbol{0}$	$\bf{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$	0.01	0.06	0.04	0.04	$\mathbf{0}$	$\mathbf{0}$	$\boldsymbol{0}$
$\overline{4}$	0.08	$\bf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	0.02	$\mathbf{0}$	$\boldsymbol{0}$	$\mathbf{0}$	$\mathbf{0}$	Ω	0.04	$\mathbf{0}$	Ω
5	0.07	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	0.02	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	0.04	0
6	0.07	$\mathbf{0}$	$\mathbf{0}$	$\overline{0}$	0.02	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\overline{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	Ω
7	0.06	$\bf{0}$	$\mathbf{0}$	0.02	$\boldsymbol{0}$	$\boldsymbol{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	0.01	Ω	$\mathbf{0}$	Ω	Ω
8	0.06	0.03	$\bf{0}$	$\boldsymbol{0}$	$\mathbf{0}$	$\mathbf{0}$	0	$\mathbf{0}$	θ						
9	0.04	0.02	0.01	$\mathbf{0}$	0.03	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	Ω						
10	$\mathbf{0}$	$\mathbf{0}$	0.06	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	Ω	Ω						
11	0.05	$\mathbf{0}$	0.04	$\mathbf{0}$	Ω	$\mathbf{0}$	0.01	$\mathbf{0}$	0.03	$\mathbf{0}$	Ω	Ω	Ω	Ω	$\mathbf{0}$
12	0.02	$\mathbf{0}$	0.04	$\mathbf{0}$	$\mathbf{0}$	$\boldsymbol{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\overline{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	0.14
13	$\mathbf{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$	0.04	$\mathbf{0}$	$\boldsymbol{0}$	$\bf{0}$	$\bf{0}$	$\boldsymbol{0}$	$\boldsymbol{0}$	$\overline{0}$	$\mathbf{0}$	0	$\mathbf{0}$	$\mathbf{0}$
14	0.02	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	0.04	$\boldsymbol{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\overline{0}$	Ω	Ω	Ω	Ω
15	$\mathbf{0}$	$\mathbf{0}$	$\overline{0}$	$\overline{0}$	$\mathbf{0}$	$\boldsymbol{0}$	θ	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	0.14	Ω	Ω	0

Table 6 Normalized membership values of link in matrix form.

Table 7 Calculation of strength of links.

				Edge(a, b) Membership values of Node a Membership values of Node b Edge membership value Minimum of node membership values Strength	
(1, 2)	$\,1$	$0.18\,$	$0.16\,$	$0.18\,$	0.029
(1, 3)	$\,$ $\,$	0.29	$0.16\,$	0.29	0.046
(1, 4)	\bf{l}	0.21	$\rm 0.08$	0.21	$0.017\,$
(1, 5)	$\,1$	0.12	$0.07\,$	0.12	$\,0.008\,$
(1, 6)	\bf{l}	0.12	$0.07\,$	0.12	0.008
(1, 7)	$\,1$	$0.07\,$	$0.06\,$	0.07	$\,0.004\,$
(1, 8)	\bf{l}	0.21	$0.06\,$	0.21	0.013
(1, 9)	\bf{l}	$0.57\,$	$\rm 0.04$	0.57	0.023
(1, 11)	\bf{l}	0.9	$0.05\,$	0.9	0.045
(1, 12)	$\,1$	0.92	$0.02\,$	0.92	0.018
(1, 14)	$\,1$	$\rm 0.04$	$0.02\,$	0.04	$0.001\,$
(2, 8)	$0.18\,$	0.21	$0.03\,$	$0.18\,$	0.005
(2, 9)	$0.18\,$	$0.57\,$	$0.02\,$	$0.18\,$	0.004
(3, 9)	0.29	$0.57\,$	$0.01\,$	0.29	0.003
(3, 10)	0.29	$\rm 0.08$	$0.06\,$	0.08	0.005
(3, 11)	0.29	0.9	$\rm 0.04$	0.29	0.012
(3, 12)	0.29	0.92	$\rm 0.04$	0.29	0.012
(4, 7)	0.21	$0.07\,$	$0.02\,$	0.07	$0.001\,$
(4, 13)	0.21	$\rm 0.04$	$\rm 0.04$	0.04	0.002
(5, 6)	0.12	0.12	$0.02\,$	0.12	0.002
(5, 14)	0.12	$\rm 0.04$	$\rm 0.04$	0.04	0.002
(7, 11)	$0.07\,$	0.9	$0.01\,$	0.07	$0.001\,$
(9, 11)	$0.57\,$	$0.9\,$	$0.03\,$	$0.57\,$	0.017
(12, 15)	0.92	0.1	0.14	$0.1\,$	$\,0.014\,$

Table 8 Final result of link prediction.

