

Social and Information Networks

CSE 3021

REVIEW--3

**Social Networking in Intelligent Health Care
Systems -Using Link Prediction to Estimate the
Chances of Occurrence of Genetic Disorders**

By –

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ABSTRACT

Genetic diseases are conditions that a person inherits from his or her parents or are caused by a spontaneous genetic alteration. A alteration or mutation in an individual's DNA causes genetic disorders.

People can inherit genetic disorders, which means they are born with them, even if they are not obvious at first. Some illnesses, on the other hand, are not inherited and arise as a result of disease-causing mutations occurring during cell division.

In link mining, link prediction is a crucial task. Based on attribute information and observed existing link information, link prediction predicts if there will be links between two nodes. Link prediction is applicable not just in the sphere of social networks, but also in other fields.

This project's major goal is to forecast a person's probability of being diagnosed with a genetic condition. In order to accomplish so, elements such as the person's family history, the environment in which he or she lives, and a variety of others will be considered.

To do so, the Firefly algorithm will be employed. The likelihood of a person being diagnosed with a specific genetic condition can be predicted using the approach described in the firefly algorithm. If a person is genetically connected to someone who has been diagnosed with the condition, he or she is more likely to be diagnosed. Various environmental factors, such as pollution, radioactive radiation, and so on, may also have a role in the disease's incidence. Taking the foregoing into account, we'd like to suggest a method for determining the likelihood of a person being diagnosed via link prediction.

INTRODUCTION

This study focuses on forecasting the likelihood of a disease manifestation in a person by analysing the family tree and a graph of environmental elements that cause disease beginning. Every member of the family is regarded a node in the binary tree for the family tree. The person under examination is the tree's root, and his or her ancestors are the nodes that follow. At each junction, a person's two parents are treated as two children on the node in the graph. Only the person's parents, their parents, and so on are considered because they have a direct link to the person's genetic make-up. Every person in the tree has either been diagnosed with a sickness or has not been. If we don't know a person's disease status, we assume that he or she hasn't been diagnosed because the chances of him or her not being diagnosed are higher. We can forecast the likelihood of an illness in a person using this graph and the firefly algorithm.

Firefly Algorithm was first developed by Xin-She Yang in late 2007 and 2008 at Cambridge University, which was based on the flashing patterns and behaviour of fireflies. This method is based on the following three idealised rules:

Fireflies are unisex so that one firefly will be attracted to other fireflies regardless of their sex;

1. Because attraction is proportional to brightness, and both diminish as distance rises, the less brilliant of two flashing fireflies will gravitate toward the brighter one. If there isn't another firefly that is brighter than it, it will migrate at random.

2. The landscape of the goal function determines the brightness of a firefly. The brightness of a firefly or a node is considered binary in this project, meaning that the firefly is either luminous or not. Either the person is diagnosed with the ailment or they are not. The distance between the firefly is equivalent to the distance between the nodes in the family tree.

As a result, the likelihood of a person being drawn to a disease is inversely related to the distance between that person and the other members in the family tree who have been diagnosed. Based on this rationale, a formula is created and utilised to forecast the likelihood of the disease occurring in that person.

PROBLEM STATEMENT

The main aim of this project is to predict the chances of a person to be diagnosed with a genetic disease. The project analyses the family tree of the person and determines the percentage chances of the person being diagnosed with a genetic disorder.

LITERATURE SURVEY

1. Firefly Algorithm for Optimization Problem

This paper reviews the applications of Firefly Algorithm (FA) in various domain of optimization problem. By decreasing or maximising the factors involved in the problems, optimization is a method of discovering the optimal solution to make something as functional and effective as feasible. Several types of optimization problems, including discrete, chaotic, multi-objective, and others, are solved by drawing inspiration from the behaviour of fireflies, as described in the literature. FA was widely used by researchers to address optimization problems in the Computer Science and Engineering sector, according to the literature.

The main update formula for any pair of two fireflies \mathbf{x}_i and \mathbf{x}_j is

$$\mathbf{x}_i^{t+1} = \mathbf{x}_i^t + \beta \exp[-\gamma r_{ij}^2](\mathbf{x}_j^t - \mathbf{x}_i^t) + \alpha_t \epsilon_t$$

where α_t is a parameter controlling the step size, while ϵ_t is a vector drawn from a Gaussian or other distribution.

