Journal of Information Systems Engineering and Management
2025, 10(41s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

An Efficient DNA Computing Model for Harmonious Colouring Problem

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ARTICLE INFO

Received: 24 Dec 2024
Revised: 18 Feb 2025
Accepted: 26 Feb 2025

ABSTRACT

DNA computation is an exceptional technique for parallel computation. It is a system suggested for finding solution to intractable computational hard problems. The complexity of NP-Complete problem upturns exponentially with the input size of the graph. This work develops a novel DNA exploring model to find the solution to the Harmonious Colouring Problem (HCP). This DNA processing model solves the HCP in polynomial time calculation.

Keywords: Harmonious, DNA, processing

Introduction

Parallel computing is an multidisciplinary research area which involves DNA molecules and biotechnologies [21] to explore the solution of NP-Complete problems. It has hope and application in solving computational hard problems. The important advantage of DNA computing are enormous storage capacity, vast parallelism and low energy consumption. It can employ DNA strands to figure out the solution of larger problems in polynomial time. The surface-based model [19], the Adleman-Lipton model [17, 18], the hairpin model [6], the sticker model, the restriction enzyme model [11], the self-assembly model [5] are recognized by researchers in recent years. Numerous papers are emerged to tackle different computational hard problems [4,10].

Graph colouring is a colouring of a graph with given colours such that same color cannot be assigned to adjacent vertices. A graph's chromatic number is the minimal number colors needed to color it. The coloring problem has many applications in networks and allocation problems. The colouring problem is one of NP-complete problem [16], thus the number of colours increases exponentially as the number of vertices increase.

The research paper [5] explores the utilization of DNA algorithms for implementing bio molecular databases on biological computers. This work delves into leveraging biological systems, particularly DNA, as a substrate for computation and data storage, offering potentially high-density and energy-efficient solutions. [6] investigates the application of quantum algorithms and mathematical formulations to address bio-molecular solutions of the vertex cover problem within the finite-dimensional Hilbert space and explores the potential of quantum computing techniques in solving

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computational problems related to bio-molecular systems, offering insights into novel computational paradigms at the intersection of quantum computing and biotechnology.

This paper [7] investigates the application of quantum algorithms and mathematical formulations to address bio-molecular solutions of the vertex cover problem within the finite-dimensional Hilbert space. [8] presents a parallel computational algorithm designed to address the Maximum k-Vertex Weighted Clique Problem. This problem involves finding the largest possible subset of vertices in a graph such that every pair of vertices in the subset is connected by an edge and has a total weight that does not exceed a given threshold. The parallel computational approach proposed in the paper aims to enhance the efficiency of solving this combinatorial optimization problem [15, 21]. The research paper [9] introduces a novel parallel computing algorithm designed to obtain the cubic sub graph for a simple graph. A cubic sub graph refers to a sub graph in which each vertex has exactly three adjacent edges. The algorithm proposed in this paper aims to efficiently identify such sub graphs using parallel computing techniques, potentially offering improvements in performance and scalability compared to traditional sequential approaches.

The DNA computing model [10] aimed at addressing the graph vertex coloring problem. Vertex coloring involves assigning colors to the vertices of a graph such that no two adjacent vertices share the same color. The proposed DNA computing model leverages the principles of molecular biology to develop a solution for this combinatorial optimization problem, utilizing DNA strands as computational agents. This approach explores the potential of DNA computing in solving complex computational problems inspired by graph theory.

[11] addresses the star coloring problem, which involves coloring the vertices of a graph such that no two adjacent vertices, including the center vertex of the star graph, share the same color and [12] introduces a fast parallel DNA solution to the oriented coloring problem. The oriented coloring problem involves coloring the vertices of a directed graph such that no two adjacent vertices have the same color, considering both the direction of the edges and the colors assigned.

The research work [13] presents a novel algorithm for efficiently solving the minimum spanning tree problem using DNA molecules computation. The minimum spanning tree problem involves finding the shortest possible tree that connects all the nodes in a graph, minimizing the total edge weight. By leveraging the properties of DNA molecules and their potential for parallel computation, the authors propose an algorithm that aims to provide a fast and efficient solution to this classic optimization problem.

[19] presents a novel approach to DNA computation that involves utilizing surfaces as a substrate for performing computations with DNA molecules. DNA computation is a field that explores the potential of using DNA strands as a medium for performing computational tasks, leveraging the immense parallelism and information storage capacity inherent in DNA molecules. Surface-based approaches offer advantages such as spatial organization and containment, potentially enhancing the efficiency and scalability of DNA computing systems. The paper discusses theoretical concepts, experimental methodologies, and potential applications of this surface-based approach to DNA computation. The paper [20] introduces a new cryptographic system designed for cyber-physical systems, leveraging the principles of DNA cryptography, hyper chaotic systems, and Moore machine generation. DNA cryptography involves using DNA sequences for encryption and decryption purposes, taking advantage of the unique properties of DNA molecules for secure communication. Hyper chaotic systems are dynamical systems characterized by multiple chaotic attractors, which can be utilized for generating complex cryptographic keys. Moore machines are finite state machines used in cryptography for various purposes, including key generation and management. The cryptosystem proposed in this paper likely integrates these components to enhance the security and resilience of cyber-physical systems, ensuring confidentiality, integrity, and authenticity of data transmission and communication within such systems.

