

# DNA Computing towards the Solution of Minimum Vertex Cover Problem

J. Kavitha

**Abstract---** DNA computing is an unconventional method for parallel computation. It is a technique proposed for finding solution to intractable computational problems. Computational hard problem in which the time complexity can increase exponentially with problem size. This work develops a new DNA exploring model to solve a minimum vertex cover problem (MVCP). This DNA processing model solve the MVCP in polynomial time calculation.

**Keywords---** Adleman-Lipton Model, Parallel Computing, MVCP, Watson-Crick Complementarity, NP-Complete Problem, DNA Computing.

---

## I. INTRODUCTION

NP complete problems [1] are computational issues which have exponential time complexity. It has challenging time complexity and no productive calculation found at this point. An energizing new research field DNA calculation has risen over the most recent twenty years as at the crossing point of engineering, science, mathematics, and biology. Two principle significant favorable circumstances of DNA calculation are huge storage capacity and massive parallelism. DNA model can execute billions of operations simultaneously in a single test tube. The huge parallelism of DNA computing originates from the huge number of molecules. These molecules synthetically interact in a little volume in a test tube.

DNA model provides an massive storage capacity since they encode the data on the sub-atomic scale. In 1994, the thought of performing sub-atomic calculation was figured it out. Adleman [2] displayed a thought of tackling the Hamiltonian path problem with  $n$  vertices in  $O(n)$  steps utilizing DNA particles. From that point forward the field has developed quickly, with huge hypothetical and test results being accounted for consistently. Lipton [3] showed that Adleman's test could be utilized to make sense of the arrangement of the NP-complete satisfiability issue. Many research papers have been published to solve the NP-Complete problem using DNA algorithm [4-9]. Parallel processing strategies are used in DNA processing model to take care of the computationally difficult issue. This exploration work develops a new processing model to solve the MVCP.

## II. MINIMUM VERTEX COVER PROBLEM

### *Definition*

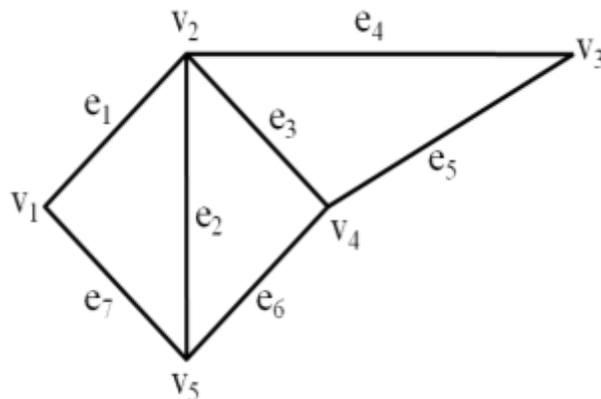
The instance of the problem is an undirected graph  $G = (V, E)$ . The subset  $M$  of a graph is said to be a vertex cover of a graph if every edge  $(s, t) \in E$  either  $s \in M$  or  $t \in M$  or both. Every edge is incident on one of the vertices in the vertex set  $M$ . Finding a set  $M$  which has minimum number of vertices of a graph  $G$  is a known as a minimum vertex cover for  $G$ .

---

J. Kavitha, Department of Mathematics, New Horizon College of Engineering, Bengaluru, India. E-mail: kavijossea@gmail.com

**Problem Description**

Consider a graph given below



This paper describes the computing model to solve the MVC. Consider undirected graph G given in Fig 1. Let V be the vertex set and E be the edge set of the given graph G. The minimum vertex cover of G is defined as a set M with minimum number of vertices such that each edge in G is incident with at least one vertex in M. The given graph has 7 edges and 5 vertices. The cover sets of the Graph G are

$M_1 = \{ v_5, v_3, v_2 \}$ ,  $M_2 = \{ v_4, v_2, v_1 \}$ ,  $M_3 = \{ v_5, v_4, v_3, v_1 \}$ ,  $M_4 = \{ v_5, v_4, v_3, v_2 \}$ ,  $M_5 = \{ v_4, v_3, v_2, v_1 \}$ ,  $M_6 = \{ v_5, v_4, v_2, v_1 \}$ ,  $M_7 = \{ v_5, v_3, v_2, v_1 \}$ ,  $M_8 = \{ v_5, v_4, v_3, v_2, v_1 \}$ , ... The cover set with minimum number of vertices are  $M_1$  and  $M_2$ . The cardinality of the MVC of the graph is 3.