The above is a objective function. In a broad sense, optimization solution methods can be categorized as exact and approximate solution methods. Exact solution methods are methods which use an exhaustive search for the exact solution in the solution space. They use mathematical and statistical arguments to get an exact solution. They mainly used calculus-based and iterative procedures. Firefly is a metaheuristic algorithm that has been optimised. Metaheuristic algorithms are approximate solution methods for optimization problems that use a randomness property with a "educated guess" in their search mechanism and attempt to improve the quality of the solutions at hand through iterations, starting with a randomly generated set of feasible solutions and exploring and exploiting the solution space.

(Johari, Nur & Zain, Azlan & Mustaffa, Noorfa & Udin, Amirmudin. (2013). Firefly Algorithm for Optimization Problem. Applied Mechanics and Materials. 421. 10.4028/www.scientific.net/AMM.421.512.)

2. An Efficient Link Prediction Technique in Social Networks based on Node Neighborhoods

The unparalleled accomplishment of social networking sites, such as Facebook, LinkedIn and Twitter have modernized and transformed the way

people communicate to each other. Nowadays, a huge amount of information is being shared by online users through these social networking sites. This paper discusses about a novel efficient link prediction technique Link-Gy and many other commonly used existing prediction techniques for suggestion of friends to online users of a social network and also carries out experimental evaluations to make a comparative analysis among each technique. The results on three real social network datasets show that the novel Link-Gy link prediction technique yields more accurate results than several existing link prediction techniques.

(Nandi, Gypsy & Das, Anjan. (2018). An Efficient Link Prediction Technique in Social Networks based on Node Neighbourhoods. International Journal of Advanced Computer Science and Applications. 9. 10.14569/IJACSA.2018.090637.)

3. Link Prediction using Supervised Learning

In recent years, social network analysis has received a lot of interest. Link prediction is a prominent research topic in this discipline. In this study, we look at link prediction as a supervised learning job. Along the way, we identify a set of properties that are crucial to the greater performance of the supervised learning configuration. The identified attributes are easy to calculate and surprisingly effective at solving the link prediction problem. The class density distribution is frequently used to explain the utility of the attributes. We next evaluate several classes of supervised learning algorithms in terms of prediction performance using various performance metrics such as accuracy, precision-recall, F-values, squared error, and so on, using a 5-fold cross validation technique.

(Hasan, Mohammad & Chaoji, Vineet & Salem, Saeed & Zaki, Mohammed. (2016). Link Prediction Using Supervised Learning.)

4. Link prediction in social networks: the state-of-the-art

Link prediction is useful for mining and evaluating the evolution of social networks because it predicts missing links in present networks and new or dissolution ties in future networks. The purpose of this study is to provide a complete evaluation, analysis, and discussion of the current state of link prediction in social networks. The link prediction techniques and difficulties are organised into a systematic category. Communication and cooperation amongst people have grown easier because to the rapid development of the internet. Online social networks such as Facebook, Twitter, and Weibo have

become a major part of our everyday lives in recent years, providing us with platforms to share information. Predicting missing or undetected links in current social networks, as well as newly added or deleted links in future social networks, is critical not just for understanding social network evolution but also for completing existing social networks.

(Wang, P., Xu, B., Wu, Y. *et al.* Link prediction in social networks: the state-of-the-art. *Sci. China Inf. Sci.* **58**, 1–38 (2015). <https://doi.org/10.1007/s11432-014-5237-y>)

5. Link Prediction in Social Networks: A Similarity score based Neural Network Approach

The ability to predict links is a crucial feature of social network analysis. Link Prediction is a function seen in many popular applications such as Facebook and LinkedIn. There will be higher accuracy in predicting the links if we have a data collection that contains more information about the author and the research paper. We suggested a technique based on the node similarity measure and the Artificial Neural Network concept in this paper. We analyse the data set's attributes or information, then assign a score to each pair of nodes and apply the Artificial Neural Network concept to the system. Link Prediction will be more accurate thanks to the presented technique.

