

New Technique Of Genetic Algorithm For Finding Maximum Clique Problem

SAVITA, CSE Department,MDU,Palwal,India-121102

SUDHA,Assistant Professor, CSE Department,LIMAT,Palwal,India-121102

Abstract— In this graph problem finding maximum clique means finding the largest subgraphs which are connected with each other. This new technique of genetic algorithm for finding the maximum clique problem (NTGAMC) is presented. The main features of the NTGAMC are a strong local optimizer to accelerate the convergence and the adaptive genetic operators to fine tune the algorithm. This algorithm is a modified genetic algorithm for solving the maximum clique problem .In this work preserved the good features of their algorithm such as preprocessing the input graph and using local optimization, but modified the local optimization algorithm, the genetic operators such as crossover and mutation to make them adaptive

Index Terms— Genetic Algorithm, Maximum Clique Problem, Np Complete Problem, Search Space.

I. INTRODUCTION

Clique means subgraphs ,so finding maximum clique means finding maximum no. of subgraphs that has higher degree of connectivity. In Clique problem there are many points these are

- A Clique which have largest number of vertices,
- A clique which have maximum weight in the weighted graph,
- Clique which is not further expandable.
- The clique problem is NP complete problem.

A **maximal** clique, sometimes called inclusion-maximal, is a clique that is not included in a larger clique.

Maximal cliques can be very small. A graph may contain a non-maximal clique with many vertices and a separate clique of size 2 which is maximal. While a maximum (i.e., largest) clique is necessarily maximal, the converse does not hold. There are some types of graphs in which every maximal clique is maximum (the complements of well-covered graphs, notably including complete graphs, triangle-free graphs without isolated vertices, complete multipartite graphs, and k-trees) but other graphs have maximal cliques that are not maximum.

Finding a maximal clique is straightforward: Starting with

an arbitrary clique (for instance, a single vertex), grow the current clique one vertex at a time by iterating over the graph's remaining vertices, adding a vertex if it is connected to each vertex in the current clique, and discarding it otherwise. genetic approaches used here.

II. METHODOLOGY AND FORMULA

A New Technique Of Genetic Algorithm(NTGAMC) For FindingMaximum Clique Problem

In this section, a new method of genetic algorithm for finding the maximum clique problem (NTGAMC) is presented. The NTGAMC basically follows the steps of a steady-state genetic algorithm, which means only a portion of the population is replaced at each generation. If the whole population is replaced at each generation, it is called a generational GA. the main features of the NTGAMC are a strong local optimizer to accelerate the convergence and the adaptive genetic operators to fine tune the algorithm. Also, graph preprocessing is used before ofalgorithm is a modified genetic algorithm for solving the maximum clique problem .In this work preserved the good features of their algorithm such as preprocessing the input graph and using local optimization, but modified the local optimization algorithm, the genetic operators such as crossover and mutation to make them adaptive. Also, the methods of extracting a clique is straight forward with more efficiency and enlarging a clique by randomizing the process of deleting or adding vertices.

11.1 Proposed Algorithm

Input: $G = (V, E)$

Output: a maximal clique in G

Preprocess the input graph

Create an initial population

Apply the local optimization to each chromosome

While (stopping condition is not met) do

Select two parents, p1 and p2, from the population
generate two offspring by crossing over
p1 and p2

Mutate the two offspring Local optimize the two offspring
 Replace a population member with a better offspring update stopping condition End while
 Return the best member of the population

A new technique of genetic algorithm (NTGA) requires the genetic representation of the solution domain and the fitness function to evaluate the resolution domain. Once the genetic representation and the fitness function are defined, a NTGA proceeds to initialize a population of solution & then to improve it.

11.2 Number of crossover and mutation is given by the formula

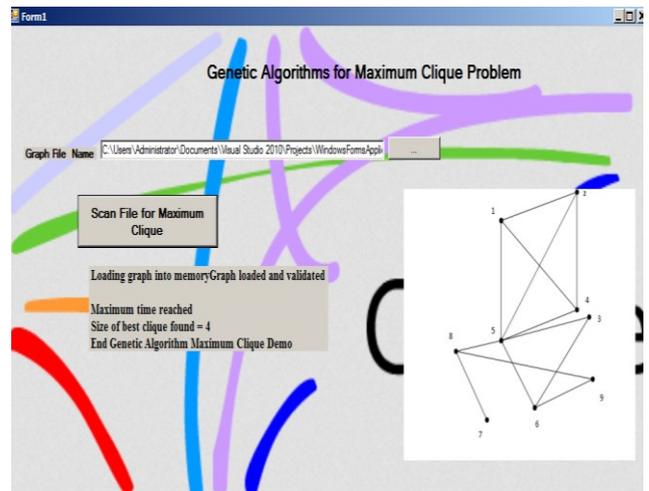


Fig.3. Maximum Clique For the first Clique File.