Fig. 5 Chart of link prediction value.

	Table 9 Link prediction score for existing and non-existing links.	
Edge(a, b)	Existence of link	Score
(2, 10)	$\boldsymbol{0}$	0.0102
(2, 13)	$\boldsymbol{0}$	0.0048
(2, 15)	$\boldsymbol{0}$	0.0236
(3, 13)	$\boldsymbol{0}$	0.0068
(4, 10)	$\boldsymbol{0}$	0.0094
(4, 15)	$\boldsymbol{0}$	0.0220
(5, 10)	$\boldsymbol{0}$	0.0074
(5, 13)	$\boldsymbol{0}$	0.0036
(5, 15)	$\boldsymbol{0}$	0.0144
(6, 10)	$\boldsymbol{0}$	0.0070
(6, 13)	$\boldsymbol{0}$	0.0068
(6, 15)	$\boldsymbol{0}$	0.0128
(7, 10)	$\boldsymbol{0}$	0.0052
(7, 15)	$\boldsymbol{0}$	0.0084
(8, 10)	$\boldsymbol{0}$	0.0086
(8, 13)	$\boldsymbol{0}$	0.0040
(8, 15)	$\boldsymbol{0}$	0.0194
(9, 13)	$\boldsymbol{0}$	0.0072
(9, 15)	$\boldsymbol{0}$	0.0336
(10, 13)	$\boldsymbol{0}$	0.0024
(10, 14)	$\boldsymbol{0}$	0.0026
(10, 15)	$\boldsymbol{0}$	0.0086
(11, 13)	$\boldsymbol{0}$	0.0104
(11, 15)	$\boldsymbol{0}$	0.0484
(12, 13)	$\boldsymbol{0}$	0.0112
(13, 14)	$\boldsymbol{0}$	0.0014
(13, 15)	$\boldsymbol{0}$	0.0040
(14, 15)	$\boldsymbol{0}$	0.0046
(1, 2)	$\,$ 1	0.0940
(1, 3)	$\mathbf 1$	0.1540
(1, 4)	$\,$ 1	0.0860
(1, 6)	ı	0.0600
(1, 8)	$\,$ 1	0.0800
(1, 9)	$\,$ 1	0.1600
(1, 11)	$\,$ 1	0.2440
(1, 12)	ı	0.2580
(1, 14)	$\mathbf 1$	0.0360
(2, 8)	1	0.0270
(2, 9)	$\mathbf 1$	0.0386
(3, 9)	$\,$ 1	0.0623
(3, 11)	$\mathbf 1$	0.1749
(3, 12)	$\,$ 1	0.0917
(4, 7)	$\mathbf 1$	0.0132
(5, 6)	$\,$ 1	0.0187
(5, 14)	$\mathbf 1$	0.0154
(7, 11)	$\,$ 1	0.0389
(9, 11)	$\,$ 1	0.1818

Table 9 Link prediction score for existing and non-existing links.

Note: In the "Existence of link" column, 0 indicates no link and 1 indicates link.

Fig. 6 AUC value of the proposed method.

threshold levels. Then, we get the AUC value by computing the area under the ROC curve. AUC values range from 0 to 1. A model with an AUC of 0.5 indicates better than random guessing. A higher AUC denotes a better-performing model.

Discussion: The suggested technique leverages the concept of fuzziness to enhance link prediction in coauthorship networks by addressing the limitations of standard algorithms, which often rely on precise definitions of relationships and clear-cut connections. Here are the ways in which fuzziness is utilized:

Fuzzy similarity measures: The technique employs fuzzy similarity measures that account for the degree of uncertainty and imprecision in the relationships between authors. Unlike binary measures that consider only the presence or absence of a link, fuzzy measures evaluate the strength and likelihood of a connection based on degrees of membership.