(Sharma, Upasana & Khatri, Sunil Kumar & Patnaik, Lalit. (2016). Link Prediction in Social Networks: A Similarity score based Neural Network Approach. 10.1145/2905055.2905149.)

6. Using Friendship Ties and Family Circles for Link Prediction

Social networks can record a wide range of interconnections between users. Friendship and family ties are both commonly examined, but most existing research looks at them separately. We look at how these networks might be overlay and suggest a link prediction feature taxonomy. We show that in a social network with tightly connected family circles, we can increase the accuracy of link prediction models. This is accomplished by utilising the family circle features, which are based on the structural equivalence of family members. On three real-world social networks, we explored the predictive potential of overlaying friendship and family links.

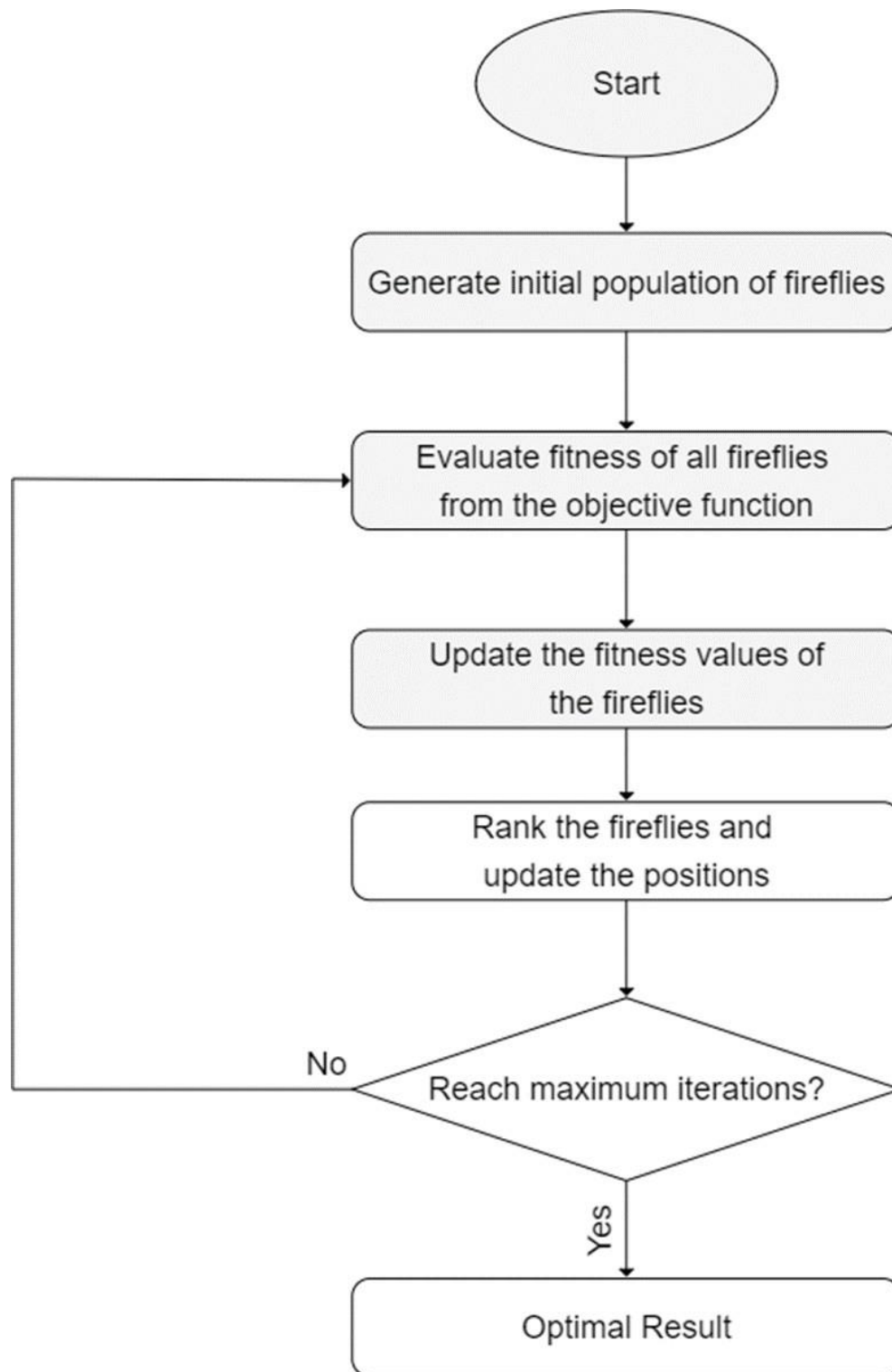
(Zheleva, Elena & Getoor, Lise & Golbeck, Jennifer & Kuter, Ugur. (2018). Using Friendship Ties and Family Circles for Link Prediction. *Advances in Social Network Mining and Analysis*. 97-113. 10.1007/978-3-642-14929-0_6.)