**III. DNA CODING OF A GRAPH**

Generate a test tube T which contains all possible solution of the graph G. The input is an undirected graph  $G = (V, E)$ , where V is the set of vertices and E is the set of edges.  $|V|$  represents the number of vertices in V and  $|E|$  represents the number of edges in E. Let  $|V| = 5$ ,  $|E| = 7$

**Encoding the Vertices**

Consider a graph G and any vertex  $v$  in G, synthesize two DNA strands. Each DNA strand is of length 10 to represent the vertex which is either ON or OFF. The vertex which is ON represented by a 5 mer DNA sequence CCCGG and OFF represented by a 5mer DNA sequence ATATA. The following DNA strands are the encoding for a given problem. The DNA strands to encode the vertex  $v_i$  which is ON and  $v_i'$  which is OFF are as follows.

$v_1$	AATTACCCGG
$v_2$	ACTGCCCCGG
$v_3$	CAGTGCCCGG
$v_4$	CTGGTCCCGG
$v_5$	GGAATCCCGG

$v_1'$	GTACGATATA
$v_2'$	TGCACATATA
$v_3'$	TTCCAATATA
$v_4'$	CCATCATATA
$v_5'$	GGTAGATATA

**Encoding the Edges**

For each undirected edge  $(v_i, v_j)$  is encoded by 8 DNA strands and each is of length 10 base consisting of 3' 5mer sequence of  $v_i$  and complementary of 5' 3mer sequence of  $v_j$  and vice-versa. The complementary seven edges are encoded as follows

<b>Edge <math>e_1: (v_1, v_2)</math></b>	
GGGCCTGACG	TATATACGTG
GGGCCTTAAT	TATATCATGC
GGGCCACGTG	TATATTGACG
TATATTTAAT	GGGCCCATGC

<b>Edge <math>e_2: (v_2, v_5)</math></b>	
GGGCCCTTA	TATATCCATC
GGGCCTGACG	TATATACGTG
GGGCCCATC	TATATCCTTA
TATATTGACG	GGGCCACGTG

<b>Edge <math>e_3: (v_2, v_4)</math></b>	
GGGCCTGACG	TATATACGTG
GGGCCGACCA	TATATGGTAG
GGGCCGGTAG	TATATGACCA
TATATTGACG	GGGCCACGTG

<b>Edge <math>e_4: (v_2, v_3)</math></b>	
GGGCCTGACG	TATATACGTG
GGGCCGTAC	TATATAAGGT
GGCCAAGGT	TATATGTCAC
TATATTGACG	GGGCCACGTG

<b>Edge <math>e_5: (v_3, v_4)</math></b>	
GGGCCGTAC	TATATAAGGT
GGGCCGACCA	TATATGGTAG
GGGCCGGTAG	TATATGACCA
TATATGTCAC	GGCCAAGGT

<b>Edge <math>e_6: (v_4, v_5)</math></b>	
GGGCCCTTA	TATATGGTAG
GGGCCGACCA	TATATCCATC
GGGCCCATC	TATATCCATC
TATATGACCA	GGGCCGGTAG

Edge $e_7: (v_1, v_5)$	
GGGCCTTAAT	TATATCATGC
GGGCCCTTA	TATATCCATC
GGGCCCATC	TATATCCTTA
TATATTTAAT	GGGCCCATGC

#### IV. DNA ALGORITHM

The DNA model proposed in this paper creates a test tube which has all paths of a given graph G. Each DNA strand in a test tube has a number of sub strands. Each sub strand is a coding for a vertex and an edge of a given graph G. Using ligation reaction all paths of the graph is generated in a test tube T [10, 11].