Path strength in fuzzy networks: The proposed method defines path strength in fuzzy terms, considering not just the existence of a path but also its strength based on the fuzzy relationships it traverses. This allows for a more nuanced assessment of potential links, especially when direct connections are absent or weak.

Handling indirect connections: By focusing on all possible paths between two nodes, the technique can predict links even when there are no common neighbours. It takes into account indirect members connected via paths, which standard methods often overlook, thus capturing a broader range of potential connections.

Robustness to dynamic changes: Fuzzy models are inherently more robust to the dynamic nature of coauthorship networks, where new collaborations can emerge and existing ones can evolve. The fuzziness accommodates these changes more gracefully than rigid binary models.

By integrating these fuzzy-based approaches, the technique can predict links with greater accuracy and provide insights that are more aligned with the complex and often ambiguous nature of human relationships in co-authorship networks.

The suggested fuzzy logic based technique offers several benefits over strategies based on crisp logic, particularly in the context of link prediction in co-authorship networks:

Handling of uncertainty: Fuzzy logic is adept at handling the uncertainty and imprecision inherent in social relationships. It allows for varying degrees of connection strength, which is more reflective of realworld social interactions.

Gradual membership: Unlike crisp logic that assigns a binary state to relationships (either a link exists or

it does not), fuzzy logic acknowledges the possibility of partial membership. This means that links can have different strengths or probabilities, offering a more nuanced view of potential connections.

Flexibility: Fuzzy logic provides flexibility in modeling complex systems where the boundaries of classes or clusters are not clearly defined. This is particularly useful in co-authorship networks where the collaboration strength between authors can vary widely.

Robustness to noise: Fuzzy systems are inherently more robust to noise and variations in data. In the context of link prediction, this means that the system can better cope with changes in the network over time, such as the addition or removal of nodes and edges.

Intuitive reasoning: Fuzzy logic mimics human reasoning by allowing for approximate values and inferences, which can be more intuitive than the rigid true/false evaluations of crisp logic. This can lead to more user-friendly systems that align better with human decision-making processes.

Complex relationship modeling: Fuzzy logic can capture complex relationships that are not easily defined by crisp logic. For example, the degree of collaboration between two authors can be influenced by various factors such as shared interests, mutual acquaintances, or historical co-authorship, which fuzzy logic can incorporate into the prediction model.

Improved decision making: By providing a range of possibilities rather than a binary decision, fuzzy logic can improve the decision-making process in link prediction. It allows for a spectrum of link strengths, which can be particularly useful for making nuanced recommendations in co-authorship networks.

5.3 Other application areas in biomedical

Link prediction in drug discovery is a rapidly growing field that uses network-based machine learning algorithms to predict drug-target interactions and identify potential drug targets. The goal is to narrow down the number of drug trials required for clinical trials by identifying potentially beneficial and harmful interactions. Another study proposed a novel link prediction methodology that employs a combination of drug-drug and protein-protein similarity networks to predict new drug-target interactions. The methodology involves feature extraction using graph embedding of networks and defining interactions by concatenating pairs of drug and target features.

Link prediction has several applications in different fields, including drug discovery, drug repositioning, drug safety, disease detection, and biomedical image processing. In drug discovery, link prediction can be used to identify potential drug targets and predict drug-drug interactions. It can also be used to predict drugtarget interactions from biomedical literature. In disease detection, link prediction can be used to predict future diseases based on existing health status, explore latent comorbidity of chronic diseases, predict diseasegene associations, and identify novel disease genes. In biomedical image processing, link prediction can be used to predict missing links in brain connectivity networks and predict protein-protein interactions from microscopy images. Deep learning based approaches have been used for biomedical image segmentation, such as the UNet architecture.

An example of biological applications in the field of bioinformatics is where link prediction can be used to understand protein-protein interactions.

Fuzzy logic, a mathematical approach that handles reasoning that is approximate rather than fixed and exact, can be applied to link prediction in protein-protein interactions (PPI) in bioinformatics.

A system called "PPIs-FuzzyKNN" has been developed that uses fuzzy logic for PPI site identification. In this system, protein sequences are transformed into numerical descriptors of equal length using the physicochemical properties of amino acids and a position-specific scoring matrix. The fuzzy logic based system then uses these descriptors to predict potential interaction sites.