7. Community Detection in Social Network with Regenerative Genetic Algorithm

The use of evolutionary algorithm-based approaches, as well as many other existing community detection techniques, is widespread. The regenerative technique is used in this research to offer a community discovery algorithm based on a genetic algorithm. The community discovery method in this technique is accomplished by population regeneration and selection. The community quality increment is utilised as a screening criterion for evolutionary operators, and the similarity of vertexes is defined as a local fitness function. Populations are classified based on their engagement and diversity, further complicating evolution. To keep the process running smoothly, a random regeneration strategy is used throughout for population diversity.

(Harish Kumar Shakya, Kuldeep Singh and Bhaskar Biswas. (2018) . Community Detection in Social Network with Regenerative Genetic Algorithm. International Journal of Pure and Applied Mathematics. Volume 118 No. 5 2018, 397-411 ISSN: 1311-8080 (printed version); ISSN: 1314-3395 (on-line version) url: <http://www.ijpam.eu>. Special Issue)

PROPOSED SYSTEM DESIGN



ANALYSIS OF PROPOSED SYSTEM MODEL

The persons in the family are treated as nodes in a binary tree in the technique utilised in this research. Every node has a key that fits the binary search tree's requirements. The person under consideration is the tree's root.

Each node will also have an illness attribute, which will be set to 1 if the person has been diagnosed with the disease in question. The sum of the reciprocals of all distances from each node to the root is total distance. Total impact distance is the total of all distances from each node with a disease attribute of 1 to the root multiplied by the reciprocal. The ratio of the total impact distance to the total distance determines the likelihood of the person being diagnosed with the condition. The percentage is calculated by multiplying the ratio by 100.

Algorithm:

Set algorithm parameters (α, γ)

Set simulation set-up (Number of initial solutions and maximum iteration ($N, MaxGen$))

Randomly generate N initial solutions

for iteration = 1 : MaxGen

 Compute the brightness, I

 Sort the solution in such a way that, $I_i \geq I_{i-1}, \forall i$

 for $i = 1 : n - 1$

 For $j = i + 1 : n$

 If $I_j > I_i$

 | move firefly i towards firefly j

 end if

 end for

 end for

 move firefly $N, (x_b)$, randomly

end for

Report the best solution,

Pseudocode:

Begin

- 1) Objective function: $f(\mathbf{x})$, $\mathbf{x}=(x_1, x_2, x_3, \dots, x_d)$;
- 2) Generate an initial population of fireflies \mathbf{x}_i ($i=1, 2, 3, \dots, n$);.
- 3) Formulate light intensity I so that it is associated with $f(\mathbf{x})$ (for example, for maximization problems, $I \propto f(\mathbf{x})$ or simply $I=f(\mathbf{x})$);
- 4) Define absorption coefficient γ

```
While (t < MaxGeneration)
  for i = 1 : n (all n fireflies)
    for j = 1 : i (n fireflies)
      if ( $I_j > I_i$ ),
        Vary attractiveness with distance r via  $\exp(-\gamma r)$ ;
        move firefly i towards j;
        Evaluate new solutions and update light intensity;
      end if
    end for j
  end for i
  Rank fireflies and find the current best;
end while
```

Post-processing the results and visualization;

end

members_of_family[31];

disease[31]; //initialize

//Build a binary tree with

members_of_family.total_distance = 0;

total_impact_distance = 0;

for(i from 1 to 31):

dist = distance_from_members_of_family[0] to members_of_family[i];

total_distance += dist;

if(disease[i] = 1) total_impact_distance += dist;

chance=(total_impact_distance/total_distance)*100;

This algorithm currently considers only the family history of a person to predict the occurrence of a disease.