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The supremacy of DNA model for finding solution to computational hard problems has been explored by researchers. DNA computing has the power to find the solution of a complex problem from the exponential solution space by applying polynomial number of biological operations with regardless of problem size. This research work, we proposed an efficient procedure to figure out the solution of the harmonious coloring problem. This algorithm is a parallel algorithm and runs in O (m^2) operations.

The flow of the paper is as follows. Introduction to Adleman-Lipton model is discussed in second section. Introduction to HCP and encoding of graph using DNA strands is explained in third section. An efficient parallel algorithm for the HCP is explained and its complexity, feasibility are discussed in fourth section. In last Section, the advantage and power of DNA computing model are discussed.

DNA computing model

This section describes the basic operation used in Adleman – Lipton model. The model first generate all possible solution to HCP, then using biological operation it will detect the solution to the problem if it exists.

2.1 Operations of Adleman-Lipton Model

Test tube T includes a set of DNA strands composed of Adenine (A), Thymine (T), Guanine (G), and Cytosine (C). For a given test tube T, the DNA model performs the following operations:

Encoding: The first step in the Adleman-Lipton model is to encode the computational problem into a biological representation using DNA strands. This encoding involves mapping the problem's inputs, operations, and outputs to sequences of DNA molecules.

Synthesis: Once the problem is encoded, DNA strands representing the problem instances are synthesized in a laboratory setting. This involves chemical processes to construct DNA sequences according to the encoding scheme.

Selection: After annealing, the test tube is subjected to various selection processes to isolate DNA strands that represent solutions to the computational problem. This may involve filtering out unwanted DNA sequences based on specific properties or performing biochemical assays to identify desired strands.

Amplification: The selected DNA strands, which represent potential solutions to the problem, are amplified through techniques such as polymerase chain reaction (PCR). This amplification process generates multiple copies of the selected DNA strands, increasing their concentration for further analysis.

Verification: The amplified DNA strands are then subjected to verification procedures to confirm whether they indeed represent valid solutions to the computational problem. This may involve sequencing techniques or other biochemical assays to validate the correctness of the solutions.

Readout: Finally, the verified DNA strands are decoded or "read out" to extract the solutions to the original computational problem. This decoding process translates the DNA sequences back into a format that represents the solutions in a human-readable form.

Detect (T): This operation detects the DNA strand in a given a test tube T and gives the output as yes if at least one DNA strand present in T. If not, this operation gives the output as NO.

Separation (T, Z, T1): For T with a set of strings Z, this operation collects all strands containing Z as a sub strand from a tube T and produces a new test tube T1.

Annealing (T): This operation produces all double stranded DNA for a given test tube with all single stranded DNA.

Denaturation (T): This operation dissociates each double stranded DNA into two single stranded DNA.

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Since the biological operations are executed in finite number of steps, each operation needs only one step and its complexity is O (1).

1. Harmonious colouring problem

The colouring of edges of proper colouring of a graph G is distinct then the graph G is having Harmonious colouring. The assignment of colours to end vertices of an edge is denoted as an ordered pair is known as the colour of an edge. Harmonious coloring [1, 2] of G refers to the use of the fewest colours necessary for such coloring. HC can be extended to directed graphs [3]. The Harmonious Coloring Problem (HCP) has several practical applications across various domains.

In wireless communication networks, nodes represent wireless devices, and interference between adjacent nodes can degrade network performance. Harmonious coloring can be used to assign frequencies or time slots to wireless channels in a way that minimizes interference between adjacent channels, thereby improving network efficiency and reducing communication errors.

Harmonious coloring can be applied to assign frequencies to radio channels in a way that minimizes interference between neighbouring channels. This is crucial in radio network planning to ensure efficient utilization of the radio spectrum and reduce co-channel interference.

In scheduling problems, harmonious coloring can be used to assign time slots or resources to tasks in a way that minimizes conflicts or overlaps. This is applicable in various contexts such as job scheduling, classroom timetabling, and task allocation in distributed systems.

In Very Large Scale Integration (VLSI) design, harmonious coloring can be used for register allocation, scheduling of hardware resources, and routing of interconnects on a chip. This helps optimize the layout of components on the chip and reduce power consumption, area usage, and signal delay.

Harmonious labeling of graphs can be used for network security applications, such as intrusion detection and prevention systems. By assigning unique labels to network nodes and edges in a way that minimizes conflicts or overlaps, it becomes easier to detect and prevent unauthorized access or malicious activities in computer networks.

Overall, the Harmonious Coloring Problem has diverse applications in optimizing resource allocation, minimizing conflicts, and improving efficiency in various real-world systems and networks.