##### *DNA Algorithm for Minimum Vertes Cover of a Graph*

This section describes the steps to filter the DNA strands which are the solution of MVCP. Consider the graph G in Fig 1. with 7 edges and 5 vertices.

##### *Algorithm*

**Step 1:** The input of the algorithm is a test tube T. T has all DNA sequence of possible paths of graph G. The paths represented have some vertices which are ON. The remaining Vertices are OFF

**Step 2:** For  $j = 1$  to  $m$

$T_1 \leftarrow + (T, e_j)$

End For

**Step 3:** If Detect ( $T_1$ ) = yes then DNA strands in the test tube  $T_1$  are the vertex cover of G.

**Step 4:** Weights of the DNA strands are determined by reading the length of the DNA sequence. The DNA strand which has minimum weight in  $T_1$  Covers entire graph. The operation read is used to describe the DNA molecule which is the minimum vertex cover of the graph if it exists.

##### *Computational Complexity*

The graph G has 7 edges and 5 vertices. The proposed algorithm generates all possible paths of the given graph in step 1 by one step and step 2 collects all the DNA strands which have all the edges as the sub strand in  $m$  steps. Steps 3 needs one step to detect the DNA strand and step 4 needs one step to read out the solution if it exists. The algorithm runs up to  $m$  steps. The time complexity of the procedure of DNA model is  $O(m)$  in worst case.

#### V. CONCLUSION

This research work develops a DNA based computing model to solve the MVCP using Adleman-Lipton model. The suggested DNA model has two advantages. Firstly, the algorithm developed in this work generates all possible solution with a lesser error rate. Secondly, the time complexity of DNA model is  $O(m)$  steps for the MVCP of an undirected simple graph.

#### REFERENCES

- [1] Garey, M.R., Johnson, D.S., Computers and Intractability: A Guide to the Theory of NP-completeness. (W. H. Freeman and Company, 1979).

- [2] L.M. Adleman, Molecular computation of solution to combinatorial problems, *Science* 1994, vol. 266, pp. 1021-1024.
- [3] R.J. Lipton, DNA solution of HARD computational problems, *Science*, 199, vol. 268, pp. 542-545.
- [4] W.X. Li, D.M. Xiao, L. He, DNA ternary addition, *Applied Mathematics and Computation* 2006, vol. 182, pp. 977-986.
- [5] D.M. Xiao, W.X. Li, J. Yu, X.D. Zhang, Z.Z. Zhang, L. He, Procedures for a dynamical system on  $\{0,1\}$  with DNA molecules, *BioSystems* 2006, vol. 84, pp. 207-216.
- [6] X.L. Wang, Z.M. Bao, J.J. Hu, S. Wang, A. Zhan, Solving the SAT problem using a DNA computing algorithm based on ligase chain reaction, *BioSystems* 2008, vol. 91, pp. 117-125.
- [7] R.M. Karp, "Reducibility among combinatorial problems," In 50 Years of Integer Programming 1958-2008, *Springer press*, 2010, pp. 219- 241.
- [8] R. Niedermeier, P. Rossmanith, "Upper bounds for vertex cover further improved," Proceedings of the 16th International Symposium on Theoretical Aspects of Computer Science (STACS), *Springer press* 1999, pp. 561-570.
- [9] S. Khuri, Th. Back, "An evolutionary heuristic for the minimum vertex cover problem," Proceedings of the 18th German Annual Conference on Artificial Intelligence, September 1998, pp. 86-904.
- [10] G. Sethuraman and J. Kavitha, "Star Coloring Problem: The DNA Solution", *International Journal of Information Technology and Computer Science* 2012, vol. 3, 31-37.
- [11] J. Kavitha, "Fast Parallel DNA Solution to Oriented Coloring Problem", *International Journal of Advanced Research in Engineering and Technology* 2017, vol. 8, 3, 12-18.