IMPLEMENTATION

```
#include
<iostream>

#include <cstdlib>
using namespace
std;

struct Family_tree
{
    struct Family_tree *left,
    *right;int key, disease;
};

//creating a new node for a family member
struct Family_tree* newMember(int key, int disease)
{
    struct Family_tree* ptr = new
    Family_tree;ptr->key = key;
    ptr->disease = disease;
    ptr->left = ptr->right =
    NULL;return ptr;
}

//inserting the family member in the family tree
struct Family_tree* insert(struct Family_tree* root, int key, int
disease)
{
    if(!root)
        root = newMember(key,
disease);else if(root->key > key)
        root->left = insert(root->left, key,
disease);else if(root->key < key)
        root->right = insert(root->right, key,
disease);return root;
}
```

```

//Calculating the distance of a node from the
rootint distance(struct Family_tree* root, int
x)
{
    if(root->key ==
        x)return 0;
    else if(root->key > x)
        return (distance(root->left, x) +
1);else
        return (distance(root->right, x) + 1);

}

void implement(int members[31], int keys[31])
{
    struct Family_tree* root = NULL;

    cout<<"The sequence:
"<<endl;for(int i=0; i<31;
i++)
{
    cout<<members[i]<<" ";
}
cout<<endl;

for(int i=0; i<31; i++)
{
    root = insert(root, keys[i], members[i]);
}

double total_distance=0,
total_impact_distance=0;for(int i=1; i<31; i++)
{
    double dist =
1/(double)distance(root,keys[i]);

```

```

        total_distance += dist;
        if (members[i]==1)
        {
            total_impact_distance += dist;
        }
    }

    double chance =
        (total_impact_distance/total_distance)*100;cout<<"The
        chances of occurrence of the disease are:
"<<chance<<"%"<<endl;;
}

```

```

int main()
{
    int
    keys[31];
    keys[0]=16;
    keys[1]=8;
    keys[2]=24;
    keys[3]=4;
    keys[4]=12;
    keys[5]=20;
    keys[6]=28;
    keys[7]=2;
    keys[8]=6;
    keys[9]=10;
    keys[10]=14;
    keys[11]=18;
    keys[12]=22;
    keys[13]=26;
    keys[14]=30;
    keys[15]=1;
    keys[16]=3;
    keys[17]=5;
    keys[18]=7;
    keys[19]=9;

```

```

keys[20]=11;
keys[21]=13;
keys[22]=15;

keys[23]=17;
keys[24]=19;
keys[25]=21;
keys[26]=23;
keys[27]=25;
keys[28]=27;
keys[29]=29;
keys[30]=31;

int members[10][31];
for(int i=0; i<10;
i++)
{
    members[i][0]=0;
    for(int j=1; j<31;
j++)
    {
        members[i][j] = rand()%2;
    }
    implement(members[i],keys);
}

/*int members1[31] =
{0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1};
implement(members1,keys);*/
}

```


RESULTS AND DISCUSSIONS

10 Random sequences were generated using random() function. The chances of getting genetic disorder has been calculated based on firefly algorithm as discussed before. The following results showed up for the 10 randomly generated sequences.