$$\text{Number of crossover} = (\text{Number of cell in a chromosome} * \text{number of chromosome} * \text{crossover rate}) / n.$$

$$\text{Number of mutation} = (\text{Number of the cell in the chromosomes} * \text{Number of the chromosomes} * \text{Mutation rate}) / 100.$$

III. FIGURES

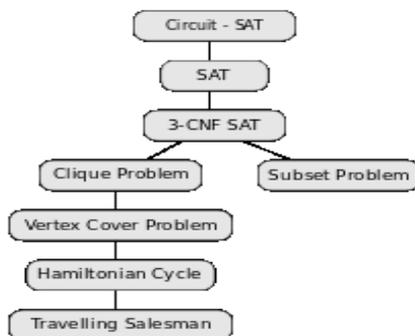


Fig.1. Some NP-complete problems, indicating the reductions typically used to prove their NP-complete

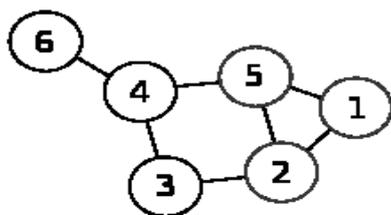


Fig.2. The graph shown has one maximum clique, the triangle {1,2,5}, and four more maximal cliques, the pairs {2,3}, {3,4}, {4,5}, and {4,6}.

IV. EXPERIMENT AND RESULT

IV.1. *DiamacsGraph.clq*

c *DimacsGraph.clq*

c number nodes, edges: 9, 13

p edge 9 13

e 1 2

e 1 4

e 1 5

e 2 4

e 2 5

e 3 5

e 3 6

e 4 5

e 5 6

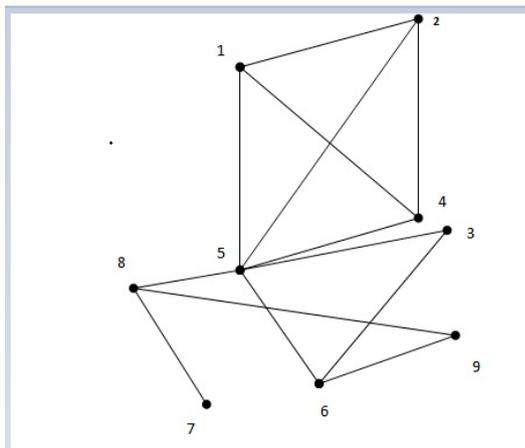
e 5 8

e 6 9

e 7 8

e 8 9

IV.2. Graph generated from this Clique File



Graph obtains from Diamacs Graph.clq.

REFERENCES

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V. CONCLUSION

Many researchers have worked on Maximum clique problem. In our work, we merged the genetic algorithm and graph theory concepts to optimize the problem. This work found that the genetic algorithm method is effective in finding global optimal or near-optimal solutions for the case study network. This algorithm could be expanded by distributing the graph across networked machines Genetic algorithm used in maximum clique can be used for a complex problem optimization field. Genetic algorithm used in maximum clique can be used for a complex problem optimization field. It merges the information of individuals in the population, selects individual with high fitness, and finds the global optima by global search in relatively short time. However, when the data is mass and sparse, time and space complexity will surge.

VI. ACKNOWLEDGMENT

I hereby declare that this submission is my own work and that, to the best of my knowledge and belief, it contains no material previously published or written by another person nor material which has been accepted for the award of any other degree or diploma of the university or other institute of higher learning, except where due acknowledgment has been made in the text.

VII. FUTURE SCOPE

This work can facilitate extremely large graphs, such as those produced by modeling the page and link structure of the World Wide Web or by modeling telephone numbers and calls made over a period of time. Tunnel edges could be designed to transport ants from one machine to another in a manner transparent to the chromosomes. Many different problems from bioinformatics have been modeled using cliques.