The fuzzy logic approach is particularly useful in dealing with the inherent uncertainty and complexity in biological systems. It allows for handling partial truths and more flexible reasoning compared to traditional binary logic.

(1) Feature extraction: The first step involves transforming protein sequences into numerical descriptors. This is done using the physicochemical properties of amino acids and a position-specific scoring matrix.

(2) Fuzzy logic application: The numerical descriptors are then input into the fuzzy logic system. Fuzzy logic allows for degrees of truth, which means it can handle the uncertainty and complexity often found in biological data.

(3) Prediction: The fuzzy logic system then outputs a prediction of whether a pair of proteins is likely to interact.

This approach has been shown to be effective, with the PPIs-FuzzyKNN model achieving high accuracy on different datasets. Therefore, fuzzy logic provides a powerful tool for link prediction in PPI networks, aiding in the understanding of complex biological systems and contributing to advancements in the field of bioinformatics.

6 Conclusion

Thus, we proposed a better way of link prediction in social networks under a fuzzy environment which is based on path and degree. We consider all possible paths between two nodes along with node membership values. So, the method is global. The application of this method was analyzed very clearly. So, the model will be helpful for the generalization of link prediction in uncertain cases.

(1) Projected relationships in biomedical applications

(a) Control systems in biomedical engineering: Control systems in biomedical engineering, such as those used in artificial organs and rehabilitation engineering, are designed to achieve a desired response even when external disturbances are present. The relationships between sensors, controllers, and actuators in these systems can be predicted using fuzzy techniques, contributing to the advancement of healthcare equipment and medical systems.

(b) Tissue engineering: Tissue engineering involves the use of biomaterials, biomolecules, and cells to replace or regenerate biological functions of tissues or organs. The relationships between these elements can be predicted to help develop new biomaterials and scaffold fabrication methods, contributing to advancements in tissue regeneration applications.

(2) Contribution to scientific knowledge or discovery

Link prediction plays a significant role in scientific collaboration networks, favourably affecting the

organization of international scientific projects. For instance, it can predict future scientific collaborations in a collaborative network, which can strengthen knowledge and idea diffusion, help researchers complement each other's advantages, and improve research productivity.

Moreover, link prediction contributes significantly to our understanding of complex biological systems, facilitating the discovery of novel biomarkers, drug targets, and insights into the intricate web of biological interactions. It also drives social media expansion and is used in a wide range of scientific research, such as predicting the interaction between genes and proteins. These predictions are used by researchers as a benchmark for testing the performance of new machine learning algorithms, thereby contributing to the advancement of scientific knowledge and discovery.

Link important less (LIL) may be future research work using the proposed work. A link may be important in many ways. It can be defined as LIL = (strength of connectedness) – (link membership value). When the strength of connectedness between two nodes is a higher value than the link membership value, then LIL predicts that the link may be deleted in the immediate future.

(3) Acknowledging research limitation

Indeed, every research study has its limitations. In the context of the model sensitivity and fuzzification technique investigation, some potential constraints could include:

(a) Data constraint: The quality and quantity of the data used to train and test the model can significantly impact its performance. If the data are noisy, incomplete, or unbalanced, they can lead to inaccurate predictions.

(b) Model assumption: Every model makes certain assumptions. For instance, a common assumption in many models is that the input features are independent. If these assumptions do not hold true, it can affect the model's accuracy.

(c) Computational constraint: Complex models and large datasets can require significant computational resources. This can limit the feasibility of certain approaches, particularly in resource-constrained settings.

(d) Future research path

To address these constraints and further refine the approach, future research could explore the following paths:

● Data augmentation and preprocessing: Techniques such as data augmentation, feature selection, and outlier detection can help improve the quality of the data and thereby enhance model performance.

● Advanced modeling technique: Exploring advanced modeling techniques, such as ensemble methods or deep learning, could potentially improve prediction accuracy.

● Model interpretability: Research into methods for improving model interpretability, such as explainable AI techniques, could help balance the trade-off between accuracy and interpretability.

● Parameter optimization: Techniques such as grid search or genetic algorithms can be used to optimize the parameters of the model, potentially improving its sensitivity.

In conclusion, acknowledging the limitations of the research and suggesting future research paths is a crucial part of any scientific investigation. It helps ensure that the research is transparent, reproducible, and continuously improving.

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