The percentage chances of occurrence of the disease are determined based on the family tree.

```
C:\Users\SHUBHAM KUMAR\Downloads\SIN Project\Sin_Project.exe
The sequence:
0 1 1 0 0 1 0 0 0 0 0 1 1 1 1 1 1 0 1 0 1 0 0 1 0 0 1
The chances of occurrence of the disease are: 54.6875%
The sequence:
0 1 0 1 0 1 0 1 1 1 0 1 1 0 1 1 0 1 1 1 0 0 1 1 1 1 0
The chances of occurrence of the disease are: 63.2813%
The sequence:
0 0 1 0 0 0 0 0 0 0 0 0 1 0 1 0 0 0 1 1 0 1 1 0 0 0 0 1 0
The chances of occurrence of the disease are: 27.3438%
The sequence:
0 0 1 0 1 1 0 0 0 1 1 1 1 1 0 0 0 1 0 1 0 1 1 0 0 0 1 1 1 0
The chances of occurrence of the disease are: 53.125%
The sequence:
0 0 0 1 0 1 1 1 0 1 0 0 0 1 0 0 0 1 1 1 1 1 1 1 1 1 0 1 0
The chances of occurrence of the disease are: 51.5625%
The sequence:
0 0 0 0 0 1 0 0 1 0 1 0 1 0 1 0 1 1 1 0 0 1 0 0 0 0 1 0 1 0 0
The chances of occurrence of the disease are: 31.25%
The sequence:
0 1 0 1 1 0 0 0 0 1 1 0 1 0 1 1 1 0 1 1 0 1 0 1 1 0 1 1 0 0 1
The chances of occurrence of the disease are: 54.6875%
The sequence:
0 0 0 0 1 1 0 1 1 1 1 1 1 0 1 0 0 0 0 0 0 0 1 1 0 1 1 0 0 0 0
The chances of occurrence of the disease are: 40.625%
The sequence:
0 0 1 0 1 0 1 1 0 0 1 0 0 0 1 0 0 0 0 1 1 1 0 0 0 1 0 0 1 1 1
The chances of occurrence of the disease are: 44.5313%
The sequence:
0 1 0 0 1 1 0 0 0 1 1 1 0 1 1 1 1 0 1 0 1 0 0 1 1 0 0 1 0 1 1
The chances of occurrence of the disease are: 55.4688%
```

Figure 1: Output for objective function by mod 2

```

C:\Users\SHUBHAM KUMAR\Downloads\SIN Project\Sin_Project.exe
The sequence:
0 1 3 2 0 1 0 2 2 2 0 1 1 1 3 1 3 3 2 3 0 3 0 2 1 0 2 1 0 2 3
The chances of occurrence of the disease are: 30.4688%
The sequence:
0 3 2 3 2 1 0 3 3 3 2 3 3 2 1 1 0 1 3 1 0 3 0 2 1 1 3 3 1 1 2
The chances of occurrence of the disease are: 24.2188%
The sequence:
0 0 3 2 2 0 2 0 0 2 1 2 1 2 2 2 1 1 0 1 3 0 2 0 0 2 0 3 0
The chances of occurrence of the disease are: 13.2813%
The sequence:
0 0 3 2 3 1 2 2 2 1 1 1 3 3 2 0 2 1 2 1 2 1 1 0 0 2 1 1 1 0
The chances of occurrence of the disease are: 32.8125%
The sequence:
0 2 2 1 0 3 3 3 2 3 0 2 2 1 0 2 2 3 3 3 1 3 1 3 1 1 1 2 1 0
The chances of occurrence of the disease are: 24.2188%
The sequence:
0 2 2 2 1 0 0 3 2 3 2 3 0 1 0 3 3 1 2 2 3 0 2 0 0 1 0 3 0 0
The chances of occurrence of the disease are: 12.5%
The sequence:
0 1 2 1 3 2 2 0 0 3 3 0 1 0 3 3 1 2 1 1 2 1 0 3 3 0 1 3 0 2 3
The chances of occurrence of the disease are: 28.9063%
The sequence:
0 0 0 0 1 1 2 3 1 1 3 3 3 2 3 0 0 2 2 0 0 2 1 1 2 1 1 0 2 2 0
The chances of occurrence of the disease are: 25%
The sequence:
0 2 3 2 1 2 3 3 0 0 3 2 2 0 3 0 2 2 2 3 1 1 2 0 0 1 2 2 3 1 3
The chances of occurrence of the disease are: 14.0625%
The sequence:
0 1 0 0 1 3 0 0 2 3 1 1 0 1 1 3 3 2 1 2 1 0 2 1 1 0 0 1 2 1 1
The chances of occurrence of the disease are: 42.9688%