Problem: Description: consider the instance given below

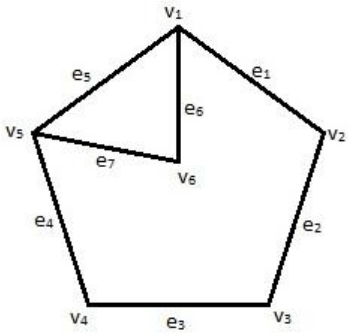

Fig. 1

3.1 DNA coding

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If G = (V, E) be a graph, where V is the set of vertices and E is a set of edges of Graph. G has six vertices and seven edges. In DNA coding the vertices and edges are encoded using DNA strands, the hybridization process generates all possible solution of G. The legal solution to the problem is filtered using biological operation.

Encoding of vertices

For each vertex synthesize DNA strands each of length 14 to represent the vertex which is colored by specific color. The vertex vi is represented by PiCsPi. Pi is a DNA sequence (length 5) represents the position of a vertex vi. Cs is a color of a vertex and it is a 4 mer DNA sequence. The following DNA strands are the encoding for a given instance. The DNA strands to encode the vertex vi are as follows

Table 1: DNA encoding of vertices of a graph

Vertex		DNA Strands
V_1	$P_1C_sP_1$	$AATTAC_sAATTA$
V_2	$P_2C_sP_2$	$ACTGCC_sACTGC$
V_3	$P_3C_sP_3$	$CAGTGC_sCAGTG$
V_4	$P_4C_sP_4$	$CTGGTC_sCTGGT$
V_5	$P_5C_sP_5$	$GGAATC_sGGAAT$
V_6	$P_6C_sP_6$	$GGCCTC_sGGCCT$

Encoding of edges

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

Table 2: DNA encoding of edges of a graph

Edge of graph	End vertices		DNA strands
Edge e_1	**(v_2, v_1)**	$\overline{P_2 P_1}$	TTAATTGACG
Edge e_2	**(v_3, v_2)**	$\overline{P_3 P_2}$	TGACGGTCAC
Edge e_3	**(v_4, v_3)**	$\overline{P_4 P_3}$	GTCACGACCA
Edge e_4	**(v_4, v_5)**	$\overline{P_4 P_5}$	GACCACCTTA
Edge e_5	**(v_1, v_5)**	$\overline{P_1 P_5}$	TTAATCCTTA
Edge e_6	**(v_5, v_6)**	$\overline{P_5 P_6}$	CCTTACCGGA
Edge e_7	**(v_1, v_6)**	$\overline{P_1 P_6}$	TTAATCCGGA

2. DNA algorithm

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This model produces DNA strands which are the encodings of colours of the vertices of G. For the given instance, using DNA strands of vertices and edges, the algorithm develops the assignment of colours to the graph G.

DNA model to solve HCP

This section describes the DNA algorithm for finding solution to HCP. This algorithm solves the HC to any given undirected graph.

Algorithm

Step1: The input of the algorithm is a test tube T. It contains all assignment of colours of the given graph represented by DNA sequence.

Step2: for s = 1, 2, 3

for t = s to 3

for every edge e = (v_i, v_j)

$T_1 \leftarrow + (T, P_iC_sP_i)$

$T_2 \leftarrow + (T_1, P_j C_t P_j)$

for all edges e = (v_x, v_y), x ≠ i, y ≠ j

$T_3 \leftarrow + (T_2, P_xC_sP_x)$

$T_4 \leftarrow + (T_3, P_yC_{s+1}P_y)$

Detect (T_4)

end for

end for

end for

end for

Step3: If Detect (T_4) = yes then

all the DNA strands in T4 are the HC of G.

Computational Complexity

The worst-case complexity of finding the solution of the harmonious coloring problem using DNA algorithm can be obtained as follows: the proposed algorithm generates solution space to the given graph in step 1 by one step and step 2 collects all the DNA strands in which all the edge colorings are distinct in $O(m^2)$ steps. Step 3 need one step to detect the DNA strand and readout the solution if it exists. This model needs $O(m^2)$ steps to figure out the solution to HCP.

5. Conclusion

DNA computing offers a promising avenue for solving complex computational problems using biological molecules. While still in its early stages, DNA computing has shown potential in certain domains due to its massive parallelism, high density, and energy efficiency. However, it also presents several challenges and limitations that need to be addressed for practical applications to become widespread. DNA computing holds great promise for revolutionizing certain areas of computation, particularly in bioinformatics, cryptography, and optimization problems. As research progresses and

technology advances, DNA-based systems playing a more significant role in solving real-world problems. It could be a field with an exceptional potential, capable to resolve computational hard problems and receives more attentions from biologists, mathematicians and computer scientists. When new challenges emerge, the sector of DNA computing and DNA Computer remains alive and promising. This research paper develops a DNA algorithm for finding solution to HCP. The algorithm proposed in this research work has couple of advantages. It generates solution space of the problem with less error rate of hybridization. Secondly, for the given graph, the algorithm run in O (m^2) steps for the HCP. The algorithm proposed in this research work proves the power of DNA parallel computation in solving NP-Complete.

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