```

Figure 2: Output for objective function by mod 4

GRAPHICAL ANALYSIS

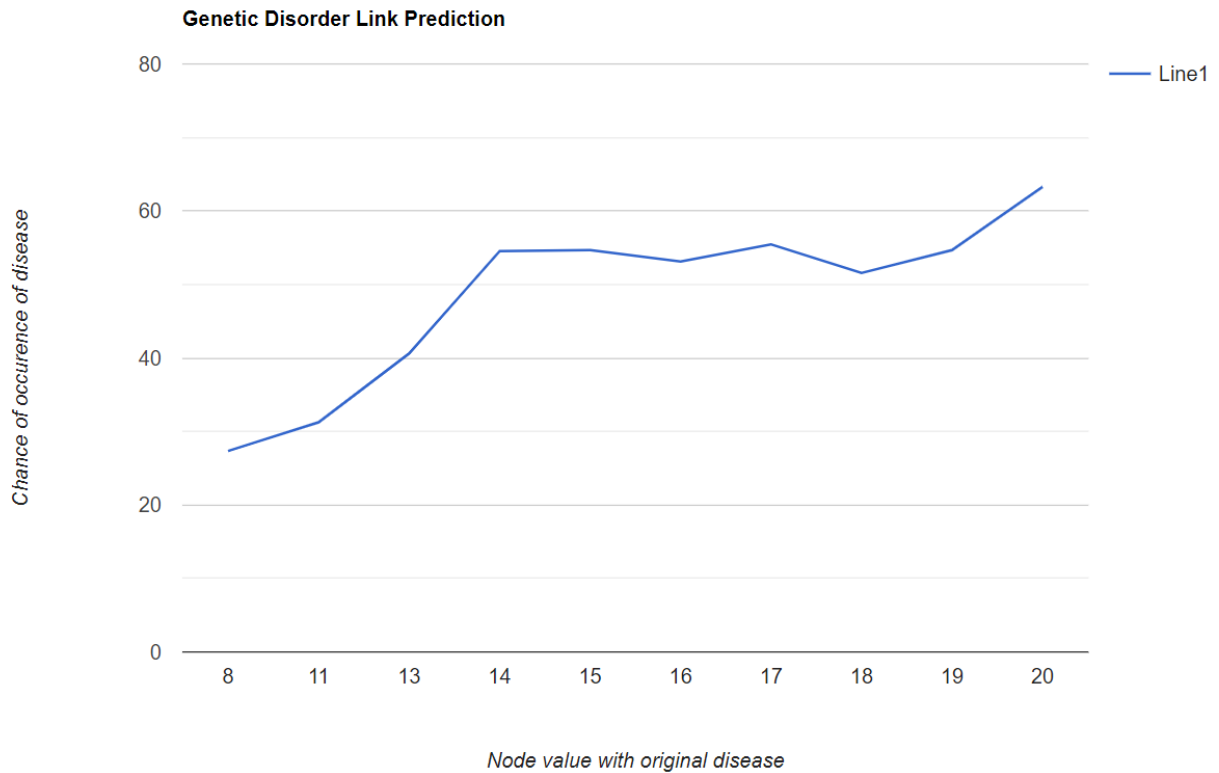


Figure 3: Genetic Disorder Line Graph

The above depicted graph shows the growth of chance of occurring a genetic disease in the forthcoming generation.

The X-axis is the number of nodes in the binary search tree (BST).

The Y-axis is the probability of occurrence of disease.

From the above graph we can conclude that growth of graph is an upward curve stating that new generation of the family are prone to genetic disorders.

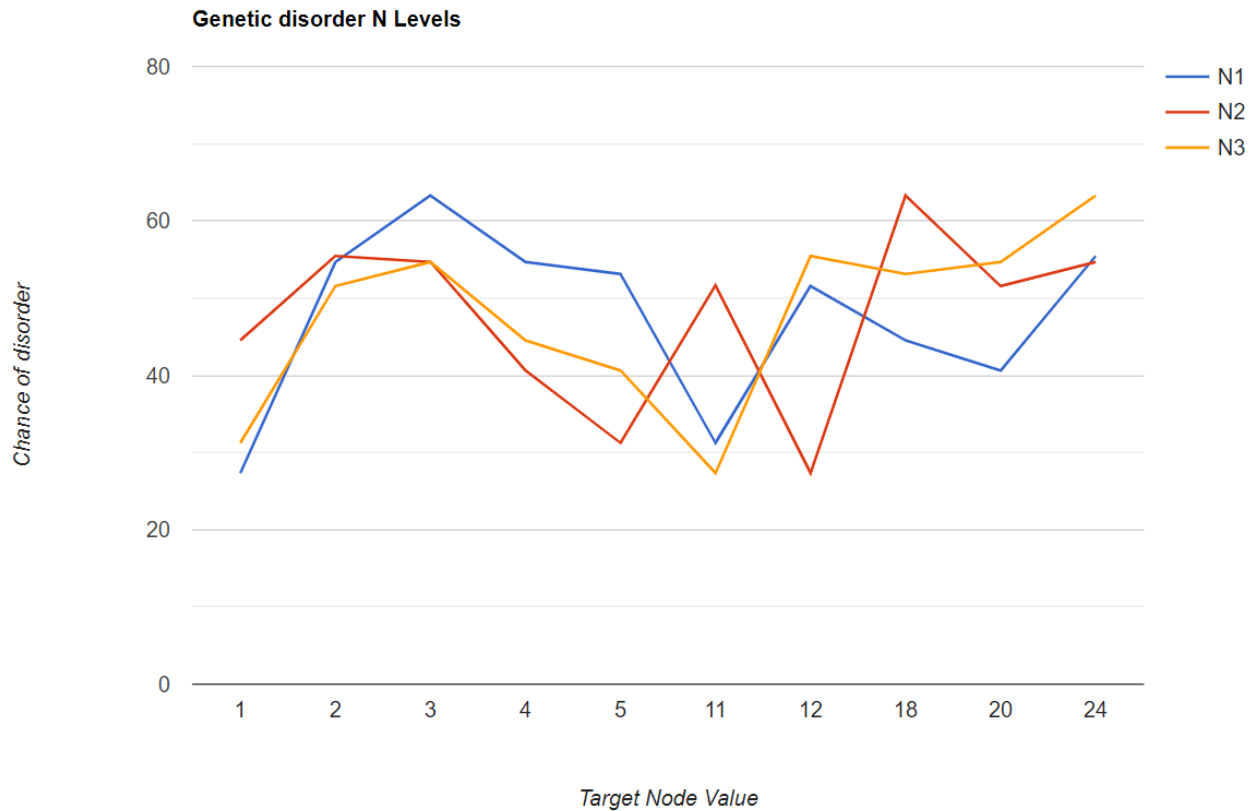


Figure 4: Genetic Disorder over N-order by factor of 2

The above depicted graph is a line graph for probability of occurrence of disease over next generation mapped over Target node value for Nth generation or Nth level in binary search tree (BST).

X-axis is the target node value of BST.

Y-axis is the probability of objective function for various generations.

The variation in the graph for the three line plots namely N1, N2, N3 are having a change factor of 2.

N1 graph has N-order factor of 2 i.e. Objective function by mod 2

N2 graph has N-order factor of 4 i.e. Objective function by mod 4

N3 graph has N-order factor of 6 i.e. Objective function by mod 6

Here Order refers to the mod factor of power 2, which is used in the code to depict other environmental factors apart from genetic construct of human gene in a family tree.

CONCLUSION

As a result, we explored the prognosis of a genetic condition for a person based on his family tree in this research. To estimate the likelihood of disease occurrence, we applied the notion of Link Prediction in social information networks and the Firefly algorithm. Other environmental variables, such as pollution, radioactive exposure, personal hygiene, exposure to dangerous gases or chemicals, and health factors, can be included in the project scope. It is possible to obtain affinities, similarities, and trends by studying these structures and relationships, as well as to make predictions or remarks about relationships in this network.

LIMITATIONS AND SCOPE FOR FUTURE WORK

The above project does not take into account the above-mentioned environmental elements, nor does it address health issues, which might also be a cause of sickness in a certain person. As a result, greater research in this area would be beneficial for future work in predicting a person's odds of developing a genetic illness.

The theories, methods, and techniques explored in this project can be used to build the analytic foundations for a new science of elucidating information from a large collection of real-time, heterogeneous, and dynamic information sources, as well as to develop the next generation of information distillation systems that extract useful information with time and quality guarantees by leveraging into common people's collective wisdom.

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